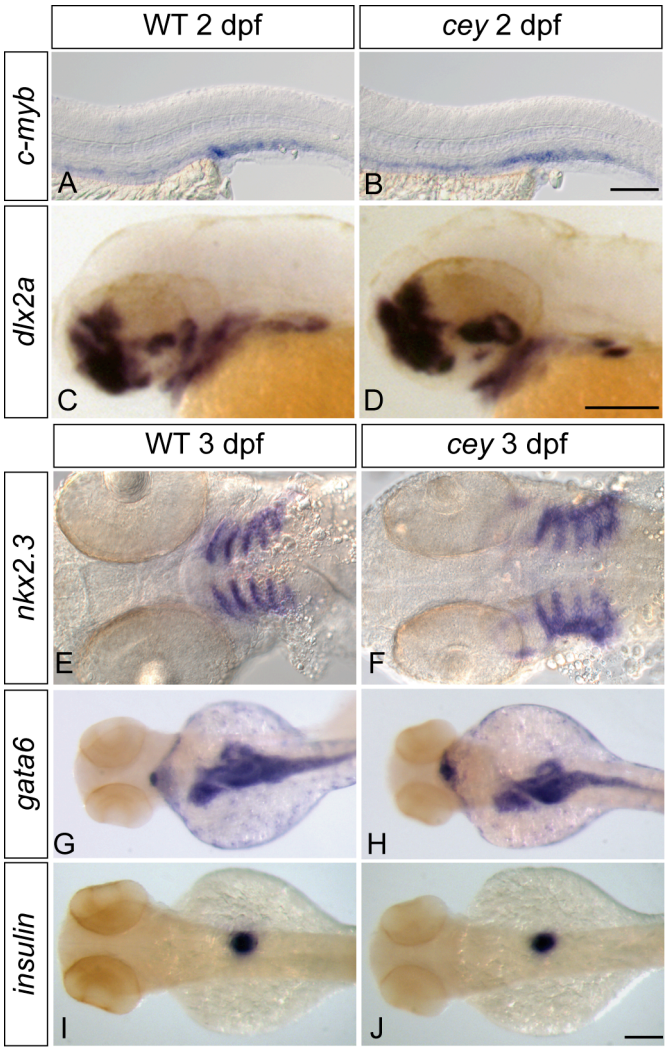
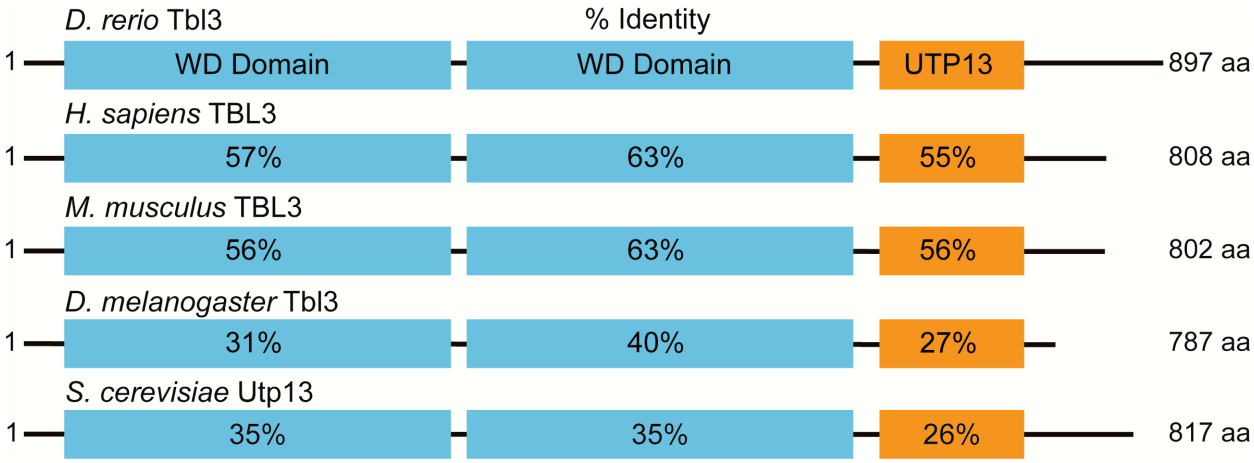


