

CORRECTION

Correction: Fission yeast polycystin Pkd2p promotes cell size expansion and antagonizes the Hippo-related SIN pathway

Debatrayee Sinha, Denisa Ivan, Ellie Gibbs, Madhurya Chetluru, John Goss and Qian Chen

There was an error in *J. Cell Sci.* (2022) **135**, jcs259046 (doi:10.1242/jcs.259046).

The article reported the identification of a novel temperature-sensitive fission yeast mutant *pkd2-B42* and its characterization that revealed the function of Pkd2 in cell growth. In it, the coding sequence of the *pkd2* gene in this mutant was determined, and the authors identified eight missense mutations at the time (Fig. 1A; Table S1).

However, the authors now report that there is an additional insertion mutation in the *pkd2* coding sequence of *pkd2-B42*, which was missed in the previous sequencing reactions. The insertion of a single guanine nucleotide (G) at the 2020 bp position of the coding sequence also changes the *pkd2* sequence from GGA to GGGA in *pkd2-B42*. This results in two additional missense mutations at the amino acid residues of 675 and 676, followed by a premature stop codon, in the open reading frame of *pkd2-B42*.

The authors have informed us that these additional mutations do not change the nature of *pkd2-B42* as a temperature-sensitive mutant, nor change the phenotype of this *pkd2* mutant (because the number of mutations in *pkd2-B42* is irrelevant to its genetic and cell biology characterization described in the study). Therefore, the authors conclude that this new finding does not change any of the conclusions reached in the paper.

The correct Fig. 1A is shown below, and has been updated in the PDF and online versions. Table S1 has also been updated to include these additional mutations:

Residue	Position	Mutation	Amino acid change
675	C terminal domain	N→K	Polar Uncharged to Positively Charged
676	C terminal domain	T→Y	Polar Uncharged to Polar Uncharged
677	C terminal	D→Stop	Truncates last 34 amino acids (677-710)

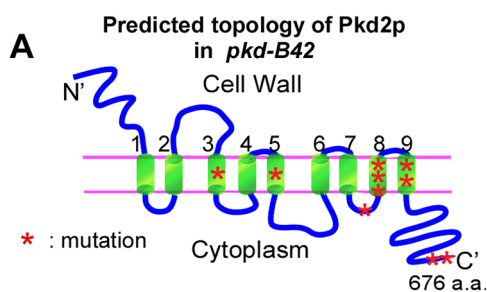


Fig. 1 (corrected panel). A novel temperature-sensitive *pkd2* mutant, *pkd2-B42*. (A) Schematic of the predicted topology of wild-type Pkd2p. The mutated residues in *pkd2-B42* are shown as red asterisks. The length is 676 amino acids owing to a truncation of the C-terminus. Numbers denote the nine transmembrane helices.

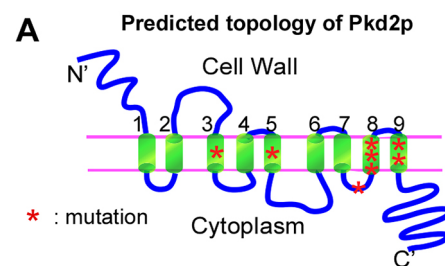


Fig. 1 (original panel). A novel temperature-sensitive *pkd2* mutant, *pkd2-B42*. (A) Schematic of the predicted topology of wild-type Pkd2p. The mutated residues in *pkd2-B42* are shown as red asterisks. Numbers denote the nine transmembrane helices.

The authors apologise for this error and any inconvenience caused.