

gene_name = SLC9A3R2

븕

main

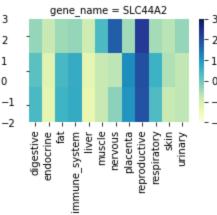
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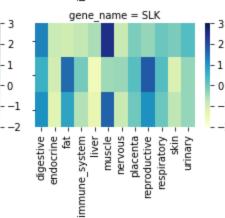
digestive

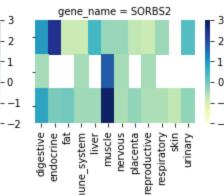
endocrine

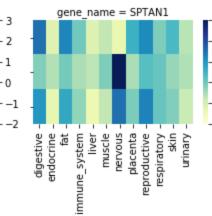
fat

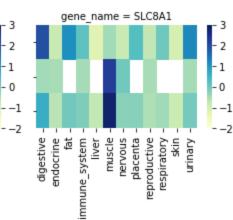
fat

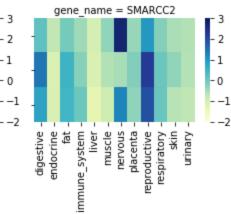


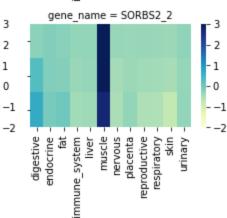


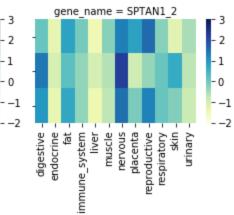


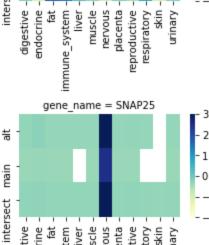




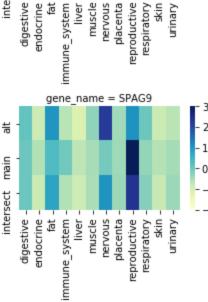


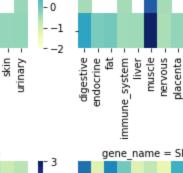


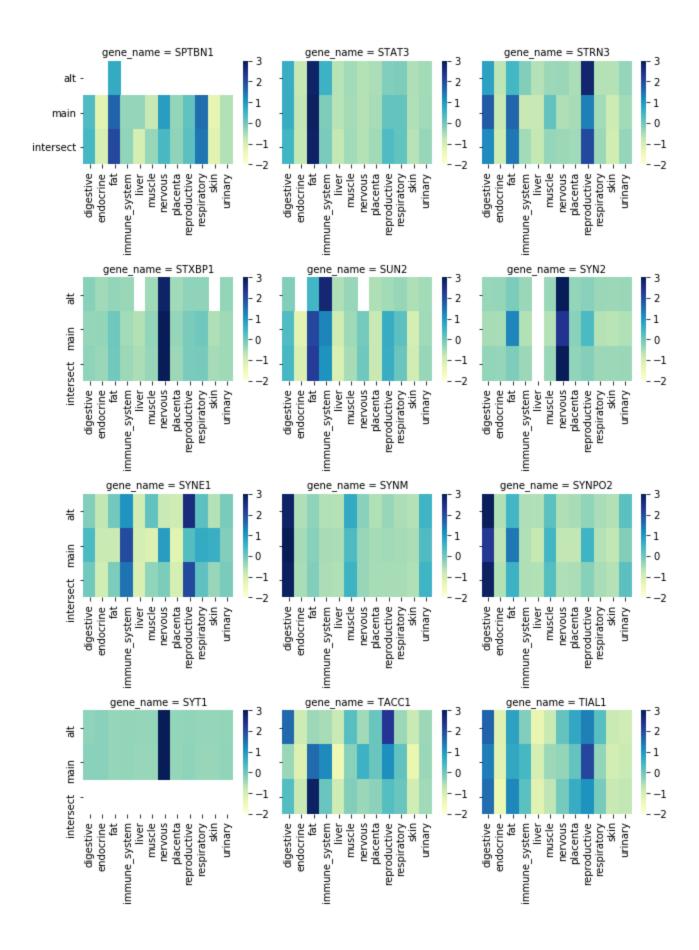


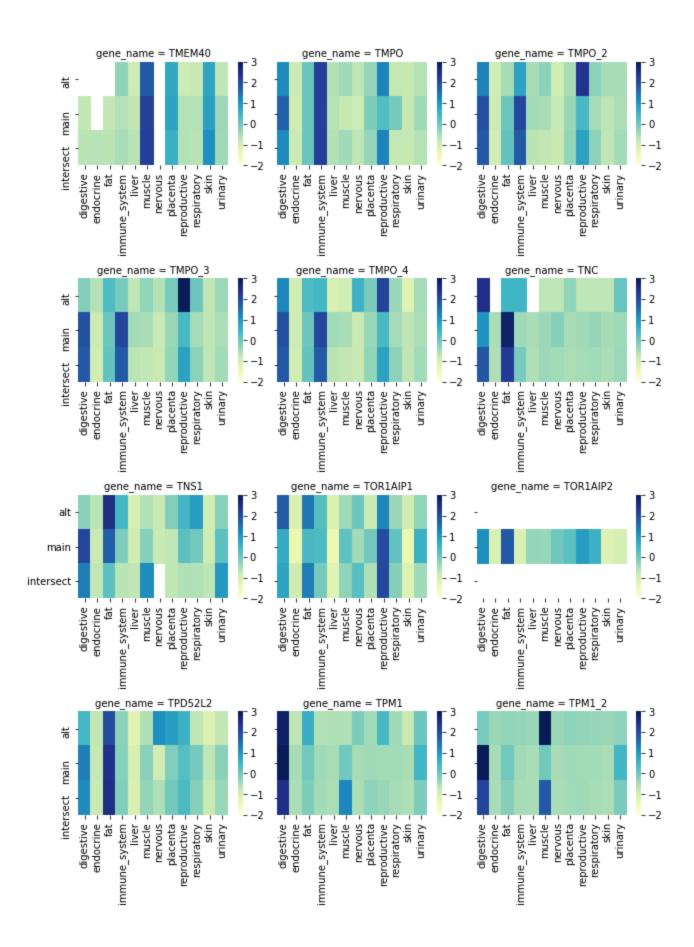


