

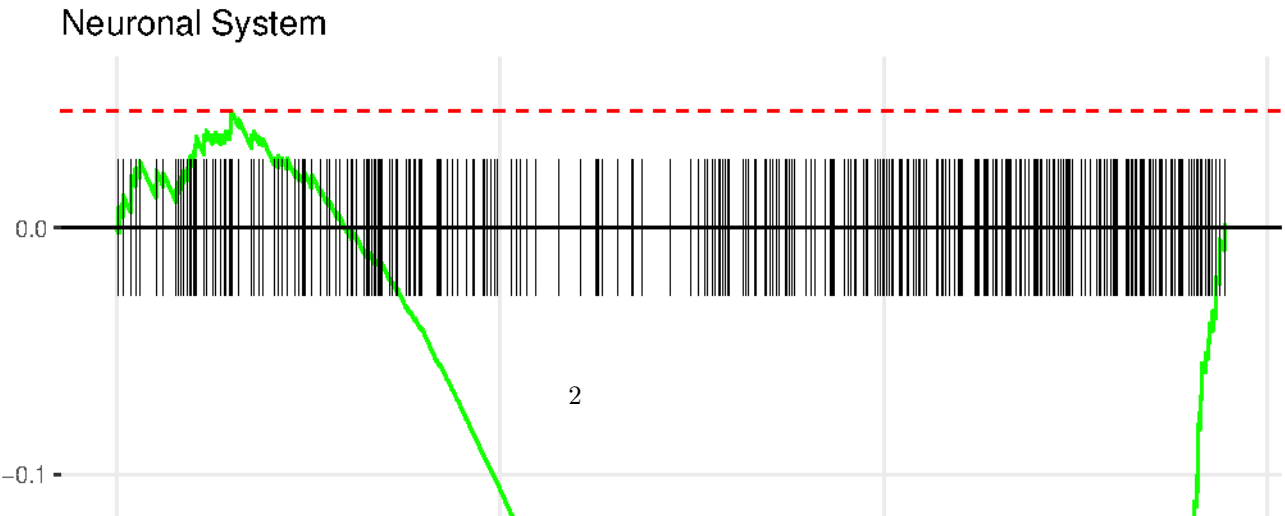
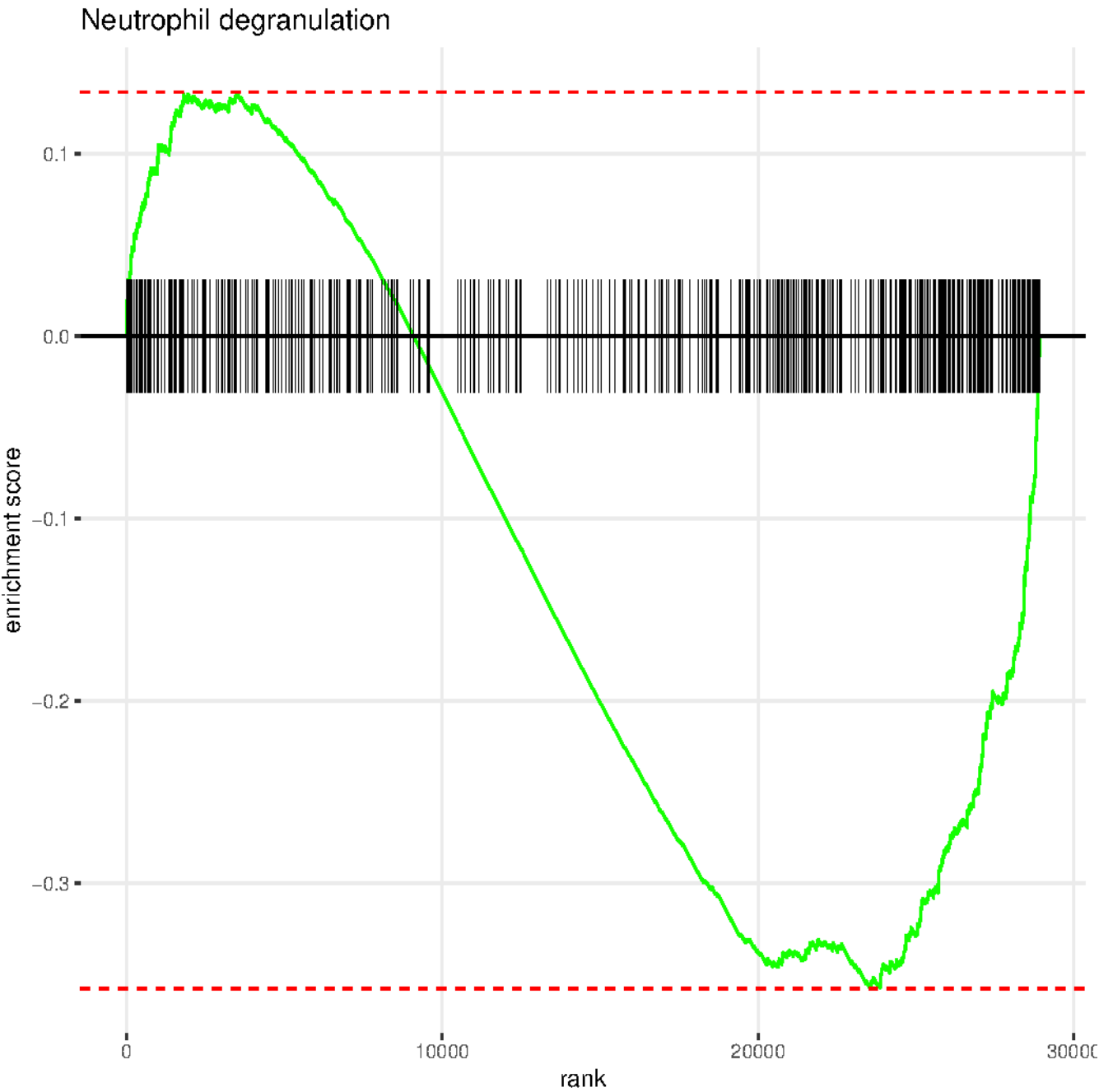
Gene Set Enrichment Analysis

RaNA-seq

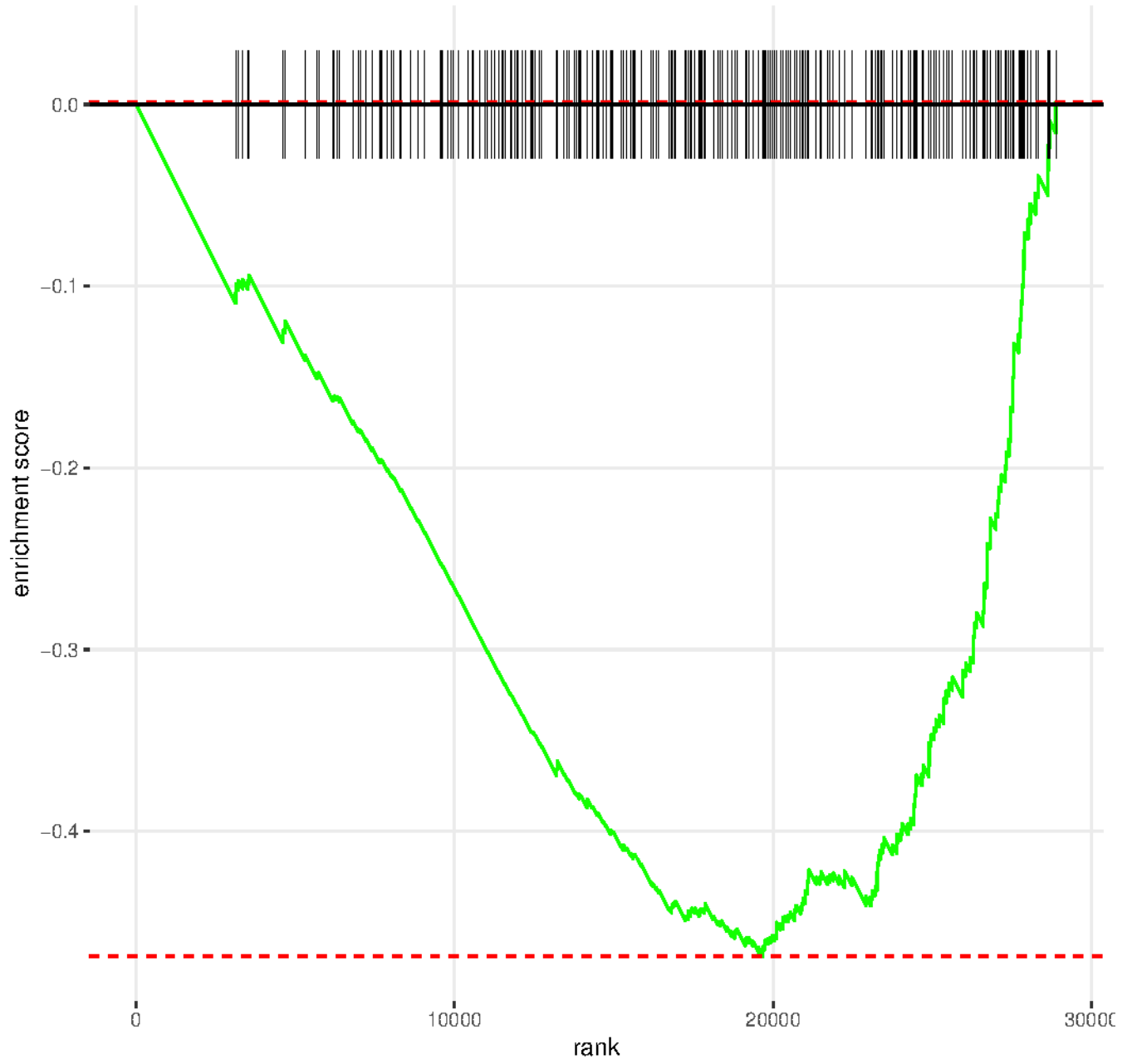
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Gene set enrichment analysis was performed with the fgsea R package (Sergushichev 2016).

