

# Genomic characterization of Wilms' tumor suppressor 1 targets in nephron progenitor cells during kidney development

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## SUMMARY

The Wilms' tumor suppressor 1 (*WT1*) gene encodes a DNA- and RNA-binding protein that plays an essential role in nephron progenitor differentiation during renal development. To identify WT1 target genes that might regulate nephron progenitor differentiation *in vivo*, we performed chromatin immunoprecipitation (ChIP) coupled to mouse promoter microarray (ChIP-chip) using chromatin prepared from embryonic mouse kidney tissue. We identified 1663 genes bound by WT1, 86% of which contain a previously identified, conserved, high-affinity WT1 binding site. To investigate functional interactions between WT1 and candidate target genes in nephron progenitors, we used a novel, modified WT1 morpholino loss-of-function model in embryonic mouse kidney explants to knock down WT1 expression in nephron progenitors *ex vivo*. Low doses of WT1 morpholino resulted in reduced WT1 target gene expression specifically in nephron progenitors, whereas high doses of WT1 morpholino arrested kidney explant development and were associated with increased nephron progenitor cell apoptosis, reminiscent of the phenotype observed in *Wt1*<sup>-/-</sup> embryos. Collectively, our results provide a comprehensive description of endogenous WT1 target genes in nephron progenitor cells *in vivo*, as well as insights into the transcriptional signaling networks controlled by WT1 that might direct nephron progenitor fate during renal development.

**KEY WORDS:** ChIP-chip, WT1, Kidney, Progenitor, Transcription factor, Mouse

## INTRODUCTION

The pediatric kidney malignancy Wilms' tumor has an incidence of 1 in 10 000 in North America (Matsunaga, 1981), making it the most common solid tumor in childhood (Bennington and Beckwith, 1975). Wilms' tumor is thought to arise from a single transformed pluripotent nephron progenitor cell whose progeny fail to undergo normal differentiation. *WT1* was the first gene identified as mutated in Wilms' tumors (Call et al., 1990; Gessler et al., 1990; Haber et al., 1990), and inactivating mutations in *Wt1* are responsible for ~10% of sporadic Wilms' tumor cases. WT1 also plays a crucial role during embryogenesis, including development of the kidneys and gonads (Kreidberg et al., 1993; Pelletier et al., 1991). At the onset of kidney development, *Wt1* is weakly expressed in the uninduced metanephric mesenchyme and increases in the cap of condensed nephrogenic progenitors surrounding the tips of the branching ureteric bud as development proceeds (Pritchard-Jones et al., 1990). Targeted mutation of *Wt1* in mice results in bilateral renal agenesis, characterized by apoptosis of the metanephric mesenchyme and failure of ureteric bud invasion into the metanephric mesenchyme

(Kreidberg et al., 1993). Importantly, nephron progenitor incompetence is the primary defect in *Wt1*<sup>-/-</sup> embryos, as evidenced by the failure of isolated *Wt1*<sup>-/-</sup> mesenchymal rudiments to differentiate when co-cultured with wild-type ureteric bud cells (Donovan et al., 1999). In the complementary gain-of-function experiment, microinjection of *Wt1*-expressing plasmids into isolated embryonic kidneys stimulates nephron development (Gao et al., 2005). Collectively, these results strongly suggest that *Wt1* promotes nephron progenitor differentiation during kidney development *in vivo*.

*Wt1* encodes a transcription factor with four Krüppel-type (Cys<sub>2</sub>-His<sub>2</sub>) zinc finger domains. In mammals, an alternative splice donor site at exon 9 inserts the amino acids lysine, threonine and serine (KTS) between the third and fourth zinc fingers, significantly diminishing the DNA-binding affinity of WT1 (Gessler et al., 1992; Haber et al., 1991). Thus, (+KTS) WT1 isoforms have a high affinity for RNA (Bor et al., 2006), whereas (-KTS) isoforms bind DNA with high affinity and function in transcriptional regulation. Several EGR1-like GC-rich DNA sequences and (TCC)<sub>n</sub> consensus sequences have been identified as cognate WT1 (-KTS) binding sites *in vitro* (Drummond et al., 1994; Rauscher et al., 1990), including a high-affinity 10-bp EGR1-like (WT1) motif (GCGTGGGCGG) associated with WT1-dependent gene transcriptional activation *in vitro* (Hamilton et al., 1995; Nakagama et al., 1995).

The identification of direct WT1 target genes will be essential to our understanding of WT1 function in the developing kidney and other developing organs. Therefore, to gain a deeper insight into the WT1-mediated regulatory networks that control kidney development *in vivo*, we initiated a systematic effort to define the genes directly regulated by WT1 during renal development. WT1-

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directed ChIP products isolated from mouse embryonic kidneys were used to interrogate mouse promoter arrays without PCR amplification prior to hybridization, to avoid the introduction of PCR amplification bias. A large number of *in vivo* target sites were identified and were validated by bioinformatics analysis, ChIP-PCR, and a novel, modified WT1 morpholino loss-of-function model in embryonic kidney explants. Essential kidney development genes *Bmp7*, *Pax2* and *Sall1* were identified as WT1 transcriptional target genes and might explain the renal agenesis phenotype observed in *Wt1*<sup>-/-</sup> embryos. Further, our data identified numerous WT1 target genes not previously studied in the developing kidney co-expressed with *Wt1* in nephron progenitors and potentially mediating its function in nephron progenitor differentiation *in vivo*. Collectively, these data provide novel insights into the signaling networks and biological processes that might be regulated by WT1 in nephron progenitors during kidney development *in vivo*.

## MATERIALS AND METHODS

### WT1 location analysis

Location analysis was performed as previously described (Lee et al., 2006), using pooled polyclonal anti-WT1 antibodies directed against the C-19 and N-180 terminal amino acids of WT1 (Santa Cruz), and optimized for chromatin extraction from embryonic mouse kidney tissue. Hybridization to Agilent mouse 244K promoter tiling arrays was performed using Agilent SureHyb hybridization chambers according to the manufacturer's Mammalian ChIP-on-chip v.9.0 Protocol ([http://www.chem.agilent.com/Library/usermanuals/Public/G4481-90010\\_ManmalianProtocol\\_10.11.pdf](http://www.chem.agilent.com/Library/usermanuals/Public/G4481-90010_ManmalianProtocol_10.11.pdf)) (Whitehead Institute Genome Technology Core, Cambridge, MA, USA). Raw ChIP-chip fluorescence intensity data were analyzed using ChIP Analytics 1.3.1 software (Boyer et al., 2005). Settings included spatial detrending of extracted array data, and dye-bias intra-array Lowess normalization. Normalized log-intensity and log ratio histograms followed a normal and symmetric distribution (see Fig. S1 in the supplementary material), indicating that the ChIP data are of high quality. The complete data set is available in the Array Express database (<http://www.ebi.ac.uk/microarray-as/ae/>, Accession No. E-TABM-872). All coordinates in this manuscript are reported in mm9.

### DNA sequence motif analysis

To identify sequence motifs in WT1-bound regions detected by ChIP-chip, sequences of all 4953 WT1-bound regions were extracted and extended 200 bp from both ends. The hypothesis-driven motif discovery algorithm THEME (Macisaac et al., 2006) tested a compendium of 233 unique sequence motifs derived from ~400 mammalian transcription factor binding specificities in the TRANSFAC and JASPAR databases, to identify the enrichment of any of these motifs in WT1-bound sequences, using 5490 randomly sampled, unbound sequences for background comparison. Motifs were ranked by their mean cross-validated prediction error on held-out-bound and unbound test sequences. The top-ranking motif identified by THEME (Fig. 1A), henceforth called the WT1 matrix, comprises multiple 8-12 bp permutations of a motif consistent with the previously reported WT1 consensus sequence: GCG(T/G)(G/A)GG(C/A)G(G/T) (Hamilton et al., 1995; Nakagama et al., 1995). The statistical significance of the WT1 matrix site was determined by randomly permuting bound and unbound sequence labels and rerunning the algorithm 25 times to obtain an empirical null distribution of cross-validation errors of ~0.38 and an associated *z*-score of 27.5, indicating that the WT1 matrix site is highly statistically significant. To map the WT1 binding site to our bound data set, each bound region was scanned for matches to the WT1 consensus sequence, permitting the defined substitutions denoted above in the fourth, fifth, eighth and tenth positions (substitutions noted in parentheses).

### Chromatin immunoprecipitation

ChIP followed by site-specific PCR (ChIP-PCR) was performed according to published protocols (Lee et al., 2006) to confirm binding of WT1 to a panel of ~40 WT1 target loci identified by ChIP-chip (see Table S1 in the supplementary material). Each PCR experiment comprised 5 PCR reactions:

no DNA, rabbit IgG ChIP, RNA Polymerase II ChIP, WT1 ChIP and input DNA, using equimolar amounts (30 ng) of starting DNA per reaction. The following antibodies were used to perform ChIP: anti-rabbit IgG and anti-WT1 (Santa Cruz), and anti-RNA polymerase II (Upstate). The linear range of amplification was determined for each PCR reaction, with the optimal cycle number semi-quantitatively determined as 2 cycles prior to the plateau phase of amplification (see Table S2 in the supplementary material).

### Wt1 vivo-morpholino treatment of embryonic kidney explants

Mouse embryonic kidneys were excised from E12.5 pregnant CD1 mice, and kidneys that had undergone 2-3 branching events were selected and transferred onto a 0.4 μM polyethylene terephthalate membrane (Falcon). Explants were cultured for 24 hours as previously described (Piscione et al., 2001), in media supplemented with either 10 μM *Wt1* antisense vivo-morpholino (5'-CAGGTCCCGCACGTCGGAACCCATG-3') or 10 μM five-base-pair-mismatched vivo-morpholino control (5'-CAGcTCCGgCACcTCGcAACCgATG-3') (Gene Tools).

### Immunofluorescence and in situ hybridization

Immunofluorescence was performed using anti-WT1 (Santa Cruz) and anti-cytokeratin (Sigma) primary antibodies and anti-rabbit Texas Red and donkey anti-mouse FITC secondary antibodies (Jackson ImmunoResearch). TUNEL staining was performed with the Apoptag Plus Fluorescein in situ Apoptosis Detection Kit, as per manufacturer's instructions (Millipore). In situ hybridization was performed as previously described (Mo et al., 1997). The following probes were generated by PCR amplification (see Table S3 in the supplementary material) and subsequently cloned into the pCRII-TOPO vector (Invitrogen): *HeyL* (exon 5), *Cxcr5* (exon 3), *Lsp1* (5' UTR), *Pbx2* (exon 9), *Plxdc2* (5' UTR), *Rps6ka3* (exon 14-20), *Scx* (exon 1-2) and *Sox11* (3' UTR). Probes encoding *Wt1* (Gao et al., 2005), *Bmp7* (Lyons et al., 1995), *Pax2* (Dressler et al., 1990) and *Sall1* (Nishinakamura et al., 2001) have been previously described.

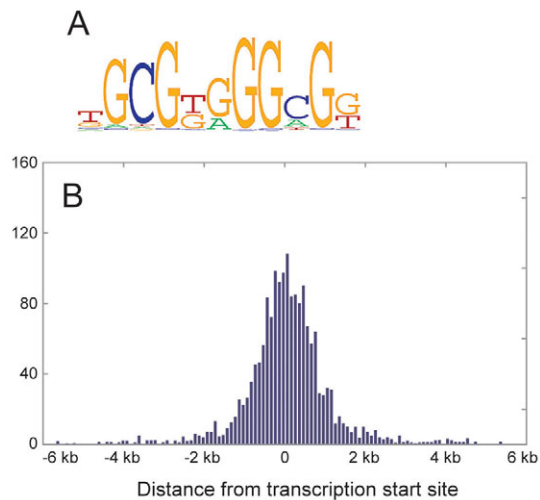
### Quantification of apoptosis in organ explants

To quantify apoptosis, the number of TUNEL-labeled cells in the general nephron progenitor cap region was first standardized to regional surface area as previously described (Hartwig et al., 2005). This was accomplished by overlaying each digital Pax2- and TUNEL-labeled confocal image with a grid and counting the number of boxes filled by the cap region. Regional apoptosis was then quantified as the ratio of TUNEL-positive cells to the total number of filled boxes in the grid, with values presented as mean fold change in WT1-morphants versus control morphant explants (*n*=3). Mean differences were examined using a Student's *t*-test (two-tailed) and significance was taken at *P*<0.05.

## RESULTS

### Identification of loci bound by WT1

WT1 is an essential kidney development gene expressed in nephron progenitor cells that plays a crucial role in nephron progenitor differentiation *in vivo*. However, a comprehensive list of the transcriptional targets of WT1 that mediate its function *in vivo* has yet to be described. As a first step towards identifying the transcriptional targets of WT1 in nephron progenitor cells *in vivo*, we performed ChIP-chip on chromatin DNA isolated from embryonic mouse kidney tissue to identify genes physically bound by WT1. Chromatin immunoprecipitated with anti-WT1 antibodies (ChIP DNA) or without ChIP (input DNA) are typically amplified by PCR in order to generate sufficient DNA for hybridization to array (~10 μg DNA per channel). However, to avoid introducing bias associated with this PCR amplification step in our experiments, we processed ~1200 E18.5 kidneys, generating sufficient ChIP DNA for array hybridization without prior PCR amplification. Applying a previously published *P*-value cut-off of 0.001 for significant WT1 binding (Boyer et al., 2005; Lee et al., 2006), 4953 bound sequences were identified, corresponding to 1663 bound genes (see Table S4 in the supplementary material). The defined



**Fig. 1. Distribution of WT1 bound promoter regions and the WT1 matrix site.** (A) Weblogo of the WT1 matrix site identified by THEME, comprising multiple permutations of a high-affinity, EGR1-like WT1 consensus site. (B) Histogram showing distribution of the defined peak regions of WT1-bound promoters identified by ChIP-chip in relation to the transcriptional start site (TSS). Most WT1-bound regions (~85%) and the WT1 matrix sites contained within these defined peak regions are localized within 1 kb of the TSS.

peak regions of WT1-bound promoters were largely localized (>90%) within 2 kb of the transcriptional start site (TSS; Fig. 1B). The close proximity of these cis-elements to the TSS indicate that WT1, possibly in conjunction with other co-factors, might act to stabilize general transcription factor machinery at the core promoter elements to regulate target gene transcription, as has been shown for other transcription factors that bind proximal promoter regions (Farnham, 2009).

### Integrated functional annotation of WT1 target genes using DAVID knowledgebase

To interpret the biological significance of WT1 binding events in the developing kidney, we used the DAVID integrative knowledgebase (Huang da et al., 2007) to identify biological processes and molecular functions enriched in our data set. DAVID identified 64 partially overlapping functional clusters (see Table S5 in the supplementary material), which were manually organized into eight unique meta-clusters (Table 1). The most highly enriched function relates to regulation of transcription, and includes transcription factors and genes involved in chromatin establishment and modification. The second-ranking meta-cluster relates to development and differentiation in multiple tissues. In fact, *Wt1* is widely expressed in many developing organs, and *Wt1* loss-of-function mouse models have established a requirement for *Wt1* in the development of multiple organ systems, including the kidney, gonads, heart, lungs (Kreidberg et al., 1993), spleen (Herzer et al., 1999), liver (Ijpenberg et al., 2007), diaphragm (Moore et al., 1998), nervous system, vasculature (Scholz et al., 2009), brain, eye (Wagner et al., 2002), olfactory system (Wagner et al., 2005), adrenal gland and mesothelial tissues (Moore et al., 1999). The large breadth of developmental processes enriched in WT1 target genes suggests that there might indeed be a common mode of action by which WT1 regulates differentiation and development of multiple organ systems during embryogenesis. The third-ranking meta-

cluster relates to cell cycle, including regulation of cell proliferation and apoptosis. The top three functional meta-clusters enriched in WT1 targets are consistent with established functions of WT1 and thus also serve as an indicator of high data set quality.

### Identification of a WT1 binding motif using THEME

ChIP-chip experiments identify transcription factor binding events at low resolution. To improve the resolution of our data set, we used the THEME algorithm (Macisaac et al., 2006) to identify a sequence motif distinguishing WT1-bound target sequences from unbound sequences. The top-ranked motif identified by THEME (visualized by WebLogo in Fig. 1A and referred to as the WT1 matrix site) was detected in 86.1% of WT1-bound sites versus 34.8% of unbound sites and was consistent with the previously published EGR1-like WT1 consensus sequence (Hamilton et al., 1995; Nakagama et al., 1995). To map the WT1 binding site to our bound data set, the core WT1 consensus sequence  $G^1C^2G^3(T/G)^4(G/A)^5G^6G^7(C/A)^8G^9(G/T)^{10}$  was used to scan genomic sequences, with defined substitutions permitted at the fourth, fifth, eighth or tenth positions (substitutions noted in parentheses). Notably, the WT1 consensus sequence occurs with higher frequency in higher-ranking WT1 target genes (presence of WT1 consensus site in WT1-bound promoters: 74% in genes enriched greater than 8-fold versus 25% in genes enriched less than 8-fold;  $P < 0.001$ , Fisher's exact test). These observations indicate that high-affinity WT1 sites, as predicted by the consensus sequence, are more likely to be highly occupied in vivo. Collectively, these results indicate that the WT1 matrix site is a strong predictor of WT1 binding events in our data set.

### Validation of ChIP-chip output by ChIP-PCR

To validate our ChIP-chip results by ChIP-PCR, we selected ~40 target genes from our array list that could potentially function downstream of WT1 in nephron progenitor cells (Table 2). Using both database-assisted (DAVID) annotations, as well as manual annotations (PubMed searches), targets were selected based on their established or potential roles (i.e. established role of other highly homologous family members) in kidney development, progenitor cell fate, organogenesis, cell signaling or transcriptional regulation. Targets were chosen from across a range of array enrichment scores (3- to 25-fold), to assist in determining an enrichment cut-off value for subsequent biological validation of our array data.

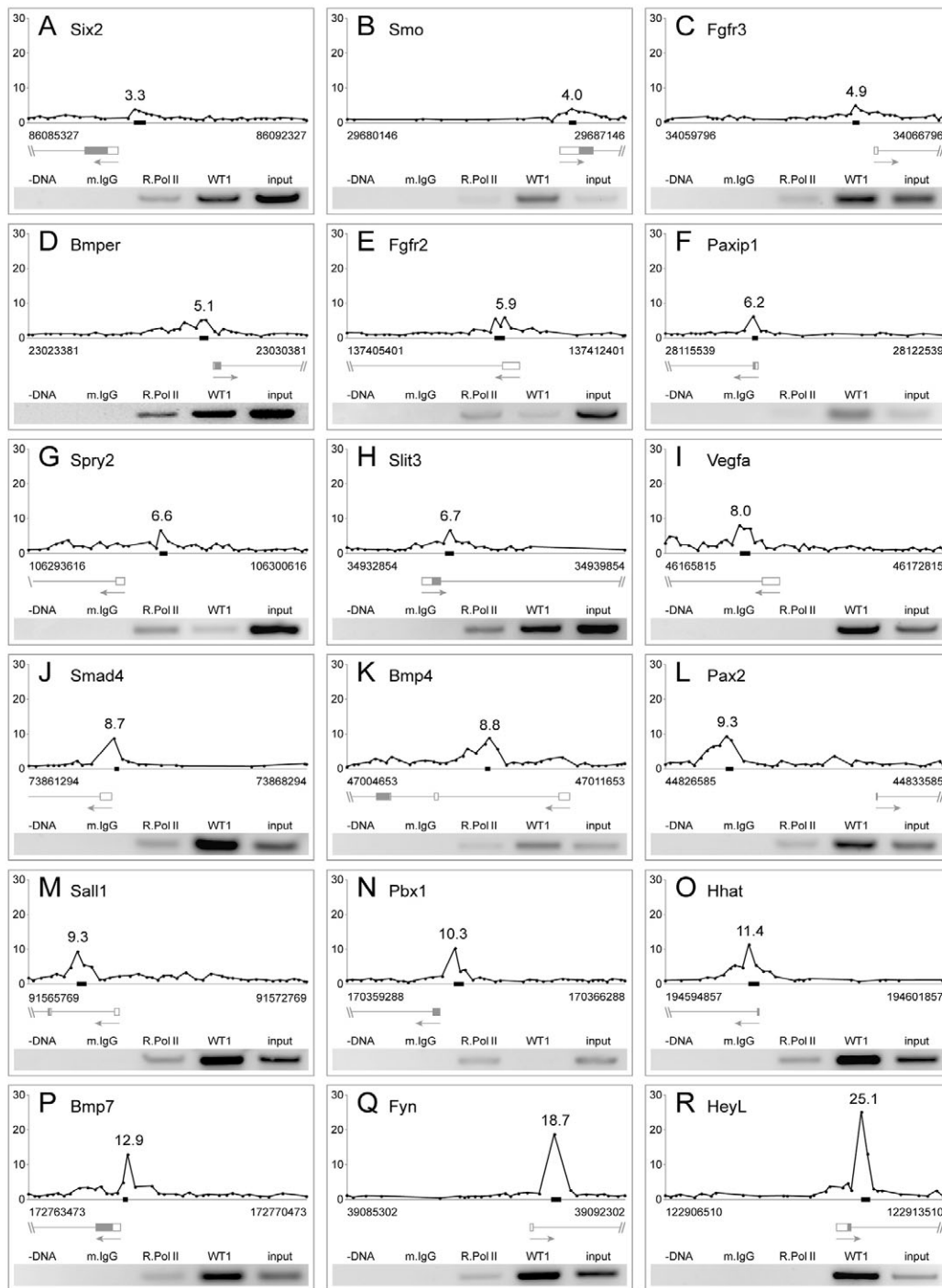
To verify WT1-specific enrichment of cis-regulatory regions identified by ChIP-chip, we adapted a standard ChIP protocol to perform ChIP using anti-WT1 antibodies in embryonic mouse kidney tissue (Lee et al., 2006). Following WT1 ChIP, enrichment of defined WT1-bound peak regions in ChIP fractions was compared with input fractions by PCR (see Fig. S2 in the supplementary material). A positive validation by ChIP-PCR was semi-quantitatively defined as a greater than 2-fold enrichment of WT1 ChIP DNA versus input DNA in each PCR reaction within the linear range of amplification, as measured by densitometry (NIS Elements statistical software; see Table S6 in the supplementary material). Numerous kidney development genes, including members of the Bmp (*Bmp4*, *Bmp7*, *Smad4*) and Hedgehog pathways (*Smo*, *Hhat*), as well as *Vegfa*, *Pax2* and *Sall1*, were validated as WT1 targets by ChIP-PCR (Fig. 2), suggesting that they might be bona fide transcriptional targets of WT1 in nephron progenitor cells in vivo.

Notably, lower-ranking WT1 binding sites enriched less than 8-fold on array were generally not validated by ChIP-PCR (4 were validated out of 15 ChIP-PCR reactions; see Fig. S2A-O in the supplementary material; Table 2). However, ChIP-PCR confirmed

Table 1. Functional annotation clustering of WT1 target genes using DAVID

| Meta cluster   |                                   | Cluster   |                                      |   |                |      |          |
|--|-----------------------------------|---|--------------------------------------|---|----------------|------|----------|
| Rank   | Term                              | Term  | Rank                                 | Enrichment score  | Median P-value |      |          |
| 1  | Transcription                     | Transcription/regulation of transcription                   | 1                                    | 20.43   | 8.64E-22       |      |          |
|  |                                   | Positive regulation (of transcription)                      | 3                                    | 9.66  | 2.94E-10       |      |          |
|  |                                   | Negative regulation (of transcription)                      | 5                                    | 7.23  | 1.14E-06       |      |          |
|  |                                   | Chromatin establishment/modification                        | 24                                   | 2.39  | 0.002          |      |          |
|  |                                   | RNA recognition/binding                                     | 31                                   | 2.05  | 0.012          |      |          |
| 2  | Development                       | (Positive) Regulation of DNA binding                        | 59                                   | 1.45  | 0.047          |      |          |
|  |                                   | Development/morphogenesis/differentiation                   | 2                                    | 16.11   | 2.87E-14       |      |          |
|  |                                   | Neuronal development/cellular morphogenesis                 | 4                                    | 7.75  | 2.84E-07       |      |          |
|  |                                   | Regulation of development/differentiation                   | 6                                    | 7.14  | 1.28E-07       |      |          |
|  |                                   | Homeobox (HOX)  | 9                                    | 4.84  | 1.38E-04       |      |          |
|  |                                   | Pattern specification                                       | 11                                   | 4.33  | 8.05E-05       |      |          |
|  |                                   | Skeletal development/remodeling/differentiation             | 12                                   | 4.06  | 7.18E-05       |      |          |
|  |                                   | Lung development/branching (tube) morphogenesis             | 13                                   | 3.88  | 3.90E-05       |      |          |
|  |                                   | Brain development   | 15                                   | 3.83  | 8.33E-05       |      |          |
|  |                                   | Embryonic development                                       | 16                                   | 3.83  | 1.07E-04       |      |          |
|  |                                   | Blood vessel development                                    | 19                                   | 2.62  | 0.003          |      |          |
|  |                                   | (Neural) Tube morphogenesis                                 | 20                                   | 2.55  | 0.004          |      |          |
|  |                                   | Muscle development/myoblast differentiation                 | 22                                   | 2.54  | 0.003          |      |          |
|  |                                   | Embryonic (limb/appendage) morphogenesis                    | 32                                   | 2.04  | 0.024          |      |          |
|  |                                   | Mesoderm/primary germ layer development/gastrulation        | 33                                   | 2   | 0.003          |      |          |
|  |                                   | Ear development/morphogenesis                               | 34                                   | 2   | 0.010          |      |          |
|  |                                   | Embryonic digestive tract development/morphogenesis         | 36                                   | 1.95  | 0.009          |      |          |
|  |                                   | Plexin/semaphorin   | 38                                   | 1.79  | 0.013          |      |          |
|  |                                   | Gastrulation  | 43                                   | 1.73  | 0.037          |      |          |
|  |                                   | Regulation of neuron differentiation                        | 48                                   | 1.68  | 0.019          |      |          |
| Osteoblast differentiation (regulation)                            | 50                                | 1.64  | 0.081                                |   |                |      |          |
| Kidney/urogenital development                                      | 52                                | 1.6   | 0.015                                |   |                |      |          |
| (Positive) Regulation of axonogenesis/neurogenesis                 | 61                                | 1.41  | 0.037                                |   |                |      |          |
| Pancreas development   | 63                                | 1.35  | 0.032                                |   |                |      |          |
| 3  | Cell cycle/cell growth            | Cell cycle (regulation)                                     | 7                                    | 5.49  | 1.92E-05       |      |          |
|  |                                   | Cell proliferation (regulation)                             | 14                                   | 3.84  | 1.14E-04       |      |          |
|  |                                   | Cell growth (regulation)                                    | 21                                   | 2.55  | 0.003          |      |          |
|  |                                   | Apoptosis (regulation)                                      | 25                                   | 2.28  | 0.007          |      |          |
|  |                                   | Epithelial cell proliferation (regulation)                  | 27                                   | 2.2   | 0.005          |      |          |
|  |                                   | (Negative) Regulation of cell growth                        | 30                                   | 3.11  | 0.011          |      |          |
|  |                                   | Mitogen/growth factor activity                              | 54                                   | 1.53  | 0.029          |      |          |
|  |                                   | Mitogen/PDGF/phosphorylation                                | 60                                   | 1.42  | 0.042          |      |          |
|  |                                   | 4   | Actin cytoskeleton                   | (Actin) Cytoskeleton organization and biogenesis                | 10             | 4.53 | 9.09E-06 |
|  |                                   |   |                                      | (Actin) Cytoskeleton binding                                    | 18             | 3.38 | 5.64E-04 |
| 5  | DNA-binding domain/protein        | Zinc finger/zinc binding                                    | 8                                    | 4.9   | 1.77E-05       |      |          |
|  |                                   | Basic leucine zipper (BZIP) domain                          | 23                                   | 2.43  | 0.004          |      |          |
|  |                                   | (Basic) Helix-loop-helix domain/motif                       | 29                                   | 2.14  | 0.012          |      |          |
|  |                                   | Dwarfin/CTF/NF-1 domain                                     | 39                                   | 1.78  | 0.035          |      |          |
|  |                                   | Chromatin binding/chromo domain                             | 47                                   | 1.71  | 0.043          |      |          |
|  |                                   | PHD-type zinc finger domain                                 | 49                                   | 1.67  | 0.030          |      |          |
|  |                                   | C2H2-type zinc finger domain                                | 53                                   | 1.55  | 0.118          |      |          |
|  |                                   | BTB/POZ domain  | 55                                   | 1.53  | 0.041          |      |          |
|  |                                   | Zinc finger nuclear receptors/COUP/RARA                     | 57                                   | 1.49  | 0.019          |      |          |
|  |                                   | 6   | Protein modification/kinase activity | Protein modification/phosphorylation/ phosphotransferase/kinase | 17             | 3.72 | 0.002    |
| Glycosylation/glycosyltransferase activity                         | 26                                |   |                                      | 2.25  | 0.006          |      |          |
| Golgi apparatus/glycosyltransferase activity                       | 28                                |   |                                      | 2.15  | 0.018          |      |          |
| Kinase (enzyme) binding  | 42                                |   |                                      | 1.75  | 0.016          |      |          |
| Glycosyltransferase activity/glycan biosynthesis/manganese binding | 44                                |   |                                      | 1.73  | 0.017          |      |          |
| (MAPK) Phosphatase/hydrolase activity                              | 56                                |   |                                      | 1.51  | 0.036          |      |          |
| cAMP-dependent activity/cAMP binding                               | 62                                |   |                                      | 1.41  | 0.058          |      |          |
| Cation transport/channel activity                                  | 64                                |   |                                      | 1.33  | 0.056          |      |          |
| 7  | Cell adhesion/migration/signaling | (Positive) Regulation of cell migration/motility/locomotion | 35                                   | 2   | 0.003          |      |          |
|  |                                   | Cell adhesion   | 37                                   | 1.86  | 0.015          |      |          |
| 8  | Miscellaneous protein domain      | (Synaptic) Cell signaling                                   | 41                                   | 1.75  | 0.024          |      |          |
|  |                                   | WH1/EVH1 domain   | 40                                   | 1.76  | 0.016          |      |          |
|  |                                   | GPCR/frizzled domain/PDZ binding                            | 45                                   | 1.72  | 0.015          |      |          |
|  |                                   | WW domain   | 46                                   | 1.71  | 0.046          |      |          |
|  |                                   | SH3 domain  | 51                                   | 1.62  | 0.017          |      |          |
| Pleckstrin homology (PH) domain                                    | 58                                | 1.48  | 0.100                                |   |                |      |          |

The DAVID integrative functional annotation database identified 64 functional clusters (see Table S1 in the supplementary material) over-represented in WT1 target genes. Related clusters were manually organized into 8 major functional meta-clusters that are enriched in WT1-bound target genes.



**Fig. 2. ChIP-PCR validation of ChIP-chip results.** (A-R) Plots of the mean fold-enrichment of WT1 ChIP versus input DNA ( $n=3$ ) for selected WT1-bound genes expressed in the developing kidney. The numeric peak fold-enrichment value from the microarray is noted above the peak. The chromosomal position of the ChIP-PCR amplicon is noted along the X axis (black box). The position of the transcript is noted below the graph. The corresponding ChIP-PCR result is shown underneath. (A-H) WT1-binding sites with fold-enrichment scores less than 8-fold were generally not validated by ChIP-PCR (see Table S6 in the supplementary material for quantification of ChIP-PCR results). (I-R) By contrast, ChIP-PCR consistently confirmed WT1-specific enrichment in >90% of target genes with enrichment scores 8-fold or higher.

WT1-specific enrichment in more than 90% of higher-ranking target genes enriched greater than 8-fold (24 validated out of 26 ChIP-PCR reactions; see Fig. S2P-O' in the supplementary material). This ChIP-PCR validation threshold of 8-fold enrichment correlates with the inflexion point of the curve identified at  $\sim 7.75$ -fold enrichment

(R Statistical Software), when all 1663 genes were plotted against their fold-enrichment scores (see Fig. S2P' in the supplementary material). Interestingly, among the target genes enriched greater than 8-fold, the only 2 target genes not validated by ChIP-PCR, *Pbx1* and *Pbx2* (see Fig. S2W,D' in the supplementary material), do not

Table 2. Summary statistics of WT1 ChIP-chip peaks in selected WT1 target genes

| Gene          | Fold-enrichment | Chromosome              | Distance to TSS | WT1 consensus site           | Validated by ChIP-PCR | Function  | Reference(s)  |
|---------------|-----------------|-------------------------|-----------------|------------------------------|-----------------------|---|---|
| <i>Heyl</i>   | 25.11           | 4: 122910233-122911555  | 372             | GCGGGGGCG                    | yes                   | <i>Notch</i> signaling pathway, cell fate determination     | (Iso et al., 2003; Steidl et al., 2000)                                 |
| <i>Egr3</i>   | 24.39           | 14: 70474926-70476048   | -2009           | GCGGAGGAG, GCGTGGGAGG        | yes                   | Cellular growth and differentiation                         | (Tourtellotte and Milbrandt, 1998)                                      |
| <i>Actn1</i>  | 23.89           | 12: 81360886-81361985   | -193            | GCGGAGGCGG, GCGGGGGAG        | yes                   | Focal adhesion, actin cytoskeleton regulation               | (Izaguirre et al., 2001)  |
| <i>Nab2</i>   | 19.58           | 10: 127103344-127103263 | 241             | GCGTGGGCG, GCGGGGG(C/A)G     | yes                   | Schwann cell differentiation, <i>Egr1/Egr2</i> co-repressor | (Le et al., 2005)   |
| <i>Fyn</i>    | 18.7            | 10: 39089847-39090342   | 708             | GCGGGGGCG                    | yes                   | Brain development, anti-apoptosis, GSD                      | (Arnaud et al., 2003; Harita et al., 2008; Tang et al., 2007)           |
| <i>Hoxd4</i>  | 16.56           | 2: 74565721-74566423    | 6012            | GCGGGGGCG                    | yes                   | Embryonic pattern formation, kidney development             | (Di-Poi et al., 2007; reviewed in Wellick, 2009)                        |
| <i>Sox11</i>  | 15.48           | 12: 28027842-28028642   | -657            | N/A                          | yes                   | Embryonic development, neural differentiation               | (Bergsland et al., 2006; Sock et al., 2004; Wurm et al., 2008)          |
| <i>Scx</i>    | 14.68           | 15: 76287234-76288113   | -86             | GCGGGGG(C/A)GGAG             | yes                   | Heart valve and Sertoli cell differentiation                | (Levy et al., 2008; Muir et al., 2005)                                  |
| <i>Sema6d</i> | 14.11           | 2: 124435389-124435389  | -248            | GCGTGGGCGTAG                 | yes                   | Myocardial patterning                                       | (Toyofuku et al., 2004a; Toyofuku et al., 2004b)                        |
| <i>Bmp7</i>   | 12.87           | 2: 172765859-172765859  | -204            | GCGGGGGAGGAG                 | yes                   | Eye, skeletal and kidney development                        | (Dudley et al., 1995; Jena et al., 1997; Kazama et al., 2008)           |
| <i>Pbx2</i>   | 12.78           | 17: 34729336-34730271   | 252             | N/A                          | no                    | Limb patterning, skeletal development                       | (Capellini et al., 2006; Capellini et al., 2008)                        |
| <i>Rest</i>   | 12.04           | 5: 77694648-77695784    | -1927           | GCGGGGG(C/A)G                | yes                   | Master negative regulator of neurogenesis                   | (Jones and Meech, 1999; Schoenherr and Anderson, 1995)                  |
| <i>Zfr</i>    | 11.96           | 15: 12047157-12047853   | -195            | GCGGGGGAG                    | yes                   | Perigastrulation growth and survival                        | (Meagher et al., 2001)  |
| <i>Hhat</i>   | 11.41           | 1: 194596974-194596864  | 219             | N/A                          | yes                   | Sonic hedgehog signaling ( <i>Shh</i> ) pathway             | (Buglino et al., 2008)  |
| <i>Zyx</i>    | 11.38           | 6: 42299668-42300772    | 388             | GCGGGGGCG                    | yes                   | Focal adhesion, cell migration, actin cytoskeleton          | (Hirata et al., 2008)   |
| <i>Arnt2</i>  | 10.9            | 7: 91557697-91558276    | 457             | GCGGGGGAG                    | yes                   | Neuronal development  | (Keith et al., 2001; Kozak et al., 1997)                                |
| <i>ErbB2</i>  | 10.75           | 11: 98273670-98274011   | 15              | GCGGAGGAGG                   | yes                   | Neural and cardiac development, oncogene                    | (Lee et al., 1995)  |
| <i>Smad7</i>  | 10.71           | 18: 75527141-75527426   | 268             | GCGGAGG(C/A)GG               | yes                   | <i>Tgfb/Bmp</i> signaling pathways                          | (Nakao et al., 1997)  |
| <i>Pbx1</i>   | 10.27           | 1: 170361694-170362190  | 341             | N/A                          | no                    | Limb patterning, skeletal and kidney development            | (Capellini et al., 2006; Capellini et al., 2008; Schnabel et al., 2003) |
| <i>Plxnb1</i> | 9.69            | 9: 108998328-109000281  | 1362            | GCGGAGGAG                    | yes                   | Sema receptor, cell migration, invasive cell growth         | (Basile et al., 2005; Giordano et al., 2002)                            |
| <i>Pax2</i>   | 9.26            | 19: 44827636-44828304   | -3729           | GCGGGGGAG                    | yes                   | Eye, inner ear and kidney development                       | (Rothenpieler et al., 1993; Torres et al., 1996)                        |
| <i>Sall1</i>  | 9.26            | 8: 91566663-91567411    | 1027            | GCGGGGGAG                    | yes                   | Limb, neural and kidney development                         | (Bohm et al., 2008; Nishinakamura et al., 2001)                         |
| <i>Bmp4</i>   | 8.8             | 14: 47007581-47008501   | 2006            | GCGGGGGAG                    | yes                   | Stem cell fate, kidney development                          | (reviewed in de Felici et al., 2009; Miyazaki et al., 2000)             |
| <i>Smad4</i>  | 8.7             | 18: 73863445-73863699   | -73             | GCGGGGGAG                    | yes                   | <i>Tgfb/Bmp</i> signaling pathways                          | (Lagna et al., 1996; Zhang et al., 1996)                                |
| <i>Smad3</i>  | 8.16            | 9: 63605810-63606524    | -423            | GCGGGGGAGGAG, GCGGAGG(C/A)GG | yes                   | <i>Tgfb/Bmp</i> signaling pathways                          | (Wu, 1997; Zhang et al., 1996)  |
| <i>Vegfa</i>  | 8.03            | 17: 46165927-46166243   | 3838            | GCGTGGGCG, GCGGGGGAG         | yes                   | Vasculogenesis, angiogenesis, kidney development            | (Gao et al., 2005; Keck et al., 1989; Leung et al., 1989)               |

Table 2 continued on next page

contain the WT1 consensus site (Table 2). In all subsequent experiments, we therefore focused on the cohort of WT1 targets exhibiting enrichment scores greater than 8-fold by array ( $n=202$ ).

### WT1 morpholino treatment arrests development in embryonic kidney explants

The absence of kidneys in *Wt1*<sup>-/-</sup> mice has precluded conventional approaches of investigating WT1 function during early renal development in vivo. Therefore, to gain insight into the role of WT1 during early kidney development, we used a novel, modified antisense, ‘vivo-morpholino’ delivery system (Gene Tools) to examine the consequences of WT1 knock-down in cultured E12.5 kidney explants. Each vivo-morpholino is a fusion moiety comprising a standard morpholino covalently fused to an octaguanidium dendramer transporter at its 5' end, permitting morpholino penetration into mouse tissue. Embryonic E12.5 mouse kidneys were cultured for 24 hours in media supplemented with WT1 antisense or 5-mismatch control vivo-morpholinos at varying dosages (10–20  $\mu$ M). Anti-WT1 immunofluorescent staining was used to determine the efficacy of WT1 antisense vivo-morpholinos

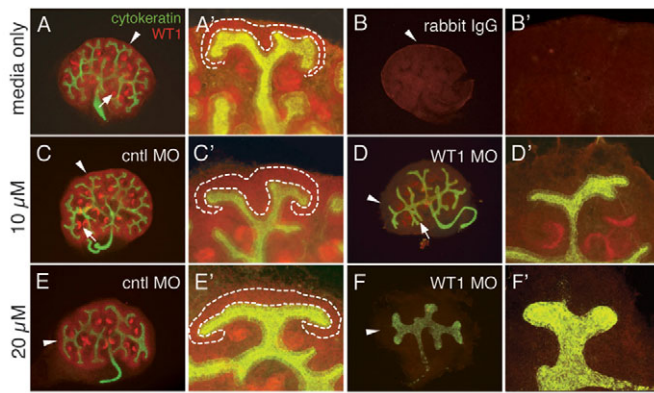
in blocking WT1 protein translation, and ureteric bud branching was visualized using anti-cytokeratin antibodies (Fig. 3). After 24 hours of culture, explants cultured with 10  $\mu$ M control vivo-morpholino (henceforth called control morphants) had undergone extensive ureteric bud branching, similar to explants cultured in media alone (Fig. 3C,C' versus A,A'). Control morphants exhibited characteristic WT1 expression in the cap of nephron progenitors surrounding the ureteric bud tips, as well as in pretubular aggregates, also similar to explants cultured in media alone. By contrast, WT1 expression in nephron progenitors was markedly reduced in explants treated with 10  $\mu$ M WT1 vivo-morpholino (hitherto referred to as WT1 morphants;  $n=6$ ; Fig. 3D,D' versus C,C'). Decreased WT1 expression in WT1 morphants was associated with moderately reduced ureteric bud branching and overall explant size.

To examine the effects of increased WT1 morpholino concentration, we next treated explants with a high dose (20  $\mu$ M) of vivo-morpholino. Control morphants treated with 20  $\mu$ M control vivo-morpholino exhibited a moderate reduction in ureteric bud branch number associated with altered terminal ureteric bud tip morphology compared with explants cultured in media alone,

Table 2. Continued

| Gene         | Fold-enrichment | Chromosome              | Distance to TSS | WT1 consensus site           | Validated by ChIP-PCR | Function  | Reference(s)   |
|--------------|-----------------|-------------------------|-----------------|------------------------------|-----------------------|---|--|
| <i>Nab1</i>  | 7.65            | 1: 52556594-52556904    | 322             | N/A                          | no                    | Schwann cell differentiation, <i>Egr1/Egr2</i> co-repressor | (Le et al., 2005)  |
| <i>Ptch1</i> | 6.87            | 13: 63665972-63666429   | 532             | GCGTGGGCG                    | no                    | <i>Shh</i> signaling pathway                                | (Murone et al., 1999; Stone et al., 1996)                  |
| <i>Slit3</i> | 6.67            | 11: 34935290-34935979   | 523             | GCGGAGGAG(T/G)               | no                    | Embryonic development, kidney development                   | (Liu et al., 2003)   |
| <i>Spry2</i> | 6.6             | 14: 106296835-106297186 | -938            | N/A                          | no                    | Embryonic development, Fgf signaling                        | (Taniguchi et al., 2007; Taketomi et al., 2005)            |
| <i>PTIP</i>  | 6.17            | 5: 28117756-28117994    | 101             | GCGGGGGCG                    | yes                   | Cell proliferation, DNA repair, Pax2-interacting            | (Cho et al., 2003)   |
| <i>Lef1</i>  | 5.95            | 3: 130814332-130815403  | 1166            | GCGGGGG(C/A)GGAG, GCGGAGGAGG | no                    | <i>Wnt</i> signaling pathway                                | (Huber et al., 1996)                                       |
| <i>Fgfr2</i> | 5.93            | 7: 137409139-137409581  | 922             | GCGGGGGCG                    | no                    | Stem cell fate, kidney development                          | (Poladia et al., 2006; Xu et al., 1998; Zhao et al., 2004) |
| <i>Sulf2</i> | 5.2             | 2: 165980866-165981075  | 262             | N/A                          | yes                   | Skeletal and renal development                              | (Ai, et al., 2007; Holst et al., 2007)                     |
| <i>Bmper</i> | 5.12            | 9: 23027603-23027893    | 351             | N/A                          | no                    | <i>Bmp</i> signaling pathway, endothelial cell migration    | (Heinke et al., 2008)                                      |
| <i>Fgfr3</i> | 4.92            | 5: 34064468-34064972    | 236             | GCGGGGGCG                    | no                    | Stem cell fate, kidney development                          | (Poladia et al., 2006; Xu et al., 1998; Zhao et al., 2004) |
| <i>Six4</i>  | 4.75            | 12: 74213237-74213712   | 972             | N/A                          | no                    | Neuronal cell survival, kidney induction                    | (Kobayashi et al., 2007; Konishi et al., 2006)             |
| <i>Stau1</i> | 4.52            | 2: 166820990-166821445  | 590             | N/A                          | no                    | RNA-binding, embryonic stem cell differentiation            | (Gautrey et al., 2008; Marion et al., 1999)                |
| <i>Smad6</i> | 4.34            | 9: 63870056-63870384    | -1103           | N/A                          | yes                   | <i>Tgfb/Bmp</i> signaling pathways                          | (Hata et al., 1998)  |
| <i>Smo</i>   | 3.97            | 6: 29685666-29686165    | 328             | N/A                          | yes                   | <i>Shh</i> signaling pathway                                | (Alcedo et al., 1996)                                      |
| <i>Six2</i>  | 3.34            | 17: 86088110-86088338   | -551            | N/A                          | no                    | Stem cell self-renewal, kidney development                  | (Kobayashi et al., 2008; Self et al., 2006)                |

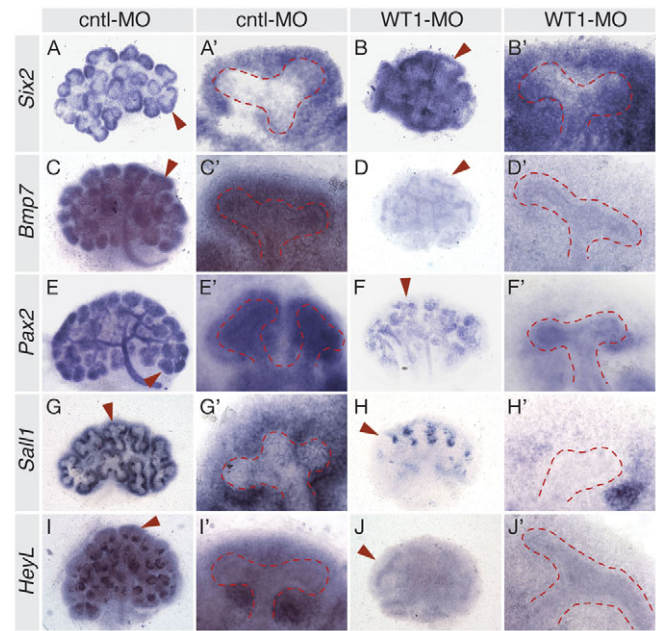
First tier peaks of 41 WT1 target genes identified by ChIP-chip ( $P < 0.001$ ) selected for subsequent ChIP-PCR validation. Genes are ranked by fold-enrichment scores on array. Locations of defined peak regions and gene functions are noted. Negative values indicate locations upstream (5') of the TSS. WT1 consensus sites were mapped to defined peak regions and, where present, are noted. Our WT1 consensus site mapping tolerates defined nucleotide substitutions within the 10 bp consensus sequence G<sup>1</sup>C<sup>2</sup>G<sup>3</sup>(T/G)<sup>4</sup>(G/A)<sup>5</sup>G<sup>6</sup>G<sup>7</sup>(C/A)<sup>8</sup>G<sup>9</sup>(G/T)<sup>10</sup> identified by the motif discovery algorithm THEME, at the fourth, fifth, eighth or tenth positions (substitutions noted in parentheses). Of the 1663 WT1 target genes identified on array, the WT1 consensus site occurs with higher frequency (74%) in target genes enriched >8-fold (versus 25% in genes enriched <8-fold;  $P < 0.0001$  by Fisher's Exact Test). Among the 41 target genes selected for ChIP-PCR validation shown here, 24 of the 26 (92%) target genes enriched >8-fold were validated by ChIP-PCR as measured by >2-fold enrichment of WT1 ChIP versus input DNA using densitometry (see Fig. S2 and Table S6 in the supplementary material), of which 22 contain the WT1 consensus site. Note that the two target genes in this cohort not validated by ChIP-PCR, namely *Pbx1* and *Pbx2*, lack the WT1 consensus site. By contrast, only 4 of 15 (27%) target genes enriched <8-fold were validated by ChIP-PCR. Within the cohort of targets enriched <8-fold, there is no correlation between the presence of a WT1 consensus site and validation by ChIP-PCR. TSS, transcriptional start site; N/A, not applicable (no WT1 consensus site present). Red font denotes positive ChIP-PCR validation. Red line marks the 8-fold enrichment threshold.



**Fig. 3. Reduced WT1 expression and arrested development in WT1 morphant kidney explants.** (A,A',C,C') E12.5 kidney explants cultured for 24 hours in media alone (A,A') or in 10  $\mu$ M control morpholino (cntl MO; C,C') exhibit strong WT1 (red) expression in the cap of nephron progenitors (dashed outlines) surrounding the tip of the ureteric bud (green), as well as in epithelialized nephrogenic structures (arrows). Arrowheads denote regions shown in high magnification in adjacent panels. (B,B') Background auto-fluorescence in negative control explants incubated with rabbit IgG. (D,D') WT1 expression is markedly reduced in the cap region and moderately reduced in epithelialized nephrogenic structures of explants treated with 10  $\mu$ M WT1 MO. The number of WT1-expressing nephrogenic tubules is also reduced in these explants. (E,E') Explants treated with 20  $\mu$ M cntl MO exhibit moderate reductions in ureteric bud branching compared with explants cultured in media alone but continue to express WT1 in nephron progenitor cells and form WT1-expressing epithelialized nephrogenic structures. (F,F') By contrast, WT1 expression is not detected in explants treated with 20  $\mu$ M WT1 MO, and explants do not undergo growth or ureteric bud branching.

indicative of a mild, general cytotoxic effect of *vivo*-morpholino treatment at this dosage, independent of effects on WT1 expression. Nevertheless, control morphants retained strong WT1 expression in nephron progenitors and epithelial tubules and underwent branching (Fig. 3E,E'). By contrast, WT1 expression was not detected in explants treated with 20  $\mu$ M antisense WT1 *vivo*-morpholino, and loss of WT1 was associated with arrested ureteric bud branching and reduced overall explant size. In all subsequent experiments, 10  $\mu$ M of WT1 *vivo*-morpholino was used, a dosage at which WT1 expression is reduced in nephron progenitors while maintaining the presence of progenitor cells.

Having demonstrated that WT1 expression is reduced in embryonic kidney explants treated with WT1 *vivo*-morpholinos, we proposed to use this *vivo*-morpholino system to examine whether WT1 target genes identified by array are indeed regulated by WT1. Loss of target gene expression in nephron progenitors of WT1 morphants could be attributable to a loss of specific regulation by WT1 or due to a general loss of progenitor cells. Therefore, we first determined whether nephron progenitor cells are still present in WT1 morphant explants. Explants were cultured for 24 hours with either 10  $\mu$ M WT1 antisense or control *vivo*-morpholino ( $n=10$ ) and *Six2* mRNA expression was assessed by RNA in situ hybridization (Fig. 4A,A'). *Six2* is a cap-specific marker of nephron progenitors surrounding ureteric bud tips (Kobayashi et al., 2008) and is downregulated in pretubular aggregates (Self et al., 2006). *Six2* was identified as a WT1 target gene (enriched 3.3-fold) by ChIP-chip. However, *Six2* was not validated by ChIP-PCR (Fig. 2A), and we therefore examined *Six2* expression in morpholino-treated explants



**Fig. 4. Expression of kidney development WT1 target genes is reduced in WT1 morphant kidney explants.** (A,A') Control morphant explants exhibit a characteristic expression pattern of *Six2*, a marker of nephron progenitors. (A') Higher magnification of region in A denoted by arrowhead. Dashed lines demarcate the ureteric bud. (B,B') The discrete pattern of cap-specific *Six2* expression is lost in WT1 morphants, which instead exhibit an expanded *Six2* expression domain. (C-J') Control morphants express *Bmp7* (C,C'), *Pax2* (E,E'), *Sall1* (G,G') and *HeyL* (I,I') in nephron progenitors and other lineages. In all cases, WT1 *vivo*-morpholino treatment results in a specific and marked reduction of gene expression in nephron progenitor cells (D,D',F,F',H,H',J,J'). Arrowheads denote regions shown in higher magnification in adjacent panels.

as a negative control. Characteristically discrete *Six2* mRNA expression was detected in the cap of nephron progenitors of control morphants, tightly condensed around ureteric bud tips (Fig. 4A,A'). *Six2* expression was also detected in WT1 morphant explants (Fig. 4B,B' versus A,A'). This was confirmed by qRT-PCR for *Six2*, which revealed no significant difference in *Six2* mRNA levels (1.1-fold higher in morphants; s.d. for WT1 morphants=0.158; s.d. for control morphants=0.136 normalized to GAPDH;  $n=3$ ). However, the *Six2* expression domain appeared less compact adjacent to ureteric bud tips in these explants, possibly reflecting a failure of nephron progenitors to undergo condensation in the absence of WT1. Although we are not able to rescue WT1 expression in morpholino-treated explants, to completely eliminate the possibility of a toxic effect specific to the WT1 morpholino, the continued expression of *Six2* makes it unlikely that the WT1 morpholino is considerably more toxic than the control morpholino.

### WT1 regulates expression of essential kidney development genes

Having established an *ex vivo* model in which to modulate WT1 expression in embryonic kidney explants while maintaining the presence of nephron progenitor cells, we next determined whether expression of essential early kidney development genes identified as WT1 targets by array are indeed regulated by WT1. In contrast to *Six2*, WT1 targets identified by array, including *Pax2* (enriched 9.3-

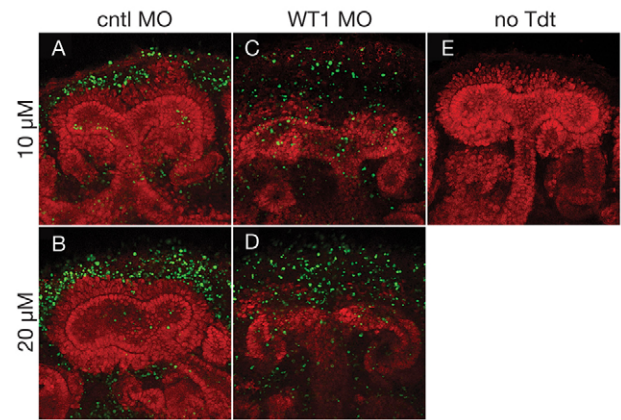


fold), *Sall1* (enriched 9.3-fold), *Bmp7* (enriched 12.9-fold) and *HeyL* (enriched 25.1-fold), were all validated by ChIP-PCR (Fig. 2L,M,P,R) and are regulated by WT1 (Fig. 4C-J'). In control morphants, *Bmp7* (Lyons et al., 1995) and *Pax2* (Dressler et al., 1990) mRNA expression was strongly detected in the ureteric bud and nephron progenitors and weakly expressed in pretubular aggregates (Fig. 4C,C',E,E'). *Sall1* expression was detected predominantly in nephron progenitors and weakly in nephrogenic tubules of control morphants (Fig. 4G,G') (Nishinakamura et al., 2001), whereas *HeyL* was expressed in nephron progenitors and ureteric bud cells (Leimeister et al., 2003), with strongest expression in pretubular aggregates (Fig. 4I,I'). In all cases, WT1 morphants exhibited a marked and specific reduction in target gene expression in nephron progenitors (Fig. 4D,D',F,F',H,H',J,J' versus C,C',E,E',G,G',I,I'), whereas residual *Bmp7* and *Pax2* expression was retained in the ureteric bud.

Importantly, the demonstration that *Six2*-expressing nephron progenitor cells are indeed present in WT1 morphants (Fig. 4B,B') indicates that loss of *Bmp7*, *Pax2*, *Sall1* and *HeyL* expression in nephron progenitors is not attributable to the absence of nephron progenitor cells. Rather, WT1-deficient nephron progenitors are present, but do not express these WT1 target genes. Collectively, these findings, which recapitulate both array and ChIP-PCR results, strongly suggest that *Bmp7*, *Pax2*, *Sall1* and *HeyL* are bona fide transcriptional targets of WT1 in embryonic kidneys. Notably, both *Pax2*<sup>-/-</sup> and *Sall1*<sup>-/-</sup> mice exhibit renal agenesis phenotypes. Our observations that these essential kidney development genes are regulated by WT1 suggest that loss of *Pax2*- and *Sall1*-dependent signaling in *Wt1*<sup>-/-</sup> embryos might account for the renal agenic phenotype in these embryos.