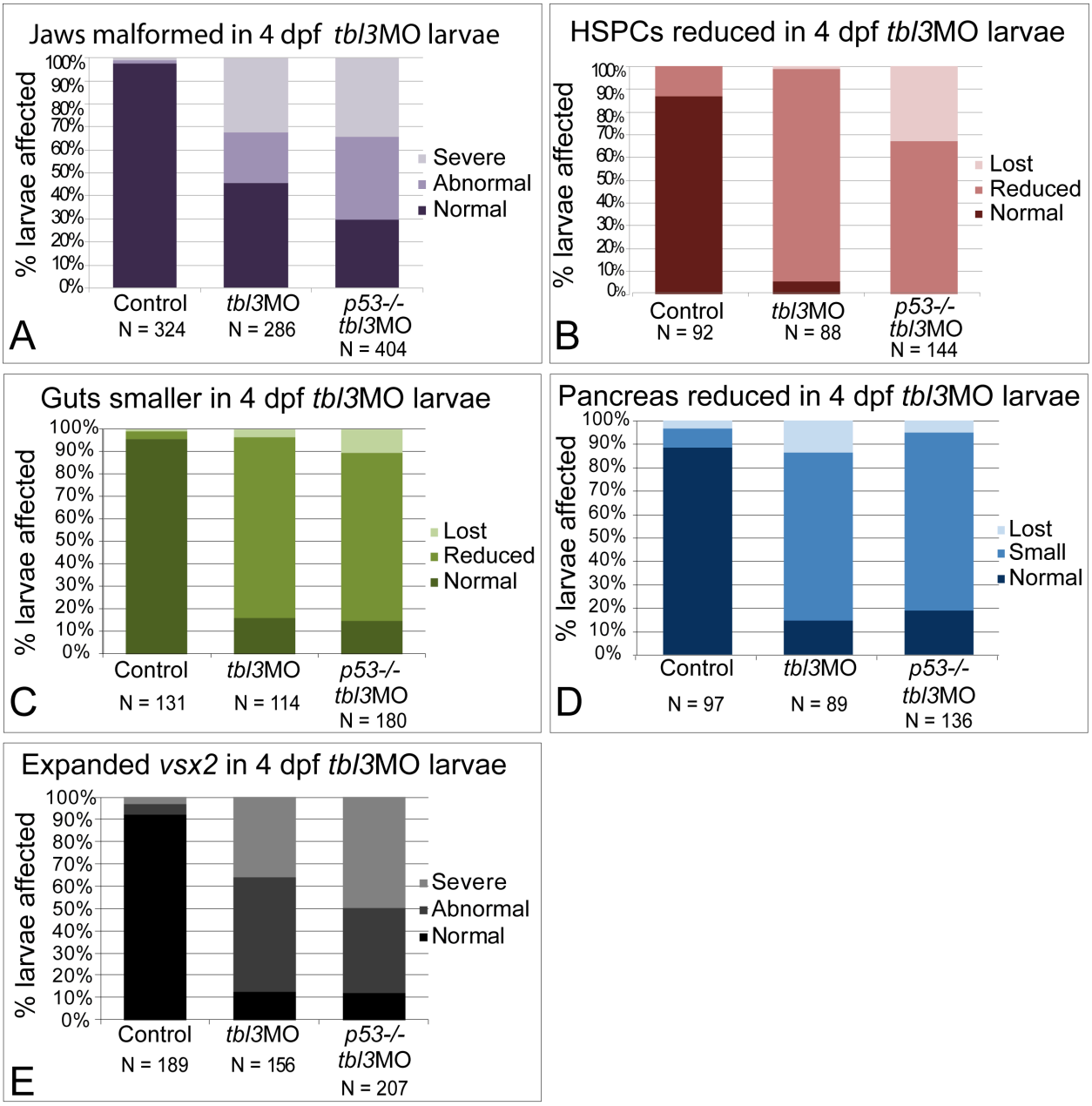
Supplementary Figure 1: Tissue specification and patterning is normal in *cey* mutants

Despite the severe reduction of HSPCs in *cey* mutants at 4 dpf, HSPCs labeled by *c-myb* in *cey* mutants at 2 dpf are comparable to wild-type (A, B). The cranial neural crest labeled by *dlx2a* gives rise to jaw cartilage and is normal at 2 dpf in *cey* mutants (C, D). At 3 dpf the endoderm that contributes to jaw formation is specified properly as indicated by *nkx2.3* staining in *cey* mutants (E, F). Patterning and size of the intestinal and pancreatic *anlage* is also normal as shown by *gata6* staining in *cey* mutants at 3 dpf (G, H). While differentiation of the exocrine pancreas is deficient, beta cells in the endocrine pancreas labeled by insulin are normal in *cey* mutants at 3 dpf (I, J). Scale bars are 125 μm.



