

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Sample IDs and Metadata

GEO IDs and metadata for all postmortem cortex transcriptomes considered in this analysis.

File Name: Supplementary Data 2

Description: Transposable Element Quantification

Transposable element raw counts for all samples considered in this analysis. TE counts reflect the application of the expectation maximization algorithm, to aid in the allocation of multi-mapping reads.

File Name: Supplementary Data 3

Description: Resource, software, and data sources

Resource, software, and data sources for the ALS patient stratification analysis performed in this study.

File Name: Supplementary Data 4

Description: Enrichment feature set

Normalized gene and TE counts for the 1681 features considered during enrichment, network development, and univariate analysis. Feature counts are provided for both the ALS and control cohorts.

File Name: Supplementary Data 5

Description: TE names corresponding to Fig. 2D

Row names for the 426 unique transposable elements presented in Fig. 2E.

File Name: Supplementary Data 6

Description: WGCNA analysis of TEs

Application of WGCNA to a feature set containing transposable elements exclusively. TE eigengenes do not show correlated expression at the subfamily, family or superfamily level – supporting the consideration of locus-specific TEs as unique molecular features.

File Name: Supplementary Data 7

Description: Eigengene membership

Eigengene memberships and gene significances are provided in the context of three clinical parameters: disease duration, age of symptom onset, and age at death.

File Name: Supplementary Data 8

Description: Eigengene enrichment for gene ontology

Enrichment of eigengenes for biological process, molecular function, and cellular component gene ontologies. Bonferroni-adjusted p -values are provided and used to assess significant associations between eigengenes and gene ontologies.

File Name: Supplementary Data 9**Description: ALS patient subtype assignment and clinical data**

Assignment of ALS patient subtype labels, using the majority agreement approach outlined in Tam et al.⁷. Clinical parameters, such as site of onset, age of onset, age at death, disease duration, fALS genetic characterization, and disease group, are provided for each ALS patient.

File Name: Supplementary Data 10**Description: Differential expression**

Pairwise differential expression analysis for ALS subtypes and controls. A multi-factor design equation was utilized for this analysis, accounting for sequencing platform, RIN, site of sample collection, and disease subgroup. A full list of subtype-associated features is also provided and provides the ALS subtype assigned to each feature during clustering with the NovaSeq and HiSeq cohorts.

File Name: Supplementary Data 11**Description: Sample subtype assignment**

Robustly assigned subtype labels are provided for all 451 ALS and control patient samples considered in this analysis.

File Name: Supplementary Data 12**Description: Network edge weights for VisANT**

WGCNA derived edge weights for eigengene network visualization in VisANT.