We counted the number of motor neurons per unit area containing a p62-positive cytoplasmic inclusion in cervical spinal cord anterior horn from 11 ALS patients including seven G93A/SN-ALS patients and four patients with sporadic ALS. Counts are plotted for each of cases 1-11 (Table 1).

Within independent tissue sections from cervical spine of ALS cases, counts of p62-positive and phosphorylated-TDP-43-positive inclusions are significantly correlated (Spearman rank correlation, p<0.05).

WGCNA analysis identified 82 network modules from genes correlated with counts of proteinaceous inclusions in diseased motor neurons. Clustering tree and heat map illustrate separation of the gene modules, a lower branch height or darker color denotes a greater Pearson correlation coefficient between pairs of genes.
Supplementary Figure 4: Survival analysis in lymphoblastoid cells from C9ORF72 (n=26) and sporadic ALS (n=20)

A

**C9ORF72-ALS**

![Survival curves for C9ORF72-ALS](image)

**Sporadic ALS**

![Survival curves for Sporadic ALS](image)

B

![Bar chart for number of cases](image)

Survival curves for patients from which lymphoblastoid cells were sampled (A). Patient samples were chosen to represent the extremes of survival in ALS. Logistic regression on disease duration identified genes from the immune module capable of distinguishing patients by rate of disease progression. Fitting binomial logistic regression with expression of ITGB2, CEBPD and ULRA2 and performing leave-one-out cross validation resulted in classification of individual patients as rapidly progressive (disease duration <2 years, labelled FAST) or slowly progressive (disease duration >4 years, labelled SLOW) independent of genetic background (3). For each sample group, columns depict, from left to right, the number of samples in the group, the number correctly classified by the model and the number of correct classifications expected by chance.