### Increased apoptosis in WT1 morphant kidneys

WT1 vivo-morpholino treatment of embryonic kidney explants reduces expression of essential kidney development genes *Bmp7*, *Pax2* and *Sall1*. Increased mesenchymal apoptosis is observed in *Bmp7*<sup>-/-</sup> (Luo et al., 1995), *Sall1*<sup>-/-</sup> (Nishinakamura et al., 2001) and *Wt1*<sup>-/-</sup> embryos (Kreidberg et al., 1993) and it has been proposed that these genes might control renal development in part via anti-apoptotic effects. To determine whether apoptosis is altered in WT1 morphants, we performed TUNEL staining in WT1 morphant explants, together with *Pax2* immunostaining to identify ureteric bud and nephron progenitor cells and visualized explants by confocal microscopy (Fig. 5). In explants treated with 10 or 20  $\mu$ M control vivo-morpholino (Fig. 5A,B), the highest concentration of TUNEL-positive cells (green) was observed in the peripheral region of metanephric mesenchyme, with low numbers of TUNEL-positive cells also observed in the ureteric bud, nephron progenitors and stromal compartment. The number of apoptotic cells in the cap region of explants treated with 10  $\mu$ M control vivo-morpholino was not significantly different from explants treated with 20  $\mu$ M control vivo-morpholino ( $P=0.62$ ,  $n=3$ ). In WT1 morphant explants, *Pax2* expression was reduced in the cap region (Fig. 5C,D), consistent with our previous results demonstrating reduced *Pax2* mRNA expression in WT1 morphant explants (Fig. 4F,F' versus E,E'). In WT1 morphants, the peripheral apoptotic zone was expanded towards the center of the explant and a dose-dependent increase in the number of TUNEL-positive cells is observed in the cap region of nephron progenitors at ureteric bud tips. Explants treated with 10  $\mu$ M WT1 vivo-morpholino exhibited a 2.5-fold increase in TUNEL-positive cells in the cap region ( $P=0.03$ ) compared with explants treated with 10  $\mu$ M control morpholino (Fig. 5C versus A;  $n=3$ ). Explants treated with 20  $\mu$ M WT1 vivo-morpholino exhibited a 4.22-fold increase in TUNEL-positive cells in the cap region



**Fig. 5. Increased apoptosis in WT1 morphant explants, shown by TUNEL labeling.** (A,B) Control morphant kidney explants treated with low (10  $\mu$ M) or higher doses (20  $\mu$ M) of control vivo-morpholino exhibit TUNEL-positive cells (green) mainly in the mesenchyme peripheral to the *Pax2* (red) expression domain of nephron progenitors and ureteric bud. (C,D) Low (C) and high (D) doses of WT1 vivo-morpholino result in an expansion of this outer apoptotic zone, which extends further in towards the centre of the explant. The number of apoptotic cells in the nephron progenitor cap region and in ureteric bud is increased in WT1 morphants (C,D versus A,B). At high doses of WT1 vivo-morpholino, a marked increase in the number of apoptotic cells is observed in the cap region adjacent to the ureteric bud (D). Note that *Pax2* expression is reduced in progenitor cells of WT1 morphant explants compared with controls (C,D versus A,B). (E) Negative control explant processed without Tdt enzyme showing absence of TUNEL-positivity.

( $P<0.0001$ ) compared with explants treated with 20  $\mu$ M control vivo-morpholino (Fig. 5D versus B;  $n=3$ ). Thus, the loss of WT1 in WT1 morphant explants is associated with reduced expression of *Bmp7*, *Pax2* and *Sall1*, together with increased apoptosis in the cap region and ureteric bud.

### Novel kidney genes are transcriptional targets of WT1

In a final series of proof-of-principle experiments, we attempted to identify novel kidney development WT1 target genes from our array target list that could mediate WT1 function in nephron progenitor differentiation. Of the 202 WT1 target genes enriched greater than 8-fold, a small cohort were selected based on established or potential roles in progenitor cell fate, development, or cell-cell signaling/cell migration. In E18.5 mouse kidneys, *Wt1* expression is not restricted to nephron progenitors, but is also strongly detected in presumptive podocytes occupying the posterior portion of developing nephrons (Pritchard-Jones et al., 1990) and in mature podocytes (Mundlos et al., 1993). As we had performed ChIP-chip in E18.5 mouse kidneys, our array target list included genes expressed in nephron progenitors, induced nephrogenic structures and mature podocytes. In order to select genes specifically expressed in early renal development, we screened the mRNA expression pattern of selected genes using the Genepaint Mouse Expression Database (<http://www.genepaint.org/index.html>) (Alvarez-Bolado and Eichele, 2006) to further select for genes expressed in E14.5 kidneys. We thus identified a panel of WT1 target genes enriched greater than 8-fold and co-expressed with WT1 in nephron progenitors in embryonic E14.5 kidney tissues, including *Cxhc5*, *Lsp1*, *Pbx2*, *Plexdc2*, *Rps6ka3* (*Rsk2*), *Scx* and *Sox11* (Table 3).

The mRNA expression pattern of *Cxnc5* (enriched 20.9-fold), *Lsp1* (enriched 24.4-fold), *Pbx2* (enriched 12.8-fold), *Plxdc2* (enriched 10.0-fold), *Rps6ka3* (enriched 11.9-fold), *Scx* (enriched 14.7-fold) and *Sox11* (enriched 15.5-fold) in control and WT1 morphant kidney explants is shown in Fig. 6. With the exception of *Plxdc2*, strong WT1 target gene expression was detected in nephron progenitors of control morphant explants, as well as in other cell lineages (Fig. 6). The expression of *Plxdc2* appeared restricted to the outer population of metanephric mesenchyme in control morphants, a more weakly *Wt1*-expressing domain, and did not appear to be expressed in cap or ureteric bud cells (Fig. 6G,G'). Similar to our previous observations (Fig. 5), WT1 morphants, in all cases, exhibited marked and specific reductions in target gene expression in nephron progenitors (Fig. 6) or metanephric mesenchyme (Fig. 6H,H' versus G,G'). Collectively, these findings illustrate the predictive quality of our array output in identifying novel kidney genes expressed in nephron progenitors of the developing kidney that might act as mediators of WT1 function in nephron progenitors in vivo.

## DISCUSSION

In the present study, we performed ChIP-chip in embryonic mouse kidney tissue without PCR amplification to identify transcriptional targets of WT1 in nephron progenitor cells during renal development in vivo. Using the THEME motif discovery algorithm, a single high-affinity WT1 binding motif was identified in 86% of the WT1-bound sequences (versus 34.8% of unbound sequences) on the array (Fig. 1). Consistent with a role for WT1 in transcriptional regulation during development, biological processes most highly enriched in WT1 target genes relate to transcription as well as development and differentiation of multiple tissues (Table 1). ChIP-

PCR and biological methods validated WT1 targets enriched greater than 8-fold by array, a threshold value that closely corresponds to the inflexion point (~7.75) of the fold-enrichment curve for our data set (see Fig. S2P' in the supplementary material).

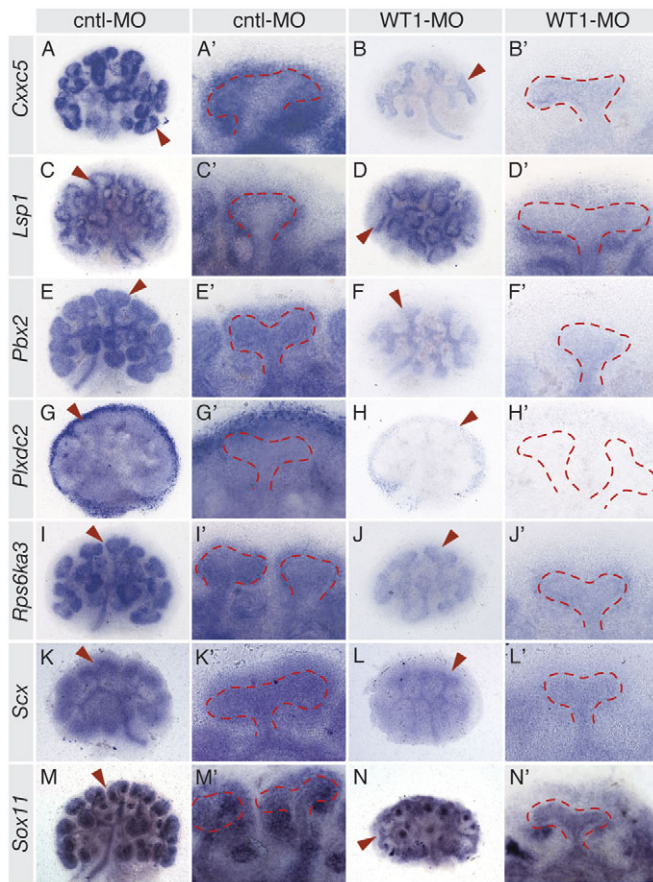
Biological validation was performed using a novel vivo-morpholino WT1 loss-of-function ex vivo model (Fig. 3-Fig.6). Embryonic kidney organ culture is a well-established model of both organogenesis in general and early kidney development in particular. WT1 vivo-morpholino treatment of embryonic kidney explants provides a powerful new biological method for validating WT1 candidate genes and characterizing both WT1 and WT1 target-gene function during renal development ex vivo. In a broader context, the core vivo-morpholino strategy should be applicable to the study of other genes that, similar to *Wt1*, exhibit early embryonic lethal organ agenesis or complex phenotypes.

Following WT1 vivo-morpholino treatment of embryonic kidney explants, RNA in situ hybridization was performed to characterize changes in renal developmental expression patterns of WT1 target genes enriched greater than 8-fold by array, including both established kidney development genes (Fig. 4), as well as genes not previously characterized in the kidney (Fig. 6). In all cases, target gene mRNA expression overlapped with the expression domain of WT1 in nephron progenitor cells and WT1 morphants uniformly exhibited decreased target gene expression in nephron progenitor cells. Collectively, these analyses suggest with considerable confidence, that WT1 target genes enriched greater than 8-fold by ChIP-chip represent bona fide WT1 transcriptional targets during renal development. Further, these results indicate a high predictive quality of our data set to identify novel WT1 target genes co-expressed with WT1 in the developing kidney that might mediate WT1 function during nephron progenitor differentiation in vivo.

**Table 3. Functions associated with novel kidney WT1 target genes**

| Gene           | Fold-enrichment | P-value | Function   | Reference  |
|----------------|-----------------|---------|--|--|
| <i>Cxnc5</i>   | 20.95           | <0.001  | <i>Bmp4</i> -dependent Wnt inhibition in neural stem cells<br>Myelopoietic progenitor differentiation<br>Related <i>Cxnc4</i> inhibits nuclear beta-catenin accumulation and Tcf signaling | (Andersson et al., 2009)<br>(Pendino et al., 2009)<br>(Hino et al., 2001; London et al., 2004) |
| <i>Lsp1</i>    | 24.46           | <0.001  | F-actin binding<br>Leukocyte cell migration  | (Jongstra-Bilen et al., 1992)<br>(Liu et al., 2005)  |
| <i>Pbx2</i>    | 12.78           | <0.001  | <i>Pbx1/Pbx2</i> coordinately regulate limb patterning and axial skeletal development<br>Related <i>Pbx1</i> regulates ureteric bud branching  | (Capellini et al., 2006; Capellini et al., 2008)<br>(Schnabel et al., 2003)                    |
| <i>Plxdc2</i>  | 10.03           | <0.001  | Potential Semaphorin growth factor receptor in neural development  | (Miller et al., 2007)  |
| <i>Rps6ka3</i> | 11.9            | <0.001  | Neurite differentiation<br><i>Fgfr3</i> -dependent hematopoietic transformation  | (Fischer et al., 2009)<br>(Kang et al., 2007; Kang et al., 2009)                               |
| <i>Scx</i>     | 14.68           | <0.001  | Tendon development<br>Heart valve development<br>Sertoli cell differentiation  | (Brent et al., 2004; Edom-Vovard et al., 2002)<br>(Levay et al., 2008)<br>(Muir et al., 2005)  |
| <i>Sox11</i>   | 15.48           | <0.001  | Tissue remodeling<br><i>Notch</i> , <i>Bmp</i> - and <i>Pax</i> -dependent signaling in eye development  | (Sock et al., 2004)<br>(Wurm et al., 2008)   |

Established or potential biological functions associated with selected WT1 target genes enriched >8-fold, expressed in E14.5 kidneys (Genepaint Mouse Expression Database), but not previously investigated in the developing kidney.



**Fig. 6. Expression of novel kidney WT1 target genes is reduced in WT1 morphant kidney explants.** Expression of *Cxhc5* (A,A'), *Lsp1* (C,C'), *Pbx2* (E,E'), *Rps6ka3* (I,I'), *Scx* (K,K') and *Sox11* (M,M') in control morphant explants, demonstrating expression in nephron progenitor cells and other lineages. *Plxdc2* (G,G') is expressed predominantly in the outer region of the metanephric mesenchyme, a weak WT1-expression domain. In all cases, WT1 vivo-morpholino treatment results in a specific and marked reduction of target gene expression in nephron progenitor cells (B,B',D,D',F,F',J,J',L,L',N,N') or in mesenchyme peripheral to the nephron progenitors (H,H'). Dashed outlines demarcate the ureteric bud. Arrowheads denote regions shown in higher magnification in adjacent panels.

### WT1 can function as a transcriptional activator in embryonic kidney explants

The transcriptional function of WT1 has been controversial. Primarily using promoter-reporter constructs in cell culture models of WT1 gain-of-function, WT1 has been shown to bind and repress GC-rich promoters of several growth-promoting genes expressed in the kidney including *Pax2* (Ryan et al., 1995), *N-myc* (Zhang et al., 1999) and *Egfr* (Englert et al., 1995). However, the biological relevance of many of these regulatory events is unknown, as GC-rich sequences are found in the promoter regions of thousands of genes, including those that have CpG islands. Moreover, major discrepancies were found when evaluating WT1 function using promoter-reporter constructs versus studies on the regulation of endogenous genes: in several cases, WT1 transfection failed to repress expression of the native gene, despite potentially repressing the activity of its corresponding

promoter-reporter constructs in transfection assays (Scharnhorst et al., 2001). For example, in the case of *Egfr*, where both endogenous gene expression and promoter activity were downregulated following WT1 transfection in Saos2 osteosarcoma cells (Englert et al., 1995), results could not be confirmed in HEK293 cells (Thate et al., 1998). Thus, WT1 transcriptional repressor activity in vitro appears to depend on promoter architecture, experimental conditions, cell line and type of expression vector (Reddy et al., 1995).

In the present study, WT1 vivo-morpholino treatment in embryonic kidney explants resulted in reduced target gene expression. These findings are consistent with the in vitro transcriptional activation function associated with the WT1 consensus site (Hamilton et al., 1995; Nakagama et al., 1995) enriched in our data set. Together with our results demonstrating physical binding of WT1 (or a WT1-containing complex) to the proximal promoter regions of these target genes, these observations indicate that WT1 can act as a transcriptional activator during embryonic renal development in vivo.

### WT1 sites and target gene binding

WT1 has been shown to bind several GC-rich and (TCC)n consensus sequences in vitro (Drummond et al., 1994; Rauscher et al., 1990). In fact, the last three zinc fingers of WT1 are highly homologous with the three zinc fingers of EGR1, which each recognize a 3 bp consensus sequence. WT1 binding specificity is influenced by specific nucleotide substitutions within the core 9-bp WT1 site GCGTGGGCG in vitro. For example, adenosine and thymidine substitutions in the eighth and tenth positions (GCGTGGGAGT), respectively, have been shown to confer 20- to 30-fold higher affinity for WT1 binding compared with EGR1 in vitro (Nakagama et al., 1995). The motif discovery algorithm THEME identified a WT1 matrix site that is highly enriched in WT1-bound sequences (present in 86.1% of WT1-bound sequences versus 34.8% of unbound sequences), consistent with the previously reported, EGR1-like, WT1 consensus site (Hamilton et al., 1995; Nakagama et al., 1995). This WT1 consensus site occurs with higher frequency in higher-ranking WT1 target genes on the array (present in 74% of genes enriched greater than 8-fold versus 25% in genes enriched less than 8-fold), indicating that highly occupied in vivo WT1 targets identified by ChIP are more likely to correspond to high affinity binding sites. However, we did not observe enrichment of WT1 consensus site variants containing adenosine at the eighth position and/or thymidine at the tenth position among higher-ranking targets on the array. This might, in part, be explained by additional factors affecting recruitment of WT1 to its targets, which could include structural characteristics of the binding site that are not well-modeled by simple matrix motif models.

In addition, the observation that a significant portion (14%) of WT1-bound genes lacked the WT1 matrix site altogether, indicates that additional factors independent of cis-sequence recognition probably mediates WT1 binding to target genes in vivo. It is possible that, similar to SWI/SNF-DNA- (Fairall et al., 1993; Schwabe et al., 1993) and GLI-DNA-binding events (Pavletich and Pabo, 1993; Vokes et al., 2007), WT1 zinc finger-DNA interactions might involve a combination of cis and trans DNA-binding sequences. In addition, cooperative or competitive interactions with other transcription factors, histone modifications and the chromatin structure in the vicinity of the binding site probably play an important role in bringing WT1 to its target site and increasing WT1 binding affinity in vivo.

### Functional annotations associated with WT1

DAVID identified eight major functional groups enriched in WT1 targets (Table 1). The three most enriched functions relate to transcription, multi-organ development and cell cycle, terms consistent with the established role of WT1 during development and in tumor biology. WT1 targets are also enriched for specific families of proteins containing conserved zinc-finger DNA-binding motifs including BZIP, BHLH, Dwarfin/CTF/NF-1, Chromo, PhD, C<sub>2</sub>H<sub>2</sub> and BTP/POZ domains, as well as zinc-finger families of nuclear receptors. Non-DNA-binding protein domains including WH1/EVH1, GPCR, Frz/PDZ, WW, SH3 and pleckstrin homology domains were also enriched in WT1 target genes. That WT1 binds conserved families of proteins suggests a model wherein WT1-dependent transcriptional regulation of a small number of ancestral genes might have been retained following gene duplication events, chromosomal segregation, and other genome reorganization events that both increased gene number and diversified gene function during evolution (Pal and Hurst, 2000).

Interestingly, WT1 target genes were also enriched for actin cytoskeleton organization, actin biogenesis and binding, as well as cell adhesion, cell migration and cell-cell signaling. In fact, three of the top ten most highly enriched WT1 targets identified by array (see Table S4 in the supplementary material), namely *Myo1B* (enriched 27.2-fold), *Lsp1* (enriched 24.5-fold) and *Actm1* (enriched 23.8-fold), are expressed during early kidney development and are involved in cytoskeletal interactions. Previously, two independent transcriptome profiling reports during pre-implantation mouse development demonstrated an obligate, transient surge in expression of genes involved in actin cytoskeleton and cell-cell signaling occurring prior to the major differentiation events in early development (Hamatani et al., 2004; Mitiku and Baker, 2007). High expression of cytoskeleton-interacting genes at this juncture is thought to relate to the dramatic morphological changes and energy requirements associated with compaction, as well as the requirement of cadherin-cytoskeleton interactions for cell-to-cell contact and adhesion during compaction (Hamatani et al., 2006). Expression of cell-cell signaling genes is thought to facilitate assembly of gap and tight junctions that enable blastomeres to lose their round shape, become tightly packed together and undergo differentiation (Watson and Barcroft, 2001).

It is intriguing to hypothesize that a similar burst of expression of genes involved in cytoskeleton and cell-cell signaling might necessarily precede the major morphologic changes associated with nephron progenitor aggregation around ureteric bud tips and differentiation. In fact, isolated *Wt1*<sup>-/-</sup> mesenchymal rudiments fail to aggregate in response to inductive signals from wild-type ureteric bud cells and instead undergo massive apoptosis (Donovan et al., 1999). This phenotype is distinct from *Sall1*<sup>-/-</sup> rudiments, which retain their competence to respond to inducing ureteric bud signals (Nishinakamura et al., 2001), suggesting that the *Wt1*<sup>-/-</sup> phenotype is not simply due to loss of *Sall1* signaling. Similarly, in WT1 morphant kidney explants, WT1-deficient nephron progenitor cells fail to become tightly packed into a discrete 'cap' around the tips of the ureteric bud. Instead, WT1-deficient nephron progenitors are loosely arranged around the ureteric bud tips, as evidenced by a diffuse rather than cap-specific expression pattern of the nephron progenitor marker *Six2* (Fig. 4B,B' versus A,A'). It is possible that one function of WT1 during early renal development is to activate genes involved in cytoskeletal-interactions, cell-cell adhesion, migration and signaling, processes that might themselves play pivotal permissive roles in nephron progenitor differentiation. In this paradigm, loss of WT1-dependent activation of cytoskeleton-

interacting genes in *Wt1*<sup>-/-</sup> mice would reduce the cellular integrity and scaffolding of individual nephron progenitor cells, thus rendering them incompetent to withstand the major morphologic changes associated with aggregation and differentiation. Similarly, loss of WT1-dependent activation of cell-cell signaling genes might prevent groups of *Wt1*<sup>-/-</sup> nephron progenitor cells from forming necessary cell-cell contacts. Thus, these cells would be unable to aggregate and undergo concerted group movement to form the cap of cells that surround the ureteric bud tips and undergo differentiation.

Recently, ChIP-chip location analysis was performed in immortalized CCG099-11 Wilms' tumor cells (Kim et al., 2009) and eight WT1 target genes were initially identified in three technical replicates. By overexpressing WT1 in inducible CCG-5.1 cells, the authors subsequently identified 643 promoter targets of WT1. The highest functional enrichment in WT1 target genes related to MAPK signaling, regulation of actin cytoskeleton and focal adhesion functional groups that were also observed in our data set, albeit at the lower range of enrichment. Major differences between this data set and our own might reflect differences in WT1-dependent tumor biology versus developmental function, as well as differences obtained by performing ChIP-chip in WT1-overexpressing immortalized cells versus in embryonic kidney tissues.

During renal development, WT1 is expressed in multiple nephrogenic compartments including the nephrogenic mesenchyme, nephron progenitors and developing tubules, as well as in glomerular podocytes. Whether WT1 regulates similar sets of gene targets in each of these cellular compartments, and at different stages of renal development, has not been explored. Recently, Brunskill et al. (Brunskill et al., 2008) have used laser capture microdissection and/or fluorescence-activated cell sorting followed by microarray profiling, to define a genome-wide gene expression atlas for the different cell lineages of the developing kidney at both late and early developmental time points (Brunskill et al., 2008). The integration of our WT1 ChIP-chip results with results from the kidney atlas and other gene expression databases will be a necessary and important first step towards a comprehensive description of WT1 function and gene targets at different stages of renal development *in vivo*.

In summary, by applying location analysis together with bioinformatics and biological approaches, we have identified WT1 target genes in embryonic mouse kidneys co-expressed with WT1 in nephron progenitor cells that could play an important role in mediating WT1 regulation of nephron progenitor differentiation *in vivo*. These data provide novel insights into biological processes that might be regulated by WT1, as well as the mechanisms by which WT1 binds and regulates target gene transcription in progenitor cells of the developing kidney and other developing organs *in vivo*.

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### Competing interests statement

The authors declare no competing financial interests.

### Supplementary material

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**Table S1. Chromosomal loci amplified in ChIP-PCR for WT1 gene targets**

| Probe chromosomal locus  | Gene         | RefSeq accession number | Fold-enrichment |
|--------------------------|--------------|-------------------------|-----------------|
| chr12:81360406-81360451  | <i>Actn1</i> | NM_134156               | 1.885162211     |
| chr12:81360886-81360931  | <i>Actn1</i> | NM_134156               | 2.123701916     |
| chr12:81361062-81361108  | <i>Actn1</i> | NM_134156               | 2.929542597     |
| chr12:81361329-81361374  | <i>Actn1</i> | NM_134156               | 3.524859728     |
| chr12:81361473-81361518  | <i>Actn1</i> | NM_134156               | 24.31048345     |
| chr12:81361601-81361646  | <i>Actn1</i> | NM_134156               | 4.263625077     |
| chr12:81361795-81361845  | <i>Actn1</i> | NM_134156               | 4.348359654     |
| chr12:81361940-81361985  | <i>Actn1</i> | NM_134156               | 1.767946788     |
| <hr/>                    |              |                         |                 |
| chr7:91557697-91557757   | <i>Arnt2</i> | NM_007488               | 3.129574932     |
| chr7:91557860-91557917   | <i>Arnt2</i> | NM_007488               | 6.569380768     |
| chr7:91557985-91558039   | <i>Arnt2</i> | NM_007488               | 10.89387706     |
| chr7:91558101-91558146   | <i>Arnt2</i> | NM_007488               | 10.08329549     |
| chr7:91558231-91558276   | <i>Arnt2</i> | NM_007488               | 7.597717035     |
| <hr/>                    |              |                         |                 |
| chr14:47007581-47007626  | <i>Bmp4</i>  | NM_007554               | 3.685465809     |
| chr14:47007693-47007740  | <i>Bmp4</i>  | NM_007554               | 5.67119259      |
| chr14:47007907-47007967  | <i>Bmp4</i>  | NM_007554               | 4.403054679     |
| chr14:47008137-47008187  | <i>Bmp4</i>  | NM_007554               | 7.004617637     |
| chr14:47008246-47008291  | <i>Bmp4</i>  | NM_007554               | 8.822840486     |
| chr14:47008451-47008501  | <i>Bmp4</i>  | NM_007554               | 5.68974169      |
| chr14:47009773-47009827  | <i>Bmp4</i>  | NM_007554               | 2.787582852     |
| <hr/>                    |              |                         |                 |
| chr2:172764762-172764807 | <i>Bmp7</i>  | NM_007557               | 3.322869114     |
| chr2:172764969-172765019 | <i>Bmp7</i>  | NM_007557               | 3.406469008     |
| chr2:172765155-172765200 | <i>Bmp7</i>  | NM_007557               | 2.779228295     |
| chr2:172765859-172765904 | <i>Bmp7</i>  | NM_007557               | 4.831320846     |
| chr2:172765976-172766021 | <i>Bmp7</i>  | NM_007557               | 12.87208012     |
| chr2:172766162-172766207 | <i>Bmp7</i>  | NM_007557               | 3.583262283     |
| chr2:172766584-172766638 | <i>Bmp7</i>  | NM_007557               | 3.844485195     |
| <hr/>                    |              |                         |                 |
| chr9:23027189-23027234   | <i>Bmper</i> | NM_028472               | 2.526008917     |
| chr9:23027603-23027648   | <i>Bmper</i> | NM_028472               | 2.809731786     |
| chr9:23027727-23027772   | <i>Bmper</i> | NM_028472               | 4.98164993      |
| chr9:23027848-23027893   | <i>Bmper</i> | NM_028472               | 5.139692259     |
| <hr/>                    |              |                         |                 |
| chr14:70474926-70474971  | <i>Egr3</i>  | NM_018781               | 3.888523381     |
| chr14:70475028-70475073  | <i>Egr3</i>  | NM_018781               | 19.40777108     |
| chr14:70475219-70475264  | <i>Egr3</i>  | NM_018781               | 24.51984838     |
| chr14:70475325-70475370  | <i>Egr3</i>  | NM_018781               | 7.660779059     |
| chr14:70475524-70475569  | <i>Egr3</i>  | NM_018781               | 1.413367113     |
| chr14:70475637-70475682  | <i>Egr3</i>  | NM_018781               | 8.821325541     |
| chr14:70475820-70475880  | <i>Egr3</i>  | NM_018781               | 8.517142461     |
| chr14:70476003-70476048  | <i>Egr3</i>  | NM_018781               | 2.7308202       |
| <hr/>                    |              |                         |                 |
| chr11:98273670-98273715  | <i>ErbB2</i> | NM_001003817            | 1.957810511     |
| chr11:98273790-98273835  | <i>ErbB2</i> | NM_001003817            | 10.86298349     |
| chr11:98273966-98274011  | <i>ErbB2</i> | NM_001003817            | 1.889541533     |
| <hr/>                    |              |                         |                 |
| chr7:137409139-137409185 | <i>Fgfr2</i> | NM_010207               | 5.53030562      |
| chr7:137409274-137409319 | <i>Fgfr2</i> | NM_010207               | 3.280239815     |
| chr7:137409376-137409424 | <i>Fgfr2</i> | NM_010207               | 5.924066939     |
| chr7:137409536-137409581 | <i>Fgfr2</i> | NM_010207               | 2.87008429      |
| <hr/>                    |              |                         |                 |
| chr5:34064468-34064513   | <i>Fgfr3</i> | NM_008010               | 2.484248062     |
| chr5:34064586-34064631   | <i>Fgfr3</i> | NM_008010               | 4.936873665     |
| chr5:34064725-34064770   | <i>Fgfr3</i> | NM_008010               | 3.615329019     |



|                           |              |           |             |
|---------------------------|--------------|-----------|-------------|
| chr5:34064927-34064972    | <i>Fgfr3</i> | NM_008010 | 2.549270022 |
| chr10:39089847-39089892   | <i>Fyn</i>   | NM_008054 | 1.564046674 |
| chr10:39090282-39090342   | <i>Fyn</i>   | NM_008054 | 18.71706365 |
| chr4:122910233-122910278  | <i>Heyl</i>  | NM_013905 | 3.692497849 |
| chr4:122910601-122910652  | <i>Heyl</i>  | NM_013905 | 3.311598782 |
| chr4:122910756-122910801  | <i>Heyl</i>  | NM_013905 | 4.55858851  |
| chr4:122910859-122910904  | <i>Heyl</i>  | NM_013905 | 2.541881335 |
| chr4:122911146-122911193  | <i>Heyl</i>  | NM_013905 | 25.1419019  |
| chr4:122911325-122911373  | <i>Heyl</i>  | NM_013905 | 13.20722708 |
| chr4:122911495-122911555  | <i>Heyl</i>  | NM_013905 | 2.981349965 |
| chr1:194596332-194596386  | <i>Hhat</i>  | NM_144881 | 2.568933819 |
| chr1:194596508-194596555  | <i>Hhat</i>  | NM_144881 | 4.514940719 |
| chr1:194596616-194596672  | <i>Hhat</i>  | NM_144881 | 5.349621816 |
| chr1:194596819-194596864  | <i>Hhat</i>  | NM_144881 | 4.681517195 |
| chr1:194596974-194597019  | <i>Hhat</i>  | NM_144881 | 11.44601784 |
| chr1:194597148-194597193  | <i>Hhat</i>  | NM_144881 | 5.40315551  |
| chr1:194597336-194597382  | <i>Hhat</i>  | NM_144881 | 3.652075846 |
| chr1:194597502-194597562  | <i>Hhat</i>  | NM_144881 | 3.593429155 |
| chr2:74565721-74565766    | <i>Hoxd4</i> | NM_010469 | 8.614434632 |
| chr2:74565868-74565918    | <i>Hoxd4</i> | NM_010469 | 6.643002341 |
| chr2:74566023-74566070    | <i>Hoxd4</i> | NM_010469 | 16.55598521 |
| chr2:74566185-74566230    | <i>Hoxd4</i> | NM_010469 | 3.883200335 |
| chr2:74566364-74566423    | <i>Hoxd4</i> | NM_010469 | 4.996171293 |
| chr3:130812572-130812629  | <i>Lef1</i>  | NM_010703 | 1.934877536 |
| chr3:130812839-130812897  | <i>Lef1</i>  | NM_010703 | 4.938118888 |
| chr3:130813037-130813083  | <i>Lef1</i>  | NM_010703 | 3.263052169 |
| chr3:130813309-130813354  | <i>Lef1</i>  | NM_010703 | 2.031235399 |
| chr3:130813444-130813489  | <i>Lef1</i>  | NM_010703 | 4.673422167 |
| chr3:130813627-130813682  | <i>Lef1</i>  | NM_010703 | 3.477142506 |
| chr3:130813795-130813855  | <i>Lef1</i>  | NM_010703 | 2.936702235 |
| chr3:130814332-130814377  | <i>Lef1</i>  | NM_010703 | 1.916384879 |
| chr3:130814529-130814579  | <i>Lef1</i>  | NM_010703 | 5.96324733  |
| chr3:130814762-130814813  | <i>Lef1</i>  | NM_010703 | 4.701323172 |
| chr3:130814942-130814987  | <i>Lef1</i>  | NM_010703 | 5.116507061 |
| chr3:130815358-130815403  | <i>Lef1</i>  | NM_010703 | 2.883503056 |
| chr1:52556594-52556640    | <i>Nab1</i>  | NM_008667 | 2.461156585 |
| chr1:52556859-52556904    | <i>Nab1</i>  | NM_008667 | 7.732770253 |
| chr1:52557045-52557090    | <i>Nab1</i>  | NM_008667 | 3.888633984 |
| chr1:52557631-52557676    | <i>Nab1</i>  | NM_008667 | 2.229038673 |
| chr10:127102470-127102530 | <i>Nab2</i>  | NM_008668 | 3.213688433 |
| chr10:127102967-127103012 | <i>Nab2</i>  | NM_008668 | 4.267911483 |
| chr10:127103213-127103263 | <i>Nab2</i>  | NM_008668 | 13.39061571 |
| chr10:127103344-127103389 | <i>Nab2</i>  | NM_008668 | 10.67535378 |
| chr10:127103495-127103540 | <i>Nab2</i>  | NM_008668 | 20.11941172 |
| chr10:127103623-127103668 | <i>Nab2</i>  | NM_008668 | 8.006574663 |
| chr19:44827636-44827681   | <i>Pax2</i>  | NM_011037 | 5.126745443 |
| chr19:44827794-44827848   | <i>Pax2</i>  | NM_011037 | 6.475285785 |
| chr19:44827957-44828002   | <i>Pax2</i>  | NM_011037 | 6.608847117 |
| chr19:44828127-44828181   | <i>Pax2</i>  | NM_011037 | 9.296241051 |
| chr19:44828244-44828304   | <i>Pax2</i>  | NM_011037 | 8.11138572  |

|                          |               |           |             |
|--------------------------|---------------|-----------|-------------|
| chr5:028122004-028122048 | <i>Paxip1</i> | NM_018878 | 6.177889802 |
| chr5:028122197-028122241 | <i>Paxip1</i> | NM_018878 | 1.961888607 |
| chr1:170361694-170361749 | <i>Pbx1</i>   | NM_183355 | 2.176399275 |
| chr1:170362020-170362076 | <i>Pbx1</i>   | NM_183355 | 10.31159147 |
| chr1:170362145-170362190 | <i>Pbx1</i>   | NM_008783 | 3.587618032 |
| chr17:34729644-34729690  | <i>Pbx2</i>   | NM_017463 | 12.8134639  |
| chr17:34729790-34729849  | <i>Pbx2</i>   | NM_017463 | 4.579223142 |
| chr17:34729960-34730009  | <i>Pbx2</i>   | NM_017463 | 4.178332977 |
| chr9:108997355-108997400 | <i>Plxnb1</i> | NM_172775 | 3.005393783 |
| chr9:108998328-108998373 | <i>Plxnb1</i> | NM_172775 | 2.802128647 |
| chr9:108998497-108998542 | <i>Plxnb1</i> | NM_172775 | 4.274904376 |
| chr9:108998726-108998781 | <i>Plxnb1</i> | NM_172775 | 3.042814622 |
| chr9:108998908-108998953 | <i>Plxnb1</i> | NM_172775 | 4.91114745  |
| chr9:108999021-108999066 | <i>Plxnb1</i> | NM_172775 | 4.082159662 |
| chr9:108999169-108999219 | <i>Plxnb1</i> | NM_172775 | 6.033638013 |
| chr9:108999301-108999360 | <i>Plxnb1</i> | NM_172775 | 5.344999505 |
| chr9:108999443-108999491 | <i>Plxnb1</i> | NM_172775 | 9.823247276 |
| chr9:108999602-108999647 | <i>Plxnb1</i> | NM_172775 | 7.401702476 |
| chr9:108999738-108999783 | <i>Plxnb1</i> | NM_172775 | 6.837802597 |
| chr9:108999867-108999919 | <i>Plxnb1</i> | NM_172775 | 9.585251157 |
| chr9:109000074-109000129 | <i>Plxnb1</i> | NM_172775 | 6.355810465 |
| chr9:109000231-109000281 | <i>Plxnb1</i> | NM_172775 | 3.376963132 |
| chr13:63665031-63665091  | <i>Ptch1</i>  | NM_008957 | 6.45134458  |
| chr13:63665293-63665340  | <i>Ptch1</i>  | NM_008957 | 3.630155535 |
| chr13:63665474-63665519  | <i>Ptch1</i>  | NM_008957 | 6.225889244 |
| chr13:63665587-63665632  | <i>Ptch1</i>  | NM_008957 | 1.855085095 |
| chr13:63665972-63666017  | <i>Ptch1</i>  | NM_008957 | 1.843057247 |
| chr13:63666138-63666193  | <i>Ptch1</i>  | NM_008957 | 5.76945033  |
| chr13:63666273-63666320  | <i>Ptch1</i>  | NM_008957 | 7.033637766 |
| chr13:63666384-63666429  | <i>Ptch1</i>  | NM_008957 | 1.520197045 |
| chr5:77694648-77694693   | <i>Rest</i>   | NM_011263 | 6.797812781 |
| chr5:77695015-77695060   | <i>Rest</i>   | NM_011263 | 11.98609536 |
| chr5:77695406-77695451   | <i>Rest</i>   | NM_011263 | 9.463158347 |
| chr5:77695615-77695673   | <i>Rest</i>   | NM_011263 | 4.787859548 |
| chr5:77695739-77695784   | <i>Rest</i>   | NM_011263 | 3.245553161 |
| chr8:91566663-91566708   | <i>Sall1</i>  | NM_021390 | 2.07127703  |
| chr8:91566838-91566883   | <i>Sall1</i>  | NM_021390 | 4.67418891  |
| chr8:91567009-91567059   | <i>Sall1</i>  | NM_021390 | 9.233639151 |
| chr8:91567167-91567212   | <i>Sall1</i>  | NM_021390 | 5.311786495 |
| chr8:91567364-91567411   | <i>Sall1</i>  | NM_021390 | 4.83002815  |
| chr15:76286655-76286702  | <i>Scx</i>    | NM_198885 | 2.203542688 |
| chr15:76287234-76287279  | <i>Scx</i>    | NM_198885 | 3.911941305 |
| chr15:76287601-76287657  | <i>Scx</i>    | NM_198885 | 12.18619789 |
| chr15:76287757-76287805  | <i>Scx</i>    | NM_198885 | 14.66848609 |
| chr15:76288068-76288113  | <i>Scx</i>    | NM_198885 | 1.909122002 |
| chr15:76288981-76289026  | <i>Scx</i>    | NM_198885 | 2.768685593 |
| chr2:124435389-124435449 | <i>Sema6d</i> | NM_172537 | 3.215933752 |
| chr2:124435597-124435642 | <i>Sema6d</i> | NM_172537 | 3.833153329 |
| chr2:124435760-124435806 | <i>Sema6d</i> | NM_172537 | 14.05544767 |
| chr2:124435951-124436003 | <i>Sema6d</i> | NM_172537 | 8.357335762 |
| chr2:124436107-124436152 | <i>Sema6d</i> | NM_172537 | 4.945232261 |

|                           |               |              |             |
|---------------------------|---------------|--------------|-------------|
| chr2:124436300-124436346  | <i>Sema6d</i> | NM_172537    | 1.556800927 |
| chr17:085597097-085597153 | <i>Six2</i>   | NM_011380    | 3.375918459 |
| chr17:085597280-085597324 | <i>Six2</i>   | NM_011380    | 2.567491338 |
| chr12:74213237-74213282   | <i>Six4</i>   | NM_011382    | 4.753794563 |
| chr12:74213466-74213511   | <i>Six4</i>   | NM_011382    | 3.909752225 |
| chr12:74213667-74213712   | <i>Six4</i>   | NM_011382    | 2.013468101 |
| chr11:34934738-34934783   | <i>Slit3</i>  | NM_011412    | 1.864892872 |
| chr11:34935290-34935335   | <i>Slit3</i>  | NM_011412    | 2.828986313 |
| chr11:34935458-34935505   | <i>Slit3</i>  | NM_011412    | 6.671547335 |
| chr11:34935603-34935648   | <i>Slit3</i>  | NM_011412    | 3.467246322 |
| chr11:34935754-34935808   | <i>Slit3</i>  | NM_011412    | 2.971228032 |
| chr11:34935923-34935979   | <i>Slit3</i>  | NM_011412    | 3.136812147 |
| chr9:63605810-63605855    | <i>Smad3</i>  | NM_016769    | 4.682243478 |
| chr9:63605972-63606017    | <i>Smad3</i>  | NM_016769    | 7.111903005 |
| chr9:63606199-63606249    | <i>Smad3</i>  | NM_016769    | 8.248561033 |
| chr9:63606311-63606356    | <i>Smad3</i>  | NM_016769    | 6.160097609 |
| chr9:63606469-63606524    | <i>Smad3</i>  | NM_016769    | 6.875655551 |
| chr18:73863445-73863490   | <i>Smad4</i>  | NM_008540    | 8.673345952 |
| chr18:73863654-73863699   | <i>Smad4</i>  | NM_008540    | 2.795492204 |
| chr9:63870056-63870101    | <i>Smad6</i>  | NM_008542    | 2.111988835 |
| chr9:63870208-63870254    | <i>Smad6</i>  | NM_008542    | 4.353732665 |
| chr9:63870339-63870384    | <i>Smad6</i>  | NM_008542    | 2.362952531 |
| chr18:75527141-75527186   | <i>Smad7</i>  | NM_001042660 | 2.478944837 |
| chr18:75527264-75527309   | <i>Smad7</i>  | NM_001042660 | 10.68378663 |
| chr18:75527381-75527426   | <i>Smad7</i>  | NM_001042660 | 3.016364783 |
| chr18:75528879-75528924   | <i>Smad7</i>  | NM_001042660 | 2.630810343 |
| chr18:75529419-75529479   | <i>Smad7</i>  | NM_001042660 | 2.362047322 |
| chr6:29685666-29685711    | <i>Smo</i>    | NM_176996    | 2.797807879 |
| chr6:29685802-29685847    | <i>Smo</i>    | NM_176996    | 4.020960332 |
| chr6:29685976-29686021    | <i>Smo</i>    | NM_176996    | 3.096481046 |
| chr6:29686120-29686165    | <i>Smo</i>    | NM_176996    | 3.08131583  |
| chr12:28027842-28027887   | <i>Sox11</i>  | NM_009234    | 2.539585452 |
| chr12:28028010-28028055   | <i>Sox11</i>  | NM_009234    | 2.09473395  |
| chr12:28028212-28028257   | <i>Sox11</i>  | NM_009234    | 15.57544715 |
| chr12:28028338-28028383   | <i>Sox11</i>  | NM_009234    | 2.929086121 |
| chr12:28028439-28028499   | <i>Sox11</i>  | NM_009234    | 10.37509824 |
| chr12:28028589-28028642   | <i>Sox11</i>  | NM_009234    | 4.998722019 |
| chr14:106294461-106294506 | <i>Spry2</i>  | NM_011897    | 3.112268827 |
| chr14:106294617-106294677 | <i>Spry2</i>  | NM_011897    | 3.743660349 |
| chr14:106296835-106296880 | <i>Spry2</i>  | NM_011897    | 1.411173652 |
| chr14:106296947-106297000 | <i>Spry2</i>  | NM_011897    | 6.615629183 |
| chr14:106297132-106297186 | <i>Spry2</i>  | NM_011897    | 3.490559634 |
| chr2:166820990-166821050  | <i>Stau1</i>  | NM_011490    | 3.089740778 |
| chr2:166821163-166821213  | <i>Stau1</i>  | NM_011490    | 4.516269924 |
| chr2:166821400-166821445  | <i>Stau1</i>  | NM_011490    | 3.405898012 |
| chr2:165980866-165980921  | <i>Sulf2</i>  | NM_028072    | 5.263198268 |
| chr2:165981030-165981075  | <i>Sulf2</i>  | NM_028072    | 1.892322462 |

|                            |              |              |             |
|----------------------------|--------------|--------------|-------------|
| chr17:46165927-46165972    | <i>Vegfa</i> | NM_001025250 | 4.799762458 |
| chr17:46166092-46166137    | <i>Vegfa</i> | NM_001025250 | 4.441552756 |
| chr17:46166198-46166243    | <i>Vegfa</i> | NM_001025250 | 2.381367448 |
| mm chr17:46167233-46167286 | <i>Vegfa</i> | NM_001025250 | 3.255572239 |
| chr17:46167362-46167407    | <i>Vegfa</i> | NM_001025250 | 3.935303472 |
| chr17:46167511-46167556    | <i>Vegfa</i> | NM_001025250 | 2.392782464 |
| chr17:46167696-46167741    | <i>Vegfa</i> | NM_001025250 | 8.130999176 |
| chr17:46167808-46167853    | <i>Vegfa</i> | NM_001025250 | 7.265683176 |
| chr17:46167969-46168014    | <i>Vegfa</i> | NM_001025250 | 7.108455984 |
| chr17:46168084-46168129    | <i>Vegfa</i> | NM_001025250 | 3.087414303 |
| chr17:46168261-46168306    | <i>Vegfa</i> | NM_001025250 | 3.711736562 |

|                         |            |           |             |
|-------------------------|------------|-----------|-------------|
| chr15:12047157-12047214 | <i>Zfr</i> | NM_011767 | 8.028833219 |
| chr15:12047388-12047433 | <i>Zfr</i> | NM_011767 | 12.01663356 |
| chr15:12047514-12047559 | <i>Zfr</i> | NM_011767 | 6.05037632  |
| chr15:12047663-12047717 | <i>Zfr</i> | NM_011767 | 10.6784367  |
| chr15:12047808-12047853 | <i>Zfr</i> | NM_011767 | 2.182854239 |

|                        |            |           |             |
|------------------------|------------|-----------|-------------|
| chr6:42299668-42299713 | <i>Zyx</i> | NM_011777 | 2.497418422 |
| chr6:42299887-42299932 | <i>Zyx</i> | NM_011777 | 5.103425692 |
| chr6:42300024-42300069 | <i>Zyx</i> | NM_011777 | 2.888080344 |
| chr6:42300192-42300237 | <i>Zyx</i> | NM_011777 | 11.54813576 |
| chr6:42300447-42300492 | <i>Zyx</i> | NM_011777 | 2.382498451 |
| chr6:42300594-42300639 | <i>Zyx</i> | NM_011777 | 2.010529457 |
| chr6:42300727-42300772 | <i>Zyx</i> | NM_011777 | 3.411675383 |

For ChIP-PCR validation of selected WT1 target genes identified by ChIP-chip, primers were designed to amplify a 150-300 bp region around the genomic location of probes that showed peak levels of immunoenrichment by WT1 ChIP-chip (highlighted in red).

**Table S2. Primer sequences for ChIP-PCR**

| Primer name | Primer sequence       | Amplicon size | Number of cycles | Annealing temperature | Q solution added |
|-------------|-----------------------|---------------|------------------|-----------------------|------------------|
| ACTN1-FRWD  | CTCTCATTGGGAATTCCTGG  | 135 bp        | 31               | 51°C                  | no               |
| ACTN1-REV   | AGGTGGTGTACATGAGCTG   |               |                  |                       |                  |
| ARNT2-FRWD  | CCTTCAGCGACATCAGACAA  | 216 bp        | 31               | 51°C                  | no               |
| ARNT2-REV   | CGCTGAGCGAGAGAAAAGTT  |               |                  |                       |                  |
| BMP4-FRWD   | TTGACCAGCTACAGAATCG   | 126 bp        | 30               | 53°C                  | yes              |
| BMP4-REV    | CGCTCCGAGGTTAGAACAG   |               |                  |                       |                  |
| BMP7-FRWD   | TACAAGTCCGGAGAGCGAGT  | 120 bp        | 31               | 55°C                  | yes              |
| BMP7-REV    | AGATCGGAAAGGGGTTTGT   |               |                  |                       |                  |
| BMPER-FRWD  | CTAGTACGCCCTCGGTCC    | 227 bp        | 30               | 53°C                  | no               |
| BMPER-REV   | AGTTGCTCTCAGCGGGTTAG  |               |                  |                       |                  |
| EGR3-FRWD   | AGAGCTAGAGGAGATCCGGG  | 230 bp        | 28               | 55°C                  | yes              |
| EGR3-REV    | GAACTTGCATCTCTCAGGGG  |               |                  |                       |                  |
| ERBB2-FRWD  | AGAAAAGTGAAGCTGGGAGCA | 165 bp        | 34               | 55°C                  | no               |
| ERBB2-REV   | GGCAATCTCAGCTCCACAA   |               |                  |                       |                  |
| FGFR2-FRWD  | GCATTCATCCACTCCTCCAT  | 261 bp        | 30               | 55°C                  | no               |
| FGFR2-REV   | TTTGGAGTTTTCTCCGAGA   |               |                  |                       |                  |
| FGFR3-FRWD  | ACTGGGACAGAGGAGACCCT  | 174 bp        | 31               | 55°C                  | yes              |
| FGFR3-REV   | CTTACGAACCGTCCACTTC   |               |                  |                       |                  |
| FYN-FRWD    | AAATAGGAATTGGCTTGGGG  | 249 bp        | 31               | 55°C                  | yes              |
| FYN-REV     | GGGAGGTTCCAGAAATAGGC  |               |                  |                       |                  |
| HEYL-FRWD   | GTAAGACAGGGTGGAGCGAG  | 219 bp        | 30               | 53°C                  | yes              |
| HEYL-REV    | CCTCCAGCTGAACTGTCCTC  |               |                  |                       |                  |
| HHAT-FRWD   | ACACACACACACACCACG    | 280 bp        | 31               | 57°C                  | yes              |
| HHAT-REV    | AAAGGCTGCCACGACTTAAC  |               |                  |                       |                  |
| HOXD4-FRWD  | GAGGACTCCATTTCCACAGC  | 106 bp        | 29               | 53°C                  | yes              |
| HOXD4-REV   | AAAGGTTCTCCCTTGCCACT  |               |                  |                       |                  |
| LEF1-FRWD   | TCAGTCATCCCGAAGAGGAG  | 295 bp        | 27               | 55°C                  | no               |
| LEF1-REV    | GCCACCGTTTAGCCATAGAA  |               |                  |                       |                  |
| NAB1-FRWD   | GCCAAGTTTCTGAAAGCCAC  | 103 bp        | 28               | 51°C                  | no               |
| NAB1-REV    | GCTGAGTCTCCGCTTTCTTC  |               |                  |                       |                  |
| NAB2-FRWD   | CACCTCCTTTGCCACTAA    | 237 bp        | 30               | 51°C                  | no               |
| NAB2-REV    | CCGAGAGAGAAGACGTGGAG  |               |                  |                       |                  |
| PAX2-FRWD   | TCCCGAGATGGGTATCAGAG  | 181 bp        | 27               | 55°C                  | no               |
| PAX2-REV    | TTGGTTGCTTTCCCTCATC   |               |                  |                       |                  |
| PAXIP-FRWD  | CCACCGCTAGTACTTGACC   | 141 bp        | 30               | 53°C                  | yes              |
| PAXIP-REV   | GGCAGTAGGCAGAGCTACGA  |               |                  |                       |                  |
| PBX1-FRWD   | GCAGGTGAGGAGCACGTTAT  | 248 bp        | 27               | 53°C                  | no               |
| PBX1-REV    | CGGCTGGTTAAGCCAATAGA  |               |                  |                       |                  |
| PBX2-FRWD   | CAAGACATCGGGGACATTCT  | 260 bp        | 32               | 55°C                  | yes              |
| PBX2-REV    | AGGAGGGAGTGAGACCACCT  |               |                  |                       |                  |
| PLXNB1-FRWD | CAGAAGAAAATGGTCTCGGG  | 134 bp        | 29               | 55°C                  | no               |

|             |                      |        |    |      |     |
|-------------|----------------------|--------|----|------|-----|
| PLXNB1-REV  | CAGCTACCAGGCCTGACCTA |        |    |      |     |
| PTCH1-FRWD  | CCGAAGATTTAAGGTGGCAA | 193 bp | 30 | 55°C | no  |
| PTCH1-REV   | GGAGGGAGCCAAAGTAAAGG |        |    |      |     |
| REST-FRWD   | TTTGAGATACTGTGGCTCG  | 212 bp | 36 | 51°C | no  |
| REST-REV    | GGGAAGTTTCAGGACCG    |        |    |      |     |
| SALL1-FRWD  | CCCATTTCGTGAGTGTTCT  | 239 bp | 35 | 53°C | yes |
| SALL1-REV   | CCTTTCCTGGGTCCTCTCT  |        |    |      |     |
| SCX-FRWD    | GCCAGGAGAGAAAGCCTCT  | 257 bp | 27 | 55°C | no  |
| SCX-REV     | CCGAGCAGTGCCTTTATAGC |        |    |      |     |
| SEMA6D-FRWD | GGAGATCTAGGGGAGCGACT | 270 bp | 30 | 55°C | no  |
| SEMA6D-REV  | TGGGCGACTGTCTTACCTCT |        |    |      |     |
| SIX2-FRWD   | GAAAAGAGGGGGACAGAAGG | 298 bp | 30 | 55°C | no  |
| SIX2-REV    | AGGGGATAGACATCTCGGGT |        |    |      |     |
| SIX4-FRWD   | AGGAGGAAAAGAAAGCTGGG | 260 bp | 27 | 55°C | no  |
| SIX4-REV    | GCGAGGAGACGGTGTATTGT |        |    |      |     |
| SLIT3-FRWD  | ACACGCTCAATAAGTTGGGG | 229 bp | 30 | 55°C | no  |
| SLIT3-REV   | TAATGGACCCCTCATACCCA |        |    |      |     |
| SMAD3-FRWD  | CCAAGTCTACGTTTCACGCA | 285 bp | 25 | 55°C | no  |
| SMAD3-REV   | AGTGCCTGTCCCTGTGAGT  |        |    |      |     |
| SMAD4-FRWD  | ACCACATCCGGGTAATTTCA | 112 bp | 35 | 53°C | yes |
| SMAD4-REV   | ACTGGGACCCTCCCTGCT   |        |    |      |     |
| SMAD6-FRWD  | CTTTGCCTCTCTGGCTTG   | 101 bp | 27 | 55°C | no  |
| SMAD6-REV   | ACGCCATTTTATTAGCCC   |        |    |      |     |
| SMAD7-FRWD  | AGAGTCTCCGAGGAAGAGGC | 144 bp | 29 | 53°C | yes |
| SMAD7-REV   | CACAGGCTAGTGTGGGGG   |        |    |      |     |
| SMO-FRWD    | AGACAGCTTCGATCTCCAGG | 188 bp | 33 | 53°C | no  |
| SMO-REV     | CGGAGGCTACTTAGGCGAC  |        |    |      |     |
| SOX11-FRWD  | CACCTTCTGGGTCATTTGCT | 251 BP | 30 | 51°C | no  |
| SOX11-REV   | TGAGCAGCCACGTTAAACAG |        |    |      |     |
| SPRY2-FRWD  | AGCGAGTCGCAGCTTTTAG  | 186 bp | 30 | 51°C | no  |
| SPRY2-REV   | ATAGCCCTCCACCTCACTT  |        |    |      |     |
| STAU1-FRWD  | TGGGTCTGGCACACTGATAA | 175 bp | 27 | 53°C | no  |
| STAU1-REV   | CCCTTCGTCACTCACTTCGT |        |    |      |     |
| SULF2-FRWD  | CTTTTCGTCCTCCTCCCTC  | 129 bp | 30 | 55°C | no  |
| SULF2-REV   | CCCTGTGAAAGCGGATAAAA |        |    |      |     |
| VEGFA-FRWD  | AACGGCAGTGACAGCAAAG  | 267 bp | 32 | 55°C | no  |
| VEGFA-REV   | AGTCACCGCACGTACGATCT |        |    |      |     |
| ZFR-FRWD    | CAACATGACCCTGAAAGGCT | 261 bp | 31 | 50°C | no  |
| ZFR-REV     | CTTTGGAAAGGGGAGGAGAC |        |    |      |     |
| ZYX-FRWD    | CGCTTAGACCGAGGAGTGTC | 195 bp | 31 | 55°C | yes |
| ZYX-REV     | GGAAAGGATTCACCTTGGGC |        |    |      |     |

Primer sequences used in ChIP-PCR experiments together with PCR reaction conditions. Each PCR was optimized for amplification within the linear range. Supplementation with Q solution (Qiagen) in the PCR reaction mixture is noted when used.

**Table S3. Primer sequences for RNA probes**

| Probe name              | Primer sequence           | Amplicon size |
|-------------------------|---------------------------|---------------|
| CXXC5 exon 3 probe FRWD | 5'TGGACAAAAGCAACCCCTACC3' | 591 bp        |
| CXXC5 exon 3 probe REV  | 5'ATCACTGAAACCACCGGAAG3'  |               |
| LSP1 5'UTR FRWD         | 5'GGCAGAGGAGAACAGAGGTG3'  | 454 bp        |
| LSP1 5'UTR REV          | 5'TCGCTTTGAGAGGGTTCAGT3'  |               |
| HEYL exon 5 FRWD        | 5'TCCACCTCAAGAGCTATGC3'   | 531 bp        |
| HEYL exon 5 REV         | 5'TCAGAAAAGCCCAATTCAG3'   |               |
| PBX2 exon 9 FRWD        | 5'GGTGAATCACTCCGACACT3'   | 500 bp        |
| PBX2 exon 9 REV         | 5'TATAAGTGGGGTGGGAACA3'   |               |
| PLXDC2 5'UTR FRWD       | 5'CCCACCTCTCTTCTGCTCAC3'  | 886 bp        |
| PLXDC2 5'UTR REV        | 5'CTGCCTTAAAAGGGTCCACA3'  |               |
| RPS6KA3 exon 14-19 FRWD | 5'TGAGTCTGAAGCCAGAGT3'    | 744 bp        |
| RPS6KA3 exon 14-19 REV  | 5'CTCTGTGAACCACCCCTTGT3'  |               |
| SCX exon1-2 FRWD        | 5'GACCCGCTTCTTCCACAG3'    | 431 bp        |
| SCX exon1-2 REV         | 5'AGGTAGAGAGCCAGCATGGA3'  |               |
| SOX11 3'UTR FRWD        | 5'GAGCCTGTACGACGAAGTGC3'  | 841 bp        |
| SOX11 3'UTR REV         | 5'TCAAAGAGCCACAAGCTTCA3'  |               |

Primer sequences used to generate RNA probes for in situ hybridization.

