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RESEARCH ARTICLE

Genome-wide assessment of differential effector gene use in embryogenesis

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ABSTRACT

Six different populations of cells were isolated by fluorescence-activated cell sorting from disaggregated late blastula- and gastrula-stage sea urchin embryos according to the regulatory states expressed in these cells, as reported by recombineered bacterial artificial chromosomes producing fluorochromes. Transcriptomes recovered from these embryonic cell populations revealed striking, early differential expression of large cohorts of effector genes. The six cell populations were presumptive pigment cells, presumptive neurogenic cells, presumptive skeletogenic cells, cells from the stomodeal region of the oral ectoderm, ciliated band cells and cells from the endoderm/ectoderm boundary that will give rise both to hindgut and to border ectoderm. Transcriptome analysis revealed that each of these domains specifically expressed several hundred effector genes at significant levels. Annotation indicated the qualitative individuality of the functional nature of each cell population, even though they were isolated from embryos only 1-2 days old. In no case was more than a tiny fraction of the transcripts enriched in one population also enriched in any other of the six populations studied. As was particularly clear in the cases of the presumptive pigment, neurogenic and skeletogenic cells, all three of which represent precociously differentiating cell types of this embryo, most specifically expressed genes of given cell types are not significantly expressed at all in the other cell types. Thus, at the effector gene level, a dramatic, cell type-specific pattern of differential gene regulation is established well before any significant embryonic morphogenesis has occurred.

KEY WORDS: Effector gene expression, Embryonic gene regulation, FACS embryonic cell populations, Sea urchin embryos

INTRODUCTION

Embryonic development is driven by the progressive establishment of spatial regulatory states, generated by the differential zygotic expression of regulatory genes encoding transcription factors. This has been demonstrated in every adequately studied experimental system, by analysis of the underlying gene regulatory networks that encode these regulatory states. A comprehensive review has recently been published (Peter and Davidson, 2015). These networks of interacting regulatory genes cause expression of much larger cohorts of protein-coding effector genes, which ultimately produce the cell's biological and morphogenetic functions, as well as the differentiated characteristics of the many cell types to which the embryo gives rise. However, we have as yet surprisingly little experimental evidence, beyond the behavior of individual genes, that directly addresses the spatial deployment of effector gene cohorts during early embryonic development. Temporally differential expression of thousands of genes during embryogenesis, i.e. of thousands of effector genes, was indicated by mRNA complexity studies as far back as the 1970s (Davidson, 1986). Evidence of the temporal progression of effector gene expression during embryogenesis has recently been fleshed out on a genome-wide scale, by staged embryo transcriptome measurements that are too numerous to mention individually, but system-level measurement of the spatial expression of effector gene cohorts has been lacking for any embryo. Large numbers of beautiful and detailed studies have illuminated the spatial activation of individual effector genes of interest in the specific domains of various embryos, but thus far the quantitative extent of this fundamental regulatory process has remained inferential.

The sea urchin embryo is an exemplar of a widespread mode of invertebrate embryogenesis particularly common in marine forms, but not confined to these, in which differentiated cell types are specified prior to gastrulation, even before any embryonic structures are manifested morphologically. Precocious (pregastrular) differentiation is characteristic of these 'mode 1' embryonic specification processes (Davidson, 1990; Peter and Davidson, 2015). It is a clear prediction from observations on individual effector genes that, early in development, batteries of such genes should be expressed differentially in the early differentiating cell types of mode 1 embryos. Nonetheless, until now, no system-level evidence on spatial effector gene deployment has been available for any kind of animal embryo.

Using a method pioneered in our laboratory, we exploit known regulatory states to mark cell types of interest fluorescently and separate them out by way of flow cytometry (akin to Defaye and Perrin, 2014; Barsi et al., 2014). Specifically, we use fluorescence-activated cell sorting (FACS) to separate out six different populations of cells from the pregastrular and early gastrula sea urchin embryo. cDNA was amplified from the mRNAs of these sorted cell populations and used to generate transcriptomes. After verification of all of the selected transcript populations, we carried out a comparative qualitative and quantitative analysis of their differential transcription of effector gene sets. A large-scale demonstration of spatially exclusive, early effector gene regulation emerges, particularly in cell populations that are fated to express given modes of differentiation.

RESULTS

Embryonic cell populations used in this study

The six cell populations isolated from sea urchin embryos and compared in this study were as follows. (1) Presumptive pigment

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cells were identified experimentally as cells expressing gcm at 45 hours postfertilization (hpf) (Ransick and Davidson, 2006; 2012). At this stage, these cells are in the blastocoel and in the process of embedding themselves in the aboral ectoderm. They were identified by sorting on the green fluorescent protein (GFP) generated by a gcm cis-regulatory reporter construct. (2) Presumptive neurogenic cells of the apical plate were identified as cells expressing lhx2/9 at 35 hpf (Lundgren et al., 1995; Farfán et al., 2009). At this stage, these cells constitute a small patch within the apical neurogenic domain of the embryo. They were identified by sorting on the GFP generated by a recombineered lhx2/9-GFP bacterial artificial chromosome (BAC). (3) Presumptive skeletogenic cells were identified as cells expressing tbrain or alx1 recombinant BACs at 24 hpf, as described at length earlier (Barsi et al., 2014). (4) Cells of the stomodeal region of the oral ectoderm were identified by expression of gsc at 35 hpf (Li et al., 2013). At this stage, these cells include the future stomodeal area and surrounding regions of the upper central oral ectoderm. They were isolated by sorting on the GFP generated by a recombineered gsc-GFP BAC. (5) Cells of the ciliated band were identified at 35 hpf as cells expressing onecut (Poustka et al., 2004; Fig. S1) and isolated by sorting on the GFP generated from a onecut GFP recombinant BAC. (6) Cells of the veg1 lineage give rise to the most posterior endoderm and the adjacent ectoderm (Peter and Davidson, 2010, 2011). They were identified by expression of the eve homeodomain regulator at 24 hpf and isolated by sorting on GFP generated by an eve-GFP recombinant BAC.

These populations of spatially confined embryonic cells fall into two biological classes and, as can be expected, the results we present below are affected by this distinction. Populations 1-3 above are essentially of unitary fate. The descendants of all gcm+ cells at this stage will become pigment cells; so far as is known, the descendants of all lhx2/9+ cells will become neurons (or neuron accessory cells); and the descendants of all alx1+ and tbrain+ cells will become skeletogenic mesenchyme cells. However, at the respective selected stages, gsc+ cells (population 4) will give rise to stomodaeum, to neurons and to the squamous oral epithelium; onecut+ ciliated band cells (population 5) include neurogenic precursors, cells that will produce the eponymous cilia, cell types of the oral posterior ectoderm, including bilateral patches of Vegf-secreting cells; and eve+ cells (population 6) will give rise to posterior ectoderm, both oral and aboral, as well as to oral and aboral posterior endoderm. Given their mixed fates, it is remarkable that, as described below, each of the populations 4-6 nonetheless expresses a unique set of effector genes, although in general with less distinct separation and more mutual overlap. In one case, the onecut+ ciliated band and the veg1 eve+ cells, some overlap could be expected because the veg1 ectoderm eventually forms the vegetal strip of the ciliated band even though as analyzed here, the veg1 cells were isolated at 24 hpf and the ciliated band cells much later, at 35 hpf. However, the cell populations of unitary fate, populations 1-3, provide clear and unequivocal results, and we focus mainly on these in the following.

Data relevant to the isolated cell populations are shown in Fig. 1. The domains of the embryo represented are indicated in row 1. In Fig. 1Aa, pigment cells are shown embedded in the aboral ectoderm wall of a late embryo, alone among all the cells in the embryo generating the orange/red echinochrome pigment. Fig. 1Ba shows a view of a late blastula embryo in which the neurogenic apical domain is marked by foxq2 expression in orange; adjacent to this domain, on the oral side, is the gsc domain of the oral ectoderm stained blue. As described below, the lhx2/9 domain is confined to a subregion of the foxq2 apical plate. In Fig. 1Ca, the now mesenchymal skeletogenic domain is highlighted by expression of tbrain (pmc, primary mesenchyme cells). In Fig. 1Da, a lateral view of an early gastrula embryo (35 hpf), the ciliated band domain that bounds the oral ectoderm can be seen in this optical section as two patches of onecut expression, one above and one below (orange), whereas the oral ectoderm at this stage is expressing gsc (blue). The view in Fig. 1Ea is oral, and the complete circular pattern of the ciliated band expressing onecut can be seen (blue), the oral ectoderm is unstained, and at the vegetal end of the embryo the anterior endoderm is marked as the domain of foxa expression (orange). Fig. 1Fa shows the eve-expressing veg1 domain (orange), immediately abutting the foxa domain (blue), again in a 24 hpf embryo. In row 2 of Fig. 1 and in Fig. S2, examples are shown of expression of the respective recombinant BACs used for isolation of the cell populations that are our subject. Rows 3 and 4 of Fig. 1 show the respective FACS separation of cells from cell fragments and small cell aggregates by forward/side scatter, and the separations of live (in each case, the vast majority) from otherwise compromised cells. The panels in row 5 of Fig. 1 show the GFP gating by which active cells were separated from those not expressing the fluorochrome.

Genes enriched in the transcriptomes of each cell population

The initial project was to assess the efficacy of separating out cell populations. This was done *in extenso* in the preceding study on skeletogenic cells (Barsi et al., 2014). In that study, virtually every one of a large number of genes indicated by transcriptome analysis of the presumed skeletogenic population to be specifically expressed was indeed shown by *in situ* hybridization to be transcribed in skeletogenic cells. This result provided proof of technological principle for the extension to the additional five populations that are the subject of this paper.

Enrichment of specifically expressed transcripts was measured in the sorted cell populations by comparing the transcriptomes of the GFP-expressing populations with those of the non-GFP-expressing cells (‘dark’ cells) from the same FACS run. Given that incorporation of the recombineered BACs generating the GFP is mosaic in the injected embryos that were used after disaggregation for the FACS separations, some cells of the same types as the GFP-expressing cells will be included in the dark control populations in these comparisons. However, although the selected cell types could constitute all of the respective GFP populations, they will constitute only a minor fraction (F) in each case of the dark populations: $F=(aT-G)/T$, where a is fraction of the total embryo accounted for by the given cell population, T is the number of cells in the total embryo at the relevant stage and G is the number of GFP-positive cells per embryo recovered. Thus, the maximal enrichment of specifically expressed transcripts that could be expected in comparing GFP-expressing with dark cell populations is F^{-1}. We know the approximate numbers of cells expressing these regulatory genes at the relevant stages from the *in situ* hybridizations and extensive other studies on expression of these genes (cf. references cited in first paragraph of Results). For the populations in this study, F values ranged from ~0.05 to ~0.085, so the maximal enrichment that could be expected on the basis of passively enhanced concentration is of the order of 10- to 20-fold [excluding, of course, any particular gene(s) that are driven by the regulatory gene overexpressed in the recombineered BAC used for selection of the experimental population]. This is completely consistent with what is observed for the overwhelming majority of the genes in the enriched populations in the scatter plots shown in the following figures, given the observed statistical spread.

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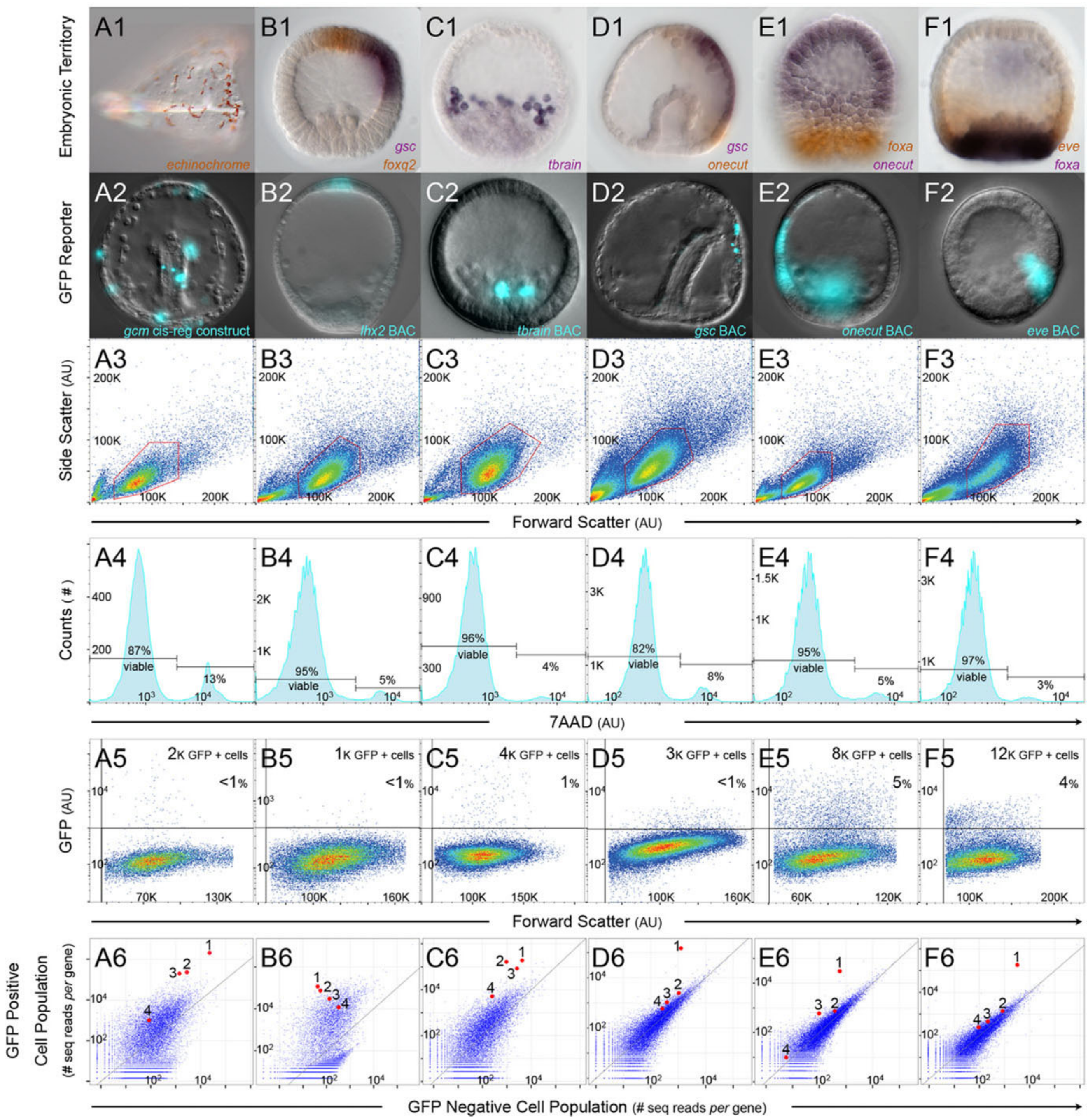

Fig. 1. See next page for legend.

An initial check is shown in row 6 of Fig. 1. Here, the positions of several transcripts known to be expressed specifically in the respective territories are highlighted on comparative transcriptome plots corresponding to each of the six cell populations (data points colored red). The only regulatory transcripts enriched $>>F^{-1}$ will be those resulting from read-through of the recombineered BACs expressing the GFP, which are injected in multiple copies per egg [although the recombineered BACs include poly(A) sequences following the GFP, these do not function efficiently enough to induce 100% chain termination, and we invariably note some read-through products in transgenic embryos expressing these BACs]. The identities of the enumerated transcripts are specified in the legend of Fig. 1, and all of them appear on the upper edge, or beyond, of the distributions in the comparative scatter plots. This indicates that, as should be the case, transcripts known to be expressed in the respective embryonic domains are enriched in the selected transcriptomes.

To obtain more comprehensive and unbiased evidence, we randomly chose transcripts that, according to the analysis, were enriched in each population, prepared *in situ* hybridization probes, and determined where in the embryo these transcripts are in fact located. These results are summarized in Fig. 2 and shown in detail in Fig. S3. The position of the data points representing transcripts chosen for whole-mount *in situ* hybridization (WMISH) examination can be seen in the scatter plots, outlined in black. Note that transcripts of different prevalence and different levels of

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Fig. 1. Diversity of embryonic cell types analyzed. (A-F) Experiments that correspond to each of the six cell types recovered: (A) pigment cells; (B) apical subdomain; (C) skeletogenic cells; (D) oral ectoderm subdomain; (E) ciliated band; and (F) veg1. (Aa-Fa) The embryonic territory of each cell type according to endogenous gene expression of key marker genes or compounds. (Aa) Pigment cells are visible from the lateral view of a larva because of the echinochrome they express. (Ba-Fa) Select marker gene expression evidenced by way of RNA *in situ* hybridization. (Ba) Lateral view of a blastula shows the apical subdomain in orange as revealed by foxq2 mRNA localization, relative to gsc expression in blue. (Ca) Oral view of a mesenchyme blastula depicts skeletogenic cells in blue as revealed by tbrain mRNA localization. (Da) Lateral view of gastrula shows the oral ectoderm in blue as revealed by gsc mRNA localization, relative to onecut expression in orange. (Ea) Oral view of gastrula shows the ciliated band in blue as revealed by onecut mRNA localization, relative to foxa expression in orange. (Fa) Oral view of blastula shows veg1 in orange as revealed by eve mRNA localization, relative to foxa expression in blue. (Ab-Fb) *In vivo* GFP expression superimposed onto differential interference contrast micrographs, demonstrating that reporter expression faithfully recapitulates each of the corresponding embryonic territories. (Ab) gcm cis-regulatory construct drives GFP expression exclusively within pigment cells. (Bb) lhx2 BAC reporter drives GFP expression exclusively within a subdomain of the apical plate. (Cb) tbrain BAC reporter drives GFP expression exclusively within skeletogenic cells. (Db) gsc BAC reporter drives GFP expression exclusively within a subdomain of the oral ectoderm. (Eb) onecut BAC reporter drives GFP expression exclusively within the ciliated band. (Fb) eve BAC reporter drives GFP expression exclusively within veg1. (Ac-Fe) Flow cytometry used for the recovery of each cell type. (Ac-Fc) Color-coded data points (orange spectrum represents higher density) are correlated with cell volume; events contained within the red demarcation were visually corroborated to constitute individual cells and chosen for subsequent fluorescence-activated cell sorting analysis. (Ad-Fd) The fraction of cells for each experiment that remained viable after disaggregation and flow cytometry, according to 7AAD incorporation. (Ad) 87% of cells derived from gcm:GFP transgenic embryos remained viable. (Bd) 95% of cells derived from lhx2:GFP transgenic embryos remained viable. (Cd) 96% of cells derived from tbrain:GFP transgenic embryos remained viable. (Dd) 82% of cells derived from gsc:GFP transgenic embryos remained viable. (Ed) 95% of cells derived from onecut:GFP transgenic embryos remained viable. (Fd) 97% of cells derived from eve:GFP transgenic embryos remained viable. (Ae-Fe) Color-coded data points (orange spectrum represents higher density) show the total number of GFP-expressing cells recovered for each embryonic territory: (Ae) 2K pigment cells; (Be) 1K apical subdomain cells; (Ce) 4K skeletogenic cells; (De) 3K oral ectoderm subdomain cells; (Ee) 8K ciliated band cells; and (Fe) 12K veg1 cells. (Af-Ff) Comparative transcriptome analysis illustrates the abundance of every mRNA species expressed in the cell type of interest, relative to control. Select data points are highlighted in red and accompanied by a numeric identifier. (Af) 1, pks1; 2, fmo3; 3, sult1c; 4, betaLi. (Bf) 1, lhx2; 2, foxq2; 3, z133; 4, ankAT-1. (Cf) 1, msp130; 2, tbrain; 3, p19; 4, alx1. (Df) 1, gsc; 2, bra; 3, lefty; 4, nodal. (Ef) 1, onecut; 2, univin; 3, slsp1; 4, pax2/5/8. (Ff) 1, eve; 2, wnt8; 3, wnt1; 4, wnt16. 7AAD, 7-aminoactinomycin D; AU, arbitrary units; BAC, bacterial artificial chromosome; GFP, green fluorescent protein; K, thousand.

enrichment were chosen for each sample. In Fig. 2, the results of such corroboration are exemplified in the three WMISH images below each scatter plot (labeled 1, 2, and 3). The expression pattern of several other transcripts subjected to *in situ* hybridization can be found in Fig. S3 (see legend for identities of these transcripts). The result is clear; exactly as in the preceding study on transcripts enriched in skeletogenic cells (Barsi et al., 2014), transcript sets isolated by this method are, by direct observation, specifically expressed in the expected spatial domains. FACS isolation of the cells expressing the respective regulatory genes thus effectively worked to separate out these embryonic cell populations, irrespective of the very distinct cell types and embryonic locations sampled. ‘Specifically expressed’ here does not necessarily mean specifically and exclusively expressed, because in some cases the WMISHs revealed that the transcript also appears in another different specific location. This will, of course, increase the value of a in the above expression, because the fraction of embryonic cells containing the given transcript would in such cases represent larger fractions of the embryo than for transcripts expressed in single differentiated cell types, thereby decreasing the possible degree of enrichment of such transcripts.

A research resource: lists of effector genes whose transcripts are significantly enriched in each isolated cell population

Preferentially expressed genes in each sorted population are listed in order of statistical improbability that their transcripts are not enriched, given the transcript read count distribution, as computed using the R packages identified in the Materials and Methods. The P value distributions shown range from $<10^{-10}$ to $<10^{-2}$ for each data set. The abbreviated gene names (for synonyms see the Echinobase genome database http://www.echinobase.org/Echinobase/Search/SpSearch/index.php), ID numbers, crude ontology assignment and enrichment significances are listed in Table S1A-E. As we show explicitly in the following description, the enriched transcript sets for all six of these preparations are almost entirely non-overlapping; that is, only a minute fraction of the genes represented in any one enriched transcript population is also represented in the enriched transcript population of another. Thus, within the confines of the measurements on these particular cell populations, these transcript sets are enriched uniquely; of course, this does not preclude preferential expression of any of these transcripts in another tissue or cell type or developmental stage than those studied here. Nonetheless, Table S1A-E provides a qualitative resource of a particular kind. For example, Table S1 could be useful for an investigator who wishes to discover what genes are specifically expressed in ciliary band cells, which generate characteristic long cilia, but are not expressed in cells that make ‘normal’ cilia, such as the epithelial veg1 cells or oral cells immediately surrounding the stomodeum among the populations studied here. Or it might be of interest to explore further the genes encoding signaling effector components that are specifically represented in the eve-expressing (veg1) cell population (Table S1E), because this domain includes the future ectoderm-endoderm boundary of the embryo.

Tables S1A and S1B represents differentiated or differentiating cell types (pigment cells and neurogenic cells, respectively), and all the effector gene transcripts that are expressed specifically in each of these cell types should be included in the enriched transcript sets, provided the genes are expressed above the one to a few transcripts per gene-cell, our minimal possible effective cut-off. Sea urchin skeletogenic effector gene sets have been previously reported by Barsi et al. (2014) and thus, are not included Table S1. Additionally, alternative methods have produced similar, albeit smaller-scale catalogs (Zhu et al., 2001; Livingston et al., 2006; Rafiq et al., 2012). Transcriptomes of various classes of neurons have been much studied elsewhere (Momčilović et al., 2014; Tu et al., 2014), although the developmental functions in neurogenesis of the apical lhx2/9 domain are scarcely resolved. However, our understanding of the overall differentiated nature of the sea urchin embryonic cells producing the napthoquinone pigment echinochrome is likely to profit greatly from the resource represented by the enriched pigment cell transcript set in Table S1A.

A relatively ‘universal’ set of effector gene transcripts

In Fig. 3 is shown the exact obverse of the enriched and depleted transcript sets indicated in red and green in Fig. 2. Here is illustrated a set of 495 transcripts no member of which is ever either enriched or underrepresented, to any statistically significant extent, in any of

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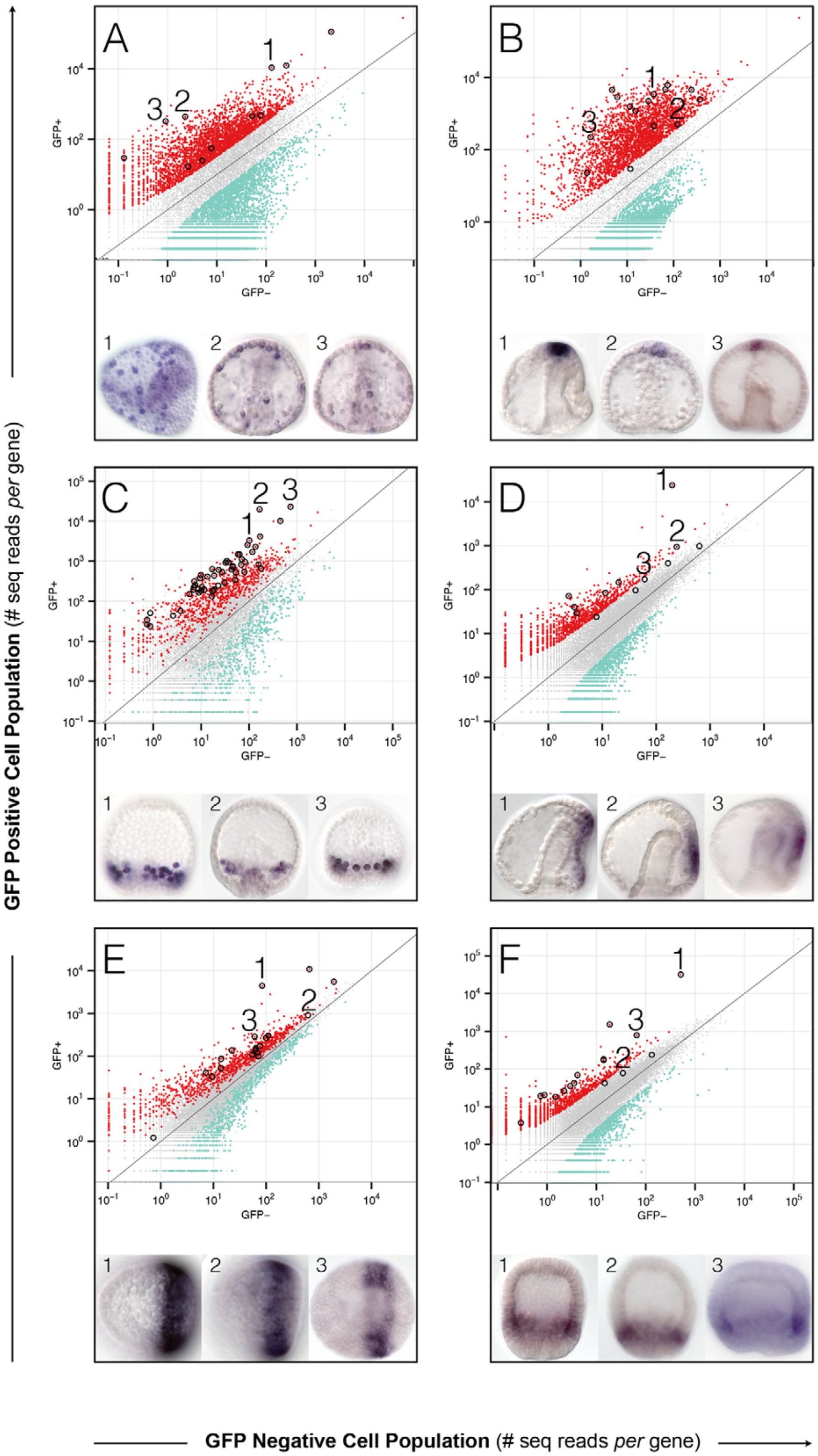

Fig. 2. Enriched populations of transcripts and WMISH corroboration. (A-F) Experiments that correspond to each of the six cell types recovered: (A) pigment cells; (B) apical subdomain; (C) skeletogenic cells; (D) oral ectoderm subdomain; (E) ciliated band; and (F) veg1. Comparative transcriptome analysis for each case is shown in the form of a scatterplot, illustrating the abundance of every mRNA species enriched to the cell type of interest (red data points), relative to control. For all cell types, underrepresented transcripts have been colored green. Data points representing mRNA species corroborated by WMISH have been outlined in black, three of which are enumerated and their corresponding pattern of expression shown immediately below. (A) 1, gcm; 2, whl22.493883; 3, gpr54l_3. (B) 1, foxq2; 2, whl22.510486; 3, kifc3L3. (C) 1, p19; 2, tbr; 3, msp130. (D) 1, gsc; 2, bra; 3, nodal. (E) 1, onecut; 2, z166; 3, slsp1. (F) 1, eve; 2, wnt1; 3, wnt16. GFP, green fluorescent protein. Note that color codes reflect the consensus among replicates, whereas the individual data points shown represent transcript abundance as observed for a single replicate.

the six selected GFP+ transcript preparations. The relative prevalence or number of sequencing reads (normalized against total reads) per locus for each transcript species varies by small factors in comparing the six different GFP+ preparations, and likewise when comparing such values for each transcript across the six control GFP– preparations. These numbers can be seen in Table S2. Most importantly, Table S2 shows no systematic enrichment or depletion in comparing the prevalence between GFP+ and GFP– preparations of the same population isolate, nor does it indicate the concentration of any particular functional category in this gene set (which could reflect the limit of such ontological categories). These details are all implied by the

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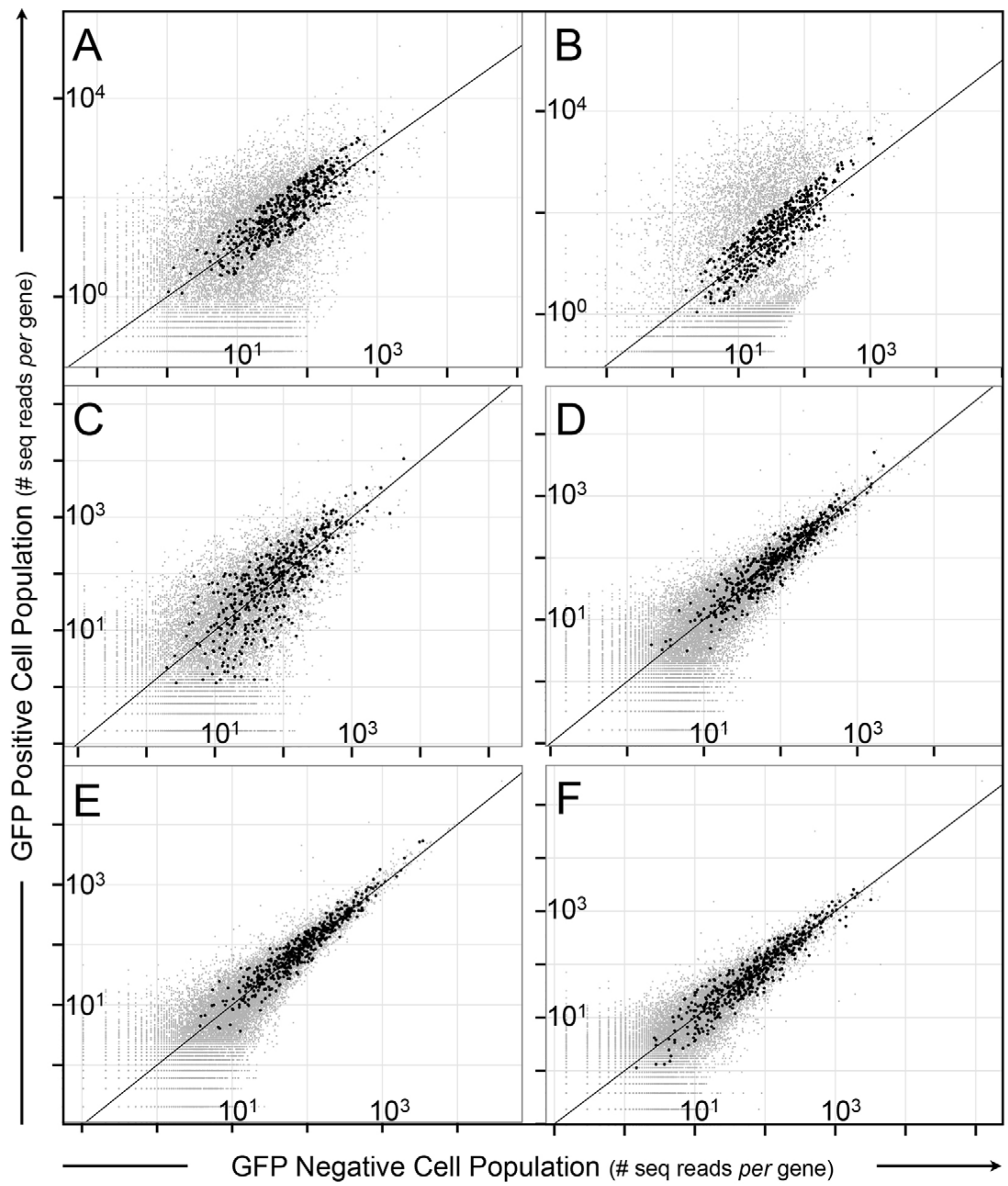

Fig. 3. Cohort of universally expressed transcripts. (A-F) Comparative transcriptome analysis for each of the six cell types recovered: (A) pigment cells; (B) apical subdomain; (C) skeletogenic cells; (D) oral ectoderm subdomain; (E) ciliated band; and (F) veg1. Illustrated in each scatterplot is the abundance of every mRNA species expressed in the cell type of interest (plotted along the ordinate), relative to control (plotted along the abscissa). Data points colored black represent 495 transcripts expressed across all six cell types analyzed.

distributions seen in Fig. 3, of which the simplest descriptor is that in every sorted sample the members of this gene set map with the unsorted majority distribution.

This is not meant to indicate the fraction of effector genes that are universally expressed, because we made no attempt to estimate the total number of transcript species behaving like those of Fig. 3, even within the six populations compared here. Furthermore, had we examined other transcript populations, some of these 495 transcripts might have displayed sharp depletion or enrichment profiles. All that can be said is that if there were genes expressed in all cells in all spatial domains of the embryo similarly (per gene, except for minor quantitative variations), their behavior would be that seen in Fig. 3 for the samples we looked at. In fact, a large fraction of the 495 transcripts are likely to be distributed universally in the embryo, with regard to spatial expression, based on another kind of comparison. Maternal transcripts in sea urchin embryos are in general universally distributed, and they are often universally expressed as ‘housekeeping’ proteins. The maternal transcriptome of these eggs has been studied in detail (Tu et al., 2014; Peter and Davidson, 2015). Out of the 495 transcript species in the set discussed here, 421 turn out also to belong to the maternal transcript component.

