

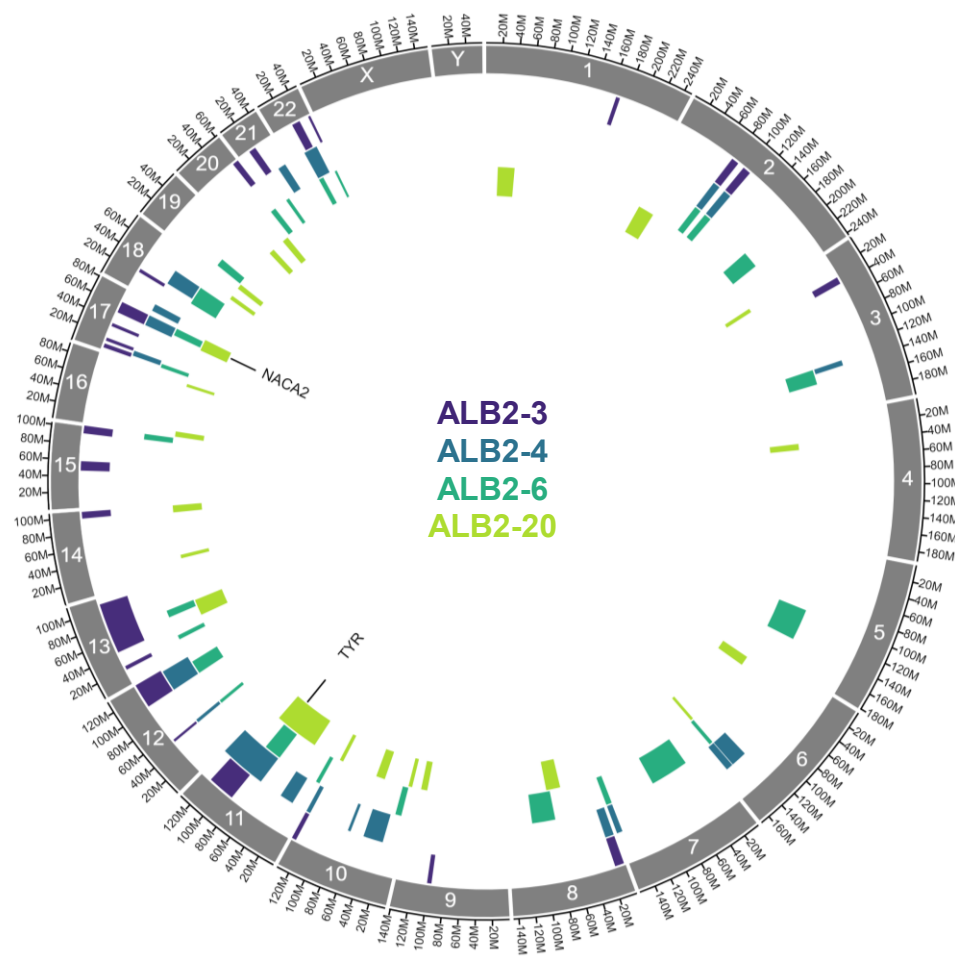


Fig. S1. Position of homozygosity-by-descent (HBD) regions in family ALB2. HBD regions from four affected family members are indicated with colour-codes. Only regions larger than 1 mbp is shown. Candidate genes in HBD regions, shared by all four affected individuals are indicated.

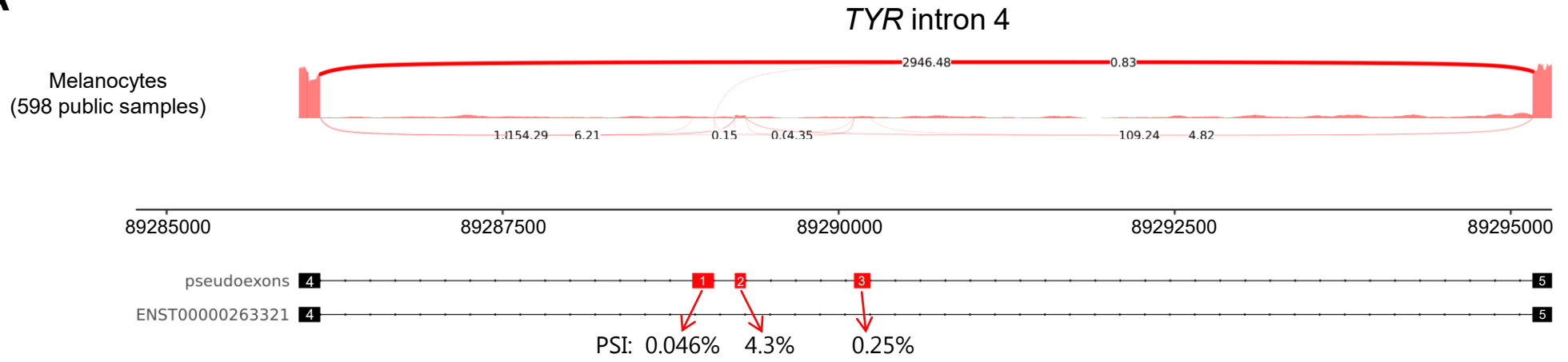
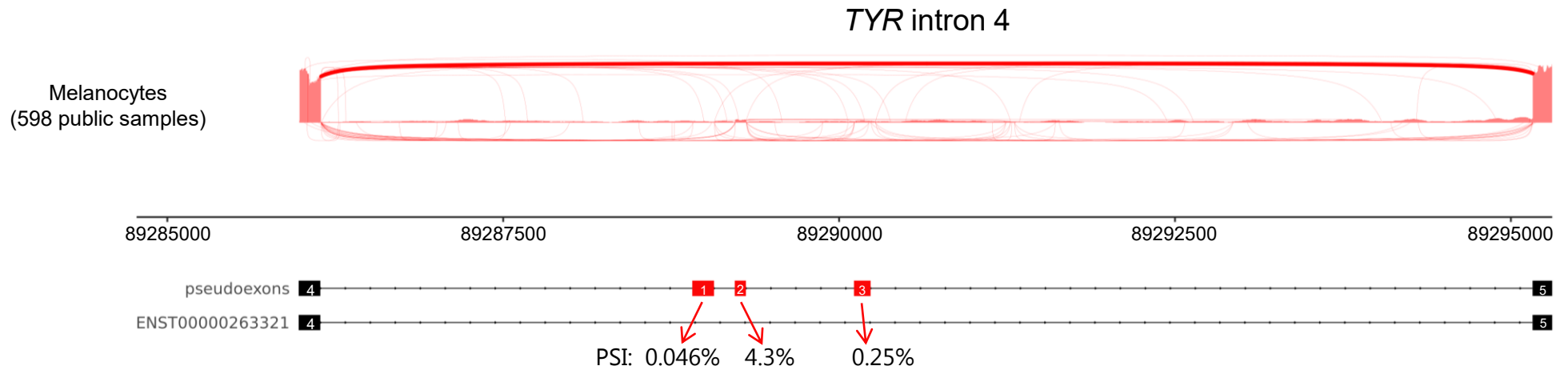
A**B**

Fig. S2. Sashimi plots of intron 4 of the *TYR* gene. Plots show mean coverage and junction count based on 598 publicly available melanocyte RNA-seq datasets. The position of exon 4, exon 5 and pseudoexons PE1-3 are indicated below each plot. Exon-inclusion ratio in *TYR* mRNA (percent spliced in, PSI) is shown for each pseudoexon. In panel (A) only the junctions matching splicing between PE1-3 and normal exons are shown, in panel (B) all junctions in the region are indicated with line thickness correlated to mean junction count.