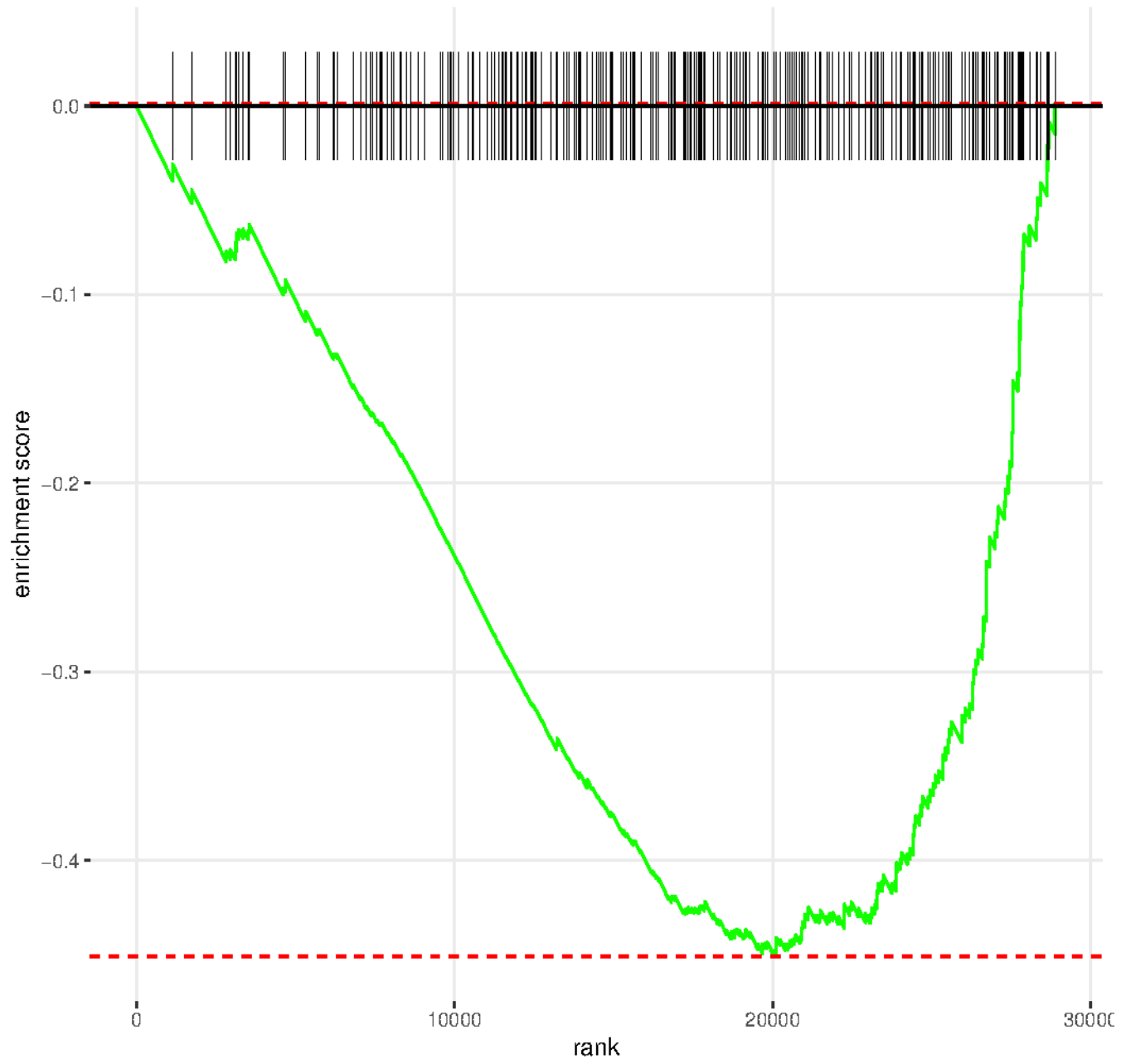
Pathway RUG plots



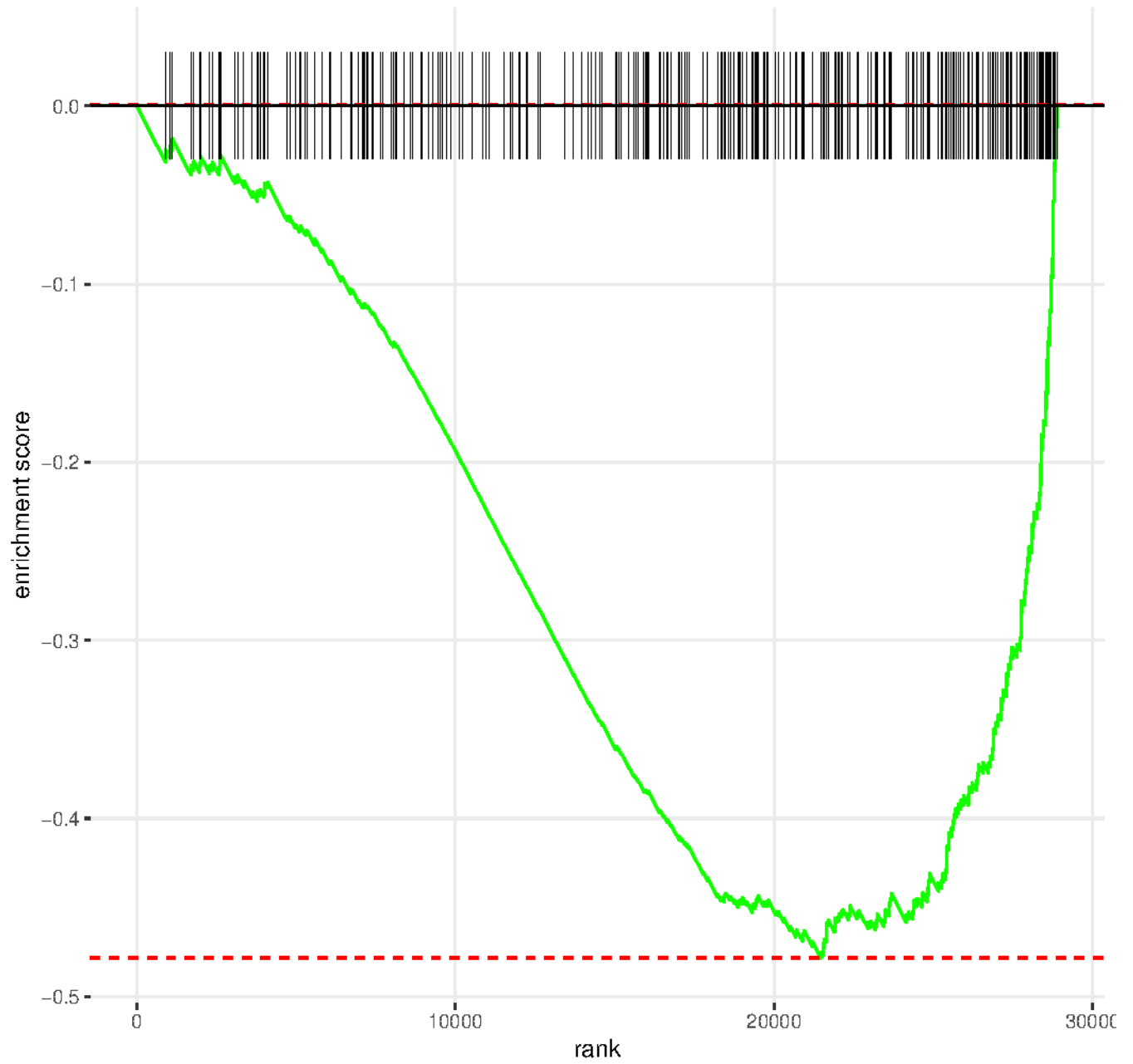
Olfactory Signaling Pathway

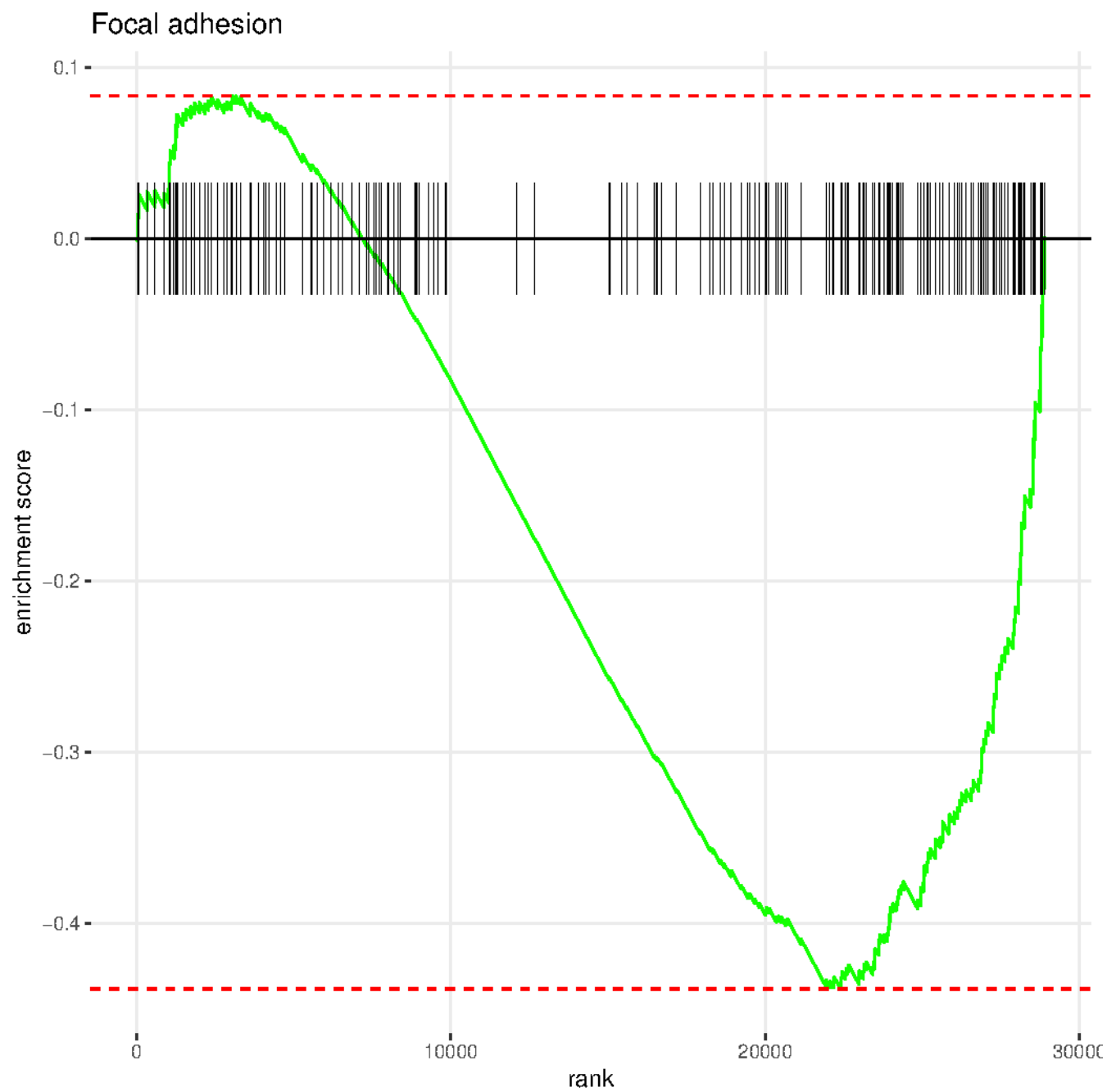