Mutual specificity of effector gene sets

The most informative demonstration of differential effector gene use is direct comparison of the specifically enriched populations of transcripts expressed in each of the three differentiated cell types. In the six panels of Fig. 4, such comparisons are shown between the

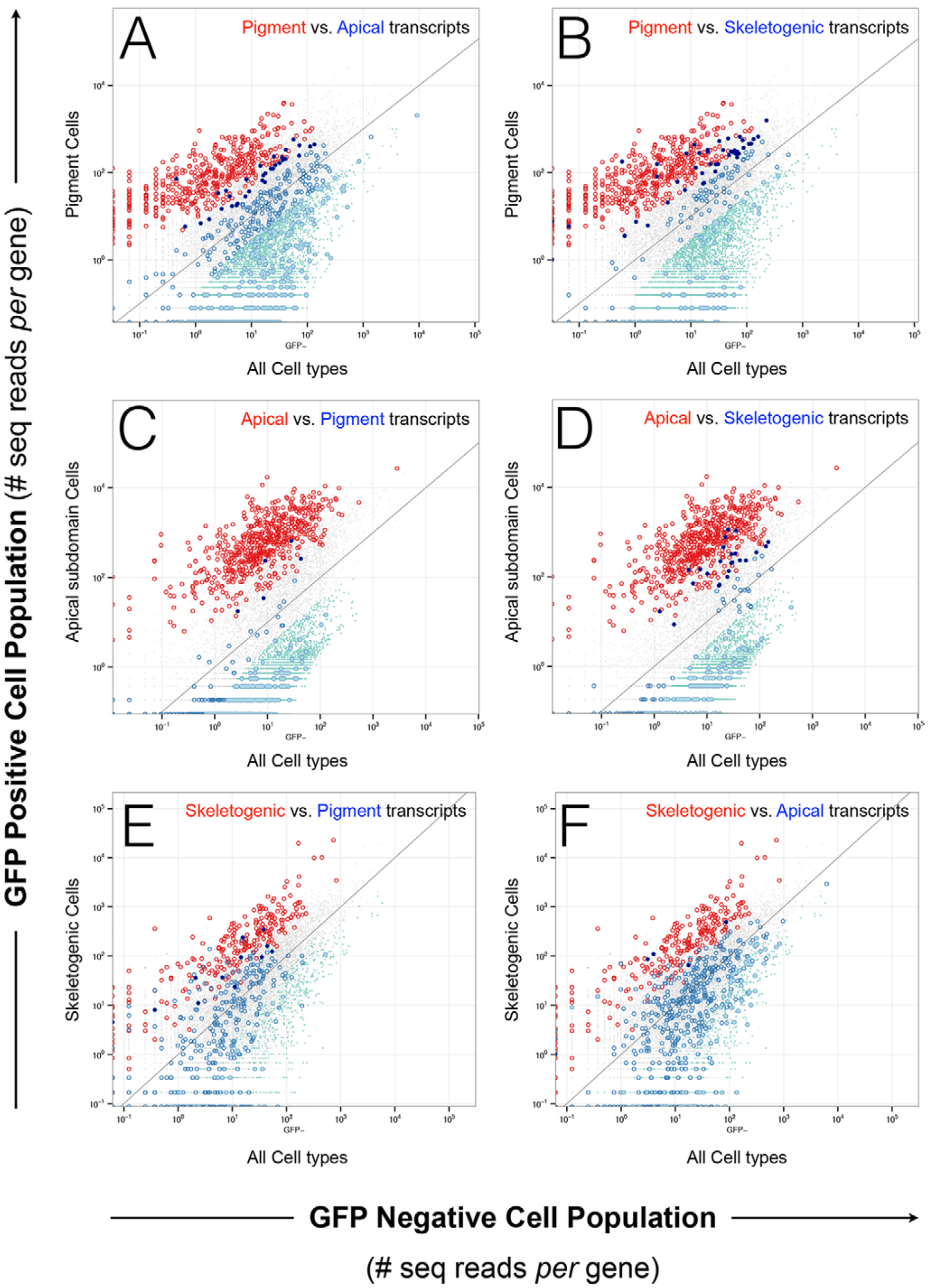

Fig. 4. Specificity of effector gene sets. (A-F) Comparative transcriptome analysis for three differentiated cell types: (A,B) pigment cells; (C,D) apical subdomain; and (E,F) skeletogenic cells. Illustrated in each scatterplot is the abundance of every mRNA species expressed in the cell type of interest (plotted and labeled along the ordinate), relative to control (plotted and labeled along the abscissa). Data points outlined in red represent transcripts uniquely expressed in the cell type specified at the top of each plot (also in red). Underrepresented transcripts are shown as green data points. Data points outlined in blue represent transcripts uniquely expressed in a different cell type, specified at the top of each plot (also in blue). Of these, those that are depleted relative to the data set shown have been shaded light blue. Likewise, those that are enriched have been shaded dark blue. All remaining data points have been colored light gray. As described in detail in the Materials and Methods, these assignments are the result of statistical prevalence analysis; the main quantitative importance of this figure is that transcripts shown in red are enriched beyond the upper bound of a ±0.05 probability envelope; depleted transcripts in light green lie beyond the lower boundary of this envelope; and the gray transcript population gives the distribution of insignificantly enriched or depleted transcripts within this envelope. Note that color codes reflect consensus among the replicates, whereas the individual data points shown represent transcript abundance as observed for a single replicate.

enriched cohorts of transcripts for each cell type (red) co-plotted in this same transcriptome with the enriched transcript cohorts of each of the other two cell types (blue). Thus, in Fig. 4A we see the distribution of the pigment cell-enriched cohort (red) compared in the same sorted pigment cell scatter plot with the distribution of those transcripts that were identified as enriched specifically in the apical neurogenic cells (blue). Likewise, in Fig. 4B the distribution of the enriched transcript cohort of the skeletogenic cells is co-plotted on the sorted pigment cell scatter plot. In Fig. 4C, the distribution of the enriched apical neurogeneic transcript cohort, as seen in the sorted lhx2/9+ cell transcriptome, is compared with that of the enriched transcript cohort of the pigment cells in the same neurogenic cell transcriptome; and in Fig. 4D the enriched apical neurogeneic transcript cohort is compared with the transcript cohort identified as enriched in the skeletogenic cells, again plotted on the neurogenic cell transcriptome distribution. In Fig. 4E, the distribution of transcripts identified as enriched in pigment cells is plotted on the transcript distribution of the sorted skeletogenic cells; and in Fig. 4F the neurogenic cell enriched cohort is plotted on the same sorted skeletogenic cell transcriptome. With minor variations, all six comparisons reveal the striking individuality of these sets of enriched transcripts with respect to one another. In each panel of Fig. 4, the dark blue dots represent transcripts recovered in the comparator enriched transcript set that co-mingle with the red dots displaying the population of enriched transcripts in that sorted sample. This would mean that the genes encoding these transcript species are preferentially transcribed in both cell types. Compared with the hundreds of transcripts enriched in each cell type, for example, there are only five transcript species of the pigment cell-enriched cohort also identified in the apical neurogenic cell-enriched cohort (Fig. 4C), and only 22 skeletogenic cell-enriched transcripts also enriched in the apical neurogenic cells (Fig. 4D). By this analysis, the enriched transcript sets of skeletogenic and pigment cells are slightly more similar (larger numbers of dark blue dots), which as we note in the Discussion is to be expected, because aspects of their functions are similar at the stages compared. Most striking, however, is the sharp depletion in each sorted population of transcripts present in the enriched transcript sets of the other two cell types, in every comparison of Fig. 4. These are indicated by the light blue symbols located below the statistical envelope within which reside the mass of gray dots representing non-selected transcripts. Many, in some cases most, of the comparator enriched population is in fact absent entirely, or these severely depleted transcripts are seen only along the abscissa or ordinate axes of the selected cell population. Thus the genes encoding the severely depleted transcripts are not transcribed significantly in each of the specific cell types or are represented at levels too low to be meaningful biologically.

DISCUSSION

The mechanistic essence of embryogenesis is installation of spatially differential regulatory gene expression. This is the fundamental process by which diverse sets of genes encoding transcription factors are respectively activated in the appropriate regions of the early embryo. Regulatory states are thus regionally formulated, and they serve as the causal determinants of embryonic fates; all developmental events downstream of the progression of regulatory states depend in each region either directly or indirectly on effector genes activated in response to these different regulatory states, i.e. on signaling genes, cell biology genes and differentiation effector genes. Much beautiful experimental analysis has now closed the circle, at least in fortuitous model systems, and demonstrated that the progression of determinant regulatory states in embryogenesis is in turn the direct read-out of the network of regulatory gene interactions encoded in the genomes of the embryo (Peter and Davidson, 2015). However, the exact course of the regulatory events that culminate in the appearance of differentiated embryonic cell types remains a challenging gray area. Considered embryo-wide, this aspect of the process is asynchronous and spatially complex, because some embryonic regions give rise uniquely and quickly to terminal cell types, whereas other domains of the same embryo are engaged in progressive specification of spatial regulatory states long in advance of resolution of terminally differentiated gene expression.

The sea urchin embryo remains the exemplar of extensive embryonic gene regulatory network analysis. Nonetheless, only two subregions of the solved networks extend to activation of at least some immediate differentiation gene drivers, and thereafter to transcription of known differentiation effector genes. One of these is the skeletogenic domain, where the specification gene regulatory network is apparently complete and where several in-depth studies have addressed activation of biomineralization and other effector genes (reflected in the tbrain domain of Fig. S4). The other is specification of pigment cells, another early differentiating lineage of this embryo, in which several genes encoding enzymes engaged in synthesis of the napthoquinone pigment are known. These two differentiating embryonic cell types are isolated and characterized in the present study. A third, also isolated and comparatively analyzed here, is the neurogenic cell population expressing the *lhx2/9* gene. This domain is one of the few embryonic domains remaining for which we still lack comprehensive knowledge of the transcriptional interactions responsible for establishment of its regulatory state (including *lhx2/9* activation).

The assays, sequence identities and validations presented in Figs 1-3 and the supplementary figures and tables of the present paper show that the transcriptomes of the six populations of embryonic cells studied here are indeed mutually unique. Three of these populations, the ciliary band cells, the veg1 cells and the circumstomodeal cells, are each a heterogeneous mixture of different future cell fates, including diverse incipient differentiations. As is to be expected, the results of intercomparisons among these populations (Fig. S5) are more nuanced than those that are so strikingly revealed in the comparisons of the enriched transcript sets shown for the three differentiated cell populations in Fig. 4. In Fig. 4, as described above, the enriched effector gene transcript set of each differentiating cell type is compared against that of each of the other two cell types. The results in each panel provide a textbook illustration of differential effector gene expression early in development. This is illustrated in three ways in each of the six panels of Fig. 4. First, each expresses several hundred transcript species in highly specific ways in respect to all the other cells in the embryo, shown in red. Second, only minute fractions of the enriched transcript set of each cell type are ever found in the enriched transcript set of another cell type, shown by the few superimposed dark blue and red points in each panel. The only minor exception is seen in comparisons of the pigment cell- and skeletogenic cell-enriched transcript populations, which is to be expected because these are both migratory cells of mesodermal embryological origin. Third, again with the quantitatively minor exception of the pigment cell- and skeletogenic cell-enriched populations, most of the genes encoding the enriched transcript populations of each cell type are not expressed at all in the other two cell types, so that their relative prevalence is negligible, or are otherwise significantly depleted in the log probability distributions, shown in light blue. Taking into account the fact that the comparisons are with unsorted cells, which include the cell types in question, these essentially mean the same thing, i.e. that the genes giving rise to the enriched transcript populations of each cell type are in general simply not being expressed in the other cell types.

The pigment cell and skeletogenic cell gene regulatory networks show that the effector genes are expressed if and when their driver regulatory genes are expressed in the differentiating cell-regulatory state. In this situation, absence of expression unequivocally means absence of the requisite sequence-specific transcriptional activators. The non-expressed genes are never turned on in the lineages leading to the pigment cells, skeletogenic cells and neurogenic cells of this study. Thus, the present study shows explicitly how the speed and power of spatially differential regulatory gene expression causes large-scale, cell type-specific deployment of effector gene cohorts in this embryo within little more than a day after fertilization.

MATERIALS AND METHODS

BAC reporters

Bacterial artificial chromosomes have been genetically engineered to express GFP in lieu of an endogenous gene, the first exon of which is replaced with a GFP cassette by way of homologous recombination. Each BAC harbors the entire locus of a gene that is exclusively expressed in the cell type of interest. The conceptual basis for using BACs as a means to label individual cell types is the assumption that they are large enough to harbor the complete cis-regulatory apparatus that governs the expression of a marker gene. This is the principle that confers spatial and temporal precision of expression to a BAC reporter. In this study, we take advantage of six BACs that have been determined to recapitulate endogenous gene expression. A library containing hundreds of genetically engineered BAC reporters can be accessed at http://www.echinobase.org/Echinobase/bac_table/bac_table.php. All BAC reporters discussed herein are publicly available upon request.

Computational procedures

Data visualization

The results were visualized predominantly in the form of scatterplots made possible by R software (R Development Core Team, 2013; version 3.1.2; http://www.r-project.org) and the ggplot2 package (Wickham, 2009; version 1.0.0; http://ggplot2.org). The online resource was generated using Shiny software (RStudio Inc. 2013; server version v1.0.0.42, R package version 0.8.0; http://www.rstudio.com/shiny/).

Differential gene expression analysis

Raw read counts for each gene locus were used to calculate differential gene expression by way of the R package known as edgeR (version 3.8.5; http://www.r-project.org). First, the effective library size for each sample was calculated by the trimmed mean of M-values method, provided in the package. Then, pairs of replicates were used to estimate the biological coefficient of variation (BCV) by way of the generalized linear model (GLM) method, also provided in the package. Differential gene expression was calculated using the GLM likelihood ratio test. A fixed value of 0.4 was found to account accurately for the BCV observed across all samples. The substitution of alternative BCV values had no effect on the vast majority of differentially expressed genes. To facilitate distinguishing between enriched and depleted gene cohorts, we expanded *P* values from [0.1] to [0.2]: for enriched gene cohorts (Count_GFP+>Count_GFP−), the *P* values were maintained; for depleted gene cohorts (Count_GFP+<Count_GFP−), the *P* values were replaced by [2 – p]. Thus, a *P* value close to 0 indicates very significantly enriched, whereas a *P* value close to 2 indicates very significantly depleted. In the case of samples with multiple replicates, the replicates were considered together for the estimation of enrichment or depletion. Conversely, the universal gene cohorts were defined by having their expanded *P* values between 0.05 and 1.95 across all cell types analyzed, and their read counts were always >1.

Mapping Illumina sequencing reads

The same pipeline described in our previous work (Barsi et al., 2014; Tu et al., 2014) was used, except that all software was upgraded to the latest version when performing analysis: STAR version 2.4.0b (Dobin et al., 2013) and HTSeq version 0.6.0 (http://www-huber.embl.de/users/anders/HTSeq/), the statistics of which can be found in Fig. S6.

Developmental model organism

Adult sea urchins were sourced locally off the coast of Southern California. They were kept at Caltech's Kerckhoff Marine Laboratory before being transferred to Caltech's main campus for experimentation purposes.

Flow cytometry

A FACS Aria Flow Cytometer Cell Sorter (BD Biosciences) was used to isolate individual cells immediately after embryo disaggregation. The only distinction from the standard operating protocol was the use of twice-filtered seawater (0.2 µm) in lieu of the regular sample diluent. This operational alternative is of biological importance when assessing live cells derived from marine model organisms.

Gene transfer

Sea urchin eggs were briefly treated in filtered seawater (FSW) containing citric acid (0.5 M) and aligned on protamine-coated Petri dishes. FSW containing para-aminobenzoic acid (300 mg/ml) was used in order to facilitate injection. Eggs were fertilized *in situ*, and the resulting zygotes were injected (1 pl/zygote) with reporter BACs (50 ng of DNA per ml of nuclease-free water). Injection needles were fabricated in house from borosilicate glass capillary tubing (1 mm outer diameter × 0.75 mm inner diameter × 100 mm long) using a Flaming/Brown P-80 (Sutter Instruments) micropipette puller. The consecutive micromanipulation of thousands of embryos was achieved on an Axiovert 40 C (Zeiss) compound microscope equipped with a single-axis oil hydraulic MM0-220 (Narishige) micromanipulator and a picospritzer III (Parker) microinjection dispense system. Transgenic embryos were cultured at 15°C in FSW containing trace amounts of penicillin and streptomycin.

Isolation and handling of specific sea urchin embryonic cell populations

The steps of this procedure are all presented in detail in the preceding publication (Barsi et al., 2014). Briefly, the sequence of steps is as follows: (1) injection of recombineered BAC reporters expressing GFP under control of specific regulatory gene cis-regulatory apparatus; (2) disaggregation of the injected embryos after they had attained the appropriate developmental stage; (3) FACS sorting to isolate the desired cell populations; (4) isolation of the sorted cell mRNA and cDNA amplification; and (5) transcriptome sequencing and analysis by standard mapping and statistical methods (Barsi et al., 2014). In the earlier work, we showed that the disaggregation and FACS procedures per se have no quantitative or qualitative effect on the transcriptomes, by comparisons with control embryos. At the time of injection, the spatial accuracy of expression of the incorporated BAC expression constructs was checked microscopically (cf. Fig. 1). Numbers of embryos used to obtain each of the populations of sorted cells analyzed in this work, and other procedural statistics, are also presented in the preceeding study.

Microscopy

Both live and fixed transgenic embryos were monitored for accurate reporter expression using an Axioskop 2 plus (Zeiss) compound microscope equipped for fluorescence and differential interference contrast microscopy. Digital images were taken using an Axiocam MRm (Zeiss) camera. Embryos shown were visualized through a 20× objective lens, whereas individual cells were imaged using a 40× objective lens.

RNA *in situ* hybridization

WMISH was performed on Sp embryos following a published method optimized in our laboratory (Ransick, 2004).

RNA processing

Total RNA was extracted from each of the various cell populations isolated by FACS using an RNeasy Plus Mini Kit (Qiagen). The only distinction from the manufacturer's recommended protocol was a twofold increase in the DNase incubation time.

Availability of raw data

All data supporting the findings communicated in this study have been submitted to the NCBI Sequence Read Archive (SRA; http://www.ncbi.nlm.nih.gov/sra) under accession number SRP052830.

Online resource for the research community

All cell-specific data originating from this study can be interrogated using purpose-built query/visualization tools or downloaded in their entirety via Echinobase (http://www.echinobase.org/SpBase/rnaseq/embryonic_territory.html).

Acknowledgements

This work is dedicated to the memory of our mentor, E.H.D. (1937-2015). Many collaborators contributed their invaluable expertise to this project. We would particularly like to acknowledge the expert assistance of Shelley Diamond and her assistants Diana Perez and Pat Koen in developing an efficacious FACS protocol for sea urchin embryonic cells; the generous provision by Dr Enhu Li of the *in situ* hybridization images in Fig. 1; Dr Andrew Ransick for kindly providing the gcm cis-reg construct used to isolate pigment cells and related micrographs used in Figs 1Aa and 2A #1; and the multiple contributions of Erika Vielmas, who authenticated the expression patterns of the injected BACs used to isolate the various cell populations by microscopic examination and assisted with miscellaneous aspects of this study.

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Competing interests

The authors declare no competing or financial interests.

Author contributions

J.C.B. and E.H.D. designed the research; J.C.B. and C.C. performed the research; J.C.B., Q.T. and E.H.D. analyzed the data; and J.C.B. and E.H.D. wrote the paper.

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Supplementary information

Supplementary information available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.127746/-/DC1

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The following document consists of supplemental information supporting the findings communicated in:

GENOME-WIDE ASSESSMENT OF DIFFERENTIAL EFFECTOR GENE USE IN EMBRYOGENESIS

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Online resources related to this study include the following:

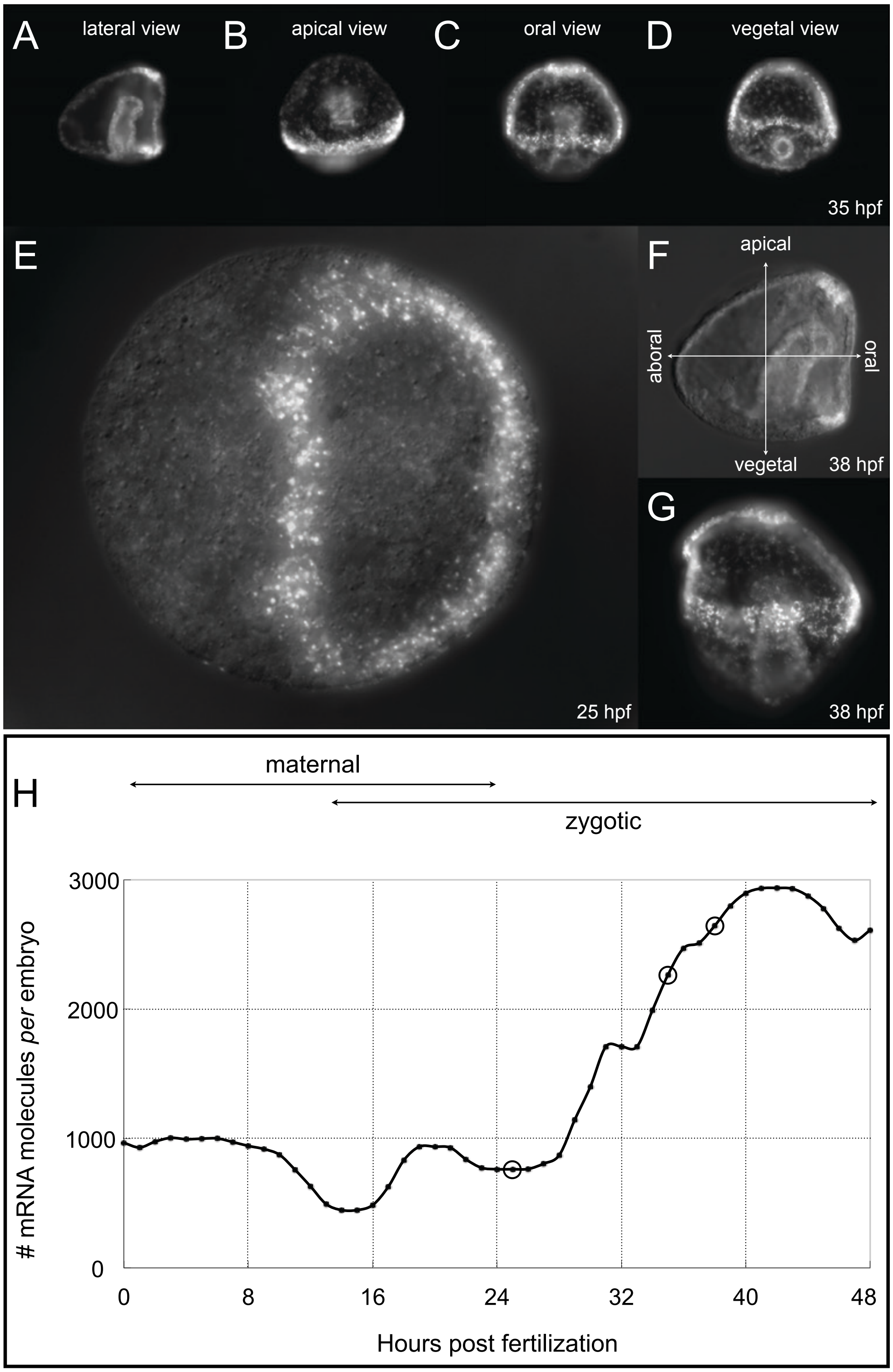
The home page of this study:
http://www.echinobase.org/SpBase/rnaseq/embryonic_territory.html

A dynamic visualization tool that allows users to interrogate all data pertaining to this study:
http://www.echinobase.org:3838/embryonic_territory/

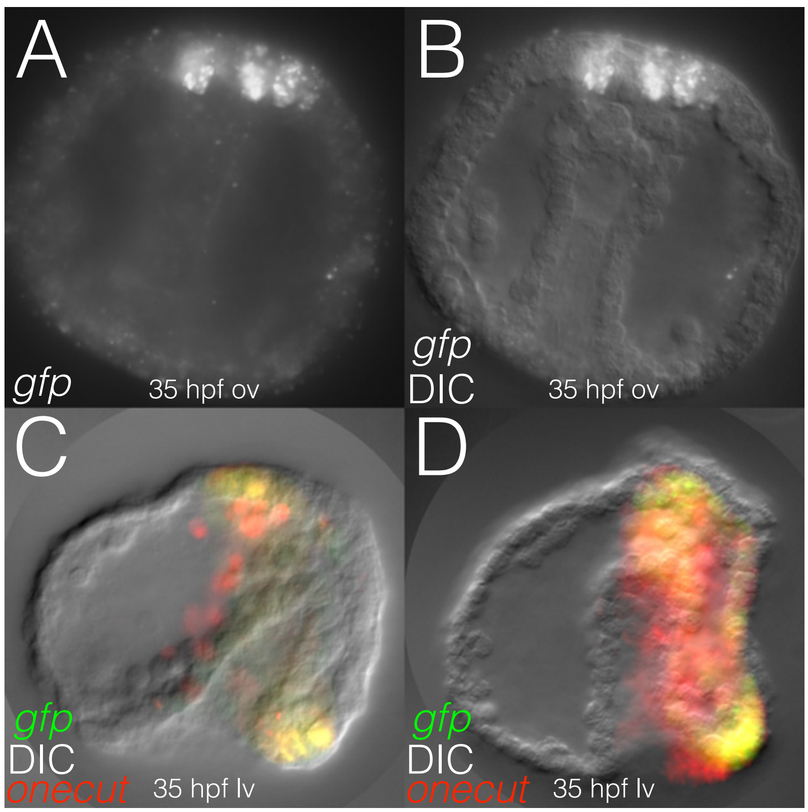
A query tool that allows users to gather additional information for any given gene:
http://www.echinobase.org/Echinobase/Search/SpSearch/

The National Sequence Read Archive, where all data has been deposited under SRP052830:
http://www.ncbi.nlm.nih.gov/sra

INDEX



Supplemental Figure 1



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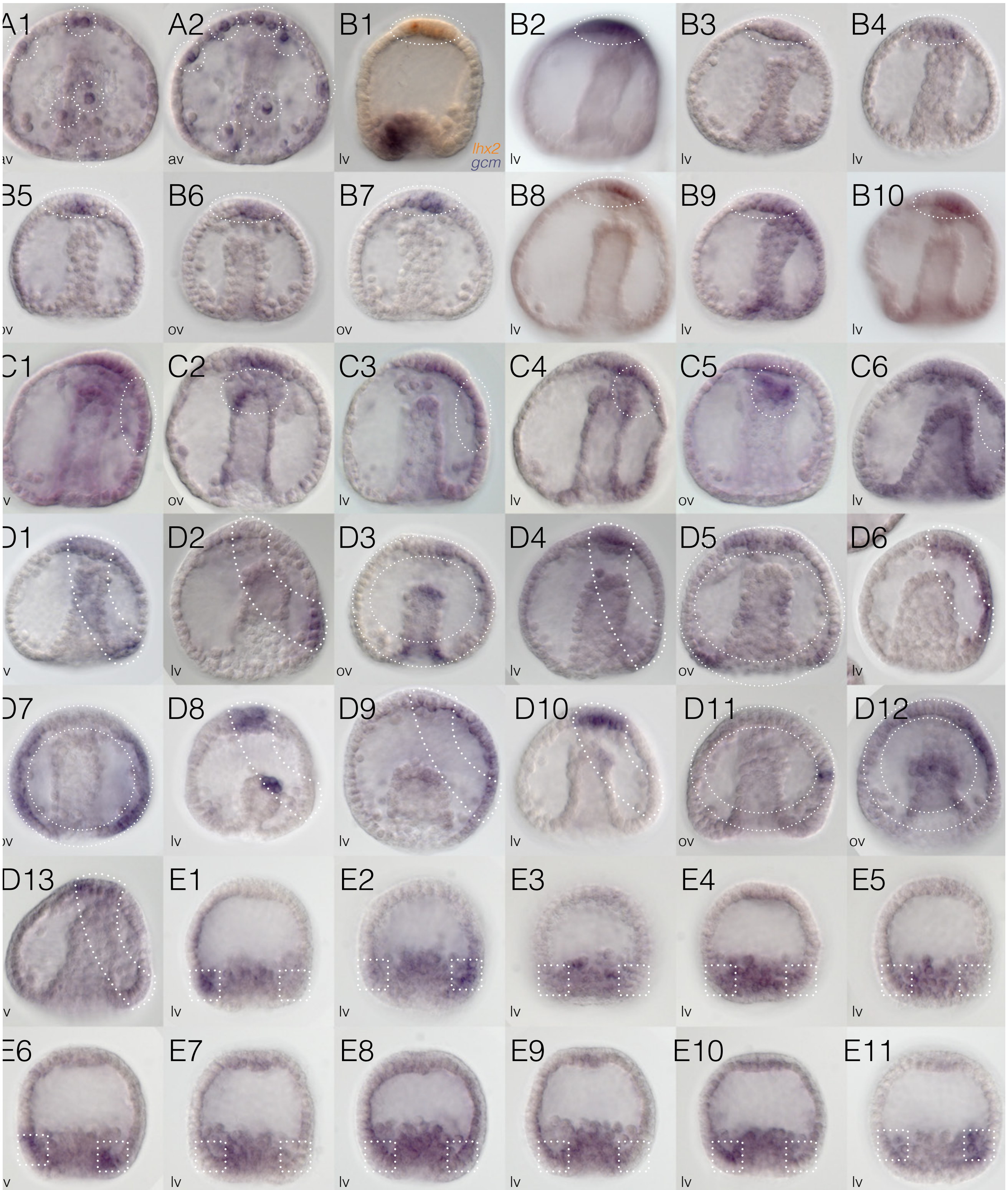

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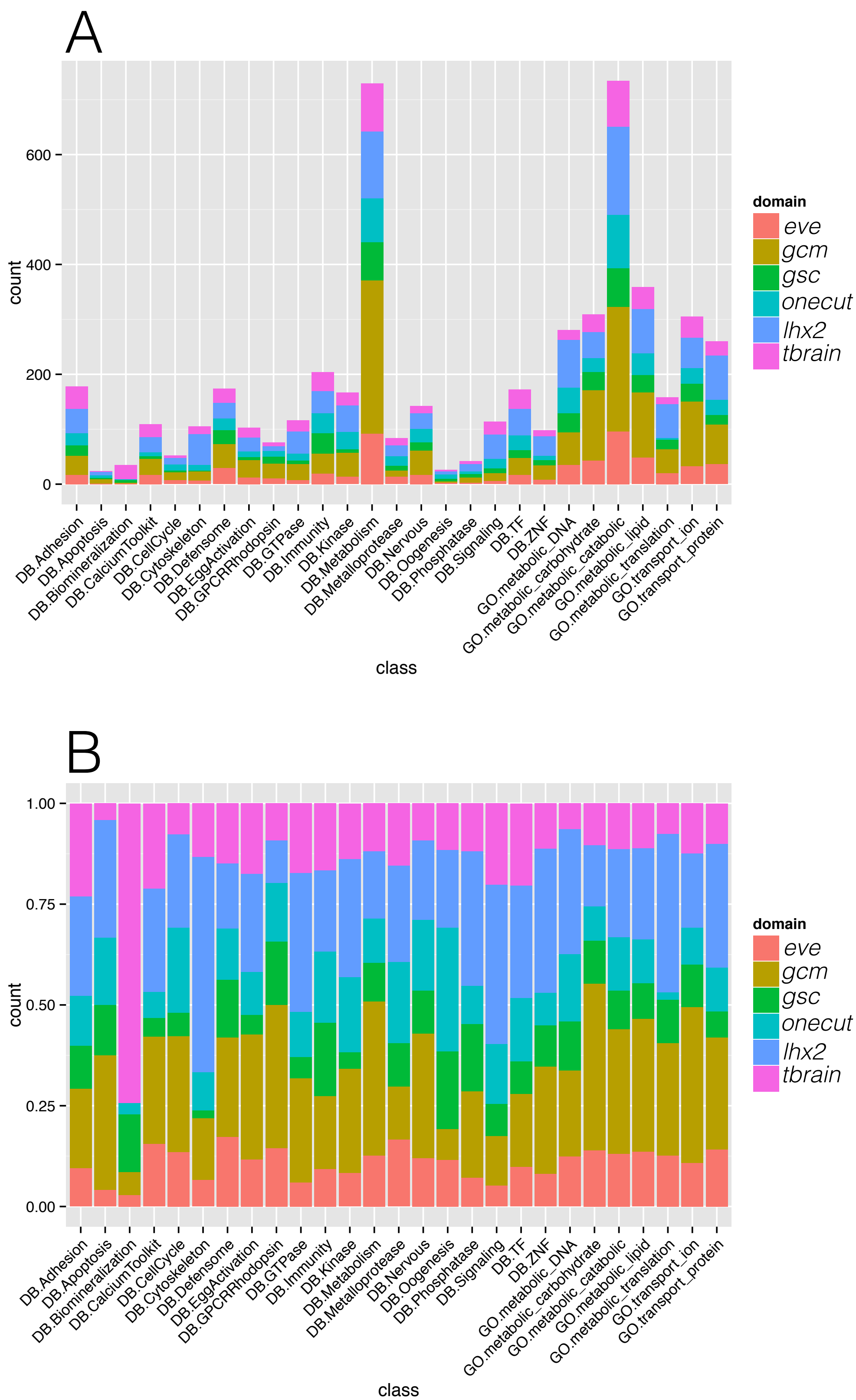

