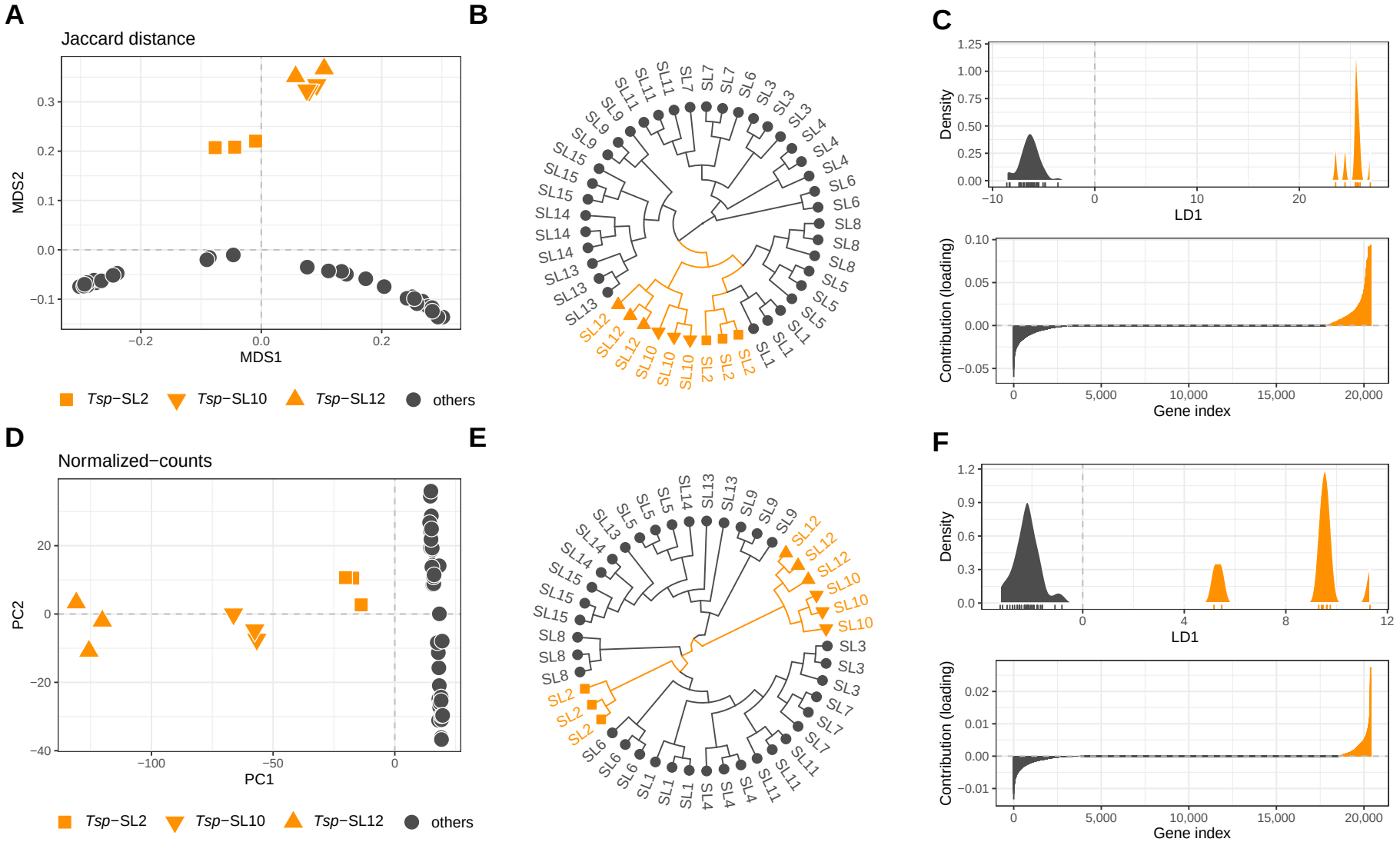

Supplemental Figure S2: Multivariate analysis of genome-wide locations of *trans*-splicing events highlights possible functional subdivision among SL2-type *trans*-spliced leaders in *T. spiralis*. (A, D) Ordination plots of Jaccard distance (multidimensional scaling, MDS) or Euclidean distance based on normalised variance-stabilised read counts (principal components analysis, PCA) among *Tsp*-SL read sets from three replicate RNAseq libraries (*Tsp*-SL1-*Tsp*-SL15). Gene annotations were derived *de novo* (BRAKER+TRINITY exon-corrected method; see main text) and *Tsp*-SL reads were classified with 10-bp match stringency. (B, E) Hierarchical clustering (Ward's method) of gene-based Jaccard or Euclidean distances among *Tsp*-SL read sets (*Tsp*-SL is abbreviated to 'SL' for simplicity). (C, F) Graphical overview of gene-specific contributions to multivariate group separation (linear discriminant analysis) between *Tsp*-SL read sets containing *Tsp*-SL2, SL10 or SL12 (orange) versus all other SLs (gray). The score of each read set in the linear discriminant function (LD1) is plotted as rug marks along the x-axis and score densities within the two groups are overlaid on the y-axis. Below, the contribution (=variable loading) of each gene to group discrimination along LD1 is plotted and coloured according to directionality (mathematical sign). Genes are ordered by contribution in ascending fashion.