Olfactory transduction

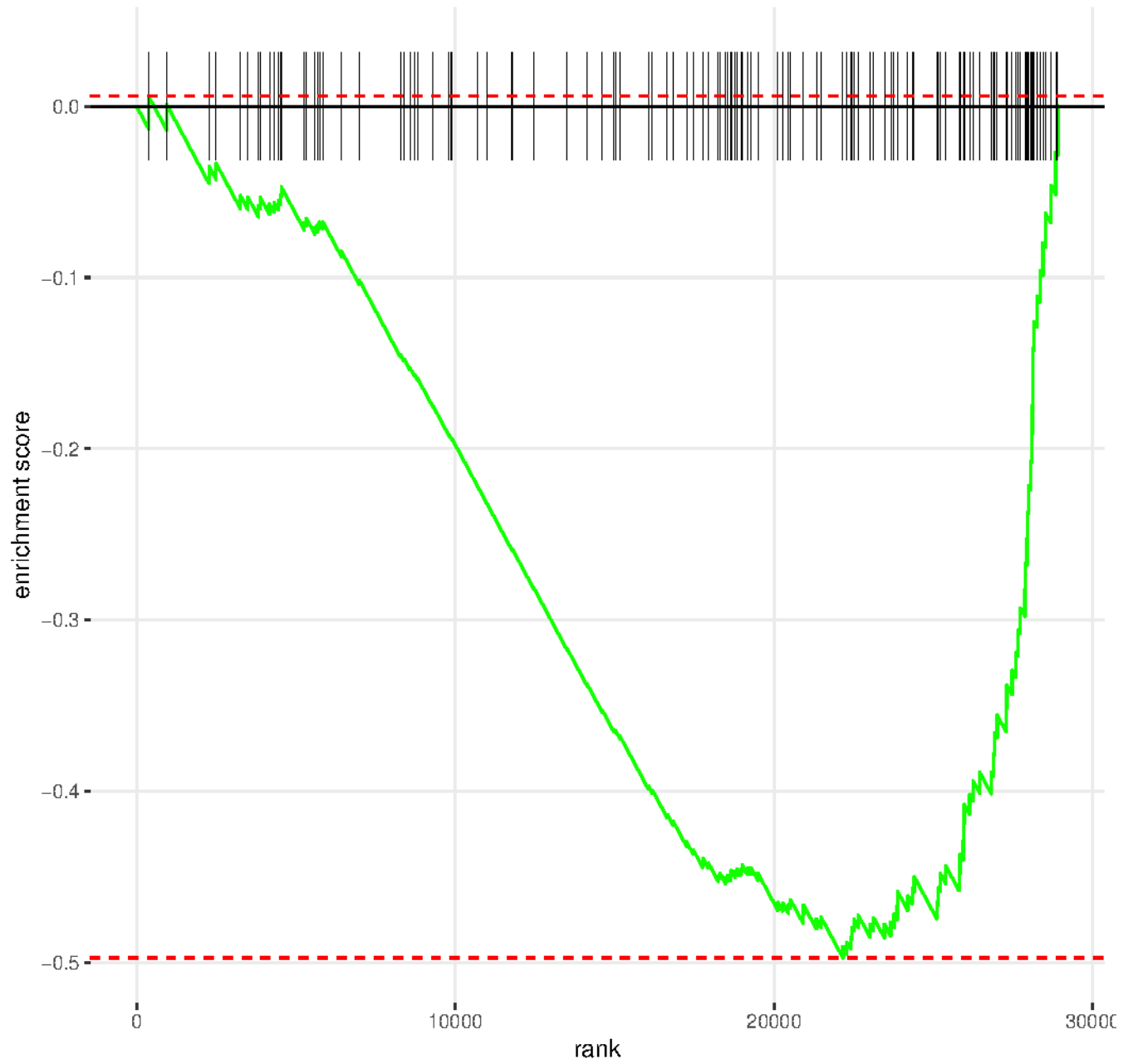


Extracellular matrix organization

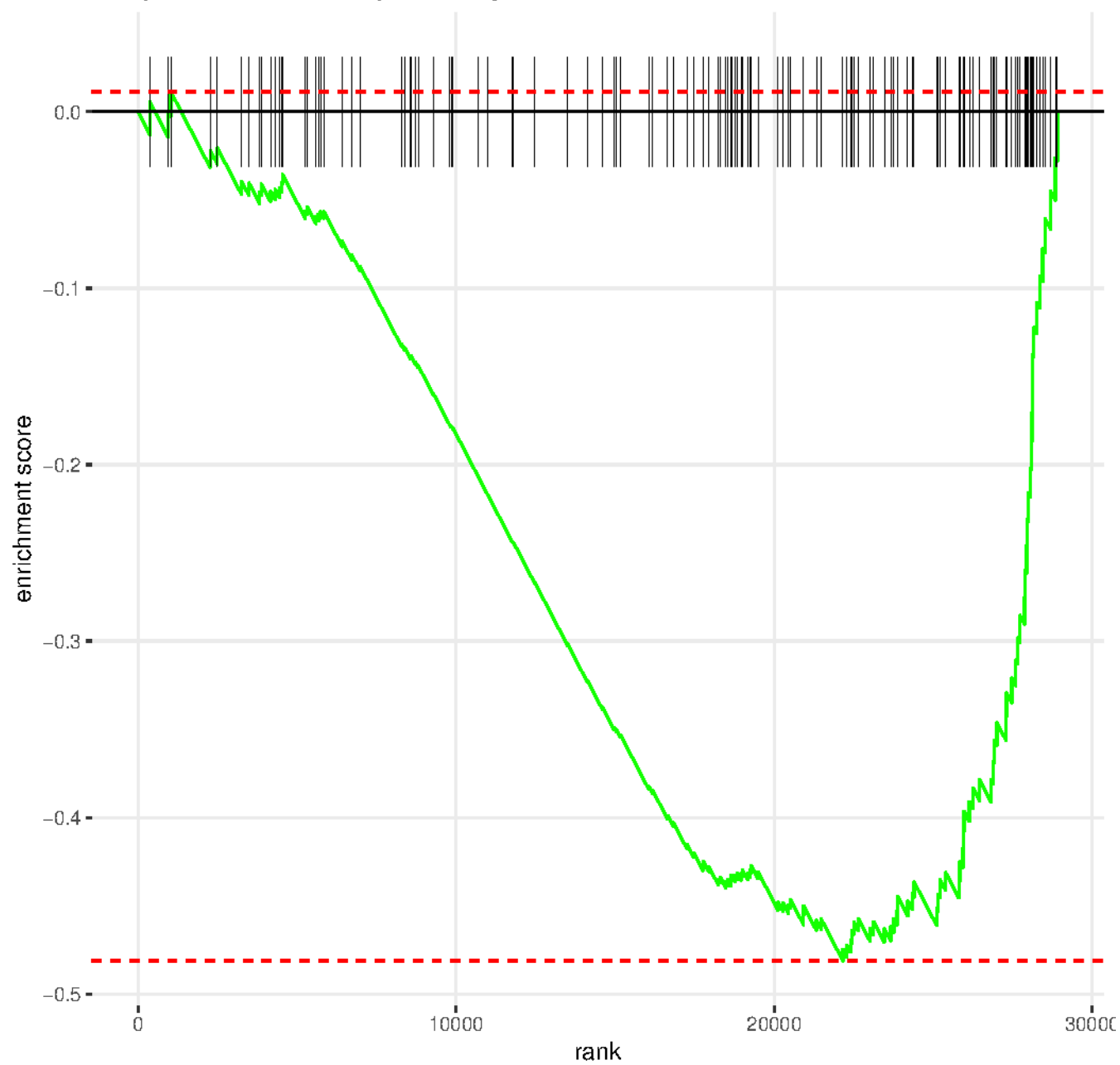


