Supplemental Material to

Generation and analysis of a mouse multi-tissue genome annotation atlas

by

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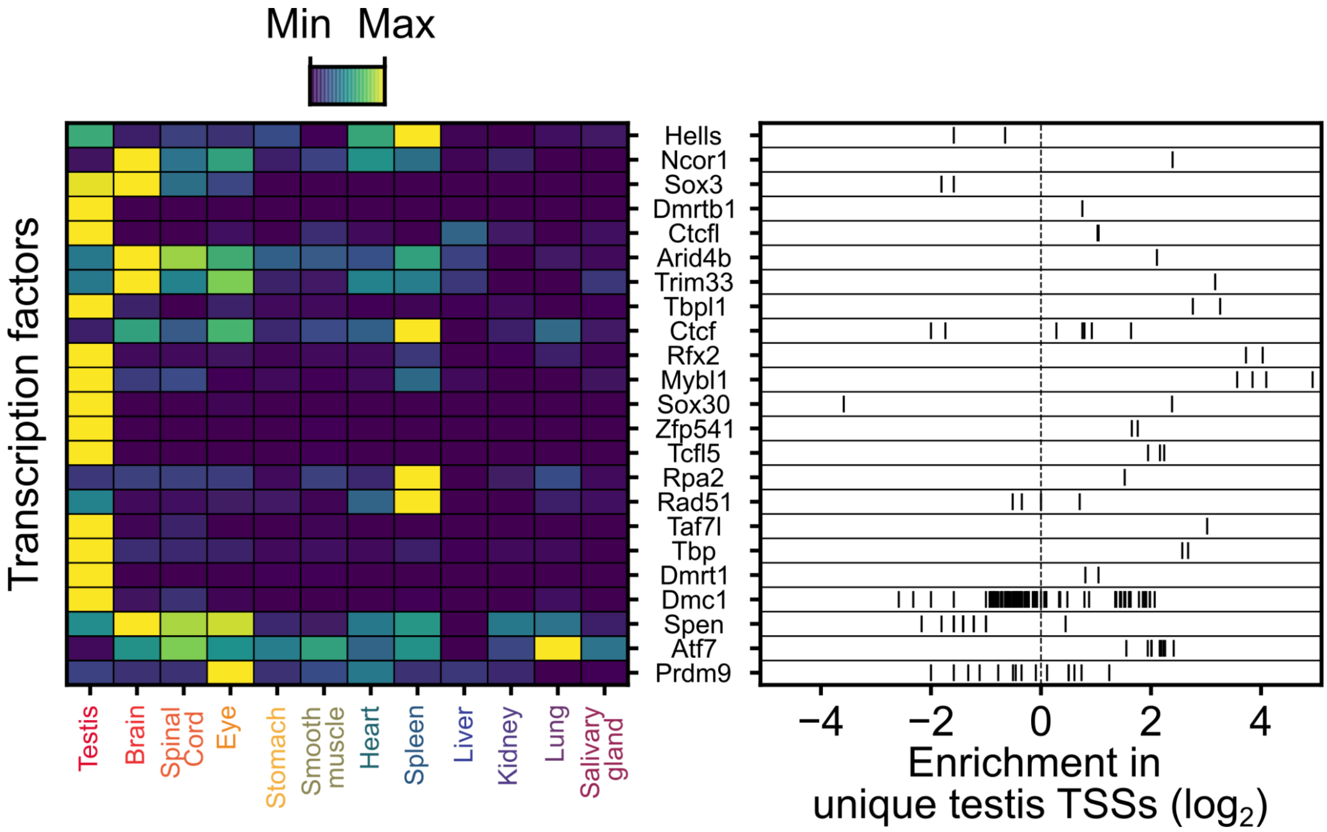

Fig. S1: Identifying testis specific transcription factors.

Left, tissue-level expression of transcription factors present in the ChIP-Atlas testis data. Right, transcription factor binding site enrichment in TSSs unique to testis. Each ChIP experiment present in the ChIP-Atlas is represented by an individual bar**.**