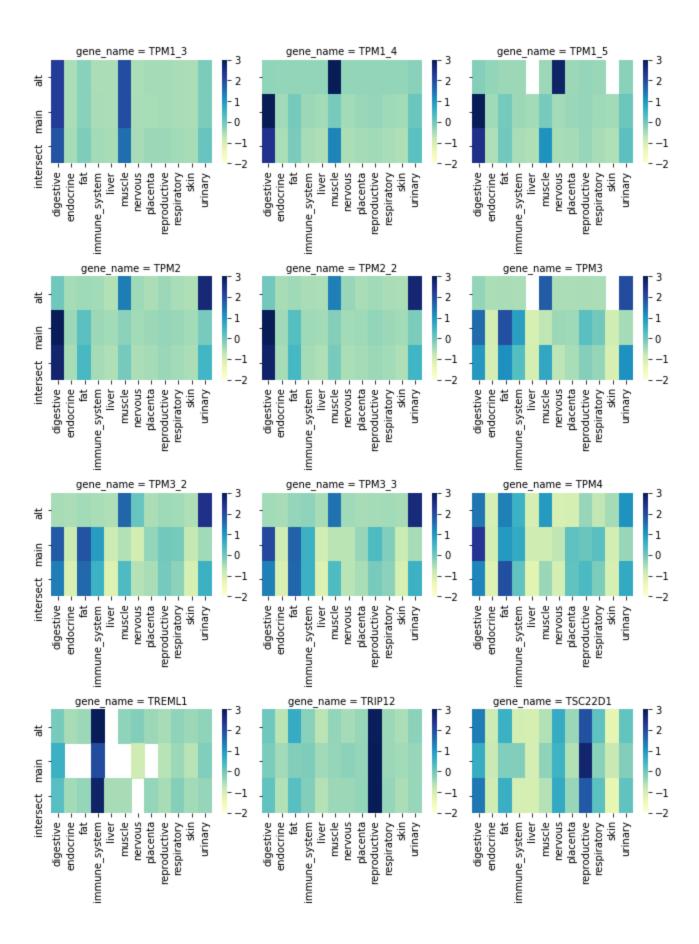
muscle nervous placenta respiratory

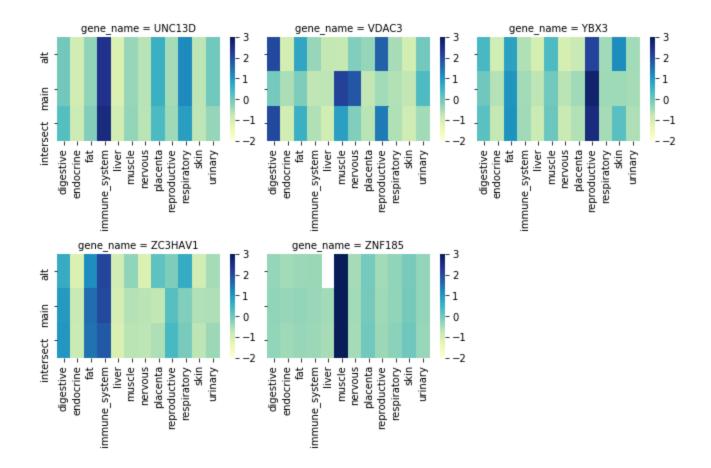












S7 Figure. Heatmaps with the standard deviation for the AS events.

We calculated the mean number of reads across all the tissue groups for each gene and used the mean to calculate standard deviations for each set of reads that mapped to each peptide. Events were counted as tissue group specific when the reads that mapped to one side of the splice event (equivalent to the main protein isoform or the alternative splice isoform) were at least one standard deviation higher than the other side of the splice event.