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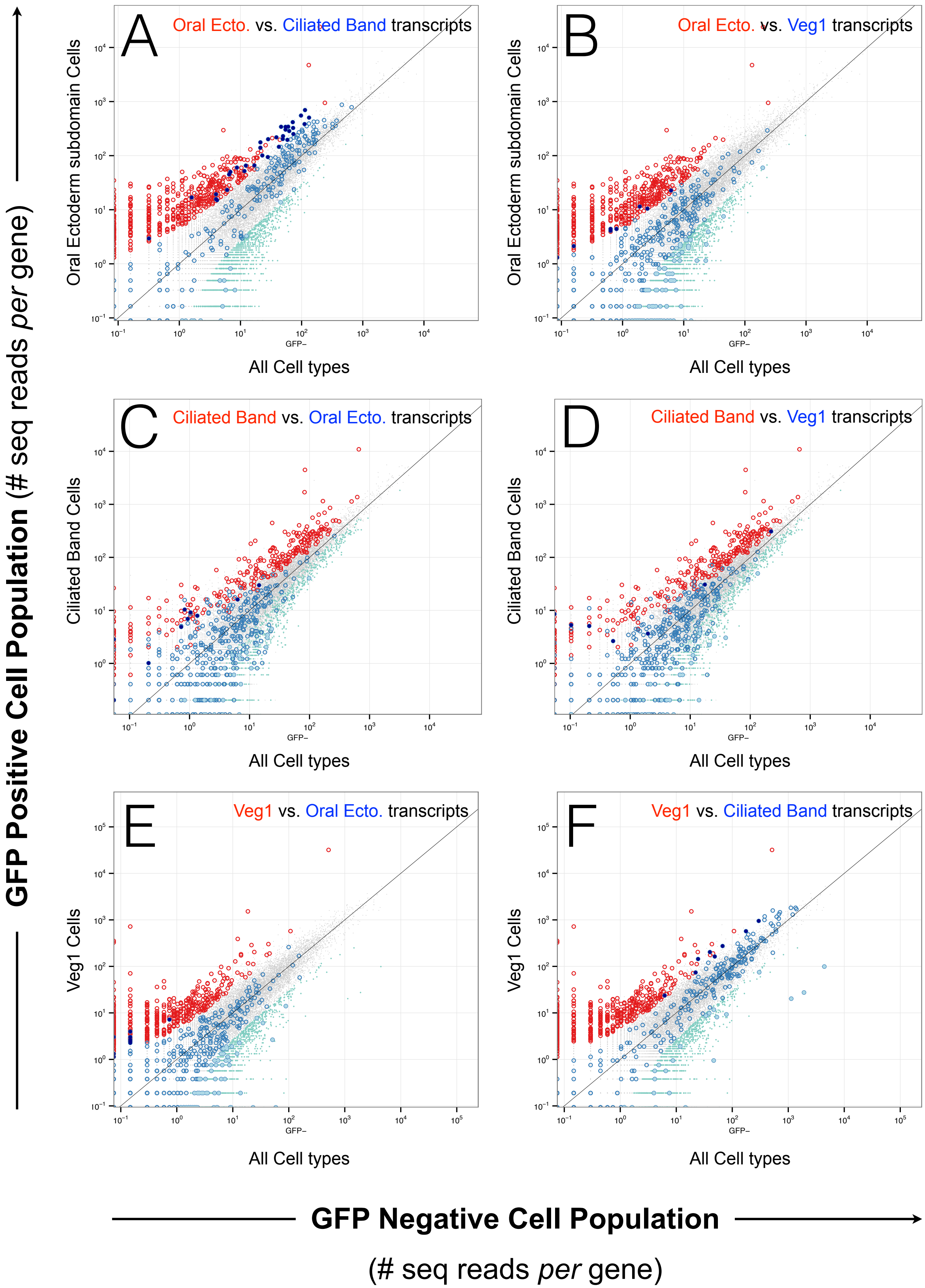
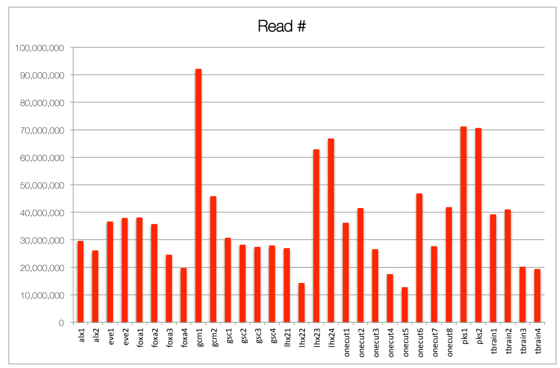
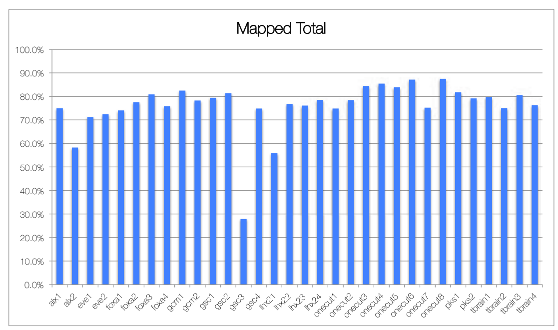


Supplemental Figure 5

Sample Name	Read #	Unmapped	Mapped Total	Mapped Unique	Mapped Multiple
alx1	29,582,297	25.0%	75.0%	55.1%	19.8%
alx2	26,144,409	41.7%	58.3%	47.6%	10.7%
eve1	36,671,651	28.7%	71.3%	55.3%	15.9%
eve2	37,947,816	27.5%	72.5%	52.8%	19.7%
foxa1	38,108,610	25.9%	74.1%	61.4%	12.7%
foxa2	35,741,746	22.4%	77.6%	60.7%	16.9%
foxa3	24,579,265	19.1%	80.9%	67.8%	13.2%
foxa4	19,724,431	24.1%	75.9%	64.8%	11.1%
gcm1	92,175,278	17.5%	82.5%	61.5%	21.0%
gcm2	45,833,688	21.7%	78.3%	63.0%	15.3%
gsc1	30,697,100	20.5%	79.5%	67.5%	12.0%
gsc2	28,208,845	18.6%	81.4%	68.3%	13.0%
gsc3	27,391,729	72.1%	27.9%	20.9%	6.9%
gsc4	27,984,642	25.1%	74.9%	60.2%	14.6%
lhx21	26,920,129	44.1%	55.9%	40.3%	15.6%
lhx22	14,294,642	23.1%	76.9%	63.4%	13.4%
lhx23	62,883,538	23.9%	76.1%	57.5%	18.6%
lhx24	66,788,914	21.4%	78.6%	62.9%	15.8%
onecut1	36,155,436	25.1%	74.9%	52.9%	22.0%
onecut2	41,521,047	21.5%	78.5%	61.1%	17.4%
onecut3	26,585,956	15.5%	84.5%	69.4%	15.1%
onecut4	17,512,935	14.5%	85.5%	73.1%	12.4%
onecut5	12,711,201	16.1%	83.9%	69.0%	14.9%
onecut6	46,827,462	12.8%	87.2%	73.1%	14.1%
onecut7	27,672,244	24.8%	75.2%	61.6%	13.6%
onecut8	41,879,554	12.5%	87.5%	73.6%	14.0%
pks1	71,217,174	18.2%	81.8%	61.2%	20.6%
pks2	70,687,515	20.8%	79.2%	60.7%	18.5%
tbrain1	39,246,895	20.2%	79.8%	59.4%	20.3%
tbrain2	41,002,846	24.9%	75.1%	61.9%	13.3%
tbrain3	20,209,687	19.4%	80.6%	67.3%	13.3%
tbrain4	19,374,435	23.7%	76.3%	62.8%	13.5%
Average	37,008,847	24%	76%	61%	15%
Total	1,184,283,117				





Supplemental Figure 6

Supplemental Table 1A	Gene transcripts uniquely enriched within Pigment Cells		
Gene	Functional Category	P-value	Identification #
rora	Transcription factor	3.10E-15	WHL22.499606
couptf1	Transcription factor	7.78E-15	WHL22.647845
slc7a6_6	Metabolism	9.09E-14	WHL22.357853
accn1	EggActivation	1.32E-13	WHL22.116455
surreal/gpcr111	GPCRRhodopsin,Nervous	1.84E-13	WHL22.252455
gpr115_5, hypp_764	Adhesion	6.73E-13	WHL22.23545
gpr54l_3	GPCRRhodopsin,Nervous	6.73E-13	WHL22.373162
npr1_5, npr1_7	Kinase,Metabolism	3.24E-12	WHL22.214967
z14	Zinc finger	5.06E-12	WHL22.376034
ugt2c1	Defensome	2.16E-11	WHL22.295528
calpn	Cytoskeleton	2.46E-11	WHL22.32815
lrr/gpcr_6	Adhesion,GPCRRhodopsin	2.87E-11	WHL22.311109
dhyg_5	Metabolism	3.06E-11	WHL22.368188
colf_8	Adhesion	5.24E-11	WHL22.72404
novel	Metabolism	5.73E-11	WHL22.727747
gyar	Metabolism	7.05E-11	WHL22.676224
kcnc1, kcnc1_1	Metabolism,Nervous	9.83E-11	WHL22.405695
ugt8_2	Defensome	1.00E-10	WHL22.632239
kcnk16	Metabolism	2.38E-10	WHL22.454139
mif5	Immunity	4.32E-10	WHL22.688866
nt5e_2, nt5e_3	Metabolism	5.49E-10	WHL22.323845
agpat1_3	Metabolism	5.77E-10	WHL22.448249
slc7a4	Metabolism	6.89E-10	WHL22.246608
slc15a4	Metabolism	7.01E-10	WHL22.242129
slc25a20, slc25a20l	Metabolism	7.21E-10	WHL22.204314
mos, mosa	EggActivation,Kinase	8.94E-10	WHL22.70110
ash2	Transcription factor	1.06E-09	WHL22.545085
sult1c_2	Defensome	1.08E-09	WHL22.555128
clect/fa58c/egf/cub/tm, echi	Adhesion,GPCRRhodopsin,Nervous	1.14E-09	WHL22.297449
acnn1	EggActivation	1.57E-09	WHL22.602919
fmo2	Defensome,Metabolism	1.60E-09	WHL22.720728
ard1	GTPase	3.06E-09	WHL22.114773
fmo5	Defensome	3.22E-09	WHL22.603788
mifl2	Immunity	3.55E-09	WHL22.660211
mocs2	Metabolism	3.60E-09	WHL22.364388

slc25a11	Metabolism	4.33E-09	WHL22.571273
fah	Metabolism	5.15E-09	WHL22.73559
ggt1	Metabolism	5.44E-09	WHL22.434952
got1	Metabolism	5.54E-09	WHL22.555933
ptprr	Phosphatase	5.94E-09	WHL22.446566
hypp_631	GPCRRhodopsin,Nervous	5.99E-09	WHL22.26454
dhyg, sdr	Metabolism	8.44E-09	WHL22.38253
unk_55	Kinase	8.72E-09	WHL22.610044
slc25a5	Metabolism	1.06E-08	WHL22.125371
bckdk	Kinase	1.15E-08	WHL22.223393
hypp_631	GPCRRhodopsin,Nervous	1.20E-08	WHL22.26442
ndufv2	Metabolism	1.29E-08	WHL22.590723
kcnk5_2	Metabolism	1.50E-08	WHL22.454155
srcr127	Immunity	1.56E-08	WHL22.146273
sult1c3	Defensome	1.57E-08	WHL22.467118
dbt	Metabolism	1.84E-08	WHL22.572991
golf	GTPase	1.95E-08	WHL22.570818
acss1	Metabolism	2.04E-08	WHL22.389777
mvd	Metabolism	3.06E-08	WHL22.290819
galr2l_4	GPCRRhodopsin,Nervous	3.53E-08	WHL22.264551
tat	Metabolism	9.37E-08	WHL22.361506
aldoaa_1	Metabolism	9.43E-08	WHL22.229888
z147	Zinc finger	9.77E-08	WHL22.370678
hrh2_3	GPCRRhodopsin	1.13E-07	WHL22.498022
cycs	Metabolism	1.19E-07	WHL22.706155
tlr029	Immunity,Metabolism	1.28E-07	WHL22.208651
atp6v1f	Metabolism	1.38E-07	WHL22.586411
cbs	Metabolism	1.54E-07	WHL22.293135
rab43, rab43_1	GTPase	1.55E-07	WHL22.374790
trpc, trpc5l	CalciumToolkit,EggActivation	1.62E-07	WHL22.75604
otcba	Metabolism,Metalloprotease	1.95E-07	WHL22.60237
acadm	Metabolism	2.03E-07	WHL22.686457
surreal/gpcr109	GPCRRhodopsin,Nervous	2.06E-07	WHL22.434825
etfdh, etfdh_1	Metabolism	2.11E-07	WHL22.70431
fn3/igf_3	Adhesion	2.43E-07	WHL22.52127
hdpx3	Immunity	2.49E-07	WHL22.155773
srcr185	Immunity	2.54E-07	WHL22.253874

surreal/gpcr106	GPCRRhodopsin,Nervous	2.55E-07	WHL22.698147
b3galt5_2, kcnk5	Metabolism	2.60E-07	WHL22.597785
opsin2	GPCRRhodopsin	2.96E-07	WHL22.272775
aprt	Metabolism	5.61E-07	WHL22.212743
acot8, acot8_1	Metabolism	6.02E-07	WHL22.229792
cdc7	DNAReplication,Kinase	7.13E-07	WHL22.618674
slc25a22	Metabolism	7.47E-07	WHL22.332096
gal/lect/lnb/7tm/gpcr	Adhesion	9.40E-07	WHL22.226348
kcnk4	Metabolism	9.49E-07	WHL22.57775
eno1, eno3	Metabolism	1.02E-06	WHL22.437753
cara2lb, cara7lb, xpapdl	Biomineralization,Metalloprotease	1.25E-06	WHL22.229209
z263	Zinc finger	1.39E-06	WHL22.429288
slc20a3	Metabolism	1.60E-06	WHL22.368906
rdh8_5	Metabolism	2.10E-06	WHL22.282937
xpapdl	Metalloprotease	2.53E-06	WHL22.229257
kcnk1	Metabolism	3.50E-06	WHL22.511917
uox	Metabolism	4.19E-06	WHL22.48702
exoc1	Nervous	4.34E-06	WHL22.277921
galr2l_12	GPCRRhodopsin,Nervous	4.39E-06	WHL22.620058
atp6v1d, atp6v1d_1	Metabolism	5.08E-06	WHL22.325567
fbw7	CellCycle	8.49E-06	WHL22.593261
pax6	Nervous,TF	1.46E-05	WHL22.585629
rar	Transcription factor	1.58E-05	WHL22.595420
gucy1b2	Metabolism,Nervous	1.64E-05	WHL22.92092
lrp1l_2, lrp4-3	Adhesion,Metabolism	1.87E-05	WHL22.185078
pkc1_1	CalciumToolkit,EggActivation,Kinase	2.05E-05	WHL22.159051
nkiras	GTPase	2.18E-05	WHL22.355329
scyl2	Kinase	2.44E-05	WHL22.63365
bmal	Nervous,TF	2.58E-05	WHL22.117405
notchl5_1	Signaling	6.50E-05	WHL22.145893
fvt1	Metabolism	6.69E-05	WHL22.657124
abcg4	Defensome	8.85E-05	WHL22.374498
stx12	Nervous	8.88E-05	WHL22.150755
z19	Zinc finger	9.80E-05	WHL22.205278
dhrsx_2	Metabolism	1.23E-04	WHL22.77314
diva, rabl2l	Apoptosis,GTPase	1.71E-04	WHL22.287461
cyp2l50	Defensome,Metabolism	1.81E-04	WHL22.136948

pkc1	CalciumToolkit,EggActivation,Kinase	2.35E-04	WHL22.343472
gcm	Transcription factor	4.51E-04	WHL22.54333
pdhb	Metabolism	4.70E-04	WHL22.521650
sema	Adhesion	5.18E-04	WHL22.648920
chst1_3	Adhesion	5.64E-04	WHL22.652484
unk_48	Zinc finger	6.58E-04	WHL22.445842
pks1	Enzyme	6.89E-04	WHL22.202707
pole, pole-3	DNAReplication	7.29E-04	WHL22.5109
hk1_1	Metabolism	7.37E-04	WHL22.576222
hypp_9, limd1	Adhesion	7.56E-04	WHL22.731445
fmo3	Defensome,Metabolism	9.86E-04	WHL22.15432
eph2, eph_1, hypp_1003	Cytoskeleton	2.74E-03	WHL22.476970
sult1a	Defensome	3.30E-03	WHL22.234536
z288	Zinc finger	3.31E-03	WHL22.568921
lhh4c	Histone	5.45E-03	WHL22.279692
acad11	Metabolism	5.60E-03	WHL22.23587
camk1	CalciumToolkit,EggActivation,Kinase	6.14E-03	WHL22.8481
sult1a	Defensome	9.79E-03	WHL22.234512
betali	Adhesion	3.09E-02	WHL22.425572
hypp_1908	Novel	1.28E-13	WHL22.690746
novel	Novel	2.47E-13	WHL22.590555
novel	Novel	8.90E-13	WHL22.623787
c20orf3_1	Novel	1.87E-12	WHL22.354482
novel	Novel	2.01E-12	WHL22.321899
hypp_211	Novel	2.16E-12	WHL22.476564
chrna9l_92	Novel	4.03E-12	WHL22.690491
pae	Novel	4.94E-12	WHL22.366513
galnac4s-6stl_2, pde6d	Novel	7.05E-12	WHL22.621157
novel	Novel	1.24E-11	WHL22.653099
novel	Novel	1.28E-11	WHL22.493883
prdx5	Novel	1.45E-11	WHL22.427634
hypp_1095	Novel	1.48E-11	WHL22.143739
novel	Novel	1.69E-11	WHL22.203678
accn1l	Novel	2.72E-11	WHL22.738446
novel	Novel	2.78E-11	WHL22.304259
hypp_456, hypp_457	Novel	2.82E-11	WHL22.608722
novel	Novel	3.03E-11	WHL22.649890
hypp_485	Novel	3.62E-11	WHL22.262714
timp1	Novel	3.72E-11	WHL22.304112

hypp_272, hypp_404	Novel	4.60E-11	WHL22.566785
novel	Novel	5.01E-11	WHL22.650426
perld1	Novel	6.13E-11	WHL22.343735
novel	Novel	7.77E-11	WHL22.90837
novel	Novel	1.01E-10	WHL22.638952
c3orf39	Novel	1.05E-10	WHL22.131526
novel	Novel	1.06E-10	WHL22.419529
gnsl	Novel	1.08E-10	WHL22.453181
novel	Novel	1.14E-10	WHL22.384931
novel	Novel	1.16E-10	WHL22.446640
hypp_7	Novel	1.23E-10	WHL22.35174
krn1	Novel	1.29E-10	WHL22.633587
hypp_1635	Novel	1.48E-10	WHL22.412691
novel	Novel	1.72E-10	WHL22.752370
novel	Novel	1.72E-10	WHL22.281721
hypp_1597	Novel	1.82E-10	WHL22.630593
novel	Novel	2.05E-10	WHL22.241626
paqr6	Novel	2.34E-10	WHL22.727619
novel	Novel	2.39E-10	WHL22.717293
syp	Novel	2.46E-10	WHL22.597595
vps37ha	Novel	2.58E-10	WHL22.90149
aqp	Novel	2.90E-10	WHL22.456167
slc10a2l_3	Novel	3.06E-10	WHL22.609344
trap5	Novel	3.20E-10	WHL22.645492
hypp_1249	Novel	3.41E-10	WHL22.480550
novel	Novel	3.54E-10	WHL22.339386
echn6	Novel	3.90E-10	WHL22.600249
novel	Novel	4.09E-10	WHL22.186266
novel	Novel	4.53E-10	WHL22.612526
hypp_862	Novel	4.60E-10	WHL22.63317
novel	Novel	5.07E-10	WHL22.623866
aifm3l	Novel	5.56E-10	WHL22.367235
novel	Novel	5.84E-10	WHL22.292197
novel	Novel	6.54E-10	WHL22.215292
novel	Novel	6.57E-10	WHL22.418830
novel	Novel	6.64E-10	WHL22.55113
ache_22	Novel	7.41E-10	WHL22.601343

novel	Novel	8.26E-10	WHL22.292564
novel	Novel	8.35E-10	WHL22.373186
novel	Novel	8.98E-10	WHL22.261559
novel	Novel	9.32E-10	WHL22.130160
novel	Novel	9.44E-10	WHL22.711542
myof	Novel	1.05E-09	WHL22.123987
novel	Novel	1.15E-09	WHL22.359826
slc24a6	Novel	1.20E-09	WHL22.83051
hdac2	Novel	1.44E-09	WHL22.580648
novel	Novel	1.63E-09	WHL22.55062
wdr27	Novel	1.88E-09	WHL22.513014
novel	Novel	1.97E-09	WHL22.605745
eme1h	Novel	1.97E-09	WHL22.605935
novel	Novel	2.08E-09	WHL22.630755
p35l	Novel	2.42E-09	WHL22.79600
novel	Novel	2.88E-09	WHL22.570525
fanca	Novel	2.94E-09	WHL22.758623
chst11_12	Novel	2.96E-09	WHL22.75001
hypp_2615	Novel	3.07E-09	WHL22.114590
atpbd4	Novel	3.13E-09	WHL22.756187
novel	Novel	3.36E-09	WHL22.448239
novel	Novel	3.41E-09	WHL22.695657
novel	Novel	4.42E-09	WHL22.38158
hypp_2909	Novel	4.81E-09	WHL22.152284
novel	Novel	4.83E-09	WHL22.740130
novel	Novel	5.19E-09	WHL22.603745
cyth1l	Novel	5.49E-09	WHL22.667648
novel	Novel	5.63E-09	WHL22.563138
prcp	Novel	5.88E-09	WHL22.306383
actr10h	Novel	6.08E-09	WHL22.377282
mect1l	Novel	6.56E-09	WHL22.222445
tor3al	Novel	6.75E-09	WHL22.452924
novel	Novel	7.10E-09	WHL22.567578
pdella	Novel	7.59E-09	WHL22.34001
novel	Novel	7.66E-09	WHL22.709598
novel	Novel	8.74E-09	WHL22.466787
cntn5l	Novel	8.85E-09	WHL22.198938

galnac4s6st	Novel	9.17E-09	WHL22.763781
ubap1l	Novel	1.05E-08	WHL22.733881
higd1a, higd1a_1	Novel	1.15E-08	WHL22.33988
novel	Novel	1.19E-08	WHL22.256310
timp3	Novel	1.33E-08	WHL22.22247
novel	Novel	1.37E-08	WHL22.768116
novel	Novel	1.46E-08	WHL22.101256
novel	Novel	1.52E-08	WHL22.716794
neurl4, neurl4-2	Novel	1.58E-08	WHL22.682681
novel	Novel	1.63E-08	WHL22.4470
calm2	Novel	1.64E-08	WHL22.4059
dioxg	Novel	1.87E-08	WHL22.156152
novel	Novel	1.92E-08	WHL22.683542
novel	Novel	2.10E-08	WHL22.458217
novel	Novel	2.16E-08	WHL22.583951
novel	Novel	2.18E-08	WHL22.649593
fn3/igf_18	Novel	2.44E-08	WHL22.392583
rbks	Novel	2.72E-08	WHL22.347104
c1orf177l	Novel	3.14E-08	WHL22.58791
cnih	Novel	3.19E-08	WHL22.440081
novel	Novel	3.73E-08	WHL22.422245
acl	Novel	3.81E-08	WHL22.733120
novel	Novel	4.07E-08	WHL22.147471
aspscr1l	Novel	4.24E-08	WHL22.693820
novel	Novel	4.68E-08	WHL22.728871
novel	Novel	4.70E-08	WHL22.615466
novel	Novel	4.72E-08	WHL22.566454
prss16, prss16l	Novel	4.98E-08	WHL22.15187
novel	Novel	5.15E-08	WHL22.412301
novel	Novel	5.20E-08	WHL22.27909
ccdc150l	Novel	5.69E-08	WHL22.728868
hypp_1375	Novel	7.32E-08	WHL22.658767
arrb2n	Novel	7.56E-08	WHL22.707285
slc2a1_1	Novel	7.81E-08	WHL22.32902
novel	Novel	7.93E-08	WHL22.23007
novel	Novel	8.09E-08	WHL22.233590
arrb1c	Novel	8.31E-08	WHL22.707282

novel	Novel	8.72E-08	WHL22.47069
novel	Novel	8.89E-08	WHL22.282838
novel	Novel	9.45E-08	WHL22.245702
novel	Novel	1.10E-07	WHL22.199772
c20orf54_1	Novel	1.11E-07	WHL22.209181
novel	Novel	1.11E-07	WHL22.642539
novel	Novel	1.16E-07	WHL22.345547
sybl1	Novel	1.30E-07	WHL22.556891
bscl2	Novel	1.31E-07	WHL22.70104
novel	Novel	1.42E-07	WHL22.108092
vps25	Novel	1.43E-07	WHL22.681316
plxnb1	Novel	1.47E-07	WHL22.194744
nfu1	Novel	1.57E-07	WHL22.538836
hypp_2914	Novel	1.77E-07	WHL22.278319
slc18a2	Novel	1.79E-07	WHL22.748659
clcn1_1	Novel	1.83E-07	WHL22.9845
novel	Novel	1.86E-07	WHL22.295925
novel	Novel	1.97E-07	WHL22.237902
bfar	Novel	2.14E-07	WHL22.29527
sug	Novel	2.39E-07	WHL22.239647
cub/so/gpcr, hypp_760	Novel	2.40E-07	WHL22.537113
c16orf62	Novel	2.66E-07	WHL22.308561
novel	Novel	2.73E-07	WHL22.421662
c2orf63	Novel	2.79E-07	WHL22.333938
tspo	Novel	2.96E-07	WHL22.508748
sspo, sspo_1	Novel	3.32E-07	WHL22.130055
novel	Novel	3.61E-07	WHL22.564440
novel	Novel	3.83E-07	WHL22.452303
novel	Novel	3.84E-07	WHL22.542829
novel	Novel	4.03E-07	WHL22.599237
ccdc76, ccdc76_1	Novel	4.12E-07	WHL22.713663
achel, bchel	Novel	4.17E-07	WHL22.453506
novel	Novel	4.63E-07	WHL22.348746
novel	Novel	4.96E-07	WHL22.377101
hypp_3001	Novel	4.97E-07	WHL22.581789
novel	Novel	5.02E-07	WHL22.443158
novel	Novel	5.08E-07	WHL22.642258

aifm3	Novel	5.66E-07	WHL22.367241
hypp_2340	Novel	5.72E-07	WHL22.263024
hypp_32	Novel	5.72E-07	WHL22.537147
znfx1-17	Novel	5.72E-07	WHL22.501840
hypp_2803	Novel	5.84E-07	WHL22.411631
echn34	Novel	5.93E-07	WHL22.682505
novel	Novel	5.94E-07	WHL22.439501
novel	Novel	6.35E-07	WHL22.284104
depdc6	Novel	7.43E-07	WHL22.107036
novel	Novel	7.44E-07	WHL22.698770
hypp_1704	Novel	7.47E-07	WHL22.532838
novel	Novel	7.58E-07	WHL22.579971
novel	Novel	7.81E-07	WHL22.363992
novel	Novel	7.83E-07	WHL22.749815
zcsl2	Novel	9.13E-07	WHL22.71376
novel	Novel	9.72E-07	WHL22.607943
banp	Novel	9.73E-07	WHL22.502001
dnahc8, ibtk	Novel	1.02E-06	WHL22.407313
hypp_806	Novel	1.08E-06	WHL22.20026
novel	Novel	1.11E-06	WHL22.404456
igcam/igcam	Novel	1.16E-06	WHL22.23785
novel	Novel	1.23E-06	WHL22.502828
mpdz-3	Novel	1.28E-06	WHL22.761611
oxa1l, oxa1l_1	Novel	1.39E-06	WHL22.658083
gaa_2	Novel	1.41E-06	WHL22.468242
novel	Novel	1.44E-06	WHL22.283905
novel	Novel	1.45E-06	WHL22.229342
novel	Novel	1.47E-06	WHL22.221085
novel	Novel	1.49E-06	WHL22.325496
hypp_1575	Novel	1.71E-06	WHL22.671637
elac2-2, elach2	Novel	1.83E-06	WHL22.557339
novel	Novel	1.91E-06	WHL22.360488
rabggtb	Novel	1.94E-06	WHL22.319512
novel	Novel	2.00E-06	WHL22.341967
cabin1l	Novel	2.01E-06	WHL22.373941
sf4	Novel	2.02E-06	WHL22.643160
ccdc149	Novel	2.14E-06	WHL22.271787

novel	Novel	2.14E-06	WHL22.22993
cramp1l	Novel	2.19E-06	WHL22.738032
novel	Novel	2.20E-06	WHL22.30333
novel	Novel	2.27E-06	WHL22.549535
smcr7l	Novel	2.35E-06	WHL22.743908
novel	Novel	2.37E-06	WHL22.7143
novel	Novel	2.37E-06	WHL22.638304
ccdc94	Novel	2.39E-06	WHL22.160352
echn6	Novel	2.47E-06	WHL22.600219
novel	Novel	2.81E-06	WHL22.285677
phol	Novel	2.81E-06	WHL22.400422
gde1	Novel	2.89E-06	WHL22.289449
novel	Novel	3.14E-06	WHL22.334349
novel	Novel	3.47E-06	WHL22.556614
nbea	Novel	4.40E-06	WHL22.52383
novel	Novel	4.41E-06	WHL22.63268
hypp_3	Novel	4.94E-06	WHL22.119611
novel	Novel	5.09E-06	WHL22.388021
wdr23_1	Novel	5.12E-06	WHL22.279666
fam114a2	Novel	5.36E-06	WHL22.702621
tatdn2	Novel	5.48E-06	WHL22.21737
scrnph2	Novel	5.49E-06	WHL22.90812
adka	Novel	6.54E-06	WHL22.18680
ganab_1	Novel	7.09E-06	WHL22.335933
novel	Novel	7.20E-06	WHL22.509814
novel	Novel	7.21E-06	WHL22.419538
novel	Novel	7.74E-06	WHL22.17568
nae1	Novel	7.79E-06	WHL22.768113
novel	Novel	7.98E-06	WHL22.452196
chst1	Novel	8.15E-06	WHL22.18155
novel	Novel	8.65E-06	WHL22.324442
novel	Novel	9.31E-06	WHL22.691910
novel	Novel	9.40E-06	WHL22.603962
clect/tm_4	Novel	9.55E-06	WHL22.424831
novel	Novel	1.04E-05	WHL22.372108
novel	Novel	1.05E-05	WHL22.498661
hypp_2261	Novel	1.15E-05	WHL22.85209

novel	Novel	1.20E-05	WHL22.421238
polq	Novel	1.26E-05	WHL22.718143
npr3	Novel	1.37E-05	WHL22.553675
novel	Novel	1.42E-05	WHL22.340296
novel	Novel	1.46E-05	WHL22.543968
dpp10	Novel	1.53E-05	WHL22.87871
hypp_2543	Novel	1.54E-05	WHL22.38796
ift122h	Novel	1.57E-05	WHL22.565476
tfiiaalp	Novel	1.57E-05	WHL22.101795
novel	Novel	1.79E-05	WHL22.440604
novel	Novel	1.80E-05	WHL22.368556
novel	Novel	1.88E-05	WHL22.656371
novel	Novel	2.00E-05	WHL22.241627
sea/ldla/cub	Novel	2.01E-05	WHL22.443501
novel	Novel	2.10E-05	WHL22.626489
lsm5	Novel	2.18E-05	WHL22.585351
ttc35	Novel	2.42E-05	WHL22.512044
arrdc3_1	Novel	2.69E-05	WHL22.734056
btbd7	Novel	3.24E-05	WHL22.609213
kiaa1772l, kiaa1772l_1	Novel	3.30E-05	WHL22.337598
seh1l	Novel	3.33E-05	WHL22.735731
novel	Novel	3.63E-05	WHL22.470876
novel	Novel	3.82E-05	WHL22.369847
novel	Novel	4.65E-05	WHL22.246573
novel	Novel	5.07E-05	WHL22.88037
pric2, triple_lim	Novel	5.46E-05	WHL22.636314
novel	Novel	6.27E-05	WHL22.63298
sil1	Novel	6.30E-05	WHL22.46984
novel	Novel	6.32E-05	WHL22.288109
ptar1	Novel	7.30E-05	WHL22.584703
novel	Novel	7.86E-05	WHL22.75664
pms1	Novel	8.07E-05	WHL22.554884
rtl_58	Novel	8.20E-05	WHL22.473256
novel	Novel	8.96E-05	WHL22.364012
hypp_210	Novel	9.24E-05	WHL22.477152
dak_2	Novel	1.06E-04	WHL22.265285
novel	Novel	1.09E-04	WHL22.562349

vps13hb	Novel	1.37E-04	WHL22.484817
novel	Novel	1.90E-04	WHL22.461248
novel	Novel	2.11E-04	WHL22.531338
gpatch2	Novel	2.16E-04	WHL22.62206
hypp_2816	Novel	2.51E-04	WHL22.635968
arsb_2	Novel	3.23E-04	WHL22.704081
aadac_6	Novel	3.41E-04	WHL22.333600
novel	Novel	3.84E-04	WHL22.50195
novel	Novel	4.04E-04	WHL22.733643
novel	Novel	4.46E-04	WHL22.367284
novel	Novel	5.22E-04	WHL22.498677
hypp_2414	Novel	6.05E-04	WHL22.639400
novel	Novel	6.53E-04	WHL22.466720
ubr2_1	Novel	6.80E-04	WHL22.329203
mett10d	Novel	6.85E-04	WHL22.731790
egf/ftp	Novel	8.04E-04	WHL22.365828
tbc1d15	Novel	1.06E-03	WHL22.322226
echn, echn20	Novel	1.07E-03	WHL22.435662
novel	Novel	1.23E-03	WHL22.331721
novel	Novel	1.24E-03	WHL22.621173
banf1	Novel	1.32E-03	WHL22.725223
c5orf34l	Novel	1.35E-03	WHL22.159495
ift140_1	Novel	1.39E-03	WHL22.434108
pitpnm, pitpnm2	Novel	1.47E-03	WHL22.387771
novel	Novel	1.75E-03	WHL22.490070
novel	Novel	1.94E-03	WHL22.101043
tpd52l2	Novel	2.20E-03	WHL22.377158
atripl	Novel	2.21E-03	WHL22.165193
sumf1	Novel	2.66E-03	WHL22.21955
mus81h	Novel	2.67E-03	WHL22.224640
pin4	Novel	2.97E-03	WHL22.530556
wdhd1	Novel	3.02E-03	WHL22.29597
eapp	Novel	3.09E-03	WHL22.2464
novel	Novel	3.87E-03	WHL22.743126
rpn2	Novel	4.47E-03	WHL22.275175
kiaa1529l	Novel	5.31E-03	WHL22.56989