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site   | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| 5830427D03Rik | 1    | 36.62           | chr15      | 98592408  | 98593528  | -577            | < 0.001 | 98593647; 98592930; 98593212; 98593644; 98593643  | yes                        |
| Myo1b         | 2    | 27.21           | chr1       | 51972665  | 51972038  | 108             | < 0.001 | 51973701; 51973701  | yes                        |
| Bcat2         | 3    | 26.35           | chr7       | 52823332  | 52824317  | -2074           | < 0.001 | 52823919; 52824027  | yes                        |
| Hey1          | 4    | 25.11           | chr4       | 122910233 | 122911555 | 372             | < 0.001 | 122911152   | yes                        |
| Lsp1          | 5    | 24.46           | chr7       | 149656912 | 149657945 | -193            | < 0.001 | 149657266; 149657864  | no                         |
| Egr3          | 6    | 24.39           | chr14      | 70474926  | 70476048  | -2009           | < 0.001 | 70475097; 70475640; 70475464; 70475222; 70475464  | yes                        |
| Actn1         | 7    | 23.89           | chr12      | 81360886  | 81361985  | -193            | < 0.001 | 81362068; 81362068; 81361341; 81362255; 81361544; 81361543  | yes                        |
| Pik3r3        | 8    | 22.67           | chr4       | 115893800 | 115894714 | -430            | < 0.001 | 115894389; 115894389  | yes                        |
| Cxhc5         | 9    | 20.95           | chr18      | 35989256  | 35990465  | 751             | < 0.001 | 35990579; 35989513; 35989513; 35990468; 35990107; 35990106  | yes                        |
| Hoxb4         | 10   | 20.76           | chr11      | 96180066  | 96181209  | 470             | < 0.001 | 96180512; 96180515  | yes                        |
| Mrc2          | 11   | 20.46           | chr11      | 105153418 | 105154743 | -257            | < 0.001 | 105154027; 105154710; 105154049; 105154049  | yes                        |
| 4933433P14Rik | 12   | 20.38           | chr12      | 106923623 | 106923883 | 85              | < 0.001 | N/A   | no                         |
| Senp8         | 13   | 19.7            | chr9       | 59598324  | 59599247  | -473            | < 0.001 | 59598660; 59598660; 59598883; 59598837; 59598837  | yes                        |
| Nab2          | 14   | 19.58           | chr10      | 127103344 | 127103263 | 241             | < 0.001 | 127104787; 127105095; 127106973; 127104790  | yes                        |
| Fyn           | 15   | 18.7            | chr10      | 39089847  | 39090342  | 708             | < 0.001 | 39090432; 39090251  | yes                        |
| BC068171      | 16   | 18.31           | chrX       | 72341212  | 72341415  | -20             | < 0.001 | N/A   | no                         |
| Igf2bp2       | 17   | 17.7            | chr16      | 22162849  | 22163052  | 342             | < 0.001 | 22161983; 22162833; 22162772  | no                         |
| Fosl2         | 18   | 17.63           | chr5       | 32437957  | 32439313  | -695            | < 0.001 | 32438608; 32438486; 32438611; 32438605; 32438304; 32438965; 32438307                              | yes                        |
| Bhlhb2        | 19   | 17.53           | chr6       | 108609800 | 108610667 | -550            | < 0.001 | 108610225; 108610225  | yes                        |
| Bri3          | 20   | 17.49           | chr5       | 145016519 | 145017300 | 620             | < 0.001 | 145016552   | yes                        |
| Bnip3         | 21   | 16.97           | chr7       | 146100844 | 146101883 | -315            | < 0.001 | 146101475; 146101211; 146101210   | yes                        |
| Fbxl19        | 22   | 16.67           | chr7       | 134889599 | 134891192 | 350             | < 0.001 | 134890215   | yes                        |
| Hoxd4         | 23   | 16.56           | chr2       | 74565721  | 74566423  | 6012            | < 0.001 | 74565827  | yes                        |
| Colla2        | 24   | 16.52           | chr6       | 4454897   | 4456114   | -200            | < 0.001 | 4455761   | yes                        |
| Wnk4          | 25   | 16.21           | chr11      | 101120919 | 101122031 | -436            | < 0.001 | 101120978; 101121644; 101120674; 101120976; 101121355; 101121524; 101121842; 101120975; 101121587 | no                         |
| Usp52         | 26   | 15.79           | chr10      | 127740614 | 127740859 | 116             | < 0.001 | 127740414   | no                         |
| Inoc1         | 27   | 15.77           | chr2       | 119303230 | 119303805 | -77             | < 0.001 | 119303668; 119303671  | yes                        |
| Sept11        | 28   | 15.71           | chr5       | 93522393  | 93523191  | 418             | < 0.001 | N/A   | yes                        |
| Mink1         | 29   | 15.61           | chr11      | 70376350  | 70377567  | 440             | < 0.001 | N/A   | no                         |
| Sox11         | 30   | 15.48           | chr12      | 28027842  | 28028642  | -657            | < 0.001 | 28028275  | no                         |
| Sp4           | 31   | 15.45           | chr12      | 119539184 | 119541019 | 112             | < 0.001 | 119539611; 119540679; 119540773; 119540645; 119540665   | no                         |
| Shf           | 32   | 15.19           | chr2       | 122194023 | 122194739 | 90              | < 0.001 | 122194677; 122194884; 122194677; 122194887  | yes                        |
| Scx           | 33   | 14.68           | chr15      | 76287234  | 76288113  | -86             | < 0.001 | 76288613; 76288613; 76287512; 76287515  | yes                        |
| Ahdcl         | 34   | 14.51           | chr4       | 132568703 | 132569015 | 1461            | < 0.001 | 132568981; 132568981  | yes                        |
| Ube2h         | 35   | 14.38           | chr6       | 30253511  | 30254074  | 293             | < 0.001 | 30253511  | no                         |
| Sox12         | 36   | 14.37           | chr2       | 152222057 | 152222715 | 1272            | < 0.001 | 152222524; 152222497  | yes                        |
| Usp14         | 37   | 14.26           | chr18      | 10029315  | 10030485  | 81              | < 0.001 | 10030089; 10029954  | yes                        |

First tier peaks of all 1663 WT1 target genes identified by ChIP-chip. Genes are ranked by fold-enrichment scores on array, and locations of defined peak regions are noted. Negative values indicate locations upstream (5') of the TSS. The motif discovery algorithm THEME identified a WT1 matrix site (tGCGtgGGcGg) in 1432 of the 1663 (86%) WT1 bound genes, consisting of multiple permutations of a core WT1 consensus site G<sup>1</sup>C<sup>2</sup>G<sup>3</sup>(T/G)<sup>4</sup>(G/A)<sup>5</sup>G<sup>6</sup>G<sup>7</sup>(C/A)<sup>8</sup>G<sup>9</sup>(G/T)<sup>10</sup>. The WT1 consensus site was mapped to defined peak regions, with defined nucleotide substitutions permitted at the 4th, 5th, 8th or 10th positions (substitutions noted in parentheses). The WT1 consensus site is present in 806 of 1663 bound genes, and occurs with higher frequency in target genes enriched >8-fold (74% vs. 25% in genes enriched < 8-fold; *P* < 0.0001 by Fisher's Exact Test). Where present, WT1 matrix and consensus site locations are noted. For WT1 matrix sites with low information content that lack an exact location assignment by THEME, the start site of the WT1 bound region is noted. (TSS) transcriptional start site. (N/A) not applicable (No WT1 site present).



**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                                       | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Sema6d        | 38   | 14.11           | chr2       | 124435389 | 124436346 | -248            | < 0.001 | 124436315; 124436315; 124436315   | yes                        |
| Stac2         | 39   | 14.06           | chr11      | 97913236  | 97915103  | 160             | < 0.001 | 97915000; 97914120  | yes                        |
| Cnot6l        | 40   | 13.88           | chr5       | 96590372  | 96591557  | -522            | < 0.001 | 96590916  | yes                        |
| Jmjd1a        | 41   | 13.77           | chr6       | 71582467  | 71583694  | -579            | < 0.001 | 71583591; 71582884; 71583611  | yes                        |
| Zfp467        | 42   | 13.72           | chr6       | 48394253  | 48395520  | 331             | < 0.001 | 48396035  | yes                        |
| Brd2          | 43   | 13.32           | chr17      | 34256834  | 34258910  | -818            | < 0.001 | 34257458; 34258484  | yes                        |
| Bahd1         | 44   | 13.31           | chr2       | 118726325 | 118728298 | -160            | < 0.001 | 118727825; 118727828  | yes                        |
| Ptbp1         | 45   | 13.19           | chr10      | 79316946  | 79317577  | 43              | < 0.001 | 79317619  | yes                        |
| Dpy19l3       | 46   | 13.14           | chr7       | 36538396  | 36539526  | 239             | < 0.001 | 36539287; 36539397; 36539397  | yes                        |
| Acp6          | 47   | 13.11           | chr3       | 96962277  | 96963022  | -77             | < 0.001 | 96962533; 96962535; 96962537; 96962542                                      | no                         |
| Wsb2          | 48   | 13.04           | chr5       | 117806468 | 117807570 | -333            | < 0.001 | 117807396; 117807370; 117807376; 117807343                                  | no                         |
| Bmp7          | 49   | 12.87           | chr2       | 172765859 | 172766638 | -204            | < 0.001 | 172766291; 172766291  | yes                        |
| Appbp2        | 50   | 12.79           | chr11      | 85047380  | 85048397  | 443             | < 0.001 | 85048523; 85048522  | yes                        |
| Arhgap18      | 50   | 12.79           | chr10      | 26492774  | 26493171  | 483             | < 0.001 | 26492693; 26492707; 26492699  | no                         |
| Gprk6         | 51   | 12.78           | chr13      | 55545945  | 55546477  | -558            | < 0.001 | 55546261; 55546261  | yes                        |
| Pbx2          | 51   | 12.78           | chr17      | 34729336  | 34730271  | 252             | < 0.001 | 34730406; 34731021; 34730103; 34730157; 34731018; 34730165                  | no                         |
| Pum1          | 52   | 12.76           | chr4       | 130219949 | 130220420 | 849             | < 0.001 | 130219924   | no                         |
| Gsr           | 53   | 12.71           | chr8       | 34764109  | 34764626  | 895             | < 0.001 | 34764236; 34764661  | yes                        |
| Des           | 54   | 12.58           | chr1       | 75356252  | 75356917  | -24             | < 0.001 | 75356961  | yes                        |
| Inpp1         | 55   | 12.56           | chr7       | 108985748 | 108986865 | -237            | < 0.001 | 108986829   | yes                        |
| Lin7b         | 56   | 12.54           | chr7       | 52625127  | 52625872  | 270             | < 0.001 | 52625959; 52625959  | yes                        |
| 5730403B10Rik | 57   | 12.53           | chr16      | 4789289   | 4790148   | 308             | < 0.001 | 4790129   | yes                        |
| Prkaca        | 58   | 12.45           | chr8       | 86496400  | 86497549  | 16              | < 0.001 | 86497063; 86497098; 86497190; 86497189                                      | yes                        |
| Cmtm3         | 59   | 12.42           | chr8       | 106864070 | 106864572 | -233            | < 0.001 | 106864105   | yes                        |
| Rest          | 60   | 12.04           | chr5       | 77694648  | 77695784  | -1927           | < 0.001 | 77695132; 77695493  | yes                        |
| Ppp3ca        | 61   | 12.03           | chr3       | 136332931 | 136335004 | 577             | < 0.001 | 136334688; 136333234; 136334124; 136333263; 136333263; 136333799; 136333799 | yes                        |
| Rsbnl         | 62   | 12.02           | chr3       | 103718356 | 103718928 | 548             | < 0.001 | 103718866; 103719000; 103718999   | yes                        |
| Baiap2        | 63   | 12.01           | chr11      | 119803386 | 119804456 | -595            | < 0.001 | 119804520; 119804253; 119804483; 119803798; 119804329                       | yes                        |
| Dbndd2        | 64   | 11.99           | chr2       | 164311170 | 164312528 | -4              | < 0.001 | 164311983; 164312479; 164312326; 164312458; 164312457                       | yes                        |
| Tesk1         | 65   | 11.98           | chr4       | 43455694  | 43456310  | 1048            | < 0.001 | 43456346  | yes                        |
| Zfr           | 66   | 11.96           | chr15      | 12047157  | 12047853  | -195            | < 0.001 | 12047523  | yes                        |
| Hsp90ab1      | 67   | 11.94           | chr17      | 45709579  | 45711348  | -996            | < 0.001 | 45709822; 45709825  | yes                        |
| Rps6ka3       | 68   | 11.9            | chrX       | 155692701 | 155693348 | -955            | < 0.001 | 155693772; 155692856; 155693292; 155693129                                  | yes                        |
| Kif23         | 69   | 11.89           | chr9       | 61793888  | 61794454  | 242             | < 0.001 | 61793888  | no                         |
| Ets2          | 70   | 11.82           | chr16      | 95923399  | 95924410  | -8              | < 0.001 | 95924137; 95924137; 95924164; 95924163                                      | yes                        |
| Tgif2         | 71   | 11.8            | chr2       | 156666586 | 156667634 | 1383            | < 0.001 | 156666842   | yes                        |
| Phf10         | 72   | 11.77           | chr17      | 15098705  | 15098858  | -599            | < 0.001 | 15098831; 15098830  | yes                        |
| Cacnb1        | 73   | 11.7            | chr11      | 97882896  | 97883825  | 232             | < 0.001 | 97883162; 97883162; 97883613  | yes                        |
| Rcor3         | 74   | 11.66           | chr1       | 193961353 | 193960970 | 601             | < 0.001 | 193962221; 193962221  | yes                        |
| 5830457O10Rik | 75   | 11.55           | chr8       | 109416395 | 109417174 | 615             | < 0.001 | N/A   | no                         |
| Hhat          | 76   | 11.41           | chr1       | 194596974 | 194596864 | 219             | < 0.001 | 194597040; 194597053; 194597440; 194597095; 194596777; 194597089            | no                         |
| Sh3md4        | 77   | 11.39           | chr10      | 58275327  | 58275609  | -356            | < 0.001 | 58275643; 58276268; 58275949; 58275949                                      | yes                        |
| Zyx           | 78   | 11.38           | chr6       | 42299668  | 42300772  | 388             | < 0.001 | 42300012  | yes                        |
| Ascl1         | 79   | 11.33           | chr10      | 86955966  | 86955851  | 417             | < 0.001 | 86956209  | yes                        |
| Vdac1         | 80   | 11.31           | chr11      | 52174874  | 52175056  | 418             | < 0.001 | N/A   | no                         |
| 1110003E01Rik | 81   | 11.3            | chr5       | 65884068  | 65885002  | -326            | < 0.001 | 65885161  | yes                        |
| Zmiz1         | 82   | 11.29           | chr14      | 26277135  | 26278605  | -777            | < 0.001 | 26277987  | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Nbl1          | 83   | 11.23           | chr4       | 138648061 | 138649348 | -63             | < 0.001 | 138649106  | yes                        |
| 6530418L21Rik | 84   | 11.11           | chr3       | 105507676 | 105508702 | 798             | < 0.001 | 105507809, 105507810, 105507816, 105507811, 105507813, 105507814, 105507808, 105507812             | no                         |
| C230071H18Rik | 85   | 11.04           | chr2       | 93028000  | 93028502  | 524             | < 0.001 | 93028345, 93027681   | no                         |
| Cxxc4         | 86   | 10.92           | chr3       | 133902077 | 133903838 | 128             | < 0.001 | 133903139; 133903593; 133903151; 133903151; 133903218; 133903217                                   | yes                        |
| Sfrs2ip       | 87   | 10.91           | chr15      | 96291693  | 96291959  | -444            | < 0.001 | 96292004; 96292004   | yes                        |
| Pddc1         | 87   | 10.91           | chr7       | 148600090 | 148600810 | -276            | < 0.001 | 148600384; 148600384; 148600429; 148600423; 148600423  | yes                        |
| Arnt2         | 88   | 10.9            | chr7       | 91557697  | 91558276  | 457             | < 0.001 | 91558033   | yes                        |
| Dcun1d4       | 89   | 10.87           | chr5       | 73882401  | 73883320  | 458             | < 0.001 | 73883068; 73883015   | yes                        |
| Ccdc92        | 90   | 10.75           | chr5       | 125343114 | 125343539 | 298             | < 0.001 | 125343552  | yes                        |
| Erb2          | 90   | 10.75           | chr11      | 98273670  | 98274011  | 15              | < 0.001 | 98273969; 98273969   | yes                        |
| Gabbr1        | 91   | 10.73           | chr17      | 37183107  | 37183956  | 358             | < 0.001 | 37183689; 37183692; 37183701; 37183700   | yes                        |
| BC003212      | 92   | 10.71           | chr13      | 12742905  | 13486616  | -499            | < 0.001 | 12743194   | yes                        |
| Smad7         | 92   | 10.71           | chr18      | 75527141  | 75527426  | 268             | < 0.001 | 75527174; 75527174; 75527165; 75527165   | yes                        |
| Raver2        | 93   | 10.65           | chr4       | 100741661 | 100742219 | 246             | < 0.001 | 100741842; 100741981; 100741801  | yes                        |
| Slc22a17      | 94   | 10.6            | chr14      | 55531699  | 55531891  | 193             | < 0.001 | 55531950; 55531801   | yes                        |
| Hivep2        | 95   | 10.56           | chr10      | 13685196  | 13685488  | -964            | < 0.001 | 13686651, 13685409   | no                         |
| 5730596B20Rik | 96   | 10.42           | chr6       | 52125537  | 52127316  | 24965           | < 0.001 | 52126090   | yes                        |
| Rchyl         | 97   | 10.32           | chr5       | 92391414  | 92391833  | 438             | < 0.001 | 92391765   | no                         |
| Rai1          | 98   | 10.3            | chr11      | 59952824  | 59953328  | -452            | < 0.001 | 59953263; 59953266; 59953740; 59953739   | yes                        |
| Tmeff2        | 98   | 10.3            | chr1       | 50984184  | 50984380  | -160            | < 0.001 | 50984184   | no                         |
| Usp16         | 99   | 10.29           | chr16      | 87454857  | 87455227  | -245            | < 0.001 | 87455363; 87455363   | yes                        |
| Pbx1          | 100  | 10.27           | chr1       | 170361694 | 170362190 | 341             | < 0.001 | 170361694  | no                         |
| Myst2         | 101  | 10.15           | chr11      | 95170829  | 95171238  | 551             | < 0.001 | 95171220; 95171223   | yes                        |
| Cend2         | 102  | 10.04           | chr6       | 127099244 | 127101942 | 1356            | < 0.001 | 127099980; 127100682; 127099983  | yes                        |
| Plxdc2        | 103  | 10.03           | chr2       | 16277188  | 16278086  | -56             | < 0.001 | 16278148; 16277617; 16278165   | yes                        |
| Ap2a1         | 103  | 10.03           | chr7       | 52184691  | 52185225  | -118            | < 0.001 | 52184691   | no                         |
| Rasa4         | 104  | 10.02           | chr5       | 136559747 | 136560117 | 139             | < 0.001 | 136559992; 136559995   | yes                        |
| BC059215      | 105  | 9.94            | chr17      | 47277983  | 47278910  | 116             | < 0.001 | N/A  | no                         |
| Man2a1        | 106  | 9.87            | chr17      | 64950234  | 64950602  | -560            | < 0.001 | 64950718   | yes                        |
| Foxl1         | 106  | 9.87            | chr8       | 123648556 | 123649438 | -2388           | < 0.001 | 123649348  | yes                        |
| Lrrn1         | 107  | 9.86            | chr6       | 107479763 | 107480926 | 648             | < 0.001 | 107479763  | no                         |
| B630005N14Rik | 108  | 9.84            | chr6       | 13627674  | 13628513  | 270             | < 0.001 | 13628358   | yes                        |
| Fytd1         | 109  | 9.76            | chr16      | 32878034  | 32878352  | 133             | < 0.001 | 32877821, 32877910, 32878180, 32877780, 32878115, 32878018, 32878202                               | no                         |
| Csnk1g3       | 110  | 9.74            | chr18      | 54022582  | 54022800  | 838             | < 0.001 | 54022596   | yes                        |
| Ilf3          | 111  | 9.72            | chr9       | 21172241  | 21172558  | 90              | < 0.001 | 21172495; 21172430   | yes                        |
| Plxnb1        | 112  | 9.69            | chr9       | 108998328 | 109000281 | 1362            | < 0.001 | 108998582  | yes                        |
| Smarca2       | 112  | 9.69            | chr19      | 26680712  | 26682169  | 2215            | < 0.001 | 26679073, 26679022, 26678971, 26681656, 26681787, 26681925, 26682057                               | no                         |
| Ankrd40       | 113  | 9.62            | chr11      | 94189669  | 94189906  | 378             | < 0.001 | 94189711, 94189254, 94189257, 94189263, 94189509, 94189506, 94189503, 94189349, 94189434, 94189500 | no                         |
| Fchsd2        | 114  | 9.61            | chr7       | 108256250 | 108257904 | -828            | < 0.001 | 108256802  | yes                        |
| Rcctb1        | 115  | 9.57            | chr14      | 59820301  | 59820521  | 427             | < 0.001 | 59820595   | yes                        |
| Fndc3b        | 116  | 9.49            | chr3       | 27609260  | 27609777  | -286            | < 0.001 | 27609684; 27609684; 27609925; 27609523   | yes                        |
| Mettl6        | 117  | 9.47            | chr14      |           | 32308161  | 281             | < 0.001 | 32307568   | no                         |
| Ikzf2         | 118  | 9.46            | chr1       | 69733419  | 69734675  | -1572           | < 0.001 | 69733995; 69734001; 69735431; 69734004; 69733998; 69735515; 69735514                               | yes                        |
| Col5a1        | 118  | 9.46            | chr2       | 27741525  | 27742110  | 12              | < 0.001 | 27741781, 27741766, 27742651   | no                         |
| Phc1          | 119  | 9.42            | chr6       | 122289333 | 122289557 | -2501           | < 0.001 | 122289333  | no                         |
| R3hdm1        | 120  | 9.41            | chr1       | 129999944 | 129999989 | 84              | < 0.001 | 130000277  | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                                       | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Ctdsp1        | 121  | 9.39            | chr1       | 74433760  | 74433573  | -4622           | < 0.001 | 74433951; 74433951; 74434160; 74434159                                      | yes                        |
| Mov10         | 122  | 9.37            | chr3       | 104620940 | 104621781 | 58              | < 0.001 | 104621573; 104621573  | yes                        |
| Nptn          | 123  | 9.35            | chr9       | 58430073  | 58430923  | 540             | < 0.001 | 58430561  | yes                        |
| Pax2          | 124  | 9.26            | chr19      | 44827636  | 44828304  | -3729           | < 0.001 | 44827776  | yes                        |
| Sall1         | 124  | 9.26            | chr8       | 91566663  | 91567411  | 1027            | < 0.001 | 91567004  | yes                        |
| Rasa3         | 125  | 9.22            | chr8       | 13677055  | 13677438  | 285             | < 0.001 | 13677467; 13677470  | yes                        |
| Phf13         | 126  | 9.2             | chr4       | 151369706 | 151370644 | -76             | < 0.001 | 151370743; 151370707; 151370707   | yes                        |
| Cyp1b1        | 126  | 9.2             | chr17      | 80114849  | 80115239  | -835            | < 0.001 | 80114849  | no                         |
| Axl           | 127  | 9.17            | chr7       | 26573402  | 26573844  | 28              | < 0.001 | 26573867; 26573866  | yes                        |
| Ptpn1         | 128  | 9.14            | chr2       | 167757840 | 167758157 | 190             | < 0.001 | 167757955; 167757958  | yes                        |
| Rreb1         | 128  | 9.14            | chr13      | 37917589  | 37918943  | -667            | < 0.001 | 37918828; 37917980; 37918874; 37918740                                      | no                         |
| Adams4        | 129  | 9.09            | chr1       | 173182266 | 173182130 | 1046            | < 0.001 | 173182977   | yes                        |
| Ncor2         | 129  | 9.09            | chr5       | 125657427 | 125658737 | 1494            | < 0.001 | 125658370   | yes                        |
| Mbnl1         | 130  | 9.07            | chr3       | 60304663  | 60305295  | -342            | < 0.001 | 60305317; 60304840  | yes                        |
| Axud1         | 131  | 9.06            | chr9       | 119891975 | 119893510 | 1588            | < 0.001 | 119892377   | no                         |
| H2afy2        | 132  | 9.05            | chr10      | 61246217  | 61246375  | 264             | < 0.001 | 61246373  | yes                        |
| Lamb1-1       | 132  | 9.05            | chr12      | 31949458  | 31950365  | -168            | < 0.001 | 31950280; 31950283  | yes                        |
| Rabepk        | 133  | 9               | chr2       | 34654951  | 34655339  | 332             | < 0.001 | 34655273; 34655210  | no                         |
| Bcor          | 134  | 8.98            | chrX       | 11656755  | 11657894  | -126            | < 0.001 | 11657334; 11657007  | yes                        |
| Txndc5        | 135  | 8.92            | chr13      | 38619884  | 38620663  | 217             | < 0.001 | 38621034  | yes                        |
| Pim1          | 135  | 8.92            | chr17      | 29626926  | 29627499  | -710            | < 0.001 | 29627513  | yes                        |
| Zbtb7b        | 136  | 8.91            | chr3       | 89197680  | 89198515  | -781            | < 0.001 | 89198233; 89197688  | yes                        |
| Btbd14a       | 137  | 8.85            | chr2       | 25978262  | 25978853  | -127            | < 0.001 | 25978539; 25978539; 25978552  | yes                        |
| Pygl          | 138  | 8.82            | chr12      | 71328236  | 71328664  | 120             | < 0.001 | 71328502; 71328217  | no                         |
| Jun           | 139  | 8.81            | chr4       | 94719458  | 94719864  | -927            | < 0.001 | 94719486; 94719737; 94719354  | no                         |
| Bmp4          | 140  | 8.8             | chr14      | 47007581  | 47008501  | 2006            | < 0.001 | 47008524  | yes                        |
| Optc          | 141  | 8.78            | chr1       | 135805382 | 135805545 | -1656           | < 0.001 | 135805727   | yes                        |
| 2900024O10Rik | 142  | 8.72            | chr13      | 81850151  | 81850611  | -61             | < 0.001 | 81850005; 81850138  | no                         |
| Smad4         | 143  | 8.7             | chr18      | 73863445  | 73863699  | -73             | < 0.001 | 73863698  | yes                        |
| B4galt6       | 144  | 8.68            | chr18      | 20904571  | 20904918  | 151             | < 0.001 | 20904869; 20904872  | yes                        |
| 1500005I02Rik | 145  | 8.66            | chr11      | 114656676 | 114656676 | 554             | < 0.001 | 114656453   | no                         |
| Ywhae         | 146  | 8.61            | chr11      | 75546761  | 75547071  | 608             | < 0.001 | 75547083  | yes                        |
| Gspt1         | 147  | 8.6             | chr16      | 11253984  | 11254415  | -177            | < 0.001 | 11254336  | yes                        |
| Lman2l        | 147  | 8.6             | chr1       | 36501895  | 36502527  | -126            | < 0.001 | 36502522  | yes                        |
| Tmem159       | 147  | 8.6             | chr7       | 127246124 | 127246953 | 427             | < 0.001 | 127246298; 127246298  | yes                        |
| Mnt           | 148  | 8.58            | chr11      | 74643609  | 74645366  | -161            | < 0.001 | 74644620; 74644620  | yes                        |
| Tpbp          | 149  | 8.57            | chr9       | 85736976  | 85737021  | 982             | < 0.001 | 85737116; 85737116  | yes                        |
| Cacnb3        | 150  | 8.54            | chr15      | 98464455  | 98465829  | -308            | < 0.001 | 98465493; 98465854; 98465267  | yes                        |
| Tnks          | 151  | 8.5             | chr8       | 36028603  | 36028823  | -56             | < 0.001 | 36028819  | yes                        |
| Susd4         | 152  | 8.48            | chr1       | 184694771 | 184694670 | -396            | < 0.001 | 184695025; 184695028; 184695274; 184695424; 184695424; 184695022; 184695021 | yes                        |
| Zfp469        | 152  | 8.48            | chr5       | 143577926 | 143579946 | -350            | < 0.001 | 143579353; 143579352; 143578264; 143578264                                  | yes                        |
| Btbd4         | 153  | 8.46            | chr2       | 181193137 | 181193592 | 539             | < 0.001 | 181194995; 181193502; 181193429   | no                         |
| Sbsn          | 154  | 8.44            | chr7       | 31536379  | 31536379  | -134            | < 0.001 | 31536331  | no                         |
| EG330503      | 155  | 8.42            | chr7       | 30954940  | 30955201  | 28              | < 0.001 | 30954913  | no                         |
| Nid1          | 156  | 8.41            | chr13      | 12794476  | 13531081  |                 | < 0.001 | 12795825; 12794773; 12794772  | yes                        |
| Setd5         | 157  | 8.39            | chr6       | 113026201 | 113026893 | -1084           | < 0.001 | 113026700; 113026703; 113026892   | yes                        |
| Gldc          | 158  | 8.38            | chr19      | 30249302  | 30250153  | 18              | < 0.001 | 30250213  | yes                        |
| Tmeff1        | 158  | 8.38            | chr4       | 48597900  | 48598090  | 4               | < 0.001 | 48598082  | yes                        |
| Nvl           | 159  | 8.37            | chr1       | 183074196 | 183074049 | 70              | < 0.001 | 183074718; 183074721  | yes                        |
| 4-Mar         | 160  | 8.36            | chr1       | 72582957  | 72583150  | 18              | < 0.001 |   | no                         |
| Mllt6         | 161  | 8.35            | chr11      | 97521073  | 97521499  | -3386           | < 0.001 | 97521227; 97523328; 97523452  | no                         |
| H2afz         | 162  | 8.34            | chr3       | 137526934 | 137527396 | -424            | < 0.001 | 137527359   | yes                        |
| Irx2          | 163  | 8.33            | chr13      | 72766019  | 72766229  | -219            | < 0.001 | 72766283; 72766282  | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site   | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Kcna3         | 164  | 8.31            | chr3       | 106838895 | 106839378 | -161            | < 0.001 | 106839230; 106839230  | yes                        |
| Asx1l         | 165  | 8.28            | chr2       | 153171881 | 153172301 | 210             | < 0.001 | 153172392; 153172256; 153172256; 153172177; 153172176   | yes                        |
| Dlgap3        | 166  | 8.26            | chr4       | 126845938 | 126846210 | -4163           | < 0.001 | 126845987   | no                         |
| Ppp1r1b       | 167  | 8.25            | chr11      | 98208997  | 98209843  | -232            | < 0.001 | 98209635; 98209820; 98209820  | yes                        |
| Slc30a1       | 168  | 8.17            | chr1       | 193730596 | 193730287 | -395            | < 0.001 | 193731253   | yes                        |
| Smad3         | 169  | 8.16            | chr9       | 63605810  | 63606524  | -423            | < 0.001 | 63606256; 63606259; 63605922; 63605922; 63606645; 63606645  | yes                        |
| Tsc22d1       | 170  | 8.15            | chr14      | 76814635  | 76814928  | -969            | < 0.001 | 76814914; 76814879; 76814878  | yes                        |
| Accn4         | 171  | 8.14            | chr1       | 75443153  | 75443341  | -3646           | < 0.001 | 75443557; 75443107  | no                         |
| Ccdc84        | 172  | 8.13            | chr9       | 44226003  | 44226544  | -252            | < 0.001 | 44226445; 44226445  | yes                        |
| Nfic          | 172  | 8.13            | chr10      | 80889430  | 80889644  | 299             | < 0.001 | 80893958; 80894361; 80889267; 80889719; 80889270; 80892755; 80892761; 80892754                    | no                         |
| Mapk3         | 173  | 8.12            | chr7       | 133903418 | 133903623 | 301             | < 0.001 | 133903333   | no                         |
| Slc27a1       | 173  | 8.12            | chr8       | 74093979  | 74094431  | 1315            | < 0.001 | 74093979  | no                         |
| Fbn2          | 174  | 8.1             | chr18      | 58369269  | 58370111  | -350            | < 0.001 | 58369526; 58370302; 58370312  | yes                        |
| Zadh2         | 175  | 8.09            | chr18      | 84256995  | 84258079  | 57              | < 0.001 | 84257589; 84257719  | yes                        |
| U2af2         | 176  | 8.06            | chr7       | 5012758   | 5013107   | -899            | < 0.001 | N/A   | no                         |
| Plekhg2       | 177  | 8.04            | chr7       | 29156402  | 29156933  | 1029            | < 0.001 | 29156988  | yes                        |
| Vegfa         | 178  | 8.03            | chr17      | 46167233  | 46168306  | -5606           | < 0.001 | 46168225; 46167783  | yes                        |
| Ptger1        | 179  | 8.02            | chr8       | 86189997  | 86190283  | -278            | < 0.001 | 86189997  | no                         |
| 2700094K13Rik | 180  | 7.99            | chr2       | 84510644  | 84510859  | 29              | < 0.001 | N/A   | no                         |
| App           | 181  | 7.98            | chr16      | 85173235  | 85173818  | 572             | < 0.001 | 85173817; 85173817  | yes                        |
| Hells         | 181  | 7.98            | chr19      | 39005816  | 39006015  | 511             | < 0.001 | 39005816  | no                         |
| Epb4.1        | 182  | 7.96            | chr4       | 131629665 | 131630271 | -1994           | < 0.001 | 131630263   | yes                        |
| Aldoa         | 183  | 7.93            | chr7       | 133943224 | 133943863 | -1136           | < 0.001 | 133943468; 133943468  | yes                        |
| Rnpc3         | 183  | 7.93            | chr3       | 113333185 | 113333562 | -148            | < 0.001 | 113333368   | yes                        |
| Tgif          | 184  | 7.91            | chr17      | 71200206  | 71201412  | -308            | < 0.001 | 71200838  | yes                        |
| Pemt1         | 185  | 7.9             | chr10      | 7382946   | 7382720   | 80              | < 0.001 | 7383811; 7383019  | yes                        |
| Rnf138        | 185  | 7.9             | chr18      | 21160096  | 21160677  | 422             | < 0.001 | 21160322; 21160322  | yes                        |
| Cdc216        | 186  | 7.88            | chr10      | 40069135  | 40069425  | 258             | < 0.001 | 40069405; 40069405  | yes                        |
| Rhpn2         | 187  | 7.87            | chr7       | 36119163  | 36119739  | 82              | < 0.001 | 36119481  | yes                        |
| Luc7l2        | 188  | 7.83            | chr6       | 38500723  | 38500911  | -630            | < 0.001 | 38500974  | yes                        |
| Ets1          | 189  | 7.82            | chr9       | 32503755  | 32504044  | 284             | < 0.001 | 32503825  | yes                        |
| Tjap1         | 190  | 7.81            | chr17      | 46419401  | 46419835  | 345             | < 0.001 | 46419674  | no                         |
| Mmp23         | 191  | 7.8             | chr4       | 155025802 | 155026537 | 1406            | < 0.001 | 155025898   | no                         |
| 0610009B22Rik | 192  | 7.78            | chr11      | 51502703  | 51502422  | -447            | < 0.001 | 51503177  | yes                        |
| Vamp8         | 193  | 7.77            | chr6       | 72340110  | 72340334  | 266             | < 0.001 | 72340349; 72340349  | yes                        |
| D10Wsu102e    | 193  | 7.77            | chr10      | 82822683  | 82822597  | -287            | < 0.001 | 82822683  | no                         |
| Phf23         | 193  | 7.77            | chr11      | 69809155  | 69810835  | 416             | < 0.001 | 69810334; 69809935; 69810472; 69810130  | no                         |
| Efna5         | 194  | 7.75            | chr17      | 63231462  | 63232326  | -1122           | < 0.001 | 63231462  | no                         |
| Kctd15        | 195  | 7.74            | chr7       | 35438431  | 35440530  | -1520           | < 0.001 | 35440262  | yes                        |
| Slmap         | 195  | 7.74            | chr14      | 27353929  | 27354274  | -894            | < 0.001 | 27354077; 27354182  | no                         |
| Mxi1          | 196  | 7.72            | chr19      | 53404584  | 53404914  | -43             | < 0.001 | 53404770; 53404818; 53404679  | no                         |
| Ptpn12        | 196  | 7.72            | chr5       | 20561278  | 20561843  | 111             | < 0.001 | 20561186; 20561584; 20561807; 20561782; 20561810; 20561574; 20561230                              | no                         |
| Ndfip1        | 197  | 7.69            | chr18      | 38579236  | 38580146  | 1140            | < 0.001 | 38580088; 38580085; 38580097; 38580096  | yes                        |
| Ralb          | 198  | 7.68            | chr1       | 121401767 | 121401436 | -425            | < 0.001 | 121402452; 121402452  | yes                        |
| Galnt12       | 198  | 7.68            | chr4       | 47104567  | 47105164  | 318             | < 0.001 | 47104766; 47104845; 47104875  | no                         |
| Npas2         | 199  | 7.67            | chr1       | 39249994  | 39250177  | -963            | < 0.001 | 39250595  | yes                        |
| Nab1          | 200  | 7.65            | chr1       | 52556594  | 52556904  | 322             | < 0.001 | 52557440; 52557615; 52556987  | no                         |
| Gli1          | 201  | 7.64            | chr10      | 126777287 | 126776612 | 1651            | < 0.001 | 126778170; 126777074; 126777080; 126777178; 126777250; 126777247; 126777245; 126777248            | no                         |
| Vps25         | 201  | 7.64            | chr11      | 101120454 | 101120642 | 558             | < 0.001 | 101121587; 101120975; 101121524; 101121644; 101120978; 101120976; 101121842; 101120674; 101121355 | no                         |
| Rmnd5a        | 202  | 7.61            | chr6       | 71390726  | 71390914  | -266            | < 0.001 | 71390729; 71390729  | yes                        |
| Ndrp1         | 202  | 7.61            | chr15      | 66799793  | 66800065  | 1165            | < 0.001 | 66799793  | no                         |
| Wwe1          | 203  | 7.6             | chr11      | 35793120  | 35792628  | 712             | < 0.001 | 35793672  | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                      | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Leng4         | 204  | 7.58            | chr7       | 3643858   | 3644537   | 967             | < 0.001 | 3644623  | yes                        |
| Vamp2         | 204  | 7.58            | chr11      | 68900583  | 68900886  | -1169           | < 0.001 | 68900798   | no                         |
| Nck2          | 205  | 7.57            | chr1       | 43502704  | 43502413  | -409            | < 0.001 | 43503339; 43503339   | yes                        |
| Tbc1d1        | 206  | 7.56            | chr5       | 64550825  | 64551602  | -79             | < 0.001 | 64551607   | yes                        |
| Olfml2a       | 207  | 7.53            | chr2       | 38789679  | 38789736  | 2209            | < 0.001 | 38789679   | no                         |
| Beam          | 208  | 7.52            | chr7       | 20353804  | 20354810  | 1223            | < 0.001 | 20354509; 20353976; 20354623; 20353982                     | no                         |
| Sosl          | 208  | 7.52            | chr17      | 80878881  | 80879263  | 889             | < 0.001 | 80879146; 80879145   | yes                        |
| Galnt4        | 209  | 7.51            | chr7       | 118922646 | 118923033 | 481             | < 0.001 | 118922932  | yes                        |
| Col18a1       | 210  | 7.5             | chr10      | 76628604  | 76628544  | 463             | < 0.001 | 76628556   | no                         |
| Itrp1         | 210  | 7.5             | chr6       | 108162562 | 108162806 | -309            | < 0.001 | 108163366; 108162909; 108163136; 108162681                 | no                         |
| Ctf1          | 211  | 7.49            | chr7       | 134856293 | 134856487 | 67              | < 0.001 | 134856215; 134856408; 134856414                            | no                         |
| Tead3         | 212  | 7.46            | chr17      | 28487625  | 28488144  | -240            | < 0.001 | 28487896; 28487896   | yes                        |
| Isoc2b        | 213  | 7.45            | chr7       | 4817625   | 4817883   | 133             | < 0.001 | 4817792  | no                         |
| Dach1         | 214  | 7.43            | chr14      | 98568757  | 98569268  | -216            | < 0.001 | 98569199; 98568845; 98569204; 98568626                     | no                         |
| Cacna1a       | 215  | 7.42            | chr8       | 86939521  | 86939726  | 442             | < 0.001 | 86939821; 86939786; 86939786                               | yes                        |
| Eif2b4        | 215  | 7.42            | chr5       | 31495305  | 31495353  | 129             | < 0.001 | 31495367   | yes                        |
| Ralgs2        | 216  | 7.41            | chr1       | 158869031 | 158868949 | 653             | < 0.001 | 158869419; 158869422; 158869421; 158869421                 | yes                        |
| Phgdh         | 216  | 7.41            | chr3       | 98143411  | 98144213  | -25             | < 0.001 | 98143956; 98143211; 98143874                               | no                         |
| Ripk5         | 217  | 7.39            | chr1       | 134314632 | 134314935 | 627             | < 0.001 | 134314896; 134314899                                       | yes                        |
| Zcchc3        | 217  | 7.39            | chr2       | 152236949 | 152237169 | 3617            | < 0.001 | 152236929; 152236817                                       | no                         |
| Gtpbp6        | 218  | 7.38            | chr5       | 110536372 | 110537341 | -102            | < 0.001 | 110537416; 110537240; 110537243; 110537416; 110537422      | yes                        |
| Casp2         | 219  | 7.37            | chr6       | 42214842  | 42215834  | -171            | < 0.001 | 42215581; 42215050; 42214977                               | no                         |
| Ibrdc2        | 220  | 7.31            | chr13      | 47217690  | 47218180  | 68              | < 0.001 | 47218253   | yes                        |
| Klf3          | 221  | 7.3             | chr5       | 65194594  | 65194824  | -145            | < 0.001 | 65194750; 65194768; 65194750                               | yes                        |
| Brwd1         | 222  | 7.27            | chr16      | 96303286  | 96303629  | 559             | < 0.001 | 96303765; 96303745; 96303745; 96303408                     | yes                        |
| Ptk7          | 223  | 7.25            | chr17      | 46766682  | 46767221  | -813            | < 0.001 | 46766558; 46766496; 46766875; 46767121; 46766556; 46766555 | no                         |
| Slco3a1       | 223  | 7.25            | chr7       | 81699147  | 81699940  | 292             | < 0.001 | 81699147   | no                         |
| Shox2         | 224  | 7.24            | chr3       | 66784590  | 66785109  | 797             | < 0.001 | 66784590   | no                         |
| 1110007L15Rik | 225  | 7.22            | chr5       | 139728644 | 139729211 | 444             | < 0.001 | 139728886; 139728886                                       | yes                        |
| Gphn          | 225  | 7.22            | chr12      | 79327206  | 79327430  | -312            | < 0.001 | 79327546   | yes                        |
| Epas1         | 226  | 7.21            | chr17      | 87153105  | 87154042  | 653             | < 0.001 | 87153628; 87153627   | yes                        |
| Lmo4          | 226  | 7.21            | chr3       | 143868006 | 143869153 | -554            | < 0.001 | 143868385; 143868382; 143868413; 143868412                 | yes                        |
| Mafb          | 226  | 7.21            | chr2       | 160193024 | 160193430 | -468            | < 0.001 | 160193138  | yes                        |
| D930015E06Rik | 227  | 7.2             | chr3       | 83843095  | 83843853  | 739             | < 0.001 | 83842919; 83843198; 83843635; 83843683                     | no                         |
| Sypl2         | 228  | 7.19            | chr3       | 108029012 | 108029751 | 286             | < 0.001 | 108029389; 108029095                                       | yes                        |
| Wipi1         | 228  | 7.19            | chr11      | 109471984 | 109472506 | 561             | < 0.001 | 109471984  | no                         |
| Pogz          | 229  | 7.18            | chr3       | 94641241  | 94641757  | -370            | < 0.001 | 94641567   | yes                        |
| Tera          | 229  | 7.18            | chr6       | 148894658 | 148896207 | -353            | < 0.001 | 148895419; 148894917                                       | yes                        |
| Tmem38a       | 230  | 7.17            | chr8       | 75096409  | 75096458  | 433             | < 0.001 | 75095822   | no                         |
| Klf16         | 231  | 7.16            | chr10      | 80040404  | 80039920  | 143             | < 0.001 | 80040873; 80040718; 80040718; 80040775; 80040775           | yes                        |
| Sox2          | 232  | 7.15            | chr3       | 34548253  | 34548969  | -328            | < 0.001 | 34548944   | yes                        |
| St3gal6       | 233  | 7.14            | chr16      | 58523710  | 58524070  | -309            | < 0.001 | 58523710   | no                         |
| Tmem106b      | 234  | 7.12            | chr6       | 13019960  | 13020361  | 289             | < 0.001 | 13020031   | yes                        |
| Slc2a1        | 235  | 7.09            | chr4       | 118781814 | 118782192 | 666             | < 0.001 | 118781955; 118782027; 118782027                            | yes                        |
| Tmem55a       | 236  | 7.06            | chr4       | 14791322  | 14791830  | 251             | < 0.001 | 14791539; 14791862; 14791862; 14791868                     | yes                        |
| Sstr3         | 237  | 7.05            | chr15      | 78374045  | 78375374  | -125            | < 0.001 | 78374933; 78375359; 78374017; 78375142; 78374679           | no                         |
| Ncam1         | 238  | 7.04            | chr9       | 49605721  | 49606397  | 1428            | < 0.001 | 49605729   | yes                        |
| Thumpd3       | 239  | 7.03            | chr6       | 112996534 | 112996799 | 348             | < 0.001 | 112996534  | no                         |
| Dnaja1        | 240  | 7.02            | chr4       | 40669340  | 40669547  | -198            | < 0.001 | 40669647   | yes                        |
| Mrgpre        | 240  | 7.02            | chr7       | 150969386 | 150969756 | 607             | < 0.001 | 150969386  | no                         |
| Dbp           | 241  | 7               | chr7       | 52961744  | 52962397  | 1629            | < 0.001 | 52963359; 52962083   | yes                        |
| Pag1          | 241  | 7               | chr3       | 9834125   | 9834886   | -716            | < 0.001 | 9834125  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                 | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Fahd1         | 242  | 6.99            | chr17      | 24986816  | 24987041  | 229             | < 0.001 | 24986816  | no                         |
| Gpd1          | 242  | 6.99            | chr15      | 99554990  | 99555395  | 7345            | < 0.001 | 99555476; 99555476                                    | yes                        |
| Tmem164       | 243  | 6.98            | chrX       | 139115480 | 139116144 | 162             | < 0.001 | 139115480   | no                         |
| Hoxb9         | 244  | 6.97            | chr11      | 96132058  | 96132549  | -121            | < 0.001 | 96133494  | yes                        |
| 4930548G07Rik | 244  | 6.97            | chr14      | 57287225  | 57287803  | 521             | < 0.001 | 57287225  | no                         |
| Cbx3          | 245  | 6.96            | chr6       | 51420739  | 51420946  | 310             | < 0.001 | 51420739  | no                         |
| Hivep1        | 246  | 6.92            | chr13      | 42146392  | 42147991  | 453             | < 0.001 | 42147574; 42147577; 42147386; 42147385                | yes                        |
| Jmjd3         | 247  | 6.91            | chr11      | 69229998  | 69229730  | -2209           | < 0.001 | 69230816  | yes                        |
| Kcna1         | 247  | 6.91            | chr6       | 126594565 | 126595206 | 635             | < 0.001 | 126595098; 126595259; 126595259                       | yes                        |
| S100a11       | 248  | 6.9             | chr3       | 93324680  | 93324922  | 479             | < 0.001 | 93324680  | no                         |
| Stag1         | 248  | 6.9             | chr9       | 100543211 | 100543473 | -597            | < 0.001 | 100543552, 100543588, 100543598, 100543624, 100543576 | no                         |
| Fgf11         | 248  | 6.9             | chr11      | 69614608  | 69614821  | 332             | < 0.001 | 69614735; 69614735                                    | yes                        |
| Ptch1         | 249  | 6.87            | chr13      | 63665972  | 63666429  | 532             | < 0.001 | 63666355  | yes                        |
| 1700025G04Rik | 250  | 6.86            | chr1       | 153937671 | 153937237 | 261             | < 0.001 | 153938716   | yes                        |
| Rhbdf1        | 251  | 6.85            | chr11      | 32121292  | 32121704  | 764             | < 0.001 | 32121609; 32121612                                    | yes                        |
| Rnf24         | 251  | 6.85            | chr2       | 131178316 | 131178836 | -247            | < 0.001 | 131179350; 131179350; 131179313; 131178960            | yes                        |
| Slc9a3r1      | 252  | 6.84            | chr11      | 115024053 | 115024332 | -348            | < 0.001 | 115024177   | no                         |
| Cbx6          | 253  | 6.83            | chr15      | 79664769  | 79665412  | -217            | < 0.001 | 79664922; 79665712; 79665749                          | yes                        |
| BC064815      | 253  | 6.83            | chr10      | 92623832  | 92624312  | 866             | < 0.001 | 92624509; 92624509                                    | yes                        |
| Mms19l        | 254  | 6.82            | chr19      | 42055086  | 42055419  | 343             | < 0.001 | 42055086  | no                         |
| Map4k4        | 255  | 6.8             | chr1       | 39959028  | 39958967  | 1301            | < 0.001 | 39959290  | yes                        |
| Tbx2          | 255  | 6.8             | chr11      | 85646086  | 85646476  | 208             | < 0.001 | 85646622; 85646625                                    | yes                        |
| Wnt1          | 255  | 6.8             | chr15      | 98619938  | 98620297  | -323            | < 0.001 | 98620360  | yes                        |
| Pitpnc1       | 256  | 6.79            | chr11      | 107330700 | 107331647 | 414             | < 0.001 | 107331214   | yes                        |
| Slain1        | 256  | 6.79            | chr14      | 104050233 | 104050393 | 799             | < 0.001 | 104050376; 104050376; 104050387                       | yes                        |
| Trim62        | 257  | 6.78            | chr4       | 128560636 | 128561129 | -449            | < 0.001 | 128560957; 128560957                                  | yes                        |
| Slc29a1       | 258  | 6.76            | chr17      | 45732419  | 45733459  | -3330           | < 0.001 | 45733088; 45733091                                    | yes                        |
| Bnip3l        | 258  | 6.76            | chr14      | 67627652  | 67628194  | -336            | < 0.001 | 67628214; 67628214                                    | yes                        |
| Fst           | 258  | 6.76            | chr13      | 115249261 | 115249777 | -634            | < 0.001 | 115249809; 115249389                                  | yes                        |
| Arf5          | 259  | 6.75            | chr6       | 28373988  | 28374033  | 371             | < 0.001 | 28374011  | yes                        |
| Ralgds        | 259  | 6.75            | chr2       | 28369914  | 28370312  | 1437            | < 0.001 | 28370449  | yes                        |
| Top1          | 259  | 6.75            | chr2       | 160472318 | 160472495 | 710             | < 0.001 | 160472619   | yes                        |
| Dedd          | 260  | 6.73            | chr1       | 173259588 | 173260212 | 169             | < 0.001 | 173259753; 173259753; 173259622                       | yes                        |
| Itpr2         | 261  | 6.71            | chr6       | 146450991 | 146451138 | -680            | < 0.001 | 146450991   | no                         |
| Vgf           | 261  | 6.71            | chr5       | 137508287 | 137508475 | 2146            | < 0.001 | N/A   | no                         |
| 4930546H06Rik | 262  | 6.7             | chr17      | 17964255  | 17965263  | -2210           | < 0.001 | 17964298  | yes                        |
| Rasal1        | 262  | 6.7             | chr5       | 121098212 | 121099052 | 200             | < 0.001 | 121098964   | yes                        |
| Isyna1        | 262  | 6.7             | chr8       | 73117265  | 73117923  | -641            | < 0.001 | 73117265  | no                         |
| Ephb1         | 263  | 6.69            | chr9       | 102257069 | 102257119 | -131            | < 0.001 | 102257069   | no                         |
| 2310033P09Rik | 264  | 6.68            | chr11      | 59021977  | 59021785  | 138             | < 0.001 | 59022271  | yes                        |
| 5033428A16Rik | 264  | 6.68            | chr8       | 90642558  | 90643265  | 105             | < 0.001 | 90643320  | yes                        |
| Cd63          | 265  | 6.67            | chr10      | 128347610 | 128347776 | 833             | < 0.001 | 128347724   | yes                        |
| Slit3         | 265  | 6.67            | chr11      | 34935290  | 34935979  | 523             | < 0.001 | 34936257; 34936257; 34935656; 34935655                | yes                        |
| Ric8b         | 266  | 6.65            | chr10      | 84380277  | 84380580  | 158             | < 0.001 | 84380608; 84380667                                    | yes                        |
| Glul          | 267  | 6.64            | chr1       | 155748095 | 155747683 | 906             | < 0.001 | 155748095   | no                         |
| BC049664      | 267  | 6.64            | chr12      | 12269302  | 12269671  | 502             | < 0.001 | 12269802  | yes                        |
| Igsf8         | 268  | 6.63            | chr1       | 174243052 | 174242684 | 289             | < 0.001 | 174243208; 174243208; 174243447; 174243446            | yes                        |
| Plat          | 268  | 6.63            | chr8       | 23868888  | 23869245  | 845             | < 0.001 | 23870348; 23869437                                    | yes                        |
| Spry2         | 269  | 6.6             | chr14      | 106296835 | 106297186 | -938            | < 0.001 | 106296835   | no                         |
| Niban         | 270  | 6.59            | chr1       | 153418364 | 153418150 | -270            | < 0.001 | 153418364   | no                         |
| Pthr1         | 270  | 6.59            | chr9       | 110644837 | 110645636 | -288            | < 0.001 | 110645092; 110645095; 110645458                       | yes                        |
| 9430071P14Rik | 271  | 6.58            | chr6       | 37999058  | 37999219  | 75390           | < 0.001 | 37999058  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| AI597468      | 271  | 6.58            | chr10      | 84566101  | 84566009  | 606             | < 0.001 | 84565322, 84565313, 84565560, 84565557, 84565283, 84565505, 84565554, 84566051, 84565767, 84565761, 84565472, 84565421, 84566200, 84565451, 84565410 | no                         |
| Prkg2         | 272  | 6.57            | chr5       | 99465568  | 99466474  | -354            | < 0.001 | 99466138, 99466119, 99466195   | no                         |
| Pwwp2         | 273  | 6.55            | chr7       | 146433827 | 146435309 | 242             | < 0.001 | 146434587; 146435237   | yes                        |
| Arvcf         | 274  | 6.54            | chr16      | 18343807  | 18344629  | -4228           | < 0.001 | 18344363; 18344366; 18344187; 18344186   | yes                        |
| Wnk1          | 275  | 6.53            | chr6       | 119987911 | 119988641 | -821            | < 0.001 | 119989173, 119988189, 119987772  | no                         |
| Snap29        | 276  | 6.5             | chr16      | 17405335  | 17405966  | -450            | < 0.001 | 17406219   | yes                        |
| Ikbkap        | 276  | 6.5             | chr4       | 56815316  | 56815744  | -377            | < 0.001 | 56815442   | no                         |
| Zbtb37        | 276  | 6.5             | chr1       | 162964732 | 162964964 | -552            | < 0.001 | 162964864, 162964647, 162964653, 162964635   | no                         |
| Abi2          | 277  | 6.49            | chr1       | 60467153  | 60466960  | 297             | < 0.001 | 60467872; 60467701   | yes                        |
| Dr1           | 277  | 6.49            | chr5       | 108697451 | 108697703 | -239            | < 0.001 | 108697451  | no                         |
| Rnd3          | 278  | 6.48            | chr2       | 51002754  | 51003691  | 1851            | < 0.001 | 51003407; 51003407   | yes                        |
| L1cam         | 278  | 6.48            | chrX       | 71125977  | 71126933  | -247            | < 0.001 | 71126411   | yes                        |
| Ube2t         | 279  | 6.45            | chr1       | 136858855 | 136859277 | -31             | < 0.001 | 136858951; 136858951   | yes                        |
| Top1111       | 280  | 6.44            | chr2       | 104552434 | 104552678 | -332            | < 0.001 | 104552558; 104552531; 104552776  | yes                        |
| Pex19         | 281  | 6.43            | chr1       | 174057179 | 174057015 | 90              | < 0.001 | 174057498  | yes                        |
| VeZF1         | 281  | 6.43            | chr11      | 87880929  | 87882755  | 533             | < 0.001 | 87882857; 87882857; 87882313; 87882036; 87882035   | yes                        |
| Lasp1         | 281  | 6.43            | chr11      | 97660313  | 97660660  | -475            | < 0.001 | 97660313   | no                         |
| 2610024E20Rik | 282  | 6.42            | chr18      | 34666560  | 34667009  | -298            | < 0.001 | 34666616; 34666616   | yes                        |
| Tex264        | 283  | 6.4             | chr9       | 106587991 | 106588781 | -341            | < 0.001 | 106588559  | yes                        |
| Ecd3          | 284  | 6.39            | chr9       | 57556329  | 57556479  | -23             | < 0.001 | 57556571   | yes                        |
| Cecr6         | 284  | 6.39            | chr6       | 120443206 | 120444687 | -275            | < 0.001 | 120444212; 120444212; 120444177; 120444218; 120444218; 120443779; 120443778  | yes                        |
| Uck2          | 284  | 6.39            | chr1       | 169214525 | 169214245 | 1038            | < 0.001 | 169215048  | yes                        |
| Wdr22         | 284  | 6.39            | chr12      | 81536375  | 81536716  | 1014            | < 0.001 | 81536317   | no                         |
| E130309F12Rik | 285  | 6.38            | chr4       | 49072026  | 49072408  | -95             | < 0.001 | 49072112, 49072122, 49072279, 49072268, 49072116   | no                         |
| Wasl          | 286  | 6.37            | chr6       | 24614170  | 24615073  | 420             | < 0.001 | 24615180; 24615212   | yes                        |
| Pum2          | 286  | 6.37            | chr12      | 8681056   | 8681641   | 132             | < 0.001 | 8681224  | yes                        |
| Nr2f6         | 287  | 6.36            | chr8       | 73904674  | 73904940  | 933             | < 0.001 | 73904928; 73904928   | yes                        |
| Ldlrad3       | 287  | 6.36            | chr2       | 102025868 | 102026104 | 452             | < 0.001 | N/A  | no                         |
| Ing2          | 288  | 6.34            | chr8       | 48759591  | 48759878  | 658             | < 0.001 | 48759433   | no                         |
| Ppm1d         | 289  | 6.32            | chr11      | 85124173  | 85124688  | -89             | < 0.001 | 85124815   | yes                        |
| Vasn          | 289  | 6.32            | chr16      | 4640187   | 4640719   | 390             | < 0.001 | 4640187  | no                         |
| AW049604      | 290  | 6.31            | chr15      | 87455391  | 87455924  | -245            | < 0.001 | 87455789; 87455792; 87455820   | yes                        |
| Gad2          | 290  | 6.31            | chr2       | 22477850  | 22478016  | 27              | < 0.001 | 22477962   | yes                        |
| Tmem53        | 290  | 6.31            | chr4       | 116924690 | 116924860 | 119             | < 0.001 | 116924574, 116924776, 116924606  | no                         |
| Pigp          | 291  | 6.29            | chr16      | 94591846  | 94592231  | -140            | < 0.001 | 94592380   | yes                        |
| Kif5c         | 291  | 6.29            | chr2       | 49475777  | 49476147  | 1284            | < 0.001 | 49475955; 49475926   | yes                        |
| Kpnb1         | 291  | 6.29            | chr11      | 97048471  | 97049080  | 328             | < 0.001 | N/A  | no                         |
| Pde10a        | 292  | 6.28            | chr17      | 8993899   | 8994191   | -441            | < 0.001 | 8994222; 8994222   | yes                        |
| Pik3r1        | 292  | 6.28            | chr13      | 102464837 | 102465254 | -2379           | < 0.001 | 102465264; 102465264   | yes                        |
| T2bp          | 292  | 6.28            | chr3       | 127492772 | 127493120 | 268             | < 0.001 | 127493156  | yes                        |
| Ngdn          | 292  | 6.28            | chr14      | 55633596  | 55633910  | -740            | < 0.001 | 55633578, 55633584   | no                         |
| Bub1b         | 293  | 6.27            | chr2       | 118423833 | 118424145 | 32              | < 0.001 | 118423937  | no                         |
| 2900093B09Rik | 294  | 6.26            | chr7       | 48154340  | 48154952  | -285            | < 0.001 | 48154461; 48154461; 48155098; 48155098   | yes                        |
| Ssx2ip        | 294  | 6.26            | chr3       | 146067207 | 146067558 | -114            | < 0.001 | 146067675  | yes                        |
| Rprc1         | 294  | 6.26            | chr4       | 125932390 | 125933014 | 689             | < 0.001 | 125932239, 125932769, 125932611, 125932617, 125933981, 125934230, 125934236  | no                         |
| Capn1         | 294  | 6.26            | chr19      | 6015069   | 6015817   | -365            | < 0.001 | 6015867; 6015523   | yes                        |
| 5730420B22Rik | 295  | 6.25            | chr14      | 45838540  | 45838940  | 151             | < 0.001 | 45839030, 45838970   | no                         |
| Pomp          | 296  | 6.24            | chr5       | 148671896 | 148672419 | 47              | < 0.001 | 148672315; 148672315   | yes                        |
| Cmtm8         | 297  | 6.23            | chr9       | 114753279 | 114753975 | -361            | < 0.001 | 114753468  | yes                        |
| Zfp191        | 297  | 6.23            | chr18      | 24179439  | 24179929  | -304            | < 0.001 | 24179581   | yes                        |