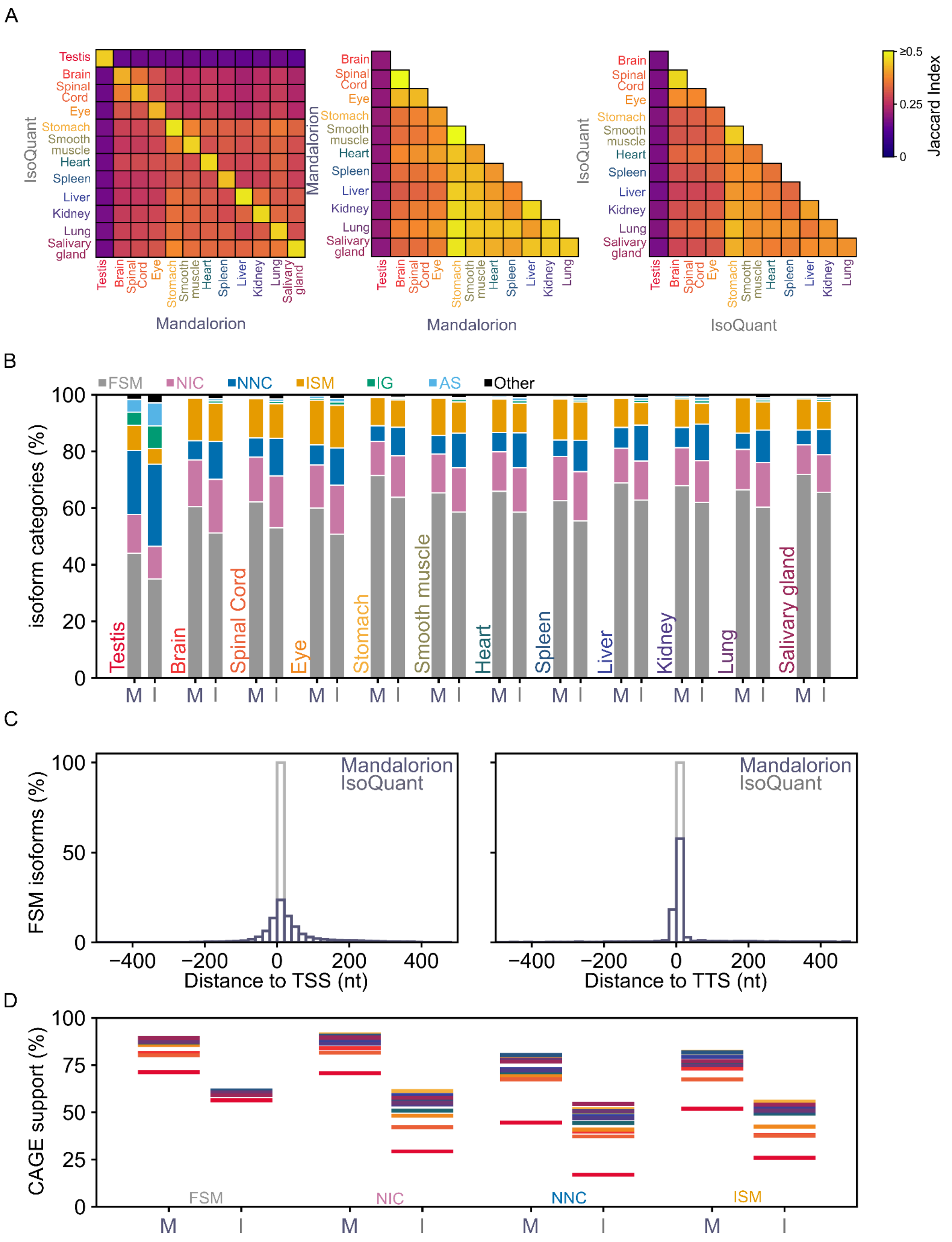

Fig. S2: Mandalorion and IsoQuant comparison. A) Isoform sets identified by Mandalorion or IsoQuant from the different tissues are compared using gffcompare to generate Jaccard Indexes.Jaccard Indexes are shown as heatmaps for comparisons of Mandalorion sets to each other (left), IsoQuant sets to each other, for comparisons between Mandalorion and IsoQuant sets. B) Isoform sets for different tissues and tools were categorized using sqanti3 and the resulting compositions are shown as stacked bars. C) The distances of transcription start sites (TSSs, left)) and transcription termination sites (TTSs, right) of isoforms categorized as ‘full_splice-match’ (FSM) by sqanti3 to the TSSs and TTSs of the annotated isoforms they are assigned to are shown as histograms. D) The percentages of isoforms whose TSS falls within a CAGE peak is shown as lines for different tissues (colors same as labels in (A)) and tools (M -> Mandalorion; I -> IsoQuant) separately for isoforms categorized as 'full-splice_match' (FSM), ’novel_in_catalog' (NIC), 'novel_not_in_catalog' (NNIC), or 'incomplete-splice_match' (ISM) by sqanti3.