Supplemental Table 1B	Gene transcripts uniquely enriched within the Apical subdomain		
Gene	Functional Category	P-value	Identification #
prxdxn	Defensome	7.40E-18	WHL22.659393
tpi1	Metabolism	1.95E-16	WHL22.644853
lhx2, limc1	Transcription factor	4.01E-16	WHL22.91758
fbgp, nlr19, nlr81	Immunity	8.11E-16	WHL22.123794
cyp2l47	Defensome,Metabolism	1.51E-15	WHL22.357752
astacin5	Metalloprotease	2.73E-15	WHL22.237823
atr	CellCycle	3.19E-15	WHL22.287064
pla2p, plaa	Metabolism	1.53E-14	WHL22.686323
reelin1	Adhesion	1.64E-14	WHL22.340762
foxq2	Nervous,TF	3.26E-14	SPU_012384
srcr54	Immunity	5.59E-14	WHL22.688649
ttrspn_18	Metabolism	5.94E-14	WHL22.31275
atr	CellCycle	1.14E-13	WHL22.287073
tmprss2l	Metabolism	1.56E-13	WHL22.275365
nalcn, vgcnl1	EggActivation	1.81E-13	WHL22.402186
h6pd	Metabolism	3.32E-13	WHL22.148153
z218	Zinc finger	3.43E-13	WHL22.478457
mapkkk12/13	EggActivation,Kinase	8.10E-13	WHL22.597870
aldh3a1	Defensome,Metabolism	9.01E-13	WHL22.519205
rab21	GTPase	9.12E-13	WHL22.103109
sfrp1/5	Signaling	1.08E-12	WHL22.146031
brn1-2-4	Nervous,TF	1.10E-12	WHL22.40221
z98	Zinc finger	1.41E-12	WHL22.670880
smurf	Signaling	1.46E-12	WHL22.474236
adrb3l_1	GPCRRhodopsin,Nervous	1.85E-12	WHL22.504386
adam/tsl5, adam/tsl6	Metalloprotease	2.78E-12	WHL22.143071
contactin2, igf_19	Adhesion,Cytoskeleton	2.94E-12	WHL22.198966
z203	Zinc finger	3.32E-12	WHL22.202593
srcr104	Immunity	4.61E-12	WHL22.253958
qrfprl	GPCRRhodopsin,Nervous	4.95E-12	WHL22.752440
slc35a3	Metabolism	5.40E-12	WHL22.761678
ilkap	EggActivation,Phosphatase	6.03E-12	WHL22.153019
hsp701g	Defensome	7.61E-12	WHL22.185050
rhobtb	GTPase	8.74E-12	WHL22.627962
rdh14_1	Metabolism	1.02E-11	WHL22.20848

glyphp1, glyphp2	Nervous	1.53E-11	WHL22.289832
ahi	Adhesion	1.97E-11	WHL22.53384
elovl7, elovl7l	Metabolism	3.89E-11	WHL22.481600
dpyd, dpyd-2	Metabolism	4.30E-11	WHL22.1286
abcf3, abcf3_1	Defensome	5.71E-11	WHL22.683993
hunk_1	Kinase	7.47E-11	WHL22.668117
foxq2_1	Nervous,TF	1.10E-10	SPU_019002
ilkap_1	Phosphatase	1.22E-10	WHL22.97994
trpm, trpm3	CalciumToolkit,EggActivation	1.69E-10	WHL22.355031
hypp_993, snrk, snrk_1	Kinase	1.87E-10	WHL22.17652
dnmbp, sh3d19l_1	GTPase	2.32E-10	WHL22.223927
rx	Nervous,TF	2.57E-10	WHL22.523971
c20orf59l	Metabolism	4.69E-10	WHL22.49716
z295, z327	Zinc finger	4.79E-10	WHL22.292281
slc10a2	Metabolism	4.91E-10	WHL22.762743
ctr9	Metabolism	6.41E-10	WHL22.323248
oda/lc7l1	Cytoskeleton	7.21E-10	WHL22.733460
btk	Kinase	7.54E-10	WHL22.240511
hairy2/4	Immunity,Signaling,TF	7.87E-10	WHL22.446908
raso	GTPase	1.06E-09	WHL22.667788
oca2	Metabolism	1.07E-09	WHL22.741771
apc3	CellCycle	1.32E-09	WHL22.339925
atf2	Immunity,Signaling,TF	1.35E-09	WHL22.59755
nacha6	CalciumToolkit,EggActivation,Nervous	1.59E-09	WHL22.694414
z133, z133_1	Zinc finger	1.85E-09	WHL22.580602
hypp_1882, nek8b, nek9-2	Kinase	1.89E-09	WHL22.122176
ugt1l_2	Defensome	2.13E-09	WHL22.221377
naalad2l_4	Metalloprotease	2.21E-09	WHL22.186833
pfkfb1	Metabolism	2.38E-09	WHL22.99469
axndhc2h, dnahc2, unk_103	Cytoskeleton	2.64E-09	WHL22.564761
smg1	Kinase	2.65E-09	WHL22.684082
fgfrl, fgfrl1	Signaling	3.12E-09	WHL22.323545
axndhc6h, dnah6, dnahc6	Cytoskeleton	3.49E-09	WHL22.689921
egfiiil_1	Adhesion	4.68E-09	WHL22.3269
rabl2, rabl2l	GTPase	6.91E-09	WHL22.287446
z45	Zinc finger	8.76E-09	WHL22.524037
lamg1	Adhesion	9.29E-09	WHL22.194092

arg99, tmtc1	Signaling	9.88E-09	WHL22.545786
cactta1hs, hypp_1585	CalciumToolkit,EggActivation	9.96E-09	WHL22.525885
cycf, hypp_819	CellCycle	1.08E-08	WHL22.149487
z116	Zinc finger	1.18E-08	WHL22.82988
reelin2	Adhesion	1.32E-08	WHL22.534858
slc7a4_3	Metabolism	1.49E-08	WHL22.468092
af9	Transcription factor	1.56E-08	WHL22.754828
irxb	Transcription factor	1.65E-08	WHL22.496846
jak1	Immunity,Kinase,Signaling	2.76E-08	WHL22.418866
reelin1, reelin3, reelinl	Adhesion	3.31E-08	WHL22.341821
kcnk3, kcnk3_1	Metabolism	4.16E-08	WHL22.674447
gmpr	Metabolism	4.38E-08	WHL22.358021
axndhc3h, dnah3	Cytoskeleton	5.48E-08	WHL22.748053
hbn	Nervous,TF	5.93E-08	WHL22.523959
tsc22d2	Transcription factor	6.52E-08	WHL22.509140
b3galt1l_3	Metabolism	6.68E-08	WHL22.172929
z94	Zinc finger	6.97E-08	WHL22.568856
ptr4	Metabolism	7.06E-08	WHL22.456407
ggt1_7	Metabolism	7.07E-08	WHL22.41537
mlh1	Oogenesis	7.79E-08	WHL22.241461
slit(n-terminus)	Adhesion	9.12E-08	WHL22.219937
galr2l_14	GPCRRhodopsin,Nervous	9.31E-08	WHL22.395150
rorl	Kinase,Signaling	1.02E-07	WHL22.77301
axndhc5h, dnah5-2	Cytoskeleton	1.17E-07	WHL22.245697
rgs12, rgs12-2, rgs12d	CalciumToolkit	1.35E-07	WHL22.329908
smad4	Immunity,Signaling,TF	1.41E-07	WHL22.57110
atp/gtpbp1_1	Metalloprotease	1.54E-07	WHL22.641632
z40_1	Zinc finger	1.84E-07	WHL22.683049
ephrin	Signaling	1.92E-07	WHL22.763086
ski, ski_1	Signaling	2.00E-07	WHL22.268154
trpc3_1	CalciumToolkit,EggActivation	2.72E-07	WHL22.563585
lhh2bj	Histone	2.90E-07	WHL22.57355
smad5	Signaling,TF	3.45E-07	WHL22.72583
axndhc5h, dnah5-2	Cytoskeleton	3.61E-07	WHL22.245700
rgn	CalciumToolkit	4.17E-07	WHL22.426420
ddr1	Kinase,Signaling	4.30E-07	WHL22.329991
ef1a_1	GTPase	4.33E-07	WHL22.620680

smooth	Signaling	4.36E-07	WHL22.589814
myt1, myt1-2	Nervous,ZNF	4.40E-07	WHL22.447009
perlc	Adhesion	4.51E-07	WHL22.374787
axndhc6h, dnah6, dnahc6	Cytoskeleton	5.66E-07	WHL22.690235
z479	Zinc finger	6.71E-07	WHL22.381988
nkx3-2	Transcription factor	7.70E-07	WHL22.329059
z114	Zinc finger	7.87E-07	WHL22.576165
cyp27l, hydin-3	Metabolism	8.85E-07	WHL22.651538
kras	GTPase	1.43E-06	WHL22.519136
dagl	Adhesion	1.59E-06	WHL22.22569
semaa	Adhesion	1.59E-06	WHL22.41191
dlc3, dlc3_1	Cytoskeleton	1.68E-06	WHL22.707717
ugt1l_11	Defensome	1.78E-06	WHL22.289883
acs13	Metabolism	3.92E-06	WHL22.230644
axndhc5h, dnah5, dnah5-2	Cytoskeleton	4.58E-06	WHL22.246805
foxj2_1	Transcription factor	7.53E-06	WHL22.767230
colf_10, colf_5	Adhesion	8.53E-06	WHL22.415047
cadherin, cadherinl3, cadher	Adhesion	1.59E-05	WHL22.359222
cytd2hc, dync2h1_2	Cytoskeleton	3.54E-05	WHL22.222366
nlr82	Immunity	3.69E-05	WHL22.355616
srcr139	Immunity	4.03E-05	WHL22.441613
srcr97	Immunity	9.67E-05	WHL22.145812
abp620h, macf1	Cytoskeleton	1.10E-04	WHL22.770360
hnf1al	Transcription factor	2.44E-04	WHL22.520179
brms1l, kif1bl1, stard9	Cytoskeleton	3.34E-04	WHL22.731792
kif9, kif9-2, kif9l1, kif9l2	Cytoskeleton	3.37E-04	WHL22.243589
awh	Transcription factor	3.41E-04	WHL22.9369
srcr95	Immunity	4.94E-04	WHL22.145902
fgfr, fn3f_67	Kinase,Signaling	5.29E-04	WHL22.323968
tektin3	Cytoskeleton	1.07E-03	WHL22.684591
axndhc15h, dnah5_1	Cytoskeleton	2.07E-03	WHL22.195413
hypp_804	GPCRRhodopsin,Nervous	2.43E-02	WHL22.49192
tph	Metabolism,Nervous	3.66E-02	WHL22.635790
ache_8	Novel	1.98E-20	WHL22.453507
ddx58_2	Novel	6.61E-19	WHL22.8118
novel	Novel	8.37E-18	WHL22.166794
adamtsl	Novel	2.00E-17	WHL22.547533
novel	Novel	2.50E-17	WHL22.659399

rabrp3	Novel	6.85E-17	WHL22.587656
novel	Novel	8.97E-17	WHL22.765839
novel	Novel	1.14E-16	WHL22.212068
fbxo4	Novel	1.25E-16	WHL22.207281
novel	Novel	5.25E-16	WHL22.511887
hypp_684	Novel	1.39E-15	WHL22.469919
novel	Novel	1.40E-15	WHL22.302750
ufc1	Novel	3.38E-15	WHL22.357801
isot	Novel	4.76E-15	WHL22.351039
novel	Novel	4.80E-15	WHL22.69988
hypp_1291, ter1	Novel	8.54E-15	WHL22.360395
novel	Novel	1.25E-14	WHL22.472720
novel	Novel	1.51E-14	WHL22.493539
trpc4l	Novel	1.78E-14	WHL22.528095
novel	Novel	2.05E-14	WHL22.271103
pcsk9l	Novel	3.05E-14	WHL22.391580
pih1d1	Novel	3.13E-14	WHL22.718047
kif14l1	Novel	3.56E-14	WHL22.502130
novel	Novel	4.83E-14	WHL22.332602
novel	Novel	7.61E-14	WHL22.276028
ripk5, sgk496	Novel	7.66E-14	WHL22.2783
hypp_169	Novel	1.12E-13	WHL22.385711
novel	Novel	1.30E-13	WHL22.146977
novel	Novel	1.64E-13	WHL22.608716
oach	Novel	1.77E-13	WHL22.741923
reps1l, reps1l_1, reps1l_2	Novel	2.81E-13	WHL22.455878
asxl3	Novel	5.45E-13	WHL22.40831
novel	Novel	5.68E-13	WHL22.515553
novel	Novel	6.14E-13	WHL22.213412
kiaa1310l	Novel	6.60E-13	WHL22.459917
fn3_23	Novel	6.86E-13	WHL22.214452
novel	Novel	8.88E-13	WHL22.131054
novel	Novel	9.13E-13	WHL22.559493
arp2/3cs3	Novel	9.99E-13	WHL22.479562
novel	Novel	1.03E-12	WHL22.258680
ip3r_5	Novel	1.19E-12	WHL22.635570
bivm, bivml	Novel	1.19E-12	WHL22.140451

gtf3c1l	Novel	1.21E-12	WHL22.239200
ubr4-4	Novel	1.38E-12	WHL22.680854
novel	Novel	1.40E-12	WHL22.198950
novel	Novel	1.73E-12	WHL22.738523
heatr1-2	Novel	1.73E-12	WHL22.581547
golga7	Novel	2.04E-12	WHL22.443691
hypp_1175	Novel	2.42E-12	WHL22.68363
c7orf25	Novel	3.04E-12	WHL22.745506
novel	Novel	3.14E-12	WHL22.203224
nubp1	Novel	3.28E-12	WHL22.535368
novel	Novel	3.78E-12	WHL22.513652
hypp_1388	Novel	3.93E-12	WHL22.523008
novel	Novel	4.24E-12	WHL22.38540
novel	Novel	5.54E-12	WHL22.182622
novel	Novel	5.82E-12	WHL22.42566
novel	Novel	5.94E-12	WHL22.500474
ppp1r10	Novel	6.91E-12	WHL22.91776
novel	Novel	8.70E-12	WHL22.156907
novel	Novel	1.05E-11	WHL22.363060
prmt5, prmt5_1	Novel	1.06E-11	WHL22.750234
fbn2	Novel	1.08E-11	WHL22.314476
dnahc5	Novel	1.14E-11	WHL22.446317
novel	Novel	1.25E-11	WHL22.622471
hypp_1532	Novel	1.40E-11	WHL22.337956
novel	Novel	1.41E-11	WHL22.368537
dnah2	Novel	1.53E-11	WHL22.299869
novel	Novel	1.53E-11	WHL22.45498
novel	Novel	1.55E-11	WHL22.535335
novel	Novel	1.63E-11	WHL22.368605
novel	Novel	1.79E-11	WHL22.692204
novel	Novel	1.90E-11	WHL22.336629
hel308	Novel	1.97E-11	WHL22.488784
hypp_1499, sgk493	Novel	2.16E-11	WHL22.354287
prei3l	Novel	2.42E-11	WHL22.192611
lonrf3	Novel	2.46E-11	WHL22.316135
c1orf222l, crhbp	Novel	2.69E-11	WHL22.437808
ap4m1	Novel	3.33E-11	WHL22.318351

novel	Novel	3.33E-11	WHL22.466257
rft1, rft_1	Novel	3.49E-11	WHL22.502677
novel	Novel	3.57E-11	WHL22.6527
b3gnt2l	Novel	3.62E-11	WHL22.580437
parp4l	Novel	3.79E-11	WHL22.616868
novel	Novel	4.27E-11	WHL22.171529
pde7al	Novel	4.58E-11	WHL22.728999
hypp_113	Novel	4.59E-11	WHL22.561018
asps, dars2	Novel	4.83E-11	WHL22.662966
novel	Novel	4.92E-11	WHL22.677489
kiaa1239	Novel	5.11E-11	WHL22.168700
rsl1d1-2	Novel	5.28E-11	WHL22.537598
trappc9	Novel	5.32E-11	WHL22.73542
dlg2, dlg2_1	Novel	5.40E-11	WHL22.495575
abtb1, abtb1_1	Novel	5.82E-11	WHL22.552518
whirlin	Novel	6.01E-11	WHL22.329331
ep300l	Novel	7.56E-11	WHL22.206287
novel	Novel	7.75E-11	WHL22.544812
hypp_1780	Novel	7.91E-11	WHL22.3338
cep78, cep78l	Novel	8.08E-11	WHL22.723897
novel	Novel	8.44E-11	WHL22.510486
serrp8	Novel	8.65E-11	WHL22.148732
hypp_65	Novel	9.15E-11	WHL22.297961
hypp_2437, lin54ll	Novel	9.40E-11	WHL22.137347
mrpl14l	Novel	9.90E-11	WHL22.725262
med12l_2	Novel	9.98E-11	WHL22.622650
zdhhc7_1	Novel	9.98E-11	WHL22.493538
vps8_2h, vps8h	Novel	1.06E-10	WHL22.220518
c9orf97l	Novel	1.17E-10	WHL22.521476
gal3st	Novel	1.18E-10	WHL22.526426
novel	Novel	1.19E-10	WHL22.198051
novel	Novel	1.19E-10	WHL22.44046
novel	Novel	1.20E-10	WHL22.83352
novel	Novel	1.22E-10	WHL22.185502
ccdc93	Novel	1.27E-10	WHL22.13233
novel	Novel	1.28E-10	WHL22.459947
novel	Novel	1.32E-10	WHL22.747300

kiaa1407l	Novel	1.33E-10	WHL22.323351
gnptab	Novel	1.36E-10	WHL22.370626
novel	Novel	1.42E-10	WHL22.197020
hypp_545	Novel	1.47E-10	WHL22.2790
novel	Novel	1.50E-10	WHL22.241719
gyg1	Novel	1.55E-10	WHL22.494169
novel	Novel	1.63E-10	WHL22.438181
c7orf42	Novel	1.81E-10	WHL22.229835
novel	Novel	1.90E-10	WHL22.541721
gga3, gga3_1	Novel	1.90E-10	WHL22.675071
mybbp1	Novel	1.97E-10	WHL22.563504
novel	Novel	2.03E-10	WHL22.140407
novel	Novel	2.06E-10	WHL22.394580
osbp, osbp2_1, osbp_1, osb	Novel	2.09E-10	WHL22.467667
bbs1	Novel	2.09E-10	WHL22.166330
hypp_2102	Novel	2.14E-10	WHL22.126336
rad50, rad50_2	Novel	2.36E-10	WHL22.494679
pionl, pionh	Novel	2.44E-10	WHL22.623577
novel	Novel	2.55E-10	WHL22.32575
tbc1d16	Novel	2.73E-10	WHL22.250559
novel	Novel	2.82E-10	WHL22.727269
pole	Novel	2.87E-10	WHL22.5154
ofd1l	Novel	2.97E-10	WHL22.65762
ankrd13	Novel	3.04E-10	WHL22.562367
novel	Novel	3.06E-10	WHL22.638866
wasf2_1	Novel	3.08E-10	WHL22.455917
c10orf97l_1	Novel	3.22E-10	WHL22.620754
tsc2	Novel	3.23E-10	WHL22.298030
fyco1	Novel	3.93E-10	WHL22.621027
novel	Novel	3.93E-10	WHL22.398797
novel	Novel	4.06E-10	WHL22.206461
novel	Novel	4.31E-10	WHL22.430748
pcnxl	Novel	4.38E-10	WHL22.146605
st6	Novel	4.38E-10	WHL22.299353
hypp_2886	Novel	4.95E-10	WHL22.432490
c9orf93l	Novel	5.13E-10	WHL22.477889
hypp_1561	Novel	5.54E-10	WHL22.124795

fam116a	Novel	6.18E-10	WHL22.486090
c4orf47	Novel	6.27E-10	WHL22.761126
pcnx, pcnx_1	Novel	6.33E-10	WHL22.520612
rvt/exn/end/pp	Novel	6.77E-10	WHL22.268159
dcun1d4	Novel	7.90E-10	WHL22.222352
veph1_1	Novel	8.93E-10	WHL22.424740
novel	Novel	9.24E-10	WHL22.120892
gtf3c4l	Novel	9.49E-10	WHL22.79487
novel	Novel	1.22E-09	WHL22.273560
c10orf112l	Novel	1.26E-09	WHL22.302303
hypp_114	Novel	1.27E-09	WHL22.350142
cubnr_3	Novel	1.35E-09	WHL22.586159
dcun1d3	Novel	1.36E-09	WHL22.61455
lrriq1	Novel	1.36E-09	WHL22.275969
novel	Novel	1.46E-09	WHL22.441227
herc2	Novel	1.49E-09	WHL22.94016
novel	Novel	1.55E-09	WHL22.241897
rad50_1	Novel	1.61E-09	WHL22.495090
wdr60	Novel	1.61E-09	WHL22.241407
hypp_1300, hypp_385	Novel	1.75E-09	WHL22.580705
novel	Novel	1.79E-09	WHL22.606904
brip1	Novel	1.99E-09	WHL22.456713
morn1	Novel	2.12E-09	WHL22.759633
novel	Novel	2.20E-09	WHL22.701606
tatdn3	Novel	2.28E-09	WHL22.364830
novel	Novel	2.28E-09	WHL22.324309
novel	Novel	2.30E-09	WHL22.528536
hypp_23, rnf165	Novel	2.50E-09	WHL22.224727
novel	Novel	2.69E-09	WHL22.550049
novel	Novel	2.78E-09	WHL22.538142
hypp_1024	Novel	2.91E-09	WHL22.33642
ift74	Novel	2.94E-09	WHL22.339234
hypp_1841	Novel	3.20E-09	WHL22.581903
iqub, uqub	Novel	3.24E-09	WHL22.5141
granln	Novel	3.27E-09	WHL22.422920
novel	Novel	3.59E-09	WHL22.126920
fam178al	Novel	3.66E-09	WHL22.314898

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hypp_3089, sorbs1	Novel	3.84E-09	WHL22.97851
ph4_1	Novel	4.01E-09	WHL22.19600
klhl29-2	Novel	4.26E-09	WHL22.32546
hypp_402	Novel	4.34E-09	WHL22.491498
sart3	Novel	4.40E-09	WHL22.541767
novel	Novel	4.50E-09	WHL22.550004
novel	Novel	4.62E-09	WHL22.123200
novel	Novel	4.73E-09	WHL22.705203
tdrd4	Novel	4.86E-09	WHL22.514151
novel	Novel	4.93E-09	WHL22.290614
pigk	Novel	5.38E-09	WHL22.134836
novel	Novel	5.53E-09	WHL22.383216
novel	Novel	5.55E-09	WHL22.113848
gnptabl	Novel	5.90E-09	WHL22.370638
novel	Novel	6.00E-09	WHL22.431471
aht1l	Novel	6.40E-09	WHL22.470543
novel	Novel	6.51E-09	WHL22.604264
trpt1	Novel	6.54E-09	WHL22.149379
novel	Novel	6.60E-09	WHL22.89123
cuzd1l_1	Novel	6.67E-09	WHL22.535819
fras1	Novel	6.79E-09	WHL22.435379
fn3f_20	Novel	6.98E-09	WHL22.303689
122c, 122c_1	Novel	7.59E-09	WHL22.491771
wdr77	Novel	7.63E-09	WHL22.462953
novel	Novel	7.74E-09	WHL22.764528
novel	Novel	7.74E-09	WHL22.454971
novel	Novel	7.82E-09	WHL22.99898
novel	Novel	7.84E-09	WHL22.254520
novel	Novel	7.95E-09	WHL22.653671
novel	Novel	8.56E-09	WHL22.364829
r/ptp/10d	Novel	9.61E-09	WHL22.575487
novel	Novel	9.78E-09	WHL22.225697
epb41l4a	Novel	1.00E-08	WHL22.322945
rapgef4_1	Novel	1.05E-08	WHL22.227137
ift122h	Novel	1.05E-08	WHL22.565494
pkd2l1, rej7	Novel	1.11E-08	WHL22.645258
novel	Novel	1.16E-08	WHL22.763128

novel	Novel	1.19E-08	WHL22.493076
nudt18	Novel	1.22E-08	WHL22.82027
novel	Novel	1.49E-08	WHL22.679679
copz1, copz1_1	Novel	1.56E-08	WHL22.621136
novel	Novel	1.59E-08	WHL22.737155
novel	Novel	1.74E-08	WHL22.405918
secisbp2l, secisbp2l_1	Novel	1.82E-08	WHL22.2531
hypp_343	Novel	1.83E-08	WHL22.95082
gtpbp3 (mitochondrial), gtpb	Novel	1.99E-08	WHL22.585451
pi4k, pi4ka	Novel	2.15E-08	WHL22.63539
novel	Novel	2.19E-08	WHL22.724320
novel	Novel	2.39E-08	WHL22.317585
mbd5	Novel	2.39E-08	WHL22.41279
hypp_2368, tsen54l_1	Novel	2.66E-08	WHL22.463479
advph	Novel	2.71E-08	WHL22.384467
novel	Novel	2.73E-08	WHL22.223252
wmp1	Novel	2.89E-08	WHL22.557562
hypp_2716	Novel	2.96E-08	WHL22.23322
hypp_2858	Novel	2.97E-08	WHL22.280947
novel	Novel	3.13E-08	WHL22.54575
ift122ap	Novel	3.18E-08	WHL22.493214
novel	Novel	3.19E-08	WHL22.502762
hypp_123	Novel	3.25E-08	WHL22.174438
hs3st6	Novel	3.36E-08	WHL22.295231
novel	Novel	3.38E-08	WHL22.141361
novel	Novel	3.39E-08	WHL22.361667
gpn1	Novel	3.73E-08	WHL22.531277
nmcp1l	Novel	3.74E-08	WHL22.464943
novel	Novel	3.76E-08	WHL22.331400
c1orf125, c1orf125l	Novel	3.86E-08	WHL22.273627
novel	Novel	3.97E-08	WHL22.253882
novel	Novel	4.20E-08	WHL22.277042
app	Novel	4.22E-08	WHL22.85379
arsb_1	Novel	4.40E-08	WHL22.105086
rps4	Novel	4.48E-08	WHL22.398258
c14orf135l	Novel	4.62E-08	WHL22.549045
fn3f_47	Novel	4.63E-08	WHL22.703471

novel	Novel	4.76E-08	WHL22.734431
non/mmyiihcph	Novel	4.79E-08	WHL22.757767
novel	Novel	4.80E-08	WHL22.305780
novel	Novel	5.19E-08	WHL22.32023
lrr_2	Novel	5.45E-08	WHL22.636066
hypp_3087	Novel	5.49E-08	WHL22.142278
hypp_586	Novel	5.52E-08	WHL22.420470
novel	Novel	5.62E-08	WHL22.157856
srrm1	Novel	5.80E-08	WHL22.620331
mdn1_2	Novel	5.84E-08	WHL22.214281
c12orf63l	Novel	5.89E-08	WHL22.609245
hypp_961	Novel	6.11E-08	WHL22.470693
novel	Novel	6.43E-08	WHL22.2178
tmed4	Novel	7.16E-08	WHL22.221549
igf2rl_1	Novel	7.42E-08	WHL22.619286
loxhd1_1	Novel	7.44E-08	WHL22.34775
hypp_11	Novel	7.53E-08	WHL22.731774
novel	Novel	7.54E-08	WHL22.684592
dtl_2, dtlh	Novel	8.28E-08	WHL22.91681
hunt(n terminal)	Novel	8.30E-08	WHL22.603736
tmc7, tmc7_1	Novel	8.33E-08	WHL22.182759
ogfod1	Novel	8.75E-08	WHL22.713782
novel	Novel	8.81E-08	WHL22.363718
th1l	Novel	8.83E-08	WHL22.212152
novel	Novel	8.98E-08	WHL22.256905
rnase3l, tatdn2l	Novel	9.96E-08	WHL22.102207
rps5	Novel	1.03E-07	WHL22.313858
nup98, nup98_2	Novel	1.05E-07	WHL22.392546
fbxl7-2	Novel	1.07E-07	WHL22.713486
novel	Novel	1.14E-07	WHL22.699846
novel	Novel	1.45E-07	WHL22.482416
wsb1	Novel	1.53E-07	WHL22.625351
novel	Novel	1.56E-07	WHL22.496227
hypp_1017	Novel	1.60E-07	WHL22.457714
ikbkap	Novel	1.62E-07	WHL22.245564
pla2g1b_1	Novel	1.95E-07	WHL22.666879
novel	Novel	2.01E-07	WHL22.331826

novel	Novel	2.06E-07	WHL22.148655
novel	Novel	2.06E-07	WHL22.171139
novel	Novel	2.10E-07	WHL22.650341
novel	Novel	2.12E-07	WHL22.296334
dnahc11, dnahc9	Novel	2.14E-07	WHL22.378478
c3orf15	Novel	2.33E-07	WHL22.498070
cks1b	Novel	2.62E-07	WHL22.108688
dsh	Novel	2.68E-07	WHL22.256185
c19orf29	Novel	2.72E-07	WHL22.458985
novel	Novel	3.01E-07	WHL22.195074
ankar_1	Novel	3.21E-07	WHL22.732448
novel	Novel	3.23E-07	WHL22.374072
novel	Novel	3.27E-07	WHL22.139068
rsu1l	Novel	3.36E-07	WHL22.34234
novel	Novel	3.36E-07	WHL22.348293
toporsl, toporsl_2	Novel	3.40E-07	WHL22.761455
novel	Novel	3.51E-07	WHL22.700776
novel	Novel	3.77E-07	WHL22.2214
anxa7_1	Novel	3.82E-07	WHL22.186269
ttc12	Novel	3.93E-07	WHL22.477635
novel	Novel	3.94E-07	WHL22.296298
novel	Novel	4.11E-07	WHL22.701601
novel	Novel	4.33E-07	WHL22.342126
novel	Novel	4.38E-07	WHL22.517885
novel	Novel	4.50E-07	WHL22.713639
bop1	Novel	4.61E-07	WHL22.377870
thegl	Novel	4.82E-07	WHL22.634523
eral1	Novel	4.86E-07	WHL22.504170
c6orf94l	Novel	5.01E-07	WHL22.565644
hypp_1706	Novel	5.32E-07	WHL22.531313
aknal	Novel	5.68E-07	WHL22.251711
hypp_2370	Novel	6.16E-07	WHL22.58437
hypp_2442	Novel	6.87E-07	WHL22.678765
novel	Novel	6.91E-07	WHL22.473501
novel	Novel	7.15E-07	WHL22.702308
novel	Novel	7.35E-07	WHL22.608201
tctn2	Novel	7.61E-07	WHL22.398527

kif1al	Novel	7.73E-07	WHL22.195393
c2orf39l	Novel	8.22E-07	WHL22.496991
novel	Novel	8.62E-07	WHL22.720114
novel	Novel	8.63E-07	WHL22.148044
hydin, hydin_2	Novel	9.34E-07	WHL22.212280
novel	Novel	9.36E-07	WHL22.520085
hypp_1863, tsnaxip1	Novel	9.61E-07	WHL22.452212
hypp_1630	Novel	9.93E-07	WHL22.3016
wdr70	Novel	1.03E-06	WHL22.582005
c14orf135l	Novel	1.03E-06	WHL22.339830
tgm1	Novel	1.34E-06	WHL22.276149
polppl-5, polppl-7, polppl-8,	Novel	1.43E-06	WHL22.491357
novel	Novel	1.56E-06	WHL22.90023
c7orf63	Novel	1.62E-06	WHL22.603522
novel	Novel	1.66E-06	WHL22.264545
novel	Novel	1.90E-06	WHL22.31294
novel	Novel	1.97E-06	WHL22.702269
unk_93	Novel	1.98E-06	WHL22.105676
kifc3l3	Novel	2.33E-06	WHL22.421412
novel	Novel	2.47E-06	WHL22.544483
novel	Novel	2.52E-06	WHL22.568033
ajpx1	Novel	2.59E-06	WHL22.317603
novel	Novel	4.03E-06	WHL22.204356
novel	Novel	4.55E-06	WHL22.13472
myst2	Novel	5.30E-06	WHL22.342382
novel	Novel	5.31E-06	WHL22.590617
rsp3h	Novel	5.90E-06	WHL22.688668
topbp1	Novel	5.95E-06	WHL22.101942
lrsam1	Novel	6.01E-06	WHL22.553550
rpn2	Novel	7.43E-06	WHL22.275181
reeler/egf/cub	Novel	8.05E-06	WHL22.224782
dis	Novel	8.40E-06	WHL22.770248
novel	Novel	8.52E-06	WHL22.124535
hypp_1332	Novel	9.02E-06	WHL22.590672
dlec1, dlec1l	Novel	9.44E-06	WHL22.644548
dkk1	Novel	1.12E-05	WHL22.342226
asphm2	Novel	1.13E-05	WHL22.591719

abhd8	Novel	1.34E-05	WHL22.756609
mat2b	Novel	1.78E-05	WHL22.640590
lrr1_1	Novel	1.94E-05	WHL22.140607
trspap1	Novel	2.07E-05	WHL22.95034
vprbp-2	Novel	2.24E-05	WHL22.482852
fbxl13	Novel	3.27E-05	WHL22.331077
novel	Novel	3.29E-05	WHL22.547686
ccdc83	Novel	4.56E-05	WHL22.34874
rptor	Novel	4.76E-05	WHL22.283863
lrrfip2	Novel	4.97E-05	WHL22.5521
hypp_1134	Novel	5.55E-05	WHL22.457378
novel	Novel	5.56E-05	WHL22.381275
grm3	Novel	6.18E-05	WHL22.497732
ttl5	Novel	7.71E-05	WHL22.423190
mre11	Novel	8.49E-05	WHL22.429507
hypp_2760	Novel	8.81E-05	WHL22.717674
novel	Novel	9.67E-05	WHL22.345699
novel	Novel	1.39E-04	WHL22.646069
socax	Novel	1.79E-04	WHL22.447834
novel	Novel	2.15E-04	WHL22.379325
hypp_1247	Novel	2.70E-04	WHL22.743718
frem1l	Novel	3.36E-04	WHL22.141951
novel	Novel	3.39E-04	WHL22.403043
cg15216pa	Novel	3.75E-04	WHL22.547520
dnahc8, hypp_2358	Novel	4.67E-04	WHL22.408041
novel	Novel	5.34E-04	WHL22.421749
unc44_308	Novel	5.57E-04	WHL22.733507
mol10l1	Novel	6.42E-04	WHL22.318218
zzz3l	Novel	6.70E-04	WHL22.624200
novel	Novel	8.04E-04	WHL22.202563
novel	Novel	8.13E-04	WHL22.708137
syne1	Novel	8.98E-04	WHL22.662846
novel	Novel	9.30E-04	WHL22.205480
rp2	Novel	9.73E-04	WHL22.569602
c20orf103l	Novel	1.87E-03	WHL22.244530
novel	Novel	2.31E-03	WHL22.730771
novel	Novel	2.36E-03	WHL22.362

hypp_3074	Novel	3.10E-03	WHL22.511987
novel	Novel	3.47E-03	WHL22.535710
novel	Novel	3.55E-03	WHL22.33967
hypp_974	Novel	3.82E-03	WHL22.521660
dystoh3, macf1l	Novel	4.67E-03	WHL22.770391
novel	Novel	6.38E-03	WHL22.454837
ccdc40	Novel	7.21E-03	WHL22.250444
hypp_3074, muc19l	Novel	8.90E-03	WHL22.511993
chaf1a	Novel	1.92E-02	WHL22.54311