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| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Ptpra         | 297  | 6.23            | chr2       | 130276039 | 130276925 | -213            | < 0.001 | 130276223, 130276352, 130276258, 130276794, 130276061, 130276157, 130276154, 130276160 | no                         |
| Ern1          | 298  | 6.22            | chr11      | 106349391 | 106350063 | -437            | < 0.001 | 106349206, 106349200, 106349276  | no                         |
| Evp1          | 298  | 6.22            | chr11      | 116103208 | 116103856 | -4062           | < 0.001 | 116103208  | no                         |
| Cobl1         | 299  | 6.21            | chr2       | 65076709  | 65077445  | -433            | < 0.001 | 65077147; 65077089; 65077450; 65077150   | yes                        |
| Crabp2        | 299  | 6.21            | chr3       | 87750927  | 87751209  | -1432           | < 0.001 | 87751337; 87751336   | yes                        |
| Thbs1         | 300  | 6.2             | chr2       | 117937259 | 117937635 | -370            | < 0.001 | 117937749; 117937615; 117937615; 117937752   | yes                        |
| Hibadh        | 301  | 6.19            | chr6       | 52590486  | 52590717  | -219            | < 0.001 | 52590543, 52590414   | no                         |
| Trim3         | 302  | 6.18            | chr7       | 112781611 | 112781962 | 235             | < 0.001 | 112781802, 112781916   | no                         |
| Paxip1        | 303  | 6.17            | chr5       | 28117756  | 28117994  | 101             | < 0.001 | 28117885; 28118140   | yes                        |
| Wdfy1         | 303  | 6.17            | chr1       | 79758128  | 79757982  | 384             | < 0.001 | 79758108   | no                         |
| Paip2         | 304  | 6.16            | chr18      | 35758346  | 35758652  | 302             | < 0.001 | 35758533   | yes                        |
| Tef           | 304  | 6.16            | chr15      | 81641068  | 81641121  | -808            | < 0.001 | 81641418   | yes                        |
| Plxdc1        | 304  | 6.16            | chr11      | 97847174  | 97847368  | 348             | < 0.001 | 97847457; 97847457   | yes                        |
| Col4a5        | 305  | 6.15            | chrX       | 137909944 | 137910926 | 237             | < 0.001 | 137909926, 137911114   | no                         |
| Myo7b         | 305  | 6.15            | chr18      | 32196506  | 32196726  | -85             | < 0.001 | 32196506   | no                         |
| D730040F13Rik | 306  | 6.13            | chr4       | 56960116  | 56960515  | -191            | < 0.001 | 56960518; 56960536; 56960536   | yes                        |
| Nt5c2         | 307  | 6.12            | chr19      | 47037017  | 47037072  | -246            | < 0.001 | 47037024; 47037027   | yes                        |
| Pcdh7         | 307  | 6.12            | chr5       | 58107160  | 58107603  | -1953           | < 0.001 | 58107892   | yes                        |
| Ncoa2         | 307  | 6.12            | chr1       | 13364474  | 13364662  | -332            | < 0.001 | 13363172, 13363221, 13364280, 13364351   | no                         |
| Ubap2l        | 307  | 6.12            | chr3       | 89855750  | 89856277  | 443             | < 0.001 | 89855677, 89855837, 89856208, 89856048, 89856043                                       | no                         |
| Igf1r         | 308  | 6.11            | chr7       | 75096138  | 75096355  | -982            | < 0.001 | 75096138   | no                         |
| Kcnj8         | 308  | 6.11            | chr6       | 142519670 | 142520325 | 40              | < 0.001 | 142520094, 142520259   | no                         |
| Elov16        | 308  | 6.11            | chr3       | 129235802 | 129236615 | 1179            | < 0.001 | N/A  | no                         |
| Alms1         | 309  | 6.1             | chr6       | 85537796  | 85538235  | 576             | < 0.001 | 85538139; 85538139; 85538146; 85538151; 85538145                                       | yes                        |
| Ninj1         | 310  | 6.08            | chr13      | 49282919  | 49283194  | 27              | < 0.001 | 49283077   | yes                        |
| Rhog          | 311  | 6.07            | chr7       | 109398502 | 109398954 | -299            | < 0.001 | 109398886; 109398775   | yes                        |
| Tubb2b        | 312  | 6.06            | chr13      | 34221621  | 34221889  | 363             | < 0.001 | 34221879   | yes                        |
| 2600010E01Rik | 312  | 6.06            | chr2       | 101637242 | 101638237 | -166            | < 0.001 | 101637479, 101637958, 101637935  | no                         |
| BC067054      | 313  | 6.05            | chr3       | 95622734  | 95623631  | -129            | < 0.001 | 95623609; 95623609   | yes                        |
| Etf1          | 314  | 6.04            | chr18      | 35091233  | 35091284  | 399             | < 0.001 | 35091355   | yes                        |
| Plec1         | 315  | 6.03            | chr15      | 76028337  | 76028933  | -163            | < 0.001 | 76028830; 76029032; 76029032   | yes                        |
| Akp2          | 315  | 6.03            | chr4       | 137352188 | 137352422 | 82              | < 0.001 | 137352443; 137352312   | yes                        |
| Sfxn3         | 315  | 6.03            | chr19      | 45119804  | 45119858  | -2332           | < 0.001 | N/A  | no                         |
| Apeh          | 316  | 6.02            | chr9       | 107997152 | 107997525 | -392            | < 0.001 | 107997457; 107997457   | yes                        |
| Phka2         | 316  | 6.02            | chrX       | 156940212 | 156940861 | -156            | < 0.001 | 156940744; 156940747   | yes                        |
| Plekhc1       | 316  | 6.02            | chr14      | 46149149  | 46150611  | 52              | < 0.001 | 46150024; 46149562   | yes                        |
| Mrpl48        | 317  | 6.01            | chr7       | 107756874 | 107757209 | 722             | < 0.001 | 107757019  | yes                        |
| Ptprg         | 318  | 6               | chr14      | 12386787  | 12387612  | 936             | < 0.001 |  | no                         |
| Ap2a2         | 319  | 5.99            | chr7       | 148748606 | 148748791 | 550             | < 0.001 | 12386787   | no                         |
| Ccdc102a      | 320  | 5.97            | chr8       | 97441560  | 97441762  | 211             | < 0.001 | 148748606  | yes                        |
| Trappc4       | 321  | 5.96            | chr9       | 44214960  | 44215412  | 649             | < 0.001 | 44214929, 44215146   | no                         |
| Nfkb2         | 321  | 5.96            | chr19      | 46380480  | 46380527  | 397             | < 0.001 | 46380594; 46380594   | yes                        |
| Myo9b         | 322  | 5.95            | chr8       | 73796754  | 73797123  | 488             | < 0.001 | 73796636; 73796583   | no                         |
| Lef1          | 322  | 5.95            | chr3       | 130814332 | 130815403 | 1166            | < 0.001 | 130815144; 130817051; 130815133; 130815647; 130815646                                  | yes                        |
| Rufy4         | 323  | 5.94            | chr1       | 74171225  | 74171389  | -748            | < 0.001 | 74171364; 74171363   | yes                        |
| B930006L02Rik | 323  | 5.94            | chr7       | 107855205 | 107855569 | 13              | < 0.001 | 107855312; 107855315   | yes                        |
| Gm266         | 323  | 5.94            | chr12      | 112724129 | 112725777 | -1527           | < 0.001 | 112725486, 112724594, 112724851  | no                         |
| Khsrp         | 323  | 5.94            | chr17      | 57170218  | 57170402  | 551             | < 0.001 | 57170218   | no                         |
| Fgfr2         | 324  | 5.93            | chr7       | 137409139 | 137409581 | 922             | < 0.001 | 137409433  | yes                        |
| D930005D10Rik | 324  | 5.93            | chr5       | 143026191 | 143026585 | 469             | < 0.001 | 143026191  | no                         |
| Frmf6         | 325  | 5.92            | chr12      | 71926104  | 71926501  | -370            | < 0.001 | 71926627; 71926627   | yes                        |
| G6pc3         | 325  | 5.92            | chr11      | 102051127 | 102051357 | 138             | < 0.001 | 102051116, 102051078, 102051062  | no                         |
| AA407270      | 326  | 5.91            | chr9       | 71439405  | 71440472  | -93             | < 0.001 | 71440347   | yes                        |



**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Fzd7          | 326  | 5.91            | chr1       | 59539423  | 59539798  | 456             | < 0.001 | 59540074; 59540037; 59540037   | yes                        |
| St3gal5       | 327  | 5.9             | chr6       | 72047426  | 72048143  | -4              | < 0.001 | 72047753; 72047756; 72047791   | yes                        |
| Hnrpk         | 327  | 5.9             | chr13      | 58503962  | 58504199  | -299            | < 0.001 | 58503962   | no                         |
| Atoh8         | 328  | 5.89            | chr6       | 72184349  | 72185966  | -35             | < 0.001 | 72185197, 72185539, 72185542, 72184775, 72184598, 72184769, 72185174, 72184673   | no                         |
| Slc4a2        | 328  | 5.89            | chr5       | 23931419  | 23932150  | 393             | < 0.001 | 23931292, 23931294   | no                         |
| Tenc1         | 328  | 5.89            | chr15      | 101932217 | 101934231 | 790             | < 0.001 | 101932936; 101932935   | yes                        |
| Ccdc58        | 329  | 5.88            | chr16      | 36071911  | 36072497  | 554             | < 0.001 | 36071597, 36072406, 36071680   | no                         |
| Homer1        | 329  | 5.88            | chr13      | 94073238  | 94073656  | -1001           | < 0.001 | 94073636   | no                         |
| Mllt7         | 330  | 5.87            | chrX       | 98450032  | 98450184  | 191             | < 0.001 | 98450974, 98451086   | no                         |
| Klf10         | 331  | 5.86            | chr15      | 38231020  | 38231764  | -892            | < 0.001 | 38231479; 38231482; 38231179; 38231340; 38231343; 38231122; 38231122   | yes                        |
| 4631426J05Rik | 332  | 5.85            | chr7       | 139507500 | 139508332 | 1064            | < 0.001 | 139508225  | yes                        |
| C2ta          | 332  | 5.85            | chr16      | 10489795  | 10490339  | 1797            | < 0.001 | 10490454; 10490454   | yes                        |
| Zfp597        | 332  | 5.85            | chr16      | 3872026   | 3872689   | 156             | < 0.001 | 3872551; 3872551   | yes                        |
| D930049A15Rik | 332  | 5.85            | chr14      | 26280054  | 26280624  | 1483            | < 0.001 | 26280335, 26280142, 26280094, 26280134, 26279869, 26276583, 26276585, 26276586, 26276584, 26276588, 26276510, 26277340 | no                         |
| Agpat7        | 333  | 5.84            | chr2       | 112080231 | 112080431 | 411             | < 0.001 | 112080339  | no                         |
| Pgm211        | 333  | 5.84            | chr7       | 107375935 | 107376343 | -156            | < 0.001 | 107376290; 107376310; 107376290  | yes                        |
| Lmo6          | 334  | 5.83            | chrX       | 7235015   | 7235698   | -192            | < 0.001 | 7235780; 7235783   | yes                        |
| Lck           | 335  | 5.82            | chr4       | 129233406 | 129233772 | 1870            | < 0.001 | 7235579  | no                         |
| Ptfr          | 336  | 5.81            | chr11      | 100830389 | 100831020 | 1239            | < 0.001 | 100830949; 100831002   | yes                        |
| Rusc1         | 336  | 5.81            | chr3       | 88897370  | 88897536  | -108            | < 0.001 | 88897308, 88897340   | no                         |
| Jag1          | 337  | 5.79            | chr2       | 136940347 | 136941094 | 1238            | < 0.001 | 136940726  | yes                        |
| Ppia          | 337  | 5.79            | chr11      | 6316475   | 6316665   | 633             | < 0.001 | 6316475  | no                         |
| Cyp46a1       | 338  | 5.78            | chr12      | 109572343 | 109572394 | -222            | < 0.001 | 109572726; 109572646   | yes                        |
| Hadhb         | 338  | 5.78            | chr5       | 30481870  | 30482020  | 31              | < 0.001 | 30481811   | no                         |
| Ppp5c         | 339  | 5.77            | chr7       | 17613374  | 17613428  | -182            | < 0.001 | 17613529; 17613532   | yes                        |
| Pdia4         | 339  | 5.77            | chr6       | 47763265  | 47763883  | -345            | < 0.001 | 47763853   | yes                        |
| Ints3         | 339  | 5.77            | chr3       | 90237084  | 90237312  | 268             | < 0.001 | 90237084   | no                         |
| Cret1         | 340  | 5.76            | chr3       | 92818464  | 92819010  | 775             | < 0.001 | 92818814   | yes                        |
| Sert1         | 341  | 5.75            | chr15      | 76350195  | 76350560  | 2341            | < 0.001 | 76350547; 76350569; 76350572; 76350550; 76350309; 76350309   | yes                        |
| St8sia2       | 342  | 5.74            | chr7       | 81157727  | 81158032  | 698             | < 0.001 | 81157727   | no                         |
| Utp18         | 342  | 5.74            | chr11      | 93748145  | 93748190  | 636             | < 0.001 | 93748145   | no                         |
| Hoxc9         | 343  | 5.72            | chr15      | 102807056 | 102808422 | 48              | < 0.001 | 102808579  | yes                        |
| Plekhl1       | 343  | 5.72            | chr7       | 39012596  | 39013276  | -133            | < 0.001 | 39013300; 39013222; 39013300   | yes                        |
| Arid5a        | 344  | 5.71            | chr1       | 36364811  | 36364659  | 238             | < 0.001 | 36365142; 36365142   | yes                        |
| Ddx6          | 345  | 5.7             | chr9       | 44413288  | 44413449  | 336             | < 0.001 | 44413383; 44413383   | yes                        |
| Klf13         | 345  | 5.7             | chr7       | 71081546  | 71082367  | 1405            | < 0.001 | 71082403; 71081723   | yes                        |
| Mtap1b        | 345  | 5.7             | chr13      | 100285079 | 100286304 | 459             | < 0.001 | 100285958; 100285958   | yes                        |
| Add3          | 345  | 5.7             | chr19      | 53216125  | 53216585  | -1924           | < 0.001 | 53216173   | no                         |
| Ppt2          | 345  | 5.7             | chr17      | 34763379  | 34763616  | 448             | < 0.001 | 34764390, 34764387, 34764384, 34764389, 34764391, 34764386, 34764388, 34764393, 34763691, 34763842                     | no                         |
| Usp11         | 346  | 5.69            | chr5       | 149996527 | 149996575 | 416             | < 0.001 | 149996527  | no                         |
| Galnt1        | 347  | 5.68            | chr18      | 24364086  | 24364131  | 167             | < 0.001 | 24364366; 24364406   | yes                        |
| Nans          | 347  | 5.68            | chr4       | 46502184  | 46502332  | 110             | < 0.001 | 46502184   | no                         |
| Xylt1         | 348  | 5.66            | chr7       | 124523655 | 124524046 | -680            | < 0.001 | N/A  | no                         |
| Bcar3         | 349  | 5.65            | chr3       | 122122542 | 122123574 | -30             | < 0.001 | 122123485; 122122975   | yes                        |
| Vamp4         | 349  | 5.65            | chr1       | 164501103 | 164501262 | 168             | < 0.001 | 164501194; 164501281   | yes                        |
| Mpp3          | 349  | 5.65            | chr11      | 101888193 | 101889124 | -345            | < 0.001 | 101888508; 101888744; 101888453; 101888452   | yes                        |
| Rod1          | 350  | 5.64            | chr4       | 59561478  | 59562167  | 2               | < 0.001 | 59561901; 59561904; 59562114   | yes                        |
| Samd4         | 350  | 5.64            | chr14      | 47502240  | 47502814  | -35             | < 0.001 | 47502721   | yes                        |
| Zbtb7a        | 350  | 5.64            | chr10      | 80601321  | 80601596  | 2329            | < 0.001 | 80601406   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene               | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                 | WT1 Consensus Site Present |
|--------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Atbf1              | 351  | 5.63            | chr8       | 111239108 | 111239153 | 587             | < 0.001 | 111239445   | yes                        |
| Atxn2              | 351  | 5.63            | chr5       | 122162420 | 122163177 | 1537            | < 0.001 | 122162543   | yes                        |
| Dnajc17            | 352  | 5.62            | chr2       | 119034386 | 119034433 | 100             | < 0.001 | 119034754   | yes                        |
| Clec11a            | 353  | 5.61            | chr7       | 51566577  | 51567261  | -4860           | < 0.001 | 51566847  | yes                        |
| Rbm39              | 353  | 5.61            | chr2       | 156005989 | 156006398 | -224            | < 0.001 | 156006324   | yes                        |
| Cbfb               | 353  | 5.61            | chr8       | 107694896 | 107695052 | 345             | < 0.001 | 107694896   | no                         |
| Cacna1h            | 354  | 5.6             | chr17      | 25571123  | 25571540  | -803            | < 0.001 | 25571481; 25571292; 25571386                          | yes                        |
| Tnpo2              | 354  | 5.6             | chr8       | 87561241  | 87561522  | 200             | < 0.001 | 87561455  | no                         |
| Ctdspl2            | 355  | 5.59            | chr2       | 121782179 | 121782373 | 161             | < 0.001 | 121782137, 121781802, 121781787, 121782072            | no                         |
| Socs7              | 356  | 5.58            | chr11      | 97224166  | 97224491  | 474             | < 0.001 | 97224197; 97224197                                    | yes                        |
| Ly6h               | 356  | 5.58            | chr15      | 75397399  | 75397741  | -176            | < 0.001 | 75397727  | yes                        |
| OTTMUSG00000003802 | 357  | 5.57            | chr11      | 117344083 | 117344611 | -1357           | < 0.001 | 117344702; 117344702                                  | yes                        |
| Foxo3a             | 358  | 5.53            | chr10      | 41997198  | 41996010  | 560             | < 0.001 | 41997543; 41997782; 41997985                          | yes                        |
| Lrfn4              | 358  | 5.53            | chr19      | 4615491   | 4615695   | -170            | < 0.001 | 4615295, 4615573                                      | no                         |
| Ubtf               | 358  | 5.53            | chr11      | 102178323 | 102178950 | -201            | < 0.001 | 102178828; 102178765; 102178347; 102178442; 102178441 | yes                        |
| Pcgf2              | 359  | 5.51            | chr11      | 97560233  | 97560593  | 1090            | < 0.001 | 97560501, 97560435, 97560444, 97560203                | no                         |
| Fbxo3              | 360  | 5.5             | chr2       | 103867763 | 103867959 | -163            | < 0.001 | 103868054   | yes                        |
| Rcsd1              | 360  | 5.5             | chr1       | 167639122 | 167638945 | -121            | < 0.001 | 167640458   | yes                        |
| Nes                | 360  | 5.5             | chr3       | 87775824  | 87776743  | 1388            | < 0.001 | 87775925, 87776369, 87775614                          | no                         |
| Pten               | 360  | 5.5             | chr19      | 32830437  | 32830640  | -1603           | < 0.001 | 32830491  | no                         |
| Poln               | 361  | 5.49            | chr5       | 34512280  | 34512448  | -206            | < 0.001 | 34512542; 34512545                                    | yes                        |
| Kcnc2              | 361  | 5.49            | chr10      | 111708034 | 111708550 | 52              | < 0.001 | 111708184   | no                         |
| Ccdc131            | 361  | 5.49            | chr10      | 114822665 | 114822522 | 304             | < 0.001 | 114822738; 114822738                                  | yes                        |
| Irs1               | 362  | 5.47            | chr1       | 82287014  | 82287407  | 521             | < 0.001 | 82288546, 82288538, 82287592                          | no                         |
| Plxna2             | 363  | 5.45            | chr1       | 196446081 | 196446000 | -46             | < 0.001 | 196446264; 196446264                                  | yes                        |
| Pura               | 363  | 5.45            | chr18      | 36440738  | 36441247  | 93              | < 0.001 | 36441820; 36441017; 36441785; 36441784                | yes                        |
| Tuba2              | 364  | 5.44            | chr15      | 98764377  | 98764619  | 225             | < 0.001 | 98764633  | yes                        |
| Gm879              | 364  | 5.44            | chr11      | 66340476  | 66340663  | -874            | < 0.001 | 66341056  | yes                        |
| Chd4               | 365  | 5.43            | chr6       | 125046851 | 125048166 | 694             | < 0.001 | 125047291   | yes                        |
| Atp5g1             | 365  | 5.43            | chr11      | 95937177  | 95937224  | -237            | < 0.001 | 95937177  | no                         |
| Calcoo1            | 365  | 5.43            | chr15      | 102552188 | 102552634 | 135             | < 0.001 | 102552430, 102552325                                  | no                         |
| AI839735           | 365  | 5.43            | chr12      | 113748938 | 113749784 | 137             | < 0.001 | 113749567   | yes                        |
| Prpf40b            | 365  | 5.43            | chr15      | 99125814  | 99126085  | 223             | < 0.001 | N/A   | no                         |
| Cox5a              | 366  | 5.42            | chr9       | 57368764  | 57368824  | -244            | < 0.001 | 57369062; 57369062                                    | yes                        |
| Pou4f1             | 366  | 5.42            | chr14      | 104866936 | 104867347 | 255             | < 0.001 | 104866969   | yes                        |
| Zhx2               | 366  | 5.42            | chr15      | 57526891  | 57527793  | 1359            | < 0.001 | 57527337  | yes                        |
| 6330442E10Rik      | 366  | 5.42            | chr12      | 80107575  | 80107827  | 460             | < 0.001 | 80107710  | no                         |
| Tdrkh              | 366  | 5.42            | chr3       | 94217113  | 94217366  | 105             | < 0.001 | 94217358; 94217301                                    | yes                        |
| Sertad4            | 367  | 5.41            | chr1       | 194681433 | 194681218 | 459             | < 0.001 | 194681700   | yes                        |
| Diap2              | 367  | 5.41            | chrX       | 126284616 | 126284864 | 308             | < 0.001 | 126285051   | yes                        |
| Mapk12             | 367  | 5.41            | chr15      | 88971258  | 88971515  | -240            | < 0.001 | 88971077  | no                         |
| Rcn1               | 367  | 5.41            | chr2       | 105239774 | 105239829 | -326            | < 0.001 | 105239774   | no                         |
| Atp11c             | 368  | 5.4             | chrX       | 57656967  | 57657012  | 166             | < 0.001 | 57657381; 57657061                                    | yes                        |
| Elk3               | 368  | 5.4             | chr10      | 92772938  | 92773360  | 706             | < 0.001 | 92773847  | yes                        |
| Cpd                | 369  | 5.39            | chr11      | 76663149  | 76663313  | -2780           | < 0.001 | 76663149  | no                         |
| Nope               | 369  | 5.39            | chr9       | 64949985  | 64950464  | 907             | < 0.001 | 64950172  | no                         |
| Ppp1r3b            | 370  | 5.38            | chr8       | 36439072  | 36439753  | 450             | < 0.001 | 36439258  | yes                        |
| Myo1c              | 370  | 5.38            | chr11      | 75465154  | 75465200  | -474            | < 0.001 | 75465154  | no                         |
| Rfc5               | 370  | 5.38            | chr5       | 117838227 | 117838761 | 296             | < 0.001 | 117838823   | yes                        |
| Trim33             | 370  | 5.38            | chr3       | 103084601 | 103084775 | 1530            | < 0.001 | N/A   | no                         |
| Nfia               | 371  | 5.37            | chr4       | 97441627  | 97442042  | -2304           | < 0.001 | 97442061; 97441743; 97441746                          | yes                        |
| Ppp1r9a            | 372  | 5.36            | chr6       | 4853505   | 4854104   | 321             | < 0.001 | 4854173; 4854167                                      | yes                        |
| Ube2v1             | 372  | 5.36            | chr2       | 167457750 | 167458058 | -267            | < 0.001 | 167457876   | yes                        |
| I300014I06Rik      | 373  | 5.35            | chr13      | 34744399  | 34745414  | -603            | < 0.001 | 34744340  | no                         |
| Anp32a             | 373  | 5.35            | chr9       | 62189900  | 62191433  | 2261            | < 0.001 | 62189851, 62189845                                    | no                         |
| Kif1a              | 373  | 5.35            | chr1       | 94997478  | 94997525  | 940             | < 0.001 | 94997321  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site            | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Mpp2          | 373  | 5.35            | chr11      | 101948727 | 101948884 | 954             | < 0.001 | 101948777, 101948769                             | no                         |
| Zfp36         | 374  | 5.34            | chr7       | 29166666  | 29166726  | -2449           | < 0.001 | 29166826   | yes                        |
| 2010305A19Rik | 374  | 5.34            | chr4       | 108000478 | 108000670 | -108            | < 0.001 | 108000609  | no                         |
| Wdr26         | 374  | 5.34            | chr1       | 183141201 | 183140911 | 460             | < 0.001 | 183141081, 183141075                             | no                         |
| Axin2         | 375  | 5.32            | chr11      | 108781745 | 108782774 | 350             | < 0.001 | 108782557; 108782556; 108782551; 108782550       | yes                        |
| Fads1         | 375  | 5.32            | chr19      | 10257651  | 10258275  | 476             | < 0.001 | 10258018   | no                         |
| Lrch1         | 376  | 5.31            | chr14      | 75346241  | 75346547  | 1284            | < 0.001 | 75346433; 75346451; 75346450                     | yes                        |
| Ntf3          | 376  | 5.31            | chr6       | 126116645 | 126117294 | -2024           | < 0.001 | 126114650, 126114694                             | no                         |
| Mgea5         | 377  | 5.3             | chr19      | 45857854  | 45858270  | -329            | < 0.001 | 45858277   | yes                        |
| Slc30a3       | 377  | 5.3             | chr5       | 31395268  | 31395598  | 295             | < 0.001 | 31395979; 31396328; 31396328; 31395600; 31395600 | yes                        |
| Dusp2         | 378  | 5.29            | chr2       | 127161409 | 127161987 | 70              | < 0.001 | 127161996  | yes                        |
| Mpp5          | 378  | 5.29            | chr12      | 79849857  | 79850008  | -23             | < 0.001 | 79849936, 79849774, 79849863, 79849840, 79849687 | no                         |
| Ints6         | 379  | 5.28            | chr14      | 63378815  | 63379656  | 907             | < 0.001 | 63378985; 63379118                               | yes                        |
| Tyro3         | 379  | 5.28            | chr2       | 119625325 | 119625935 | 521             | < 0.001 | 119625413; 119625661; 119625660                  | yes                        |
| Hoxb6         | 379  | 5.28            | chr11      | 96161421  | 96161907  | 1400            | < 0.001 | 96161824   | no                         |
| Kctd11        | 379  | 5.28            | chr11      | 69694712  | 69694984  | -249            | < 0.001 | 69694634, 69694539, 69694808, 69694677           | no                         |
| Gkap1         | 380  | 5.27            | chr13      | 58375084  | 58375316  | 443             | < 0.001 | 58375491   | yes                        |
| Sertad1       | 381  | 5.26            | chr7       | 28272063  | 28272858  | 642             | < 0.001 | 28272520; 28272479; 28272550; 28272549           | yes                        |
| Hpcal4        | 381  | 5.26            | chr4       | 122859739 | 122860478 | -705            | < 0.001 | 122859881; 122859880                             | yes                        |
| Igf2bp3       | 381  | 5.26            | chr6       | 49165518  | 49165881  | -1025           | < 0.001 | 49165683; 49165682                               | yes                        |
| Pou2f2        | 381  | 5.26            | chr7       | 25918281  | 25918686  | -965            | < 0.001 | 25918591   | yes                        |
| Cacna2d1      | 381  | 5.26            | chr5       | 15439997  | 15440330  | -346            | < 0.001 | 15439997   | no                         |
| Hnrp1         | 381  | 5.26            | chr7       | 29593539  | 29593872  | -2204           | < 0.001 | 29593539   | no                         |
| Rheb          | 382  | 5.25            | chr5       | 24348289  | 24348721  | -353            | < 0.001 | 24348904; 24348531; 24349269                     | yes                        |
| D10Erd438e    | 382  | 5.25            | chr10      | 52137141  | 52137081  | -241            | < 0.001 | 52137141   | no                         |
| Wwtr1         | 382  | 5.25            | chr3       | 57380244  | 57380544  | -594            | < 0.001 | 57379870, 57379745, 57379847                     | no                         |
| Tlx3          | 382  | 5.25            | chr11      | 33102179  | 33102095  | 1257            | < 0.001 | N/A  | no                         |
| BC005624      | 383  | 5.24            | chr2       | 30837543  | 30837588  | -160            | < 0.001 | 30837979; 30837684; 30837683                     | yes                        |
| Smpd3         | 383  | 5.24            | chr8       | 108861929 | 108862287 | -215            | < 0.001 | 108862330; 108862330                             | yes                        |
| Ppargc1b      | 384  | 5.23            | chr18      | 61558576  | 61558621  | 1487            | < 0.001 | 61560380; 61560380                               | yes                        |
| Ppp2r2c       | 384  | 5.23            | chr5       | 37260106  | 37260563  | 321             | < 0.001 | 37260106   | no                         |
| Egr1          | 385  | 5.22            | chr18      | 35020016  | 35020422  | -628            | < 0.001 | 35020459   | yes                        |
| Gabrb3        | 385  | 5.22            | chr7       | 64846708  | 64847207  | 324             | < 0.001 | 64847212; 64846730; 64846729                     | yes                        |
| Pias4         | 385  | 5.22            | chr10      | 80630047  | 80630403  | 253             | < 0.001 | 80630047   | no                         |
| Etv6          | 386  | 5.21            | chr6       | 133985469 | 133986127 | 377             | < 0.001 | 133986129; 133985764; 133986123                  | yes                        |
| Zdhhc2        | 386  | 5.21            | chr8       | 41508575  | 41509176  | -270            | < 0.001 | 41509322; 41509322                               | yes                        |
| Arid3b        | 386  | 5.21            | chr9       | 57683934  | 57684101  | -1923           | < 0.001 | 57683934   | no                         |
| Dido1         | 386  | 5.21            | chr2       | 180444403 | 180444638 | -7621           | < 0.001 | N/A  | no                         |
| Epb4.114a     | 387  | 5.2             | chr18      | 34165806  | 34166361  | 738             | < 0.001 | 34166468; 34166468                               | yes                        |
| Sf3b3         | 387  | 5.2             | chr8       | 113369864 | 113370397 | 631             | < 0.001 | 113370201  | yes                        |
| BC013481      | 387  | 5.2             | chr5       | 66542255  | 66542793  | -116            | < 0.001 | 66542670   | no                         |
| Sulf2         | 387  | 5.2             | chr2       | 165980866 | 165981075 | 262             | < 0.001 | 165981049, 165980692                             | no                         |
| Pde3b         | 388  | 5.18            | chr7       | 121558833 | 121559020 | 89              | < 0.001 | 121558912; 121558912                             | yes                        |
| Mobk1b        | 388  | 5.18            | chr6       | 83276116  | 83276267  | 106             | < 0.001 | 83276192, 83275720                               | no                         |
| Icosl         | 389  | 5.17            | chr10      | 77532388  | 77532646  | 176             | < 0.001 | 77532817   | yes                        |
| Daam2         | 389  | 5.17            | chr17      | 49702626  | 49703051  | 739             | < 0.001 | 49702609   | no                         |
| Tmem11        | 389  | 5.17            | chr11      | 60691957  | 60691884  | 554             | < 0.001 | 60692094, 60692008, 60692223, 60692082           | no                         |
| Zmym2         | 389  | 5.17            | chr14      | 57506275  | 57506320  | -332            | < 0.001 | 57506473   | no                         |
| Odz4          | 390  | 5.15            | chr7       | 103361142 | 103361202 | 2026            | < 0.001 | N/A  | no                         |
| Eef2k         | 391  | 5.14            | chr7       | 127986710 | 127987359 | 778             | < 0.001 | 127987235; 127987235                             | yes                        |
| Jup           | 391  | 5.14            | chr11      | 100256776 | 100257104 | 2252            | < 0.001 | 100256949  | yes                        |
| I500003O03Rik | 391  | 5.14            | chr2       | 119373457 | 119374014 | 368             | < 0.001 | 119373431  | no                         |
| Wbser17       | 391  | 5.14            | chr5       | 131783249 | 131783415 | 0               | < 0.001 | N/A  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Cdh24         | 392  | 5.13            | chr14      | 55260165  | 55260523  | -229            | < 0.001 | 55260496; 55260499; 55260615   | yes                        |
| Chic2         | 392  | 5.13            | chr5       | 75443087  | 75443278  | -2597           | < 0.001 | 75443226   | yes                        |
| Gpd2          | 392  | 5.13            | chr2       | 57090393  | 57090708  | -159            | < 0.001 | 57090969; 57090553; 57090553   | yes                        |
| Plcb3         | 392  | 5.13            | chr19      | 7043747   | 7044203   | 252             | < 0.001 | 7044032  | yes                        |
| Mmd           | 392  | 5.13            | chr11      | 90111015  | 90111366  | 249             | < 0.001 | 90111015   | no                         |
| 4930402H24Rik | 393  | 5.12            | chr2       | 130665974 | 130666183 | -150            | < 0.001 | 130666731; 130666731; 130666800  | yes                        |
| Bmper         | 393  | 5.12            | chr9       | 23027603  | 23027893  | 351             | < 0.001 | 23027446; 23027770; 23027452   | no                         |
| Coro1b        | 393  | 5.12            | chr19      | 4150908   | 4151239   | 2408            | < 0.001 | 4150908  | no                         |
| Arhgef10      | 393  | 5.12            | chr8       | 14911602  | 14911647  | -92             | < 0.001 | N/A  | no                         |
| Pdlim7        | 394  | 5.11            | chr13      | 55614169  | 55614732  | 435             | < 0.001 | 55614789; 55614789   | yes                        |
| Tanc1         | 394  | 5.11            | chr2       | 59451322  | 59451561  | 1436            | < 0.001 | 59451322   | no                         |
| Tnfrsf12a     | 394  | 5.11            | chr17      | 23813504  | 23814391  | 260             | < 0.001 | 23813795; 23813468   | no                         |
| Prkar1a       | 395  | 5.1             | chr11      | 109512375 | 109513396 | 304             | < 0.001 | 109512888; 109512891; 109512885; 109512884                                     | yes                        |
| Rab10         | 395  | 5.1             | chr12      | 3310084   | 3310486   | -173            | < 0.001 | 3310331; 3310246; 3310246  | yes                        |
| Vldlr         | 395  | 5.1             | chr19      | 27291700  | 27292079  | 3               | < 0.001 | 27292055; 27291848   | yes                        |
| 2700049P18Rik | 395  | 5.1             | chr1       | 133422324 | 133421940 | 1774            | < 0.001 | 133421781; 133421802; 133421951  | no                         |
| Srf           | 395  | 5.1             | chr17      | 46691961  | 46692222  | 1127            | < 0.001 | 46692143   | no                         |
| Foxf1a        | 395  | 5.1             | chr8       | 123607850 | 123608553 | -375            | < 0.001 | 123608220; 123608348   | yes                        |
| Kremen2       | 396  | 5.09            | chr17      | 23882279  | 23882719  | 248             | < 0.001 | 23882638; 23882638   | yes                        |
| Eif5a         | 396  | 5.09            | chr11      | 69734598  | 69735016  | -3              | < 0.001 | 69734741; 69734738; 69734585; 69734765; 69734747; 69734750; 69734744; 69734875 | no                         |
| Lpp           | 397  | 5.08            | chr16      | 24394018  | 24394634  | 607             | < 0.001 | 24394036; 24394098   | no                         |
| Mbnl3         | 398  | 5.07            | chrX       | 48558593  | 48559102  | 235             | < 0.001 | 48559125   | yes                        |
| Inhbb         | 398  | 5.07            | chr1       | 121318885 | 121318133 | 537             | < 0.001 | 121319306; 121319524; 121319524  | yes                        |
| Relb          | 398  | 5.07            | chr7       | 20214601  | 20215151  | -69             | < 0.001 | 20214985; 20214985   | yes                        |
| D0H4S114      | 399  | 5.06            | chr18      | 33623472  | 33623890  | -11             | < 0.001 | 33624498; 33624498; 33623631; 33623631   | yes                        |
| Igf2          | 399  | 5.06            | chr7       | 149844045 | 149845885 | -1288           | < 0.001 | 149845527; 149845720   | yes                        |
| Pdgfc         | 399  | 5.06            | chr3       | 80840715  | 80841681  | 875             | < 0.001 | 80841235   | yes                        |
| Trps1         | 399  | 5.06            | chr15      | 50720784  | 50720954  | 655             | < 0.001 | N/A  | no                         |
| Ypel4         | 399  | 5.06            | chr2       | 84582715  | 84582760  | 8378            | < 0.001 | N/A  | no                         |
| Stk39         | 400  | 5.05            | chr2       | 68309161  | 68310554  | 504             | < 0.001 | 68309469; 68309494; 68310332; 68310332; 68310533                               | yes                        |
| Tmem19        | 400  | 5.05            | chr10      | 114799442 | 114799120 | 14              | < 0.001 | 114800063; 114800066   | yes                        |
| 2810006K23Rik | 400  | 5.05            | chr5       | 124778046 | 124778091 | -29             | < 0.001 | 124778136; 124778013   | no                         |
| Wipf2         | 400  | 5.05            | chr11      | 98725425  | 98725591  | 444             | < 0.001 | 98725264; 98725266; 98725315; 98725342   | no                         |
| Msh6          | 401  | 5.04            | chr17      | 88374662  | 88374825  | 261             | < 0.001 | 88374918; 88374917   | yes                        |
| Ppp2r1a       | 401  | 5.04            | chr17      | 21082517  | 21082721  | 123             | < 0.001 | 21082517   | no                         |
| Rspo1         | 401  | 5.04            | chr4       | 124662308 | 124663155 | -883            | < 0.001 | 124662219  | no                         |
| E230022H04Rik | 402  | 5.02            | chr18      | 31920138  | 31920183  | 627             | < 0.001 | 31920425   | yes                        |
| Rgag4         | 402  | 5.02            | chrX       | 99265848  | 99266418  | 770             | < 0.001 | 99266489   | yes                        |
| Lrrc3         | 402  | 5.02            | chr10      | 77365418  | 77365728  | -159            | < 0.001 | 77365500; 77365278   | no                         |
| Pjal          | 403  | 4.99            | chrX       | 96665570  | 96665989  | 108             | < 0.001 | N/A  | no                         |
| Zfp3611       | 404  | 4.98            | chr12      | 81214980  | 81216163  | -1322           | < 0.001 | 81216078   | yes                        |
| 2900073G15Rik | 404  | 4.98            | chr17      | 71351873  | 71352192  | -291            | < 0.001 | 71352040; 71352103   | yes                        |
| Aebp1         | 404  | 4.98            | chr11      | 5761539   | 5761330   | -88             | < 0.001 | 5761539  | no                         |
| Padi2         | 404  | 4.98            | chr4       | 140462651 | 140462923 | 402             | < 0.001 | 140462651  | no                         |
| Wdr23         | 404  | 4.98            | chr14      | 56179566  | 56179791  | 722             | < 0.001 | 56179668   | no                         |
| Wwc2          | 405  | 4.97            | chr8       | 49076064  | 49076419  | -317            | < 0.001 | 49076249   | yes                        |
| Tmc6          | 406  | 4.96            | chr11      | 117640684 | 117640983 | 1090            | < 0.001 | N/A  | no                         |
| 9130227C08Rik | 407  | 4.95            | chr14      | 56503797  | 56504117  | 15              | < 0.001 | 56503960; 56504125; 56503960; 56504128   | yes                        |
| Tefe3         | 407  | 4.95            | chrX       | 7340437   | 7340991   | 1068            | < 0.001 | N/A  | no                         |
| Tle1          | 407  | 4.95            | chr4       | 71861536  | 71861765  | 395             | < 0.001 | N/A  | no                         |
| Leprel2       | 408  | 4.93            | chr6       | 124806558 | 124807411 | 629             | < 0.001 | 124806655  | yes                        |
| Dctn6         | 408  | 4.93            | chr8       | 35171140  | 35171417  | 103             | < 0.001 | 35171346   | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Midn          | 408  | 4.93            | chr10      | 79611757  | 79611980  | 924             | < 0.001 | 79611757   | no                         |
| Pfkp          | 408  | 4.93            | chr13      | 6647781   | 6647942   | 51              | < 0.001 | 6647755  | no                         |
| Fgfr3         | 409  | 4.92            | chr5       | 34064468  | 34064972  | 236             | < 0.001 | 34064509   | yes                        |
| Ppp1r9b       | 409  | 4.92            | chr11      | 94853879  | 94854310  | 1629            | < 0.001 | 94854205; 94854205   | yes                        |
| Dusp6         | 409  | 4.92            | chr10      | 98725164  | 98725613  | -278            | < 0.001 | 98724644, 98725087, 98725092, 98724439, 98724643, 98725396, 98724430   | no                         |
| Syvn1         | 409  | 4.92            | chr19      | 6046613   | 6046849   | 165             | < 0.001 | 6046613  | no                         |
| Alcam         | 410  | 4.9             | chr16      | 52452310  | 52452702  | 550             | < 0.001 | 52452393   | yes                        |
| Tbc1d2b       | 410  | 4.9             | chr9       | 90164939  | 90165411  | 641             | < 0.001 | 90165229   | no                         |
| Hoxd11        | 410  | 4.9             | chr2       | 74519648  | 74520583  | -152            | < 0.001 | 74520044   | yes                        |
| Ptn           | 411  | 4.89            | chr6       | 36760031  | 36760353  | 1035            | < 0.001 | 36759990, 36759943, 36760217   | no                         |
| Zfp148        | 411  | 4.89            | chr16      | 33381561  | 33381736  | 724             | < 0.001 | 33381561   | no                         |
| Ust           | 411  | 4.89            | chr10      | 8238334   | 8238633   | 267             | < 0.001 | N/A  | no                         |
| D230005D02Rik | 412  | 4.88            | chr14      | 77557088  | 77557301  | 488             | < 0.001 | 77557088   | no                         |
| E130014J05Rik | 412  | 4.88            | chr3       | 133207920 | 133208200 | -588            | < 0.001 | N/A  | no                         |
| Ldlrap1       | 413  | 4.87            | chr4       | 134323115 | 134323630 | 539             | < 0.001 | 134324115; 134324118   | yes                        |
| A630054L15Rik | 413  | 4.87            | chr14      | 27399494  | 27399677  | 601             | < 0.001 | 27399338   | no                         |
| Zfyve21       | 413  | 4.87            | chr12      | 113054524 | 113054709 | 2206            | < 0.001 | 113054524  | no                         |
| Pygo1         | 413  | 4.87            | chr9       | 72773727  | 72773986  | 294             | < 0.001 | N/A  | no                         |
| Fjx1          | 414  | 4.86            | chr2       | 102292363 | 102292412 | -439            | < 0.001 | 102292399; 102292385   | yes                        |
| 2310005N03Rik | 414  | 4.86            | chr1       | 180248794 | 180248839 | -467            | < 0.001 | 180249200; 180249200   | yes                        |
| Hfm1          | 415  | 4.85            | chr5       | 107354836 | 107355472 | -81             | < 0.001 | 107355428  | yes                        |
| Sdcbp         | 415  | 4.85            | chr4       | 6292974   | 6293391   | 348             | < 0.001 | 6293015  | yes                        |
| Rps10         | 415  | 4.85            | chr17      | 27773770  | 27773820  | -1608           | < 0.001 | 27773936; 27773936   | yes                        |
| Crim1         | 415  | 4.85            | chr17      | 78599189  | 78601018  | -26             | < 0.001 | 78600020, 78600023, 78599366, 78600473, 78599939, 78599936, 78599297, 78599541, 78599200, 78599774, 78599880, 78599945, 78600582, 78599498, 78600088, 78600091, 78599425, 78600014, 78599642 | no                         |
| Fign          | 415  | 4.85            | chr2       | 63936624  | 63936824  | -734            | < 0.001 | 63936508   | no                         |
| Phf12         | 415  | 4.85            | chr11      | 77797218  | 77797947  | 852             | < 0.001 | 77797218   | no                         |
| Satb2         | 416  | 4.84            | chr1       | 57029173  | 57029053  | -852            | < 0.001 | 57030638; 57029240; 57030653; 57030653; 57029240   | yes                        |
| Trp53i11      | 416  | 4.84            | chr2       | 93027427  | 93027748  | -288            | < 0.001 | 93027882   | yes                        |
| Snapc2        | 416  | 4.84            | chr8       | 4253502   | 4253661   | 535             | < 0.001 | 4253572, 4253323, 4253317, 4253436, 4253559  | no                         |
| Zbtb7c        | 416  | 4.84            | chr18      | 75979393  | 75979716  | -409            | < 0.001 | 75979566, 75979656, 75979530   | no                         |
| Crk           | 417  | 4.83            | chr11      | 75493062  | 75493537  | 463             | < 0.001 | 75493466; 75493113; 75493113   | yes                        |
| Osbpl5        | 417  | 4.83            | chr7       | 150925452 | 150925894 | 2132            | < 0.001 | 150925837, 150924691   | no                         |
| Zfp143        | 417  | 4.83            | chr7       | 117204705 | 117204757 | -484            | < 0.001 | 117204881  | yes                        |
| Tpd52l1       | 418  | 4.82            | chr10      | 31165205  | 31165483  | 499             | < 0.001 | 31165224; 31165589; 31165224   | yes                        |
| BC021881      | 418  | 4.82            | chr13      | 117814004 | 117814364 | 294             | < 0.001 | N/A  | no                         |
| 1110054O05Rik | 419  | 4.81            | chr4       | 59799694  | 59799874  | -2989           | < 0.001 | 59799885   | yes                        |
| Gpsm3         | 419  | 4.81            | chr17      | 34728329  | 34728513  | 1597            | < 0.001 | N/A  | no                         |
| Bach2         | 420  | 4.8             | chr4       | 32325550  | 32326252  | -242            | < 0.001 | 32326064   | yes                        |
| Atp2b1        | 420  | 4.8             | chr10      | 98378400  | 98378277  | 171             | < 0.001 | 98378849; 98378865; 98378489; 98378489; 98378576; 98378575   | yes                        |
| Golph2        | 420  | 4.8             | chr13      | 59776523  | 59777478  | -129            | < 0.001 | 59777186   | yes                        |
| Grb14         | 420  | 4.8             | chr2       | 64860180  | 64861175  | 111             | < 0.001 | 64861077; 64861077; 64861066; 64861083; 64861083   | yes                        |
| Igfbp2        | 420  | 4.8             | chr1       | 72870420  | 72870855  | -368            | < 0.001 | 72871858, 72870318, 72870931, 72870946, 72870950, 72870891, 72870935, 72870321, 72870961, 72870963   | no                         |
| Tusc3         | 420  | 4.8             | chr8       | 40069097  | 40069489  | 544             | < 0.001 | 40069486; 40069154; 40069153   | yes                        |
| 6430527G18Rik | 421  | 4.79            | chr12      | 88224806  | 88225141  | 771             | < 0.001 | 88225142; 88224957; 88224956   | yes                        |
| Metnl         | 421  | 4.79            | chr11      | 121563705 | 121564015 | -12             | < 0.001 | 121563852; 121563852   | yes                        |
| Rhobtb3       | 421  | 4.79            | chr13      | 76080946  | 76081607  | -98             | < 0.001 | 76081459; 76081387; 76081403   | yes                        |
| Kpna1         | 421  | 4.79            | chr16      | 35983190  | 35983468  | -228            | < 0.001 | 35983387   | no                         |
| Xpo1          | 421  | 4.79            | chr11      | 23156809  | 23157077  | 1007            | < 0.001 | N/A  | no                         |
| Actg1         | 422  | 4.78            | chr11      | 120211623 | 120211785 | -1964           | < 0.001 | 120212751; 120213057   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                                | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Gpr81         | 422  | 4.78            | chr5       | 124329917 | 124330107 | -72             | < 0.001 | 124329917  | no                         |
| Laptm5        | 422  | 4.78            | chr4       | 130465053 | 130465241 | -4034           | < 0.001 | 130465053  | no                         |
| Zdhhc20       | 423  | 4.77            | chr14      | 58508582  | 58508963  | 159             | < 0.001 | 58508873   | yes                        |
| E330009J07Rik | 423  | 4.77            | chr6       | 40385320  | 40385873  | 784             | < 0.001 | 40385976   | yes                        |
| Mapk9         | 423  | 4.77            | chr11      | 49660665  | 49661225  | 650             | < 0.001 | 49661258; 49661257   | yes                        |
| Car11         | 423  | 4.77            | chr7       | 52955835  | 52956092  | 522             | < 0.001 | 52962335, 52961521, 52961434   | no                         |
| Mxra8         | 423  | 4.77            | chr4       | 155213761 | 155214147 | 125             | < 0.001 | 155213822, 155213930   | no                         |
| Npdcl         | 424  | 4.76            | chr2       | 25258199  | 25258571  | -175            | < 0.001 | 25258747   | yes                        |
| Xrn2          | 424  | 4.76            | chr2       | 146838724 | 146839192 | 119             | < 0.001 | 146839306; 146839309   | yes                        |
| Ppfbp1        | 425  | 4.75            | chr6       | 146837166 | 146837211 | 153             | < 0.001 | 146837309  | yes                        |
| Rtkn          | 425  | 4.75            | chr6       | 83085678  | 83085978  | -1126           | < 0.001 | 83086089   | yes                        |
| Hoxd9         | 425  | 4.75            | chr2       | 74536394  | 74536995  | 981             | < 0.001 | 74536490, 74536578, 74536466, 74536251, 74536382                     | no                         |
| Six4          | 425  | 4.75            | chr12      | 74213237  | 74213712  | 972             | < 0.001 | 74213112, 74213061   | no                         |
| Tmem16f       | 425  | 4.75            | chr15      | 95621053  | 95621270  | -195            | < 0.001 | 95621236, 95621215, 95621242   | no                         |
| Tmtc2         | 425  | 4.75            | chr10      | 105011424 | 105011585 | 359             | < 0.001 | 105011597  | no                         |
| Calm1         | 426  | 4.74            | chr12      | 101438774 | 101439053 | 1046            | < 0.001 | 101438964; 101438964   | yes                        |
| Ldhb          | 426  | 4.74            | chr6       | 142456328 | 142456663 | -63             | < 0.001 | 142457099  | yes                        |
| Tubb5         | 426  | 4.74            | chr17      | 35974396  | 35974456  | 751             | < 0.001 | 35974438   | yes                        |
| Chka          | 427  | 4.73            | chr19      | 3851424   | 3852236   | 78              | < 0.001 | 3851960  | yes                        |
| Wee1          | 427  | 4.73            | chr7       | 117265588 | 117266265 | 354             | < 0.001 | 117266358; 117266103   | yes                        |
| Sh3tc2        | 427  | 4.73            | chr18      | 62112255  | 62112647  | -104            | < 0.001 | 62112575   | no                         |
| Ube2d3        | 427  | 4.73            | chr3       | 135101384 | 135101547 | -314            | < 0.001 | 135101450  | no                         |
| Atp8b1        | 428  | 4.71            | chr18      | 64820245  | 64820915  | 122             | < 0.001 | 64820370   | yes                        |
| Eed           | 428  | 4.71            | chr7       | 97128456  | 97128960  | 886             | < 0.001 | 97128651   | no                         |
| Eif4ebp1      | 428  | 4.71            | chr8       | 28371727  | 28371903  | 953             | < 0.001 | 28371554   | no                         |
| Pip5k2c       | 428  | 4.71            | chr10      | 126636116 | 126636005 | 12458           | < 0.001 | N/A  | no                         |
| Senn1g        | 429  | 4.7             | chr7       | 128878166 | 128878453 | 294             | < 0.001 | 128878433  | yes                        |
| Zfp316        | 429  | 4.7             | chr5       | 144031254 | 144031446 | 194             | < 0.001 | 144031350; 144031445; 144031445                                      | yes                        |
| 2210010L05Rik | 429  | 4.7             | chr1       | 52783434  | 52783709  | 476             | < 0.001 | 52783522, 52783939, 52783366, 52783933, 52783790, 52783797, 52783708 | no                         |
| Hoxd10        | 429  | 4.7             | chr2       | 74525395  | 74526090  | -4194           | < 0.001 | 74525931, 74525513   | no                         |
| Setd7         | 429  | 4.7             | chr3       | 51364536  | 51364968  | -21             | < 0.001 | 128878232  | no                         |
| Cdc69         | 429  | 4.7             | chr11      | 54891047  | 54891245  | 411             | < 0.001 | N/A  | no                         |
| Usp28         | 430  | 4.69            | chr9       | 48793374  | 48794080  | 399             | < 0.001 | 48793815; 48793627; 48793449; 48793449; 48793658                     | yes                        |
| Ppp2r5b       | 430  | 4.69            | chr19      | 6233771   | 6233936   | 2046            | < 0.001 | 6233771  | no                         |
| Rbms3         | 430  | 4.69            | chr9       | 117162749 | 117162800 | -1177           | < 0.001 | 117162749  | no                         |
| Sh3bgrl3      | 431  | 4.68            | chr4       | 133684961 | 133685134 | -317            | < 0.001 | 133684961  | no                         |
| Vac14         | 431  | 4.68            | chr8       | 113142668 | 113142874 | 313             | < 0.001 | 113142706  | no                         |
| Ddx11         | 431  | 4.68            | chr17      | 66473037  | 66473247  | 358             | < 0.001 | 66473251; 66473251   | yes                        |
| Elf1          | 432  | 4.67            | chr14      | 79880949  | 79880994  | -28             | < 0.001 | 79880905   | no                         |
| Gabra4        | 433  | 4.65            | chr5       | 72048292  | 72049893  | -128            | < 0.001 | 72048197   | no                         |
| Inpp5f        | 433  | 4.65            | chr7       | 135754416 | 135754595 | -306            | < 0.001 | 135754416  | no                         |
| Sncap         | 433  | 4.65            | chr18      | 52927766  | 52927928  | 426             | < 0.001 | 52927894   | yes                        |
| Serinc2       | 433  | 4.65            | chr4       | 129951574 | 129951804 | 1052            | < 0.001 | N/A  | no                         |
| Usp11         | 434  | 4.64            | chrX       | 20281290  | 20281663  | 281             | < 0.001 | 20281800   | yes                        |
| Scd2          | 434  | 4.64            | chr19      | 44369288  | 44369339  | 737             | < 0.001 | 44369383; 44369383   | yes                        |
| Dyrk2         | 434  | 4.64            | chr10      | 118306688 | 118306740 | -755            | < 0.001 | 118306688  | no                         |
| Pin1          | 435  | 4.63            | chr9       | 20456272  | 20456457  | -139            | < 0.001 | 20456633   | yes                        |
| Gpr124        | 435  | 4.63            | chr8       | 28196115  | 28196276  | -174            | < 0.001 | 28195981, 28196047, 28196108   | no                         |
| Socs1         | 435  | 4.63            | chr16      | 10785131  | 10785901  | -89             | < 0.001 | 10785388, 10785683, 10785382   | no                         |
| Ddx5          | 436  | 4.62            | chr11      | 106649658 | 106649703 | 128             | < 0.001 | 106649927  | yes                        |
| Mgat4b        | 436  | 4.62            | chr11      | 50038324  | 50038496  | -787            | < 0.001 | 50038383; 50038386   | yes                        |
| Zfp238        | 436  | 4.62            | chr1       | 179373229 | 179372896 | -1539           | < 0.001 | 179373501  | yes                        |
| Aprt          | 436  | 4.62            | chr8       | 125100387 | 125100793 | 287             | < 0.001 | 125100387  | no                         |
| Hoxa10        | 436  | 4.62            | chr6       | 52184912  | 52185132  | 10              | < 0.001 | 52184769, 52184753, 52184775   | no                         |
| Ccn11         | 437  | 4.61            | chr3       | 65761070  | 65762137  | 819             | < 0.001 | 65761814; 65762188; 65762188; 65761604; 65761603                     | yes                        |
| Hdac2         | 437  | 4.61            | chr10      | 36695100  | 36695015  | 431             | < 0.001 | 36695414; 36695506; 36695506   | yes                        |
| Ptov1         | 437  | 4.61            | chr7       | 52124141  | 52124739  | 580             | < 0.001 | 52124221; 52124536   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene                  | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                      | WT1 Consensus Site Present |
|-----------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| 4933421E11Rik         | 437  | 4.61            | chr3       | 106524955 | 106525012 | 385             | < 0.001 | 106524942, 106525051                                       | no                         |
| B3gnt2                | 438  | 4.6             | chr11      | 22759831  | 22760338  | -174            | < 0.001 | 22759950; 22760186   | yes                        |
| Klf15                 | 438  | 4.6             | chr6       | 90412019  | 90412286  | -361            | < 0.001 | 90412019   | no                         |
| Nin                   | 438  | 4.6             | chr12      | 71212459  | 71212907  | -8641           | < 0.001 | 71212835; 71212643; 71212838                               | yes                        |
| Spag8                 | 439  | 4.59            | chr4       | 43664480  | 43664525  | 1922            | < 0.001 | 43664480   | no                         |
| ENSMUST0000010037.3.1 | 439  | 4.59            | chr2       | 20890076  | 20890420  | -478            | < 0.001 | 20890468; 20890467   | yes                        |
| Enpp1                 | 440  | 4.58            | chr10      | 24432089  | 24432016  | -85             | < 0.001 | 24432175; 24432178   | yes                        |
| Peaf                  | 440  | 4.58            | chr17      | 53706456  | 53706912  | 251             | < 0.001 | 53706746; 53706746; 53706897                               | yes                        |
| Galnt7                | 441  | 4.57            | chr8       | 60131634  | 60131795  | 28              | < 0.001 | 60131709   | yes                        |
| Cd302                 | 441  | 4.57            | chr2       | 60121880  | 60122312  | 573             | < 0.001 | 60122461   | yes                        |
| 1810030007Rik         | 441  | 4.57            | chrX       | 12250526  | 12250936  | 124             | < 0.001 | 12250837, 12250716, 12250681                               | no                         |
| Bbc3                  | 441  | 4.57            | chr7       | 16895637  | 16896014  | 1002            | < 0.001 | 16895648, 16895752, 16895620, 16895617, 16895604, 16895623 | no                         |
| Agpat3                | 442  | 4.56            | chr10      | 77815379  | 77815697  | -957            | < 0.001 | 77815380; 77815380   | yes                        |
| Dync1li2              | 442  | 4.56            | chr8       | 106966424 | 106966469 | 459             | < 0.001 | 106966424  | no                         |
| Lrrc42                | 442  | 4.56            | chr4       | 106925356 | 106925582 | 578             | < 0.001 | 106925504  | no                         |
| BC005537              | 443  | 4.55            | chr13      | 24893097  | 24893700  | 29              | < 0.001 | 24893795; 24893819; 24893818                               | yes                        |
| Gse1                  | 443  | 4.55            | chr8       | 123012258 | 123012445 | -483            | < 0.001 | 123012066  | no                         |
| Nrf1                  | 443  | 4.55            | chr6       | 29998820  | 29999001  | 991             | < 0.001 | 29998703, 29998642, 29998621, 29998935                     | no                         |
| Wdtd1                 | 444  | 4.54            | chr4       | 132895180 | 132895419 | 28              | < 0.001 | 132895288  | yes                        |
| Bai1                  | 444  | 4.54            | chr15      | 74346178  | 74346878  | 45              | < 0.001 | 74346905; 74346446; 74346445                               | yes                        |
| Usp5                  | 444  | 4.54            | chr6       | 124779296 | 124779341 | 147             | < 0.001 | 124779296  | no                         |
| Clstn1                | 445  | 4.53            | chr4       | 148961706 | 148961926 | 1154            | < 0.001 | 148962108; 148962107                                       | yes                        |
| Siah2                 | 445  | 4.53            | chr3       | 58496413  | 58496813  | -354            | < 0.001 | 58496532; 58496532; 58496678; 58496532                     | yes                        |
| D030011010Rik         | 445  | 4.53            | chr6       | 149049572 | 149049775 | 606             | < 0.001 | 149049572  | no                         |
| Ube2r2                | 445  | 4.53            | chr4       | 41083112  | 41083452  | 81              | < 0.001 | 41083355, 41083085, 41083071, 41083088, 41082965           | no                         |
| Lfng                  | 446  | 4.52            | chr5       | 141082442 | 141082654 | -663            | < 0.001 | 141082691  | yes                        |
| Stau1                 | 446  | 4.52            | chr2       | 166820990 | 166821445 | 590             | < 0.001 | 166821315  | no                         |
| Crsp2                 | 447  | 4.51            | chrX       | 12339112  | 12339644  | -35             | < 0.001 | 12339477   | yes                        |
| Orc3l                 | 447  | 4.51            | chr4       | 34561937  | 34562092  | 233             | < 0.001 | 34561937   | no                         |
| Olfrl323              | 447  | 4.51            | chrX       | 47365442  | 47365704  | -2060           | < 0.001 | N/A  | no                         |
| Tpm4                  | 448  | 4.5             | chr8       | 74659216  | 74659364  | 152             | < 0.001 | 74659334   | yes                        |
| Impa2                 | 448  | 4.5             | chr18      | 67449049  | 67449094  | 196             | < 0.001 | 67449418; 67449418   | yes                        |
| 2610027C15Rik         | 448  | 4.5             | chr4       | 125824948 | 125825193 | -276            | < 0.001 | 125825093  | no                         |
| Baz2b                 | 448  | 4.5             | chr2       | 59963598  | 59963648  | 174             | < 0.001 | 59963538, 59963478, 59963486                               | no                         |
| Gas1                  | 448  | 4.5             | chr13      | 60278795  | 60278852  | -98             | < 0.001 | 60278788   | no                         |
| Sod3                  | 448  | 4.5             | chr5       | 52754533  | 52755360  | -370            | < 0.001 | 52755137, 52754912   | no                         |
| Usp9x                 | 448  | 4.5             | chrX       | 12649526  | 12650318  | 1083            | < 0.001 | 12650481; 12650458; 12650007; 12650006                     | yes                        |
| Fusip1                | 448  | 4.5             | chr4       | 135411913 | 135412846 | 202             | < 0.001 | 135412431; 135412623                                       | yes                        |
| Anks1                 | 449  | 4.49            | chr17      | 28046337  | 28046723  | 76              | < 0.001 | 28046406   | yes                        |
| Rad54l2               | 450  | 4.47            | chr9       | 106690522 | 106690861 | 998             | < 0.001 | 106690705  | yes                        |
| Cdh11                 | 450  | 4.47            | chr8       | 105309277 | 105309691 | -489            | < 0.001 | 105309162  | no                         |
| Itga5                 | 450  | 4.47            | chr15      | 103196073 | 103196778 | 704             | < 0.001 | 103196375, 103195967                                       | no                         |
| Kcns3                 | 450  | 4.47            | chr12      | 11157270  | 11157846  | -351            | < 0.001 | 11157463, 11157085, 11157079                               | no                         |
| Rmnd1                 | 450  | 4.47            | chr10      | 5916639   | 5916878   | 2460            | < 0.001 | 5916730  | no                         |
| Kcns2                 | 451  | 4.46            | chr15      | 34767119  | 34767825  | 7               | < 0.001 | 34767467   | yes                        |
| Ras110b               | 451  | 4.46            | chr11      | 83223001  | 83223225  | -549            | < 0.001 | 83223149, 83223042, 83223158, 83223049                     | no                         |
| Egff9                 | 451  | 4.46            | chr17      | 46434422  | 46434467  | 75              | < 0.001 | N/A  | no                         |
| Fbxo32                | 452  | 4.45            | chr15      | 58046562  | 58046916  | -345            | < 0.001 | 58046483, 58046485, 58046477, 58046482                     | no                         |
| Lcorl                 | 452  | 4.45            | chr5       | 46247624  | 46247838  | 144             | < 0.001 | 46247624   | no                         |
| Prr15                 | 452  | 4.45            | chr6       | 54277297  | 54277992  | 505             | < 0.001 | 54277864, 54277229   | no                         |
| BC057022              | 453  | 4.44            | chr5       | 115021439 | 115021484 | 3203            | < 0.001 | 115021825  | yes                        |
| Cltc                  | 453  | 4.44            | chr11      | 86571183  | 86571860  | -560            | < 0.001 | 86571797   | yes                        |
| Hoxa4                 | 453  | 4.44            | chr6       | 52140959  | 52141019  | 713             | < 0.001 | 52141133, 52141131, 52141115                               | no                         |
| Plekha2               | 453  | 4.44            | chr8       | 26212043  | 26212088  | 138             | < 0.001 | 26212256   | no                         |
| Lrp8                  | 453  | 4.44            | chr4       | 107474320 | 107474547 | -517            | < 0.001 | N/A  | no                         |
| Thns12                | 453  | 4.44            | chr6       | 71093909  | 71094057  | 437             | < 0.001 | N/A  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Gnai1         | 454  | 4.43            | chr5       | 17866634  | 17866916  | -430            | < 0.001 | 17866682; 17866682                     | yes                        |
| AW548124      | 454  | 4.43            | chr17      | 83613490  | 83614123  | -644            | < 0.001 | 83613586                               | no                         |
| Car15         | 454  | 4.43            | chr16      | 17835728  | 17836105  | 2389            | < 0.001 | 17835728                               | no                         |
| Man1a         | 454  | 4.43            | chr10      | 53796079  | 53796318  | -504            | < 0.001 | 53796227                               | no                         |
| Mtss1         | 454  | 4.43            | chr15      | 58912323  | 58912527  | 1046            | < 0.001 | 58912428                               | no                         |
| Wdr1          | 454  | 4.43            | chr5       | 38952316  | 38952472  | 492             | < 0.001 | 38952226                               | no                         |
| Hmga2         | 454  | 4.43            | chr10      | 119911676 | 119911836 | 2293            | < 0.001 | 119911802                              | yes                        |
| Slc6a9        | 455  | 4.42            | chr4       | 117507699 | 117508024 | 13              | < 0.001 | 117508003                              | yes                        |
| Rrad          | 455  | 4.42            | chr8       | 107154872 | 107155237 | 325             | < 0.001 | 107154872                              | no                         |
| Arid1a        | 455  | 4.42            | chr4       | 133313088 | 133313593 | -3590           | < 0.001 | N/A                                    | no                         |
| Cys1          | 455  | 4.42            | chr12      | 25365988  | 25366336  | 349             | < 0.001 | N/A                                    | no                         |
| Cd24a         | 456  | 4.41            | chr10      | 43298507  | 43299162  | 166             | < 0.001 | 43299079; 43299023; 43299395; 43299395 | yes                        |
| Slc2a12       | 456  | 4.41            | chr10      | 22364807  | 22365200  | 242             | < 0.001 | 22365400                               | yes                        |
| Epn3          | 456  | 4.41            | chr11      | 94360501  | 94361087  | 485             | < 0.001 | 94360319; 94360324; 94361026; 94360330 | no                         |
| Scamp1        | 456  | 4.41            | chr13      | 95055651  | 95055704  | -442            | < 0.001 | 95055651                               | no                         |
| Runx1         | 457  | 4.4             | chr16      | 92697152  | 92697330  | 399             | < 0.001 | 92697394; 92697394                     | yes                        |
| 2310016M24Rik | 457  | 4.4             | chr15      | 99555501  | 99555561  | -546            | < 0.001 | 99555501                               | no                         |
| Narg1         | 457  | 4.4             | chr3       | 51220820  | 51220866  | 780             | < 0.001 | 51220820                               | no                         |
| Spsb4         | 458  | 4.39            | chr9       | 96918644  | 96919073  | -126            | < 0.001 | 96918900                               | yes                        |
| Ppp2r5e       | 458  | 4.39            | chr12      | 76696396  | 76696950  | 387             | < 0.001 | 76696572; 76696893; 76696575; 76696569 | yes                        |
| Dusp4         | 458  | 4.39            | chr8       | 35870340  | 35870515  | -171            | < 0.001 | 35870340                               | no                         |
| Ptpn5         | 459  | 4.38            | chr7       | 54387791  | 54388490  | 780             | < 0.001 | 54387980; 54388353                     | yes                        |
| Sgcb          | 459  | 4.38            | chr5       | 74042368  | 74042911  | -3614           | < 0.001 | 74042818                               | yes                        |
| Gpr126        | 460  | 4.37            | chr10      | 14264835  | 14265035  | -170            | < 0.001 | 14265165                               | yes                        |
| Mettl9        | 460  | 4.37            | chr7       | 128177892 | 128178229 | 94              | < 0.001 | 128178330; 128178333                   | yes                        |
| St6galnac5    | 460  | 4.37            | chr3       | 152644009 | 152644662 | 947             | < 0.001 | 152644267; 152644474                   | yes                        |
| Utx           | 460  | 4.37            | chrX       | 17741044  | 17741577  | 1755            | < 0.001 | 17741350; 17741330                     | no                         |
| Megf9         | 461  | 4.36            | chr4       | 70197620  | 70197929  | -1688           | < 0.001 | 70197620                               | no                         |
| Wdr46         | 461  | 4.36            | chr17      | 34078066  | 34078111  | 421             | < 0.001 | 34078066                               | no                         |
| Mical1        | 462  | 4.35            | chr10      | 41197249  | 41197180  | 1216            | < 0.001 | 41197354                               | yes                        |
| Patz1         | 462  | 4.35            | chr11      | 3192132   | 3192053   | 1564            | < 0.001 | 3192132                                | no                         |
| BC030378      | 462  | 4.35            | chr15      | 96471902  | 96472318  | -252            | < 0.001 | 96472157                               | yes                        |
| Kcnk3         | 462  | 4.35            | chr5       | 30889596  | 30889990  | -576            | < 0.001 | N/A                                    | no                         |
| Smad6         | 463  | 4.34            | chr9       | 63870056  | 63870384  | -1103           | < 0.001 | 63870022; 63870008                     | no                         |
| Edg5          | 464  | 4.33            | chr9       | 20780150  | 20780678  | 917             | < 0.001 | 20780611; 20780610                     | yes                        |
| Ankrd15       | 465  | 4.32            | chr19      | 25312676  | 25312951  | 1235            | < 0.001 | 25312676                               | no                         |
| Yrdc          | 465  | 4.32            | chr4       | 124527182 | 124527556 | -821            | < 0.001 | 124527182                              | no                         |
| Gpr45         | 466  | 4.31            | chr1       | 43010157  | 43010377  | 373             | < 0.001 | 43010862                               | yes                        |
| Ifngr1        | 466  | 4.31            | chr10      | 19311282  | 19311334  | -455            | < 0.001 | 19311669; 19311672                     | yes                        |
| Mertk         | 466  | 4.31            | chr2       | 25312676  | 128524274 | -484            | < 0.001 | 25312676                               | no                         |
| Parva         | 466  | 4.31            | chr7       | 124527182 | 119571581 | 173             | < 0.001 | 124527182                              | no                         |
| Zfp691        | 466  | 4.31            | chr4       | 25312676  | 118846562 | 165             | < 0.001 | 25312676                               | no                         |
| 1700020C11Rik | 467  | 4.3             | chr11      | 3995090   | 3995361   | 97              | < 0.001 | 3995404; 3995404                       | yes                        |
| Ttyh2         | 467  | 4.3             | chr11      | 114537181 | 114537451 | 423             | < 0.001 | 114537181                              | no                         |
| Ubr1          | 467  | 4.3             | chr2       | 120795970 | 120796254 | 219             | < 0.001 | 120795970                              | no                         |
| Spa17         | 468  | 4.29            | chr9       | 37420985  | 37421191  | 191             | < 0.001 | 37421131                               | yes                        |
| Zc3h7a        | 468  | 4.29            | chr16      | 11176059  | 11176248  | 299             | < 0.001 | 11176397                               | yes                        |
| Cacng2        | 468  | 4.29            | chr15      | 77950039  | 77950203  | -470            | < 0.001 | 77949972; 77949969; 77950005           | no                         |
| Cdh22         | 468  | 4.29            | chr2       | 165061020 | 165061440 | -1029           | < 0.001 | 165061020                              | no                         |
| Uchl3         | 468  | 4.29            | chr14      | 102052989 | 102053160 | -168            | < 0.001 | N/A                                    | no                         |
| Lrrc8b        | 469  | 4.28            | chr5       | 105844006 | 105844619 | -531            | < 0.001 | 105844006                              | no                         |
| Dnm1          | 469  | 4.28            | chr2       | 32173566  | 32174026  | 35236           | < 0.001 | N/A                                    | no                         |
| 0710008K08Rik | 470  | 4.27            | chr8       | 11497566  | 11497847  | 119             | < 0.001 | 11497817                               | yes                        |
| Fhod1         | 470  | 4.27            | chr8       | 107870866 | 107871140 | 713             | < 0.001 | 107870866                              | no                         |
| Gsto1         | 471  | 4.26            | chr19      | 47929479  | 47929653  | 24              | < 0.001 | 47929639                               | yes                        |
| Sipa1         | 471  | 4.26            | chr19      | 5663337   | 5663386   | 258             | < 0.001 | 5663337                                | no                         |
| D15Mgi27      | 471  | 4.26            | chr15      | 102100868 | 102101071 | -8838           | < 0.001 | 102101133; 102101136                   | yes                        |
| D1Erd622e     | 472  | 4.25            | chr1       | 99558143  | 99558073  | 136             | < 0.001 | 99558486                               | yes                        |
| Tmem106c      | 473  | 4.24            | chr15      | 97794876  | 97795060  | 329             | < 0.001 | 97795032; 97794879                     | yes                        |
| Dmpk          | 473  | 4.24            | chr7       | 19668310  | 19669086  | -1006           | < 0.001 | N/A                                    | no                         |
| Cyp2d22       | 474  | 4.22            | chr15      | 82210496  | 82210651  | -4067           | < 0.001 | 82210496                               | no                         |