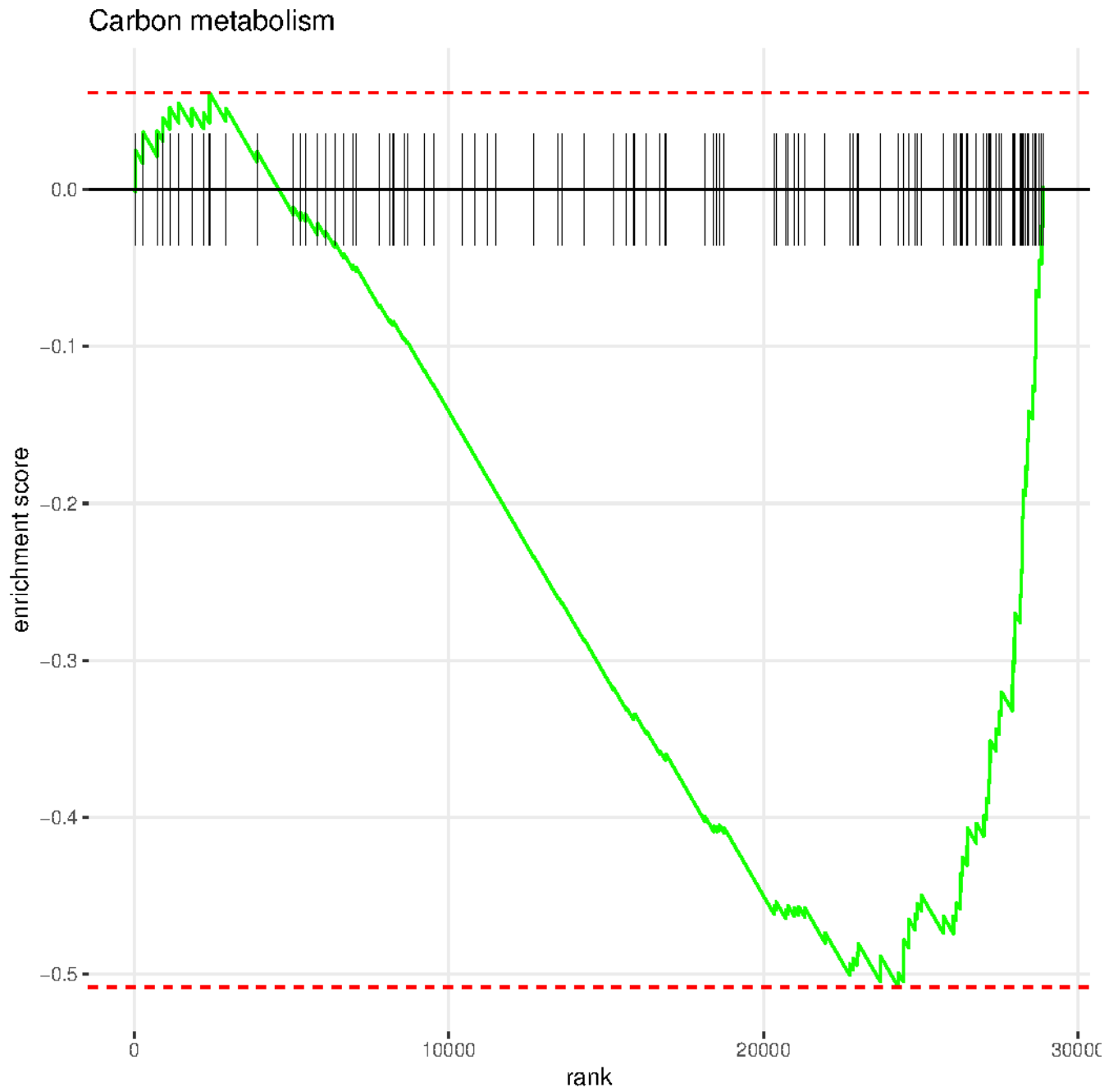


Platelet degranulation



Response to elevated platelet cytosolic Ca²⁺

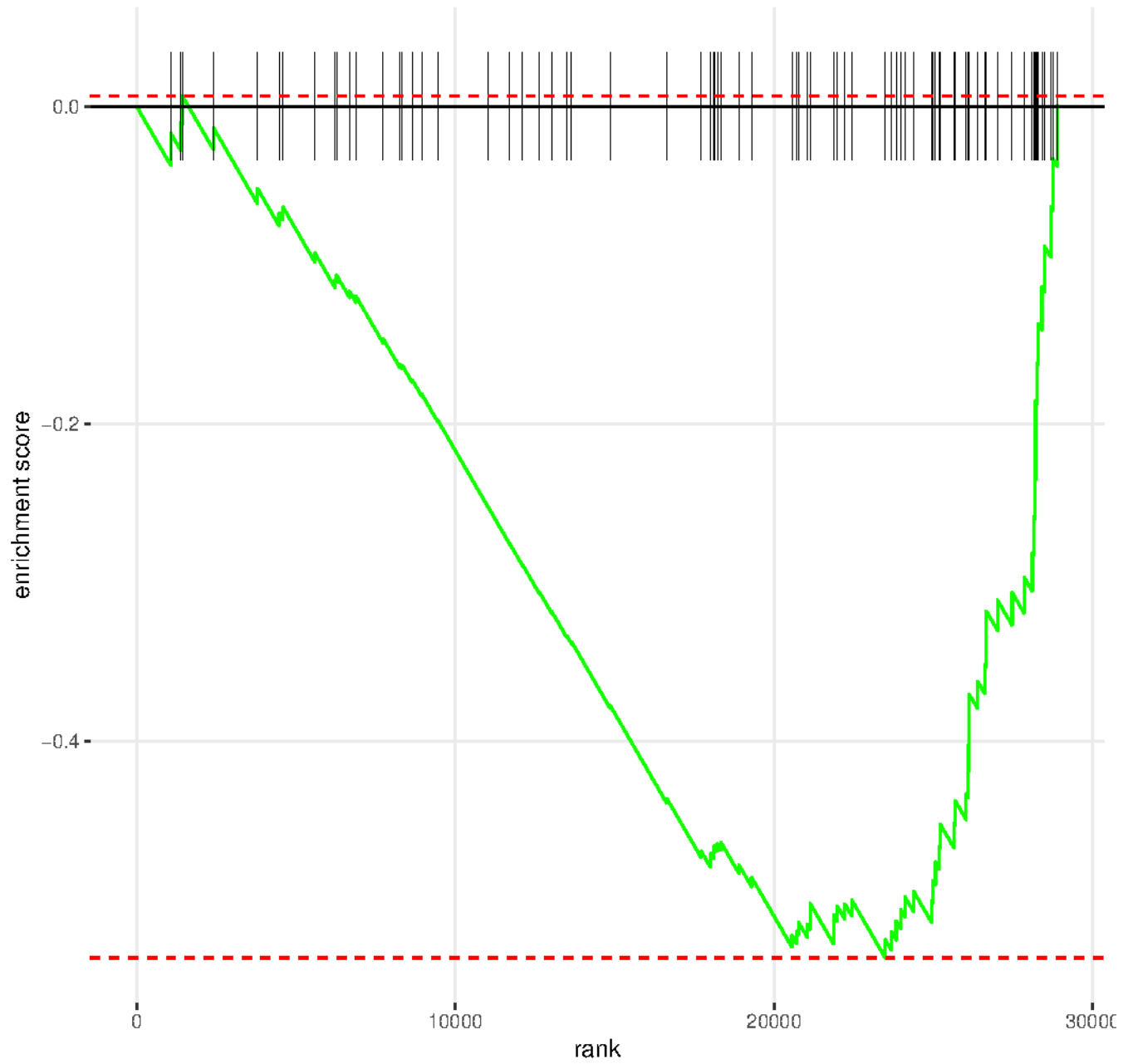