Supplemental Table 1C	Gene transcripts uniquely enriched within the Oral Ectoderm subdomain		
Gene	Functional Category	P-value	Identification #
gsc	Transcription factor	1.13E-10	WHL22.531818
myod3	Transcription factor	2.44E-08	WHL22.531810
masp	Metabolism	3.17E-08	WHL22.91488
dlst	Metabolism	1.81E-07	WHL22.531995
pmar1c	Transcription factor	2.46E-07	WHL22.462256
nacha4, nacha4_1	CalciumToolkit,EggActivation,Nervous	5.03E-07	WHL22.653834
srcr12_1, srcr77	Immunity	1.41E-06	WHL22.344665
cyp2l42	Defensome,Metabolism	1.52E-06	WHL22.610666
nlr13	Immunity	2.27E-06	WHL22.286025
lct_11	Metabolism	2.41E-06	WHL22.107148
drd2l_12	GPCRRhodopsin	2.86E-06	WHL22.315797
nlr148	Immunity	5.39E-06	WHL22.377207
yp301	Oogenesis	6.61E-06	WHL22.476018
cf5/8l1	Immunity	1.18E-05	WHL22.6050
srcr217	Immunity	1.43E-05	WHL22.524652
srcr15, srcr17, srcr183	Immunity,Adhesion	1.67E-05	WHL22.231695
sc4mol_2	Metabolism	3.21E-05	WHL22.306166
hypp_2672	GPCRRhodopsin	3.74E-05	WHL22.538160
abcg9	Defensome,Metabolism	4.93E-05	WHL22.627067
sm30d	Biomineralization	5.71E-05	WHL22.517513
fb3	Immunity	7.04E-05	WHL22.177238
htr1l_1	GPCRRhodopsin,Nervous	8.09E-05	WHL22.151560
fn3_7, lh2/fn3	Adhesion	9.14E-05	WHL22.688376
srcr138	Immunity	9.36E-05	WHL22.546129
apn6	Metalloprotease	9.36E-05	WHL22.237456
gnbp1/2/3b_1	Immunity	1.06E-04	WHL22.741917
glyctk1	Metabolism	1.08E-04	WHL22.317454
zhangfei	Transcription factor	1.21E-04	WHL22.126947
cthpsn6, cts8	Immunity	1.26E-04	WHL22.471134
galr2l_17	GPCRRhodopsin,Nervous	1.82E-04	WHL22.5611
novel	Metabolism	2.04E-04	WHL22.650480
apc11	CellCycle	4.53E-04	WHL22.239616
lmpt	Transcription factor	4.54E-04	WHL22.543989
slc16a6l_2	Metabolism	5.12E-04	WHL22.197173
mmp18/19l6	Metalloprotease	5.63E-04	WHL22.24854

uros	Metabolism	6.01E-04	WHL22.117874
slc15a4_2	Metabolism	7.79E-04	WHL22.278808
srcr218	Immunity	9.36E-04	WHL22.6041
b4galt6_7	Metabolism	1.09E-03	WHL22.591523
vtgn1	Oogenesis	1.11E-03	WHL22.512739
slc25a19	Metabolism	1.12E-03	WHL22.127558
nlr80	Immunity	1.39E-03	WHL22.661376
aldh5a1, aldh5a1_2	Defensome,Metabolism	1.67E-03	WHL22.534731
ugt2b22, ugt2b33_5	Defensome	2.04E-03	WHL22.749272
st8sia1, st8sia1_1	Metabolism	2.18E-03	WHL22.219385
novel	Defensome	2.22E-03	WHL22.346668
msp130r4	Biomineralization	2.25E-03	WHL22.405743
gst_pi, hypp_2591	Defensome	3.01E-03	WHL22.116692
abcb10a	Defensome	3.03E-03	WHL22.1844
abca1_1	Defensome	3.34E-03	WHL22.25485
cycc	CellCycle	3.36E-03	WHL22.125893
cyp2u	Defensome,Metabolism	3.59E-03	WHL22.107174
fadd	Apoptosis,Immunity	3.60E-03	WHL22.125355
slc45a2_2	Metabolism	4.00E-03	WHL22.521635
nr1h6	Defensome,TF	4.19E-03	WHL22.41011
nacha3	CalciumToolkit,EggActivation,Nervous	4.33E-03	WHL22.290503
hypp_143	Metabolism	4.43E-03	WHL22.275390
pkm2	Metabolism	4.63E-03	WHL22.334205
echl2	Immunity	5.00E-03	WHL22.120246
unk_50, z434	Zinc finger	6.53E-03	WHL22.358726
mgst3	Defensome	6.86E-03	WHL22.719693
myd88l2	Immunity	7.05E-03	WHL22.412836
ku86l	Immunity	7.34E-03	WHL22.505497
c1ql	Immunity	7.43E-03	WHL22.644401
cyb5r3, rheb	GTPase	7.46E-03	WHL22.248463
serrp1, t1tnf	Metalloprotease	8.19E-03	WHL22.179675
slc5a9	Metabolism	8.56E-03	WHL22.702636
tmprss4	Metabolism	8.56E-03	WHL22.235692
hsd17b8	Metabolism	1.03E-02	WHL22.383188
gpr112l_3	Adhesion	1.05E-02	WHL22.81256
mafs	Defensome	1.06E-02	WHL22.250411
fuca2_1	Metabolism	1.08E-02	WHL22.468276

z57	Zinc finger	1.16E-02	WHL22.376080
srcr199	Immunity	1.25E-02	WHL22.525442
dscam/dccl	Adhesion	1.35E-02	WHL22.129057
siat7e	Metabolism	1.35E-02	WHL22.19353
tulp4l	Transcription factor	1.45E-02	WHL22.608876
slc35a4	Metabolism	1.47E-02	WHL22.182098
diras	GTPase	1.52E-02	WHL22.254745
aqp3	Metabolism	1.53E-02	WHL22.528654
saa-a	Immunity	1.62E-02	WHL22.494907
cyp2l17	Defensome	2.01E-02	WHL22.722107
chordin	Signaling	2.19E-02	WHL22.124093
pruneh	Metabolism	2.54E-02	WHL22.425756
tmem195-2	Metabolism	2.56E-02	WHL22.63441
gsto1	Defensome	3.22E-02	WHL22.590704
z365	Zinc finger	3.28E-02	WHL22.10526
ugt1l_3	Defensome	3.42E-02	WHL22.349363
srcr203	Immunity	3.48E-02	WHL22.306001
slc39a11	Metabolism	3.82E-02	WHL22.466490
egf/ig/fn3, fn3/egf/ig, ptp69d	Adhesion,EggActivation,Phosphatase	4.27E-02	WHL22.255858
ugt1l_11	Defensome	4.32E-02	WHL22.289880
slc16	Novel	2.96E-09	WHL22.722801
egas	Novel	4.96E-08	WHL22.313228
novel	Novel	9.04E-08	WHL22.660350
sned1_4	Novel	9.14E-08	WHL22.595503
c6orf192l_2	Novel	1.97E-07	WHL22.24448
novel	Novel	3.90E-07	WHL22.607504
slc13a2_2	Novel	4.00E-07	WHL22.763423
novel	Novel	4.83E-07	WHL22.576686
novel	Novel	5.41E-07	WHL22.41312
endrvt65	Novel	6.62E-07	WHL22.446551
lim2l	Novel	1.37E-06	WHL22.535241
hypp_1320	Novel	2.14E-06	WHL22.137541
novel	Novel	2.27E-06	WHL22.692159
novel	Novel	2.75E-06	WHL22.349513
cerkll	Novel	3.02E-06	WHL22.258455
novel	Novel	3.39E-06	WHL22.8378
novel	Novel	3.58E-06	WHL22.464693

novel	Novel	4.03E-06	WHL22.752190
egf/zp	Novel	4.13E-06	WHL22.129863
novel	Novel	4.48E-06	WHL22.324538
novel	Novel	4.82E-06	WHL22.384247
novel	Novel	4.82E-06	WHL22.340178
novel	Novel	5.44E-06	WHL22.232496
slc46a1l	Novel	6.73E-06	WHL22.8502
novel	Novel	7.21E-06	WHL22.593603
hypp_104	Novel	7.47E-06	WHL22.436211
novel	Novel	9.26E-06	WHL22.687449
novel	Novel	9.49E-06	WHL22.181276
hypp_2144	Novel	9.63E-06	WHL22.610819
novel	Novel	1.04E-05	WHL22.133665
ado	Novel	1.04E-05	WHL22.279764
slsp_24	Novel	1.21E-05	WHL22.538031
novel	Novel	1.43E-05	WHL22.45015
novel	Novel	1.52E-05	WHL22.612688
bcatl, hypp_2696	Novel	1.55E-05	WHL22.194379
novel	Novel	1.60E-05	WHL22.383989
novel	Novel	1.76E-05	WHL22.267666
clect/tm_9	Novel	1.79E-05	WHL22.35396
grm3, grm_2	Novel	1.79E-05	WHL22.18837
novel	Novel	2.06E-05	WHL22.150496
cspl	Novel	2.24E-05	WHL22.445817
tprg1l	Novel	2.66E-05	WHL22.283130
kiaa1147	Novel	3.20E-05	WHL22.146279
thap9l	Novel	3.25E-05	WHL22.699678
novel	Novel	3.54E-05	WHL22.619525
b3galnt2	Novel	3.63E-05	WHL22.249649
novel	Novel	3.86E-05	WHL22.708564
novel	Novel	4.03E-05	WHL22.229667
sfxn1_1	Novel	4.26E-05	WHL22.213447
eaf2l	Novel	5.25E-05	WHL22.204513
novel	Novel	5.54E-05	WHL22.120292
chrna9_4	Novel	6.09E-05	WHL22.694407
alox12bl	Novel	6.38E-05	WHL22.662890
novel	Novel	6.92E-05	WHL22.583930

cubn	Novel	7.68E-05	WHL22.603616
novel	Novel	8.15E-05	WHL22.342155
hypp_523	Novel	8.57E-05	WHL22.688505
timp2	Novel	9.36E-05	WHL22.304115
novel	Novel	9.52E-05	WHL22.118423
hypp_591	Novel	1.05E-04	WHL22.277728
snx17	Novel	1.11E-04	WHL22.73718
novel	Novel	1.14E-04	WHL22.134912
mmr2l_1	Novel	1.17E-04	WHL22.541474
hypp_1556	Novel	1.24E-04	WHL22.35403
echnl_3, hypp_181	Novel	1.24E-04	WHL22.210000
novel	Novel	1.26E-04	WHL22.437339
selpl_4	Novel	1.44E-04	WHL22.6985
novel	Novel	1.52E-04	WHL22.501968
vps15	Novel	1.60E-04	WHL22.455203
novel	Novel	1.73E-04	WHL22.59816
egf/zp_3	Novel	1.80E-04	WHL22.499903
r/ptp/r	Novel	1.89E-04	WHL22.417763
cpn2l	Novel	1.98E-04	WHL22.34429
novel	Novel	1.98E-04	WHL22.307407
hypp_362	Novel	2.00E-04	WHL22.602
novel	Novel	2.10E-04	WHL22.216465
gckr	Novel	2.11E-04	WHL22.719036
novel	Novel	2.17E-04	WHL22.472815
nat13	Novel	2.22E-04	WHL22.711417
c6orf84l	Novel	2.26E-04	WHL22.184159
novel	Novel	2.36E-04	WHL22.567027
kiaa1161l_1	Novel	2.40E-04	WHL22.243206
novel	Novel	2.40E-04	WHL22.486844
angptl1, angptl1l	Novel	2.41E-04	WHL22.485012
ercc3	Novel	2.54E-04	WHL22.479681
tpcn3	Novel	2.69E-04	WHL22.265048
novel	Novel	2.80E-04	WHL22.61425
fic	Novel	2.84E-04	WHL22.114164
hypp_1441	Novel	2.86E-04	WHL22.150808
hypp_2285, hypp_2651	Novel	2.86E-04	WHL22.324916
novel	Novel	2.86E-04	WHL22.637579

hypp_1432	Novel	3.10E-04	WHL22.64170
hypp_853	Novel	3.27E-04	WHL22.564005
dhps_3	Novel	3.41E-04	WHL22.570543
novel	Novel	3.41E-04	WHL22.711320
novel	Novel	3.41E-04	WHL22.597646
novel	Novel	3.48E-04	WHL22.586193
novel	Novel	3.59E-04	WHL22.758984
slc24a6_1	Novel	3.66E-04	WHL22.238669
novel	Novel	3.80E-04	WHL22.557986
novel	Novel	3.99E-04	WHL22.566576
novel	Novel	4.04E-04	WHL22.768414
novel	Novel	4.10E-04	WHL22.272804
hypp_1294	Novel	4.10E-04	WHL22.652182
hypp2715	Novel	4.10E-04	WHL22.753588
actr5h	Novel	4.27E-04	WHL22.610156
cenpp	Novel	4.35E-04	WHL22.533557
novel	Novel	4.42E-04	WHL22.414524
dak_1	Novel	4.45E-04	WHL22.169282
mtch2l	Novel	4.61E-04	WHL22.355981
novel	Novel	4.74E-04	WHL22.504145
novel	Novel	4.85E-04	WHL22.455182
sgsm1_1	Novel	4.94E-04	WHL22.690366
novel	Novel	5.09E-04	WHL22.480022
kiaa1033, kiaa1033_1	Novel	5.45E-04	WHL22.33947
hypp_1028	Novel	5.50E-04	WHL22.678683
ehh4_65	Novel	5.54E-04	WHL22.164536
xrcc2, xrcc2l	Novel	5.54E-04	WHL22.713824
hypp_1364	Novel	6.00E-04	WHL22.579064
hypp_2465	Novel	6.00E-04	WHL22.142479
novel	Novel	6.12E-04	WHL22.479670
abp34l	Novel	6.42E-04	WHL22.445246
hypp_486	Novel	6.48E-04	WHL22.3051
chst11l_3	Novel	6.66E-04	WHL22.478670
novel	Novel	6.97E-04	WHL22.580540
hypp_2354	Novel	7.29E-04	WHL22.195200
novel	Novel	7.33E-04	WHL22.403134
fam48a	Novel	7.64E-04	WHL22.347651

solh	Novel	7.83E-04	WHL22.28700
novel	Novel	7.96E-04	WHL22.300779
hypp_2640	Novel	8.13E-04	WHL22.34337
mgst5	Novel	8.17E-04	WHL22.687133
novel	Novel	8.69E-04	WHL22.613012
adprhl2	Novel	8.75E-04	WHL22.189070
pecr	Novel	8.83E-04	WHL22.346828
novel	Novel	9.01E-04	WHL22.104354
ints2_1	Novel	9.31E-04	WHL22.510496
novel	Novel	9.36E-04	WHL22.730951
pex13	Novel	9.36E-04	WHL22.350010
trim2	Novel	9.71E-04	WHL22.109181
wdr8	Novel	1.01E-03	WHL22.282897
hypp_288	Novel	1.05E-03	WHL22.341131
dis3l	Novel	1.08E-03	WHL22.503816
hypp_803	Novel	1.09E-03	WHL22.34997
novel	Novel	1.09E-03	WHL22.222044
novel	Novel	1.12E-03	WHL22.131467
novel	Novel	1.12E-03	WHL22.182390
novel	Novel	1.17E-03	WHL22.213251
novel	Novel	1.17E-03	WHL22.587548
novel	Novel	1.19E-03	WHL22.446968
gnptgl	Novel	1.20E-03	WHL22.693829
novel	Novel	1.28E-03	WHL22.412333
hypp_300	Novel	1.28E-03	WHL22.464546
nr1_1	Novel	1.32E-03	WHL22.91739
pms2	Novel	1.35E-03	WHL22.468333
dgat2	Novel	1.36E-03	WHL22.309028
novel	Novel	1.39E-03	WHL22.540301
novel	Novel	1.39E-03	WHL22.462258
novel	Novel	1.41E-03	WHL22.644855
fut4_5	Novel	1.46E-03	WHL22.767394
hypp_1773	Novel	1.46E-03	WHL22.619809
c8orf41l	Novel	1.51E-03	WHL22.164575
novel	Novel	1.75E-03	WHL22.111124
tenal	Novel	1.75E-03	WHL22.239128
novel	Novel	1.76E-03	WHL22.165239

mrps2l_1	Novel	1.80E-03	WHL22.475690
novel	Novel	1.81E-03	WHL22.134696
novel	Novel	1.83E-03	WHL22.755596
novel	Novel	1.90E-03	WHL22.323946
novel	Novel	1.98E-03	WHL22.603799
tmem209	Novel	2.03E-03	WHL22.33898
novel	Novel	2.08E-03	WHL22.595360
novel	Novel	2.14E-03	WHL22.686659
novel	Novel	2.18E-03	WHL22.6651
sarox_4	Novel	2.21E-03	WHL22.269621
novel	Novel	2.22E-03	WHL22.114714
novel	Novel	2.22E-03	WHL22.278748
novel	Novel	2.32E-03	WHL22.562312
uchl3	Novel	2.35E-03	WHL22.224105
php	Novel	2.37E-03	WHL22.547322
tmem39a	Novel	2.40E-03	WHL22.608839
tex261l	Novel	2.44E-03	WHL22.388441
phf14	Novel	2.51E-03	WHL22.458780
novel	Novel	2.52E-03	WHL22.255109
exdl1	Novel	2.53E-03	WHL22.83095
novel	Novel	2.53E-03	WHL22.44169
novel	Novel	2.53E-03	WHL22.594005
hebp2	Novel	2.72E-03	WHL22.77498
tmem106l	Novel	2.96E-03	WHL22.701709
pald_1	Novel	3.03E-03	WHL22.538229
novel	Novel	3.05E-03	WHL22.734061
novel	Novel	3.27E-03	WHL22.682553
novel	Novel	3.37E-03	WHL22.414479
taf9	Novel	3.37E-03	WHL22.110295
novel	Novel	3.43E-03	WHL22.476409
fam62b	Novel	3.45E-03	WHL22.737962
novel	Novel	3.61E-03	WHL22.235479
novel	Novel	3.65E-03	WHL22.50873
novel	Novel	3.68E-03	WHL22.200401
rbx2	Novel	3.74E-03	WHL22.402249
novel	Novel	3.93E-03	WHL22.74684
wrb	Novel	4.00E-03	WHL22.163280

novel	Novel	4.02E-03	WHL22.480705
lrr/gpcr_1	Novel	4.03E-03	WHL22.297229
esterased	Novel	4.15E-03	WHL22.533094
novel	Novel	4.26E-03	WHL22.604746
tpcn2	Novel	4.31E-03	WHL22.726834
novel	Novel	4.34E-03	WHL22.537566
novel	Novel	4.43E-03	WHL22.164280
c14orf148l	Novel	4.48E-03	WHL22.472469
novel	Novel	4.60E-03	WHL22.336945
novel	Novel	4.64E-03	WHL22.451169
novel	Novel	4.68E-03	WHL22.223317
casp2l	Novel	4.82E-03	WHL22.325720
gabbr2l_1	Novel	4.82E-03	WHL22.36689
chst11l_3	Novel	4.86E-03	WHL22.478673
kctd12b	Novel	4.86E-03	WHL22.391565
novel	Novel	5.02E-03	WHL22.462857
angel	Novel	5.02E-03	WHL22.326578
novel	Novel	5.18E-03	WHL22.102859
novel	Novel	5.19E-03	WHL22.77483
novel	Novel	5.19E-03	WHL22.105041
hypp_1161	Novel	5.33E-03	WHL22.235916
notchl_11	Novel	5.35E-03	WHL22.298992
lacl_3, lacl_4	Novel	5.37E-03	WHL22.692656
novel	Novel	5.40E-03	WHL22.171869
slc20a1_3	Novel	5.42E-03	WHL22.351237
usp52_2	Novel	5.42E-03	WHL22.448609
novel	Novel	5.54E-03	WHL22.472728
pog_1	Novel	5.62E-03	WHL22.538056
hif1an	Novel	5.65E-03	WHL22.545028
novel	Novel	5.70E-03	WHL22.373204
novel	Novel	5.74E-03	WHL22.382414
hypp_288	Novel	5.78E-03	WHL22.341135
novel	Novel	5.78E-03	WHL22.668869
novel	Novel	5.78E-03	WHL22.759729
polr3b	Novel	5.93E-03	WHL22.341132
vta1	Novel	5.97E-03	WHL22.640491
coq6, coq6_1	Novel	6.19E-03	WHL22.532167

novel	Novel	6.21E-03	WHL22.443231
rrp8l	Novel	6.30E-03	WHL22.398390
mysm1	Novel	6.33E-03	WHL22.336913
sulf1_1	Novel	6.59E-03	WHL22.34009
novel	Novel	6.79E-03	WHL22.620669
novel	Novel	6.93E-03	WHL22.735572
dish2(dab2)	Novel	7.73E-03	WHL22.481587
nup133, nup133-2	Novel	7.86E-03	WHL22.378950
ubr7	Novel	8.15E-03	WHL22.335883
hbp1	Novel	8.20E-03	WHL22.50301
bcs1l	Novel	8.21E-03	WHL22.308983
hypp_1819	Novel	8.56E-03	WHL22.240331
novel	Novel	8.56E-03	WHL22.746736
novel	Novel	8.69E-03	WHL22.708966
clect_79	Novel	8.96E-03	WHL22.677821
phscd1	Novel	9.03E-03	WHL22.731935
novel	Novel	9.19E-03	WHL22.133060
flj20433l_1	Novel	9.52E-03	WHL22.272615
novel	Novel	9.72E-03	WHL22.226065
novel	Novel	9.93E-03	WHL22.83102
arfgef1_1	Novel	1.00E-02	WHL22.285652
novel	Novel	1.02E-02	WHL22.173777
novel	Novel	1.05E-02	WHL22.32435
ttrspn_14	Novel	1.13E-02	WHL22.263631
novel	Novel	1.14E-02	WHL22.608714
med23_1	Novel	1.16E-02	WHL22.379328
novel	Novel	1.16E-02	WHL22.202276
hypp_2017	Novel	1.17E-02	WHL22.97577
novel	Novel	1.17E-02	WHL22.538853
mrpl19	Novel	1.21E-02	WHL22.129263
hypp_1172	Novel	1.21E-02	WHL22.10745
fuzzy1, fuzzy2	Novel	1.23E-02	WHL22.566624
ankrd27l	Novel	1.24E-02	WHL22.312215
atpaf1	Novel	1.24E-02	WHL22.761770
cntnap4l_2	Novel	1.28E-02	WHL22.70552
novel	Novel	1.29E-02	WHL22.522586
selcysl	Novel	1.35E-02	WHL22.96873

novel	Novel	1.39E-02	WHL22.488474
novel	Novel	1.42E-02	WHL22.413127
novel	Novel	1.42E-02	WHL22.255677
novel	Novel	1.46E-02	WHL22.322514
novel	Novel	1.51E-02	WHL22.471432
novel	Novel	1.57E-02	WHL22.571548
novel	Novel	1.62E-02	WHL22.414943
flj37953l	Novel	1.62E-02	WHL22.42486
fbxl8_1	Novel	1.64E-02	WHL22.421159
novel	Novel	1.64E-02	WHL22.729714
gst	Novel	1.65E-02	WHL22.687001
hypp_1297	Novel	1.66E-02	WHL22.258506
mib2-4	Novel	1.66E-02	WHL22.304675
hypp_1878	Novel	1.69E-02	WHL22.296782
nup62	Novel	1.70E-02	WHL22.65170
novel	Novel	1.71E-02	WHL22.70492
ranbp2	Novel	1.71E-02	WHL22.283467
foxred1	Novel	1.71E-02	WHL22.413246
actg1	Novel	1.80E-02	WHL22.158834
cd2bp2	Novel	1.83E-02	WHL22.441758
novel	Novel	1.83E-02	WHL22.504392
hypp_262	Novel	1.85E-02	WHL22.756714
novel	Novel	1.90E-02	WHL22.645298
novel	Novel	1.93E-02	WHL22.510504
ccdc57, hypp_2016	Novel	2.03E-02	WHL22.362482
ghdc2	Novel	2.07E-02	WHL22.61789
novel	Novel	2.07E-02	WHL22.42204
novel	Novel	2.09E-02	WHL22.395166
nupb2	Novel	2.10E-02	WHL22.426293
novel	Novel	2.18E-02	WHL22.426103
hypp_468	Novel	2.23E-02	WHL22.243656
novel	Novel	2.23E-02	WHL22.280578
foxred1	Novel	2.26E-02	WHL22.413258
nat10	Novel	2.28E-02	WHL22.591769
novel	Novel	2.28E-02	WHL22.400924
novel	Novel	2.28E-02	WHL22.420337
clect_103	Novel	2.29E-02	WHL22.87875

pppl_272	Novel	2.31E-02	WHL22.8218
novel	Novel	2.31E-02	WHL22.290347
novel	Novel	2.34E-02	WHL22.147320
kntc1l	Novel	2.40E-02	WHL22.151608
novel	Novel	2.41E-02	WHL22.532323
novel	Novel	2.58E-02	WHL22.763745
novel	Novel	2.63E-02	WHL22.524985
ankrd53	Novel	2.71E-02	WHL22.388448
novel	Novel	2.71E-02	WHL22.252490
novel	Novel	2.71E-02	WHL22.564651
novel	Novel	2.73E-02	WHL22.314005
hypp_2365	Novel	2.79E-02	WHL22.535206
novel	Novel	2.80E-02	WHL22.437914
hypp_812	Novel	2.86E-02	WHL22.314676
novel	Novel	2.93E-02	WHL22.36349
zdhhc6	Novel	2.95E-02	WHL22.116431
novel	Novel	3.10E-02	WHL22.29497
novel	Novel	3.13E-02	WHL22.75318
novel	Novel	3.21E-02	WHL22.566047
bhmt_6, bhmt_7	Novel	3.28E-02	WHL22.678720
hypp_1480	Novel	3.28E-02	WHL22.761166
novel	Novel	3.28E-02	WHL22.617781
novel	Novel	3.28E-02	WHL22.9709
egfl	Novel	3.37E-02	WHL22.618665
hypp_1070	Novel	3.37E-02	WHL22.278919
novel	Novel	3.41E-02	WHL22.145282
novel	Novel	3.44E-02	WHL22.544880
cub/zp	Novel	3.56E-02	WHL22.663363
novel	Novel	3.74E-02	WHL22.760219
solh, solh-2	Novel	3.75E-02	WHL22.28690
novel	Novel	3.88E-02	WHL22.489019
novel	Novel	3.88E-02	WHL22.558794
txndc15	Novel	3.92E-02	WHL22.381210
unc44_184	Novel	3.98E-02	WHL22.263435
abca7l	Novel	4.07E-02	WHL22.25560
varsia	Novel	4.10E-02	WHL22.496167
notchh1_7	Novel	4.13E-02	WHL22.251789

dus4l	Novel	4.42E-02	WHL22.369439
tmem14c	Novel	4.48E-02	WHL22.467028
preb	Novel	4.52E-02	WHL22.371950
novel	Novel	4.58E-02	WHL22.735081
novel	Novel	4.59E-02	WHL22.479779
dnhd1l_2	Novel	4.64E-02	WHL22.290368
hypp_2444	Novel	4.71E-02	WHL22.498241
novel	Novel	4.95E-02	WHL22.232753
novel	Novel	4.98E-02	WHL22.700825
grm4l, grm8	Novel	4.99E-02	WHL22.566045

Supplemental Table 1D	Gene transcripts uniquely enriched within the Ciliated Band		
Gene	Functional Category	P-value	Identification #
onecut	Nervous,TF	2.41E-43	WHL22.288683
clvhh2a	Histone	1.46E-18	WHL22.104163
he1, he2	Metalloprotease	1.52E-12	WHL22.99505
ldla/egf/ig/gpcr, lrp1b	Adhesion	1.75E-12	WHL22.292017
he1	Metalloprotease	3.89E-11	WHL22.99508
lct_3	Metabolism	6.16E-11	WHL22.107154
macpfc3	Immunity	5.20E-10	WHL22.310563
uco2	EggActivation,Oogenesis	1.45E-08	WHL22.198221
zc3h12bl	GPCRRhodopsin,Nervous	3.59E-08	WHL22.669839
bak	Apoptosis	7.66E-07	WHL22.700645
soxf	Transcription factor	9.28E-07	WHL22.57106
dna_pkcs	Immunity,Kinase	1.07E-06	WHL22.748235
ppm1d	Phosphatase	1.20E-06	WHL22.480876
hypp_119, klkb1l1, st14l_29	Immunity,Metabolism	1.37E-06	WHL22.374795
shpk	Immunity,Kinase	1.65E-06	WHL22.183228
tnfrsf_cl2	Apoptosis,Immunity	2.57E-06	WHL22.394084
anl5	Metalloprotease	4.14E-06	WHL22.162209
rrm2_1	Metabolism	5.65E-06	WHL22.491689
cyca, cyca_1	CellCycle	6.70E-06	WHL22.595411
wnt8	Signaling	7.64E-06	WHL22.8923
spc39l	Metabolism	1.18E-05	WHL22.652723
dhfr	Metabolism	1.55E-05	WHL22.626923
plcd, plcd_1, plcd_2	CalciumToolkit,EggActivation	2.01E-05	WHL22.87965
cycb	CellCycle	3.12E-05	WHL22.675293
macpfe.3	Immunity	8.21E-05	WHL22.727726
bmp1/tldl1	Metalloprotease,Signaling	3.09E-04	WHL22.549400
tcp1	Immunity	3.66E-04	WHL22.186788
an, anl1	Metalloprotease	3.80E-04	WHL22.619773
tropmph	Cytoskeleton	4.12E-04	WHL22.553426
lrr/gpcr_6	Adhesion,GPCRRhodopsin	5.03E-04	WHL22.311137
ost	Adhesion	5.90E-04	WHL22.103791
srcr128	Immunity	7.44E-04	WHL22.655930
meid1	Oogenesis	7.65E-04	WHL22.606315
dna_pkcs_1	Immunity	8.17E-04	WHL22.443760
rhogef10	GTPase	8.96E-04	WHL22.745588