**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene                  | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|-----------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Gria3                 | 474  | 4.22            | chrX       | 38753273  | 38753324  | -1182           | < 0.001 | 38753273   | no                         |
| Shoc2                 | 474  | 4.22            | chr19      | 54018617  | 54018809  | -584            | < 0.001 | 54018617   | no                         |
| Cebpa                 | 475  | 4.21            | chr7       | 35903869  | 35903922  | -415            | < 0.001 | 35904248   | yes                        |
| Zfp503                | 475  | 4.21            | chr14      | 22805389  | 22805704  | 3304            | < 0.001 | 22805652; 22805655; 22805670; 22805669   | yes                        |
| Notch1                | 475  | 4.21            | chr2       | 26358537  | 26358854  | 325             | < 0.001 | 26359271; 26358729; 26358729   | yes                        |
| Osbpl9                | 475  | 4.21            | chr4       | 108790484 | 108790529 | 18              | < 0.001 | 108790834  | yes                        |
| Fgf20                 | 475  | 4.21            | chr8       | 41371379  | 41371618  | 465             | < 0.001 | N/A  | no                         |
| Zc3h13                | 476  | 4.2             | chr14      | 75683917  | 75684379  | -235            | < 0.001 | 75684188; 75684342; 75684342; 75684188   | yes                        |
| Adprh                 | 476  | 4.2             | chr16      | 38452240  | 38452536  | 370             | < 0.001 | 38452240   | no                         |
| Col4a3bp              | 476  | 4.2             | chr13      | 97312886  | 97312931  | 208             | < 0.001 | 97312951, 97313081, 97312962, 97312945, 97312948   | no                         |
| Calm2                 | 477  | 4.19            | chr17      | 87845920  | 87846305  | 113             | < 0.001 | 87846085; 87846853; 87846852   | yes                        |
| Icam5                 | 477  | 4.19            | chr9       | 20836015  | 20836466  | -205            | < 0.001 | 20836132; 20836132   | yes                        |
| Zbtb1                 | 477  | 4.19            | chr12      | 77471356  | 77471994  | 126             | < 0.001 | 77471492, 77470990, 77470909, 77471414, 77471098, 77471447, 77470924, 77471404, 77471298, 77471129 | no                         |
| Satb1                 | 478  | 4.18            | chr17      | 51972864  | 51973092  | -1108           | < 0.001 | 51973185; 51973185   | yes                        |
| Cul5                  | 478  | 4.18            | chr9       | 53475432  | 53475477  | 128             | < 0.001 | 53475802   | yes                        |
| Mtag2                 | 478  | 4.18            | chr7       | 52622935  | 52623318  | -784            | < 0.001 | 52623071; 52623070   | yes                        |
| Kcnj2                 | 479  | 4.17            | chr11      | 110926612 | 110926888 | -835            | < 0.001 | 110926612  | no                         |
| Rbbp5                 | 480  | 4.16            | chr1       | 134373612 | 134373829 | -144            | < 0.001 | 134374121  | yes                        |
| Cic                   | 480  | 4.16            | chr7       | 26068017  | 26068199  | 845             | < 0.001 | 26068017   | no                         |
| Fzd10                 | 480  | 4.16            | chr5       | 129105459 | 129106137 | -1054           | < 0.001 | 129105459  | no                         |
| Rnf180                | 480  | 4.16            | chr13      | 106084400 | 106084445 | -1328           | < 0.001 | 106084722  | yes                        |
| Gnb4                  | 481  | 4.15            | chr3       | 32515791  | 32515988  | -505            | < 0.001 | 32515921   | yes                        |
| Lgals1                | 481  | 4.15            | chr15      | 78758690  | 78758884  | 1560            | < 0.001 | 78758983   | yes                        |
| Zfp637                | 482  | 4.14            | chr6       | 117791617 | 117791847 | 387             | < 0.001 | 117791705  | yes                        |
| 2210412D01Rik         | 482  | 4.14            | chr7       | 91300289  | 91300334  | 91              | < 0.001 | 91300465, 91300171   | no                         |
| Slc25a5               | 482  | 4.14            | chrX       | 34336171  | 34336330  | 548             | < 0.001 | 34336171   | no                         |
| Dpysl5                | 483  | 4.13            | chr5       | 31014236  | 31014676  | 191             | < 0.001 | 31014561; 31014560   | yes                        |
| Lass6                 | 483  | 4.13            | chr2       | 68699542  | 68699871  | 235             | < 0.001 | 68699600   | yes                        |
| Oaf                   | 483  | 4.13            | chr9       | 43047730  | 43048502  | -245            | < 0.001 | 43047750; 43048380   | yes                        |
| Camk2g                | 483  | 4.13            | chr14      | 21612948  | 21613162  | 170             | < 0.001 | 21613038, 21613008, 21612883, 21612779   | no                         |
| Gabra1                | 483  | 4.13            | chr11      | 41996285  | 41996085  | 117             | < 0.001 | 41995762, 41996415   | no                         |
| Tial1                 | 483  | 4.13            | chr7       | 135604204 | 135604249 | 801             | < 0.001 | 135604204  | no                         |
| Pcdcd4                | 484  | 4.12            | chr19      | 53978213  | 53978607  | 11858           | < 0.001 | 53978447; 53978446   | yes                        |
| Phldb1                | 484  | 4.12            | chr9       | 44543144  | 44543809  | -111            | < 0.001 | 44543647   | yes                        |
| Gm962                 | 484  | 4.12            | chr19      | 5568063   | 5568108   | 13              | < 0.001 | 5567955, 5567929, 5567821, 5568006, 5567981  | no                         |
| M6prbp1               | 484  | 4.12            | chr17      | 56429044  | 56429922  | 191             | < 0.001 | 56429044   | no                         |
| Tmem142a              | 484  | 4.12            | chr5       | 123465983 | 123466255 | 930             | < 0.001 | 123465983  | no                         |
| Tgfb1                 | 484  | 4.12            | chr13      | 56710721  | 56710887  | -99             | < 0.001 | N/A  | no                         |
| Dusp7                 | 485  | 4.1             | chr9       | 106270464 | 106270690 | -296            | < 0.001 | 106270464  | no                         |
| Msi2                  | 485  | 4.1             | chr11      | 88578858  | 88579090  | 481             | < 0.001 | 88578858   | no                         |
| Prep                  | 485  | 4.1             | chr7       | 100023176 | 100023362 | -466            | < 0.001 | 100022993, 100023033   | no                         |
| Robo2                 | 485  | 4.1             | chr16      | 74411465  | 74412068  | -538            | < 0.001 | 74411931   | yes                        |
| Ep400                 | 486  | 4.09            | chr5       | 111200099 | 111200144 | -386            | < 0.001 | 111200289  | yes                        |
| ENSMUST0000008365.8.1 | 486  | 4.09            | chr18      | 61812765  | 61813570  | -4632           | < 0.001 | N/A  | no                         |
| Dhrs3                 | 487  | 4.08            | chr4       | 144482503 | 144482558 | -449            | < 0.001 | 144482503  | no                         |
| Mgat1                 | 487  | 4.08            | chr11      | 49058202  | 49058422  | -2748           | < 0.001 | 49057969, 49057741, 49058255   | no                         |
| Tnfrsf1a              | 487  | 4.08            | chr6       | 125300164 | 125300639 | 730             | < 0.001 | 125300164  | no                         |
| Tsga2                 | 487  | 4.08            | chr17      | 31414099  | 31414251  | 75              | < 0.001 | 31414099   | no                         |
| Lrba                  | 488  | 4.07            | chr3       | 86027336  | 86027802  | -955            | < 0.001 | N/A  | no                         |
| Trp73                 | 489  | 4.06            | chr4       | 153514287 | 153514332 | 7               | < 0.001 | 153514464; 153514463   | yes                        |
| Tgfb1                 | 489  | 4.06            | chr7       | 26472469  | 26473055  | 635             | < 0.001 | 26472469   | no                         |
| Socs3                 | 490  | 4.05            | chr11      | 117830448 | 117831034 | -536            | < 0.001 | 117831052; 117830972   | yes                        |
| Nfil3                 | 491  | 4.04            | chr13      | 53075458  | 53075958  | 476             | < 0.001 | 53075587   | yes                        |
| C430014K11Rik         | 491  | 4.04            | chr15      | 98662411  | 98663415  | -720            | < 0.001 | 98662411   | no                         |
| Fem1b                 | 492  | 4.03            | chr9       | 62659838  | 62660122  | -518            | < 0.001 | 62660230   | yes                        |
| Twist1                | 492  | 4.03            | chr12      | 34643154  | 34643388  | 641             | < 0.001 | 34643337; 34643280; 34643280   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Camta2        | 492  | 4.03            | chr11      | 70483346  | 70483551  | 18062           | < 0.001 | N/A  | no                         |
| Slc25a19      | 492  | 4.03            | chr11      | 115476279 | 115476339 | 13144           | < 0.001 | N/A  | no                         |
| Centg2        | 493  | 4.02            | chr1       | 91351073  | 91350809  | -472            | < 0.001 | 91351006, 91351054   | no                         |
| Enpep         | 493  | 4.02            | chr3       | 129035572 | 129035747 | 73              | < 0.001 | 129035572  | no                         |
| Aqp11         | 494  | 4.01            | chr7       | 104886416 | 104886762 | 17              | < 0.001 | 104886779; 104886779   | yes                        |
| Gpre5c        | 494  | 4.01            | chr11      | 114712308 | 114712705 | -314            | < 0.001 | 114712314; 114712721; 114712720  | yes                        |
| Prdx5         | 494  | 4.01            | chr19      | 6983822   | 6984079   | 286             | < 0.001 | 6984372; 6984375   | yes                        |
| Fcho1         | 494  | 4.01            | chr8       | 74249221  | 74249419  | 302             | < 0.001 | 74249221   | no                         |
| Slc9a3r2      | 494  | 4.01            | chr17      | 24786885  | 24787046  | -5122           | < 0.001 | 24786885   | no                         |
| I500004A08Rik | 495  | 4               | chr11      | 3232268   | 3232459   | 1703            | < 0.001 | 3232268  | no                         |
| Gng12         | 495  | 4               | chr6       | 66846685  | 66846953  | 481             | < 0.001 | 66846685   | no                         |
| Rbpms2        | 495  | 4               | chr9       | 65477991  | 65478163  | -367            | < 0.001 | 65477918, 65477924, 65477915   | no                         |
| Qk            | 495  | 4               | chr17      | 10512925  | 10513269  | -229            | < 0.001 | 10513115; 10513347   | yes                        |
| C78409        | 495  | 4               | chr10      | 126617542 | 126617072 | 9807            | < 0.001 | 126618161; 126618160   | yes                        |
| Fbxl14        | 495  | 4               | chr6       | 119429216 | 119429735 | -275            | < 0.001 | 119429632; 119429893; 119429500  | yes                        |
| Mtdh          | 496  | 3.99            | chr15      | 34012013  | 34012204  | -291            | < 0.001 | 34012013   | no                         |
| Nr1i2         | 496  | 3.99            | chr16      | 38295612  | 38295868  | -930            | < 0.001 | 38295612   | no                         |
| Rev3l         | 497  | 3.98            | chr10      | 39451113  | 39451421  | -829            | < 0.001 | 39451547; 39451495; 39451495   | yes                        |
| Acss1         | 497  | 3.98            | chr2       | 150493460 | 150493885 | 271             | < 0.001 | 150493460  | no                         |
| Map3k12       | 497  | 3.98            | chr15      | 102347067 | 102347112 | 153             | < 0.001 | 102347501, 102347459, 102347108  | no                         |
| Klh2          | 497  | 3.98            | chr8       | 67374469  | 67374624  | -782            | < 0.001 | N/A  | no                         |
| Kpna4         | 498  | 3.97            | chr3       | 68931187  | 68931232  | -196            | < 0.001 | 68931187   | no                         |
| Smo           | 498  | 3.97            | chr6       | 29685666  | 29686165  | 328             | < 0.001 | 29685624, 29685622, 29685620, 29685591, 29685589, 29685625, 29685628, 29685623, 29685626 | no                         |
| Wbscr16       | 498  | 3.97            | chr5       | 134652198 | 134652422 | 237             | < 0.001 | 134652198  | no                         |
| Ppm1e         | 499  | 3.96            | chr11      | 87171290  | 87171994  | 890             | < 0.001 | 87171459; 87171459   | yes                        |
| Dnajb12       | 499  | 3.96            | chr10      | 59342424  | 59342469  | 108             | < 0.001 | 59342424   | no                         |
| Lmbrd1        | 500  | 3.95            | chr1       | 24685213  | 24685422  | 18              | < 0.001 | 24685565   | yes                        |
| BC057627      | 501  | 3.94            | chr7       | 16986075  | 16986231  | -439            | < 0.001 | 16986207, 16986172   | no                         |
| Erc2          | 501  | 3.94            | chr14      | 28435955  | 28436188  | 351             | < 0.001 | 28435802, 28435922   | no                         |
| Atp6v1f       | 502  | 3.93            | chr6       | 29417825  | 29418213  | 202             | < 0.001 | 29417964; 29417964   | yes                        |
| Gabpb1        | 502  | 3.93            | chr2       | 126501010 | 126501295 | 186             | < 0.001 | 126501314  | yes                        |
| Pdzd4         | 503  | 3.92            | chrX       | 71070453  | 71070732  | -168            | < 0.001 | 71070525   | yes                        |
| Bcl10         | 503  | 3.92            | chr3       | 145587439 | 145587956 | 591             | < 0.001 | 145587914, 145587744, 145587738  | no                         |
| Ss18l1        | 504  | 3.91            | chr2       | 179777224 | 179777717 | 341             | < 0.001 | 179777608; 179777611   | yes                        |
| E130310K16Rik | 504  | 3.91            | chr4       | 20705805  | 20706116  | -277            | < 0.001 | 20705805   | no                         |
| Grm7          | 504  | 3.91            | chr6       | 110595642 | 110595790 | 177             | < 0.001 | 110595642  | no                         |
| Sema3f        | 504  | 3.91            | chr9       | 107609828 | 107610571 | 2954            | < 0.001 | 107609828  | no                         |
| Slc45a3       | 504  | 3.91            | chr1       | 133868973 | 133869172 | 1811            | < 0.001 | 133868973  | no                         |
| Mat2b         | 505  | 3.9             | chr11      | 40505902  | 40505837  | 191             | < 0.001 | 40505902   | no                         |
| Pter          | 506  | 3.89            | chr2       | 12845700  | 12845745  | 55              | < 0.001 | 12845700   | no                         |
| Zfp142        | 506  | 3.89            | chr1       | 74634217  | 74634404  | 220             | < 0.001 | 74634461   | yes                        |
| Smurf2        | 507  | 3.88            | chr11      | 106781142 | 106781549 | 335             | < 0.001 | 106781142  | no                         |
| Dll1          | 508  | 3.87            | chr17      | 15512518  | 15513430  | 0               | < 0.001 | 15513054   | yes                        |
| Tbc1d10a      | 509  | 3.86            | chr11      | 4086908   | 4087084   | 227             | < 0.001 | 4087002  | yes                        |
| Etfb          | 509  | 3.86            | chr7       | 50699045  | 50699100  | -440            | < 0.001 | 50699045   | no                         |
| Ucp2          | 509  | 3.86            | chr7       | 107642264 | 107642784 | 557             | < 0.001 | 107642264  | no                         |
| Enah          | 510  | 3.85            | chr1       | 183949274 | 183949458 | 679             | < 0.001 | 183949373  | yes                        |
| H3f3a         | 510  | 3.85            | chr1       | 182744336 | 182744381 | -624            | < 0.001 | 182744336  | no                         |
| Rcc2          | 511  | 3.84            | chr4       | 140258422 | 140259215 | 1554            | < 0.001 | 140259129; 140258559   | yes                        |
| Itga3         | 511  | 3.84            | chr11      | 94937831  | 94938562  | -504            | < 0.001 | 94937831   | no                         |
| Crtc1         | 512  | 3.83            | chr8       | 72962605  | 72963289  | 568             | < 0.001 | 72963469; 72963472   | yes                        |
| Ctbp2         | 512  | 3.83            | chr7       | 140313851 | 140314515 | 878             | < 0.001 | 140314975; 140314975; 140314137  | yes                        |
| Gli3          | 512  | 3.83            | chr13      | 15554941  | 15555462  | -299            | < 0.001 | 15555284; 15555284   | yes                        |
| Adamts18      | 512  | 3.83            | chr8       | 116372745 | 116373043 | -281            | < 0.001 | 116372906  | yes                        |
| Ddx50         | 513  | 3.82            | chr10      | 62114274  | 62114457  | -78             | < 0.001 | 62115221; 62115224   | yes                        |
| Chr1l         | 513  | 3.82            | chr11      | 103993958 | 103994849 | 491             | < 0.001 | 103994224; 103994224   | yes                        |
| A230074B11Rik | 513  | 3.82            | chr1       | 37086340  | 37086528  | 340             | < 0.001 | 37086289, 37086090   | no                         |
| Cry2          | 514  | 3.81            | chr2       | 92274279  | 92274671  | -415            | < 0.001 | 92274688   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Clef1         | 515  | 3.8             | chr19      | 4214010   | 4214749   | -93             | < 0.001 | 4214728; 4214731   | yes                        |
| Rgma          | 515  | 3.8             | chr7       | 80519767  | 80520067  | -365            | < 0.001 | 80520030   | yes                        |
| Galnt11       | 515  | 3.8             | chr5       | 24728812  | 24729006  | 274             | < 0.001 | 24728784; 24728901   | no                         |
| Gtpbp3        | 515  | 3.8             | chr8       | 74009933  | 74010488  | -1677           | < 0.001 | 74009996; 74009920; 74009992; 74009874   | no                         |
| Maged1        | 515  | 3.8             | chrX       | 91786121  | 91786515  | 1093            | < 0.001 | 91785946; 91786228; 91786424   | no                         |
| Nfatc4        | 515  | 3.8             | chr14      | 56443786  | 56444042  | 176             | < 0.001 | 56443830; 56443759; 56443724; 56443622; 56443936   | no                         |
| Cer10         | 515  | 3.8             | chr11      | 101034756 | 101034962 | 1971            | < 0.001 | N/A  | no                         |
| Pdpn          | 516  | 3.79            | chr4       | 142888759 | 142889091 | 454             | < 0.001 | N/A  | no                         |
| Mllt3         | 517  | 3.78            | chr4       | 87677901  | 87678193  | 1386            | < 0.001 | 87677952; 87678171   | yes                        |
| Hdlbp         | 517  | 3.78            | chr1       | 95375092  | 95375391  | 125             | < 0.001 | 95375185; 95374962   | no                         |
| Sfrs7         | 518  | 3.77            | chr17      | 80606235  | 80606426  | 221             | < 0.001 | 80606560; 80606563   | yes                        |
| Clqtnf7       | 518  | 3.77            | chr5       | 43906881  | 43907173  | 85              | < 0.001 | 43906881   | no                         |
| Prss12        | 519  | 3.76            | chr3       | 123149643 | 123150008 | 36              | < 0.001 | 123150183; 123150013   | yes                        |
| Insm1         | 519  | 3.76            | chr2       | 146043905 | 146044069 | -3802           | < 0.001 | 146043838; 146043836; 146043108  | no                         |
| Rapgef3       | 519  | 3.76            | chr15      | 97597793  | 97598298  | -1              | < 0.001 | 97597748; 97598189   | no                         |
| Tcf2          | 520  | 3.75            | chr11      | 83666802  | 83666847  | 2454            | < 0.001 | 83667045; 83667045   | yes                        |
| Pgep1         | 521  | 3.73            | chr8       | 73183037  | 73184206  | 166             | < 0.001 | 73183067; 73183067   | yes                        |
| 4930543L23Rik | 521  | 3.73            | chr11      | 58977070  | 58977115  | 152             | < 0.001 | 58977268; 58977232; 58977174; 58977235; 58977238; 58977244; 58977241                               | no                         |
| Hic1          | 521  | 3.73            | chr11      | 74983538  | 74983708  | -2031           | < 0.001 | 74983538   | no                         |
| Ppp1r1a       | 522  | 3.72            | chr15      | 103367759 | 103368134 | 507             | < 0.001 | 103367759  | no                         |
| Sox4          | 522  | 3.72            | chr13      | 29043054  | 29050299  | 2471            | < 0.001 | 29050075; 29050064; 29043150; 29043041   | no                         |
| 6330512M04Rik | 523  | 3.71            | chr7       | 149557396 | 149557939 | 568             | < 0.001 | 149557396  | no                         |
| BC020002      | 523  | 3.71            | chr6       | 8159471   | 8159622   | 266             | < 0.001 | 8159471  | no                         |
| 9430078G10Rik | 524  | 3.7             | chr19      | 4397704   | 4397883   | -783            | < 0.001 | N/A  | no                         |
| Osbp16        | 525  | 3.69            | chr2       | 76244452  | 76245242  | 232             | < 0.001 | 76245410; 76245409   | yes                        |
| Abcf2         | 525  | 3.69            | chr5       | 24082546  | 24083087  | 295             | < 0.001 | 24082546   | no                         |
| BC021395      | 525  | 3.69            | chr18      | 24688267  | 24688749  | 251             | < 0.001 | 24688267   | no                         |
| Copz2         | 525  | 3.69            | chr11      | 96711201  | 96711578  | 195             | < 0.001 | 96711154; 96711240; 96711280; 96711257; 96711268   | no                         |
| D130059P03Rik | 525  | 3.69            | chr6       | 38383301  | 38383498  | -448            | < 0.001 | 38383301   | no                         |
| Igfbp6        | 525  | 3.69            | chr15      | 101974940 | 101975408 | 554             | < 0.001 | 101973868; 101975101   | no                         |
| Ptgs1         | 525  | 3.69            | chr2       | 36085913  | 36085958  | -9              | < 0.001 | 36085913   | no                         |
| Dek           | 526  | 3.68            | chr13      | 47200560  | 47201480  | 640             | < 0.001 | 47200719; 47201562   | yes                        |
| Tmsb4x        | 526  | 3.68            | chrX       | 163645680 | 163646772 | 1440            | < 0.001 | 163645940; 163646649; 163645943  | yes                        |
| Adamts19      | 527  | 3.67            | chr18      | 58997329  | 58997518  | 1079            | < 0.001 | 58997691; 58997691   | yes                        |
| BC005764      | 527  | 3.67            | chr10      | 79336789  | 79337086  | 315             | < 0.001 | 79337293; 79337399   | yes                        |
| Hexim1        | 527  | 3.67            | chr11      | 102977872 | 102977922 | 259             | < 0.001 | 102977872  | no                         |
| Trap1         | 528  | 3.66            | chr16      | 4077929   | 4077979   | -144            | < 0.001 | 4078034  | yes                        |
| Gfra1         | 529  | 3.65            | chr19      | 58528940  | 58529251  | -132            | < 0.001 | 58529353   | yes                        |
| 1200009O22Rik | 529  | 3.65            | chr6       | 53771016  | 53771062  | -351            | < 0.001 | 53770994; 53770988   | no                         |
| 9930021D14Rik | 529  | 3.65            | chr17      | 24610550  | 24611004  | -32             | < 0.001 | 24610550   | no                         |
| Tspan4        | 529  | 3.65            | chr7       | 148662496 | 148662544 | 1382            | < 0.001 | 148662496  | no                         |
| Anapc5        | 530  | 3.64            | chr5       | 123271427 | 123271478 | -104            | < 0.001 | N/A  | no                         |
| Foxd2         | 531  | 3.63            | chr4       | 114580611 | 114581050 | 475             | < 0.001 | 114580517; 114580542   | no                         |
| lkbke         | 531  | 3.63            | chr1       | 133173777 | 133173957 | 2336            | < 0.001 | 133173777  | no                         |
| Hmg20b        | 532  | 3.62            | chr10      | 80812912  | 80813089  | 89              | < 0.001 | 80813537   | yes                        |
| Sfrs9         | 532  | 3.62            | chr5       | 115777146 | 115777191 | -17             | < 0.001 | 115777338; 115777408; 115777458; 115777458   | yes                        |
| Tbl2          | 532  | 3.62            | chr5       | 135625600 | 135625863 | 42              | < 0.001 | 135625733  | yes                        |
| Clic1         | 532  | 3.62            | chr17      | 35187226  | 35187271  | 61              | < 0.001 | 35187134; 35187335; 38825161; 38825381; 38825167   | no                         |
| Hipk2         | 532  | 3.62            | chr6       | 38825227  | 38826773  | -561            | < 0.001 | 38826790; 38826669   | no                         |
| Aftph         | 533  | 3.6             | chr11      | 20641433  | 20641726  | 31              | < 0.001 | 20641730; 20641729; 20641745; 20641744   | yes                        |
| Hpc4          | 533  | 3.6             | chr4       | 128798571 | 128798746 | -2722           | < 0.001 | 128798822; 128798825   | yes                        |
| Arf3          | 533  | 3.6             | chr15      | 98593655  | 98593700  | -129            | < 0.001 | 98592726; 98593446; 98593440; 98593437; 98592577; 98593011; 98593085; 98593209; 98592929; 98592485 | no                         |
| BC055324      | 533  | 3.6             | chr1       | 165924509 | 165924671 | 265             | < 0.001 | 165924509  | no                         |
| Lrn3          | 533  | 3.6             | chr12      | 42211651  | 42212093  | 660             | < 0.001 | 42211651   | no                         |
| Slc9a2        | 533  | 3.6             | chr1       | 40737661  | 40737835  | -746            | < 0.001 | 40737661   | no                         |
| Trpm4         | 534  | 3.59            | chr7       | 52588589  | 52588811  | 362             | < 0.001 | 52588589   | no                         |
| Ifngr2        | 535  | 3.58            | chr16      | 91546993  | 91547369  | -315            | < 0.001 | 91547448; 91547448   | yes                        |
| Irf3          | 535  | 3.58            | chr7       | 52256148  | 52256376  | 3141            | < 0.001 | 52256472; 52256472   | yes                        |
| Efnal         | 535  | 3.58            | chr3       | 89083818  | 89084174  | -282            | < 0.001 | 89083818   | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                                       | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Slc12a4       | 535  | 3.58            | chr8       | 108489489 | 108489726 | 427             | < 0.001 | 108489489   | no                         |
| Lmna          | 535  | 3.58            | chr3       | 88305881  | 88306466  | -8897           | < 0.001 | 88306256  | yes                        |
| Eif1a         | 536  | 3.57            | chr18      | 46757254  | 46757753  | 125             | < 0.001 | 46757505  | yes                        |
| Arhgef7       | 536  | 3.57            | chr8       | 11758430  | 11758673  | 123             | < 0.001 | 11758760; 11758493; 11758766  | yes                        |
| Ntn4          | 537  | 3.56            | chr10      | 93103940  | 93103985  | 17              | < 0.001 | 93104038; 93104038  | yes                        |
| Hk2           | 537  | 3.56            | chr6       | 82722578  | 82723248  | 1554            | < 0.001 | 82722578  | no                         |
| Fzd4          | 538  | 3.55            | chr7       | 96552793  | 96552838  | -87             | < 0.001 | 96553040; 96553043  | yes                        |
| H1fx          | 538  | 3.55            | chr6       | 87930395  | 87930780  | 1058            | < 0.001 | 87930851; 87930560  | yes                        |
| Smek1         | 538  | 3.55            | chr12      | 102321738 | 102321783 | -150            | < 0.001 | 102322025; 102322025  | yes                        |
| Hectd2        | 538  | 3.55            | chr19      | 36628499  | 36628992  | -747            | < 0.001 | 36628499  | no                         |
| Dlat          | 539  | 3.54            | chr9       | 50467607  | 50468021  | 23              | < 0.001 | 50468015  | yes                        |
| Irf2          | 539  | 3.54            | chr8       | 47825107  | 47825305  | 33              | < 0.001 | 47825069; 47825053  | no                         |
| Orc4l         | 539  | 3.54            | chr2       | 48805177  | 48805467  | -545            | < 0.001 | 48805008; 48805100  | no                         |
| Hmga1         | 539  | 3.54            | chr17      | 27694412  | 27694630  | 908             | < 0.001 | 27694589; 27694630  | yes                        |
| Yap1          | 540  | 3.53            | chr9       | 8003576   | 8003912   | 982             | < 0.001 | 8003888   | yes                        |
| Cgml1         | 540  | 3.53            | chr9       | 71619204  | 71619249  | 183             | < 0.001 | 71619330; 71619330  | yes                        |
| Atf2          | 540  | 3.53            | chr2       | 73730863  | 73731396  | -476            | < 0.001 | 73731039; 73731269; 73731269; 73731039; 73731249                            | yes                        |
| Sbno2         | 540  | 3.53            | chr10      | 79564908  | 79565120  | 349             | < 0.001 | 79564908  | no                         |
| Vps26b        | 540  | 3.53            | chr9       | 26836819  | 26837012  | 652             | < 0.001 | 26836819  | no                         |
| BCO62109      | 541  | 3.52            | chr5       | 100587581 | 100587632 | 1221            | < 0.001 | 100587581   | no                         |
| Sync          | 541  | 3.52            | chr4       | 128964591 | 128964858 | -250            | < 0.001 | 128964458; 128964456; 128964773; 128964544; 128964744; 128964486; 128964788 | no                         |
| Nr4a2         | 541  | 3.52            | chr2       | 56967817  | 56967862  | -174            | < 0.001 | 56967833  | yes                        |
| Smarca5       | 542  | 3.51            | chr8       | 83262579  | 83262637  | 750             | < 0.001 | 83262667  | yes                        |
| Timm8b        | 542  | 3.51            | chr9       | 50412490  | 50412550  | 515             | < 0.001 | 50412500  | yes                        |
| Dkk1          | 542  | 3.51            | chr19      | 30624062  | 30624253  | -98             | < 0.001 | 30624007; 30624118  | no                         |
| Rbm4b         | 543  | 3.49            | chr19      | 4756056   | 4756312   | -234            | < 0.001 | 4756056   | no                         |
| Rce1          | 543  | 3.49            | chr19      | 4625115   | 4625283   | 357             | < 0.001 | 4625115   | no                         |
| Rara          | 543  | 3.49            | chr11      | 98800369  | 98800602  | 1566            | < 0.001 | 98800563  | yes                        |
| Pi4k2a        | 544  | 3.48            | chr19      | 42164890  | 42165423  | 476             | < 0.001 | 42164982; 42164781; 42165191; 42165104                                      | yes                        |
| Usp21         | 545  | 3.47            | chr1       | 173218313 | 173218362 | -281            | < 0.001 | 173218313   | no                         |
| Rbp1          | 546  | 3.46            | chr9       | 98322119  | 98322488  | -1089           | < 0.001 | 98322119  | no                         |
| Als2cr4       | 547  | 3.45            | chr1       | 59176967  | 59177012  | -50             | < 0.001 | 59177242  | yes                        |
| Arl6ip6       | 548  | 3.44            | chr2       | 53051317  | 53051566  | 196             | < 0.001 | 53051391  | yes                        |
| Vdr           | 548  | 3.44            | chr15      | 97738015  | 97738571  | 179             | < 0.001 | 97738601; 97738601  | yes                        |
| Svil          | 549  | 3.43            | chr18      | 4921809   | 4922006   | 1420            | < 0.001 | 4922091   | yes                        |
| Ube2c         | 550  | 3.42            | chr2       | 164595335 | 164595380 | -70             | < 0.001 | 164595746   | yes                        |
| Nrd1          | 550  | 3.42            | chr4       | 108673549 | 108673747 | 315             | < 0.001 | 108673553; 108673553  | yes                        |
| Tomm20        | 550  | 3.42            | chr8       | 129468612 | 129468775 | 984             | < 0.001 | 129468612   | no                         |
| Rab3a         | 550  | 3.42            | chr8       | 73278541  | 73278586  | -844            | < 0.001 | 73278841; 73278840  | yes                        |
| Dock11        | 551  | 3.41            | chrX       | 33429456  | 33429699  | 654             | < 0.001 | 33429535  | yes                        |
| Hoxd3         | 551  | 3.41            | chr2       | 74578842  | 74578900  | 28822           | < 0.001 | 74578949; 74578948  | yes                        |
| Tbcc          | 551  | 3.41            | chr17      | 47026766  | 47027173  | -775            | < 0.001 | 47026948  | yes                        |
| I110059P08Rik | 551  | 3.41            | chr10      | 14425387  | 14425445  | -121            | < 0.001 | 14425387  | no                         |
| Pla2g12a      | 551  | 3.41            | chr3       | 129581951 | 129581996 | -2127           | < 0.001 | N/A   | no                         |
| Srebf2        | 552  | 3.4             | chr15      | 81977689  | 81977844  | 124             | < 0.001 | 81977976; 81977975  | yes                        |
| Kif2a         | 552  | 3.4             | chr13      | 107811684 | 107811851 | 366             | < 0.001 | 107811684   | no                         |
| Map3k1        | 552  | 3.4             | chr13      | 112599486 | 112599961 | -747            | < 0.001 | 112599486   | no                         |
| Nradd         | 553  | 3.38            | chr9       | 110526725 | 110527161 | 31              | < 0.001 | 110527205   | yes                        |
| Fasn          | 553  | 3.38            | chr11      | 120685592 | 120686117 | 63              | < 0.001 | 120685960; 120685501; 120685630; 120685718; 120685652                       | no                         |
| Grec10        | 553  | 3.38            | chr6       | 124690842 | 124690887 | 233             | < 0.001 | 124690842   | no                         |
| Ugp2          | 553  | 3.38            | chr11      | 21271281  | 21270990  | -490            | < 0.001 | 21271211; 21271335; 21270939; 21270882; 21271397                            | no                         |
| Tmem86a       | 554  | 3.37            | chr7       | 54306288  | 54306567  | 301             | < 0.001 | 54306526; 54306525  | yes                        |
| D11Bwg0517e   | 554  | 3.37            | chr11      | 118769006 | 118769363 | 1852            | < 0.001 | N/A   | no                         |
| Csnk2a1       | 555  | 3.36            | chr2       | 152052291 | 152052336 | -261            | < 0.001 | 152052291   | no                         |
| Pdlim4        | 555  | 3.36            | chr11      | 53882568  | 53882434  | 244             | < 0.001 | 53882568  | no                         |
| Phka1         | 556  | 3.35            | chrX       | 99839836  | 99839886  | -276            | 0.01    | 99840206; 99840206  | yes                        |
| Sh3glb1       | 556  | 3.35            | chr3       | 144382973 | 144383018 | 291             | < 0.001 | 144383376   | yes                        |
| Atf3          | 556  | 3.35            | chr1       | 193007729 | 193007774 | -540            | < 0.001 | 193007688; 193007850  | no                         |
| Six2          | 557  | 3.34            | chr17      | 86088110  | 86088338  | -551            | < 0.001 | 86088110  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Mlst2         | 558  | 3.33            | chr7       | 120657497 | 120657542 | 145             | < 0.001 | 120657759; 120657791; 120657762  | yes                        |
| Tex2          | 558  | 3.33            | chr11      | 106473732 | 106473908 | 360             | < 0.001 | 106473732  | no                         |
| Neo1          | 558  | 3.33            | chr9       | 58883355  | 58883809  | 602             | < 0.001 | N/A  | no                         |
| Trpc4         | 559  | 3.32            | chr3       | 53959829  | 53960072  | -173            | < 0.001 | 53960141   | yes                        |
| Pias3         | 559  | 3.32            | chr3       | 96500489  | 96500536  | -2833           | < 0.001 | N/A  | no                         |
| Nptx1         | 560  | 3.31            | chr11      | 119408322 | 119408368 | 789             | < 0.001 | 119408322  | no                         |
| Rbbp7         | 560  | 3.31            | chrX       | 159197594 | 159197654 | -679            | < 0.001 | 159197978, 159197987, 159197975, 159198056, 159197969, 159197981, 159197972, 159197984 | no                         |
| Cd151         | 560  | 3.31            | chr7       | 148653743 | 148653993 | -721            | < 0.001 | 148653907  | yes                        |
| Eif2c1        | 560  | 3.31            | chr4       | 126145099 | 126145144 | 543             | < 0.001 | N/A  | no                         |
| Dbi           | 561  | 3.3             | chr1       | 122017064 | 122016936 | 410             | < 0.001 | 122017064  | no                         |
| Gadd45g       | 561  | 3.3             | chr13      | 51940890  | 51941166  | -919            | < 0.001 | 51940890   | no                         |
| Jub           | 561  | 3.3             | chr14      | 55197111  | 55197289  | -1007           | < 0.001 | 55197111   | no                         |
| 1700040103Rik | 561  | 3.3             | chr6       | 85401101  | 85401146  | 118             | < 0.001 | 85401640; 85401643   | yes                        |
| Sqstm1        | 562  | 3.29            | chr11      | 50023991  | 50024036  | 278             | < 0.001 | 50023994; 50024218   | yes                        |
| Fzd8          | 562  | 3.29            | chr18      | 9212568   | 9212827   | -116            | < 0.001 | N/A  | no                         |
| Ier2          | 563  | 3.28            | chr8       | 87184590  | 87185065  | 1716            | < 0.001 | 87184590   | no                         |
| 2700081015Rik | 564  | 3.27            | chr19      | 7496954   | 7497452   | 2040            | < 0.001 | 7497572  | yes                        |
| Sema4g        | 564  | 3.27            | chr19      | 45064365  | 45064697  | 838             | < 0.001 | 45064646; 45064649   | yes                        |
| Smpd1         | 565  | 3.26            | chr7       | 112702921 | 112703261 | 194             | < 0.001 | 112702921  | no                         |
| Ctcf          | 565  | 3.26            | chr8       | 108159946 | 108159991 | -469            | < 0.001 | 108160364; 108160363   | yes                        |
| Boc           | 566  | 3.25            | chr16      | 44558931  | 44558990  | 23              | < 0.001 | 44559048, 44559034, 44559104, 44559107, 44559102, 44559105, 44559100                   | no                         |
| Kiss1r        | 566  | 3.25            | chr10      | 79383229  | 79383277  | 3538            | < 0.001 | 79383229   | no                         |
| Selm          | 566  | 3.25            | chr11      | 3417367   | 3417077   | 2689            | < 0.001 | N/A  | no                         |
| Rybp          | 567  | 3.24            | chr6       | 100237002 | 100237047 | 328             | < 0.001 | 100237073; 100237348   | yes                        |
| Bbx           | 567  | 3.24            | chr16      | 50431167  | 50431354  | 1301            | < 0.001 | 50431167   | no                         |
| Frzb          | 567  | 3.24            | chr2       | 80287642  | 80288229  | -225            | < 0.001 | 80287642   | no                         |
| Nuak1         | 568  | 3.23            | chr10      | 83903495  | 83903799  | -78             | < 0.001 | 83903880; 83903621   | yes                        |
| Stx16         | 568  | 3.23            | chr2       | 173900894 | 173900941 | -1633           | < 0.001 | 173901013, 173900790   | no                         |
| 2810002009Rik | 568  | 3.23            | chrX       | 92640105  | 92640511  | -117            | < 0.001 | N/A  | no                         |
| Rims2         | 569  | 3.22            | chr15      | 39029769  | 39030067  | 165             | < 0.001 | 39029796; 39030166; 39030165   | yes                        |
| Dcbld2        | 569  | 3.22            | chr16      | 58408637  | 58408682  | 13              | < 0.001 | 58408734, 58408604   | no                         |
| Syt12         | 569  | 3.22            | chr19      | 4476572   | 4476880   | 285             | < 0.001 | 4476572  | no                         |
| Clock         | 570  | 3.21            | chr5       | 76733017  | 76733063  | 533             | < 0.001 | 76733174   | yes                        |
| Sgtb          | 570  | 3.21            | chr13      | 104900312 | 104900372 | 473             | < 0.001 | 104900312  | no                         |
| Tro           | 570  | 3.21            | chrX       | 147091449 | 147091638 | 503             | < 0.001 | 147091250, 147091251, 147091249, 147091253   | no                         |
| Dhx29         | 570  | 3.21            | chr13      | 113718231 | 113718282 | 256             | < 0.001 | N/A  | no                         |
| Ar            | 571  | 3.19            | chrX       | 95344313  | 95344358  | -752            | < 0.001 | 95344313   | no                         |
| D15Wsu169e    | 571  | 3.19            | chr15      | 76648086  | 76648131  | 473             | < 0.001 | 76648086   | no                         |
| Smarcc1       | 571  | 3.19            | chr9       | 110034235 | 110034295 | -262            | < 0.001 | 110034167, 110034183, 110034181  | no                         |
| Prkar2b       | 572  | 3.18            | chr12      | 32745554  | 32745599  | 568             | < 0.001 | 32745604, 32745741   | no                         |
| Pcd6ip        | 572  | 3.18            | chr9       | 113617010 | 113617055 | 193             | < 0.001 | 113617113  | yes                        |
| Ascl2         | 573  | 3.17            | chr7       | 150154892 | 150154940 | 216             | < 0.001 | 150154919  | yes                        |
| Lcmt1         | 573  | 3.17            | chr7       | 130521550 | 130521859 | 78              | < 0.001 | 130521501, 130521512   | no                         |
| Pfn2          | 573  | 3.17            | chr3       | 57651976  | 57652021  | -539            | < 0.001 | 57651896, 57651852, 57651831   | no                         |
| Til           | 573  | 3.17            | chr2       | 128892133 | 128892188 | 433             | < 0.001 | 128892331, 128892325   | no                         |
| EG329763      | 574  | 3.16            | chr3       | 137729003 | 137729052 | 1324            | < 0.001 | 137729175  | yes                        |
| Rbm35a        | 574  | 3.16            | chr4       | 11314286  | 11314331  | -378            | < 0.001 | 11314550   | yes                        |
| Unc84a        | 574  | 3.16            | chr5       | 139676493 | 139676538 | -107            | < 0.001 | 139676493  | no                         |
| B3gnt8        | 574  | 3.16            | chr7       | 26412258  | 26412311  | -358            | < 0.001 | 26412332; 26412335   | yes                        |
| 1700012H17Rik | 575  | 3.15            | chr4       | 5571046   | 5571510   | 33              | < 0.001 | 5571542  | yes                        |
| Larp2         | 575  | 3.15            | chr3       | 40753322  | 40753367  | -1208           | < 0.001 | 40753737; 40753742; 40753736   | yes                        |
| Dnajc7        | 576  | 3.14            | chr11      | 100480323 | 100480711 | 794             | < 0.001 | 100480747; 100480750   | yes                        |
| Nr0b1         | 576  | 3.14            | chrX       | 83437053  | 83437098  | -37             | < 0.001 | 83437053   | no                         |
| Atxn2l        | 577  | 3.13            | chr7       | 133647017 | 133647062 | -224            | < 0.001 | 133647202; 133647428; 133647428  | yes                        |
| Tspan5        | 577  | 3.13            | chr3       | 138405783 | 138406005 | 648             | < 0.001 | 138405976  | yes                        |
| Klhl23        | 578  | 3.12            | chr2       | 69660693  | 69660738  | 187             | < 0.001 | 69661062; 69661062   | yes                        |
| Zmat3         | 578  | 3.12            | chr3       | 32264530  | 32264575  | 35              | < 0.001 | 32264819; 32264819   | yes                        |
| Sph1          | 579  | 3.11            | chr19      | 44144104  | 44144514  | -476            | < 0.001 | 44144395   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene              | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                      | WT1 Consensus Site Present |
|-------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Lmx1b             | 579  | 3.11            | chr2       | 33492022  | 33492082  | 3979            | < 0.001 | N/A  | no                         |
| Perld1            | 579  | 3.11            | chr11      | 98249743  | 98249790  | 12038           | < 0.001 | N/A  | no                         |
| Ncoa7             | 580  | 3.09            | chr10      | 30522818  | 30522713  | 223             | < 0.001 | 30522991   | yes                        |
| C230021P08Rik     | 580  | 3.09            | chr15      | 99288146  | 99288191  | 11              | < 0.001 | 99288146   | no                         |
| Pfkl              | 581  | 3.08            | chr10      | 77472235  | 77472281  | 283             | < 0.001 | 77472524   | yes                        |
| BC054817          | 581  | 3.08            | chr8       | 55615454  | 55615499  | -125            | < 0.001 | N/A  | no                         |
| Top3b             | 582  | 3.07            | chr16      | 16871155  | 16871200  | 195             | < 0.001 | 16871211   | yes                        |
| Fip1l1            | 582  | 3.07            | chr5       | 74931848  | 74931893  | 329             | < 0.001 | 74932188; 74932187   | yes                        |
| Ccher1            | 582  | 3.07            | chr17      | 35654277  | 35654322  | 240             | < 0.001 | 35653835; 35653837   | no                         |
| Fgf18             | 582  | 3.07            | chr11      | 33048071  | 33048261  | -694            | < 0.001 | 33048071   | no                         |
| Lhx1              | 582  | 3.07            | chr11      | 84339400  | 84339799  | -736            | < 0.001 | 84339400   | no                         |
| Mif4gd            | 582  | 3.07            | chr11      | 115475848 | 115476198 | -2359           | < 0.001 | 115475848  | no                         |
| Tep11l2           | 582  | 3.07            | chr10      | 84039720  | 84040043  | 169             | < 0.001 | 84039720   | no                         |
| Mltl1             | 583  | 3.06            | chr17      | 57074994  | 57075039  | -205            | < 0.001 | 57074994   | no                         |
| Sh3pxd2a          | 583  | 3.06            | chr19      | 47539365  | 47539423  | -493            | < 0.001 | 47539365   | no                         |
| Pip5k1c           | 584  | 3.05            | chr10      | 80756000  | 80756159  | 298             | < 0.001 | 80756251; 80756137   | yes                        |
| Tob1              | 584  | 3.05            | chr11      | 94071952  | 94072012  | -785            | < 0.001 | 94071952   | no                         |
| Lhx2              | 585  | 3.03            | chr2       | 38206287  | 38206342  | -513            | 0.01    | 38206287   | no                         |
| Rpp25             | 585  | 3.03            | chr9       | 57351125  | 57351185  | -753            | < 0.001 | 57351125   | no                         |
| Atp11a            | 586  | 3.02            | chr8       | 12756785  | 12756958  | -79             | < 0.001 | 12757075   | yes                        |
| Dnajb5            | 586  | 3.02            | chr4       | 42963544  | 42963777  | -2399           | < 0.001 | 42964161; 42964161; 42964071; 42963662; 42963662; 42964015 | yes                        |
| Klf6              | 587  | 3.01            | chr13      | 5860614   | 5860659   | -98             | < 0.001 | 5860918; 5860918   | yes                        |
| Mapk1             | 588  | 2.99            | chr16      | 16983413  | 16983591  | -38             | < 0.001 | 16983551   | yes                        |
| Echdc3            | 589  | 2.98            | chr2       | 6134339   | 6134384   | -322            | 0.01    | 6134609  | yes                        |
| Pea15             | 589  | 2.98            | chr1       | 174137321 | 174137370 | -434            | 0.01    | 174137321  | no                         |
| Smyd3             | 589  | 2.98            | chr1       | 181446979 | 181447039 | 1125            | 0.01    | 181446979  | no                         |
| Llg1l             | 590  | 2.97            | chr11      | 60512523  | 60512568  | -795            | < 0.001 | 60512695; 60512695   | yes                        |
| I600021P15Rik     | 590  | 2.97            | chr16      | 28930318  | 28930365  | -558            | < 0.001 | 28930318   | no                         |
| Arhgap10          | 590  | 2.97            | chr8       | 80041309  | 80041475  | 354             | 0.01    | 80041309   | no                         |
| Dusp23            | 590  | 2.97            | chr1       | 174562756 | 174562801 | 327             | 0.01    | 174562684; 174562678                                       | no                         |
| Teerg1l           | 590  | 2.97            | chr7       | 145591790 | 145591837 | -2401           | 0.01    | 145591790  | no                         |
| Tcf7l2            | 590  | 2.97            | chr19      | 55817291  | 55817338  | 555             | < 0.001 | 55817291   | no                         |
| Cdc14a            | 590  | 2.97            | chr3       | 116126767 | 116126922 | 50              | 0.01    | N/A  | no                         |
| Six5              | 591  | 2.96            | chr7       | 19680549  | 19680799  | 884             | 0.01    | 19681178; 19681126; 19680977; 19681132; 19680971           | yes                        |
| Nsg1              | 592  | 2.95            | chr5       | 38550211  | 38550979  | 46              | 0.01    | 38550907; 38550907; 38550957; 38550956                     | yes                        |
| Irx3              | 592  | 2.95            | chr8       | 94326130  | 94326318  | -1023           | 0.01    | 94326192   | yes                        |
| Sfrs6             | 592  | 2.95            | chr2       | 162757568 | 162757613 | 310             | 0.01    | 162757845  | yes                        |
| Marveld1          | 592  | 2.95            | chr19      | 42222908  | 42223347  | -522            | < 0.001 | 42222974; 42222956   | no                         |
| Mst1r             | 593  | 2.94            | chr9       | 107808929 | 107808975 | -267            | < 0.001 | 107809157; 107808873; 107808879                            | no                         |
| Zfyve19           | 593  | 2.94            | chr2       | 119034894 | 119034939 | 224             | 0.01    | 119034547; 119034553                                       | no                         |
| Coll2a1           | 594  | 2.93            | chr9       | 79566742  | 79567134  | -279            | < 0.001 | 79566924; 79566923   | yes                        |
| Peolce            | 595  | 2.92            | chr5       | 138052181 | 138052231 | 426             | 0.01    | N/A  | no                         |
| Ptprv             | 595  | 2.92            | chr1       | 137025771 | 137025816 | 3358            | 0.01    | N/A  | no                         |
| Arid5b            | 596  | 2.91            | chr10      | 67739915  | 67739510  | 1688            | < 0.001 | 67739915   | no                         |
| Gnb2              | 596  | 2.91            | chr5       | 137972966 | 137973011 | 1469            | 0.01    | 137972966  | no                         |
| Mars2             | 597  | 2.9             | chr1       | 55293773  | 55293828  | -220            | 0.01    | 55294138   | yes                        |
| Rcor1             | 597  | 2.9             | chr12      | 112276678 | 112276723 | -1308           | < 0.001 | 112276816; 112276815                                       | yes                        |
| Pcm1              | 597  | 2.9             | chr8       | 42326141  | 42326192  | 1054            | 0.01    | 42326141   | no                         |
| Rnd1              | 597  | 2.9             | chr15      | 98507899  | 98508182  | -32             | < 0.001 | 98507899   | no                         |
| Rnf152            | 597  | 2.9             | chr1       | 107252019 | 107252079 | 1198            | 0.01    | N/A  | no                         |
| St6galnac6        | 598  | 2.89            | chr2       | 32463323  | 32463371  | 867             | 0.01    | 32463401   | yes                        |
| Aldh4a1           | 598  | 2.89            | chr4       | 139180613 | 139180673 | 1719            | 0.01    | N/A  | no                         |
| Bcl2l11           | 599  | 2.88            | chr2       | 127953786 | 127953833 | 2037            | 0.01    | 127953786  | no                         |
| Crtc3             | 600  | 2.86            | chr7       | 87833192  | 87833237  | 549             | 0.01    | 87833391; 87833407; 87833247; 87833410; 87833413           | no                         |
| Ripk3             | 600  | 2.86            | chr14      | 56407647  | 56407702  | -51             | 0.01    | 56407647   | no                         |
| Chek1             | 601  | 2.85            | chr9       | 36533706  | 36533751  | 484             | < 0.001 | 36533766; 36533820   | no                         |
| ENSMUST0000008366 | 601  | 2.85            | chr14      | 65208893  | 65208938  | -578            | 0.01    | N/A  | no                         |
| 3.1               |      |                 |            |           |           |                 |         |  |                            |
| Ung               | 601  | 2.85            | chr5       | 114581338 | 114581383 | 196             | 0.01    | N/A  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site            | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Bmp2k         | 602  | 2.84            | chr5       | 97425958  | 97426018  | -719            | 0.01    | 97426366; 97426369; 97426363                     | yes                        |
| Atp6v1b2      | 603  | 2.83            | chr8       | 71612286  | 71612346  | -366            | 0.01    | 71612721   | yes                        |
| Hnrp11        | 603  | 2.83            | chr17      | 80460974  | 80461019  | 678             | 0.01    | 80461439   | yes                        |
| Rnf135        | 603  | 2.83            | chr11      | 79997610  | 79997655  | 259             | 0.01    | 79997929   | yes                        |
| 2900010M23Rik | 603  | 2.83            | chr17      | 27268579  | 27268629  | 2232            | 0.01    | 27268579   | no                         |
| Hsd11b2       | 603  | 2.83            | chr8       | 108042457 | 108042502 | -165            | 0.01    | N/A  | no                         |
| Casp9         | 604  | 2.82            | chr4       | 141349557 | 141349776 | 228             | 0.01    | 141349900  | yes                        |
| Ap4s1         | 604  | 2.82            | chr12      | 52792066  | 52792111  | 136             | 0.01    | 52792182   | yes                        |
| Klhl26        | 604  | 2.82            | chr8       | 73001755  | 73001801  | -930            | 0.01    | 73001650, 73001708                               | no                         |
| Slc25a39      | 604  | 2.82            | chr11      | 102269280 | 102269326 | -517            | 0.01    | 102269280  | no                         |
| Lnpep         | 605  | 2.81            | chr17      | 17761820  | 17761865  | -389            | 0.01    | 17761663, 17761621, 17761644                     | no                         |
| Pim3          | 605  | 2.81            | chr15      | 88694593  | 88694639  | 1993            | 0.01    | 88694593   | no                         |
| Unc5c         | 605  | 2.81            | chr3       | 141128216 | 141128261 | -289            | 0.01    | 141128322, 141128077                             | no                         |
| Ppm2c         | 605  | 2.81            | chr4       | 11893616  | 11893661  | -41             | 0.01    | N/A  | no                         |
| Bnip1         | 606  | 2.8             | chr17      | 26918234  | 26918282  | 223             | 0.01    | 26918597; 26918597                               | yes                        |
| Perl          | 606  | 2.8             | chr11      | 68910469  | 68910517  | -1957           | 0.01    | 68910651   | yes                        |
| Sphk1         | 606  | 2.8             | chr11      | 116393916 | 116393961 | -722            | 0.01    | 116394216  | yes                        |
| Slc32a1       | 606  | 2.8             | chr2       | 158438762 | 158438822 | 2299            | 0.01    | 158439442; 158439060; 158439059                  | yes                        |
| Cnn3          | 606  | 2.8             | chr3       | 121130496 | 121130548 | 1064            | 0.01    | 121130496  | no                         |
| Eya4          | 606  | 2.8             | chr10      | 23068134  | 23068191  | 1547            | 0.01    | 23068134   | no                         |
| Klf9          | 606  | 2.8             | chr19      | 23216509  | 23216554  | 817             | 0.01    | 23216509   | no                         |
| Ppic          | 606  | 2.8             | chr18      | 53577975  | 53578026  | -339            | 0.01    | 53577975   | no                         |
| Wbp4          | 606  | 2.8             | chr14      | 79881066  | 79881111  | -13             | 0.01    | 79881066   | no                         |
| Pdgfb         | 607  | 2.79            | chr15      | 79845530  | 79845575  | -314            | 0.01    | 79845565   | yes                        |
| Islr          | 607  | 2.79            | chr9       | 58006612  | 58006659  | 313             | 0.01    | 58006612   | no                         |
| Pold4         | 607  | 2.79            | chr19      | 4231607   | 4231659   | -303            | 0.01    | 4231607  | no                         |
| Pitx2         | 607  | 2.79            | chr3       | 128917636 | 128917685 | 806             | 0.01    | N/A  | no                         |
| Zfp28         | 607  | 2.79            | chr7       | 6336307   | 6336359   | 306             | 0.01    | N/A  | no                         |
| 2310057D15Rik | 608  | 2.78            | chr5       | 100469514 | 100469561 | 506             | 0.01    | 100469514  | no                         |
| D4Ert429e     | 608  | 2.78            | chr4       | 149111492 | 149111540 | 627             | 0.01    | 149111492  | no                         |
| Pafah1b3      | 608  | 2.78            | chr7       | 26082495  | 26082540  | 456             | 0.01    | 26082495   | no                         |
| Spin1         | 609  | 2.77            | chr13      | 51196711  | 51196756  | 468             | 0.01    | 51196871; 51196783; 51196871; 51196766; 51196898 | yes                        |
| Tb11xr1       | 609  | 2.77            | chr3       | 21975835  | 21975880  | 285             | 0.01    | 21976122; 21975957                               | yes                        |
| Wt1           | 609  | 2.77            | chr2       | 104967268 | 104967313 | 605             | 0.01    | 104967697; 104967544; 104967543                  | yes                        |
| Lox3          | 609  | 2.77            | chr6       | 82984198  | 82984250  | 7               | 0.01    | 82983462, 82984029, 82984023, 82983514           | no                         |
| Mtf2          | 609  | 2.77            | chr5       | 108495220 | 108495271 | 486             | 0.01    | 108495220  | no                         |
| ORF19         | 609  | 2.77            | chr17      | 66461035  | 66461080  | 74              | 0.01    | 66461413   | yes                        |
| Lamc1         | 610  | 2.76            | chr1       | 155180081 | 155180126 | -188            | 0.01    | 155180262  | yes                        |
| Ssr3          | 610  | 2.76            | chr3       | 65196135  | 65196183  | 316             | 0.01    | 65196319   | yes                        |
| Utp14b        | 610  | 2.76            | chr1       | 78654844  | 78654889  | 418             | 0.01    | 78655133; 78655132                               | yes                        |
| 2810451A06Rik | 610  | 2.76            | chr15      | 98928265  | 98928314  | -1624           | 0.01    | 98927578, 98927062, 98928078                     | no                         |
| Cerk          | 610  | 2.76            | chr15      | 86019375  | 86019428  | -2831           | 0.01    | 86019375   | no                         |
| Fblim1        | 610  | 2.76            | chr4       | 141154340 | 141154385 | 7585            | 0.01    | 141154340  | no                         |
| Cdkn1a        | 611  | 2.75            | chr17      | 29231458  | 29231503  | 764             | 0.01    | 29231811   | yes                        |
| Dkk2          | 611  | 2.75            | chr3       | 131748415 | 131748460 | 174             | 0.01    | 131748693  | yes                        |
| C79267        | 611  | 2.75            | chr4       | 139155120 | 139155165 | 24092           | 0.01    | 139155120  | no                         |
| Itrp3         | 611  | 2.75            | chr17      | 27195780  | 27195835  | 1560            | 0.01    | 27195780   | no                         |
| Nckap1        | 611  | 2.75            | chr2       | 80421892  | 80421952  | -800            | 0.01    | 80421892   | no                         |
| Tbx15         | 611  | 2.75            | chr3       | 99058121  | 99058170  | 464             | 0.01    | 99058121   | no                         |
| B4galnt3      | 611  | 2.75            | chr6       | 120244677 | 120244722 | -123            | 0.01    | N/A  | no                         |
| Tnfrsf25      | 612  | 2.74            | chr4       | 151490094 | 151490139 | -335            | 0.01    | 151490261  | yes                        |
| Rad51c        | 612  | 2.74            | chr11      | 87217969  | 87218014  | -51             | 0.01    | 87218225   | yes                        |
| Celsr3        | 612  | 2.74            | chr9       | 108729017 | 108729062 | 390             | 0.01    | 108729017  | no                         |
| Ing1          | 613  | 2.73            | chr8       | 11557333  | 11557378  | 1291            | 0.01    | 11557501   | yes                        |
| Fads3         | 613  | 2.73            | chr19      | 10116032  | 10116077  | 17              | 0.01    | 10115985, 10116106, 10116004                     | no                         |
| Tmem4         | 613  | 2.73            | chr10      | 127760070 | 127760125 | 584             | 0.01    | 127760070  | no                         |
| Cldn12        | 614  | 2.72            | chr5       | 5514598   | 5514644   | 252             | 0.01    | 5514598  | no                         |
| EG622320      | 614  | 2.72            | chr7       | 104481288 | 104481341 | 482             | 0.01    | 104481288  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                 | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Tfrc          | 614  | 2.72            | chr16      | 32609095  | 32609140  | 12              | 0.01    | 32609095  | no                         |
| Col27a1       | 614  | 2.72            | chr4       | 62875997  | 62876048  | -423            | 0.01    | N/A   | no                         |
| Slc4a4        | 614  | 2.72            | chr5       | 89358861  | 89358910  | 42602           | 0.01    | N/A   | no                         |
| Tmem178       | 614  | 2.72            | chr17      | 81343388  | 81343444  | -555            | 0.01    | N/A   | no                         |
| Arpc5         | 615  | 2.71            | chr1       | 154613675 | 154613720 | -84             | 0.01    | 154613855; 154613750; 154613855; 154613753            | yes                        |
| Btg2          | 615  | 2.71            | chr1       | 135974801 | 135974847 | 908             | 0.01    | 135974801   | no                         |
| Bhlhb3        | 616  | 2.7             | chr6       | 145812432 | 145814359 | -476            | 0.01    | 145812771; 145812549; 145812549                       | yes                        |
| Mcam          | 616  | 2.7             | chr9       | 43939819  | 43939867  | -2897           | 0.01    | 43940359  | yes                        |
| A930012O16Rik | 616  | 2.7             | chr2       | 57091009  | 57091054  | 325             | 0.01    | 57090807; 57090352                                    | no                         |
| Col11a1       | 616  | 2.7             | chr3       | 113734164 | 113734224 | 737             | 0.01    | 113734164   | no                         |
| Siva1         | 616  | 2.7             | chr12      | 113883685 | 113883735 | 588             | 0.01    | 113883685   | no                         |
| Adam11        | 617  | 2.69            | chr11      | 102624273 | 102624333 | 1551            | 0.01    | 102624233; 102624232                                  | no                         |
| Cryz1         | 617  | 2.69            | chr16      | 91728741  | 91728791  | 78              | 0.01    | 91728741  | no                         |
| Rai14         | 617  | 2.69            | chr15      | 10644922  | 10644982  | -1657           | 0.01    | 10644922  | no                         |
| Rps20         | 617  | 2.69            | chr4       | 3763103   | 3763157   | -383            | 0.01    | 3763103   | no                         |
| Adora1        | 617  | 2.69            | chr1       | 136132844 | 136132893 | -860            | 0.01    | N/A   | no                         |
| Notch3        | 618  | 2.68            | chr17      | 32303094  | 32303139  | 681             | 0.01    | 32303230  | yes                        |
| Chml          | 618  | 2.68            | chr1       | 177622081 | 177622127 | -3620           | 0.01    | 177622081   | no                         |
| Exoc6         | 618  | 2.68            | chr19      | 37625608  | 37625668  | 731             | 0.01    | 37625608  | no                         |
| Gpc4          | 618  | 2.68            | chrX       | 49517356  | 49517405  | 1049            | 0.01    | 49517339; 49517441                                    | no                         |
| Cdh2          | 619  | 2.67            | chr18      | 16968053  | 16968098  | -518            | 0.01    | 16968144  | yes                        |
| D8Erd82e      | 619  | 2.67            | chr8       | 37157736  | 37157781  | -123            | 0.01    | 37158016  | yes                        |
| Nedd4         | 619  | 2.67            | chr9       | 72510243  | 72510438  | 263             | 0.01    | 72510291; 72510459; 72510458                          | yes                        |
| AB041550      | 619  | 2.67            | chr6       | 87680838  | 87680883  | -2              | 0.01    | 87680838  | no                         |
| Magi1         | 619  | 2.67            | chr6       | 94234327  | 94234492  | -452            | 0.01    | 94234327  | no                         |
| Tpp1          | 619  | 2.67            | chr7       | 112900439 | 112900487 | 258             | 0.01    | 112900439   | no                         |
| Klc2          | 619  | 2.67            | chr19      | 5117799   | 5118023   | 408             | 0.01    | 5118093; 5118096                                      | yes                        |
| Hnrpd         | 619  | 2.67            | chr5       | 100407017 | 100407075 | 911             | 0.01    | N/A   | no                         |
| Pebp4         | 619  | 2.67            | chr9       | 106355355 | 106355400 | -842            | 0.01    | N/A   | no                         |
| Trpv4         | 620  | 2.66            | chr5       | 115108145 | 115108190 | 228             | 0.01    | 115108271; 115108271                                  | yes                        |
| Usp1          | 620  | 2.66            | chr4       | 98590973  | 98591018  | 496             | 0.01    | 98591003  | yes                        |
| Efnb3         | 620  | 2.66            | chr11      | 69373973  | 69374018  | -316            | 0.01    | 69373973  | no                         |
| Kenj5         | 620  | 2.66            | chr9       | 32152335  | 32152381  | -536            | 0.01    | 32152335  | no                         |
| Rnf150        | 620  | 2.66            | chr8       | 85388301  | 85388346  | 1070            | 0.01    | 85388406; 85389108; 85389107                          | yes                        |
| Psip1         | 621  | 2.65            | chr4       | 83132050  | 83132095  | 222             | 0.01    | 83132356; 83132356                                    | yes                        |
| AK122525      | 621  | 2.65            | chr10      | 43198487  | 43198369  | -435            | 0.01    | 43198487  | no                         |
| Mlnt10        | 621  | 2.65            | chr2       | 17978287  | 17978332  | 1413            | 0.01    | 17977968; 17977824; 17977962                          | no                         |
| Spes1         | 621  | 2.65            | chr14      | 31814428  | 31814476  | 97              | 0.01    | 31814428  | no                         |
| Gad1          | 622  | 2.64            | chr2       | 70404492  | 70406550  | 4296            | 0.01    | 70404492  | no                         |
| Zfyve1        | 622  | 2.64            | chr12      | 84937526  | 84937586  | 541             | 0.01    | 84937526  | no                         |
| 4930566A11Rik | 623  | 2.63            | chr8       | 112230471 | 112230530 | 513             | 0.01    | 112231005   | yes                        |
| Anxa5         | 623  | 2.63            | chr3       | 36375565  | 36375616  | -970            | 0.01    | 36375827  | yes                        |
| Mib1          | 623  | 2.63            | chr18      | 10726494  | 10726539  | 894             | 0.01    | 10726763  | yes                        |
| 4930483J18Rik | 623  | 2.63            | chr15      | 81021469  | 81021517  | -306            | 0.01    | 81021469  | no                         |
| Has2          | 623  | 2.63            | chr15      | 56525132  | 56525184  | 943             | 0.01    | 56525132  | no                         |
| Hoxa6         | 623  | 2.63            | chr6       | 52158636  | 52158696  | -43             | 0.01    | 52158636  | no                         |
| Hs3st3b1      | 623  | 2.63            | chr11      | 63734619  | 63734664  | 1144            | 0.01    | 63734619  | no                         |
| Mapre3        | 623  | 2.63            | chr5       | 31117505  | 31117550  | 400             | 0.01    | 31117505  | no                         |
| Hist1h1c      | 624  | 2.62            | chr13      | 23831404  | 23831458  | 756             | 0.01    | 23831404  | no                         |
| Prkce         | 624  | 2.62            | chr17      | 86566207  | 86566564  | -1387           | 0.01    | 86566207  | no                         |
| Mark4         | 624  | 2.62            | chr7       | 20043645  | 20043690  | 175             | 0.01    | N/A   | no                         |
| Sms           | 625  | 2.61            | chrX       | 153928957 | 153929003 | 998             | 0.01    | 153928984; 153928984                                  | yes                        |
| Fgf16         | 625  | 2.61            | chrX       | 102959541 | 102959598 | -245            | 0.01    | 102959955   | yes                        |
| 3732412D22Rik | 625  | 2.61            | chr5       | 67137351  | 67137396  | 296             | 0.01    | N/A   | no                         |
| Jarid1b       | 626  | 2.6             | chr1       | 136457887 | 136457932 | 1156            | 0.01    | 136457960; 136457958; 136457955; 136457880; 136457957 | no                         |
| Tmem42        | 626  | 2.6             | chr9       | 122930322 | 122930367 | -99             | 0.01    | 122930322   | no                         |
| Ghr           | 626  | 2.6             | chr15      | 3532152   | 3532207   | 1050            | 0.01    | N/A   | no                         |
| Extl2         | 627  | 2.59            | chr3       | 115710429 | 115710476 | 58              | 0.01    | 115710542; 115710542                                  | yes                        |



