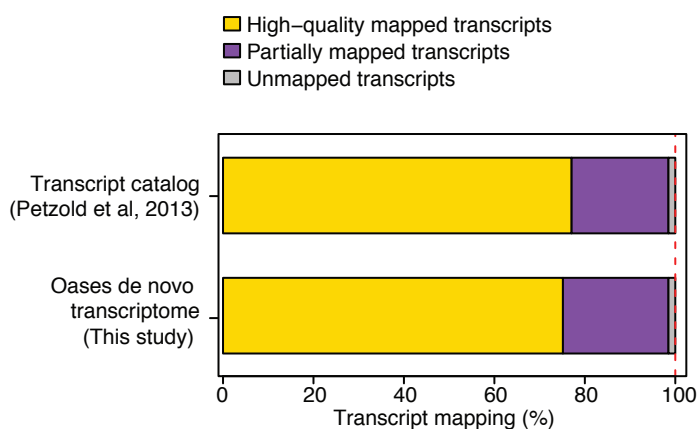


Figure S1

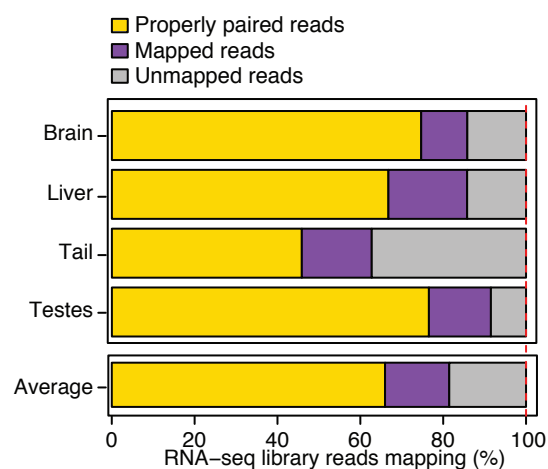
A Regions with excess coverage in the turquoise killifish genome assembly

Regions with excess coverage	Length (Mb)	Portion of assembly (%)	Proportion of reads (%)	Over-representation
> 2 times the expected coverage	455	44.5	70.1	1.6X
> 3 times the expected coverage	47	4.6	26.0	5.7X
> 4 times the expected coverage	21	2.0	20.1	10.4X
> 10 times the expected coverage	10	1.0	17.4	17.4X

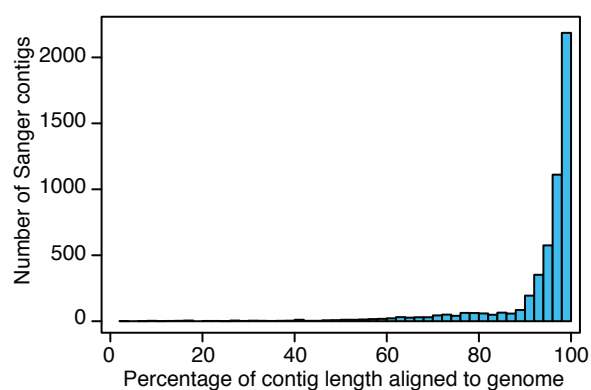
B Assembled transcript mapping



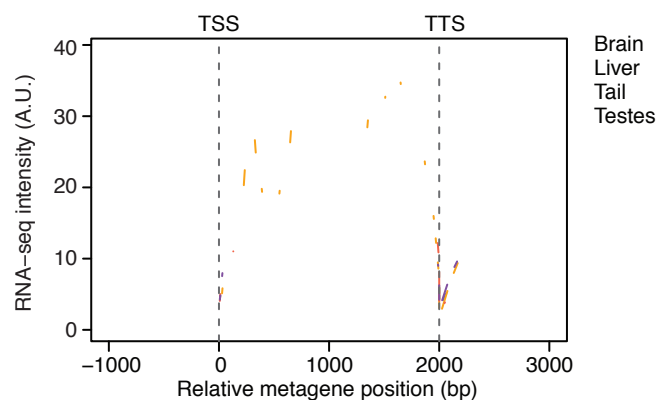
C Paired-end RNA-seq mapping



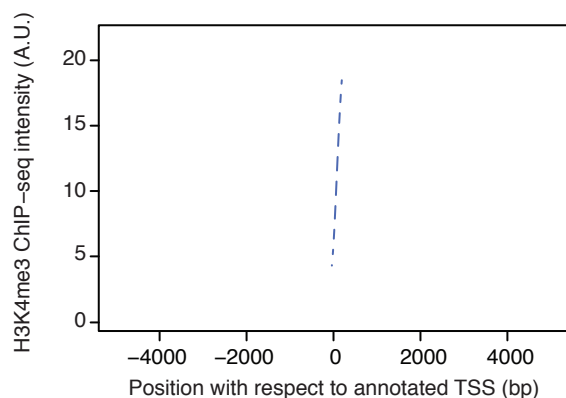
D Alignment of Sanger-sequenced genome shotgun contigs



E Gene body RNA-seq support



F Promoter annotation quality



G Nomenclature for protein-coding genes