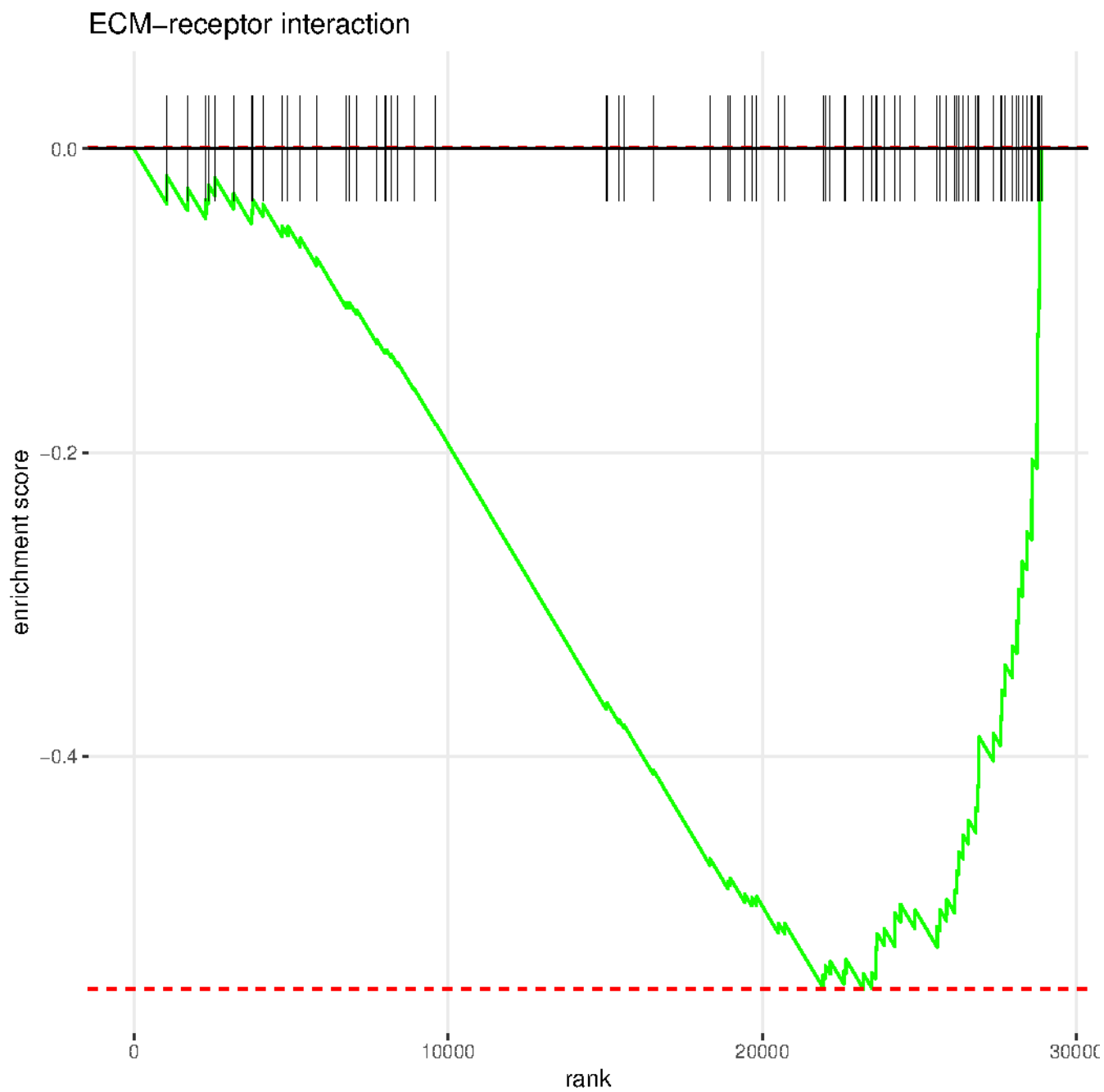


Collagen formation

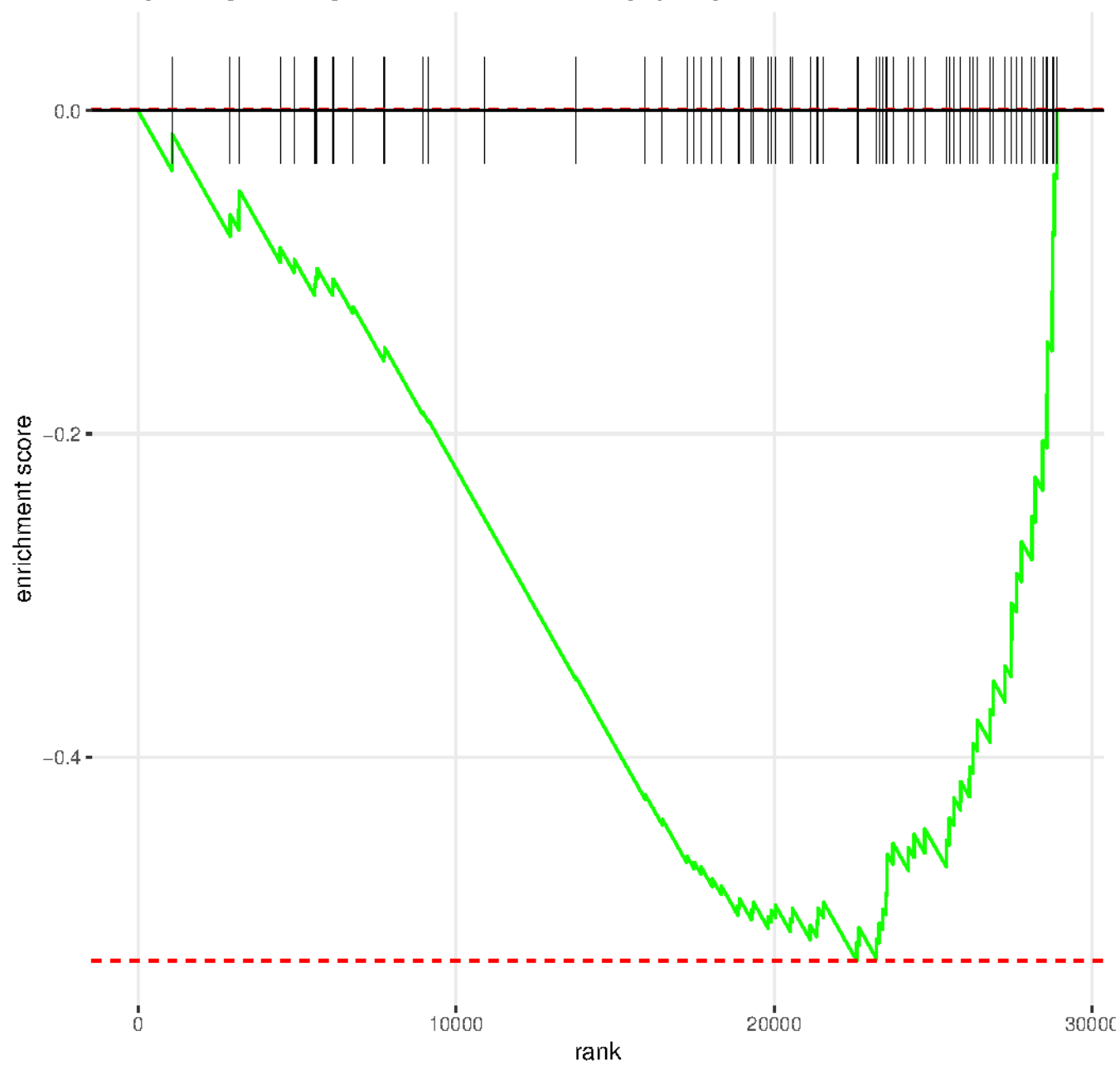


Cell junction organization

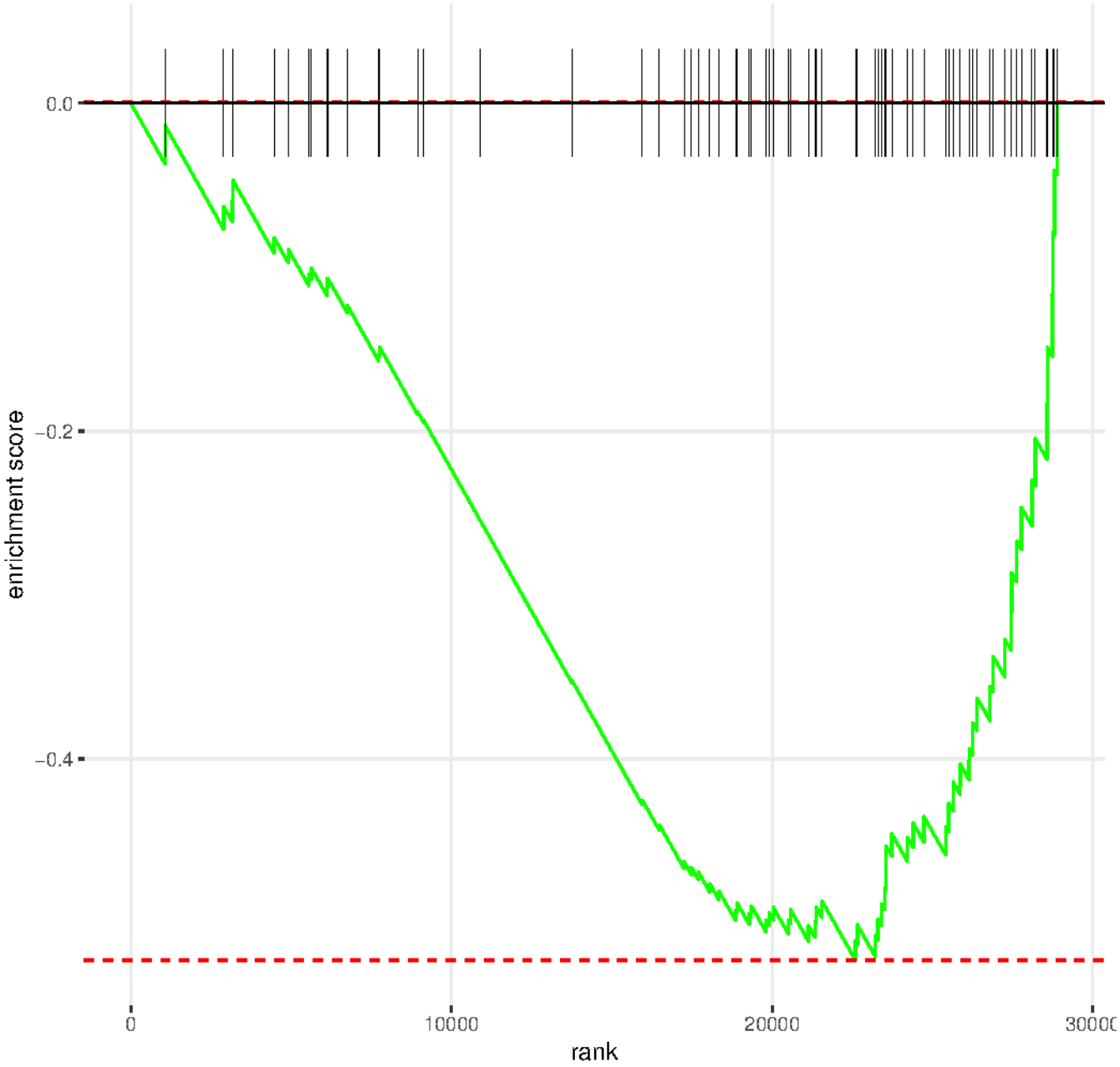