Development • Supplementary information

ccp/lnb/7tm/gpcr	Adhesion	9.03E-04	WHL22.643837
sstr4l_1	GPCRRhodopsin,Nervous	1.04E-03	WHL22.235655
sra	GTPase	1.09E-03	WHL22.654882
gnbp1/2/3b	Immunity,Oogenesis	1.12E-03	WHL22.59278
ppp4c	Phosphatase	1.29E-03	WHL22.504357
slc30a3	Metabolism	1.44E-03	WHL22.578679
z197	Zinc finger	1.80E-03	WHL22.520690
syt15-2a, syt15-2b	Nervous	2.21E-03	WHL22.369954
cyp1l1	Defensome,Metabolism	2.22E-03	WHL22.641036
slc38a3	Metabolism	2.48E-03	WHL22.717191
agrin, agrin_1	Adhesion,Signaling	2.59E-03	WHL22.595204
coll	Adhesion,Biomineralization	2.70E-03	WHL22.271968
foxm, foxm_1	Nervous,TF	2.86E-03	WHL22.548104
ptk7	Kinase,Signaling	3.14E-03	WHL22.541169
mif1	Immunity	3.35E-03	WHL22.357870
lim1	Nervous,TF	3.44E-03	WHL22.720614
trk	Kinase,Nervous,Signaling	3.73E-03	WHL22.78748
thrombb1	Adhesion	3.73E-03	WHL22.723435
runt2	CellCycle,Immunity,TF	4.76E-03	WHL22.425096
slc5a12_7	Metabolism	5.51E-03	WHL22.665691
lct_12, lct_5, lct_7	Metabolism	5.91E-03	WHL22.238985
sgpl1	Metabolism	6.82E-03	WHL22.544363
gramarl2	Immunity,Metabolism	7.11E-03	WHL22.297648
kifc3l1	Cytoskeleton	7.60E-03	WHL22.421202
adss2, adssl1	Metabolism	8.50E-03	WHL22.568281
z215	Zinc finger	8.66E-03	WHL22.111895
slco4a1_10	Defensome,Metabolism	9.00E-03	WHL22.507273
rhogap8	GTPase	9.26E-03	WHL22.351944
adam/tsl3, vwde	Metalloprotease	9.69E-03	WHL22.581093
mad	Transcription factor	9.81E-03	WHL22.80541
err	Defensome,TF	1.04E-02	WHL22.91797
tecp4	Immunity	1.06E-02	WHL22.487599
racgap1	GTPase	1.10E-02	WHL22.716841
rigil6	Immunity	1.11E-02	WHL22.243301
twi	Transcription factor	1.19E-02	WHL22.118674
unk_42	Adhesion	1.26E-02	WHL22.476619
hypp_270	Adhesion	1.29E-02	WHL22.657921

lppr	Metabolism	1.32E-02	WHL22.417168
spr_1	Metabolism	1.40E-02	WHL22.109000
spr_2	Metabolism	1.40E-02	WHL22.554821
rhogef10	GTPase	1.44E-02	WHL22.745567
srcr45	Immunity	1.44E-02	WHL22.763590
abcb1a, abcb1_3	Defensome,Metabolism	1.44E-02	WHL22.426823
nudt9	Metabolism	1.49E-02	WHL22.393127
axndhc2h, unk_103, unk_10	Cytoskeleton	1.50E-02	WHL22.564539
cyce	CellCycle	1.52E-02	WHL22.279708
ace_2	Metalloprotease	1.54E-02	WHL22.106352
furin	Signaling	1.55E-02	WHL22.215692
birc1	Apoptosis	1.64E-02	WHL22.425609
spz12	Transcription factor, Zinc finger	1.74E-02	WHL22.446293
nacha2	CalciumToolkit,EggActivation,Nervous	1.74E-02	WHL22.446232
hypp_3079	Adhesion	1.76E-02	WHL22.541274
pdss2	Metabolism	1.96E-02	WHL22.513673
smocl	Adhesion	2.19E-02	WHL22.370629
slco5a1	Defensome,Metabolism	2.20E-02	WHL22.289793
slc7	Metabolism	2.26E-02	WHL22.282635
cts11	Immunity	2.29E-02	WHL22.57377
srcr105	Immunity	2.36E-02	WHL22.441763
cbpddl_1	Metalloprotease	2.40E-02	WHL22.69709
nkx2.5	Transcription factor	2.58E-02	WHL22.680396
novel	GPCRRhodopsin	2.58E-02	WHL22.335733
novel	GPCRRhodopsin,Nervous	2.71E-02	WHL22.60722
nacha2	CalciumToolkit,EggActivation,Nervous	3.03E-02	WHL22.446214
cyp2l55	Defensome,Metabolism	3.08E-02	WHL22.610334
prx1	Transcription factor	3.14E-02	WHL22.486796
srcr168	Immunity	3.29E-02	WHL22.744005
pou4f2	Nervous,TF	3.44E-02	WHL22.738139
tbx20	Transcription factor	3.73E-02	WHL22.730224
abca1	Defensome	4.11E-02	WHL22.89747
gpc35_2	Adhesion,Signaling	4.30E-02	WHL22.626708
hypp_70	Novel	7.41E-43	WHL22.288330
hypp_70	Novel	2.02E-21	WHL22.288327
chd1l	Novel	1.69E-14	WHL22.731753
parp3	Novel	5.80E-14	WHL22.735506

novel	Novel	7.04E-14	WHL22.252632
parp2l	Novel	5.07E-12	WHL22.658024
novel	Novel	5.91E-12	WHL22.36637
dnl3	Novel	2.80E-11	WHL22.305916
fn3/igf_25	Novel	2.47E-10	WHL22.583890
egf/hyalinl14, hypp_475	Novel	3.56E-10	WHL22.757746
nampt	Novel	1.43E-09	WHL22.521505
hypp_3046, setxl	Novel	3.02E-09	WHL22.640153
novel	Novel	3.15E-09	WHL22.361559
hypp_2295	Novel	7.89E-09	WHL22.615763
novel	Novel	9.36E-09	WHL22.522987
tmlhe	Novel	1.23E-08	WHL22.488438
novel	Novel	1.53E-08	WHL22.234491
hypp_3042	Novel	2.40E-08	WHL22.543310
novel	Novel	2.96E-08	WHL22.54608
fut4l_2	Novel	3.71E-08	WHL22.49779
hypp_2295	Novel	7.81E-08	WHL22.615757
alox12b	Novel	8.26E-08	WHL22.524047
c1ql_7, c1ql_8	Novel	9.33E-08	WHL22.208335
lrrc47	Novel	1.08E-07	WHL22.235937
novel	Novel	1.28E-07	WHL22.252500
mmp1/3l1	Novel	1.99E-07	WHL22.717538
trp53bp1	Novel	2.13E-07	WHL22.657244
novel	Novel	2.81E-07	WHL22.357502
ehd3	Novel	3.97E-07	WHL22.708867
novel	Novel	4.26E-07	WHL22.626829
slsp_1	Novel	6.26E-07	WHL22.550133
dnajhc4l	Novel	7.89E-07	WHL22.370870
novel	Novel	1.85E-06	WHL22.457258
polb	Novel	2.10E-06	WHL22.84737
novel	Novel	3.19E-06	WHL22.457236
helbl	Novel	4.06E-06	WHL22.179491
sacsl_10	Novel	5.70E-06	WHL22.358189
ythdc2_1	Novel	7.66E-06	WHL22.555297
hypp_2774	Novel	8.23E-06	WHL22.281790
hypp_191	Novel	8.67E-06	WHL22.68849
psat1, psat1_1	Novel	1.06E-05	WHL22.387632

novel	Novel	5.36E-05	WHL22.59127
polyq	Novel	6.10E-05	WHL22.720265
serrp14	Novel	6.48E-05	WHL22.52137
novel	Novel	9.01E-05	WHL22.252879
manrc1a	Novel	1.25E-04	WHL22.621623
mmp2l	Novel	1.52E-04	WHL22.717540
slc7a2	Novel	1.60E-04	WHL22.145534
gelsolin, gsn	Novel	1.77E-04	WHL22.323869
lama5lf	Novel	1.89E-04	WHL22.690203
novel	Novel	2.16E-04	WHL22.384077
hypp_1181	Novel	2.19E-04	WHL22.747257
sf3a2	Novel	2.33E-04	WHL22.668923
nphp4	Novel	2.92E-04	WHL22.235758
hypp_1465, parp1_1, unc44	Novel	2.96E-04	WHL22.319397
incenpl	Novel	3.30E-04	WHL22.605564
novel	Novel	3.69E-04	WHL22.595500
novel	Novel	3.70E-04	WHL22.50922
novel	Novel	3.92E-04	WHL22.173954
adarb1	Novel	3.99E-04	WHL22.626947
hypp_2090	Novel	4.00E-04	WHL22.536
hypp_1687	Novel	4.13E-04	WHL22.27354
armc9-2	Novel	4.32E-04	WHL22.216200
hypp_2436	Novel	4.38E-04	WHL22.576155
rnf32	Novel	4.42E-04	WHL22.737594
novel	Novel	4.45E-04	WHL22.633512
dur3	Novel	5.35E-04	WHL22.22923
novel	Novel	5.65E-04	WHL22.240863
novel	Novel	5.95E-04	WHL22.698932
novel	Novel	6.86E-04	WHL22.514703
so/gpcr	Novel	6.93E-04	WHL22.143613
gpld1	Novel	7.00E-04	WHL22.104053
bdnf	Novel	7.65E-04	WHL22.626989
efcab8l, wdr49_3	Novel	7.83E-04	WHL22.65843
novel	Novel	7.85E-04	WHL22.523233
ccp/sea	Novel	8.10E-04	WHL22.26434
akrl_1	Novel	8.43E-04	WHL22.394234
gluld1_5	Novel	8.76E-04	WHL22.739922

slc7a5	Novel	9.04E-04	WHL22.536576
notch1	Novel	9.62E-04	WHL22.667366
novel	Novel	1.01E-03	WHL22.345235
novel	Novel	1.03E-03	WHL22.573769
trabd	Novel	1.11E-03	WHL22.415934
novel	Novel	1.18E-03	WHL22.406641
hypp_1414	Novel	1.29E-03	WHL22.5156
nup50l	Novel	1.36E-03	WHL22.706357
pura	Novel	1.41E-03	WHL22.728994
tanc2_1	Novel	1.42E-03	WHL22.578943
hypp_1955	Novel	1.42E-03	WHL22.497035
novel	Novel	1.60E-03	WHL22.42160
novel	Novel	1.62E-03	WHL22.639306
novel	Novel	1.77E-03	WHL22.571084
novel	Novel	2.25E-03	WHL22.404194
novel	Novel	2.36E-03	WHL22.525353
kiaa1751l	Novel	2.72E-03	WHL22.437832
scpep1	Novel	2.73E-03	WHL22.367710
bbox1_1	Novel	2.78E-03	WHL22.711689
novel	Novel	2.80E-03	WHL22.230167
novel	Novel	2.92E-03	WHL22.358324
novel	Novel	3.05E-03	WHL22.508202
novel	Novel	3.13E-03	WHL22.555760
novel	Novel	3.19E-03	WHL22.556352
akirin2	Novel	3.30E-03	WHL22.587097
tep1-2	Novel	3.38E-03	WHL22.760326
novel	Novel	3.53E-03	WHL22.744681
novel	Novel	3.59E-03	WHL22.478999
hypp_18	Novel	3.62E-03	WHL22.351025
polr2c	Novel	3.71E-03	WHL22.442626
novel	Novel	3.73E-03	WHL22.757223
maob	Novel	3.74E-03	WHL22.237619
kif18al3	Novel	3.91E-03	WHL22.67000
hypp_721	Novel	4.04E-03	WHL22.452988
ggh	Novel	4.18E-03	WHL22.542904
hypp_2179, hypp_36	Novel	4.21E-03	WHL22.68199
sirt3	Novel	4.41E-03	WHL22.471515

hnrpul1, hnrpul1_1	Novel	4.45E-03	WHL22.378640
pex2	Novel	4.50E-03	WHL22.110786
novel	Novel	4.66E-03	WHL22.107138
pcbp3	Novel	4.77E-03	WHL22.515058
ser/thrpp2b/dirsigc	Novel	4.77E-03	WHL22.137367
novel	Novel	5.35E-03	WHL22.535857
e2f7	Novel	5.68E-03	WHL22.755786
novel	Novel	5.86E-03	WHL22.636230
novel	Novel	5.90E-03	WHL22.717167
dnajhc10	Novel	5.93E-03	WHL22.84690
novel	Novel	5.94E-03	WHL22.490171
novel	Novel	5.96E-03	WHL22.635052
ptcd1	Novel	6.03E-03	WHL22.334728
ctps2	Novel	6.36E-03	WHL22.62114
dpp9	Novel	6.44E-03	WHL22.171845
novel	Novel	6.50E-03	WHL22.228100
hypp_485	Novel	6.72E-03	WHL22.262720
novel	Novel	6.76E-03	WHL22.391930
snx4	Novel	7.05E-03	WHL22.191104
rpgr	Novel	7.06E-03	WHL22.452516
cub/zp_1	Novel	7.08E-03	WHL22.141701
novel	Novel	7.31E-03	WHL22.162976
hypp_811	Novel	7.41E-03	WHL22.314679
anxa7	Novel	7.53E-03	WHL22.296106
fam119a	Novel	7.62E-03	WHL22.658884
novel	Novel	7.86E-03	WHL22.138288
hypp_356	Novel	8.14E-03	WHL22.161798
pot1h	Novel	8.18E-03	WHL22.552801
ccdc135	Novel	8.48E-03	WHL22.493663
c17orf66l	Novel	8.55E-03	WHL22.293424
novel	Novel	8.73E-03	WHL22.17057
novel	Novel	8.76E-03	WHL22.656534
novel	Novel	9.00E-03	WHL22.567385
hypp_1229, susd2	Novel	9.02E-03	WHL22.187447
novel	Novel	9.02E-03	WHL22.68941
novel	Novel	9.30E-03	WHL22.409819
crhr2l_1	Novel	9.51E-03	WHL22.216477

herc1l	Novel	9.95E-03	WHL22.661898
novel	Novel	1.03E-02	WHL22.762181
novel	Novel	1.04E-02	WHL22.345205
hypp_2406	Novel	1.06E-02	WHL22.77253
nkapl	Novel	1.11E-02	WHL22.226324
mucl_5	Novel	1.11E-02	WHL22.563495
ccndbp1	Novel	1.13E-02	WHL22.341048
novel	Novel	1.14E-02	WHL22.466892
syf2h	Novel	1.14E-02	WHL22.72479
novel	Novel	1.21E-02	WHL22.77298
hypp_1502, hypp_2360	Novel	1.23E-02	WHL22.544157
novel	Novel	1.32E-02	WHL22.119801
novel	Novel	1.32E-02	WHL22.68290
novel	Novel	1.36E-02	WHL22.451259
novel	Novel	1.38E-02	WHL22.63051
a2mgl	Novel	1.40E-02	WHL22.487656
lrp6	Novel	1.42E-02	WHL22.120474
novel	Novel	1.42E-02	WHL22.282601
hypp_2812	Novel	1.42E-02	WHL22.27834
tmem127	Novel	1.44E-02	WHL22.385949
novel	Novel	1.46E-02	WHL22.388168
clca1_3	Novel	1.48E-02	WHL22.59523
novel	Novel	1.48E-02	WHL22.400623
cub/zp	Novel	1.54E-02	WHL22.663285
novel	Novel	1.54E-02	WHL22.142680
plxnb1l_3	Novel	1.54E-02	WHL22.194717
edd	Novel	1.56E-02	WHL22.243622
pofut2	Novel	1.58E-02	WHL22.553119
sea/ccp_1	Novel	1.59E-02	WHL22.69027
syt9l	Novel	1.61E-02	WHL22.342914
novel	Novel	1.66E-02	WHL22.44118
c2orf21l_2	Novel	1.72E-02	WHL22.332174
novel	Novel	1.74E-02	WHL22.72982
grm4l, grm8	Novel	1.75E-02	WHL22.566039
novel	Novel	1.77E-02	WHL22.556088
st8sia_2	Novel	1.78E-02	WHL22.457585
wdr51a	Novel	1.83E-02	WHL22.49843

novel	Novel	1.83E-02	WHL22.345874
treh, treh_1	Novel	1.84E-02	WHL22.617259
novel	Novel	1.88E-02	WHL22.467975
novel	Novel	1.90E-02	WHL22.363021
novel	Novel	1.92E-02	WHL22.642229
novel	Novel	1.94E-02	WHL22.615431
aox	Novel	1.99E-02	WHL22.258947
thoc4	Novel	2.06E-02	WHL22.364444
capn5, capn5l	Novel	2.16E-02	WHL22.295643
fbf1	Novel	2.16E-02	WHL22.31468
novel	Novel	2.19E-02	WHL22.119385
novel	Novel	2.28E-02	WHL22.402600
novel	Novel	2.36E-02	WHL22.704445
c9orf102l	Novel	2.42E-02	WHL22.79158
novel	Novel	2.45E-02	WHL22.348685
novel	Novel	2.45E-02	WHL22.600698
novel	Novel	2.45E-02	WHL22.498297
akrl	Novel	2.48E-02	WHL22.564328
novel	Novel	2.58E-02	WHL22.400974
novel	Novel	2.58E-02	WHL22.333226
novel	Novel	2.69E-02	WHL22.566812
chst11_9	Novel	2.71E-02	WHL22.478902
novel	Novel	2.72E-02	WHL22.585851
novel	Novel	2.79E-02	WHL22.768654
bud13	Novel	3.00E-02	WHL22.376040
hypp_388, hypp_66, pmfbp	Novel	3.03E-02	WHL22.365606
novel	Novel	3.08E-02	WHL22.160426
aspl, slsp_14	Novel	3.14E-02	WHL22.662201
cxorf22l, cxorf30l_1	Novel	3.26E-02	WHL22.425197
hypp_2485	Novel	3.30E-02	WHL22.104948
novel	Novel	3.36E-02	WHL22.336080
hypp_1015, hypp_908	Novel	3.37E-02	WHL22.221179
novel	Novel	3.43E-02	WHL22.514359
hsf5l	Novel	3.49E-02	WHL22.678800
reeler/egf/cub_1	Novel	3.55E-02	WHL22.382468
novel	Novel	3.77E-02	WHL22.365453
novel	Novel	3.96E-02	WHL22.621690

novel	Novel	4.14E-02	WHL22.54928
novel	Novel	4.48E-02	WHL22.310995
novel	Novel	4.68E-02	WHL22.318801

Supplemental Table 1E	Gene transcripts uniquely enriched within Veg1		
Gene	Functional Category	P-value	Identification #
eve	Transcription factor	6.65E-09	WHL22.442145
dscaml, dscaml_1, igcam	Adhesion	8.03E-08	WHL22.199355
sfe1	Oogenesis	2.74E-07	WHL22.106873
abcg2b	Defensome,Metabolism	4.72E-07	WHL22.642741
hadhsc	Metabolism	2.41E-06	WHL22.28327
mt1-4/mmpl7	Metalloprotease	4.39E-06	WHL22.312033
kmanl, rxfp1_1	GPCRRhodopsin,Adhesion	6.74E-06	WHL22.636279
gucy1b2, gucy1b2_5	Metabolism,Nervous	1.14E-05	WHL22.92113
cnga3_2	CalciumToolkit,EggActivation	1.43E-05	WHL22.92304
scavrbiiil, scavrbiiil_1	Immunity	1.45E-05	WHL22.36490
cecr1	Metabolism	2.24E-05	WHL22.225613
rdh1_1	Metabolism	2.30E-05	WHL22.214632
fn3/igf_32, fn3/igf_9	Adhesion	3.21E-05	WHL22.572040
neurmdnr	GPCRRhodopsin,Nervous	4.12E-05	WHL22.737431
macpfd1	Immunity	4.71E-05	WHL22.722785
adrb2_1, htr1b_1	GPCRRhodopsin	5.18E-05	WHL22.625476
galk2_1	Metabolism	6.13E-05	WHL22.265537
slc10a2_5	Metabolism	6.83E-05	WHL22.348669
cd38	CalciumToolkit,EggActivation	6.98E-05	WHL22.756176
opo	Defensome,EggActivation,Oogenesis	9.89E-05	WHL22.230227
tlr120	Immunity	1.14E-04	WHL22.676604
cca2da	CalciumToolkit,EggActivation	1.23E-04	WHL22.317750
stom_5	Metabolism	1.54E-04	WHL22.576658
hk1_2	Metabolism	2.05E-04	WHL22.576216
apc10	CellCycle	2.09E-04	WHL22.132817
gpr133l_2	Adhesion	2.34E-04	WHL22.689148
nlr173	Immunity	2.55E-04	WHL22.728233
hyr/egf/lnb/7tm/gpcr	Adhesion	3.62E-04	WHL22.230519
slco_1	Defensome,Metabolism	3.71E-04	WHL22.501536
cyp3l6	Defensome,Metabolism	4.10E-04	WHL22.534656
n_wasp_bp	Cytoskeleton	4.64E-04	WHL22.180622
hypp_2080	GPCRRhodopsin,Nervous	5.22E-04	WHL22.717062
novel	Defensome	5.73E-04	WHL22.487291
ris	GTPase	7.49E-04	WHL22.53701
fn3f_9	Adhesion	9.01E-04	WHL22.53011

trpc5_7	CalciumToolkit,EggActivation	9.01E-04	WHL22.582371
slco3a1_1	Defensome,Metabolism	9.01E-04	WHL22.673931
mftc	Metabolism	9.62E-04	WHL22.77638
srd5a2l	Metabolism	9.64E-04	WHL22.633190
atm_1, atm_2	CellCycle,Kinase	1.06E-03	WHL22.25282
lphn2l	Adhesion	1.12E-03	WHL22.193334
st8sia4_1, st8sia4_2	Metabolism	1.12E-03	WHL22.738095
acel_8	Metabolism,Metalloprotease	1.12E-03	WHL22.106388
ache_7, ache_9	Nervous	1.12E-03	WHL22.23305
aacy1	Metabolism,Metalloprotease	1.13E-03	WHL22.486005
hypp_1033, srcr100	Immunity,Adhesion	1.51E-03	WHL22.372632
z379	Zinc finger	1.66E-03	WHL22.316175
slc16a6l_11	Metabolism	1.72E-03	WHL22.359107
z308	Zinc finger	2.01E-03	WHL22.334412
glur6_1, grik1	CalciumToolkit	2.12E-03	WHL22.184130
chrm3l	GPCRRhodopsin	2.12E-03	WHL22.578634
slc16a6l_6	Metabolism	2.22E-03	WHL22.47726
pi3kp110	CalciumToolkit,Signaling	2.30E-03	WHL22.62907
eif2ba	EggActivation,TranslationFactor,ZNF	3.02E-03	WHL22.367428
sstr4l_2	GPCRRhodopsin	3.87E-03	WHL22.32177
phyh	Metabolism	4.43E-03	WHL22.377076
novel	Defensome	4.82E-03	WHL22.374833
lyplal1	Metabolism	4.82E-03	WHL22.422905
tmprss3_1	Metabolism	4.82E-03	WHL22.431002
selb, selb_1, selb_2	GTPase	5.40E-03	WHL22.768402
pcs_2	Defensome	5.40E-03	WHL22.256119
lyk5, papk	Kinase	5.58E-03	WHL22.735197
slc17	Metabolism	6.21E-03	WHL22.747311
rgn_2	CalciumToolkit	6.38E-03	WHL22.415265
atm_3	Kinase	6.38E-03	WHL22.25279
dhyd	Metabolism	6.86E-03	WHL22.687989
dynamnp50ph	Cytoskeleton	7.98E-03	WHL22.472075
sec14l2	Metabolism	8.13E-03	WHL22.664046
chat, vacht	Nervous,Metabolism	8.20E-03	WHL22.544208
siat7b	Metabolism	8.56E-03	WHL22.216573
siat7e	Metabolism	8.77E-03	WHL22.19179
orc1	DNAReplication	9.56E-03	WHL22.348359

z27	Zinc finger	9.96E-03	WHL22.129245
hnf1	Transcription factor	1.05E-02	WHL22.83266
ash3l	Transcription factor	1.17E-02	WHL22.523564
rasgrf1, rasgrf2	GTPase	1.28E-02	WHL22.480581
cyp17a1, cyp1r4	Defensome	1.41E-02	WHL22.614000
tf	Defensome,Oogenesis	1.48E-02	WHL22.652241
phgdh, phgdh_2	Metabolism	1.51E-02	WHL22.178838
z431	Zinc finger	1.52E-02	WHL22.146052
tk7	Kinase	1.54E-02	WHL22.491225
slc17a5_7	Metabolism	1.62E-02	WHL22.326605
slc24a3	CalciumToolkit	1.79E-02	WHL22.668748
z447	Zinc finger	1.79E-02	WHL22.78034
fdxr	Metabolism	1.82E-02	WHL22.264899
srcr159	Immunity	2.04E-02	WHL22.434989
ectdrn	Kinase,Signaling	2.07E-02	WHL22.587073
pi3kp110_2	CalciumToolkit,Signaling	2.28E-02	WHL22.62937
orct_1	Defensome	2.29E-02	WHL22.69926
sorl1l, tmprss6	Metabolism	2.71E-02	WHL22.208581
bhmt_1	Metabolism	3.05E-02	WHL22.445251
slco4c1, slco4c1_1	Defensome,Metabolism	3.07E-02	WHL22.143217
crot_2	Metabolism	3.10E-02	WHL22.426109
myd88	Immunity	3.26E-02	WHL22.224767
rit1	GTPase	4.24E-02	WHL22.195879
mucd	Novel	2.07E-16	WHL22.47503
amidl_2	Novel	2.36E-15	WHL22.630200
amds_3	Novel	3.90E-15	WHL22.630178
clect_112	Novel	3.54E-10	WHL22.580606
novel	Novel	7.37E-10	WHL22.246251
novel	Novel	1.48E-09	WHL22.522365
hypp_1592	Novel	7.01E-09	WHL22.247480
novel	Novel	4.38E-08	WHL22.283064
novel	Novel	4.49E-08	WHL22.448577
novel	Novel	5.75E-08	WHL22.129368
novel	Novel	6.01E-08	WHL22.158456
pnlip_10	Novel	7.22E-08	WHL22.555949
novel	Novel	2.08E-07	WHL22.236424
novel	Novel	2.71E-07	WHL22.163765

novel	Novel	4.85E-07	WHL22.522368
slc14, slc14_1	Novel	6.10E-07	WHL22.93800
novel	Novel	7.96E-07	WHL22.436142
novel	Novel	1.11E-06	WHL22.677860
hypp_1077	Novel	1.17E-06	WHL22.446356
zanl_2	Novel	1.41E-06	WHL22.461391
novel	Novel	2.43E-06	WHL22.125362
elft	Novel	3.70E-06	WHL22.600551
novel	Novel	4.41E-06	WHL22.164767
novel	Novel	5.12E-06	WHL22.697401
hypp_1743, hypp_1744	Novel	6.37E-06	WHL22.363039
c20orf152l_1	Novel	9.43E-06	WHL22.175424
novel	Novel	1.16E-05	WHL22.81664
novel	Novel	1.36E-05	WHL22.499574
novel	Novel	1.60E-05	WHL22.685586
hypp_1138	Novel	1.86E-05	WHL22.585972
notch2_12	Novel	2.00E-05	WHL22.249031
novel	Novel	2.00E-05	WHL22.360310
dtwd1, dtwd1_1	Novel	2.05E-05	WHL22.589802
ddx59_1	Novel	2.14E-05	WHL22.218454
novel	Novel	2.41E-05	WHL22.355401
udg	Novel	2.94E-05	WHL22.53517
novel	Novel	3.21E-05	WHL22.608249
idua	Novel	3.38E-05	WHL22.134892
novel	Novel	3.48E-05	WHL22.263373
choldhl	Novel	3.51E-05	WHL22.508782
novel	Novel	3.54E-05	WHL22.20032
novel	Novel	4.12E-05	WHL22.124698
redt-aldo/keta	Novel	4.12E-05	WHL22.325529
znfx1-16, znfx1-18, znfx1_6	Novel	4.69E-05	WHL22.483900
tmem144	Novel	5.05E-05	WHL22.17476
novel	Novel	5.18E-05	WHL22.705188
novel	Novel	5.36E-05	WHL22.130263
novel	Novel	5.36E-05	WHL22.292801
myo1b	Novel	5.86E-05	WHL22.422980
gnmt_3	Novel	6.13E-05	WHL22.231889
mylkl	Novel	6.31E-05	WHL22.23804

novel	Novel	6.31E-05	WHL22.142993
hypp_1231	Novel	6.33E-05	WHL22.51988
novel	Novel	7.04E-05	WHL22.525132
agrnl	Novel	7.26E-05	WHL22.218459
act_1	Novel	7.50E-05	WHL22.350285
veb4	Novel	7.50E-05	WHL22.506142
pdia5	Novel	7.87E-05	WHL22.630176
novel	Novel	8.85E-05	WHL22.647933
novel	Novel	9.36E-05	WHL22.435066
novel	Novel	9.36E-05	WHL22.722146
novel	Novel	9.36E-05	WHL22.418136
c1orf124l	Novel	9.76E-05	WHL22.535888
brrn1	Novel	1.06E-04	WHL22.438400
novel	Novel	1.14E-04	WHL22.79723
novel	Novel	1.14E-04	WHL22.623450
novel	Novel	1.26E-04	WHL22.555967
hypp_537	Novel	1.28E-04	WHL22.700861
novel	Novel	1.36E-04	WHL22.419718
novel	Novel	1.36E-04	WHL22.106094
rbbp5	Novel	1.36E-04	WHL22.754914
hypp_1929	Novel	1.42E-04	WHL22.22407
novel	Novel	1.47E-04	WHL22.712423
novel	Novel	1.48E-04	WHL22.147275
novel	Novel	1.48E-04	WHL22.367778
pigw	Novel	1.49E-04	WHL22.402132
gdap1l	Novel	1.73E-04	WHL22.142378
suv420h1l	Novel	1.73E-04	WHL22.412199
novel	Novel	1.81E-04	WHL22.520054
cuzd1, ly/cub/sr/zp	Novel	2.04E-04	WHL22.143059
novel	Novel	2.04E-04	WHL22.330214
novel	Novel	2.04E-04	WHL22.161076
novel	Novel	2.04E-04	WHL22.552578
mpg	Novel	2.17E-04	WHL22.537641
novel	Novel	2.17E-04	WHL22.512169
novel	Novel	2.29E-04	WHL22.540227
mib_8	Novel	2.30E-04	WHL22.20701
novel	Novel	2.36E-04	WHL22.497993

hypp_1363	Novel	2.41E-04	WHL22.579061
novel	Novel	2.41E-04	WHL22.721969
galk2	Novel	2.86E-04	WHL22.607252
novel	Novel	2.86E-04	WHL22.72640
novel	Novel	3.00E-04	WHL22.261974
p4html	Novel	3.01E-04	WHL22.157159
novel	Novel	3.06E-04	WHL22.701106
novel	Novel	3.24E-04	WHL22.369483
myo1b	Novel	3.41E-04	WHL22.422989
c6orf192l	Novel	3.41E-04	WHL22.3943
hypp_1289	Novel	3.41E-04	WHL22.8561
novel	Novel	3.59E-04	WHL22.633722
novel	Novel	3.79E-04	WHL22.642327
hypp_1178	Novel	3.99E-04	WHL22.551404
aifm2	Novel	4.10E-04	WHL22.23539
novel	Novel	4.10E-04	WHL22.65581
novel	Novel	4.10E-04	WHL22.568446
hypp_1656	Novel	4.22E-04	WHL22.455608
unk_6	Novel	4.24E-04	WHL22.47693
polypl_4	Novel	4.45E-04	WHL22.230844
pipox_1	Novel	4.54E-04	WHL22.88333
hypp_513	Novel	4.64E-04	WHL22.566307
hypp_854	Novel	4.67E-04	WHL22.399505
novel	Novel	4.86E-04	WHL22.481437
hypp_272	Novel	4.96E-04	WHL22.566803
cub/egf	Novel	4.98E-04	WHL22.316785
novel	Novel	5.07E-04	WHL22.479525
clect_112	Novel	5.12E-04	WHL22.580609
stac3	Novel	5.12E-04	WHL22.646588
wscd1	Novel	5.54E-04	WHL22.731197
dak_3	Novel	6.00E-04	WHL22.265243
hypp_2913	Novel	6.00E-04	WHL22.278346
tin/ag	Novel	6.00E-04	WHL22.172784
tm2d2_1	Novel	6.00E-04	WHL22.670237
cyp46l7	Novel	6.20E-04	WHL22.110354
bbox1_7	Novel	6.21E-04	WHL22.734267
novel	Novel	6.21E-04	WHL22.511856

novel	Novel	7.20E-04	WHL22.418802
novel	Novel	7.25E-04	WHL22.592840
arh/ldl	Novel	7.33E-04	WHL22.108974
naglu_2	Novel	7.43E-04	WHL22.572323
slspl	Novel	7.49E-04	WHL22.325703
novel	Novel	7.83E-04	WHL22.159853
cbwd3	Novel	8.04E-04	WHL22.42051
novel	Novel	8.27E-04	WHL22.374860
scai	Novel	8.31E-04	WHL22.609083
usp20l	Novel	8.63E-04	WHL22.479869
tert	Novel	8.83E-04	WHL22.694332
lyz	Novel	9.01E-04	WHL22.685592
novel	Novel	9.01E-04	WHL22.749719
novel	Novel	9.01E-04	WHL22.320423
prps1_1	Novel	9.01E-04	WHL22.297332
trit1l	Novel	9.15E-04	WHL22.58483
hypp_600	Novel	9.97E-04	WHL22.55311
pus3	Novel	1.04E-03	WHL22.296469
adsda	Novel	1.05E-03	WHL22.544293
novel	Novel	1.12E-03	WHL22.487702
slspl	Novel	1.12E-03	WHL22.325697
endrvt100	Novel	1.12E-03	WHL22.523618
novel	Novel	1.18E-03	WHL22.765852
novel	Novel	1.28E-03	WHL22.579814
novel	Novel	1.28E-03	WHL22.503339
wbscr27	Novel	1.31E-03	WHL22.420317
novel	Novel	1.34E-03	WHL22.487676
p4html	Novel	1.39E-03	WHL22.157153
hypp_1661	Novel	1.39E-03	WHL22.616561
novel	Novel	1.39E-03	WHL22.316234
novel	Novel	1.39E-03	WHL22.114344
susd2-4	Novel	1.39E-03	WHL22.273060
c5orf44	Novel	1.45E-03	WHL22.315305
novel	Novel	1.46E-03	WHL22.618402
sec14l_2	Novel	1.46E-03	WHL22.110710
novel	Novel	1.51E-03	WHL22.130939
pigw_1	Novel	1.55E-03	WHL22.581594

novel	Novel	1.63E-03	WHL22.527120
hypp_1555	Novel	1.66E-03	WHL22.35381
vwc	Novel	1.75E-03	WHL22.674165
ilf2	Novel	1.75E-03	WHL22.553591
novel	Novel	1.75E-03	WHL22.756412
novel	Novel	1.90E-03	WHL22.451823
novel	Novel	1.90E-03	WHL22.659682
novel	Novel	1.92E-03	WHL22.223320
hypp_9771	Novel	1.93E-03	WHL22.458031
hypp_259	Novel	1.97E-03	WHL22.749044
hypp_2400	Novel	2.10E-03	WHL22.373721
novel	Novel	2.10E-03	WHL22.207186
novel	Novel	2.14E-03	WHL22.705122
fam167a	Novel	2.18E-03	WHL22.13601
hypp_1162	Novel	2.18E-03	WHL22.607361
lyrm5	Novel	2.19E-03	WHL22.117384
novel	Novel	2.22E-03	WHL22.451252
novel	Novel	2.22E-03	WHL22.420621
novel	Novel	2.22E-03	WHL22.389596
wdr79	Novel	2.22E-03	WHL22.308928
novel	Novel	2.50E-03	WHL22.603568
novel	Novel	2.51E-03	WHL22.124709
novel	Novel	2.52E-03	WHL22.294939
ids_3, ids_8	Novel	2.52E-03	WHL22.172853
echn3	Novel	2.60E-03	WHL22.191686
hypp_987	Novel	2.62E-03	WHL22.167416
fam20b	Novel	2.73E-03	WHL22.670817
bbs4	Novel	2.84E-03	WHL22.732443
novel	Novel	2.84E-03	WHL22.73869
novel	Novel	2.84E-03	WHL22.132987
novel	Novel	2.84E-03	WHL22.190958
novel	Novel	2.84E-03	WHL22.752127
novel	Novel	2.84E-03	WHL22.643683
novel	Novel	2.84E-03	WHL22.287400
novel	Novel	2.84E-03	WHL22.450420
hypp_2086	Novel	3.09E-03	WHL22.693020
novel	Novel	3.09E-03	WHL22.499200