**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site      | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Dnajc4        | 627  | 2.59            | chr19      | 7062390   | 7062440   | 4347            | 0.01    | 7062452; 7062452; 7062441; 7062441         | yes                        |
| Eml4          | 627  | 2.59            | chr17      | 83750364  | 83750409  | 116             | 0.01    | 83750432; 83750462; 83750432               | yes                        |
| Zfp3612       | 627  | 2.59            | chr17      | 84587416  | 84587786  | -477            | 0.01    | 84587781                                   | yes                        |
| 4930570C03Rik | 627  | 2.59            | chr15      | 97612834  | 97612882  | -1937           | 0.01    | 97612834                                   | no                         |
| 4933439F18Rik | 627  | 2.59            | chr11      | 60231764  | 60231809  | 982             | 0.01    | 60231764                                   | no                         |
| Cd72          | 627  | 2.59            | chr4       | 43466819  | 43466872  | 652             | 0.01    | 43466819                                   | no                         |
| Arl5a         | 628  | 2.58            | chr2       | 52280113  | 52280158  | 258             | 0.01    | 52280113                                   | no                         |
| Bccip         | 628  | 2.58            | chr7       | 140901040 | 140901085 | 47              | 0.01    | 140901040                                  | no                         |
| Sema3e        | 628  | 2.58            | chr5       | 14025556  | 14025601  | 303             | 0.01    | 14025556                                   | no                         |
| 5730410I19Rik | 629  | 2.57            | chr12      | 103995793 | 103995838 | -368            | 0.01    | 103995932; 103995935                       | yes                        |
| Foxe3         | 629  | 2.57            | chr4       | 114598323 | 114598368 | 272             | 0.01    | 114598323                                  | no                         |
| Siae          | 629  | 2.57            | chr9       | 37421778  | 37421838  | 377             | 0.01    | 37420930; 37420968                         | no                         |
| Slc31a2       | 629  | 2.57            | chr4       | 61948074  | 61948126  | 622             | 0.01    | 61947992; 61947970                         | no                         |
| Syncrip       | 629  | 2.57            | chr9       | 88378054  | 88378101  | -843            | 0.01    | 88378054                                   | no                         |
| Rasgrf1       | 629  | 2.57            | chr9       | 89805071  | 89805116  | 482             | 0.01    | N/A  | no                         |
| Hspa12b       | 630  | 2.56            | chr2       | 130950169 | 130950218 | -2953           | 0.01    | 130950253; 130950252                       | yes                        |
| Kif21b        | 630  | 2.56            | chr1       | 138025110 | 138025159 | -2843           | 0.01    | 138025110                                  | no                         |
| 4831426I19Rik | 630  | 2.56            | chr12      | 106248179 | 106248224 | -183            | 0.01    | 106248608; 106248611                       | yes                        |
| Matr3         | 631  | 2.55            | chr18      | 35722226  | 35722271  | 437             | 0.01    | 35722493                                   | yes                        |
| 4930471M23Rik | 631  | 2.55            | chr5       | 30951036  | 30951093  | 729             | 0.01    | 30951036                                   | no                         |
| Lrp1          | 631  | 2.55            | chr10      | 127058554 | 127058604 | -375            | 0.01    | 127058554                                  | no                         |
| Kctd14        | 631  | 2.55            | chr7       | 104602038 | 104602086 | 138             | 0.01    | 104602310                                  | yes                        |
| Il17ra        | 632  | 2.54            | chr6       | 120413667 | 120413712 | 439             | 0.01    | 120413667                                  | no                         |
| Brd4          | 633  | 2.53            | chr17      | 32420767  | 32420819  | 261             | 0.01    | 32420767                                   | no                         |
| Gab1          | 633  | 2.53            | chr8       | 83403659  | 83403704  | 696             | 0.01    | 83403659                                   | no                         |
| Loxl1         | 633  | 2.53            | chr9       | 58159975  | 58160020  | 995             | 0.01    | 58159975                                   | no                         |
| 4933406E20Rik | 633  | 2.53            | chr9       | 108481412 | 108481457 | 18497           | 0.01    | N/A  | no                         |
| Tmem2         | 633  | 2.53            | chr19      | 21853510  | 21853560  | 704             | 0.01    | N/A  | no                         |
| Dusp1         | 634  | 2.52            | chr17      | 26645406  | 26645451  | -22             | 0.01    | 26645406                                   | no                         |
| Tnrc9         | 635  | 2.51            | chr8       | 92871435  | 92871494  | 687             | 0.01    | 92871739                                   | yes                        |
| Prkci         | 635  | 2.51            | chr3       | 30895370  | 30895430  | 708             | 0.01    | 30895370                                   | no                         |
| Ywhaz         | 635  | 2.51            | chr15      | 36722413  | 36722458  | 1563            | 0.01    | 36722499; 36722546; 36722304               | no                         |
| Aff4          | 636  | 2.5             | chr11      | 53164022  | 53164067  | -290            | 0.01    | 53164313                                   | yes                        |
| Pou2f1        | 636  | 2.5             | chr1       | 167933593 | 167933638 | -851            | 0.01    | 167933773; 167933773                       | yes                        |
| D830007B15Rik | 636  | 2.5             | chr5       | 67998427  | 67998487  | -664            | 0.01    | 67998427                                   | no                         |
| Prrx1         | 637  | 2.49            | chr1       | 165243230 | 165243290 | 521             | 0.01    | 165243381                                  | yes                        |
| Scube3        | 637  | 2.49            | chr17      | 28278566  | 28278886  | -882            | 0.01    | 28278900                                   | yes                        |
| 2610018G03Rik | 637  | 2.49            | chrX       | 48194857  | 48194902  | 268             | 0.01    | 48194857                                   | no                         |
| Ube3a         | 637  | 2.49            | chr7       | 66484303  | 66484348  | 205             | 0.01    | 66484303                                   | no                         |
| 2810025M15Rik | 638  | 2.48            | chr1       | 159342555 | 159342600 | -509            | 0.01    | 159342984; 159342984                       | yes                        |
| D230039L06Rik | 638  | 2.48            | chr1       | 180459213 | 180459268 | -15             | 0.01    | 180459037; 180459014                       | no                         |
| Impdh1        | 638  | 2.48            | chr6       | 29161861  | 29161906  | 387             | 0.01    | 29161861                                   | no                         |
| Clmn          | 638  | 2.48            | chr12      | 106103083 | 106103128 | 180             | 0.01    | 106103137; 106103140; 106103139; 106103139 | yes                        |
| Tpm3          | 638  | 2.48            | chr3       | 89884090  | 89884135  | 7497            | 0.01    | N/A  | no                         |
| Wbp1          | 638  | 2.48            | chr6       | 83071607  | 83071659  | -178            | 0.01    | N/A  | no                         |
| Csnk1a1       | 639  | 2.47            | chr18      | 61714747  | 61714792  | -465            | 0.01    | 61714741; 61714840                         | no                         |
| Fus           | 639  | 2.47            | chr7       | 135112108 | 135112166 | 1145            | 0.01    | 135112108                                  | no                         |
| Gjb5          | 639  | 2.47            | chr4       | 127035334 | 127035389 | 46              | 0.01    | 127035334                                  | no                         |
| Tbl1x         | 639  | 2.47            | chrX       | 74755641  | 74755698  | -895            | 0.01    | 74755641                                   | no                         |
| 1110007A13Rik | 640  | 2.46            | chr7       | 135883760 | 135883805 | 161             | 0.01    | 135884021; 135884011; 135884011            | yes                        |
| Ddit3         | 640  | 2.46            | chr10      | 126727841 | 126727899 | 22              | 0.01    | 126727614; 126727555; 126727569            | no                         |
| Golph3        | 640  | 2.46            | chr15      | 12251784  | 12251829  | 556             | 0.01    | 12251784                                   | no                         |
| Itpka         | 640  | 2.46            | chr2       | 119567113 | 119567168 | -932            | 0.01    | 119567113                                  | no                         |
| Serpinf2      | 640  | 2.46            | chr11      | 75257506  | 75257701  | -4701           | 0.01    | 75257506                                   | no                         |
| Tcf23         | 640  | 2.46            | chr5       | 31271100  | 31271147  | 75              | 0.01    | 31271100                                   | no                         |
| Gabarapl1     | 641  | 2.45            | chr6       | 129483763 | 129483808 | 577             | 0.01    | 129484023; 129484172; 129484172            | yes                        |
| Efcab2        | 642  | 2.44            | chr1       | 180336712 | 180336765 | 727             | 0.01    | 180336850; 180336849                       | yes                        |
| Csnk1g1       | 642  | 2.44            | chr9       | 65757469  | 65757514  | 676             | 0.01    | 65757469                                   | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site  | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| ORF61         | 642  | 2.44            | chr10      | 79446969  | 79447014  | 83              | 0.01    | 79446939, 79446823, 79446820, 79446936, 79446955, 79446952, 79446949, 79446942         | no                         |
| Parp1         | 642  | 2.44            | chr1       | 182499354 | 182499399 | 271             | 0.01    | 182499354  | no                         |
| Trim8         | 642  | 2.44            | chr19      | 46578552  | 46578604  | 2441            | 0.01    | 46578552   | no                         |
| BC049834      | 642  | 2.44            | chr1       | 157589636 | 157589681 | -501            | 0.01    | N/A  | no                         |
| Rbm26         | 642  | 2.44            | chr14      | 105576359 | 105576404 | 162             | 0.01    | N/A  | no                         |
| Snx9          | 642  | 2.44            | chr17      | 5940354   | 5940406   | -899            | 0.01    | N/A  | no                         |
| Mobk12b       | 643  | 2.43            | chr4       | 35104308  | 35104353  | 385             | 0.01    | 35104564; 35104564   | yes                        |
| Ntn1          | 643  | 2.43            | chr11      | 68200097  | 68200151  | 204             | 0.01    | 68200295   | yes                        |
| Ap1g2         | 643  | 2.43            | chr14      | 55724155  | 55724201  | 924             | 0.01    | 55724155   | no                         |
| Cx3cl1        | 643  | 2.43            | chr8       | 97296262  | 97296307  | 205             | 0.01    | 97296340, 97296301   | no                         |
| Grin2a        | 643  | 2.43            | chr16      | 9993307   | 9993353   | -704            | 0.01    | 9993307  | no                         |
| Scotin        | 643  | 2.43            | chr9       | 108940937 | 108940982 | -180            | 0.01    | 108940937  | no                         |
| Dpf3          | 643  | 2.43            | chr12      | 84828992  | 84829051  | -364            | 0.01    | N/A  | no                         |
| D18Ert653e    | 644  | 2.42            | chr18      | 68093054  | 68093099  | 166             | 0.01    | 68093302; 68093165   | yes                        |
| Impdh2        | 644  | 2.42            | chr9       | 108462617 | 108462662 | -191            | 0.01    | 108462735; 108462735; 108462741  | yes                        |
| Grifin        | 644  | 2.42            | chr5       | 141041664 | 141041709 | -665            | 0.01    | N/A  | no                         |
| Zfand5        | 645  | 2.41            | chr19      | 21346974  | 21347246  | 229             | 0.01    | 21347211; 21347214   | yes                        |
| Atxn1         | 645  | 2.41            | chr13      | 46059468  | 46059513  | 855             | 0.01    | 46059602, 46059301, 46059307   | no                         |
| Bcat1         | 645  | 2.41            | chr6       | 145024191 | 145024238 | 837             | 0.01    | 145024191  | no                         |
| Pitpna        | 645  | 2.41            | chr11      | 75402224  | 75402270  | 638             | 0.01    | N/A  | no                         |
| 5730469M10Rik | 646  | 2.4             | chr14      | 41827057  | 41827102  | -16             | 0.01    | 41827357; 41827321   | yes                        |
| D130058121Rik | 646  | 2.4             | chr11      | 72227461  | 72227825  | -2269           | 0.01    | 72227461   | no                         |
| Otx1          | 646  | 2.4             | chr11      | 21901663  | 21901708  | -32             | 0.01    | 21901663   | no                         |
| Rhoq          | 646  | 2.4             | chr17      | 87363663  | 87363709  | 1236            | 0.01    | 87363663   | no                         |
| Socs2         | 646  | 2.4             | chr10      | 94879962  | 94880007  | -529            | 0.01    | 94879962   | no                         |
| Slc4a3        | 647  | 2.39            | chr1       | 75543580  | 75543635  | 768             | 0.01    | 75543830   | yes                        |
| Farp2         | 647  | 2.39            | chr1       | 95408479  | 95408524  | -199            | 0.01    | 95408864; 95408864; 95408982   | yes                        |
| Cbx4          | 647  | 2.39            | chr11      | 118947634 | 118947824 | -251            | 0.01    | 118947435, 118947738, 118947476, 118947441, 118947479, 118947714, 118947473, 118947482 | no                         |
| Pdgfa         | 647  | 2.39            | chr5       | 139473699 | 139473744 | -2815           | 0.01    | 139473699  | no                         |
| Vps37d        | 647  | 2.39            | chr5       | 135553361 | 135553421 | 745             | 0.01    | 135553361  | no                         |
| Wdr34         | 647  | 2.39            | chr2       | 29904621  | 29904666  | -245            | 0.01    | 29904621   | no                         |
| Igsf9         | 647  | 2.39            | chr1       | 174412825 | 174412884 | 407             | 0.01    | N/A  | no                         |
| Mef2d         | 648  | 2.38            | chr3       | 87943128  | 87943179  | -3162           | 0.01    | 87943260; 87943263   | yes                        |
| Igf2bp1       | 648  | 2.38            | chr11      | 95866555  | 95866600  | 680             | 0.01    | 95866555   | no                         |
| Nr2f1         | 648  | 2.38            | chr13      | 78341408  | 78341465  | -3193           | 0.01    | 78341408   | no                         |
| Ptpn9         | 648  | 2.38            | chr9       | 56842904  | 56842949  | 152             | 0.01    | 56842904   | no                         |
| Cnot6         | 649  | 2.37            | chr11      | 49525901  | 49525946  | 288             | 0.01    | 49526162   | yes                        |
| Ube2e2        | 649  | 2.37            | chr14      | 19726109  | 19726154  | 9               | 0.01    | 19726192; 19726521; 19726192; 19726524; 19726358; 19726357                             | yes                        |
| Mos           | 649  | 2.37            | chr4       | 3802604   | 3802664   | -3382           | 0.01    | 3802738  | yes                        |
| Apbb1         | 650  | 2.35            | chr7       | 112729410 | 112729456 | 616             | 0.02    | 112729593; 112729596   | yes                        |
| Prpf4b        | 650  | 2.35            | chr13      | 34966102  | 34966147  | -1238           | 0.01    | 34966497; 34966500; 34966499; 34966499; 34966436; 34966436                             | yes                        |
| AU041783      | 650  | 2.35            | chr19      | 57081772  | 57082017  | 869             | 0.01    | 57081772   | no                         |
| Car14         | 650  | 2.35            | chr3       | 95709491  | 95709539  | -953            | 0.02    | 95709491   | no                         |
| Celsr1        | 650  | 2.35            | chr15      | 85865187  | 85865247  | -1010           | 0.01    | 85865187   | no                         |
| Gpr176        | 650  | 2.35            | chr2       | 118200157 | 118200216 | -1139           | 0.02    | 118200157  | no                         |
| Tgfb3         | 650  | 2.35            | chr5       | 107718440 | 107718485 | 77              | 0.02    | 107718312, 107718602   | no                         |
| Rbpms         | 650  | 2.35            | chr8       | 35039595  | 35039646  | 693             | 0.02    | N/A  | no                         |
| Nfat5         | 651  | 2.34            | chr8       | 109817620 | 109817665 | 273             | 0.02    | 109817816, 109817829, 109817621, 109817808, 109817533, 109817827, 109817665            | no                         |
| Slc35b2       | 651  | 2.34            | chr17      | 45701033  | 45701078  | -44             | 0.01    | N/A  | no                         |
| Stk10         | 651  | 2.34            | chr11      | 32433540  | 32433585  | 297             | 0.01    | N/A  | no                         |
| Hoxa2         | 652  | 2.33            | chr6       | 52114976  | 52115036  | -176            | 0.02    | 52115375   | yes                        |
| Emp1          | 652  | 2.33            | chr6       | 135312720 | 135312778 | -199            | 0.02    | 135312720  | no                         |
| Slc38a2       | 653  | 2.32            | chr15      | 96529511  | 96529556  | 595             | 0.01    | 96529590   | yes                        |
| Usp25         | 653  | 2.32            | chr16      | 77013828  | 77013873  | -463            | 0.01    | 77014094; 77014094   | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene                     | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                 | WT1 Consensus Site Present |
|--------------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Zfp367                   | 653  | 2.32            | chr13      | 64253572  | 64253617  | 913             | 0.01    | 64254002  | yes                        |
| B4galt2                  | 653  | 2.32            | chr4       | 117555686 | 117555731 | 366             | 0.02    | 117555686   | no                         |
| Dhx35                    | 653  | 2.32            | chr2       | 158620321 | 158620366 | -211            | 0.02    | 158620468, 158620466, 158620511, 158620464, 158620520 | no                         |
| Vipr1                    | 653  | 2.32            | chr9       | 121552322 | 121552367 | 511             | 0.01    | 121552322   | no                         |
| ENSMUST0000002686<br>5.5 | 653  | 2.32            | chr3       | 41367883  | 41367943  | -933            | 0.02    | N/A   | no                         |
| C030014K22Rik            | 654  | 2.31            | chr1       | 168930753 | 168930798 | -829            | 0.02    | 168931227   | yes                        |
| Tomm34                   | 654  | 2.31            | chr2       | 163895975 | 163896035 | 833             | 0.02    | 163896255   | yes                        |
| Arpc5l                   | 654  | 2.31            | chr2       | 38864630  | 38864690  | 1002            | 0.02    | 38863799; 38863799; 38864031                          | yes                        |
| 1700021F05Rik            | 654  | 2.31            | chr10      | 43260359  | 43260404  | 418             | 0.01    | 43260700; 43260700                                    | yes                        |
| B630019A10Rik            | 654  | 2.31            | chr16      | 23225406  | 23225451  | 594             | 0.01    | 23225406  | no                         |
| Ccdc115                  | 655  | 2.3             | chr1       | 34492016  | 34492076  | 4471            | 0.02    | 34492100  | yes                        |
| 2900046G09Rik            | 655  | 2.3             | chr16      | 20695572  | 20695632  | 473             | 0.01    | 20695572  | no                         |
| Git1                     | 655  | 2.3             | chr11      | 77307608  | 77307653  | 717             | 0.01    | 77307562, 77307438                                    | no                         |
| Rnf139                   | 655  | 2.3             | chr15      | 58721011  | 58721056  | 182             | 0.02    | 58720870, 58721172                                    | no                         |
| Zfp330                   | 656  | 2.29            | chr8       | 85298783  | 85298841  | -787            | 0.02    | 85298783  | no                         |
| Ggnbp2                   | 657  | 2.28            | chr11      | 84683595  | 84683761  | 502             | 0.02    | N/A   | no                         |
| Poren                    | 658  | 2.27            | chrX       | 7783641   | 7783687   | -37             | 0.02    | 7783776   | yes                        |
| Sh3rf2                   | 658  | 2.27            | chr18      | 42212196  | 42212245  | -1143           | 0.02    | 42212196  | no                         |
| Tmem132a                 | 658  | 2.27            | chr19      | 10943282  | 10943338  | 959             | 0.02    | 10943282  | no                         |
| Slc37a2                  | 658  | 2.27            | chr9       | 37055602  | 37055656  | 7370            | 0.02    | N/A   | no                         |
| Lzts2                    | 659  | 2.26            | chr19      | 45090397  | 45090451  | -5455           | 0.02    | 45090400  | yes                        |
| Zfand3                   | 659  | 2.26            | chr17      | 30141559  | 30141604  | -449            | 0.02    | 30141923  | yes                        |
| Rasgrp2                  | 659  | 2.26            | chr19      | 6399998   | 6400043   | -562            | 0.02    | 6399823, 6399812                                      | no                         |
| Lonrf3                   | 660  | 2.25            | chrX       | 33870057  | 33870102  | 1677            | 0.02    | 33870318  | yes                        |
| Csdc2                    | 660  | 2.25            | chr15      | 81766993  | 81767048  | -352            | 0.02    | 81766993  | no                         |
| Nanos1                   | 660  | 2.25            | chr19      | 60831621  | 60831667  | -245            | 0.02    | 60831621  | no                         |
| Ovol1                    | 660  | 2.25            | chr19      | 5558456   | 5558509   | 2093            | 0.02    | 5558456   | no                         |
| Sesn3                    | 660  | 2.25            | chr9       | 14081602  | 14081662  | 888             | 0.02    | 14081602  | no                         |
| Grina                    | 661  | 2.24            | chr15      | 76077932  | 76077977  | 718             | 0.02    | 76077932  | no                         |
| Mybpc2                   | 661  | 2.24            | chr7       | 51780386  | 51780435  | -386            | 0.02    | 51780386  | no                         |
| Sh3bp1                   | 662  | 2.23            | chr15      | 78730527  | 78730572  | 335             | 0.02    | N/A   | no                         |
| 0610038D11Rik            | 663  | 2.22            | chr19      | 6984302   | 6984347   | 137             | 0.02    | 6984302   | no                         |
| Arhgef2                  | 663  | 2.22            | chr3       | 88424753  | 88425046  | -3              | 0.02    | 88424753  | no                         |
| C530043G21Rik            | 664  | 2.21            | chr1       | 158648556 | 158648601 | 463             | 0.02    | 158648556   | no                         |
| Pnkd                     | 664  | 2.21            | chr1       | 74331737  | 74331785  | 154             | 0.02    | 74331400, 74331573                                    | no                         |
| Tac2                     | 664  | 2.21            | chr10      | 127158953 | 127159004 | -3469           | 0.02    | 127158953   | no                         |
| Timeless                 | 664  | 2.21            | chr10      | 127669131 | 127669176 | -5966           | 0.02    | 127669545; 127669311; 127669545; 127669314            | yes                        |
| Skil                     | 665  | 2.2             | chr3       | 30994640  | 30994685  | 680             | 0.02    | 30994595, 30994571                                    | no                         |
| Pim2                     | 665  | 2.2             | chrX       | 7456020   | 7456072   | 615             | 0.02    | N/A   | no                         |
| Ncdn                     | 666  | 2.19            | chr4       | 126429827 | 126429872 | 841             | 0.02    | 126430113   | yes                        |
| Nr2f2                    | 666  | 2.19            | chr7       | 77505956  | 77506001  | -499            | 0.02    | 77506079  | yes                        |
| Ddx26b                   | 666  | 2.19            | chrX       | 53707733  | 53707791  | -291            | 0.02    | 53708061  | yes                        |
| Xpr1                     | 666  | 2.19            | chr1       | 157264566 | 157264611 | -14             | 0.02    | 157264683; 157264682; 157264791; 157264790            | yes                        |
| Pard6g                   | 666  | 2.19            | chr18      | 80243584  | 80243629  | -96             | 0.02    | 80243723; 80243723                                    | yes                        |
| Nxph3                    | 666  | 2.19            | chr11      | 95375185  | 95375230  | 671             | 0.02    | 95375185  | no                         |
| Rmi1                     | 666  | 2.19            | chr13      | 58503739  | 58503784  | 115             | 0.02    | 58503739  | no                         |
| Srpk1                    | 666  | 2.19            | chr17      | 28759236  | 28759281  | 141             | 0.02    | 28759189, 28759156, 28759450                          | no                         |
| Stk24                    | 666  | 2.19            | chr14      | 121779021 | 121779066 | -592            | 0.02    | 121778616, 121778558, 121778564, 121778748            | no                         |
| E130319B15Rik            | 667  | 2.18            | chr2       | 4639147   | 4639193   | -20             | 0.02    | 4639365   | yes                        |
| Jph4                     | 667  | 2.18            | chr14      | 55735772  | 55735817  | -679            | 0.02    | 55735772  | no                         |
| Npr2                     | 667  | 2.18            | chr4       | 43644615  | 43644660  | -168            | 0.02    | 43644615  | no                         |
| 2310028H24Rik            | 667  | 2.18            | chr4       | 41516021  | 41516066  | 498             | 0.02    | N/A   | no                         |
| Tle3                     | 667  | 2.18            | chr9       | 61220667  | 61220712  | 518             | 0.02    | N/A   | no                         |
| Prr14                    | 668  | 2.17            | chr7       | 134615244 | 134615289 | 139             | 0.02    | 134615593   | yes                        |
| Adams15                  | 669  | 2.16            | chr9       | 30729777  | 30729822  | 237             | 0.02    | 30729777  | no                         |
| Tmem166                  | 669  | 2.16            | chr6       | 81991640  | 81991685  | -4              | 0.02    | 81991640  | no                         |
| 1500005A01Rik            | 670  | 2.15            | chr14      | 56204072  | 56204117  | -3              | 0.02    | 56204429; 56204428                                    | yes                        |
| Mgat3                    | 670  | 2.15            | chr15      | 80003752  | 80003797  | -376            | 0.02    | 80004133; 80004133; 80004111                          | yes                        |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                 | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|---|----------------------------|
| Src           | 670  | 2.15            | chr2       | 157250456 | 157250501 | 450             | 0.02    | 157250403, 157250421                                  | no                         |
| Eps15         | 671  | 2.14            | chr4       | 108953155 | 108953200 | 271             | 0.03    | 108953486; 108953489                                  | yes                        |
| Mageb3        | 671  | 2.14            | chr2       | 121781671 | 121781716 | 134             | 0.02    | 121782338; 121782338; 121782276; 121782006; 121782005 | yes                        |
| Dtnb          | 671  | 2.14            | chr12      | 3572721   | 3572766   | 222             | 0.02    | 3572566, 3572522                                      | no                         |
| Nudt4         | 671  | 2.14            | chr10      | 95025929  | 95025974  | 849             | 0.02    | 95025929  | no                         |
| Gpr146        | 671  | 2.14            | chr5       | 139857004 | 139857050 | -8830           | 0.02    | N/A   | no                         |
| Ubl3          | 672  | 2.13            | chr5       | 149364038 | 149364083 | 304             | 0.03    | 149364410; 149364409                                  | yes                        |
| Zfp668        | 672  | 2.13            | chr7       | 135020107 | 135020152 | 207             | 0.03    | 135020346; 135020346                                  | yes                        |
| Abcd2         | 672  | 2.13            | chr15      | 91022148  | 91022201  | 64              | 0.02    | 91022484; 91022484                                    | yes                        |
| Foxg1         | 672  | 2.13            | chr12      | 50485979  | 50486024  | 2009            | 0.02    | 50485979  | no                         |
| Ptgir         | 672  | 2.13            | chr7       | 17491240  | 17491290  | -573            | 0.02    | 17491240  | no                         |
| Scyl3         | 672  | 2.13            | chr1       | 165859586 | 165859646 | -578            | 0.02    | 165859586   | no                         |
| Palm          | 673  | 2.12            | chr10      | 79256745  | 79256790  | 308             | 0.02    | 79256745  | no                         |
| Faf1          | 674  | 2.11            | chr4       | 109349260 | 109349305 | 51              | 0.03    | 109349397; 109349397; 109349421; 109349421            | yes                        |
| Fn3k          | 674  | 2.11            | chr11      | 121296260 | 121296305 | -3              | 0.02    | 121296205, 121296250, 121296098                       | no                         |
| Oxct1         | 674  | 2.11            | chr15      | 3977736   | 3977792   | 1337            | 0.02    | 3977736   | no                         |
| Vasp          | 674  | 2.11            | chr7       | 19857388  | 19857446  | -214            | 0.03    | N/A   | no                         |
| Actr10        | 675  | 2.1             | chr12      | 72039245  | 72039290  | 375             | 0.02    | 72039245  | no                         |
| Ankrd25       | 675  | 2.1             | chr9       | 21602380  | 21602425  | 588             | 0.03    | 21602380  | no                         |
| Cnmm4         | 676  | 2.09            | chr1       | 36528307  | 36528352  | -111            | 0.03    | 36528679  | yes                        |
| Unc13a        | 676  | 2.09            | chr8       | 74195045  | 74195090  | 478             | 0.03    | 74195459  | yes                        |
| Wbscr27       | 676  | 2.09            | chr5       | 135408558 | 135408603 | 338             | 0.03    | 135408719; 135408718                                  | yes                        |
| Fbxo6         | 676  | 2.09            | chr4       | 147524933 | 147524993 | 1054            | 0.03    | 147524933   | no                         |
| Jph1          | 676  | 2.09            | chr1       | 17087383  | 17087428  | 473             | 0.03    | 17087383  | no                         |
| BC021523      | 677  | 2.08            | chr15      | 85889266  | 85889311  | 1152            | 0.03    | 85889430; 85889429                                    | yes                        |
| BC046404      | 677  | 2.08            | chr11      | 62462072  | 62462117  | -69             | 0.02    | 62462208; 62462347; 62462208; 62462350                | yes                        |
| Pknox2        | 677  | 2.08            | chr9       | 36953462  | 36953512  | 1364            | 0.02    | 36953462  | no                         |
| Slc8a2        | 677  | 2.08            | chr7       | 16715197  | 16715242  | -428            | 0.03    | 16715197  | no                         |
| Cdk5r1        | 678  | 2.07            | chr11      | 80291109  | 80291154  | 585             | 0.02    | 80291304, 80290971                                    | no                         |
| Fbxl10        | 678  | 2.07            | chr5       | 123438549 | 123438594 | -30             | 0.03    | 123438526, 123438352                                  | no                         |
| Ormdl3        | 679  | 2.06            | chr11      | 98449721  | 98449766  | -1185           | 0.03    | 98449771, 98449777                                    | no                         |
| Rab38         | 679  | 2.06            | chr7       | 95578501  | 95578551  | -256            | 0.03    | 95578501  | no                         |
| B230317C12Rik | 679  | 2.06            | chr2       | 26483394  | 26483447  | -556            | 0.03    | N/A   | no                         |
| 0610010K14Rik | 680  | 2.05            | chr11      | 70051050  | 70051095  | 344             | 0.03    | 70051050  | no                         |
| Tmem35        | 680  | 2.05            | chrX       | 130829983 | 130830028 | 243             | 0.03    | 130829983   | no                         |
| Chd1          | 681  | 2.04            | chr17      | 15841675  | 15841720  | -555            | 0.03    | 15842040; 15842043                                    | yes                        |
| Myen          | 681  | 2.04            | chr12      | 12947500  | 12947546  | 1119            | 0.03    | 12947500  | no                         |
| Tgfb3         | 681  | 2.04            | chr12      | 87418005  | 87418060  | 1452            | 0.03    | 87418005  | no                         |
| Crtc2         | 682  | 2.03            | chr3       | 90058505  | 90058550  | 311             | 0.03    | 90058741  | yes                        |
| Ube2e1        | 682  | 2.03            | chr14      | 19164414  | 19164459  | -78             | 0.03    | 19164592  | yes                        |
| Glrx          | 682  | 2.03            | chr13      | 75977775  | 75977820  | 465             | 0.03    | 75977775  | no                         |
| Itgb1         | 682  | 2.03            | chr8       | 131209308 | 131209353 | -350            | 0.03    | 131209308   | no                         |
| Mmp14         | 683  | 2.02            | chr14      | 55050322  | 55050377  | -105            | 0.03    | 55050617; 55050617; 55050623                          | yes                        |
| Dynl1         | 683  | 2.02            | chr5       | 115749703 | 115749763 | 1210            | 0.03    | 115749703   | no                         |
| Slc29a2       | 683  | 2.02            | chr19      | 5023854   | 5023899   | -2229           | 0.03    | 5023854   | no                         |
| Uap1          | 683  | 2.02            | chr1       | 172105270 | 172105315 | -215            | 0.03    | 172105228, 172105206, 172105222                       | no                         |
| Dab1          | 684  | 2.01            | chr4       | 104039835 | 104039880 | -306            | 0.03    | 104040123   | yes                        |
| Abec4         | 685  | 2               | chr14      | 119105539 | 119105584 | -135            | 0.03    | 119105910; 119105933                                  | yes                        |
| Gdf10         | 685  | 2               | chr14      | 34736672  | 34736717  | -78             | 0.03    | 34736761  | yes                        |
| Pepd          | 685  | 2               | chr7       | 35695580  | 35695627  | -1821           | 0.03    | 35695768; 35695768                                    | yes                        |
| Nfib          | 685  | 2               | chr4       | 82153048  | 82153102  | -1863           | 0.03    | 82153048  | no                         |
| Pdzd3         | 685  | 2               | chr9       | 44058602  | 44058647  | 923             | 0.03    | 44058602  | no                         |
| Stac3         | 685  | 2               | chr10      | 126947580 | 126947625 | -4392           | 0.03    | N/A   | no                         |
| BC018371      | 686  | 1.99            | chr11      | 94463254  | 94463299  | -176            | 0.03    | 94463254  | no                         |
| Mapt          | 686  | 1.99            | chr11      | 104094269 | 104094320 | 1545            | 0.03    | 104094269   | no                         |
| Rab11fip5     | 686  | 1.99            | chr6       | 85324150  | 85324195  | 456             | 0.03    | 85324150  | no                         |
| Pnmt          | 686  | 1.99            | chr11      | 98249630  | 98249675  | 1707            | 0.03    | N/A   | no                         |
| Foxp4         | 687  | 1.98            | chr17      | 48059926  | 48059971  | 1633            | 0.03    | 48059926  | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene                     | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site            | WT1 Consensus Site Present |
|--------------------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Slc41a3                  | 687  | 1.98            | chr6       | 90571491  | 90571545  | 2309            | 0.03    | 90571491   | no                         |
| Diras2                   | 688  | 1.97            | chr13      | 52625649  | 52625697  | 532             | 0.03    | 52625649   | no                         |
| Ssfa2                    | 688  | 1.97            | chr2       | 79475980  | 79476025  | 306             | 0.04    | N/A  | no                         |
| Prkar1b                  | 689  | 1.96            | chr5       | 139605206 | 139605251 | 417             | 0.04    | 139605206  | no                         |
| Arhgap8                  | 689  | 1.96            | chr15      | 84512032  | 84512077  | 627             | 0.03    | N/A  | no                         |
| Zfp161                   | 690  | 1.95            | chr17      | 69732893  | 69732938  | -401            | 0.04    | 69733278; 69733281; 69733236                     | yes                        |
| Brsk1                    | 691  | 1.94            | chr7       | 4642903   | 4642948   | 397             | 0.04    | 4643042; 4643042; 4642913                        | yes                        |
| Sirt5                    | 691  | 1.94            | chr13      | 43461294  | 43461339  | -4768           | 0.03    | 43461294   | no                         |
| Zfp574                   | 691  | 1.94            | chr7       | 25862319  | 25862364  | 40              | 0.04    | 25858024, 25857809, 25858022, 25857997           | no                         |
| Dnajb10                  | 692  | 1.93            | chr1       | 75233022  | 75233067  | -17             | 0.04    | 75233177; 75233165                               | yes                        |
| 6330505N24Rik            | 692  | 1.93            | chr3       | 84283948  | 84283993  | 381             | 0.04    | 84283948   | no                         |
| Spred2                   | 692  | 1.93            | chr11      | 19823978  | 19824025  | -442            | 0.04    | 19823978   | no                         |
| Kdelc1                   | 692  | 1.93            | chr1       | 44158703  | 44158762  | 16886           | 0.04    | N/A  | no                         |
| E130114P18Rik            | 693  | 1.92            | chr4       | 97444652  | 97444697  | 358             | 0.04    | 97444895   | yes                        |
| Nr4a1                    | 693  | 1.92            | chr15      | 101097227 | 101097272 | -42             | 0.04    | 101097416  | yes                        |
| Pgrmc1                   | 693  | 1.92            | chrX       | 34138703  | 34138748  | 507             | 0.04    | 34138701, 34138681                               | no                         |
| 5730442P18Rik            | 693  | 1.92            | chr11      | 103225340 | 103225390 | -667            | 0.04    | N/A  | no                         |
| Sorcs1                   | 694  | 1.91            | chr19      | 50752933  | 50752978  | 146             | 0.04    | 50752947; 50753294; 50753294                     | yes                        |
| 4930412M03Rik            | 694  | 1.91            | chr11      | 59928402  | 59928452  | 9913            | 0.04    | 59928402   | no                         |
| X99384                   | 694  | 1.91            | chr10      | 60845390  | 60845435  | 859             | 0.04    | 60845390   | no                         |
| Lgr6                     | 695  | 1.9             | chr1       | 137001675 | 137001720 | 155             | 0.04    | 137002037  | yes                        |
| Bin1                     | 695  | 1.9             | chr18      | 32537327  | 32537372  | 480             | 0.04    | 32537703   | yes                        |
| Cdkn1c                   | 695  | 1.9             | chr7       | 150647382 | 150647431 | -505            | 0.04    | 150647234, 150647215, 150647240, 150647241       | no                         |
| Tax1bp3                  | 695  | 1.9             | chr11      | 72991021  | 72991066  | 460             | 0.04    | 72991021   | no                         |
| Tbx3                     | 695  | 1.9             | chr5       | 120120713 | 120120758 | 59              | 0.04    | 120120713  | no                         |
| Zfp3                     | 695  | 1.9             | chr11      | 70577737  | 70577782  | -188            | 0.04    | 70577737   | no                         |
| Vti1b                    | 696  | 1.89            | chr12      | 80273135  | 80273180  | 206             | 0.04    | 80273392; 80273507; 80273507                     | yes                        |
| Slc35e1                  | 696  | 1.89            | chr8       | 75016979  | 75017026  | -489            | 0.04    | 75016979   | no                         |
| Fxyd5                    | 697  | 1.88            | chr7       | 31827214  | 31827259  | -399            | 0.05    | 31827185, 31827147                               | no                         |
| Mbc2                     | 697  | 1.88            | chr10      | 127962196 | 127962241 | 697             | 0.04    | 127962196  | no                         |
| Plekhh3                  | 697  | 1.88            | chr11      | 101032141 | 101032186 | 452             | 0.04    | 101032141  | no                         |
| Tbcd1f6                  | 698  | 1.87            | chr11      | 119089660 | 119089705 | 131             | 0.04    | 119090040; 119089742; 119090032; 119090031       | yes                        |
| Lrrc4                    | 698  | 1.87            | chr6       | 28782622  | 28782667  | -897            | 0.05    | 28782687, 28782705, 28782681, 28782740, 28782592 | no                         |
| ENSMUST0000008358<br>2.1 | 698  | 1.87            | chr1       | 164147100 | 164147151 | 261035          | 0.05    | N/A  | no                         |
| Larp6                    | 699  | 1.86            | chr9       | 60560773  | 60560818  | -131            | 0.04    | 60561140; 60561031                               | yes                        |
| Slc25a37                 | 699  | 1.86            | chr14      | 69902684  | 69902729  | 454             | 0.04    | 69902684   | no                         |
| Ccnt2                    | 700  | 1.85            | chr1       | 129671054 | 129671100 | 337             | 0.05    | 129671054  | no                         |
| Galnt2                   | 700  | 1.85            | chr8       | 126755926 | 126755971 | 655             | 0.05    | 126755926  | no                         |
| Ppap2b                   | 700  | 1.85            | chr4       | 104830209 | 104830254 | 281             | 0.05    | 104830209  | no                         |
| Ddr1                     | 700  | 1.85            | chr17      | 35841379  | 35841434  | -322            | 0.04    | N/A  | no                         |
| Gtf2i                    | 700  | 1.85            | chr5       | 134790010 | 134790055 | 584             | 0.05    | N/A  | no                         |
| Syn2                     | 701  | 1.84            | chr6       | 115084796 | 115084841 | -101            | 0.05    | 115085078; 115085078                             | yes                        |
| Ak3l1                    | 701  | 1.84            | chr4       | 101092775 | 101092820 | 435             | 0.05    | 101092745, 101092671                             | no                         |
| Rap2a                    | 701  | 1.84            | chr14      | 120877052 | 120877097 | -608            | 0.05    | 120877052  | no                         |
| Zfp53                    | 701  | 1.84            | chr17      | 21625888  | 21625933  | -41             | 0.05    | 21625888   | no                         |
| Ap1s3                    | 701  | 1.84            | chr1       | 79668400  | 79668445  | 125             | 0.05    | N/A  | no                         |
| Chrd                     | 702  | 1.83            | chr16      | 20732670  | 20732715  | -507            | 0.05    | 20732670   | no                         |
| Rorc                     | 702  | 1.83            | chr3       | 94177233  | 94177278  | 549             | 0.06    | 94177233   | no                         |
| Skap2                    | 703  | 1.82            | chr6       | 51962155  | 51962200  | 370             | 0.05    | 51962491   | yes                        |
| Yeats4                   | 703  | 1.82            | chr10      | 116661501 | 116661546 | 5               | 0.05    | 116661748  | yes                        |
| Anp32b                   | 703  | 1.82            | chr4       | 46465201  | 46465246  | 1236            | 0.05    | 46465201   | no                         |
| C130026L21Rik            | 703  | 1.82            | chr5       | 112010630 | 112010686 | -106            | 0.05    | 112010630  | no                         |
| Fbxw7                    | 703  | 1.82            | chr3       | 84756093  | 84756143  | -14             | 0.05    | 84756093   | no                         |
| C1qdc2                   | 704  | 1.81            | chr4       | 155336917 | 155336962 | 514             | 0.06    | 155336917  | no                         |
| Kctd9                    | 704  | 1.81            | chr14      | 68334564  | 68334609  | 432             | 0.05    | 68334450, 68334378, 68334293, 68334316           | no                         |
| Sema6a                   | 704  | 1.81            | chr18      | 47528068  | 47528115  | 430             | 0.05    | 47528068   | no                         |
| Tmem126b                 | 705  | 1.8             | chr7       | 97624417  | 97624462  | 65              | 0.05    | 97624417   | no                         |

