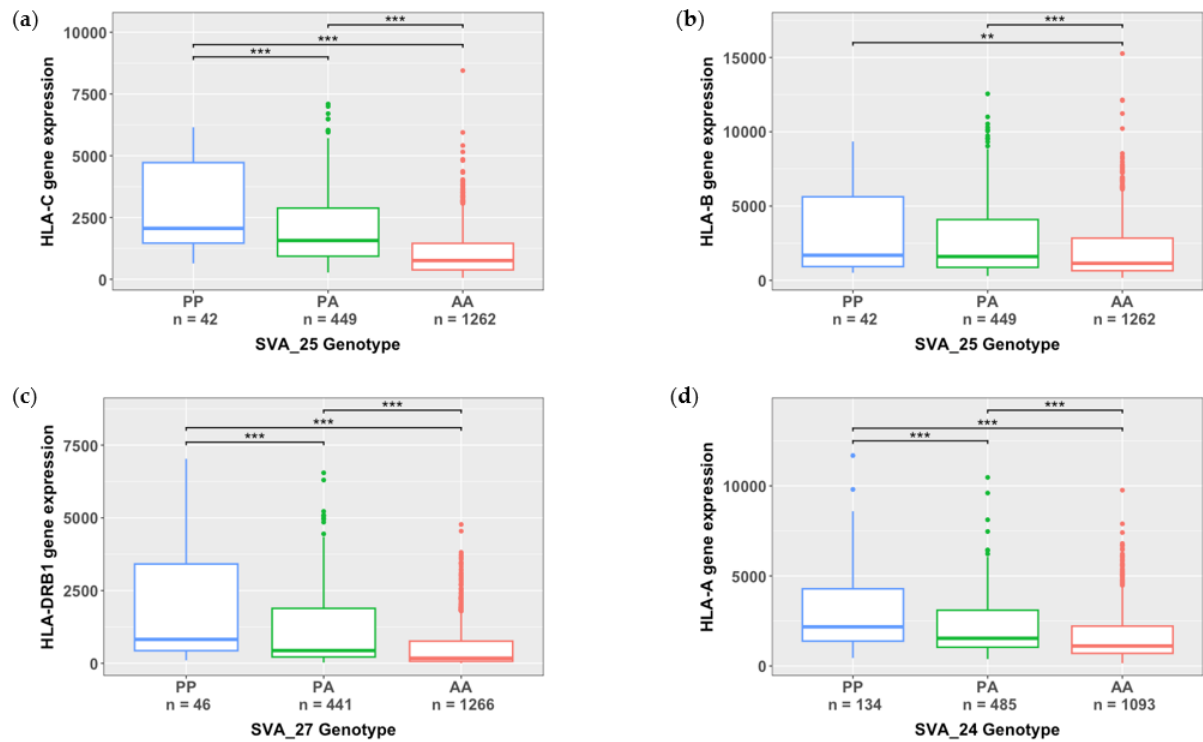
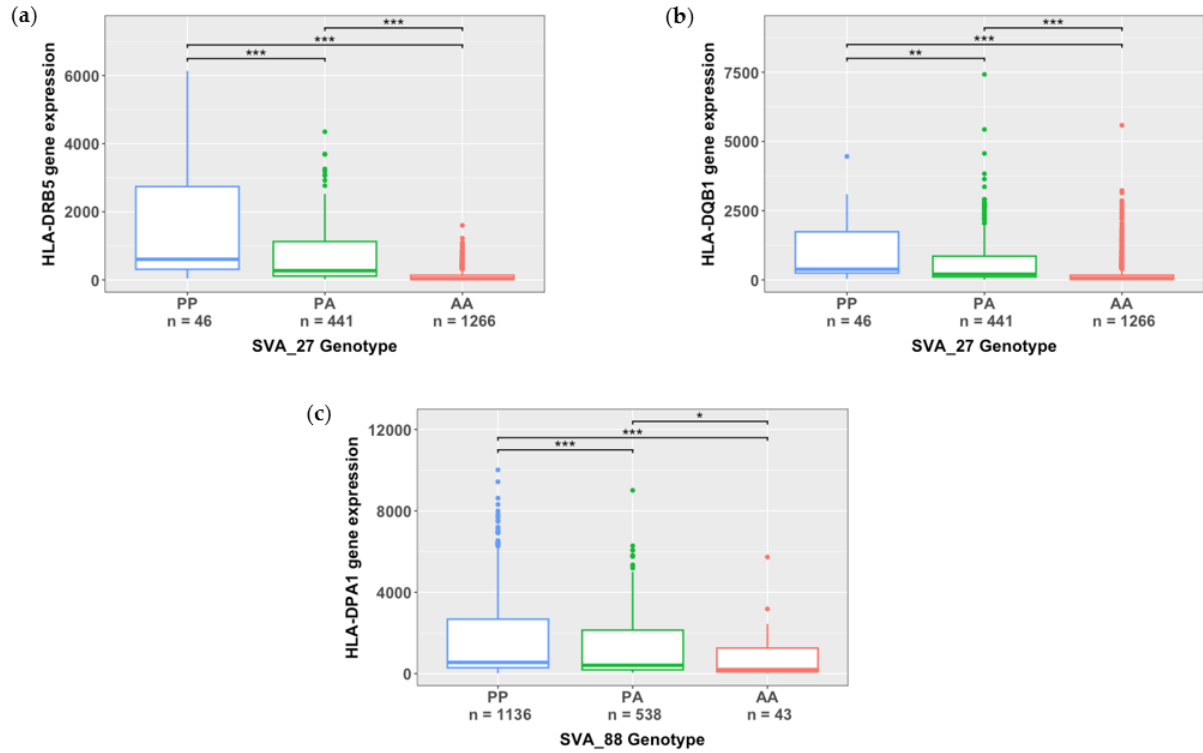


**Figure S1.** Boxplots of *cis*-acting SVA RIPs displaying the top two hits for largest effect size on both gene upregulation and downregulation. Datapoints from both ALS individuals and healthy controls across all CNS tissues were combined and the significance of gene expression changes between groups (PP, PA, and AA) was determined using the Wilcoxon pairwise comparison with FDR adjusted *p*-values (FDR<0.05). (a) Boxplot of *LRRC37A4P* gene expression stratified by SVA\_67 genotype. Significant differences were observed between all genotype groups, displaying a 447.3-fold ( $p=1.04E-40$ ), 214.4-fold ( $p=2.55E-38$ ) and 2.1-fold ( $p=8.70E-77$ ) increase in *LRRC37A4P* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_67 significantly upregulated *LRRC37A4P* gene expression. (b) Boxplot of *MAPT* gene expression stratified by SVA\_67 genotype. Significant differences were observed between all genotype groups, displaying a 1.4-fold ( $p=2.53E-09$ ), 1.2-fold ( $p=2.51E-04$ ) and 1.2-fold ( $p=2.14E-12$ ) increase in *MAPT* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_67 significantly upregulated *MAPT* gene expression. (c) Boxplot of *FCGBP* gene expression stratified by SVA\_73 genotype. Significant differences were observed between all genotype groups, displaying a 3.7-fold ( $p=3.61E-02$ ) and 10-fold ( $p=2.61E-03$ ) increase in *FCGBP* gene expression between the PP vs AA and PA vs AA genotype groups, whilst *FCGBP* gene expression was repressed by 63% ( $p=3.29E-08$ ) in the PP vs PA genotype group. (d) Boxplot of *FCGBP* gene expression stratified by SVA\_72 genotype. Significant differences were only observed between the PP vs AA and PP vs PA genotype groups demonstrating a 23% reduction ( $p=5.74E-03$ ) and 32% ( $p=1.85E-05$ ) reduction in *FCGBP* gene expression, respectively. A 1.2-fold ( $p=4.23E-01$ ) increase in *FCGBP* gene expression was indicated between the PA vs AA genotype groups, however no statistical significance was found. \* $p<0.05$ , \*\* $p<0.01$ , \*\*\* $p<0.001$ .