novel	Novel	3.09E-03	WHL22.137634
ndufa11	Novel	3.27E-03	WHL22.6583
c10orf118l	Novel	3.28E-03	WHL22.437409
novel	Novel	3.65E-03	WHL22.631831
polr3c	Novel	3.92E-03	WHL22.488354
2ogfeii	Novel	3.97E-03	WHL22.38348
hypp_717	Novel	4.08E-03	WHL22.280141
thtpa	Novel	4.16E-03	WHL22.369871
novel	Novel	4.34E-03	WHL22.487741
ship	Novel	4.37E-03	WHL22.457785
unc44_184	Novel	4.43E-03	WHL22.263438
novel	Novel	4.43E-03	WHL22.24574
novel	Novel	4.57E-03	WHL22.608544
fads1	Novel	4.57E-03	WHL22.52203
hypp_2262	Novel	4.57E-03	WHL22.728211
novel	Novel	4.57E-03	WHL22.180300
novel	Novel	4.57E-03	WHL22.380387
arpc1a	Novel	4.82E-03	WHL22.468324
novel	Novel	4.82E-03	WHL22.86565
novel	Novel	4.82E-03	WHL22.660893
novel	Novel	4.82E-03	WHL22.733553
novel	Novel	4.86E-03	WHL22.333975
mtif3l	Novel	4.90E-03	WHL22.738050
hemk1	Novel	5.35E-03	WHL22.533478
novel	Novel	5.35E-03	WHL22.531302
novel	Novel	5.40E-03	WHL22.593200
smicl_1	Novel	5.63E-03	WHL22.517191
pdcl3	Novel	5.90E-03	WHL22.742000
ngrnl	Novel	5.97E-03	WHL22.287040
lars2, lars2_1	Novel	6.30E-03	WHL22.82957
novel	Novel	6.30E-03	WHL22.683545
piga	Novel	6.30E-03	WHL22.496885
novel	Novel	6.34E-03	WHL22.299107
akrl_2	Novel	6.38E-03	WHL22.564274
chst8l	Novel	6.38E-03	WHL22.243692
clcn2	Novel	6.38E-03	WHL22.9839
clect_61	Novel	6.38E-03	WHL22.24025

novel	Novel	6.38E-03	WHL22.143910
novel	Novel	6.38E-03	WHL22.347132
novel	Novel	6.38E-03	WHL22.107394
novel	Novel	6.38E-03	WHL22.415137
novel	Novel	6.38E-03	WHL22.368101
sirt5	Novel	6.38E-03	WHL22.329177
trappc3	Novel	6.45E-03	WHL22.621030
mitd1	Novel	6.77E-03	WHL22.246004
novel	Novel	6.79E-03	WHL22.724130
novel	Novel	7.43E-03	WHL22.433669
bxdc1_1	Novel	7.72E-03	WHL22.586550
kcna	Novel	8.14E-03	WHL22.76994
novel	Novel	8.38E-03	WHL22.665898
asp_8	Novel	8.56E-03	WHL22.117491
fam55c_5	Novel	8.56E-03	WHL22.618366
hnmtl_2	Novel	8.56E-03	WHL22.556422
hypp_736	Novel	8.56E-03	WHL22.413543
novel	Novel	8.56E-03	WHL22.518887
pign, pign_1	Novel	8.56E-03	WHL22.657678
tsp1_2	Novel	8.56E-03	WHL22.114983
novel	Novel	8.83E-03	WHL22.398627
cathepsinl	Novel	9.12E-03	WHL22.741594
epb41l4a	Novel	1.01E-02	WHL22.322978
novel	Novel	1.01E-02	WHL22.733136
hypp_1674	Novel	1.02E-02	WHL22.744693
mtif2l1, mtif2l2	Novel	1.02E-02	WHL22.493260
novel	Novel	1.05E-02	WHL22.704958
novel	Novel	1.05E-02	WHL22.706909
novel	Novel	1.05E-02	WHL22.500574
pcid2	Novel	1.06E-02	WHL22.508067
pil6l	Novel	1.07E-02	WHL22.209615
trappc10_1	Novel	1.14E-02	WHL22.582122
novel	Novel	1.17E-02	WHL22.382193
hypp_1242	Novel	1.18E-02	WHL22.69534
hypp_1782	Novel	1.18E-02	WHL22.316634
c3orf19	Novel	1.21E-02	WHL22.327117
commd6	Novel	1.21E-02	WHL22.113163

novel	Novel	1.21E-02	WHL22.642523
novel	Novel	1.22E-02	WHL22.226516
inpp5d, inpp5dl	Novel	1.28E-02	WHL22.676498
novel	Novel	1.28E-02	WHL22.682724
novel	Novel	1.29E-02	WHL22.447813
mrpl15	Novel	1.35E-02	WHL22.116486
act, actb	Novel	1.35E-02	WHL22.349195
impf	Novel	1.37E-02	WHL22.200876
novel	Novel	1.39E-02	WHL22.294369
b3galtnt2	Novel	1.44E-02	WHL22.362419
fbxw9	Novel	1.47E-02	WHL22.253846
hpse	Novel	1.49E-02	WHL22.535878
novel	Novel	1.50E-02	WHL22.661716
mamdc4-13	Novel	1.52E-02	WHL22.327304
mrps16l_1	Novel	1.52E-02	WHL22.351827
novel	Novel	1.52E-02	WHL22.140797
novel	Novel	1.52E-02	WHL22.762187
fancgl	Novel	1.62E-02	WHL22.747472
fdps	Novel	1.62E-02	WHL22.84233
hypp_2157	Novel	1.62E-02	WHL22.145698
novel	Novel	1.62E-02	WHL22.296836
novel	Novel	1.62E-02	WHL22.455735
novel	Novel	1.62E-02	WHL22.44640
novel	Novel	1.62E-02	WHL22.320268
tm2d2	Novel	1.62E-02	WHL22.417569
dedd	Novel	1.64E-02	WHL22.356741
gpr112l_5	Novel	1.67E-02	WHL22.7479
hypp_1450	Novel	1.80E-02	WHL22.572386
novel	Novel	1.83E-02	WHL22.695208
timm9	Novel	1.83E-02	WHL22.442366
wdr3	Novel	1.83E-02	WHL22.425458
hypp_1343	Novel	1.84E-02	WHL22.286421
dpy19l1	Novel	2.01E-02	WHL22.5237
novel	Novel	2.04E-02	WHL22.246060
novel	Novel	2.07E-02	WHL22.677495
novel	Novel	2.09E-02	WHL22.270463
hypp_3010	Novel	2.10E-02	WHL22.177408

novel	Novel	2.17E-02	WHL22.410201
varsib(fragments)	Novel	2.23E-02	WHL22.763228
kctd21	Novel	2.23E-02	WHL22.171348
ache_18	Novel	2.28E-02	WHL22.589238
novel	Novel	2.28E-02	WHL22.49226
novel	Novel	2.28E-02	WHL22.374851
novel	Novel	2.28E-02	WHL22.621701
novel	Novel	2.28E-02	WHL22.602924
novel	Novel	2.28E-02	WHL22.496427
slc16a7l_2	Novel	2.28E-02	WHL22.587457
novel	Novel	2.31E-02	WHL22.303063
novel	Novel	2.31E-02	WHL22.465788
wrnl_2	Novel	2.43E-02	WHL22.263402
c1ql_5	Novel	2.46E-02	WHL22.244527
novel	Novel	2.51E-02	WHL22.205815
novel	Novel	2.67E-02	WHL22.20866
novel	Novel	2.71E-02	WHL22.77201
novel	Novel	2.72E-02	WHL22.573980
exoc4	Novel	2.73E-02	WHL22.221093
scdfr2l_1	Novel	2.73E-02	WHL22.29584
timp3	Novel	2.82E-02	WHL22.22250
novel	Novel	2.88E-02	WHL22.343869
tbrg1	Novel	2.97E-02	WHL22.373316
mrpl24	Novel	3.03E-02	WHL22.508016
wdr79	Novel	3.22E-02	WHL22.308933
ptcd1l	Novel	3.22E-02	WHL22.600671
novel	Novel	3.25E-02	WHL22.447703
novel	Novel	3.28E-02	WHL22.627063
novel	Novel	3.28E-02	WHL22.408565
novel	Novel	3.28E-02	WHL22.393658
oxch_3	Novel	3.28E-02	WHL22.552569
novel	Novel	3.34E-02	WHL22.304647
ttrl	Novel	3.34E-02	WHL22.679950
mapko1	Novel	3.37E-02	WHL22.33567
novel	Novel	3.37E-02	WHL22.694285
rnf207	Novel	3.56E-02	WHL22.174498
ttll9	Novel	3.56E-02	WHL22.535846

novel	Novel	3.68E-02	WHL22.320265
pak1ip1	Novel	3.73E-02	WHL22.665154
novel	Novel	3.85E-02	WHL22.252242
hypp_2281, hypp_2282, me	Novel	3.90E-02	WHL22.347032
hypp_2698	Novel	4.07E-02	WHL22.435971
novel	Novel	4.18E-02	WHL22.188749
rwdd1	Novel	4.38E-02	WHL22.548966
ecd	Novel	4.47E-02	WHL22.468421
deth1	Novel	4.52E-02	WHL22.321971
terfal	Novel	4.52E-02	WHL22.242370
novel	Novel	4.76E-02	WHL22.758306
appbp2_1	Novel	4.82E-02	WHL22.480837
novel	Novel	4.82E-02	WHL22.442656
dcdsh_2	Novel	4.83E-02	WHL22.43827

Supplemental Table 2	Universally Expressed Transcripts	A		B		C		D		E		F		
Gene	Functional Category	GFP +	Control	GFP +	Control	GFP +	Control	GFP +	Control	GFP +	Control	GFP +	Control	Identification #
tcp1, wap/ty/egf	Immunity	2171	1263	2862	948	3308	2671	5068	1659	5346	3468	2028	1729	WHL22.190274
slc4a2_1, slc4a3	Metabolism	916	308	2906	1034	1167	3600	3046	2195	5124	3125	1799	1891	WHL22.49246
spalt	Transcription factor, Zinc finger	367	711	736	381	3319	1648	1384	1494	2762	1967	1191	1419	WHL22.150131
hdlbp	Metabolism	1465	552	226	535	2402	818	1119	1337	1370	1548	720	703	WHL22.338109
brd, brd2	Kinase	279	350	972	363	1290	1689	715	916	1047	873	2205	2051	WHL22.673823
pum	EggActivation,GermLineDeterminant	1188	429	1047	512	753	829	938	936	1133	1091	1523	1160	WHL22.745377
nfe2	Defensome,Immunity,Nervous,TF	1178	651	467	205	660	701	587	487	576	622	809	549	WHL22.621478
smc1l1, smc1l1_1	CellCycle,Oogenesis	1183	438	703	316	469	633	525	635	641	444	764	732	WHL22.529863
moesin, radxh	Cytoskeleton	454	471	869	372	267	731	590	611	694	536	622	652	WHL22.373529
dag1	Adhesion	386	401	412	293	237	607	886	911	884	705	531	550	WHL22.372217
ctnnb	Signaling	323	363	439	283	432	530	911	576	1229	761	421	354	WHL22.589082
hsp40d	Defensome	426	151	116	136	826	589	315	299	345	333	1286	1012	WHL22.81793
rhoa	GTPase	351	220	158	132	838	1211	218	169	234	243	1246	810	WHL22.583759
eif1	TranslationFactor	425	164	302	152	1257	591	483	340	380	264	846	446	WHL22.45712
gi, gi[cterm]	GTPase	892	299	77	167	896	624	380	353	369	342	606	420	WHL22.762062
etif4bl	TranslationFactor	111	131	178	112	848	710	297	253	219	163	1056	1038	WHL22.225876
arf1	GTPase	201	179	166	68	672	429	324	193	326	215	604	628	WHL22.91473
rab8	GTPase	215	81	64	31	1335	534	80	62	146	100	744	523	WHL22.561690
cycd	CellCycle	623	220	268	113	212	212	472	394	444	417	127	185	WHL22.727579
pmca	CalciumToolkit,EggActivation,Metabolism	361	195	101	112	789	463	231	235	234	225	368	308	WHL22.769600
hypp_766, unk_85	Metabolism	342	209	52	117	641	368	293	275	362	356	191	379	WHL22.553940
z75	Zinc finger	230	201	205	111	522	384	353	222	214	201	329	421	WHL22.173514
bmpr2, bmpr2_1	Kinase,Signaling	454	217	338	126	615	350	233	216	174	236	172	238	WHL22.248672
cd109l, cd109l_2	Immunity	110	182	148	172	196	214	510	368	503	413	273	251	WHL22.675133
tropmy1	Cytoskeleton	198	142	81	88	231	340	292	341	351	378	413	287	WHL22.483284
hypp_2193, mib1_1, satb1	Transcription factor	162	218	141	122	604	191	288	516	315	261	184	133	WHL22.589656
rad21	Oogenesis	346	125	102	121	369	183	233	285	504	256	368	230	WHL22.177493
fra2	Immunity,Signaling,TF	502	285	105	75	40	202	452	194	402	389	258	179	WHL22.538597
abcf2	Defensome	145	131	59	112	345	216	349	252	386	342	370	353	WHL22.200752
slc25a3_2	Metabolism	135	124	48	130	238	142	545	381	543	416	216	137	WHL22.624240
z156	Zinc finger	97	145	116	94	556	300	277	245	273	325	219	184	WHL22.33721
hypp_936, mprot1l	Metalloprotease	255	97	110	116	254	471	231	215	201	221	260	311	WHL22.660166
slc7a6_2, slc7a6_7, slc7a7	Metabolism	107	162	237	112	417	255	172	310	238	241	183	251	WHL22.384271
syt14	Nervous	413	169	219	118	93	191	314	392	198	217	114	125	WHL22.108947
cyct	CellCycle	165	171	267	86	329	190	116	284	265	297	157	182	WHL22.168610
erf3	GTPase,TranslationFactor	130	146	98	97	248	291	325	217	180	213	268	278	WHL22.228287
mst	Kinase	221	124	174	62	461	187	193	128	166	215	301	136	WHL22.78158
id	Immunity,TF	246	80	101	69	132	303	158	191	264	269	153	259	WHL22.467043
xbp1	Immunity,TF	380	150	164	93	41	90	191	273	306	362	58	98	WHL22.490709
pak7, pak7_1	Kinase	49	136	204	104	199	206	191	220	183	193	222	227	WHL22.208401
ran	GTPase	60	127	66	63	202	206	163	248	159	202	349	256	WHL22.446899
z64	Signaling,ZNF	76	207	49	90	340	93	264	268	257	297	78	71	WHL22.732653
rab11	GTPase	214	116	32	68	432	276	113	83	55	78	247	338	WHL22.652208
pum	EggActivation,GermLineDeterminant	265	157	116	70	113	102	168	186	294	282	80	163	WHL22.746215
centd, hypp_3110	GTPase	187	260	24	68	154	133	247	194	225	242	99	94	WHL22.393414
zir1, zir2	GTPase	132	138	67	48	376	85	255	212	179	186	124	120	WHL22.579690
eif5b_1, eif5bl, tif2l	GTPase,TranslationFactor	133	89	78	39	185	275	108	85	103	122	315	378	WHL22.554715
ptpr1, ptprg/z1	Phosphatase,Immunity	273	122	81	68	320	137	105	198	166	218	117	78	WHL22.552532
seawi	GermLineDeterminant	146	173	126	87	173	101	100	175	153	150	276	194	WHL22.338712
dock180, dock180_1	GTPase	348	158	47	54	145	142	174	225	180	198	58	83	WHL22.695305
slka, stk10	Kinase	181	175	227	93	83	128	142	134	173	130	188	137	WHL22.684862
z154	Zinc finger	58	66	47	40	497	220	81	67	88	64	246	299	WHL22.682998
z145	Defensome,ZNF	193	87	22	36	211	302	102	75	148	119	227	231	WHL22.719692
smekh1	Metabolism	73	43	38	43	138	169	121	127	157	106	466	266	WHL22.12679
betadi	Adhesion	112	133	201	86	115	68	260	237	191	129	122	56	WHL22.197596
muskl	Adhesion,Kinase,Signaling	107	160	200	88	51	143	249	186	163	182	64	96	WHL22.580001
gmps	Metabolism	37	66	124	65	87	176	304	126	144	123	240	172	WHL22.767555
skp1	CellCycle	56	31	103	45	229	102	136	140	147	165	311	167	WHL22.139582
z220	Zinc finger	73	35	29	35	244	186	121	121	154	124	228	236	WHL22.362083
hh3.3	Histone	227	137	79	58	26	40	230	215	249	205	31	65	WHL22.568244
smad6/7, smad6/7_1	Signaling,TF	105	252	323	106	28	38	153	210	123	145	23	21	WHL22.579194
eif2g	GTPase,TranslationFactor	288	95	215	76	86	87	103	155	97	153	87	71	WHL22.669828
foxn1/4	Transcription factor	37	104	107	83	147	176	182	155	119	151	77	106	WHL22.604594
srp54	GTPase	112	67	21	36	559	136	32	67	59	58	128	153	WHL22.668850
mrck	Kinase	71	175	42	66	70	51	180	201	189	215	62	52	WHL22.1863
abca3, abca3_1	Defensome	71	121	25	66	78	87	228	171	201	159	54	104	WHL22.741880
lhh2ba	Histone	84	45	122	60	104	182	95	86	111	144	107	185	WHL22.273077
hspd1	Defensome	319	117	92	71	93	101	115	74	82	122	61	66	WHL22.192596
abcc9d, abcc9j	Defensome,Metabolism	132	58	28	51	155	78	237	82	129	182	57	81	WHL22.581027
wee1, wee1_1	CellCycle,Kinase	93	63	58	54	28	100	223	197	168	118	78	84	WHL22.139065
dnm2	GTPase	155	53	66	40	208	127	85	62	87	72	169	114	WHL22.721840
dnm1, dnm2	GTPase	66	74	74	36	252	111	143	73	84	85	107	126	WHL22.721874
pola, pola1	DNAReplication	226	119	152	51	15	119	56	143	74	81	67	84	WHL22.676756
alk3-6	Kinase,Signaling	48	71	47	44	106	114	108	96	93	113	179	154	WHL22.531157
eb1ph	Cytoskeleton	49	48	56	30	270	175	95	56	41	52	162	115	WHL22.25898
ck1d	Kinase,Signaling	22	55	19	34	182	130	136	137	137	111	57	95	WHL22.557027
cyc1, cyc1_1	Metabolism	66	111	104	84	51	94	141	122	101	105	68	61	WHL22.99960
lamg1f	Adhesion	161	55	50	48	64	98	95	91	80	77	87	104	WHL22.711452
ampd	Metabolism	38	35	11	21	278	114	40	28	69	60	159	126	WHL22.391236
cts5	Immunity	29	21	118	43	94	95	105	80	162	93	76	35	WHL22.323131
zizimin1	GTPase	151	66	40	23	66	53	110	107	100	103	80	44	WHL22.486240
z257	Zinc finger	73	44	84	42	101	70	46	114	64	56	135	112	WHL22.744369
kif4_1	Cytoskeleton	23	61	64	46	41	118	83	89	98	81	72	105	WHL22.314263
c3-2	Immunity	35	55	91	30	30	42	198	128	104	94	23	49	WHL22.668496
flj46688l2, hypp_1631	GTPase	49	90	43	43	5	67	123	120	112	121	34	57	WHL22.3012
hypp_165, swift	Signaling	31	35	24	32	102	72	95	140	77	59	52	111	WHL22.229272
kifc1, kifc1l	Cytoskeleton	39	52	30	55	26	82	65	141	108	92	27	60	WHL22.525887

khc	Cytoskeleton	93	57	49	30	64	57	95	80	71	85	50	45	WHL22.471932
agxt2l, agxt2l1	Metabolism	53	35	51	40	78	50	109	65	87	87	64	53	WHL22.761131
mthfd1	Metabolism	102	93	84	33	14	39	141	64	70	49	28	41	WHL22.594625
z129, z144	Zinc finger	67	41	41	22	223	40	46	42	27	58	53	81	WHL22.205291
aof2	Metabolism	39	91	103	35	22	56	108	98	63	61	27	36	WHL22.719655
tyms	Metabolism	51	24	25	16	197	48	49	75	56	55	86	56	WHL22.28181
eif3a	TranslationFactor	98	38	10	32	132	71	52	83	35	56	43	81	WHL22.626908
z28	Zinc finger	23	15	19	11	324	66	40	46	27	36	62	60	WHL22.594922
slit1(c-terminus)	Adhesion	93	47	43	26	134	80	22	16	32	29	97	97	WHL22.219243
raf	EggActivation,Kinase	52	23	7	17	93	136	65	56	40	41	57	127	WHL22.200072
contactin2, igf_19	Adhesion,Cytoskeleton	40	65	19	29	45	57	104	87	56	75	55	80	WHL22.199353
ppib	Biomineralization	112	40	22	41	52	31	82	71	73	68	53	48	WHL22.556199
ldb2	Transcription factor	36	23	6	19	215	64	57	30	48	66	56	64	WHL22.386521
lycat_2	Metabolism	78	39	67	21	47	70	32	28	75	57	87	63	WHL22.680318
pkg2	Kinase	78	67	11	29	94	16	93	86	70	59	13	14	WHL22.28224
g12	GTPase	48	45	22	28	15	52	67	70	71	62	76	55	WHL22.442689
ark2	CellCycle,EggActivation	21	13	11	34	22	77	84	58	62	72	73	72	WHL22.457797
z150	Zinc finger	17	15	24	25	107	102	29	38	44	39	47	95	WHL22.368440
kcnj4	Metabolism	78	43	47	26	9	30	119	83	48	41	12	22	WHL22.747080
keap1	Defensome	35	35	26	31	39	56	23	41	98	88	44	35	WHL22.686707
slc31a1	Metabolism	30	25	69	21	44	61	30	44	74	61	40	33	WHL22.618634
vinph	TranslationFactor,Cytoskeleton	82	81	15	21	68	32	29	40	51	85	7	17	WHL22.151079
fn3_28, igf_17, nfascl, nfasc	Adhesion	19	24	18	11	38	38	92	105	62	51	28	34	WHL22.165444
atp5c1	Metabolism	79	38	51	24	5	12	41	99	62	70	5	8	WHL22.623237
st6galnac4	Metabolism	76	29	6	15	23	46	22	51	88	83	28	22	WHL22.89142
novel	Metabolism	62	20	6	13	98	29	60	51	33	59	21	27	WHL22.364613
ppef2, ppef2_1, ppef2_2	Phosphatase	32	31	12	15	1	38	108	57	47	36	43	43	WHL22.469735
man2b1	Metabolism	45	64	37	18	39	15	61	27	66	43	26	16	WHL22.262947
hypp_2810, mapk15_1, ma	EggActivation,Kinase	18	23	12	19	11	36	69	62	57	67	38	32	WHL22.313504
atp5g1	Metabolism	80	27	21	17	91	13	29	42	27	55	4	4	WHL22.119525
ectdrn	Kinase,Signaling	65	36	39	18	12	28	30	49	47	37	29	10	WHL22.587103
cdt1, cdt1l	DNAReplication	7	4	19	9	7	53	13	17	27	16	130	77	WHL22.640181
ndufs2	Metabolism	65	41	36	28	36	20	21	28	41	13	19	27	WHL22.123524
rhogef2	GTPase	54	19	15	8	32	53	17	18	26	22	53	57	WHL22.749978
rsk1, rsk2	EggActivation,Kinase	14	16	14	13	97	17	63	53	37	30	14	6	WHL22.368522
hypp_142	Transcription factor	8	15	14	10	51	23	103	37	42	43	6	19	WHL22.755982
fn3_16, fn3_22, fn3_36, ptp	Phosphatase	17	21	31	20	10	28	37	62	50	65	12	15	WHL22.769903
pfas, pfas_1	Metabolism	36	25	43	16	29	19	47	66	17	38	9	17	WHL22.347666
zpd	Metalloprotease	32	20	10	24	14	40	32	32	36	51	32	37	WHL22.741591
rab18	GTPase	10	20	2	7	5	6	87	44	53	39	37	36	WHL22.258438
sema6d	Adhesion	22	33	13	11	49	25	38	27	31	35	38	19	WHL22.226117
cyp46l2, cyp46l9	Metabolism	30	21	11	11	44	29	44	38	43	45	9	9	WHL22.616
dbi	Metabolism	14	13	12	12	11	12	64	37	55	73	22	7	WHL22.647233
fgd6	GTPase	36	35	8	19	22	19	49	42	29	35	6	10	WHL22.533518
kif3a, krp85	Cytoskeleton,Signaling	6	16	30	21	7	36	30	32	29	14	27	50	WHL22.335711
kif21a	Cytoskeleton	3	9	5	5	62	29	26	23	15	20	5	12	WHL22.305559
z472	Zinc finger	3	6	12	4	30	30	14	14	34	20	19	21	WHL22.582275
prss12l	Metabolism	16	7	8	7	19	12	24	39	14	19	19	17	WHL22.193534
ndufa12	Metabolism	10	10	2	6	9	28	17	22	5	9	52	19	WHL22.51675
dpdpalphab, pola2, pola2_1	DNAReplication	30	20	7	13	9	15	16	20	8	24	5	11	WHL22.2612
rbl1	CellCycle	3	7	20	6	16	21	16	24	16	13	12	17	WHL22.678129
z189	Zinc finger	15	18	9	8	9	20	12	14	11	25	5	15	WHL22.548929
egfib_5	Adhesion	5	6	3	5	2	13	9	7	10	6	18	14	WHL22.483837
auh	Metabolism	5	10	21	8	13	4	8	12	4	4	1	3	WHL22.485992
adck5	Kinase	13	5	3	2	9	8	3	3	10	8	15	14	WHL22.104285
hmg2	Transcription factor	1	2	4	3	6	10	4	2	6	4	13	12	SPU_005572
ndufs4	Metabolism	3	6	3	4	2	2	11	11	4	13	2	5	WHL22.643191
novel	Defensome	4	6	1	2	4	3	5	4	9	10	5	10	WHL22.325446
gage1	Novel	741	1164	2278	1121	10791	5734	1571	1533	1731	1762	1644	3207	WHL22.415416
fibcystl_1, pkhd1l1	Novel	326	895	900	548	737	972	1881	1367	1783	931	521	1414	WHL22.562775
nucb2	Novel	551	190	650	331	2653	1116	701	439	744	448	2557	1822	WHL22.529220
tropmyh	Novel	1016	356	879	320	1633	1650	600	707	928	814	782	1421	WHL22.432759
hypp_93	Novel	262	257	354	182	761	1426	785	704	977	971	677	1163	WHL22.585089
bctg1	Novel	1302	510	483	197	478	384	1055	540	912	647	498	619	WHL22.504151
novel	Novel	345	228	56	165	500	491	806	510	864	753	845	599	WHL22.17913
ankhd1, ankrd17	Novel	429	241	457	166	1007	728	386	410	451	478	642	599	WHL22.106647
hypp_194, myst3l	Novel	132	400	85	200	1291	505	653	599	658	819	248	274	WHL22.139911
hypp_2375	Novel	409	145	240	164	834	830	372	311	448	316	908	763	WHL22.290835
polr2a, polr2a-2	Novel	667	364	144	176	314	185	1230	667	821	615	189	217	WHL22.235505
med1	Novel	499	183	297	127	610	357	691	460	643	622	475	463	WHL22.221161
myx	Novel	1593	523	282	195	111	247	459	513	380	353	147	424	WHL22.282796
bptf	Novel	361	334	462	217	442	463	558	628	551	649	245	260	WHL22.297412
gata2a	Novel	178	329	756	323	243	444	664	521	507	476	337	265	WHL22.555721
ranbp1	Novel	246	90	219	123	796	681	234	179	240	169	1026	910	WHL22.65641
novel	Novel	316	157	160	115	646	297	596	553	776	607	278	309	WHL22.506733
flot2h	Novel	629	270	72	202	749	383	419	305	395	350	527	373	WHL22.505296
ttrspn_12	Novel	284	300	298	171	150	516	636	468	445	337	552	493	WHL22.739969
camsap1l	Novel	346	266	417	150	1244	385	304	402	291	369	230	224	WHL22.323943
novel	Novel	555	399	493	175	590	285	333	259	383	247	405	349	WHL22.478918
mpc2	Novel	126	157	171	98	451	415	211	131	172	104	1509	901	WHL22.357949
bat2	Novel	136	219	49	103	1147	501	231	249	217	252	608	618	WHL22.18009
tropmy2	Novel	211	218	327	150	308	312	661	432	509	288	486	344	WHL22.510117
rbm12l	Novel	433	233	55	154	466	420	439	467	504	524	241	301	WHL22.217966
capsl	Novel	967	325	234	109	241	338	380	395	323	323	224	333	WHL22.116291
hypp_207, serp5	Novel	318	240	587	193	280	423	368	367	403	362	277	374	WHL22.283651
nup153	Novel	196	367	119	178	588	293	607	482	468	502	178	212	WHL22.364351
sfrs2, sfrs2_1	Novel	307	177	54	156	646	397	373	286	399	291	508	510	WHL22.299492
sfrs3	Novel	75	189	57	149	491	846	208	227	337	178	665	665	WHL22.692671
hypp_693, phf3	Novel	220	179	221	129	780	451	242	269	243	250	406	661	WHL22.173528

rpl8, rpl8_1	Novel	438	328	247	205	106	115	589	760	390	536	101	111	WHL22.198933
ssr1, ssr1_1	Novel	205	92	73	118	674	457	280	256	233	292	642	390	WHL22.51596
hypp_2383, ppp1r16b	Novel	72	87	51	54	1588	394	175	153	179	183	366	332	WHL22.759049
novel	Novel	132	53	75	45	658	682	194	111	190	120	593	627	WHL22.129324
slc28a3_1	Novel	522	316	168	131	90	193	533	330	349	318	195	313	WHL22.323554
hypp_267	Novel	100	180	134	114	874	423	237	163	229	147	377	422	WHL22.55352
clpx	Novel	136	149	169	99	645	371	307	249	270	207	380	361	WHL22.435163
hypp_208	Novel	258	191	239	129	218	261	345	364	365	424	225	227	WHL22.437292
larp1	Novel	323	224	143	154	266	175	379	362	372	485	169	134	WHL22.335959
hypp_1182	Novel	185	175	82	109	962	377	231	196	182	190	204	258	WHL22.328527
snd1, snd1_1	Novel	286	129	68	99	893	223	329	217	242	213	266	152	WHL22.463224
brca1l	Novel	378	211	101	110	297	378	421	325	273	280	164	172	WHL22.602855
clip170ph	Novel	553	184	86	88	323	188	338	271	325	357	156	173	WHL22.662909
hnrph1	Novel	171	140	288	123	693	367	132	211	173	172	195	305	WHL22.141621
pnn	Novel	174	73	24	71	442	469	111	84	111	67	826	504	WHL22.659641
novel	Novel	44	93	82	92	273	425	306	207	321	202	355	442	WHL22.381228
hypp_3037	Novel	124	105	164	86	530	416	92	119	181	146	322	525	WHL22.155817
caprin1l	Novel	210	183	219	120	133	99	412	469	386	380	121	70	WHL22.591714
hypp_179	Novel	191	258	102	138	317	192	268	336	292	335	195	176	WHL22.369392
cubn-4, cubn2, cubnr_3	Novel	103	240	131	102	104	187	490	340	292	461	126	178	WHL22.586162
pb1, pb1_1	Novel	131	141	241	109	458	228	249	249	320	254	150	188	WHL22.316946
pabpc1	Novel	200	242	192	152	207	57	286	292	376	548	80	58	WHL22.512017
cenpc1, hypp_935	Novel	224	95	66	69	139	439	245	113	185	139	501	426	WHL22.58367
pb1	Novel	215	183	272	210	199	177	393	218	278	235	111	138	WHL22.316940
phf12	Novel	281	140	59	83	325	181	333	235	192	185	247	281	WHL22.480908
thymbh	Novel	526	265	292	106	55	66	248	405	198	215	66	35	WHL22.424734
hypp_3073, vparpf	Novel	271	98	61	21	241	144	295	185	380	340	228	202	WHL22.688834
sept6	Novel	386	217	96	139	99	148	324	299	209	230	155	158	WHL22.227277
hypp_2225	Novel	26	57	46	119	737	599	73	55	131	158	210	199	WHL22.549050
pacrg	Novel	203	64	56	110	53	187	436	345	258	347	191	143	WHL22.523709
ssbp3l	Novel	61	147	163	100	246	114	308	396	314	265	109	165	WHL22.502025
serrp1	Novel	117	121	42	69	90	272	396	306	331	365	104	124	WHL22.180607
nova1	Novel	350	216	43	96	345	137	239	287	200	268	78	75	WHL22.170210
helz	Novel	257	178	110	79	299	100	276	209	315	341	79	92	WHL22.476604
hypp_91	Novel	200	104	92	63	205	125	292	266	370	400	93	120	WHL22.617626
tial1	Novel	142	90	71	53	385	426	118	78	107	94	371	373	WHL22.79179
c1orf9l	Novel	101	78	31	90	178	353	193	170	183	183	393	345	WHL22.281926
cnot3, cnot3_1	Novel	163	94	102	73	341	194	341	210	179	199	161	167	WHL22.159299
hook3	Novel	126	95	60	41	367	175	135	142	209	157	385	277	WHL22.116741
xpo1_1, xpo1h	Novel	103	54	142	55	80	134	368	262	401	280	157	118	WHL22.499160
aff3, hypp_2533	Novel	84	110	81	62	431	248	141	184	221	187	127	268	WHL22.316579
ncbp1	Novel	246	138	192	86	297	153	107	163	164	96	315	154	WHL22.699772
fjx1l	Novel	106	225	178	155	82	170	208	238	231	217	175	107	WHL22.406692
ubqln1	Novel	107	102	37	57	391	179	139	138	311	203	221	201	WHL22.401640
ttc3, ttc3l	Novel	295	230	73	75	97	188	207	175	189	219	158	178	WHL22.450938
prpf8	Novel	41	71	100	83	193	157	294	276	286	309	155	101	WHL22.446251
hnrpcl	Novel	138	135	377	157	146	178	106	163	108	143	187	150	WHL22.88073
aco1	Novel	167	129	254	81	73	80	247	223	289	206	96	83	WHL22.586460
stt3hb	Novel	217	101	278	103	287	197	150	138	97	105	63	181	WHL22.553454
hagb	Novel	7	16	43	21	312	397	63	38	84	39	415	443	WHL22.65838
iswi	Novel	76	147	41	68	293	216	113	115	144	77	353	208	WHL22.77519
gbf1, gbf1l	Novel	398	168	179	103	94	43	155	179	224	243	19	31	WHL22.686481
sf3b2, sf3b2_1	Novel	99	55	221	98	105	94	246	242	113	143	211	168	WHL22.726029
usp8	Novel	291	96	195	64	194	72	131	152	180	193	121	96	WHL22.369453
psmd3	Novel	195	76	35	52	336	112	299	156	120	136	151	85	WHL22.423553
gsn_1	Novel	334	115	115	91	8	155	215	185	154	108	132	127	WHL22.280583
slc6a9	Novel	107	133	16	45	134	192	157	192	135	111	314	182	WHL22.342488
znrf3	Novel	148	75	25	42	52	253	195	120	163	184	235	193	WHL22.645661
jip3_2	Novel	45	67	110	35	538	183	75	76	121	91	171	148	WHL22.580730
novel	Novel	41	62	23	44	571	291	22	39	29	48	272	199	WHL22.675865
ddx6	Novel	134	100	16	50	349	137	87	171	200	172	50	130	WHL22.357809
nef3	Novel	187	88	57	62	138	226	38	101	147	163	192	182	WHL22.659796
ttrspn_21	Novel	296	125	79	62	15	80	247	126	134	271	51	60	WHL22.337669
hypp_1195	Novel	67	63	33	54	88	208	103	124	91	103	330	275	WHL22.292951
c5orf42l, hypp_1096, hypp_	Novel	221	87	71	61	122	60	146	153	195	176	96	120	WHL22.2847
pppl_270	Novel	21	8	6	4	73	366	129	108	77	79	301	328	WHL22.321570
osgin1	Novel	158	162	126	93	40	73	244	85	135	198	78	85	WHL22.759750
ppp2adirsb56	Novel	174	123	195	64	48	87	224	151	122	174	60	51	WHL22.198321
kif21a	Novel	39	57	51	34	482	237	113	83	62	79	132	88	WHL22.305565
zc3h15	Novel	11	27	52	31	167	91	192	124	143	151	272	194	WHL22.69973
ddx23, ddx23_1, unk_5	Novel	37	68	55	64	66	162	202	134	127	98	159	265	WHL22.154262
sec63h	Novel	17	49	94	59	321	131	107	157	124	135	110	95	WHL22.401912
atrnl1, atrnl1_1	Novel	111	93	44	32	227	132	198	166	128	160	37	66	WHL22.109980
strn	Novel	100	55	18	34	75	160	108	116	110	99	301	213	WHL22.610149
hnrph2l	Novel	65	88	42	36	254	234	53	53	83	77	155	244	WHL22.141671
mycbp2	Novel	68	157	132	51	98	85	174	191	176	162	23	38	WHL22.299783
hypp_3108	Novel	76	56	121	68	125	223	90	95	85	113	162	142	WHL22.212879
myef2, safb2l	Novel	38	59	138	57	118	168	114	87	74	80	196	205	WHL22.270423
ddx48	Novel	30	42	28	47	154	86	222	161	141	112	197	110	WHL22.436683
wdr35	Novel	84	82	31	68	296	102	193	127	122	80	72	63	WHL22.77634
cir	Novel	26	44	41	38	94	206	54	78	78	64	355	227	WHL22.669859
hypp_2362, tacc	Novel	39	96	20	33	188	117	222	99	127	150	110	97	WHL22.627977
adcy9, adcy9_1	Novel	367	138	89	50	17	89	71	98	63	95	137	76	WHL22.580865
rbm8a	Novel	33	23	35	28	154	182	42	67	128	75	307	206	WHL22.464156
ero1l	Novel	65	70	110	64	127	196	88	81	35	32	281	116	WHL22.476526
kiaa1324l	Novel	86	89	109	79	48	82	200	105	153	101	106	105	WHL22.759814
novel	Novel	70	46	104	51	106	90	146	103	137	115	204	82	WHL22.384500
novel	Novel	152	55	91	49	127	65	153	153	134	121	51	91	WHL22.96976
ccdc41	Novel	21	41	15	35	22	182	69	92	126	71	347	219	WHL22.198471