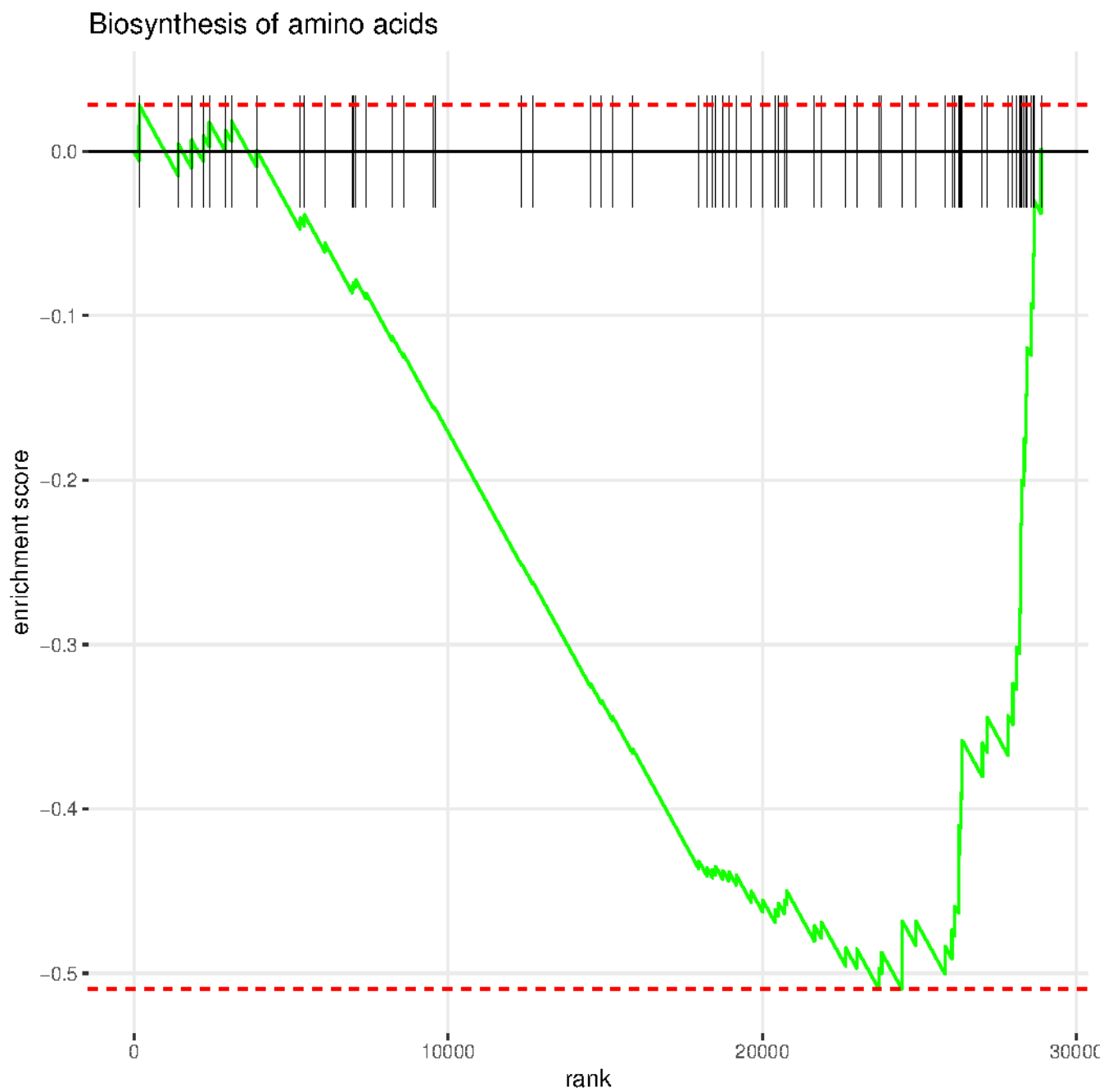


Arrhythmogenic Right Ventricular Cardiomyopathy



Arrhythmogenic right ventricular cardiomyopathy (ARVC)