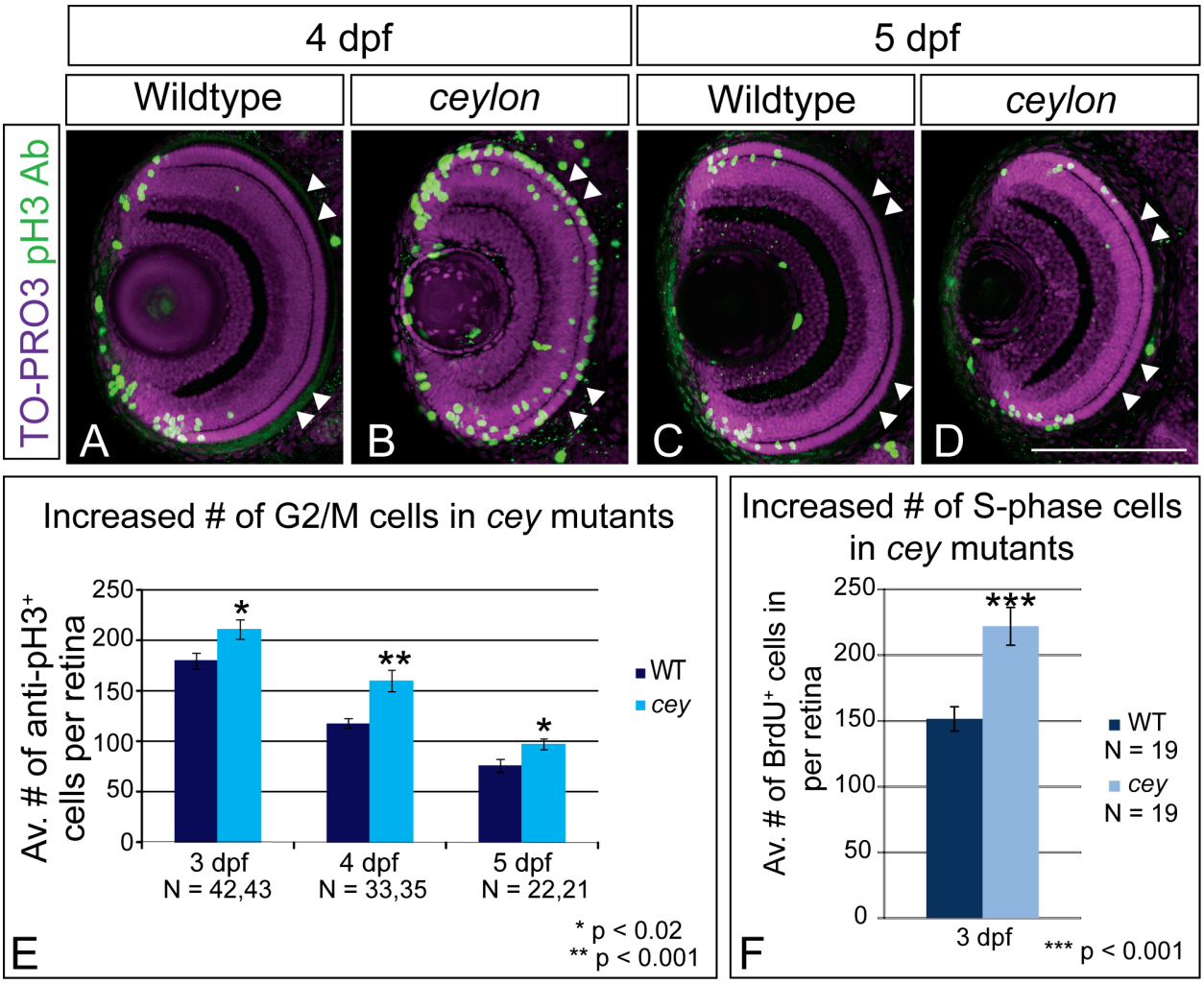
Supplementary Figure 2: The WD-repeat protein Tbl3 is highly conserved

Tbl3 is a WD-repeat protein that contains two WD-repeat regions (blue) in the N-terminal end of the protein. The C-terminal end contains an Utp13 (orange) homology domain that was first identified in the yeast Utp13 protein. The protein is highly conserved across species in both the WD domains and the UTP13 domain.