atg2bl, atg2hb	Novel	217	112	59	54	105	67	128	137	124	98	63	75	WHL22.64051
sin3a	Novel	27	83	68	31	109	46	289	167	166	173	37	42	WHL22.172891
eif4enif1	Novel	129	155	53	76	11	69	115	134	186	165	54	62	WHL22.28634
ckap5, map215prh	Novel	30	90	121	45	167	79	186	128	131	122	49	38	WHL22.527473
gpr128l, hypp_1631	Novel	191	143	16	50	62	103	170	111	103	89	71	59	WHL22.3020
msl1l	Novel	107	68	20	55	51	107	158	160	109	85	139	103	WHL22.346078
ncoa4	Novel	164	54	12	32	103	46	169	162	181	163	29	44	WHL22.678301
novel	Novel	69	93	158	53	191	64	85	74	100	104	91	76	WHL22.517925
unc119hb	Novel	14	24	57	32	92	77	232	121	170	155	113	71	WHL22.480864
hypp_3069, pragmin	Novel	301	98	23	28	182	42	135	129	72	55	37	48	WHL22.759837
novel	Novel	21	24	29	21	248	247	28	43	46	51	237	155	WHL22.656456
ppppp2arsa, pr65a	Novel	25	80	14	44	40	48	270	205	138	163	61	52	WHL22.11441
fryl_2	Novel	48	65	26	36	158	121	78	77	109	85	195	142	WHL22.444086
phf10	Novel	28	48	142	61	130	72	113	128	124	107	88	79	WHL22.434699
rps8	Novel	54	124	178	65	12	92	121	132	105	123	36	60	WHL22.215386
pip5k1a	Novel	203	65	58	44	127	71	117	98	118	116	43	42	WHL22.119644
gdi1_1, gdi1_2	Novel	70	76	11	35	71	76	167	71	71	60	195	197	WHL22.683578
hypp_3116	Novel	28	54	18	29	104	188	82	80	75	53	167	222	WHL22.264530
mycbp2-2	Novel	45	60	64	28	409	57	113	107	97	77	19	22	WHL22.756954
narg1	Novel	28	56	161	56	128	149	145	130	42	55	36	97	WHL22.190108
rps13	Novel	161	89	123	52	1	10	124	154	127	174	4	10	WHL22.595201
kiaa1731l	Novel	49	72	125	72	76	120	82	86	70	110	74	90	WHL22.115244
hypp_12	Novel	23	37	30	40	161	154	103	131	87	78	84	98	WHL22.620802
dnajc7	Novel	92	74	78	27	222	82	59	49	60	78	82	111	WHL22.130821
hypp_342	Novel	18	57	22	22	150	165	60	94	95	100	90	131	WHL22.32809
smarce1	Novel	39	69	21	55	165	121	54	74	105	56	132	105	WHL22.713308
dnajc3, dnajc3l	Novel	32	54	87	65	71	134	70	81	86	55	144	105	WHL22.297128
smc6, smc6-2, smc6-3	Novel	26	58	67	53	96	78	151	135	79	91	69	77	WHL22.143883
tchp	Novel	21	52	46	43	181	106	29	52	69	86	151	140	WHL22.524850
znf593	Novel	7	10	4	9	257	144	15	18	18	28	271	191	WHL22.414388
narg1	Novel	46	51	25	44	166	109	97	109	115	85	30	74	WHL22.190105
qprt	Novel	80	90	48	44	60	42	234	129	67	86	37	29	WHL22.690504
hypp_1188	Novel	67	24	14	22	164	174	87	52	62	40	165	73	WHL22.511945
trafd1	Novel	60	54	17	40	44	108	96	115	59	119	81	141	WHL22.303732
hdac4, hdac4l	Novel	89	73	33	19	144	77	104	77	123	107	33	36	WHL22.710167
cecr2l, cecr2l_2	Novel	23	21	39	35	149	153	20	28	58	33	194	153	WHL22.313788
hypp_390	Novel	222	74	57	40	98	70	35	49	65	100	33	51	WHL22.732295
novel	Novel	118	105	9	29	21	20	122	65	180	121	45	48	WHL22.310170
ptprtfpipa1, ptprtfpipa1_1	Novel	70	72	89	33	57	153	29	80	50	82	85	75	WHL22.650058
cpsf6l	Novel	35	57	37	44	174	69	68	79	95	112	40	61	WHL22.323428
rbm17l	Novel	25	30	87	47	43	104	98	63	62	64	131	99	WHL22.49878
novel	Novel	62	66	28	18	127	43	112	103	84	128	35	43	WHL22.588903
git1_1	Novel	18	32	16	29	194	92	47	41	46	74	83	174	WHL22.233762
hypp_148	Novel	70	57	11	34	80	40	94	75	98	149	58	68	WHL22.557673
myxviii, myo18a_3	Novel	137	78	42	25	107	97	49	47	36	48	94	70	WHL22.179516
novel	Novel	11	21	104	45	40	88	49	100	108	121	46	92	WHL22.374764
rab3gap2	Novel	29	56	63	34	256	86	35	60	59	47	40	49	WHL22.147372
sel1l	Novel	18	19	21	25	114	119	53	65	92	52	110	122	WHL22.561375
ndfip1l	Novel	34	28	50	27	70	59	134	92	130	111	39	32	WHL22.373445
hypp_1200	Novel	92	30	19	22	56	94	104	92	53	73	82	86	WHL22.704121
tbc1d30	Novel	189	78	17	28	54	53	44	78	113	96	25	30	WHL22.565465
ube2e	Novel	50	46	32	20	19	68	124	88	111	96	89	61	WHL22.682558
hypp_175	Novel	51	80	106	38	68	75	61	69	49	47	64	79	WHL22.494614
cd109l_2	Novel	13	40	18	34	49	166	70	69	70	53	103	101	WHL22.675136
hypp_1374	Novel	47	76	66	32	71	98	54	86	66	52	60	70	WHL22.336882
chmp4b	Novel	13	12	4	10	159	114	24	14	86	32	152	152	WHL22.12207
daxx	Novel	111	45	59	25	25	73	36	55	60	78	115	76	WHL22.331083
thoc2	Novel	68	59	41	34	7	81	88	106	70	104	68	31	WHL22.640388
hypp_277	Novel	20	62	85	34	25	83	64	107	66	77	65	63	WHL22.744667
mlf2	Novel	100	54	8	14	219	58	47	28	52	59	54	41	WHL22.617157
hyou1	Novel	71	95	71	61	50	38	36	106	54	58	41	41	WHL22.143536
tmem214, tmem214_1	Novel	48	24	10	28	51	23	99	98	142	107	46	45	WHL22.701839
hdlbp_1	Novel	53	26	9	18	162	32	112	105	71	78	18	10	WHL22.562051
alms1l	Novel	20	35	34	31	92	96	27	63	83	72	69	59	WHL22.221190
kif4	Novel	27	35	24	26	25	57	106	90	86	67	80	49	WHL22.66529
tkyr	Novel	18	31	45	21	179	42	85	79	49	57	37	31	WHL22.233768
tmc7	Novel	54	36	31	25	86	73	71	78	72	60	47	41	WHL22.182732
nf1	Novel	91	38	30	38	27	39	138	81	72	76	20	21	WHL22.126992
wdfy3_1	Novel	88	69	59	20	29	24	100	70	55	114	24	14	WHL22.526295
ap1gbp1l	Novel	68	21	40	23	97	50	47	81	120	71	16	32	WHL22.308994
hypp_2746	Novel	133	100	6	16	5	14	50	64	78	99	38	63	WHL22.691075
cct7, cct7_1	Novel	100	98	46	27	19	23	79	102	64	71	11	10	WHL22.762548
tmc7, tmc7_1	Novel	71	42	25	15	95	31	96	47	88	49	44	37	WHL22.182750
wdr43	Novel	32	25	89	28	55	57	71	59	35	55	74	54	WHL22.154338
kiaa0368l	Novel	68	31	14	25	116	46	53	75	104	68	10	23	WHL22.618101
ttrspn_13, ttrspn_21	Novel	23	38	64	20	33	37	70	77	96	57	54	53	WHL22.337666
tep1l_6	Novel	14	28	81	34	23	32	95	59	133	91	14	21	WHL22.147551
sfrs16, sfrs16_1	Novel	27	57	18	18	26	102	79	72	41	60	35	78	WHL22.128732
rin2l	Novel	36	26	40	18	69	47	54	48	90	57	53	64	WHL22.597950
unk	Novel	46	48	44	17	32	54	87	49	63	76	28	53	WHL22.17392
trrap_2	Novel	14	27	33	17	74	25	80	80	112	92	15	16	WHL22.614482
hypp_291, ttc3, ttc3l	Novel	99	69	24	16	7	29	35	50	94	97	29	31	WHL22.450633
pwwp2bl	Novel	18	24	41	15	18	61	65	58	98	91	47	38	WHL22.134762
smarca3, swi/snf	Novel	35	30	31	18	125	87	26	24	73	34	32	41	WHL22.15177
lrrc48	Novel	34	17	95	40	9	39	80	68	34	50	46	39	WHL22.641737
snx6, snx6_1	Novel	48	26	33	20	104	57	46	64	37	55	26	25	WHL22.2463
brwd1	Novel	22	30	48	21	62	31	59	36	60	106	28	31	WHL22.128720
hypp_1390, hypp_201	Novel	12	10	4	11	60	70	55	60	70	48	58	61	WHL22.58116
spast	Novel	38	31	6	11	43	19	86	63	44	31	97	47	WHL22.235359

c1orf58	Novel	90	32	9	12	41	35	92	37	39	36	37	49	WHL22.511927
hypp_185	Novel	11	29	7	18	42	41	74	40	50	74	42	63	WHL22.26462
hydin_2	Novel	18	31	81	26	13	19	118	74	33	51	6	15	WHL22.212186
usp19, usp19_1	Novel	97	69	36	12	48	38	39	22	18	34	39	27	WHL22.553434
rpl11, rpl11_1	Novel	110	52	41	19	6	14	32	71	35	72	10	12	WHL22.480857
ter1	Novel	16	32	24	32	47	34	39	42	58	45	62	29	WHL22.360389
novel	Novel	10	18	28	16	16	20	42	31	111	100	44	24	WHL22.580447
copa, copa_1	Novel	41	59	23	30	31	20	66	58	56	58	10	6	WHL22.395777
pdia3	Novel	26	31	17	37	84	25	49	64	42	49	12	19	WHL22.762798
jip3_1	Novel	51	24	7	18	98	20	37	53	57	49	19	15	WHL22.580754
rt25	Novel	42	47	35	28	42	48	12	32	27	28	53	54	WHL22.163671
novel	Novel	104	61	6	15	6	55	25	40	33	40	21	42	WHL22.600051
crtapl, hypp_2994	Novel	36	29	30	16	11	18	81	42	42	42	66	31	WHL22.328367
fam126a	Novel	61	24	38	16	26	31	67	26	46	47	34	21	WHL22.551269
novel	Novel	50	32	29	14	59	33	29	32	37	31	41	45	WHL22.443784
c10orf93l	Novel	110	36	20	16	10	47	48	57	20	31	15	19	WHL22.547837
ddx20	Novel	3	9	9	10	97	26	51	43	61	42	31	44	WHL22.180831
nippbl	Novel	16	38	18	10	117	40	33	24	35	25	22	44	WHL22.145766
myst2_1	Novel	5	7	14	7	139	46	33	20	38	25	31	53	WHL22.702344
cttnbp2	Novel	12	26	16	9	25	57	35	35	45	31	66	46	WHL22.712342
novel	Novel	13	29	9	17	65	8	66	77	47	29	11	22	WHL22.445214
agps	Novel	23	22	21	22	1	57	53	56	48	36	15	34	WHL22.167941
novel	Novel	50	67	16	13	24	28	19	49	30	41	12	38	WHL22.632383
novel	Novel	11	11	16	6	69	35	14	21	10	12	71	103	WHL22.350013
sfrs11	Novel	26	25	64	21	5	14	96	45	22	44	12	8	WHL22.717329
pabct	Novel	19	12	12	10	13	42	29	28	37	26	103	48	WHL22.653759
kiaa0090l	Novel	37	15	9	14	80	27	72	33	18	32	17	25	WHL22.631609
gne, gne_1	Novel	42	42	47	17	26	29	34	36	13	28	28	32	WHL22.567497
dlg1	Novel	32	19	3	7	132	32	21	22	17	22	50	16	WHL22.580907
tagln2	Novel	22	20	12	10	100	14	31	35	39	16	50	19	WHL22.309575
novel	Novel	7	18	5	14	53	47	38	30	28	25	44	57	WHL22.767350
bcdin3	Novel	10	28	33	14	42	27	36	28	54	32	21	41	WHL22.98540
tsc2, tsc2_1	Novel	12	15	15	14	84	32	22	43	50	45	15	17	WHL22.298027
acad9	Novel	39	21	29	22	13	15	32	33	49	53	28	22	WHL22.665658
flj13072l	Novel	9	19	22	15	3	24	22	42	67	63	35	36	WHL22.536973
slbp_1	Novel	68	28	7	17	64	22	31	24	27	25	22	19	WHL22.385492
novel	Novel	10	19	7	7	32	25	28	46	51	92	17	19	WHL22.440771
muc4dl2	Novel	18	35	17	20	4	23	27	42	54	64	32	18	WHL22.68953
pgbtpasel	Novel	20	25	10	15	44	17	89	30	36	43	6	13	WHL22.452200
tgshl	Novel	8	14	26	17	3	45	26	51	55	30	26	46	WHL22.456243
c12orf51l	Novel	14	14	50	17	67	11	39	43	44	24	4	10	WHL22.361373
raph1l	Novel	13	30	13	8	29	23	41	34	28	33	62	23	WHL22.711035
apeh, apeh-2	Novel	16	31	16	27	16	45	43	39	29	43	10	21	WHL22.317361
tcea1	Novel	9	14	22	12	15	43	54	17	42	21	38	42	WHL22.544172
novel	Novel	16	21	4	13	34	45	26	31	28	42	40	30	WHL22.61221
rnase3l_1	Novel	13	20	19	29	81	56	13	14	12	13	21	32	WHL22.61727
miox	Novel	31	13	5	12	1	7	58	63	56	55	10	11	WHL22.477283
rad23	Novel	4	9	5	12	93	28	37	29	23	24	33	23	WHL22.686696
brd7	Novel	3	10	34	20	10	48	14	32	41	17	38	49	WHL22.358228
med23	Novel	29	13	31	14	4	13	49	42	44	59	9	6	WHL22.82057
tdrd1	Novel	19	22	11	14	3	19	67	59	23	27	20	21	WHL22.566979
paf1	Novel	25	11	7	17	2	24	27	24	36	20	77	31	WHL22.549292
trrap_2	Novel	34	21	20	8	46	10	37	26	24	39	17	12	WHL22.614479
senp1, senp1_1	Novel	20	23	22	15	7	30	27	35	38	29	33	11	WHL22.107922
spg20	Novel	34	30	24	8	44	14	45	19	19	18	23	7	WHL22.738733
hypp_228	Novel	19	38	8	12	17	11	24	28	58	42	14	9	WHL22.88918
psmd12	Novel	33	10	11	6	77	40	11	9	19	15	30	17	WHL22.456017
novel	Novel	17	16	3	7	7	54	12	37	44	49	18	14	WHL22.58273
ubp24	Novel	61	21	3	7	6	34	26	26	32	22	22	15	WHL22.289771
novel	Novel	6	9	7	6	11	28	59	35	27	25	31	31	WHL22.572668
clect/cub	Novel	52	22	17	15	11	12	22	29	27	36	13	17	WHL22.450542
oaf	Novel	9	3	23	8	54	32	17	14	23	16	41	27	WHL22.754882
trnt1, trnt1_1	Novel	3	7	7	3	40	6	16	17	32	28	26	78	WHL22.294897
hypp_2735	Novel	6	16	9	15	6	29	30	51	42	21	16	22	WHL22.118642
btf3l4	Novel	12	9	11	8	59	19	43	20	23	20	18	17	WHL22.584491
mgrn1	Novel	15	21	29	16	16	20	28	23	30	23	18	16	WHL22.667684
upf2	Novel	19	26	25	9	18	19	19	29	21	23	28	18	WHL22.170212
prpf39	Novel	14	8	2	6	11	9	30	62	37	22	39	13	WHL22.224813
xpmc2hl	Novel	16	6	3	9	53	14	10	26	21	18	25	46	WHL22.566192
ddx19a	Novel	20	15	12	9	21	13	44	33	26	23	9	16	WHL22.10570
tubgcp3, tubgcp3_1	Novel	24	17	16	8	15	19	32	42	18	32	7	11	WHL22.368691
novel	Novel	11	11	3	7	44	27	3	6	25	7	31	61	WHL22.631511
vps13c	Novel	4	6	7	15	4	25	53	45	23	22	10	19	WHL22.41321
xpo4, xpo4_1	Novel	29	28	8	4	90	5	10	19	20	16	1	1	WHL22.513397
vps54	Novel	6	12	3	8	43	16	29	31	15	32	13	10	WHL22.170253
hypp_1385, lekr1l	Novel	4	12	21	10	5	57	19	16	12	8	25	30	WHL22.291547
cuedc1	Novel	20	12	4	4	36	35	13	12	19	9	34	21	WHL22.110691
man2a1	Novel	9	8	27	10	20	6	36	15	29	16	25	17	WHL22.652149
tmem67	Novel	22	11	2	5	26	18	20	15	29	22	18	28	WHL22.657101
flna	Novel	33	29	2	3	2	9	54	31	22	16	6	5	WHL22.739162
novel	Novel	16	9	8	9	5	25	31	11	17	15	27	37	WHL22.304981
hesbl	Novel	8	11	18	7	3	16	13	17	53	33	13	10	WHL22.265084
nudt18	Novel	4	10	5	14	12	35	13	19	14	18	22	27	WHL22.82036
rska2	Novel	8	10	11	4	69	9	20	22	12	16	3	7	WHL22.368528
novel	Novel	16	10	6	7	8	17	18	7	28	33	12	15	WHL22.21131
depdc1, depdc1b	Novel	12	7	5	6	2	15	15	10	12	14	46	30	WHL22.714590
cbr1_1	Novel	15	13	6	11	3	13	29	12	21	42	4	3	WHL22.259275
bms1	Novel	7	5	6	8	47	11	11	24	14	20	11	6	WHL22.397454
asph, asphl	Novel	4	4	5	6	4	10	12	14	28	23	37	19	WHL22.35714

hypp_2828	Novel	4	6	5	5	6	28	13	17	14	15	31	24	WHL22.393807
pgap1	Novel	7	10	7	3	13	11	29	14	25	18	19	9	WHL22.338475
rbm19	Novel	19	6	5	9	2	20	12	9	9	12	33	25	WHL22.114255
rspry1-2, rspry1l	Novel	15	13	2	7	1	12	30	20	24	22	4	3	WHL22.237524
mov10l_2, mov10l	Novel	5	4	3	7	12	10	23	18	21	18	16	14	WHL22.74839
c1orf55	Novel	4	1	6	8	16	22	17	13	13	14	18	18	WHL22.5447
wdr55, wdr55_1	Novel	8	9	5	7	4	20	10	8	7	4	23	37	WHL22.614961
novel	Novel	12	5	2	4	31	5	4	4	12	8	18	35	WHL22.196082
usp22	Novel	10	8	5	7	23	13	17	16	10	17	2	4	WHL22.748468
fam160a2l	Novel	9	18	4	6	2	14	13	8	13	10	11	22	WHL22.487373
kcnk10, kcnk5_1, kcnk9	Novel	3	2	5	5	2	19	9	17	11	15	30	10	WHL22.580025
zranb1	Novel	7	5	5	5	11	11	6	13	26	18	10	5	WHL22.13037
kif27l2	Novel	21	10	16	6	2	8	13	14	10	5	3	8	WHL22.340094
psmb1	Novel	3	8	3	6	8	4	19	17	8	10	16	8	WHL22.255746
novel	Novel	20	8	2	9	14	5	14	5	18	5	3	5	WHL22.764504
herc4-5	Novel	9	6	3	4	6	5	10	9	26	18	3	3	WHL22.674334
cerkll	Novel	1	1	6	3	2	15	11	14	17	12	6	11	WHL22.258410
c2orf29	Novel	4	6	2	4	8	12	7	16	10	16	8	5	WHL22.500122
pomgnt1	Novel	20	12	10	3	1	3	4	3	4	7	7	8	WHL22.149935
novel	Novel	345	348	357	195	737	461	487	562	716	466	820	875	WHL22.499079
novel	Novel	193	195	120	105	1139	427	462	418	600	527	287	346	WHL22.500411
novel	Novel	19	58	171	61	285	629	196	251	368	523	967	655	WHL22.682450
novel	Novel	124	292	396	274	97	238	356	424	410	534	179	235	WHL22.701051
novel	Novel	325	170	72	82	520	295	195	233	283	184	141	103	WHL22.702012
novel	Novel	35	104	59	47	138	207	171	149	186	214	302	161	WHL22.744627
novel	Novel	85	58	77	46	266	196	46	69	92	90	263	314	WHL22.400358
novel	Novel	44	39	32	27	82	98	242	221	156	147	30	97	WHL22.78949
novel	Novel	161	58	170	77	12	18	78	141	151	97	9	12	WHL22.94265
novel	Novel	139	95	60	22	70	49	113	106	52	102	45	86	WHL22.375245
novel	Novel	57	44	66	31	146	49	137	111	118	63	55	55	WHL22.490402
novel	Novel	23	68	29	39	17	104	140	92	112	118	78	89	WHL22.122101
novel	Novel	40	33	12	5	186	85	51	32	66	67	52	165	WHL22.701496
novel	Novel	42	31	99	35	13	134	30	56	32	75	133	89	WHL22.738808
novel	Novel	76	27	76	34	90	88	21	28	30	22	137	140	WHL22.19393
novel	Novel	21	29	73	27	72	50	56	49	87	44	55	81	WHL22.223249
novel	Novel	185	67	17	37	28	17	58	86	31	54	4	5	WHL22.302939
novel	Novel	3	9	15	22	60	38	101	111	41	51	26	10	WHL22.476823
novel	Novel	26	10	8	6	85	21	75	38	82	62	16	20	WHL22.640166
novel	Novel	17	38	24	21	24	15	65	57	63	53	16	11	WHL22.316666
novel	Novel	23	21	21	9	76	45	15	20	20	21	48	66	WHL22.418583
novel	Novel	14	32	39	16	14	39	20	25	39	31	32	20	WHL22.174204
novel	Novel	20	17	14	8	95	26	21	21	21	19	31	21	WHL22.591243
novel	Novel	27	23	21	14	16	14	46	21	53	37	16	13	WHL22.457344
novel	Novel	26	23	10	16	7	15	43	41	24	26	7	15	WHL22.260865
novel	Novel	11	18	7	11	30	12	43	41	22	25	5	13	WHL22.351683
novel	Novel	31	26	2	4	4	9	40	20	28	23	1	4	WHL22.316144
novel	Novel	14	6	3	5	25	18	22	27	17	19	15	16	WHL22.283688
novel	Novel	8	4	10	6	13	31	18	19	18	27	11	19	WHL22.538069
novel	Novel	35	13	11	4	9	8	11	12	4	7	38	14	WHL22.520878
novel	Novel	5	6	24	9	4	7	38	23	24	12	2	4	WHL22.702777
novel	Novel	34	11	7	6	16	15	3	12	21	14	8	10	WHL22.205285
novel	Novel	7	7	2	4	12	16	15	25	20	23	4	10	WHL22.95669

FIGURE LEGENDS

Supplemental Figure 1. Onecut gene expression. (A-G) Fluorescent RNA in situ hybridization reveals onecut mRNA spatial localization during early embryogenesis. (A) Gene expression pattern of onecut at 35 hpf observed from different angles: lateral, apical, oral and vegetal view (A, B, C and D, respectively). (E) The embryonic territory from which the ciliated band will arise is first delineated at 25 hpf by onecut zygotic expression. (F) Spatial coordinates overlaid onto the lateral view of a 38 hpf embryo, illustrate that onecut's expression pattern separates oral from aboral ectoderm and generates similar polarity at the apical plate. (G) Three-quarters perspective, relative to the vegetal pole of a 38 hpf embryo, reveals that onecut expression remains circular after gastrulation. Note: True RNA in situ signal is strong and bright whereas baseline fluorescence vaguely reveals the archenteron/blastopore on account of the relative thickness of that particular tissue. (H) mRNA abundance profile throughout early embryogenesis, as quantified by the nCounter Analysis System. Maternal onecut mRNA is ubiquitously distributed throughout the embryo until it's complete decay by 24 hpf. Zygotic transcription of onecut begins approximately at 14 hpf and may be observed ten hours later. Each of the encircled data points reflects one of the developmental stages shown above (25 hpf, 35 hpf and 38 hpf, respectively).

Supplemental Figure 2. BAC reporters recapitulate endogenous expression. (A-D) RNA in situ hybridization. (A) Transgenic gfp expression from a lhx2/9::BAC reporter. (B) Same image as in A overlaid onto a DIC image of the corresponding embryo. (C) Endogenous onecut expression in red; transgenic gfp expression in green. Co-localization between the two, appears yellow. Fluorescent signal is overlaid onto a DIC image of the corresponding embryo. (D) Same description as in C, but visualized in an embryo from a different batch. Abbreviations: hfp, hours post fertilization; ov, oral view; lv, lateral view.

Supplemental Figure 3. WMISH corroboration. A1-E11 reflect the expression pattern of random genes chosen from among the population of transcripts enriched in each of the following cell types, (A) Pigment cells, (B) Apical subdomain, (C) Oral ectoderm subdomain, (D) Ciliated band, and (E) Veg1; all of which are outlined in black in Fig.2. (A1) gpr54l_3, (A2) whl22.493883, (B1) lhx2, (B2) whl22.510486, (B3) ctr9, (B4) nek8b, (B5) iqub, (B6) whl22.273560, (B7) whirlin, (B8) axndhc15h, (B9) dis, (B10) chaf1a, (C1) c8orf41l, (C2) whl22.446968, (C3) melkl, (C4) clect/fn3_10, (C5) whl22.327392, (C6) herc1l_2, (D1) cdc6, (D2) slsp1, (D3) hypp_70, (D4) psat1, (D5) whl22.522987, (D6) bmp1/tldl1, (D7) wnt8, (D8) soxf, (D9) rel, (D10) vtgn2, (D11) bpr, (D12) frizz1/2/7, (D13) whl22.539554, (E1) whl22.522365, (E2) pdia5, (E3) udg, (E4) dtwd1, (E5) hk1_2, (E6) idua, (E7) brrn1, (E8) whl22.261974, (E9) apc10, (E10) hypp_513, (E11) gcn1l1. For novel genes, WHL identification # has been used in lieu of a name. Notice that in several instances the pattern of expression may represent only a fraction of the overall embryonic territory from which it was derived (indicated by a dotted white line), or alternatively, despite being expressed throughout the outlined territory, may in addition be expressed in another, not yet addressed domain. Abbreviations: av, aboral view; lv, lateral view; ov, oral view.

Supplemental Figure 4. Functional categories per cell type. (A-B) Histogram reflecting the fraction of genes corresponding to functional categories analyzed, for each of the six cell types recovered. (A) Number of genes found in each category, according to cell-type/domain. (B) Percent of genes that make up each category compared across cell-types/domains. Note the overrepresentation of biomineralizetion genes in the tbrain positive domain, in accordance with what is known from previous reports.

FIGURE LEGENDS (…*continued*)

Supplemental Figure 5. Specificity of effector gene sets. A-F reflect comparative transcriptome analysis for three differentiated cell types: (A-B) Oral ectoderm cells, (C-D) Ciliated band, and (E-F) Veg1 cells. Illustrated in each scatterplot is the abundance of every mRNA species expressed in the cell type of interest (plotted/labeled along the ordinate), relative to control (plotted/labeled along the abscissa). Data points outlined in red represent transcripts uniquely expressed in the cell type specified at the top of each plot (also in red). Underrepresented transcripts are shown as green colored data points. Data points outlined in blue represent transcripts uniquely expressed in a different cell type; specified at the top of each plot (also in blue). Of these, those that are depleted relative to the dataset shown, have been shaded light blue. Likewise, those that are enriched have been shaded dark blue. All remaining data points have been colored light grey. As described in detail in Methods these assignments are the result of statistical prevalence analysis; the main quantitative import of this figure is that transcripts shown in red are enriched beyond the upper bound of a +/-.05 probability envelope; depleted transcripts in light green lie beyond the lower boundary of this envelope; and the gray transcript population gives the distribution of insignificantly enriched or depleted transcripts within this envelope.

Supplemental Figure 6. Mapping statistics. Table and corresponding histograms describing the number of sequencing reads obtained from each of the 33 samples/replicates and associated statistics of how such reads mapped to the genome.

Supplemental Table 1. Catalog of transcripts unique to each cell type. (A) Pigment cells, (B) Apical subdomain, (C) Oral ectoderm subdomain, (D) Ciliated band, and (E) Veg1. The first two columns list gene names and the functional category to which they belong, respectively. The third column reveals the statistical significance associated with each gene, in terms of P-value. The last column is the identification # by which each and every gene listed can be looked up; information such as genomic coordinates, expression profile, peptide sequence, etc. may be accessed at http://www.spbase.org:3838/quantdev/. Red text denotes genes whose expression pattern has been independently corroborated to coincide with the territory specified at the top of each table, during the developmental stage in question.

Supplemental Table 2. Catalog of transcripts expressed across all cell types. The first two columns list gene names and the functional category to which they belong, respectively. Columns three through eight display the relative abundance (in terms of seq reads per gene) of transcripts as observed for each cell type, alongside that of their respective control. (A) Pigment cells, (B) Apical subdomain, (C) Skeletogenic cells, (D) Oral ectoderm subdomain, (E) Ciliated band, and (F) Veg1. The last column is the identification # by which each and every gene listed can be looked up; information such as genomic coordinates, expression profile, peptide sequence, etc. may be accessed at http://www.spbase.org:3838/quantdev/.