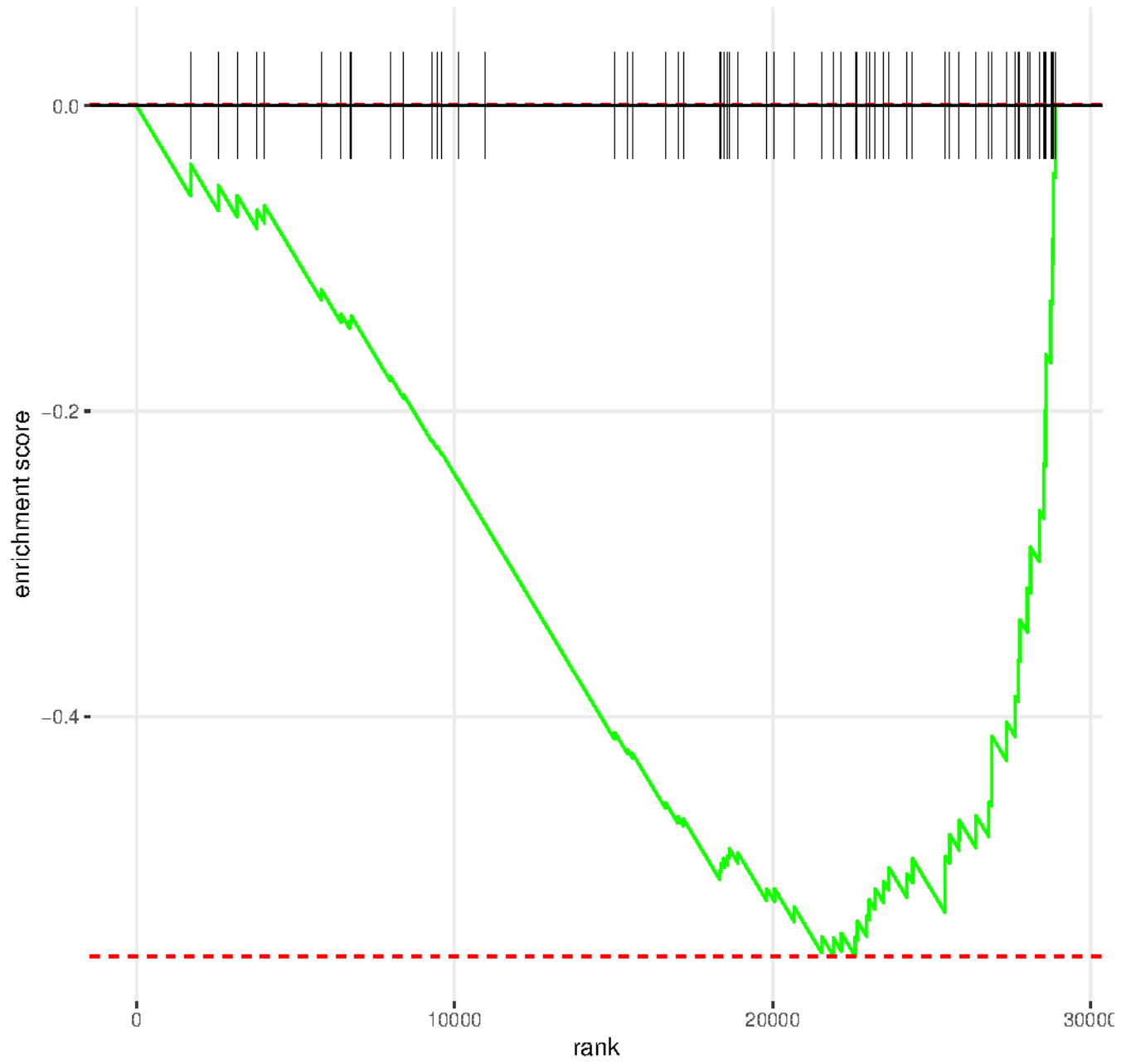


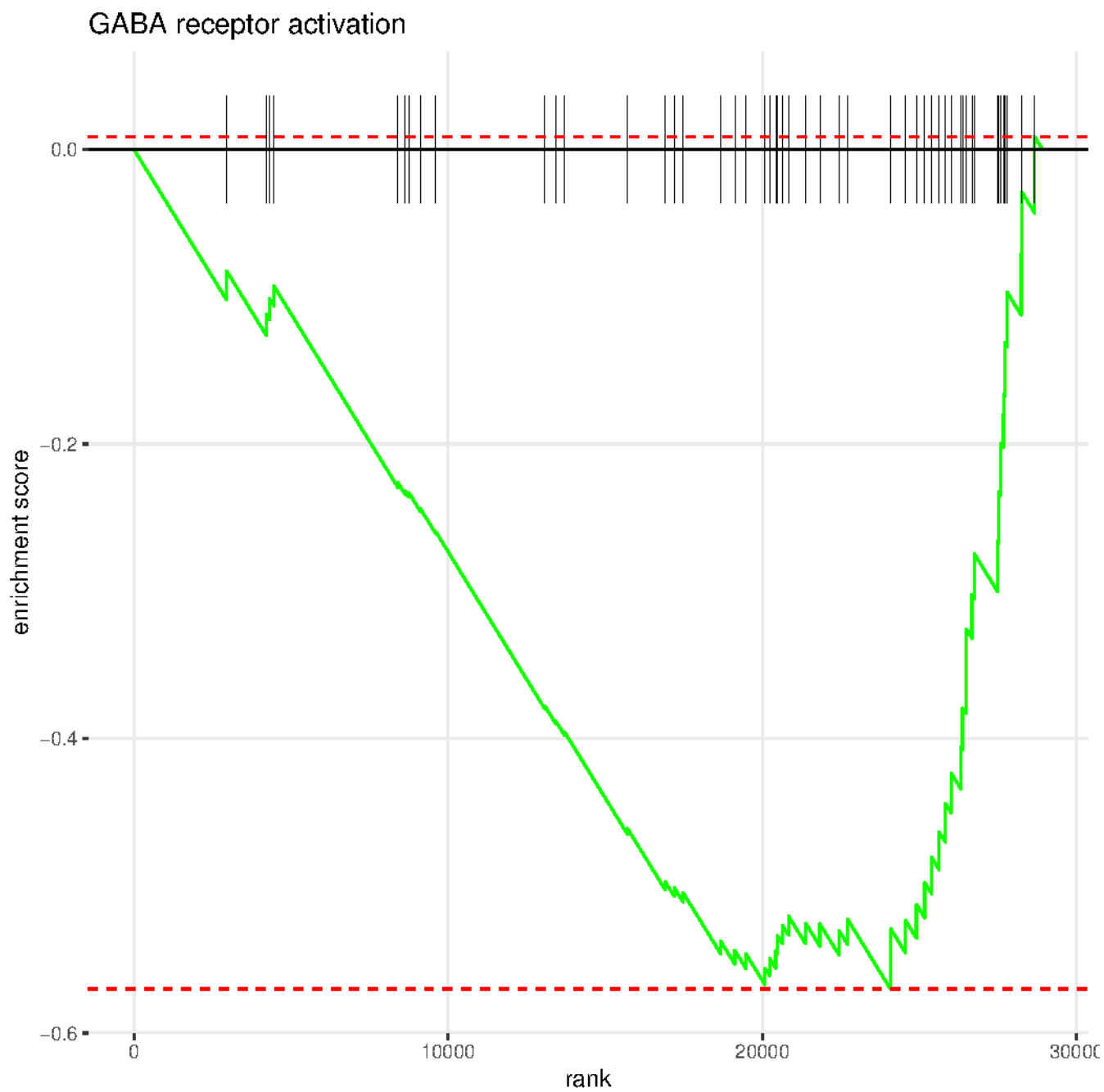


Collagen biosynthesis and modifying enzymes

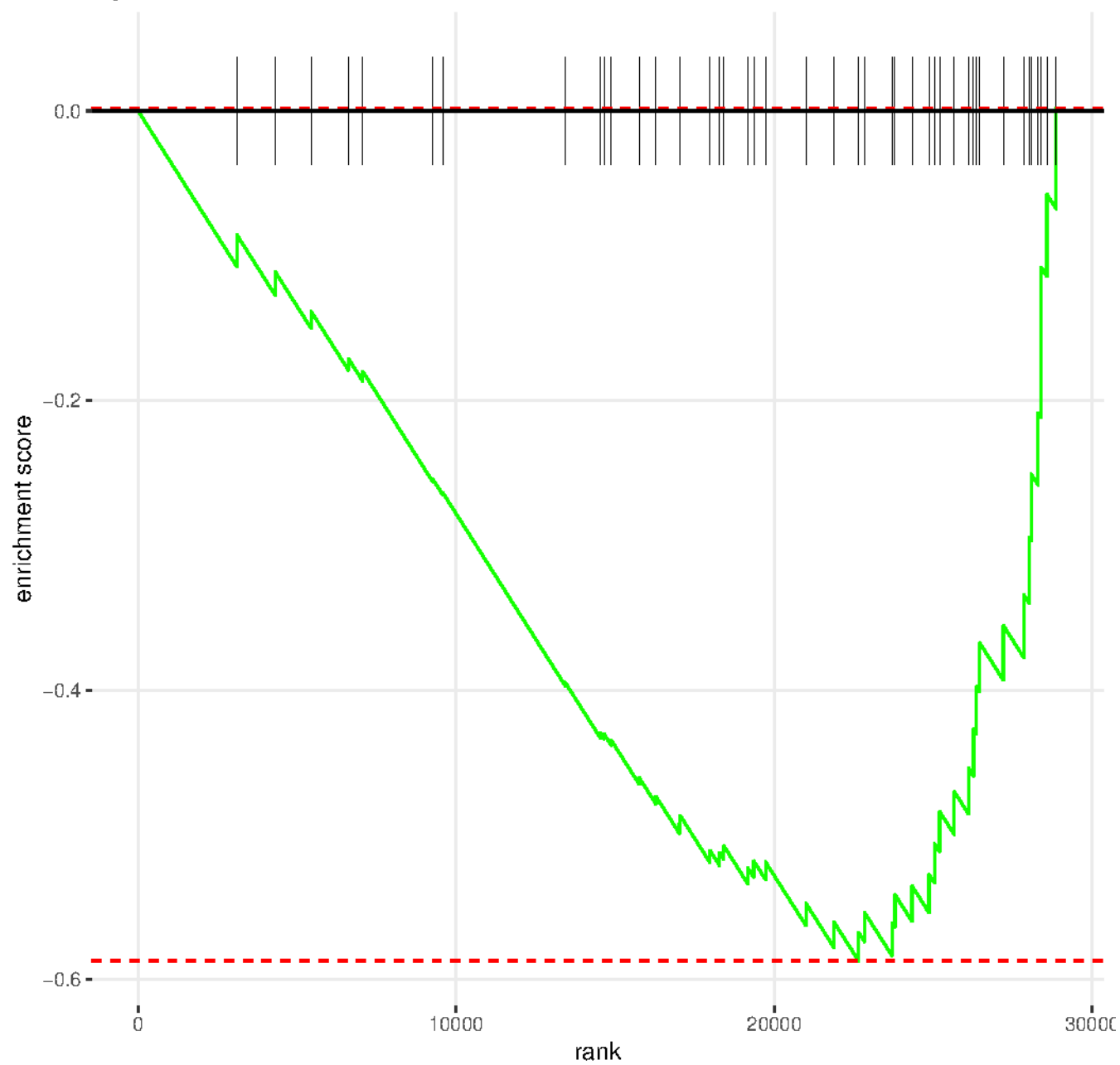


