**Supplemental figure captions**

**Figure supplement 1:** *ScISOr-Seq improved gene models by extending the 3’ UTRs illustrated by tyr (ENSGACG00000007960), foxd3 (ENSGACG00000006933), and gata5 (ENSGACG00000003649).* scRNAseq reads are shown at the top for each gene in grey.The label to the right of the scRNAseq reads indicate the scale of the reads. The existing Ensembl models are shown in dark blue. The ScISOr-Seq reads (in grey) are shown above the respective gene models (in red) that they generated. Colored lines on the ScISOr-Seq and scRNAseq reads indicate a different base pair in the read than the stickleback reference genome (BROAD S1, 104.1 database version). The scale bar at the bottom indicates the position of each gene model. The ScISOr-Seq generated gene models capture the majority of the scRNAseq reads.

**Figure supplement 2**: *Expression patterns of sox9a and sox9b recapitulate expression seen in Cresko et al. 2003*. The two paralogs are plotted on separate Dot plots due to an order of magnitude difference in expression. A) as observed in Cresko *et al.* 2003, *sox9a* is expressed in the pharyngeal arches, brain, and somites. B) We found *sox9b* expression in the pharyngeal arches, retina, brain, and weakly in somites, similar to Cresko *et al.* 2003.

**Supplementary file captions**

**Supplementalfile1\_CellRangerOutputInformation.xlsx:** A table containing detailed Cell Ranger results for each annotation that was used.

**Supplementalfile2\_Annotation1\_scISOrSeq.gtf**: The genome annotations that originated from the scISOrSeq sequencing reads and was produced from SQANTI3.

**Supplementalfile3\_Annotation2\_Bulk\_Iso\_Seq.gtf**: The genome annotations that originated from the bulk Iso-Seq sequencing reads from Naftaly et al. (2021) and was produced from SQANTI3.

**Supplementalfile4\_Annotation3\_Pooled\_Iso\_Seqs\_merged\_with\_ensembl.gtf**: The genome annotations from ensembl (BROAD S1, 104.1) merged with the gtf file produced by SQANTI3’s file that originated from the bulk Iso-Seq and scISOrSeq data.

**Supplementalfile5\_Annotation4\_Pooled\_Iso\_Seqs\_merged\_with\_ensembl\_for\_cellranger.gtf**: The genome annotations from ensembl (BROAD S1, 104.1) merged with the gtf file produced by SQANTI3’s file that originated from the bulk Iso-Seq and scISOrSeq data. The file is the same as the annotation 4 file with the exception of mitochondrial genes which have gene names that start with MT.

**Supplementalfile6\_IsoSeq\_Processing\_Data.xlsx**: The processing information (reads retained and lost at each step) for the Bulk Iso-seq and ScISOr-Seq datasets.

**Supplementalfile7\_EnsemblModified\_manual\_changes.xlsx**: The 3’ UTR modifications made to the ensembl genome for select marker genes and *fgf*/*fgfr* genes.

**Supplementalfile8\_Annotation5\_ensembl\_modified.gtf**: The genome annotations from ensembl (BROAD S1, 104.1) with 3’ UTRs extended in select marker genes and *fgf*/*fgfr* genes as described in **EnsemblModified\_manual\_changes.xlsx**.