

File Name: supplementary_data_1_list_sequenced_samples.xlsx

Description: Sequenced samples for all neuron types.

File Name: supplementary_data_2_novel_junctions.xlsx

Description: Novel splice junctions detected. For each putative novel junction, the neighbor genes are reported, as well as the neuron types in which this junction is expressed.

File Name: supplementary_data_3_genes_DAS_in_neurons_literature.xlsx

Description: Known AS genes compiled from literature.

File Name: supplementary_data_4_all_comparisons_sequence_features.xlsx

Description: Features of binary events that were tested, medians, and p-values, comparing non-DAS to DAS events. Chi-square tests with Holm correction for multiple comparisons.

File Name: supplementary_data_5_list_putative_splice_factors_for_network.xlsx

Description: Putative splice factors and RBPs included in the network.

File Name: supplementary_data_6_SF_expressions.xlsx

Description: Transcript quantifications of putative splice factors, used in the network.

File Name: supplementary_data_7_ground_truth_interactions_for_network.xlsx

Description: List of “ground truth” splicing regulatory interactions, indicating the ID and symbol of the Splice Factor and ID and symbol of its putative target.

File Name: supplementary_data_8_metrics_hyperparameters.xlsx

Description: Network metrics for various hyperparameters during Cross Validation. The column starting with “run” indicate the hyperparameters for this run, the column “fold” corresponds to the CV fold, the following columns indicate the value of the metrics.

File Name: supplementary_data_9_metrics_permutations.xlsx

Description: Network metrics for permutation test on best model. The model type (glasso, PSI, knn, k=4) was selected from previous runs. The column “permutation” is 0 for unpermuted data, otherwise corresponds to the permutation number.

File Name: supplementary_data_10_splicing_network_adjacency.xlsx

Description: Network adjacency matrix. Each row corresponds to an edge between a target event (indicated by its event_id, along with the ID and symbol of the gene it belongs to) and a Splice Factor (indicated by its transcript name, along with the ID and symbol of the gene it belongs to). The “degree” indicates the weight of the edge.