**Supplemental Table 4. Summary Statistics of WT1 ChIP-chip Peaks and Motif Discovery.**

| Gene          | Rank | Fold-Enrichment | Chromosome | Start     | End       | Distance to TSS | P-Value | Location of WT1 Matrix/Consensus Site                      | WT1 Consensus Site Present |
|---------------|------|-----------------|------------|-----------|-----------|-----------------|---------|--|----------------------------|
| Jundm2        | 706  | 1.79            | chr12      | 86939998  | 86940043  | -345            | 0.05    | 86940362; 86940322   | yes                        |
| Eda           | 706  | 1.79            | chrX       | 97170352  | 97170399  | -568            | 0.05    | 97170352   | no                         |
| Fxyd6         | 706  | 1.79            | chr9       | 45178515  | 45178560  | 271             | 0.05    | 45178515   | no                         |
| Mrp155        | 706  | 1.79            | chr11      | 59015808  | 59015853  | -188            | 0.05    | 59015808   | no                         |
| Oxr1          | 706  | 1.79            | chr15      | 41620566  | 41620611  | -472            | 0.05    | 41620654; 41620497   | no                         |
| Trappc5       | 706  | 1.79            | chr8       | 3672225   | 3672270   | -4228           | 0.06    | 3672225  | no                         |
| Mfn1          | 707  | 1.77            | chr3       | 32428792  | 32428852  | 415             | 0.06    | 32428876; 32428875   | yes                        |
| Gm71          | 707  | 1.77            | chr12      | 70683994  | 70684039  | -1              | 0.05    | 70684216; 70684215; 70684215                               | yes                        |
| Dock4         | 708  | 1.76            | chr12      | 41173034  | 41173079  | 417             | 0.06    | 41173034   | no                         |
| Cggbp1        | 709  | 1.75            | chr16      | 64851125  | 64851170  | -762            | 0.06    | 64851344; 64851329; 64851040                               | no                         |
| Nkx6-1        | 709  | 1.75            | chr5       | 102094435 | 102094480 | -728            | 0.06    | 102094435  | no                         |
| 1700012A16Rik | 710  | 1.74            | chr1       | 155271882 | 155271935 | -430            | 0.07    | 155272469; 155272444                                       | yes                        |
| Col13a1       | 710  | 1.74            | chr10      | 61441987  | 61442032  | -154            | 0.06    | 61442140; 61442139   | yes                        |
| Grtp1         | 710  | 1.74            | chr8       | 13199869  | 13199915  | 732             | 0.07    | 13200038   | yes                        |
| Usf2          | 710  | 1.74            | chr7       | 31741410  | 31741455  | 366             | 0.07    | 31741410   | no                         |
| Pan3          | 711  | 1.73            | chr5       | 148241873 | 148241918 | -568            | 0.07    | 148241873  | no                         |
| Lbx2          | 712  | 1.72            | chr6       | 83034247  | 83034298  | -2086           | 0.07    | 83034247   | no                         |
| Ehbp1         | 713  | 1.7             | chr11      | 22186735  | 22186780  | -917            | 0.07    | 22187168   | yes                        |
| Hspb8         | 714  | 1.68            | chr5       | 116873217 | 116873267 | -369            | 0.08    | 116873295; 116873298                                       | yes                        |
| Card10        | 714  | 1.68            | chr15      | 78634102  | 78634150  | -654            | 0.07    | 78634102   | no                         |
| Lrrc8d        | 714  | 1.68            | chr5       | 106128040 | 106128095 | -919            | 0.08    | 106128040  | no                         |
| Cnot4         | 715  | 1.67            | chr6       | 35083695  | 35083740  | -3              | 0.08    | 35083380; 35083388   | no                         |
| Trim46        | 715  | 1.67            | chr3       | 89047691  | 89047736  | 1407            | 0.08    | 89047691   | no                         |
| Gprc5a        | 716  | 1.65            | chr6       | 135015349 | 135015394 | -335            | 0.08    | 135015349  | no                         |
| Prkch         | 717  | 1.62            | chr12      | 74685598  | 74685643  | -407            | 0.08    | 74685943; 74685943   | yes                        |
| Slc35f2       | 717  | 1.62            | chr9       | 53619543  | 53619588  | 225             | 0.08    | 53619630; 53619630   | yes                        |
| Etv5          | 718  | 1.6             | chr16      | 22439533  | 22439578  | 87              | 0.09    | 22439672; 22439620; 22439619                               | yes                        |
| Wnt11         | 718  | 1.6             | chr7       | 105986752 | 105986802 | -577            | 0.1     | 105986763  | yes                        |
| Pank1         | 719  | 1.59            | chr19      | 34953561  | 34953606  | -1177           | 0.09    | 34953640; 34953551   | no                         |
| Mareks11      | 720  | 1.57            | chr4       | 129191319 | 129191365 | 455             | 0.11    | 129191471  | yes                        |
| BC079880      | 720  | 1.57            | chr8       | 108130344 | 108130389 | 1238            | 0.1     | N/A  | no                         |
| B3galnt2      | 721  | 1.53            | chr13      | 14047084  | 14047129  | 166             | 0.11    | 14047168; 14047089   | yes                        |
| Hip1r         | 722  | 1.51            | chr5       | 124423962 | 124424007 | 337             | 0.13    | 124423888; 124423894                                       | no                         |
| Ece1          | 723  | 1.49            | chr4       | 137417821 | 137417866 | -367            | 0.13    | 137417821  | no                         |
| Btbd12        | 724  | 1.45            | chr16      | 4003484   | 4003529   | -1826           | 0.14    | 4003885  | yes                        |
| Lass5         | 725  | 1.44            | chr15      | 99603245  | 99603290  | -322            | 0.14    | 99603245   | no                         |
| Antxr2        | 726  | 1.43            | chr5       | 98459520  | 98459565  | 439             | 0.15    | 98459520-98459565  | no                         |
| B3galnt4      | 726  | 1.43            | chr17      | 34088230  | 34088275  | 181             | 0.15    | 34088230-34088275  | no                         |
| 4121402D02Rik | 727  | 1.37            | chr11      | 98656629  | 98656674  | -430            | 0.18    | 98656763; 98656521; 98656587; 98656757; 98656621; 98656845 | no                         |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score   | Median P-Value | Geometric Mean | Category        | Term  | Count    | % of Total | P-Value       | Bonferroni   | Benjamini | FDR      | Information Content (bits) |          |          |          |      |
|------------------|--|----------------|----------------|-----------------|---|----------|------------|---------------|--|-----------|----------|----------------------------|----------|----------|----------|------|
| 1                | 20.43  | 8.64E-22       | 3.70E-21       | SP_PIR_KEYWORDS | Transcription regulation  | 216      | 13.4%      | 1.06E-24      | 9.18E-22   | 4.59E-22  | 1.64E-21 | 3.80                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006355~regulation of transcription, DNA-dependent   | 308      | 19.1%      | 1.76E-23      | 9.15E-20   | 1.14E-20  | 3.37E-20 | 3.19                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006351~transcription, DNA-dependent   | 308      | 19.1%      | 1.12E-22      | 5.80E-19   | 5.28E-20  | 2.14E-19 | 3.17                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process          | 321      | 19.9%      | 1.43E-22      | 7.42E-19   | 6.18E-20  | 2.73E-19 | 3.05                       |          |          |          |      |
|                  |  |                |                | SP_PIR_KEYWORDS | Transcription   | 213      | 13.2%      | 1.50E-22      | 1.30E-19   | 4.35E-20  | 2.33E-19 | 3.63                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0032774~RNA biosynthetic process   | 308      | 19.1%      | 1.61E-22      | 8.35E-19   | 6.42E-20  | 3.07E-19 | 3.17                       |          |          |          |      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0030528~transcription regulator activity   | 208      | 12.9%      | 1.82E-22      | 4.92E-19   | 1.64E-19  | 3.24E-19 | 3.89                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045449~regulation of transcription  | 314      | 19.5%      | 8.64E-22      | 4.49E-18   | 2.80E-19  | 1.65E-18 | 3.11                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006350~transcription  | 318      | 19.7%      | 1.08E-20      | 5.61E-17   | 2.95E-18  | 2.06E-17 | 3.06                       |          |          |          |      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0003677~DNA binding  | 278      | 17.3%      | 7.11E-19      | 1.92E-15   | 4.81E-16  | 1.27E-15 | 3.26                       |          |          |          |      |
|                  |  |                |                | SP_PIR_KEYWORDS | dna-binding   | 204      | 12.7%      | 8.89E-18      | 7.70E-15   | 1.93E-15  | 1.38E-14 | 3.75                       |          |          |          |      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0003700~transcription factor activity  | 151      | 9.4%       | 2.23E-16      | 6.01E-13   | 1.20E-13  | 4.00E-13 | 4.38                       |          |          |          |      |
|                  |  |                |                | 2               | 16.11   | 2.87E-14 | 7.82E-17   | GOTERM_BP_ALL | GO:0048856~anatomical structure development          | 292       | 18.1%    | 2.91E-23                   | 1.51E-19 | 1.68E-20 | 5.57E-20 | 3.20 |
|                  |  |                |                |                 |   |          |            | GOTERM_BP_ALL | GO:0007275~multicellular organismal development      | 313       | 19.4%    | 4.93E-23                   | 2.56E-19 | 2.56E-20 | 9.42E-20 | 3.06 |
| GOTERM_BP_ALL    | GO:0048731~system development                            | 257            | 15.9%          |                 |   |          |            | 2.17E-22      | 1.13E-18   | 8.06E-20  | 4.15E-19 | 3.41                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0009653~anatomical structure morphogenesis            | 194            | 12.0%          |                 |   |          |            | 1.06E-21      | 5.48E-18   | 3.22E-19  | 2.02E-18 | 3.92                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0007399~nervous system development                    | 121            | 7.5%           |                 |   |          |            | 8.82E-17      | 5.76E-13   | 2.51E-14  | 2.11E-13 | 4.76                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048869~cellular developmental process                | 240            | 14.9%          |                 |   |          |            | 5.74E-14      | 2.98E-10   | 1.03E-11  | 1.10E-10 | 3.17                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0030154~cell differentiation                          | 240            | 14.9%          |                 |   |          |            | 5.74E-14      | 2.98E-10   | 1.03E-11  | 1.10E-10 | 3.32                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0009887~organ morphogenesis                           | 97             | 6.0%           |                 |   |          |            | 5.76E-14      | 2.99E-10   | 9.97E-12  | 1.10E-10 | 4.77                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048513~organ development                             | 194            | 12.0%          |                 |   |          |            | 2.25E-13      | 1.17E-09   | 3.66E-11  | 4.31E-10 | 3.68                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048468~cell development                              | 173            | 10.7%          |                 |   |          |            | 7.73E-13      | 4.02E-09   | 1.15E-10  | 1.48E-09 | 3.91                       |          |          |          |      |
| 3                | 9.66   | 2.94E-10       | 2.21E-10       |                 |   |          |            | GOTERM_BP_ALL | GO:0048522~positive regulation of cellular process   | 143       | 8.9%     | 5.07E-15                   | 2.65E-11 | 1.02E-12 | 9.76E-12 | 4.26 |
|                  |  |                |                |                 |   |          |            | GOTERM_BP_ALL | GO:0048518~positive regulation of biological process | 150       | 9.3%     | 1.26E-12                   | 6.55E-09 | 1.77E-10 | 2.41E-09 | 4.11 |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045941~positive regulation of transcription   | 68       | 4.2%       | 6.39E-12      | 3.32E-08   | 8.29E-10  | 1.22E-08 | 5.76                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 68       | 4.2%       | 1.93E-11      | 1.00E-07   | 2.39E-09  | 3.69E-08 | 5.71                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006366~transcription from RNA polymerase II promoter  | 80       | 5.0%       | 2.69E-10      | 1.40E-06   | 3.04E-08  | 5.15E-07 | 5.30                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006357~regulation of transcription from RNA polymerase II promoter                                  | 74       | 4.6%       | 2.94E-10      | 1.52E-06   | 3.18E-08  | 5.61E-07 | 5.45                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0031325~positive regulation of cellular metabolic process  | 75       | 4.7%       | 3.99E-10      | 2.07E-06   | 4.23E-08  | 7.62E-07 | 5.35                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0009893~positive regulation of metabolic process   | 77       | 4.8%       | 1.07E-09      | 5.57E-06   | 1.07E-07  | 2.05E-06 | 5.30                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045893~positive regulation of transcription, DNA-dependent  | 54       | 3.4%       | 5.60E-09      | 2.91E-05   | 5.19E-07  | 1.07E-05 | 6.04                       |          |          |          |      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045944~positive regulation of transcription from RNA polymerase II promoter                         | 45       | 2.8%       | 1.48E-08      | 7.69E-05   | 1.35E-06  | 2.83E-05 | 6.40                       |          |          |          |      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016563~transcription activator activity   | 37       | 2.3%       | 2.77E-05      | 0.072  | 0.005     | 0.049    | 6.43                       |          |          |          |      |
|                  |  |                |                | 4               | 7.75  | 2.84E-07 | 1.79E-08   | GOTERM_BP_ALL | GO:0022008~neurogenesis                              | 76        | 4.7%     | 1.86E-13                   | 9.67E-10 | 3.12E-11 | 3.56E-10 | 5.52 |
|                  |  |                |                |                 |   |          |            | GOTERM_BP_ALL | GO:0048699~generation of neurons                     | 71        | 4.4%     | 7.76E-13                   | 4.03E-09 | 1.12E-10 | 1.48E-09 | 5.60 |
| GOTERM_BP_ALL    | GO:0030182~neuron differentiation                        | 65             | 4.0%           |                 |   |          |            | 1.37E-12      | 7.11E-09   | 1.87E-10  | 2.62E-09 | 5.77                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0032989~cellular structure morphogenesis              | 89             | 5.5%           |                 |   |          |            | 1.07E-10      | 5.56E-07   | 1.26E-08  | 2.05E-07 | 5.04                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0000902~cell morphogenesis                            | 89             | 5.5%           |                 |   |          |            | 1.07E-10      | 5.56E-07   | 1.26E-08  | 2.05E-07 | 5.13                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048666~neuron development                            | 51             | 3.2%           |                 |   |          |            | 5.81E-10      | 3.02E-06   | 6.04E-08  | 1.11E-06 | 6.21                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0016477~cell migration                                | 59             | 3.7%           |                 |   |          |            | 6.92E-10      | 3.59E-06   | 7.05E-08  | 1.32E-06 | 5.99                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0006928~cell motility                                 | 65             | 4.0%           |                 |   |          |            | 3.81E-09      | 1.98E-05   | 3.74E-07  | 7.29E-06 | 5.72                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0051674~localization of cell                          | 65             | 4.0%           |                 |   |          |            | 3.81E-09      | 1.98E-05   | 3.74E-07  | 7.29E-06 | 5.72                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0031175~neurite development                           | 41             | 2.5%           |                 |   |          |            | 5.64E-07      | 0.003  | 4.37E-05  | 0.001    | 6.53                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0032990~cell part morphogenesis                       | 51             | 3.2%           |                 |   |          |            | 7.54E-07      | 0.004  | 5.60E-05  | 0.001    | 5.94                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048858~cell projection morphogenesis                 | 51             | 3.2%           |                 |   |          |            | 7.54E-07      | 0.004  | 5.60E-05  | 0.001    | 5.98                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0030030~cell projection organization and biogenesis   | 51             | 3.2%           |                 |   |          |            | 7.54E-07      | 0.004  | 5.60E-05  | 0.001    | 5.98                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0007411~axon guidance                                 | 22             | 1.4%           |                 |   |          |            | 6.27E-06      | 0.032  | 3.87E-04  | 0.012    | 7.89                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0007409~axonogenesis                                  | 32             | 2.0%           |                 |   |          |            | 1.89E-05      | 0.094  | 0.001     | 0.036    | 6.87                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0000904~cellular morphogenesis during differentiation | 36             | 2.2%           |                 |   |          |            | 2.22E-05      | 0.109  | 0.001     | 0.042    | 6.54                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048812~neurite morphogenesis                         | 32             | 2.0%           |                 |   |          |            | 6.62E-05      | 0.291  | 0.003     | 0.126    | 6.77                       |          |          |          |      |
| GOTERM_BP_ALL    | GO:0048667~neuron morphogenesis during differentiation   | 32             | 2.0%           |                 |   |          |            | 6.62E-05      | 0.291  | 0.003     | 0.126    | 6.77                       |          |          |          |      |

The DAVID Functional Annotation tool identified 64 functional groups enriched in WT1 bound genes. Geometric means for each functional group were negative log-transformed to generate an enrichment score which ranks each functional group by overall importance (enrichment). The absolute (count) and relative frequency (% of total) of each term within a given functional group is given, together with its associated P-Value and information content. Multiple testing correction techniques were applied to control family-wise error rate (Bonferroni) and false discovery rate (FDR) (Benjamini-Hochberg).

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score   | Median P-Value | Geometric Mean | Category        | Term   | Count    | % of Total | P-Value       | Bonferroni                                      | Benjamini | FDR      | Information Content (bits) |
|------------------|--|----------------|----------------|-----------------|--|----------|------------|---------------|---|-----------|----------|----------------------------|
| 5                | 7.23   | 1.14E-06       | 5.92E-08       | GOTERM_BP_ALL   | GO:0048519--negative regulation of biological process  | 160      | 9.9%       | 9.78E-16      | 5.19E-12  | 2.08E-13  | 1.91E-12 | 4.08                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048523--negative regulation of cellular process  | 150      | 9.3%       | 7.88E-15      | 4.09E-11  | 1.52E-11  | 1.51E-11 | 4.20                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0016481--negative regulation of transcription   | 49       | 3.0%       | 8.14E-07      | 0.004   | 5.87E-05  | 0.002    | 6.00                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0031324--negative regulation of cellular metabolic process  | 57       | 3.5%       | 1.00E-06      | 0.005   | 7.11E-05  | 0.002    | 5.51                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045934--negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 51       | 3.2%       | 1.14E-06      | 0.006   | 7.99E-05  | 0.002    | 5.90                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0009892--negative regulation of metabolic process   | 62       | 3.9%       | 1.33E-06      | 0.007   | 9.21E-05  | 0.003    | 5.41                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016564--transcription repressor activity   | 33       | 2.1%       | 9.54E-06      | 0.025   | 0.003     | 0.017    | 6.72                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045892--negative regulation of transcription, DNA-dependent  | 36       | 2.2%       | 4.59E-05      | 0.212   | 0.002     | 0.088    | 6.43                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0000122--negative regulation of transcription from RNA polymerase II promoter                         | 24       | 1.5%       | 0.002         | 1   | 0.069     | 3.999    | 6.93                       |
|                  |  |                |                | 6               | 7.14   | 1.28E-07 | 7.17E-08   | GOTERM_BP_ALL | GO:0050793--regulation of developmental process | 57        | 3.5%     | 4.03E-09                   |
| GOTERM_BP_ALL    | GO:0045596--negative regulation of cell differentiation  | 26             | 1.6%           |                 |  |          |            | 8.97E-08      | 4.65E-04  | 7.76E-06  | 1.71E-04 | 7.35                       |
| GOTERM_BP_ALL    | GO:0045595--regulation of cell differentiation           | 38             | 2.4%           |                 |  |          |            | 1.66E-07      | 8.59E-04  | 1.36E-05  | 3.16E-04 | 6.16                       |
| GOTERM_BP_ALL    | GO:0051093--negative regulation of developmental process | 28             | 1.7%           |                 |  |          |            | 4.42E-07      | 0.002   | 3.48E-05  | 8.44E-04 | 5.80                       |
| 7                | 5.49   | 1.92E-05       | 3.25E-06       | GOTERM_BP_ALL   | GO:0000074--regulation of progression through cell cycle   | 62       | 3.9%       | 1.14E-07      | 5.91E-04  | 9.69E-06  | 2.17E-04 | 5.64                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0051726--regulation of cell cycle   | 62       | 3.9%       | 1.49E-07      | 7.74E-04  | 1.25E-05  | 2.85E-04 | 5.64                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007049--cell cycle   | 94       | 5.8%       | 1.92E-05      | 0.095   | 0.001     | 0.037    | 4.66                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0022402--cell cycle process   | 79       | 4.9%       | 2.28E-05      | 0.112   | 0.001     | 0.044    | 5.00                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045786--negative regulation of progression through cell cycle  | 27       | 1.7%       | 4.90E-05      | 0.225   | 0.003     | 0.094    | 7.00                       |
| 8                | 4.90   | 1.77E-05       | 1.25E-05       | SP_PIR_KEYWORDS | zinc   | 198      | 12.3%      | 1.27E-06      | 0.001   | 1.00E-04  | 0.002    | 3.54                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0008270--zinc ion binding   | 227      | 14.1%      | 1.68E-06      | 0.005   | 5.05E-04  | 0.003    | 3.33                       |
|                  |  |                |                | SP_PIR_KEYWORDS | zinc-finger  | 156      | 9.7%       | 2.31E-05      | 0.020   | 0.002     | 0.036    | 3.96                       |
|                  |  |                |                | SP_PIR_KEYWORDS | metal-binding  | 243      | 15.1%      | 1.39E-04      | 0.114   | 0.008     | 0.216    | 3.10                       |
| 9                | 4.84   | 1.38E-04       | 1.46E-05       | GOTERM_MF_ALL   | GO:0043565--sequence-specific DNA binding  | 87       | 5.4%       | 1.21E-11      | 3.26E-08  | 5.44E-09  | 2.15E-08 | 5.28                       |
|                  |  |                |                | INTERPRO        | IPR012287:Homeodomain-related  | 34       | 2.1%       | 2.68E-05      | 0.145   | 0.145     | 0.052    | 6.52                       |
|                  |  |                |                | INTERPRO        | IPR001356:Homeobox   | 34       | 2.1%       | 1.24E-04      | 0.516   | 0.305     | 0.239    | 6.51                       |
|                  |  |                |                | SP_PIR_KEYWORDS | Homeobox   | 41       | 2.5%       | 1.52E-04      | 0.124   | 0.008     | 0.236    | 6.24                       |
|                  |  |                |                | UP_SEQ_FEATURE  | DNA-binding region:Homeobox  | 31       | 1.9%       | 5.28E-04      | 1   | 0.670     | 1.113    | 6.70                       |
|                  |  |                |                | SMART           | SM00389:HOX  | 37       | 2.3%       | 0.003         | 0.842   | 0.842     | 4.404    | 6.39                       |
| 10               | 4.53   | 9.09E-06       | 2.95E-05       | GOTERM_BP_ALL   | GO:0030029--actin filament-based process   | 38       | 2.4%       | 4.97E-06      | 0.025   | 3.19E-04  | 0.010    | 6.50                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0030036--actin cytoskeleton organization and biogenesis   | 36       | 2.2%       | 9.09E-06      | 0.046   | 5.42E-04  | 0.017    | 6.57                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007010--cytoskeleton organization and biogenesis   | 67       | 4.2%       | 5.70E-04      | 0.948   | 0.022     | 1.083    | 5.29                       |
| 11               | 4.33   | 8.05E-05       | 4.64E-05       | GOTERM_BP_ALL   | GO:0007389--pattern specification process  | 44       | 2.7%       | 7.27E-07      | 0.004   | 5.55E-05  | 0.001    | 6.31                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0003002--regionalization  | 28       | 1.7%       | 8.05E-05      | 0.342   | 0.004     | 0.154    | 6.96                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0009952--anterior/posterior pattern formation   | 18       | 1.1%       | 0.002         | 1   | 0.060     | 3.213    | 7.63                       |
| 12               | 4.06   | 7.18E-05       | 8.66E-05       | GOTERM_BP_ALL   | GO:0001501--skeletal development   | 35       | 2.2%       | 8.13E-06      | 0.041   | 4.91E-04  | 0.016    | 6.63                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0046849--bone remodeling  | 23       | 1.4%       | 2.95E-05      | 0.142   | 0.002     | 0.056    | 7.40                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0001503--ossification   | 21       | 1.3%       | 6.14E-05      | 0.273   | 0.003     | 0.117    | 7.55                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0031214--biomineral formation   | 21       | 1.3%       | 7.18E-05      | 0.311   | 0.004     | 0.137    | 7.52                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0009888--tissue development   | 45       | 2.8%       | 1.30E-04      | 0.491   | 0.006     | 0.248    | 5.06                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048771--tissue remodeling  | 24       | 1.5%       | 1.47E-04      | 0.534   | 0.007     | 0.281    | 7.16                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0001649--osteoblast differentiation   | 9        | 0.6%       | 0.002         | 1   | 0.061     | 3.381    | 9.30                       |
| 13               | 3.88   | 3.90E-05       | 1.31E-04       | GOTERM_BP_ALL   | GO:0030324--lung development   | 19       | 1.2%       | 2.99E-06      | 0.015   | 1.96E-04  | 0.006    | 8.13                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0030323--respiratory tube development   | 19       | 1.2%       | 3.80E-06      | 0.020   | 2.47E-04  | 0.007    | 8.11                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0035295--tube development   | 35       | 2.2%       | 3.90E-05      | 0.183   | 0.002     | 0.075    | 6.47                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0001763--morphogenesis of a branching structure   | 13       | 0.8%       | 0.008         | 1   | 0.179     | 13.737   | 8.02                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048754--branching morphogenesis of a tube  | 12       | 0.7%       | 0.011         | 1   | 0.234     | 19.451   | 8.11                       |
| 14               | 3.84   | 1.14E-04       | 1.46E-04       | GOTERM_BP_ALL   | GO:0008283--cell proliferation   | 71       | 4.4%       | 7.12E-05      | 0.309   | 0.004     | 0.136    | 5.09                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0042127--regulation of cell proliferation   | 53       | 3.3%       | 1.14E-04      | 0.446   | 0.005     | 0.217    | 5.63                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0008284--positive regulation of cell proliferation  | 32       | 2.0%       | 3.86E-04      | 0.865   | 0.016     | 0.734    | 6.51                       |
| 15               | 3.83   | 8.33E-05       | 1.48E-04       | GOTERM_BP_ALL   | GO:0007417--central nervous system development   | 41       | 2.5%       | 6.06E-05      | 0.270   | 0.003     | 0.116    | 6.26                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007420--brain development  | 34       | 2.1%       | 8.33E-05      | 0.351   | 0.004     | 0.159    | 6.58                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0030900--forebrain development  | 20       | 1.2%       | 6.40E-04      | 0.964   | 0.025     | 1.217    | 7.52                       |