**Figure S2.** Boxplots of *cis*-acting SVA RIPs displaying four hits for the greatest effect size on gene upregulation. Datapoints from both ALS individuals and healthy controls across all CNS tissues were combined and the significance of gene expression changes between groups (PP, PA, and AA) was determined using the Wilcoxon pairwise comparison with FDR adjusted *p*-values (FDR<0.05). (a) Boxplot of *HLA-C* gene expression stratified by SVA\_25 genotype. Significant differences were observed between all genotype groups, displaying a 3.1-fold ( $p=1.83E-13$ ), 2.1-fold ( $p=1.82E-52$ ) and 1.5-fold ( $p=3.18E-03$ ) increase in *HLA-C* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_25 significantly upregulated *HLA-C* gene expression. (b) Boxplot of *HLA-B* gene expression stratified by SVA\_25 genotype. Significant differences were only observed between the PP vs AA and PA vs AA genotype groups demonstrating a 1.8-fold ( $p=2.84E-03$ ), and 1.4-fold ( $p=1.16E-10$ ) increase in *HLA-B* gene expression, respectively. A 1.3-fold increase in *HLA-B* gene expression was indicated between the PP vs PA genotype groups, however no statistical significance was found. (c) Boxplot of *HLA-DRB1* gene expression stratified by SVA\_27 genotype. Significant differences were observed between all genotype groups, displaying a 5.1-fold ( $p=1.01E-10$ ), 2.8-fold ( $p=1.84E-34$ ) and 1.8-fold ( $p=7.26E-04$ ) increase in *HLA-DRB1* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_27 significantly upregulated *HLA-DRB1* gene expression. (d) Boxplot of *HLA-A* gene expression stratified by SVA\_24 genotype. Significant differences were observed between all genotype groups, displaying a 1.9-fold ( $p=3.40E-18$ ), 1.4-fold ( $p=3.40E-18$ ) and 1.4-fold ( $p=3.44E-06$ ) increase in *HLA-A* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_24 significantly upregulated *HLA-A* gene expression. \*\* $p<0.01$ , \*\*\* $p<0.001$ .



**Figure S3.** Boxplots of *cis*-acting SVA RIPs displaying three hits for the greatest effect size on gene upregulation. Datapoints from both ALS individuals and healthy controls across all CNS tissues were combined and the significance of gene expression changes between groups (PP, PA, and AA) was determined using the Wilcoxon pairwise comparison with FDR adjusted *p*-values (FDR<0.05). **(a)** Boxplot of *HLA-DRB5* gene expression stratified by SVA\_27 genotype. Significant differences were observed between all genotype groups, displaying a 23.3-fold ( $p=7.51E-22$ ), 10.4-fold ( $p=5.38E-100$ ) and 2.3-fold ( $p=1.01E-04$ ) increase in *HLA-DRB5* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_27 significantly upregulated *HLA-DRB5* gene expression. **(b)** Boxplot of *HLA-DQB1* gene expression stratified by SVA\_27 genotype. Significant differences were observed between all genotype groups, displaying a 12.4-fold ( $p=1.07E-14$ ), 6.4-fold ( $p=1.17E-57$ ) and 1.9-fold ( $p=2.06E-03$ ) increase in *HLA-DQB1* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_27 significantly upregulated *HLA-DQB1* gene expression. **(c)** Boxplot of *HLA-DPA1* gene expression stratified by SVA\_88 genotype. Significant differences were observed between all genotype groups, displaying a 2.3-fold ( $p=7.63E-06$ ), 1.8-fold ( $p=1.05E-03$ ) and 1.3-fold ( $p=2.49E-07$ ) increase in *HLA-DQB1* gene expression between the PP vs AA, PA vs AA, and PP vs PA genotype groups. Presence of SVA\_88 significantly upregulated *HLA-DPA1* gene expression. \* $p<0.05$ , \*\* $p<0.01$ , \*\*\* $p<0.001$ .