Supplementary information

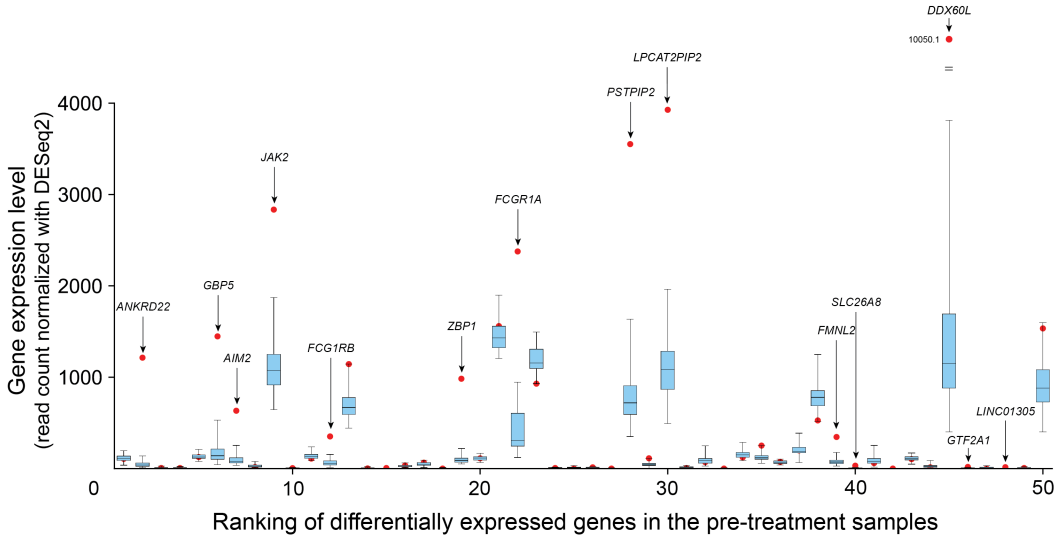
Comparative transcriptome analysis of Parkinson's disease focusing on the efficacy of zonisamide

Naito T et al.

Supplementary Note 1. Sample removal in transcriptome data

We initially performed differential gene expression analysis between SRs and NRs for each test set; however, we identified that there was significant enrichment of immune-related genes in the top differentially expressed genes in the pre-treatment samples. We detected that this trend was caused by abnormally high gene expression levels in one sample (**Supplementary Fig. 1**). The abnormally high expressions totally disappeared in the other timing (i.e., post-treatment). Most such genes were reported to be upregulated in viral infection: listed in a previous study of differential gene expression analysis of viral infection (e.g., *ANKRD22*, *AIM2*, *JAK2*, *FCGR1B*, *ZBP1*, *FCGR1A*, *SLC26A8*, and *GLS*),[1] or in GEO signatures of differentially expressed genes for viral infections (e.g., *GBP5*, *PSTPIP2*, *LPCAT2, FMNL2*, *SLC26A8*, *DDX60L*, and *GTF2A1*).[2] Therefore, we considered that the sample was likely to be infected with a virus or in some other transient immune active condition and excluded it from subsequent analyses.

Supplementary Fig. 1. Top differentially expressed genes between SRs and NRs in the pre-treatment samples before sample removal



The gene expression levels of top 50 differentially expressed genes between SRs and NRs in the pre-treatment samples are shown in the box plots. For individual genes on the horizontal axis, the lower and upper limits of the boxes represent the maximum and minimum values within 1.5 × interquartile range from the hinge, respectively, and the top and bottom whiskers represent the 5% and 95% percentiles, respectively. The red dots represent the expression levels of the removed sample. Genes with outlier expression levels in the removed sample were indicated by arrows with the names.

References

1. Zarei Ghobadi M, Mozhgani SH, Farzanehpour M, Behzadian F. Identifying novel biomarkers of the pediatric influenza infection by weighted co-expression network analysis. Virol. J. 2019;16(1):1–10.
2. Barrett T, Wilhite SE, Ledoux P, et al. NCBI GEO: archive for functional genomics data sets—update. Nucleic Acids Res. 2012;41(D1):D991–D995.