**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value  | Bonferroni | Benjamini | FDR      | Information Content (bits) |
|------------------|------------------|----------------|----------------|-----------------|--|-------|------------|----------|------------|-----------|----------|----------------------------|
| 16               | 3.83             | 1.07E-04       | 1.48E-04       | GOTERM_BP_ALL   | GO:0009790~embryonic development   | 66    | 4.1%       | 7.97E-06 | 0.041      | 4.87E-04  | 0.015    | 5.40                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048598~embryonic morphogenesis   | 35    | 2.2%       | 2.04E-05 | 0.101      | 0.001     | 0.039    | 6.32                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0021915~neural tube development   | 15    | 0.9%       | 8.25E-05 | 0.348      | 0.004     | 0.157    | 8.47                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0043009~chordate embryonic development                                  | 36    | 2.2%       | 1.32E-04 | 0.495      | 0.006     | 0.251    | 6.43                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0009792~embryonic development ending in birth or egg hatching           | 36    | 2.2%       | 1.73E-04 | 0.592      | 0.008     | 0.329    | 6.42                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001701~in utero embryonic development                                  | 18    | 1.1%       | 0.035    | 1          | 0.463     | 48.883   | 7.25                       |
| 17               | 3.72             | 0.002          | 1.92E-04       | GOTERM_BP_ALL   | GO:0006464~protein modification process                                    | 214   | 13.3%      | 2.24E-12 | 1.16E-08   | 2.98E-10  | 4.27E-09 | 3.50                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0043412~biopolymer modification   | 219   | 13.6%      | 6.87E-12 | 3.57E-08   | 8.70E-10  | 1.31E-08 | 3.45                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0043687~post-translational protein modification                         | 188   | 11.7%      | 3.16E-11 | 1.64E-07   | 3.82E-09  | 6.04E-08 | 3.71                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0006468~protein amino acid phosphorylation                              | 96    | 6.0%       | 3.54E-08 | 1.84E-04   | 3.16E-06  | 6.75E-05 | 4.83                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0006793~phosphorus metabolic process                                    | 120   | 7.4%       | 1.73E-07 | 8.98E-04   | 1.38E-05  | 3.30E-04 | 4.39                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0006796~phosphate metabolic process                                     | 120   | 7.4%       | 1.73E-07 | 8.98E-04   | 1.38E-05  | 3.30E-04 | 4.39                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0016310~phosphorylation   | 101   | 6.3%       | 1.71E-06 | 0.009      | 1.15E-04  | 0.003    | 4.65                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016301~kinase activity   | 113   | 7.0%       | 3.36E-05 | 0.087      | 0.006     | 0.060    | 4.40                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016773~phosphotransferase activity, alcohol group as acceptor          | 92    | 5.7%       | 7.24E-05 | 0.178      | 0.011     | 0.129    | 4.73                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0004672~protein kinase activity   | 80    | 5.0%       | 1.23E-04 | 0.283      | 0.017     | 0.219    | 4.97                       |
|                  |                  |                |                | INTERPRO        | IPR000719:Protein kinase, core   | 50    | 3.1%       | 1.58E-04 | 0.604      | 0.265     | 0.305    | 5.71                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | kinase   | 90    | 5.6%       | 7.23E-04 | 0.466      | 0.029     | 1.115    | 4.33                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016772~transferase activity, transferring phosphorus-containing groups | 119   | 7.4%       | 0.001    | 0.943      | 0.108     | 1.869    | 4.21                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0000166~nucleotide binding  | 207   | 12.8%      | 0.002    | 0.986      | 0.138     | 2.788    | 3.24                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0004674~protein serine/threonine kinase activity                        | 62    | 3.9%       | 0.002    | 0.993      | 0.145     | 3.240    | 5.26                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016740~transferase activity  | 191   | 11.9%      | 0.002    | 0.999      | 0.175     | 4.225    | 3.38                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0004713~protein-tyrosine kinase activity                                | 42    | 2.6%       | 0.004    | 1.000      | 0.251     | 6.608    | 5.87                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:Protein kinase  | 54    | 3.4%       | 0.004    | 1          | 0.982     | 8.370    | 5.69                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | nucleotide-binding   | 144   | 8.9%       | 0.005    | 0.980      | 0.119     | 6.777    | 3.76                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0032553~ribonucleotide binding  | 173   | 10.7%      | 0.007    | 1          | 0.355     | 11.400   | 3.51                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0032555~purine ribonucleotide binding                                   | 173   | 10.7%      | 0.007    | 1          | 0.355     | 11.400   | 3.51                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | binding site:ATP   | 56    | 3.5%       | 0.008    | 1          | 0.994     | 15.038   | 5.61                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | Serine/threonine-protein kinase  | 45    | 2.8%       | 0.017    | 1          | 0.282     | 22.923   | 5.73                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0032559~adenyl ribonucleotide binding                                   | 141   | 8.8%       | 0.018    | 1          | 0.539     | 27.459   | 3.82                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0017076~purine nucleotide binding                                       | 175   | 10.9%      | 0.018    | 1          | 0.542     | 28.048   | 3.45                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | active site:Proton acceptor  | 67    | 4.2%       | 0.019    | 1          | 1.000     | 33.256   | 5.26                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | transferase  | 135   | 8.4%       | 0.024    | 1          | 0.333     | 31.413   | 3.69                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | nucleotide phosphate-binding region:ATP                                    | 80    | 5.0%       | 0.028    | 1          | 1.000     | 45.609   | 4.90                       |
|                  |                  |                |                | INTERPRO        | IPR002290:Serine/threonine protein kinase                                  | 27    | 1.7%       | 0.032    | 1          | 0.978     | 46.786   | 6.48                       |
|                  |                  |                |                | INTERPRO        | IPR008271:Serine/threonine protein kinase, active site                     | 31    | 1.9%       | 0.038    | 1          | 0.979     | 52.671   | 6.21                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0005524~ATP binding   | 135   | 8.4%       | 0.046    | 1          | 0.766     | 56.466   | 3.84                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0030554~adenyl nucleotide binding                                       | 143   | 8.9%       | 0.047    | 1          | 0.770     | 57.269   | 3.75                       |
| SP_PIR_KEYWORDS  | atp-binding      | 105            | 6.5%           | 0.081           | 1  | 0.632 | 72.920     | 4.18     |            |           |          |                            |
| SMART            | SM00220:S_TKc    | 45             | 2.8%           | 0.108           | 1  | 0.923 | 81.616     | 5.69     |            |           |          |                            |
| 18               | 3.38             | 5.64E-04       | 4.13E-04       | SP_PIR_KEYWORDS | cytoskeleton   | 47    | 2.9%       | 1.01E-04 | 0.084      | 0.006     | 0.156    | 5.24                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0008092~cytoskeletal protein binding                                    | 55    | 3.4%       | 1.40E-04 | 0.316      | 0.018     | 0.249    | 5.58                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0003779~actin binding   | 39    | 2.4%       | 9.88E-04 | 0.931      | 0.105     | 1.745    | 6.08                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | actin-binding  | 28    | 1.7%       | 0.002    | 0.837      | 0.067     | 3.191    | 6.37                       |
| 19               | 2.62             | 0.003          | 0.002          | GOTERM_BP_ALL   | GO:0048646~anatomical structure formation                                  | 34    | 2.1%       | 1.35E-04 | 0.505      | 0.006     | 0.259    | 5.99                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001944~vasculature development   | 33    | 2.1%       | 0.002    | 1          | 0.063     | 3.568    | 6.27                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001568~blood vessel development  | 32    | 2.0%       | 0.003    | 1          | 0.092     | 5.503    | 6.29                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048514~blood vessel morphogenesis                                      | 28    | 1.7%       | 0.005    | 1          | 0.127     | 8.472    | 6.51                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001525~angiogenesis  | 21    | 1.3%       | 0.024    | 1          | 0.365     | 36.690   | 6.85                       |
| 20               | 2.55             | 0.004          | 0.003          | GOTERM_BP_ALL   | GO:0021915~neural tube development   | 15    | 0.9%       | 8.25E-05 | 0.348      | 0.004     | 0.157    | 8.47                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0035239~tube morphogenesis  | 25    | 1.6%       | 8.60E-04 | 0.989      | 0.032     | 1.630    | 6.93                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001841~neural tube formation   | 11    | 0.7%       | 0.002    | 1          | 0.079     | 4.653    | 8.81                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001839~neural plate morphogenesis                                      | 11    | 0.7%       | 0.003    | 1          | 0.092     | 5.527    | 8.77                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001840~neural plate development  | 11    | 0.7%       | 0.004    | 1          | 0.105     | 6.521    | 8.77                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001838~embryonic epithelial tube formation                             | 11    | 0.7%       | 0.004    | 1          | 0.117     | 7.645    | 8.70                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001843~neural tube closure   | 9     | 0.6%       | 0.005    | 1          | 0.137     | 9.611    | 9.25                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0002009~morphogenesis of an epithelium                                  | 19    | 1.2%       | 0.007    | 1          | 0.178     | 13.349   | 7.11                       |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score                             | Median P-Value | Geometric Mean | Category        | Term                                     | Count  | % of Total | P-Value  | Bonferroni | Benjamini | FDR    | Information Content (bits) |        |
|------------------|--|----------------|----------------|-----------------|--|--|------------|----------|------------|-----------|--------|----------------------------|--------|
| 20               | 2.55   | 0.004          | 0.003          | GOTERM_BP_ALL   | GO:0014020~primary neural tube formation | 9  | 0.6%       | 0.008    | 1          | 0.180     | 13.560 | 9.11                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0016331~morphogenesis of embryonic epithelium                                 | 12         | 0.7%     | 0.013      | 1         | 0.256  | 21.603                     | 8.33   |
| 21               | 2.55   | 0.003          | 0.003          | GOTERM_BP_ALL   | GO:0016049~cell growth                   | 24   | 1.5%       | 1.89E-04 | 0.625      | 0.008     | 0.360  | 7.18                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0008361~regulation of cell size   | 25         | 1.6%     | 3.35E-04   | 0.824     | 0.014  | 0.638                      | 7.00   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0040007~growth  | 39         | 2.4%     | 0.002      | 1         | 0.060  | 3.261                      | 6.07   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0001558~regulation of cell growth   | 18         | 1.1%     | 0.005      | 1         | 0.126  | 8.357                      | 7.43   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0040008~regulation of growth  | 24         | 1.5%     | 0.018      | 1         | 0.319  | 29.928                     | 6.68   |
|                  |  |                |                |                 | SP_PIR_KEYWORDS                          | growth regulation  | 8          | 0.5%     | 0.057      | 1         | 0.554  | 59.732                     | 8.73   |
| 22               | 2.54   | 0.003          | 0.003          | GOTERM_BP_ALL   | GO:0014706~striated muscle development   | 25   | 1.6%       | 3.35E-04 | 0.824      | 0.014     | 0.638  | 7.07                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0007517~muscle development  | 29         | 1.8%     | 0.001      | 0.997     | 0.042  | 2.155                      | 6.68   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0048747~muscle fiber development  | 15         | 0.9%     | 0.002      | 1         | 0.059  | 3.101                      | 8.04   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0048741~skeletal muscle fiber development                                     | 15         | 0.9%     | 0.002      | 1         | 0.059  | 3.101                      | 8.04   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0007519~skeletal muscle development   | 19         | 1.2%     | 0.003      | 1         | 0.081  | 4.841                      | 7.43   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0045662~negative regulation of myoblast differentiation                       | 4          | 0.3%     | 0.005      | 1         | 0.129  | 8.865                      | 12.06  |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0042692~muscle cell differentiation   | 14         | 0.9%     | 0.006      | 1         | 0.150  | 10.789                     | 7.93   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0045661~regulation of myoblast differentiation                                | 5          | 0.3%     | 0.009      | 1         | 0.203  | 16.330                     | 11.06  |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0045445~myoblast differentiation  | 9          | 0.6%     | 0.019      | 1         | 0.325  | 30.925                     | 8.81   |
| 23               | 2.43   | 0.004          | 0.004          | INTERPRO        | IPR011700:Basic leucine zipper           | 8  | 0.5%       | 3.26E-04 | 0.852      | 0.380     | 0.629  | 9.77                       |        |
|                  |  |                |                |                 | INTERPRO                                 | IPR004827:Basic-leucine zipper (bZIP) transcription factor domain:Leucine-zipper | 12         | 0.7%     | 0.001      | 1         | 0.539  | 2.520                      | 8.39   |
|                  |  |                |                |                 | UP_SEQ_FEATURE                           | domain:Leucine-zipper  | 19         | 1.2%     | 0.004      | 1         | 0.972  | 8.889                      | 7.58   |
|                  |  |                |                |                 | SMART                                    | SM00338:BRLZ   | 12         | 0.7%     | 0.012      | 1         | 0.828  | 15.773                     | 8.31   |
|                  |  |                |                |                 | INTERPRO                                 | IPR000837:Fos transforming protein   | 4          | 0.3%     | 0.031      | 1         | 0.977  | 45.489                     | 10.77  |
| 24               | 2.39   | 0.002          | 0.004          | GOTERM_BP_ALL   | GO:0016568~chromatin modification        | 31   | 1.9%       | 1.43E-04 | 0.524      | 0.006     | 0.273  | 6.73                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006323~DNA packaging   | 40         | 2.5%     | 8.08E-04   | 0.985     | 0.031  | 1.532                      | 5.89   |
|                  |  |                |                |                 | SP_PIR_KEYWORDS                          | Chromatin regulator  | 20         | 1.2%     | 0.001      | 0.691     | 0.048  | 2.082                      | 7.46   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006325~establishment and/or maintenance of chromatin architecture            | 38         | 2.4%     | 0.002      | 1         | 0.061  | 3.353                      | 6.04   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006259~DNA metabolic process   | 66         | 4.1%     | 0.113      | 1         | 0.786  | 89.812                     | 4.81   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0051276~chromosome organization and biogenesis                                | 40         | 2.5%     | 0.156      | 1         | 0.862  | 96.047                     | 5.69   |
| 25               | 2.28   | 0.007          | 0.005          | GOTERM_BP_ALL   | GO:0012501~programmed cell death         | 84   | 5.2%       | 3.61E-04 | 0.846      | 0.015     | 0.687  | 4.73                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0008219~cell death  | 86         | 5.3%     | 4.63E-04   | 0.910     | 0.019  | 0.882                      | 4.68   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043068~positive regulation of programmed cell death                          | 33         | 2.1%     | 4.66E-04   | 0.911     | 0.019  | 0.887                      | 6.47   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0016265~death   | 86         | 5.3%     | 5.04E-04   | 0.927     | 0.020  | 0.958                      | 4.68   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006915~apoptosis   | 82         | 5.1%     | 5.25E-04   | 0.935     | 0.021  | 0.999                      | 4.76   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043065~positive regulation of apoptosis                                      | 31         | 1.9%     | 0.002      | 1         | 0.057  | 2.954                      | 6.49   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006917~induction of apoptosis  | 24         | 1.5%     | 0.007      | 1         | 0.175  | 12.925                     | 6.84   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0012502~induction of programmed cell death                                    | 24         | 1.5%     | 0.007      | 1         | 0.175  | 12.925                     | 6.84   |
|                  |  |                |                |                 | SP_PIR_KEYWORDS                          | apoptosis  | 35         | 2.2%     | 0.009      | 1         | 0.200  | 13.723                     | 5.76   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043067~regulation of programmed cell death                                   | 54         | 3.4%     | 0.010      | 1         | 0.211  | 17.080                     | 5.32   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0042981~regulation of apoptosis   | 53         | 3.3%     | 0.011      | 1         | 0.236  | 19.765                     | 5.35   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043066~negative regulation of apoptosis                                      | 22         | 1.4%     | 0.095      | 1         | 0.743  | 85.055                     | 6.57   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043069~negative regulation of programmed cell death                          | 22         | 1.4%     | 0.107      | 1         | 0.776  | 88.474                     | 6.54   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006916~anti-apoptosis  | 9          | 0.6%     | 0.605      | 1         | 0.997  | 100                        | 7.47   |
|                  |  |                |                |                 | SP_PIR_KEYWORDS                          | glycosyltransferase  | 29         | 1.8%     | 0.003      | 0.936     | 0.088  | 4.804                      | 6.56   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006486~protein amino acid glycosylation                                      | 16         | 1.0%     | 0.004      | 1         | 0.105  | 6.615                      | 7.68   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043413~biopolymer glycosylation  | 16         | 1.0%     | 0.005      | 1         | 0.132  | 9.152                      | 7.63   |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0009100~glycoprotein metabolic process  | 19         | 1.2%     | 0.006      | 1         | 0.156  | 11.295                     | 6.96   |
|                  |  |                |                |                 | GOTERM_MF_ALL                            | GO:0016757~transferase activity, transferring glycosyl groups                    | 32         | 2.0%     | 0.009      | 1         | 0.401  | 14.669                     | 6.21   |
| GOTERM_BP_ALL    | GO:0009101~glycoprotein biosynthetic process | 16             | 1.0%           | 0.010           | 1  | 0.217  | 17.792     | 7.28     |            |           |        |                            |        |
| 26               | 2.25   | 0.006          | 0.006          | SP_PIR_KEYWORDS | glycosyltransferase                      | 29   | 1.8%       | 0.003    | 0.936      | 0.088     | 4.804  | 6.5599                     |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0006486~protein amino acid glycosylation                                      | 16         | 1.0%     | 0.004      | 1         | 0.105  | 6.615                      | 7.6846 |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0043413~biopolymer glycosylation  | 16         | 1.0%     | 0.005      | 1         | 0.132  | 9.152                      | 7.6333 |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0009100~glycoprotein metabolic process  | 19         | 1.2%     | 0.006      | 1         | 0.156  | 11.295                     | 6.9616 |
|                  |  |                |                |                 | GOTERM_MF_ALL                            | GO:0016757~transferase activity, transferring glycosyl groups                    | 32         | 2.0%     | 0.009      | 1         | 0.401  | 14.669                     | 6.2078 |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0009101~glycoprotein biosynthetic process                                     | 16         | 1.0%     | 0.010      | 1         | 0.217  | 17.792                     | 7.2782 |
| 27               | 2.20   | 0.005          | 0.006          | GOTERM_BP_ALL   | GO:0050673~epithelial cell proliferation | 11   | 0.7%       | 2.79E-04 | 0.765      | 0.012     | 0.532  | 8.97                       |        |
|                  |  |                |                |                 | GOTERM_BP_ALL                            | GO:0050678~regulation of epithelial cell proliferation                           | 8          | 0.5%     | 0.005      | 1         | 0.132  | 9.212                      | 9.30   |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value  | Bonferroni | Benjamini | FDR    | Information Content (bits) |
|------------------|------------------|----------------|----------------|-----------------|--|-------|------------|----------|------------|-----------|--------|----------------------------|
| 27               | 2.20             | 0.005          | 0.006          | GOTERM_BP_ALL   | GO:0050679--positive regulation of epithelial cell proliferation | 4     | 0.3%       | 0.179    | 1          | 0.884     | 97.698 | 9.81                       |
| 28               | 2.15             | 0.018          | 0.007          |                 |  |       |            |          |            |           |        |                            |
|                  |                  |                |                | SP_PIR_KEYWORDS | golgi apparatus  | 60    | 3.7%       | 1.57E-04 | 0.127      | 0.008     | 0.243  | 5.36                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0008194--UDP-glycosyltransferase activity                     | 20    | 1.2%       | 5.09E-04 | 0.748      | 0.058     | 0.903  | 7.49                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | glycosyltransferase  | 29    | 1.8%       | 0.003    | 0.936      | 0.088     | 4.804  | 6.56                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016757--transferase activity, transferring glycosyl groups   | 32    | 2.0%       | 0.009    | 1          | 0.401     | 14.669 | 6.21                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | Manganese  | 19    | 1.2%       | 0.018    | 1          | 0.299     | 24.901 | 7.23                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0016758--transferase activity, transferring hexosyl groups    | 22    | 1.4%       | 0.020    | 1          | 0.559     | 30.691 | 6.85                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | signal-anchor  | 42    | 2.6%       | 0.028    | 1          | 0.366     | 36.088 | 5.68                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | topological domain:Luminal                                       | 37    | 2.3%       | 0.035    | 1          | 1         | 53.440 | 6.09                       |
|                  |                  |                |                | KEGG_PATHWAY    | mmu01030:Glycan structures - biosynthesis 1                      | 19    | 1.2%       | 0.054    | 1          | 0.314     | 50.292 | 7.40                       |
| 29               | 2.14             | 0.012          | 0.007          | INTERPRO        | IPR011598:Helix-loop-helix DNA-binding                           | 16    | 1.0%       | 0.001    | 0.997      | 0.631     | 1.952  | 7.73                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | DNA-binding region:Basic motif                                   | 24    | 1.5%       | 0.001    | 1          | 0.862     | 3.087  | 7.22                       |
|                  |                  |                |                | INTERPRO        | IPR001092:Basic helix-loop-helix dimerisation region bHLH        | 16    | 1.0%       | 0.012    | 1          | 0.897     | 21.311 | 7.39                       |
|                  |                  |                |                | SMART           | SM00353:HLH  | 18    | 1.1%       | 0.031    | 1          | 0.798     | 37.377 | 7.31                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:Helix-loop-helix motif                                    | 15    | 0.9%       | 0.033    | 1          | 1         | 50.744 | 7.79                       |
| 30               | 3.11             | 0.011          | 0.008          | GOTERM_BP_ALL   | GO:0045926--negative regulation of growth                        | 11    | 0.7%       | 0.001    | 0.997      | 0.042     | 2.172  | 8.74                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001558--regulation of cell growth                            | 18    | 1.1%       | 0.005    | 1          | 0.126     | 8.357  | 7.43                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0030308--negative regulation of cell growth                   | 7     | 0.4%       | 0.017    | 1          | 0.300     | 27.374 | 9.36                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0045792--negative regulation of cell size                     | 7     | 0.4%       | 0.043    | 1          | 0.521     | 56.863 | 9.02                       |
| 31               | 2.05             | 0.012          | 0.009          | INTERPRO        | IPR000504:RNA recognition motif, RNP-1                           | 27    | 1.7%       | 0.001    | 0.998      | 0.536     | 2.007  | 6.87                       |
|                  |                  |                |                | INTERPRO        | IPR012677:Nucleotide-binding, alpha-beta plait                   | 27    | 1.7%       | 0.001    | 0.998      | 0.536     | 2.007  | 6.87                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | rna-binding  | 48    | 3.0%       | 0.012    | 1          | 0.236     | 17.522 | 5.58                       |
|                  |                  |                |                | SMART           | SM00360:RRM  | 29    | 1.8%       | 0.032    | 1          | 0.776     | 37.781 | 6.71                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0003723--RNA binding  | 60    | 3.7%       | 0.126    | 1          | 0.948     | 90.907 | 4.92                       |
| 32               | 2.04             | 0.024          | 0.009          | GOTERM_BP_ALL   | GO:0048598--embryonic morphogenesis                              | 35    | 2.2%       | 2.04E-05 | 0.101      | 0.001     | 0.039  | 6.32                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0030326--embryonic limb morphogenesis                         | 12    | 0.7%       | 0.016    | 1          | 0.293     | 26.307 | 8.18                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0035113--embryonic appendage morphogenesis                    | 12    | 0.7%       | 0.016    | 1          | 0.293     | 26.307 | 8.18                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048736--appendage development                                | 13    | 0.8%       | 0.024    | 1          | 0.372     | 37.682 | 7.99                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0060173--limb development                                     | 13    | 0.8%       | 0.024    | 1          | 0.372     | 37.682 | 7.99                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0035107--appendage morphogenesis                              | 12    | 0.7%       | 0.041    | 1          | 0.513     | 55.386 | 8.06                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0035108--limb morphogenesis                                   | 12    | 0.7%       | 0.041    | 1          | 0.513     | 55.386 | 8.06                       |
| 33               | 2.00             | 0.003          | 0.010          | GOTERM_BP_ALL   | GO:0048332--mesoderm morphogenesis                               | 9     | 0.6%       | 0.002    | 1          | 0.061     | 3.381  | 9.42                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001704--formation of primary germ layer                      | 9     | 0.6%       | 0.002    | 1          | 0.061     | 3.381  | 9.42                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0007498--mesoderm development                                 | 12    | 0.7%       | 0.002    | 1          | 0.067     | 3.821  | 8.57                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0007369--gastrulation   | 13    | 0.8%       | 0.002    | 1          | 0.073     | 4.237  | 8.36                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001707--mesoderm formation                                   | 8     | 0.5%       | 0.004    | 1          | 0.117     | 7.402  | 9.54                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048729--tissue morphogenesis                                 | 13    | 0.8%       | 0.038    | 1          | 0.485     | 51.894 | 6.48                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048340--paraxial mesoderm morphogenesis                      | 3     | 0.2%       | 0.165    | 1          | 0.868     | 96.790 | 10.89                      |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048339--paraxial mesoderm development                        | 3     | 0.2%       | 0.258    | 1          | 0.935     | 99.664 | 10.60                      |
| 34               | 2.00             | 0.010          | 0.010          | GOTERM_BP_ALL   | GO:0007423--sensory organ development                            | 27    | 1.7%       | 0.006    | 1          | 0.156     | 11.316 | 6.70                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0042471--ear morphogenesis                                    | 12    | 0.7%       | 0.009    | 1          | 0.199     | 15.562 | 8.23                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0043583--ear development                                      | 14    | 0.9%       | 0.010    | 1          | 0.219     | 18.144 | 7.93                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0042472--inner ear morphogenesis                              | 11    | 0.7%       | 0.013    | 1          | 0.258     | 22.038 | 8.39                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048839--inner ear development                                | 13    | 0.8%       | 0.014    | 1          | 0.265     | 22.946 | 8.06                       |
| 35               | 2.00             | 0.003          | 0.010          | GOTERM_BP_ALL   | GO:0030334--regulation of cell migration                         | 14    | 0.9%       | 0.002    | 1          | 0.056     | 2.918  | 8.13                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0051270--regulation of cell motility                          | 15    | 0.9%       | 0.002    | 1          | 0.063     | 3.557  | 7.87                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0040011--locomotion   | 16    | 1.0%       | 0.003    | 1          | 0.097     | 5.904  | 5.49                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0040012--regulation of locomotion                             | 15    | 0.9%       | 0.003    | 1          | 0.097     | 5.949  | 7.72                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0030335--positive regulation of cell migration                | 5     | 0.3%       | 0.045    | 1          | 0.537     | 58.666 | 9.89                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0051272--positive regulation of cell motility                 | 5     | 0.3%       | 0.088    | 1          | 0.719     | 82.730 | 9.60                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0040017--positive regulation of locomotion                    | 5     | 0.3%       | 0.088    | 1          | 0.719     | 82.730 | 9.20                       |
| 36               | 1.95             | 0.009          | 0.011          | GOTERM_BP_ALL   | GO:0048546--digestive tract morphogenesis                        | 7     | 0.4%       | 5.07E-04 | 0.928      | 0.020     | 0.964  | 10.36                      |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048557--embryonic digestive tract morphogenesis              | 5     | 0.3%       | 0.004    | 1          | 0.115     | 7.462  | 10.74                      |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048565--gut development                                      | 7     | 0.4%       | 0.004    | 1          | 0.120     | 7.841  | 9.89                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048568--embryonic organ development                          | 10    | 0.6%       | 0.004    | 1          | 0.121     | 7.978  | 8.93                       |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score                                 | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value  | Bonferroni | Benjamini | FDR    | Information Content (bits) |
|------------------|--|----------------|----------------|-----------------|--|-------|------------|----------|------------|-----------|--------|----------------------------|
| 36               | 1.95   | 0.009          | 0.011          | GOTERM_BP_ALL   | GO:0048562--embryonic organ morphogenesis                          | 7     | 0.4%       | 0.007    | 1          | 0.174     | 12.773 | 9.60                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048567--ectodermal gut morphogenesis                           | 5     | 0.3%       | 0.009    | 1          | 0.203     | 16.330 | 10.89                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007439--ectodermal gut development                             | 5     | 0.3%       | 0.009    | 1          | 0.203     | 16.330 | 10.89                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048547--gut morphogenesis                                      | 5     | 0.3%       | 0.013    | 1          | 0.258     | 22.181 | 10.60                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048566--embryonic gut development                              | 5     | 0.3%       | 0.018    | 1          | 0.312     | 28.816 | 10.36                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048558--embryonic gut morphogenesis                            | 4     | 0.3%       | 0.023    | 1          | 0.358     | 35.267 | 10.89                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007440--foregut morphogenesis                                  | 3     | 0.2%       | 0.057    | 1          | 0.603     | 67.308 | 11.74                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048613--embryonic ectodermal gut morphogenesis                 | 3     | 0.2%       | 0.081    | 1          | 0.704     | 79.966 | 11.47                      |
| GOTERM_BP_ALL    | GO:0048611--embryonic ectodermal gut development | 3              | 0.2%           | 0.081           | 1  | 0.704 | 79.966     | 11.47    |            |           |        |                            |
| 37               | 1.86   | 0.015          | 0.014          | GOTERM_BP_ALL   | GO:0022610--biological adhesion                                    | 76    | 4.7%       | 0.005    | 1          | 0.128     | 8.626  | 4.89                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007155--cell adhesion  | 76    | 4.7%       | 0.005    | 1          | 0.128     | 8.626  | 4.89                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0016337--cell-cell adhesion                                     | 32    | 2.0%       | 0.026    | 1          | 0.385     | 39.221 | 6.27                       |
|                  |  |                |                | SP_PIR_KEYWORDS | cell adhesion  | 39    | 2.4%       | 0.064    | 1          | 0.573     | 63.923 | 5.71                       |
| 38               | 1.79   | 0.013          | 0.016          | INTERPRO        | IPR003659:Plexin/semaphorin/integrin                               | 11    | 0.7%       | 0.003    | 1          | 0.637     | 5.199  | 8.88                       |
|                  |  |                |                | INTERPRO        | IPR002165:Plexin   | 8     | 0.5%       | 0.009    | 1          | 0.886     | 15.757 | 9.51                       |
|                  |  |                |                | INTERPRO        | IPR001627:Semaphorin/CD100 antigen                                 | 8     | 0.5%       | 0.011    | 1          | 0.893     | 18.657 | 9.45                       |
|                  |  |                |                | SMART           | SM00423:PSI  | 11    | 0.7%       | 0.013    | 1          | 0.726     | 17.266 | 8.88                       |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:Sema  | 7     | 0.4%       | 0.029    | 1          | 1         | 46.201 | 9.84                       |
|                  |  |                |                | SMART           | SM00630:Sema   | 8     | 0.5%       | 0.032    | 1          | 0.755     | 38.166 | 9.45                       |
|                  |  |                |                | PIR_SUPERFAMILY | PIRSF005526:semaphorin   | 4     | 0.3%       | 0.104    | 1          | 1         | 86.177 | 10.63                      |
| 39               | 1.78   | 0.035          | 0.017          | INTERPRO        | IPR003619:MAD homology 1, Dwarf-fin-type                           | 6     | 0.4%       | 0.003    | 1          | 0.636     | 4.880  | 10.39                      |
|                  |  |                |                | SMART           | SM00523:DWA  | 6     | 0.4%       | 0.007    | 0.983      | 0.871     | 9.505  | 10.39                      |
|                  |  |                |                | INTERPRO        | IPR000647:CTF/NF-I   | 3     | 0.2%       | 0.035    | 1          | 0.978     | 50.147 | 11.51                      |
|                  |  |                |                | PIR_SUPERFAMILY | PIRSF018476:nuclear factor 1                                       | 3     | 0.2%       | 0.037    | 1          | 1         | 49.151 | 11.51                      |
|                  |  |                |                | UP_SEQ_FEATURE  | DNA-binding region:CTF/NF-I  | 3     | 0.2%       | 0.058    | 1          | 1         | 71.818 | 11.77                      |
| 40               | 1.76   | 0.016          | 0.017          | INTERPRO        | IPR000697:EVH1   | 5     | 0.3%       | 0.013    | 1          | 0.895     | 21.721 | 10.39                      |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:WH1   | 5     | 0.3%       | 0.016    | 1          | 1         | 28.187 | 10.51                      |
|                  |  |                |                | SMART           | SM00461:WH1  | 5     | 0.3%       | 0.027    | 1          | 0.869     | 32.789 | 10.39                      |
| 41               | 1.75   | 0.024          | 0.018          | GOTERM_BP_ALL   | GO:0007267--cell-cell signaling                                    | 56    | 3.5%       | 1.29E-05 | 0.065      | 0.001     | 0.025  | 5.65                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0019226--transmission of nerve impulse                          | 34    | 2.1%       | 0.006    | 1          | 0.143     | 10.140 | 6.20                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0007268--synaptic transmission                                  | 27    | 1.7%       | 0.024    | 1          | 0.366     | 36.905 | 6.47                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0050877--neurological system process                            | 47    | 2.9%       | 1        | 1          | 1         | 100    | 3.61                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0003008--system process   | 56    | 3.5%       | 1        | 1          | 1         | 100    | 3.48                       |
| 42               | 1.75   | 0.016          | 0.018          | GOTERM_MF_ALL   | GO:0019901--protein kinase binding                                 | 13    | 0.8%       | 0.015    | 1          | 0.506     | 23.923 | 8.13                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0019900--kinase binding   | 14    | 0.9%       | 0.016    | 1          | 0.513     | 24.698 | 7.95                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0019899--enzyme binding   | 28    | 1.7%       | 0.023    | 1          | 0.580     | 34.051 | 6.46                       |
| 43               | 1.73   | 0.037          | 0.019          | GOTERM_BP_ALL   | GO:0007369--gastrulation   | 13    | 0.8%       | 0.002    | 1          | 0.073     | 4.237  | 8.36                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0010003--gastrulation (sensu Mammalia)                          | 6     | 0.4%       | 0.016    | 1          | 0.294     | 26.762 | 9.47                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048276--gastrulation (sensu Vertebrata)                        | 6     | 0.4%       | 0.057    | 1          | 0.599     | 67.392 | 9.47                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0001702--gastrulation with mouth forming second                 | 6     | 0.4%       | 0.057    | 1          | 0.599     | 67.392 | 9.47                       |
| 44               | 1.73   | 0.017          | 0.019          | GOTERM_MF_ALL   | GO:0008194--UDP-glycosyltransferase activity                       | 20    | 1.2%       | 5.09E-04 | 0.748      | 0.058     | 0.903  | 7.49                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0004653--polypeptide N-acetylgalactosaminyltransferase activity | 7     | 0.4%       | 0.001    | 0.959      | 0.116     | 2.083  | 10.25                      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0008376--acetylgalactosaminyltransferase activity               | 9     | 0.6%       | 0.002    | 0.993      | 0.147     | 3.190  | 9.36                       |
|                  |  |                |                | UP_SEQ_FEATURE  | region of interest:Catalytic subdomain A                           | 7     | 0.4%       | 0.004    | 1          | 0.982     | 8.814  | 10.28                      |
|                  |  |                |                | UP_SEQ_FEATURE  | region of interest:Catalytic subdomain B                           | 7     | 0.4%       | 0.004    | 1          | 0.982     | 8.814  | 10.28                      |
|                  |  |                |                | INTERPRO        | IPR000772:Ricin B lectin   | 8     | 0.5%       | 0.005    | 1          | 0.737     | 8.826  | 9.63                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0030145--manganese ion binding                                  | 21    | 1.3%       | 0.005    | 1          | 0.317     | 9.338  | 7.13                       |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:Ricin B-type lectin   | 7     | 0.4%       | 0.006    | 1          | 0.986     | 12.201 | 10.18                      |
|                  |  |                |                | SMART           | SM00458:RICIN  | 8     | 0.5%       | 0.015    | 1          | 0.739     | 20.487 | 9.63                       |
|                  |  |                |                | SP_PIR_KEYWORDS | Manganese  | 19    | 1.2%       | 0.018    | 1          | 0.299     | 24.901 | 7.23                       |
|                  |  |                |                | INTERPRO        | IPR001173:Glycosyl transferase, family 2                           | 6     | 0.4%       | 0.019    | 1          | 0.939     | 31.446 | 9.84                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016758--transferase activity, transferring hexosyl groups      | 22    | 1.4%       | 0.020    | 1          | 0.559     | 30.691 | 6.85                       |
|                  |  |                |                | KEGG_PATHWAY    | mmu01030:Glycan structures - biosynthesis 1                        | 19    | 1.2%       | 0.054    | 1          | 0.314     | 50.292 | 7.40                       |
|                  |  |                |                | KEGG_PATHWAY    | mmu00512:O-Glycan biosynthesis                                     | 7     | 0.4%       | 0.067    | 1          | 0.346     | 58.054 | 9.39                       |
|                  |  |                |                | PIR_SUPERFAMILY | PIRSF005670:polypeptide N-acetylgalactosaminyltransferase          | 3     | 0.2%       | 0.198    | 1          | 1         | 98.163 | 11.09                      |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006493--protein amino acid O-linked glycosylation              | 3     | 0.2%       | 0.441    | 1          | 0.986     | 99.999 | 9.97                       |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value  | Bonferroni | Benjamini | FDR    | Information Content (bits) |
|------------------|------------------|----------------|----------------|-----------------|--|-------|------------|----------|------------|-----------|--------|----------------------------|
| 44               | 1.73             | 0.017          | 0.019          | SP_PIR_KEYWORDS | lectin   | 13    | 0.8%       | 0.783    | 1          | 0.999     | 100    | 5.94                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0005529-sugar binding                                     | 14    | 0.9%       | 0.892    | 1          | 1         | 100    | 6.49                       |
| 45               | 1.72             | 0.015          | 0.019          | INTERPRO        | IPR000832:GPCR, family 2, secretin-like                      | 13    | 0.8%       | 0.001    | 0.998      | 0.505     | 2.067  | 8.63                       |
|                  |                  |                |                | INTERPRO        | IPR000539:Frizzled protein                                   | 5     | 0.3%       | 0.009    | 1          | 0.879     | 15.969 | 10.77                      |
|                  |                  |                |                | INTERPRO        | IPR015526:Frizzled related                                   | 6     | 0.4%       | 0.009    | 1          | 0.873     | 16.781 | 10.18                      |
|                  |                  |                |                | INTERPRO        | IPR000024:Frizzled CRD region                                | 7     | 0.4%       | 0.011    | 1          | 0.885     | 18.685 | 9.63                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:FZ  | 7     | 0.4%       | 0.015    | 1          | 1         | 26.702 | 9.77                       |
|                  |                  |                |                | SMART           | SM00063:FRI  | 7     | 0.4%       | 0.029    | 1          | 0.861     | 35.138 | 9.63                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | short sequence motif:Lys-Thr-X-X-Trp motif                   | 4     | 0.3%       | 0.061    | 1          | 1         | 73.613 | 11.09                      |
|                  |                  |                |                | UP_SEQ_FEATURE  | short sequence motif:PDZ-binding                             | 11    | 0.7%       | 0.081    | 1          | 1         | 83.367 | 8.42                       |
|                  |                  |                |                | PIR_SUPERFAMILY | PIRSF006696:fruit fly frizzled protein                       | 3     | 0.2%       | 0.167    | 1          | 1         | 96.357 | 11.09                      |
| 46               | 1.71             | 0.046          | 0.019          | INTERPRO        | IPR001202:WW/Rsp5/WWP  | 12    | 0.7%       | 0.002    | 1          | 0.633     | 3.569  | 8.63                       |
|                  |                  |                |                | SMART           | SM00456:WW   | 12    | 0.7%       | 0.012    | 1          | 0.828     | 15.773 | 8.60                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:WW 1  | 5     | 0.3%       | 0.081    | 1          | 1         | 83.194 | 10.18                      |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:WW 2  | 5     | 0.3%       | 0.081    | 1          | 1         | 83.194 | 10.18                      |
| 47               | 1.71             | 0.043          | 0.020          | GOTERM_MF_ALL   | GO:0003682-chromatin binding                                 | 21    | 1.3%       | 0.001    | 0.970      | 0.122     | 2.279  | 7.32                       |
|                  |                  |                |                | INTERPRO        | IPR000953:Chromo   | 7     | 0.4%       | 0.019    | 1          | 0.940     | 30.996 | 9.51                       |
|                  |                  |                |                | SMART           | SM00298:CHROMO   | 7     | 0.4%       | 0.066    | 1          | 0.862     | 63.721 | 9.51                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:Chromo 1  | 3     | 0.2%       | 0.090    | 1          | 1         | 86.451 | 12.09                      |
| 48               | 1.68             | 0.019          | 0.021          | GOTERM_BP_ALL   | GO:0045665-negative regulation of neuron differentiation     | 6     | 0.4%       | 0.016    | 1          | 0.294     | 26.762 | 9.81                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0045664-regulation of neuron differentiation              | 8     | 0.5%       | 0.019    | 1          | 0.318     | 30.022 | 7.93                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0048663-neuron fate commitment                            | 6     | 0.4%       | 0.030    | 1          | 0.423     | 43.964 | 9.60                       |
| 49               | 1.67             | 0.030          | 0.022          | INTERPRO        | IPR001965:Zinc finger, PHD-type                              | 16    | 1.0%       | 0.003    | 1          | 0.631     | 5.435  | 8.18                       |
|                  |                  |                |                | SMART           | SM00249:PHD  | 16    | 1.0%       | 0.030    | 1          | 0.839     | 35.916 | 8.11                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | zinc finger region:PHD-type                                  | 6     | 0.4%       | 0.117    | 1          | 1         | 92.904 | 8.77                       |
| 50               | 1.64             | 0.081          | 0.023          | GOTERM_BP_ALL   | GO:0001649-osteoblast differentiation                        | 9     | 0.6%       | 0.002    | 1          | 0.061     | 3.381  | 9.30                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0045668-negative regulation of osteoblast differentiation | 3     | 0.2%       | 0.081    | 1          | 0.704     | 79.966 | 11.47                      |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0045667-regulation of osteoblast differentiation          | 4     | 0.3%       | 0.085    | 1          | 0.714     | 81.531 | 10.47                      |
| 51               | 1.62             | 0.017          | 0.024          | INTERPRO        | IPR011511:Variant SH3  | 11    | 0.7%       | 0.011    | 1          | 0.877     | 18.707 | 8.51                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | SH3 domain   | 27    | 1.7%       | 0.016    | 1          | 0.276     | 21.522 | 6.59                       |
|                  |                  |                |                | INTERPRO        | IPR001452:Src homology-3                                     | 25    | 1.6%       | 0.017    | 1          | 0.946     | 27.916 | 6.70                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:SH3   | 19    | 1.2%       | 0.054    | 1          | 1         | 68.887 | 7.15                       |
|                  |                  |                |                | SMART           | SM00326:SH3  | 28    | 1.7%       | 0.056    | 1          | 0.827     | 57.561 | 6.63                       |
| 52               | 1.60             | 0.015          | 0.025          | GOTERM_BP_ALL   | GO:0001655-urogenital system development                     | 14    | 0.9%       | 0.013    | 1          | 0.256     | 21.831 | 7.83                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001656-metanephros development                           | 10    | 0.6%       | 0.015    | 1          | 0.281     | 24.760 | 8.51                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001822-kidney development                                | 13    | 0.8%       | 0.015    | 1          | 0.285     | 25.145 | 7.99                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001657-ureteric bud development                          | 8     | 0.5%       | 0.019    | 1          | 0.318     | 30.022 | 8.97                       |
|                  |                  |                |                | GOTERM_BP_ALL   | GO:0001658-ureteric bud branching                            | 4     | 0.3%       | 0.201    | 1          | 0.902     | 98.612 | 9.74                       |
| 53               | 1.55             | 0.118          | 0.028          | UP_SEQ_FEATURE  | zinc finger region:C2H2-type 2                               | 29    | 1.8%       | 2.05E-04 | 0.951      | 0.778     | 0.433  | 7.10                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | zinc finger region:C2H2-type 3                               | 27    | 1.7%       | 5.31E-04 | 1          | 0.623     | 1.120  | 7.18                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | zinc finger region:C2H2-type 1                               | 27    | 1.7%       | 0.001    | 1          | 0.805     | 2.327  | 7.10                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | zinc finger region:C2H2-type 4                               | 20    | 1.2%       | 0.006    | 1          | 0.988     | 11.415 | 7.54                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | zinc finger region:C2H2-type 5                               | 13    | 0.8%       | 0.118    | 1          | 1         | 92.969 | 7.86                       |
|                  |                  |                |                | INTERPRO        | IPR007087:Zinc finger, C2H2-type                             | 51    | 3.2%       | 0.209    | 1          | 1         | 98.939 | 5.44                       |
|                  |                  |                |                | INTERPRO        | IPR015880:Zinc finger, C2H2-like                             | 33    | 2.1%       | 0.688    | 1          | 1         | 100    | 5.88                       |
|                  |                  |                |                | INTERPRO        | IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding      | 24    | 1.5%       | 0.884    | 1          | 1         | 100    | 6.16                       |
|                  |                  |                |                | SMART           | SM00355:ZnF_C2H2   | 35    | 2.2%       | 0.983    | 1          | 1         | 100    | 5.74                       |
| 54               | 1.53             | 0.029          | 0.029          | SP_PIR_KEYWORDS | mitogen  | 8     | 0.5%       | 0.023    | 1          | 0.325     | 30.118 | 8.11                       |
|                  |                  |                |                | SP_PIR_KEYWORDS | growth factor  | 18    | 1.1%       | 0.029    | 1          | 0.356     | 36.144 | 6.13                       |
|                  |                  |                |                | GOTERM_MF_ALL   | GO:0008083-growth factor activity                            | 21    | 1.3%       | 0.039    | 1          | 0.720     | 50.546 | 6.77                       |
| 55               | 1.53             | 0.041          | 0.030          | INTERPRO        | IPR011333:BTB/POZ fold                                       | 23    | 1.4%       | 0.005    | 1          | 0.750     | 9.557  | 7.07                       |
|                  |                  |                |                | INTERPRO        | IPR000210:BTB/POZ-like                                       | 22    | 1.4%       | 0.009    | 1          | 0.871     | 16.099 | 7.10                       |
|                  |                  |                |                | SMART           | SM00225:BTB  | 24    | 1.5%       | 0.041    | 1          | 0.775     | 46.185 | 7.06                       |
|                  |                  |                |                | INTERPRO        | IPR013069:BTB/POZ  | 15    | 0.9%       | 0.054    | 1          | 0.979     | 65.802 | 7.67                       |
|                  |                  |                |                | UP_SEQ_FEATURE  | domain:BTB   | 9     | 0.6%       | 0.222    | 1          | 1         | 99.507 | 8.42                       |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score                         | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value         | Bonferroni                                  | Benjamini | FDR    | Information Content (bits) |   |       |        |       |
|------------------|--|----------------|----------------|-----------------|--|-------|------------|-----------------|---|-----------|--------|----------------------------|---|-------|--------|-------|
| 56               | 1.51                                     | 0.036          | 0.031          | SP_PIR_KEYWORDS | protein phosphatase  | 21    | 1.3%       | 4.59E-04        | 0.328                                       | 0.020     | 0.710  | 6.94                       |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR008343:MAP kinase phosphatase   | 5     | 0.3%       | 0.004           | 1   | 0.701     | 7.280  | 10.92                      |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR014393:Dual specificity protein phosphatase (MAP kinase phosphatase)              | 4     | 0.3%       | 0.005           | 1   | 0.749     | 8.718  | 11.77                      |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0004721~phosphoprotein phosphatase activity                                       | 24    | 1.5%       | 0.005           | 1   | 0.323     | 9.294  | 7.00                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity                 | 5     | 0.3%       | 0.006           | 1   | 0.350     | 10.728 | 10.89                      |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0033549~MAP kinase phosphatase activity   | 5     | 0.3%       | 0.006           | 1   | 0.350     | 10.728 | 10.89                      |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0042578~phosphoric ester hydrolase activity                                       | 40    | 2.5%       | 0.007           | 1   | 0.358     | 12.044 | 5.94                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016791~phosphoric monoester hydrolase activity                                   | 33    | 2.1%       | 0.009           | 1   | 0.399     | 14.849 | 6.31                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0004725~protein tyrosine phosphatase activity                                     | 16    | 1.0%       | 0.010           | 1   | 0.425     | 16.932 | 7.77                       |   |       |        |       |
|                  |  |                |                | UP_SEQ_FEATURE  | active site:Phosphocysteine intermediate   | 13    | 0.8%       | 0.011           | 1   | 0.999     | 20.883 | 8.51                       |   |       |        |       |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:Rhodanese   | 5     | 0.3%       | 0.031           | 1   | 1         | 48.450 | 10.28                      |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006470~protein amino acid dephosphorylation                                      | 18    | 1.1%       | 0.032           | 1   | 0.444     | 46.635 | 7.25                       |   |       |        |       |
|                  |  |                |                | BIOCARTA        | m_dspPathway:Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases | 5     | 0.3%       | 0.034           | 1   | 0.802     | 36.418 | 10.63                      |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR000340:Protein-tyrosine phosphatase, dual specificity                             | 7     | 0.4%       | 0.036           | 1   | 0.977     | 50.676 | 9.18                       |   |       |        |       |
|                  |  |                |                | PIR_SUPERFAMILY | PIRSF000939:dual specificity protein phosphatase (MAP kinase phosphatase)            | 3     | 0.2%       | 0.037           | 1   | 1         | 49.151 | 12.09                      |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR000387:Protein-tyrosine phosphatase, Tyr-specific/dual-specificity type           | 13    | 0.8%       | 0.041           | 1   | 0.979     | 55.667 | 7.90                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0016311~dephosphorylation   | 19    | 1.2%       | 0.050           | 1   | 0.567     | 62.559 | 7.11                       |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR001763:Rhodanese-like   | 5     | 0.3%       | 0.053           | 1   | 0.982     | 64.942 | 9.92                       |   |       |        |       |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:Tyrosine-protein phosphatase  | 9     | 0.6%       | 0.088           | 1   | 1         | 85.656 | 8.54                       |   |       |        |       |
|                  |  |                |                | SMART           | SM00195:DSPc   | 7     | 0.4%       | 0.098           | 1   | 0.918     | 78.243 | 9.14                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0008138~protein tyrosine/serine/threonine phosphatase activity                    | 7     | 0.4%       | 0.106           | 1   | 0.938     | 86.431 | 8.85                       |   |       |        |       |
|                  |  |                |                | SMART           | SM00450:RHOD   | 5     | 0.3%       | 0.118           | 1   | 0.922     | 84.483 | 9.84                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016788~hydrolase activity, acting on ester bonds                                 | 66    | 4.1%       | 0.121           | 1   | 0.943     | 89.915 | 4.89                       |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type                   | 6     | 0.4%       | 0.284           | 1   | 1         | 99.844 | 9.05                       |   |       |        |       |
|                  |  |                |                | SP_PIR_KEYWORDS | phosphoric monoester hydrolase   | 6     | 0.4%       | 0.323           | 1   | 0.918     | 99.763 | 8.67                       |   |       |        |       |
|                  |  |                |                | SP_PIR_KEYWORDS | tyrosine-specific phosphatase  | 4     | 0.3%       | 0.362           | 1   | 0.941     | 99.907 | 9.51                       |   |       |        |       |
|                  |  |                |                | SMART           | SM00194:PTPc   | 6     | 0.4%       | 0.483           | 1   | 0.986     | 99.994 | 9.05                       |   |       |        |       |
|                  |  |                |                | 57              | 1.49   | 0.019 | 0.032      | INTERPRO        | IPR013088:Zinc finger, NHR/GATA-type        | 9         | 0.6%   | 0.012                      | 1 | 0.892 | 20.377 | 8.77  |
|                  |  |                |                |                 |  |       |            | INTERPRO        | IPR013629:Zinc finger-associated region     | 3         | 0.2%   | 0.019                      | 1 | 0.946 | 30.556 | 12.09 |
|                  |  |                |                |                 |  |       |            | PIR_SUPERFAMILY | PIRSF500849:orphan nuclear receptor COUP-TF | 3         | 0.2%   | 0.019                      | 1 | 1     | 29.851 | 12.09 |
|                  |  |                |                |                 |  |       |            | INTERPRO        | IPR003068:Transcription factor COUP         | 3         | 0.2%   | 0.035                      | 1 | 0.978 | 50.147 | 11.77 |
| PIR_SUPERFAMILY  | PIRSF002534:retinoic acid receptor alpha | 3              | 0.2%           |                 |  |       |            | 0.230           | 1   | 1         | 99.110 | 10.51                      |   |       |        |       |
| 58               | 1.48                                     | 0.100          | 0.033          | INTERPRO        | IPR011993:Pleckstrin homology-type   | 36    | 2.2%       | 4.62E-04        | 0.934                                       | 0.419     | 0.890  | 6.31                       |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR001849:Pleckstrin-like  | 25    | 1.6%       | 0.06            | 1   | 0.980     | 70.064 | 6.57                       |   |       |        |       |
|                  |  |                |                | SMART           | SM00233:PH   | 29    | 1.8%       | 0.14            | 1   | 0.908     | 89.062 | 6.47                       |   |       |        |       |
|                  |  |                |                | UP_SEQ_FEATURE  | domain:PH  | 14    | 0.9%       | 0.30            | 1   | 1         | 99.954 | 7.27                       |   |       |        |       |
| 59               | 1.45                                     | 0.047          | 0.036          | GOTERM_BP_ALL   | GO:0051098~regulation of binding   | 8     | 0.5%       | 0.01            | 1   | 0.203     | 16.386 | 8.39                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0051101~regulation of DNA binding   | 5     | 0.3%       | 0.01            | 1   | 0.258     | 22.181 | 8.85                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0043388~positive regulation of DNA binding  | 3     | 0.2%       | 0.08            | 1   | 0.704     | 79.966 | 9.30                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0051099~positive regulation of binding  | 3     | 0.2%       | 0.16            | 1   | 0.868     | 96.790 | 9.15                       |   |       |        |       |
| 60               | 1.42                                     | 0.042          | 0.038          | SP_PIR_KEYWORDS | mitogen  | 8     | 0.5%       | 0.02            | 1   | 0.325     | 30.118 | 8.11                       |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR000072:Platelet-derived growth factor (PDGF)                                      | 4     | 0.3%       | 0.03            | 1   | 0.977     | 45.489 | 10.51                      |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0050730~regulation of peptidyl-tyrosine phosphorylation                           | 8     | 0.5%       | 0.05            | 1   | 0.583     | 64.481 | 8.93                       |   |       |        |       |
|                  |  |                |                | SMART           | SM00141:PDGF   | 4     | 0.3%       | 0.05            | 1   | 0.832     | 56.266 | 10.51                      |   |       |        |       |
| 61               | 1.41                                     | 0.037          | 0.039          | GOTERM_BP_ALL   | GO:0050770~regulation of axonogenesis  | 9     | 0.6%       | 0.008           | 1   | 0.180     | 13.560 | 8.93                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0050767~regulation of neurogenesis  | 10    | 0.6%       | 0.027           | 1   | 0.400     | 40.854 | 7.62                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0030516~regulation of axon extension  | 5     | 0.3%       | 0.037           | 1   | 0.479     | 51.223 | 9.81                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0050772~positive regulation of axonogenesis                                       | 5     | 0.3%       | 0.037           | 1   | 0.479     | 51.223 | 10.15                      |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0048675~axon extension  | 6     | 0.4%       | 0.049           | 1   | 0.564     | 61.863 | 9.36                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0050769~positive regulation of neurogenesis                                       | 5     | 0.3%       | 0.088           | 1   | 0.719     | 82.730 | 9.11                       |   |       |        |       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0045773~positive regulation of axon extension                                     | 3     | 0.2%       | 0.107           | 1   | 0.776     | 88.493 | 11.06                      |   |       |        |       |
| 62               | 1.41                                     | 0.058          | 0.039          | GOTERM_MF_ALL   | GO:0008603~cAMP-dependent protein kinase regulator activity                          | 6     | 0.4%       | 0.002           | 0.992                                       | 0.150     | 3.153  | 10.47                      |   |       |        |       |
|                  |  |                |                | INTERPRO        | IPR002373:cAMP/cGMP-dependent protein kinase   | 5     | 0.3%       | 0.002           | 1   | 0.621     | 4.384  | 10.92                      |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0019887~protein kinase regulator activity   | 14    | 0.9%       | 0.003           | 1   | 0.221     | 5.580  | 8.06                       |   |       |        |       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0016208~AMP binding   | 6     | 0.4%       | 0.008           | 1   | 0.365     | 12.566 | 10.25                      |   |       |        |       |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score                           | Median P-Value | Geometric Mean | Category        | Term   | Count | % of Total | P-Value       | Bonferroni                      | Benjamini | FDR    | Information Content (bits) |
|------------------|--|----------------|----------------|-----------------|--|-------|------------|---------------|---------------------------------|-----------|--------|----------------------------|
| 62               | 1.41                                       | 0.058          | 0.039          | INTERPRO        | IPR003117:cAMP-dependent protein kinase regulator, type II PKA R subunit | 4     | 0.3%       | 0.022         | 1                               | 0.951     | 34.824 | 11.28                      |
|                  |  |                |                | INTERPRO        | IPR012198:cAMP-dependent protein kinase regulatory subunit               | 3     | 0.2%       | 0.035         | 1                               | 0.978     | 50.147 | 12.09                      |
|                  |  |                |                | PIR_SUPERFAMILY | PIRSF000548:cAMP-dependent protein kinase, regulatory subunit            | 3     | 0.2%       | 0.037         | 1                               | 1.000     | 49.151 | 12.09                      |
|                  |  |                |                | SMART           | SM00394:RIIa   | 4     | 0.3%       | 0.039         | 1                               | 0.780     | 44.590 | 11.28                      |
|                  |  |                |                | UP_SEQ_FEATURE  | binding site:cAMP 2  | 3     | 0.2%       | 0.058         | 1                               | 1         | 71.818 | 12.09                      |
|                  |  |                |                | UP_SEQ_FEATURE  | binding site:cAMP 1  | 3     | 0.2%       | 0.058         | 1                               | 1         | 71.818 | 12.09                      |
|                  |  |                |                | UP_SEQ_FEATURE  | region of interest:Dimerization and phosphorylation                      | 3     | 0.2%       | 0.058         | 1                               | 1         | 71.818 | 12.09                      |
|                  |  |                |                | SP_PIR_KEYWORDS | camp-binding   | 4     | 0.3%       | 0.061         | 1                               | 0.575     | 62.468 | 10.77                      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0030552~cAMP binding  | 4     | 0.3%       | 0.069         | 1                               | 0.868     | 72.223 | 10.74                      |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0030551~cyclic nucleotide binding                                     | 5     | 0.3%       | 0.088         | 1                               | 0.912     | 80.687 | 9.81                       |
|                  |  |                |                | UP_SEQ_FEATURE  | nucleotide phosphate-binding region:cAMP 1                               | 3     | 0.2%       | 0.090         | 1                               | 1         | 86.451 | 11.77                      |
|                  |  |                |                | UP_SEQ_FEATURE  | nucleotide phosphate-binding region:cAMP 2                               | 3     | 0.2%       | 0.090         | 1                               | 1         | 86.451 | 11.77                      |
|                  |  |                |                | SP_PIR_KEYWORDS | camp   | 5     | 0.3%       | 0.113         | 1                               | 0.707     | 84.512 | 9.05                       |
|                  |  |                |                | INTERPRO        | IPR014710:RmlC-like jelly roll fold                                      | 5     | 0.3%       | 0.156         | 1                               | 0.999     | 96.207 | 9.63                       |
|                  |  |                |                | INTERPRO        | IPR000595:Cyclic nucleotide-binding                                      | 5     | 0.3%       | 0.188         | 1                               | 0.999     | 98.235 | 9.39                       |
|                  |  |                |                | SMART           | SM00100:cNMP   | 5     | 0.3%       | 0.360         | 1                               | 0.972     | 99.865 | 9.34                       |
|                  |  |                |                | 63              | 1.35   | 0.032 | 0.045      | GOTERM_BP_ALL | GO:0031016~pancreas development | 5         | 0.3%   | 0.023                      |
| GOTERM_BP_ALL    | GO:0031018~endocrine pancreas development  | 4              | 0.3%           |                 |  |       |            | 0.032         | 1                               | 0.441     | 45.995 | 10.89                      |
| GOTERM_BP_ALL    | GO:0035270~endocrine system development    | 8              | 0.5%           |                 |  |       |            | 0.121         | 1                               | 0.804     | 91.509 | 8.42                       |
| 64               | 1.33                                       | 0.056          | 0.046          | GOTERM_MF_ALL   | GO:0005262~calcium channel activity                                      | 15    | 0.9%       | 0.002         | 0.995                           | 0.146     | 3.376  | 8.15                       |
|                  |  |                |                | SP_PIR_KEYWORDS | Calcium channel  | 12    | 0.7%       | 0.002         | 0.826                           | 0.068     | 3.081  | 8.70                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006816~calcium ion transport   | 19    | 1.2%       | 0.009         | 1                               | 0.199     | 15.658 | 7.35                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0046873~metal ion transmembrane transporter activity                  | 38    | 2.4%       | 0.010         | 1                               | 0.414     | 15.820 | 5.93                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022843~voltage-gated cation channel activity                         | 20    | 1.2%       | 0.011         | 1                               | 0.426     | 17.278 | 7.16                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005261~cation channel activity                                       | 33    | 2.1%       | 0.014         | 1                               | 0.478     | 21.986 | 6.17                       |
|                  |  |                |                | SP_PIR_KEYWORDS | calcium transport  | 12    | 0.7%       | 0.019         | 1                               | 0.303     | 25.659 | 8.23                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005244~voltage-gated ion channel activity                            | 24    | 1.5%       | 0.020         | 1                               | 0.563     | 30.192 | 6.74                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022832~voltage-gated channel activity                                | 24    | 1.5%       | 0.020         | 1                               | 0.563     | 30.192 | 6.74                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022836~gated channel activity  | 34    | 2.1%       | 0.021         | 1                               | 0.556     | 30.858 | 6.09                       |
|                  |  |                |                | SP_PIR_KEYWORDS | Ionic channel  | 36    | 2.2%       | 0.021         | 1                               | 0.311     | 27.848 | 5.98                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005216~ion channel activity  | 42    | 2.6%       | 0.022         | 1                               | 0.573     | 32.798 | 5.70                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022838~substrate specific channel activity                           | 43    | 2.7%       | 0.023         | 1                               | 0.577     | 33.445 | 5.65                       |
|                  |  |                |                | INTERPRO        | IPR003131:Potassium channel, voltage dependent, Kv, tetramerisation      | 9     | 0.6%       | 0.024         | 1                               | 0.956     | 36.986 | 8.63                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0015674~di-, tri-valent inorganic cation transport                    | 21    | 1.3%       | 0.028         | 1                               | 0.415     | 42.424 | 6.96                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005245~voltage-gated calcium channel activity                        | 6     | 0.4%       | 0.036         | 1                               | 0.700     | 47.822 | 9.81                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005249~voltage-gated potassium channel activity                      | 14    | 0.9%       | 0.050         | 1                               | 0.790     | 59.872 | 7.55                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0015267~channel activity  | 44    | 2.7%       | 0.054         | 1                               | 0.808     | 62.742 | 5.52                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022803~passive transmembrane transporter activity                    | 44    | 2.7%       | 0.054         | 1                               | 0.808     | 62.742 | 5.52                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006811~ion transport   | 78    | 4.8%       | 0.054         | 1                               | 0.591     | 65.566 | 4.59                       |
|                  |  |                |                | SP_PIR_KEYWORDS | ion transport  | 51    | 3.2%       | 0.056         | 1                               | 0.553     | 59.099 | 5.22                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0030955~potassium ion binding   | 15    | 0.9%       | 0.062         | 1                               | 0.843     | 68.209 | 7.32                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0030001~metal ion transport   | 46    | 2.9%       | 0.068         | 1                               | 0.653     | 74.119 | 5.44                       |
|                  |  |                |                | INTERPRO        | IPR003968:Potassium channel, voltage dependent, Kv                       | 5     | 0.3%       | 0.098         | 1                               | 0.996     | 86.339 | 9.63                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022892~substrate-specific transporter activity                       | 96    | 6.0%       | 0.107         | 1                               | 0.938     | 86.616 | 4.22                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0022891~substrate-specific transmembrane transporter activity         | 77    | 4.8%       | 0.114         | 1                               | 0.942     | 88.419 | 4.55                       |
|                  |  |                |                | SP_PIR_KEYWORDS | voltage-gated channel  | 16    | 1.0%       | 0.119         | 1                               | 0.714     | 86.084 | 7.17                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0008324~cation transmembrane transporter activity                     | 52    | 3.2%       | 0.121         | 1                               | 0.943     | 89.830 | 5.06                       |
|                  |  |                |                | GOTERM_BP_ALL   | GO:0006812~cation transport  | 53    | 3.3%       | 0.126         | 1                               | 0.814     | 92.289 | 5.15                       |
|                  |  |                |                | INTERPRO        | IPR005821:Ion transport  | 13    | 0.8%       | 0.129         | 1                               | 0.998     | 93.157 | 7.57                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0005267~potassium channel activity                                    | 16    | 1.0%       | 0.148         | 1                               | 0.967     | 94.254 | 7.09                       |
|                  |  |                |                | GOTERM_MF_ALL   | GO:0015075~ion transmembrane transporter activity                        | 66    | 4.1%       | 0.154         | 1                               | 0.971     | 94.950 | 4.71                       |
|                  |  |                |                | SP_PIR_KEYWORDS | potassium  | 13    | 0.8%       | 0.161         | 1                               | 0.795     | 93.424 | 7.20                       |
| GOTERM_MF_ALL    | GO:0031420~alkali metal ion binding        | 20             | 1.2%           | 0.172           | 1  | 0.976 | 96.539     | 6.61          |                                 |           |        |                            |
| SP_PIR_KEYWORDS  | transport                                  | 121            | 7.5%           | 0.233           | 1  | 0.869 | 98.368     | 3.66          |                                 |           |        |                            |
| PIR_SUPERFAMILY  | PIRSF002449:potassium channel protein Drk1 | 3              | 0.2%           | 0.261           | 1  | 1     | 99.585     | 10.51         |                                 |           |        |                            |
| UP_SEQ_FEATURE   | short sequence motif:Selectivity filter    | 7              | 0.4%           | 0.282           | 1  | 1     | 99.909     | 8.70          |                                 |           |        |                            |
| GOTERM_MF_ALL    | GO:0005215~transporter activity            | 120            | 7.4%           | 0.294           | 1  | 0.997 | 99.796     | 3.82          |                                 |           |        |                            |

**Supplemental Table 5. Functional Mapping of WT1 Target Genes using DAVID.**

| Functional Group | Enrichment Score | Median <i>P</i> -Value | Geometric Mean | Category        | Term   | Count | % of Total | <i>P</i> -Value | Bonferroni | Benjamini | FDR    | Information Content (bits) |
|------------------|------------------|------------------------|----------------|-----------------|--|-------|------------|-----------------|------------|-----------|--------|----------------------------|
| 64               | 1.33             | 0.056                  | 0.046          | INTERPRO        | IPR003091:Voltage-dependent potassium channel    | 5     | 0.3%       | 0.315           | 1          | 1         | 99.934 | 9.09                       |
|                  |                  |                        |                | GOTERM_BP_ALL   | GO:0006813~potassium ion transport               | 17    | 1.1%       | 0.328           | 1          | 0.962     | 99.949 | 6.77                       |
|                  |                  |                        |                | SP_PIR_KEYWORDS | Potassium channel                                | 7     | 0.4%       | 0.377           | 1          | 0.944     | 99.935 | 7.26                       |
|                  |                  |                        |                | SP_PIR_KEYWORDS | potassium transport                              | 10    | 0.6%       | 0.401           | 1          | 0.953     | 99.964 | 7.51                       |
|                  |                  |                        |                | GOTERM_MF_ALL   | GO:0022857~transmembrane transporter activity    | 80    | 5.0%       | 0.405           | 1          | 1         | 100    | 4.35                       |
|                  |                  |                        |                | GOTERM_BP_ALL   | GO:0015672~monovalent inorganic cation transport | 25    | 1.6%       | 0.808           | 1          | 1         | 100    | 5.84                       |



**Table S6. Densitometric measurement of ChIP-PCR enrichment**

| Gene          | Fold-enrichment on array | ChIP-PCR group    | Normalized amplicon density | Normalized density ratio (WT1 ChIP:Input) |
|---------------|--------------------------|-------------------|-----------------------------|---|
| <i>HeyL</i>   | 25.1                     | WT1 ChIP<br>Input | 2296.35<br>199.82           | 11.49                                     |
| <i>Egr3</i>   | 24.4                     | WT1 ChIP<br>Input | 18014.45<br>156.93          | 114.79                                    |
| <i>Actn1</i>  | 23.8                     | WT1 ChIP<br>Input | 2685.29<br>181.1            | 14.83                                     |
| <i>Nab2</i>   | 19.6                     | WT1 ChIP<br>Input | 14795.4<br>618.88           | 23.91                                     |
| <i>Fyn</i>    | 18.7                     | WT1 ChIP<br>Input | 11488.66<br>1591.68         | 7.22                                      |
| <i>Zfr</i>    | 16.7                     | WT1 ChIP<br>Input | 1466.03<br>549.27           | 2.67                                      |
| <i>Hoxd4</i>  | 16.6                     | WT1 ChIP<br>Input | 1008.15<br>127.38           | 7.91                                      |
| <i>Sox11</i>  | 15.5                     | WT1 ChIP<br>Input | 2751.63<br>983.17           | 2.80                                      |
| <i>Scx</i>    | 14.7                     | WT1 ChIP<br>Input | 901.83<br>31.65             | 28.49                                     |
| <i>Sema6D</i> | 14.1                     | WT1 ChIP<br>Input | 2564.21<br>339.43           | 7.55                                      |
| <i>Bmp7</i>   | 12.9                     | WT1 ChIP<br>Input | 6621.97<br>605.59           | 10.93                                     |
| <i>Pbx2</i>   | 12.8                     | WT1 ChIP<br>Input | 10891.67<br>10208.41        | 1.07                                      |
| <i>Rest</i>   | 12.0                     | WT1 ChIP<br>Input | 2263.24<br>286.15           | 7.91                                      |
| <i>Zyx</i>    | 11.4                     | WT1 ChIP<br>Input | 873.16<br>345.94            | 2.52                                      |
| <i>Hhat</i>   | 11.4                     | WT1 ChIP<br>Input | 3356.92<br>1431.72          | 2.34                                      |
| <i>Arnt2</i>  | 10.9                     | WT1 ChIP<br>Input | 3395.57<br>77.35            | 43.90                                     |
| <i>Smad7</i>  | 10.7                     | WT1 ChIP<br>Input | 2870.59<br>281.77           | 10.19                                     |
| <i>ErbB2</i>  | 10.7                     | WT1 ChIP<br>Input | 754.17<br>130.34            | 5.79                                      |
| <i>Pbx1</i>   | 10.3                     | WT1 ChIP<br>Input | 44.11<br>310.45             | 0.14                                      |
| <i>Plxnb1</i> | 9.7                      | WT1 ChIP<br>Input | 1936.22<br>164.78           | 11.75                                     |
| <i>Sall1</i>  | 9.3                      | WT1 ChIP          | 14471.44                    | 5.38                                      |

|               |     |          |          |       |
|---------------|-----|----------|----------|-------|
|               |     | Input    | 2692.25  |       |
| <i>Pax2</i>   | 9.3 | WT1 ChIP | 1353.66  | 2.71  |
|               |     | Input    | 499.9    |       |
| <i>Bmp4</i>   | 8.8 | WT1 ChIP | 456.48   | 2.01  |
|               |     | Input    | 226.82   |       |
| <i>Smad4</i>  | 8.7 | WT1 ChIP | 3380.86  | 3.61  |
|               |     | Input    | 935.24   |       |
| <i>Smad3</i>  | 8.1 | WT1 ChIP | 1839.33  | 10.32 |
|               |     | Input    | 178.25   |       |
| <i>Vegfa</i>  | 8.0 | WT1 ChIP | 2085.11  | 3.17  |
|               |     | Input    | 658.4    |       |
| <i>Nab1</i>   | 7.6 | WT1 ChIP | 1780.31  | 0.95  |
|               |     | Input    | 1878.21  |       |
| <i>Ptch1</i>  | 6.9 | WT1 ChIP | 960.31   | 1.22  |
|               |     | Input    | 786.26   |       |
| <i>Slit3</i>  | 6.7 | WT1 ChIP | 2001.28  | 0.72  |
|               |     | Input    | 2772.54  |       |
| <i>Spry2</i>  | 6.6 | WT1 ChIP | 110.65   | 0.04  |
|               |     | Input    | 2752.32  |       |
| <i>Paxip1</i> | 6.2 | WT1 ChIP | 435.03   | 4.90  |
|               |     | Input    | 88.74    |       |
| <i>Lef1</i>   | 6.0 | WT1 ChIP | 206.99   | 0.61  |
|               |     | Input    | 337.36   |       |
| <i>Fgfr2</i>  | 5.9 | WT1 ChIP | 76.05    | 0.06  |
|               |     | Input    | 1242.78  |       |
| <i>Sulf2</i>  | 5.2 | WT1 ChIP | 1679.07  | 2.95  |
|               |     | Input    | 569.06   |       |
| <i>Bmper</i>  | 5.1 | WT1 ChIP | 9837.24  | 0.66  |
|               |     | Input    | 14870.88 |       |
| <i>Fgfr3</i>  | 4.9 | WT1 ChIP | 1385.57  | 1.60  |
|               |     | Input    | 868.63   |       |
| <i>Six4</i>   | 4.8 | WT1 ChIP | 358.4    | 0.54  |
|               |     | Input    | 662.27   |       |
| <i>Stau1</i>  | 4.5 | WT1 ChIP | 52.44    | 0.30  |
|               |     | Input    | 173.65   |       |
| <i>Smad6</i>  | 4.3 | WT1 ChIP | 297.31   | 22.47 |
|               |     | Input    | 13.23    |       |
| <i>Smo</i>    | 4.0 | WT1 ChIP | 562.07   | 7.63  |
|               |     | Input    | 73.63    |       |
| <i>Six2</i>   | 3.3 | WT1 ChIP | 1221.98  | 0.46  |
|               |     | Input    | 2660.44  |       |