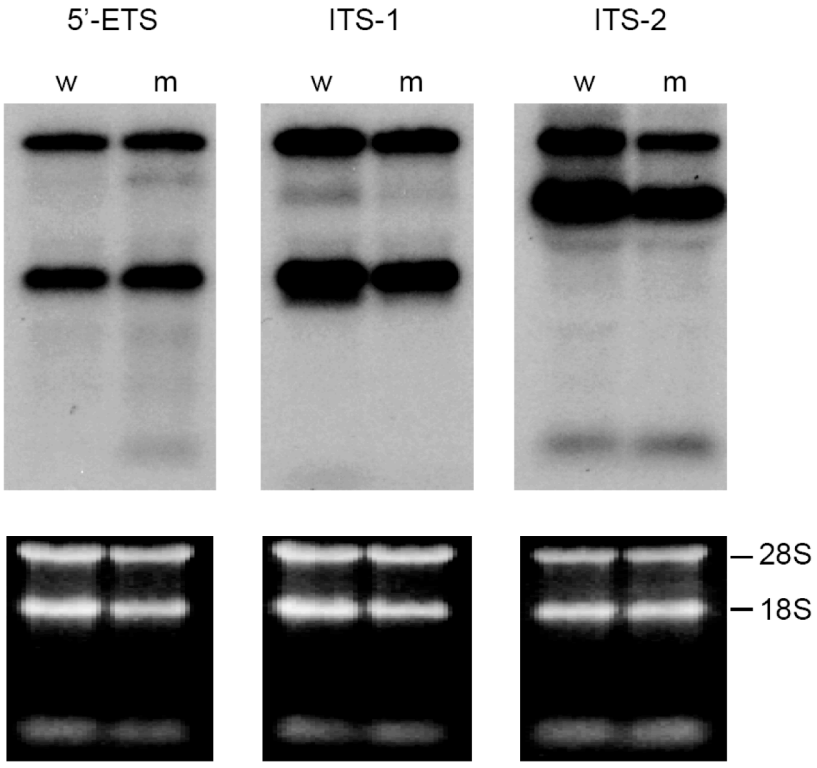
Supplementary Figure 3: *tbl3*MO larvae phenocopy *cey* in wild-type and *p53*$^{-/-}$ larvae

Injection of *tbl3*MO into wild-type or *p53*$^{-/-}$ recapitulated the *cey* mutant phenotype in a large percentage of the larvae. All injections were repeated three times and the phenotypes were divided into three categories with the most severe being the *cey* phenotype at 4 dpf. Jaws were malformed when *tbl3*MO was injected (A). HSPCs labeled by *c-myb* (B), the gut labeled by *ifabp* (C), and the exocrine pancreas labeled by *trypsin* (D) were all severely reduced in *tbl3* morphants. Also in correlation with the *cey* mutant phenotype, *vsx2* expression was expanded into the central retina in *tbl3* morphants (E). N is the number of embryos.



Supplementary Figure 4: *cey* mutants have increased proliferation in the retina

Proliferation is expanded in *cey* mutant retinas. At 4 dpf there are more pH3$^+$ (G2/M) cells in *cey* mutants (B) as compared to wild-type (A). In addition these cells are not confined to the peripheral CMZ region, but are throughout the central retina (white arrowheads; B). By 5 dpf the number of pH3$^+$ cells is reduced and confined in *cey* larvae (D), more closely resembling wild-type larvae (C). Quantification shows that *cey* mutants have significantly more pH3$^+$ cells than wild-type at 3, 4 and 5 dpf, although the number of cells decreases over time in both wild-type and *cey* mutants (E). Whole Z-stacks of dorsal view retinas were projected and the number of pH3$^+$ cells were counted and then averaged to determine the average number of mitotic cells in wild-type and *cey* larvae at 3, 4 and 5 dpf (E, see methods for more details on quantification). *cey* mutants also have an increased number of cells in S-phase as compared to wild-type (F) indicating there are more proliferating cells at 3 dpf. The average number of BrdU positive cells in five lateral view sections was calculated for each retina (F, see methods for more details). Scale Bars are 130μm.



Supplementary Figure 5: rRNA processing is normal in *cey* mutants

At 4 dpf, rRNA precursors identified by 5’ external transcribed spacer (5'ETS), first internal transcribed spacer (ITS-1) and second internal transcribed spacer (ITS-2) probes on a Northern blot are indistinguishable between *cey* mutants (m) and wild-type (w) (top panels). Equal RNA loading is shown by ethidium bromide stain of 28S and 18s rRNA (lower panels).