Integrin cell surface interactions





Cysteine and methionine metabolism



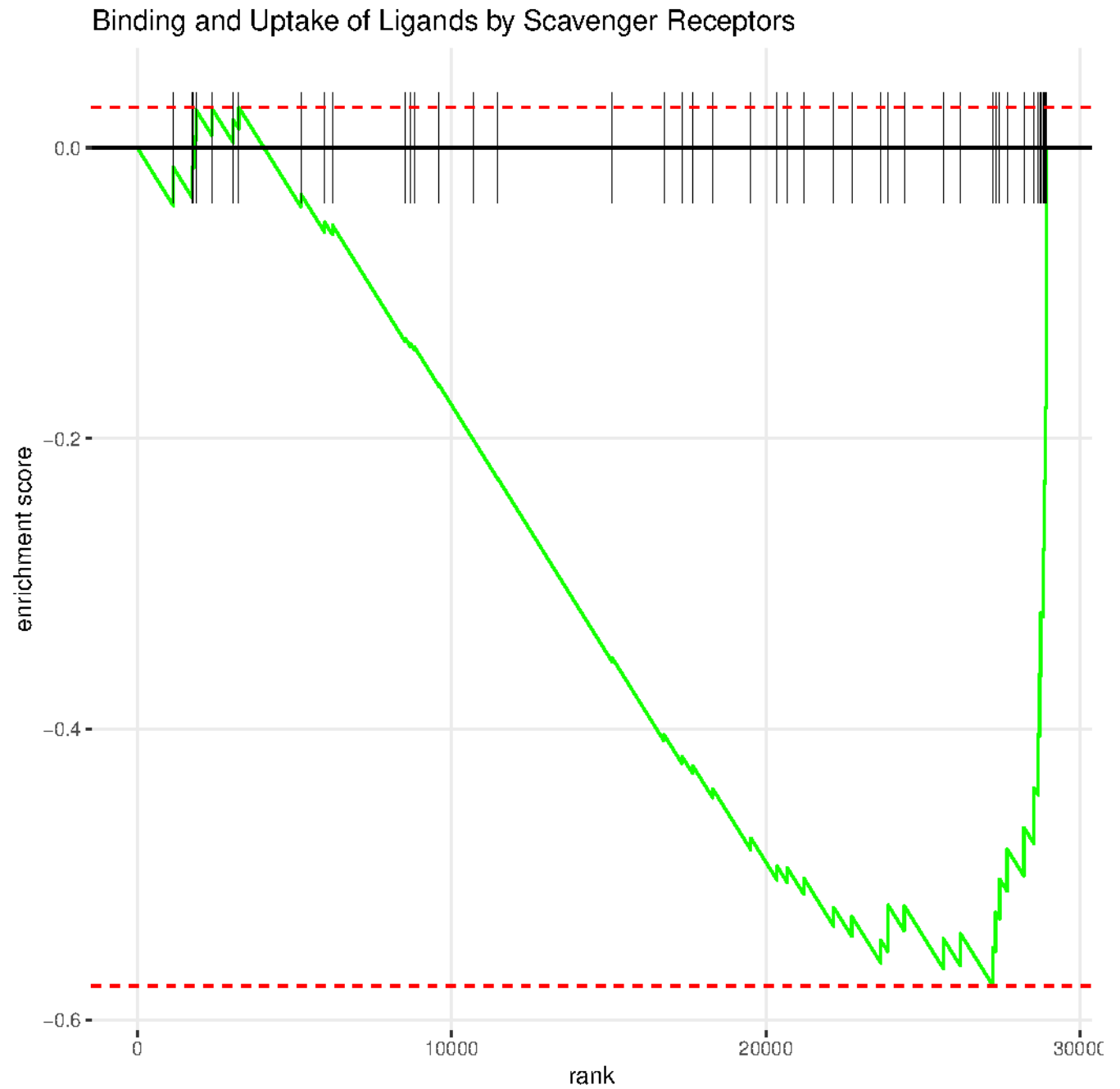
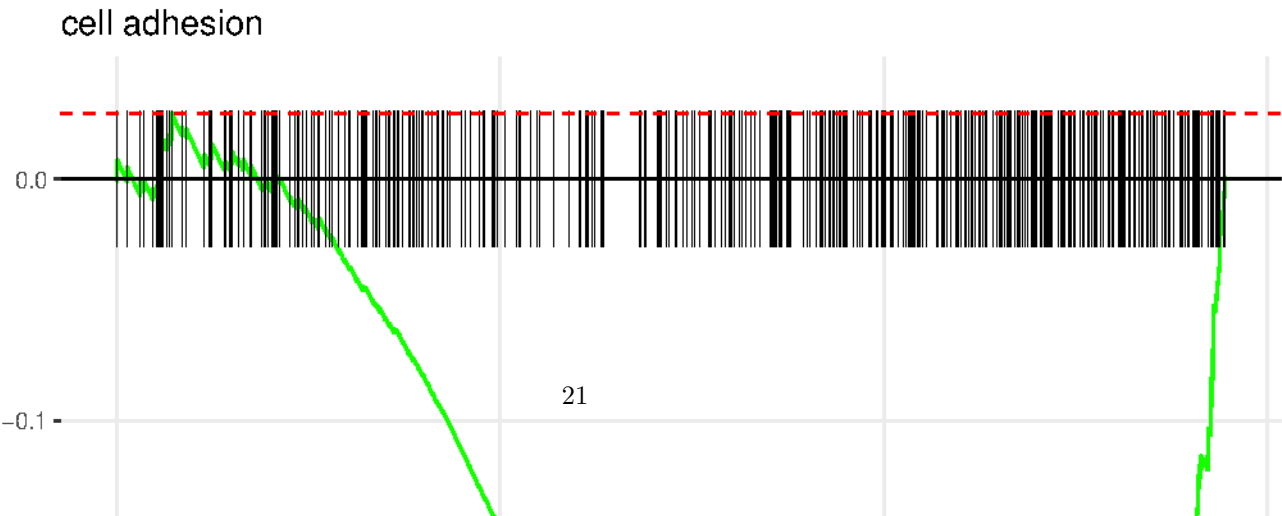
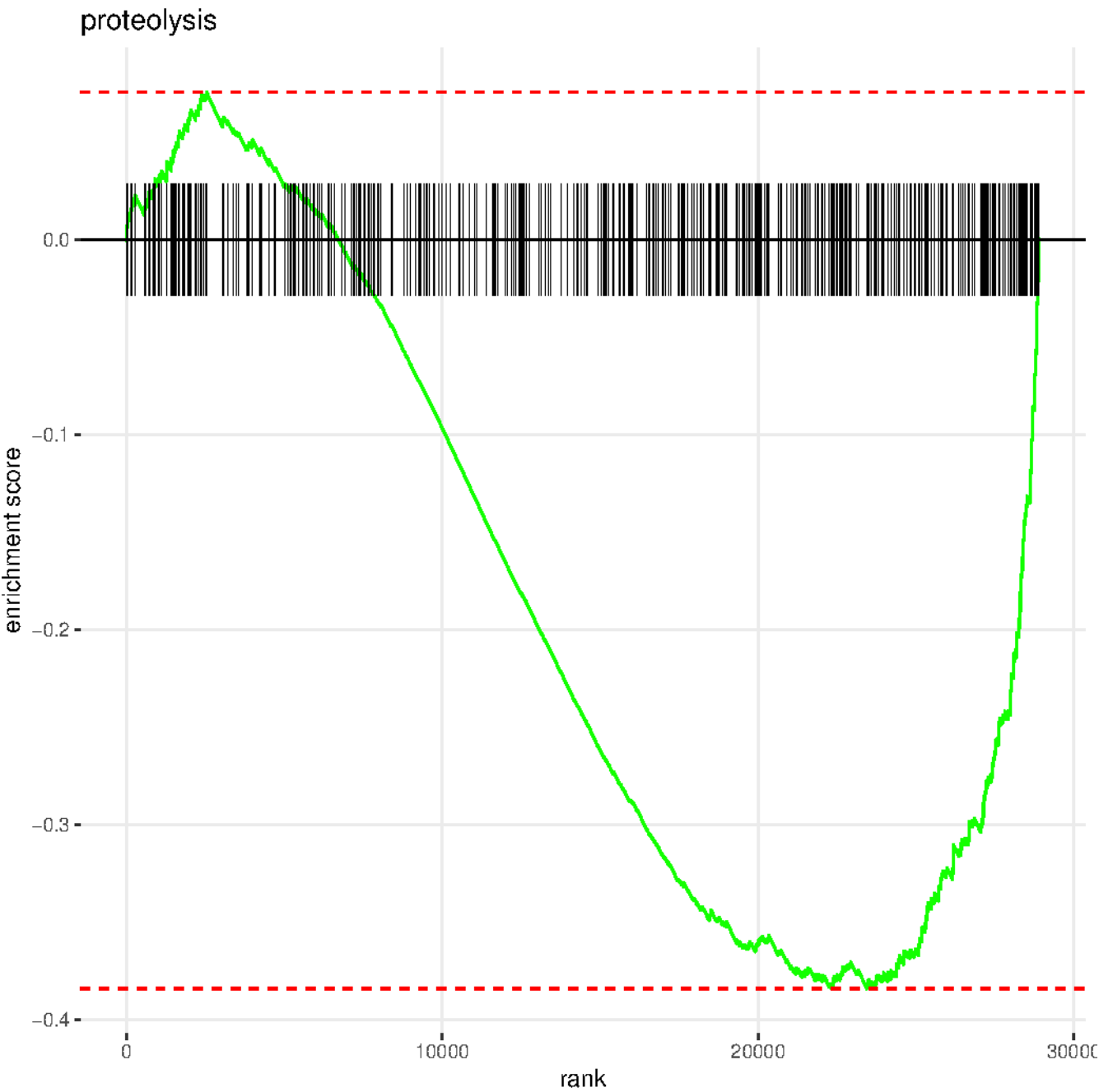
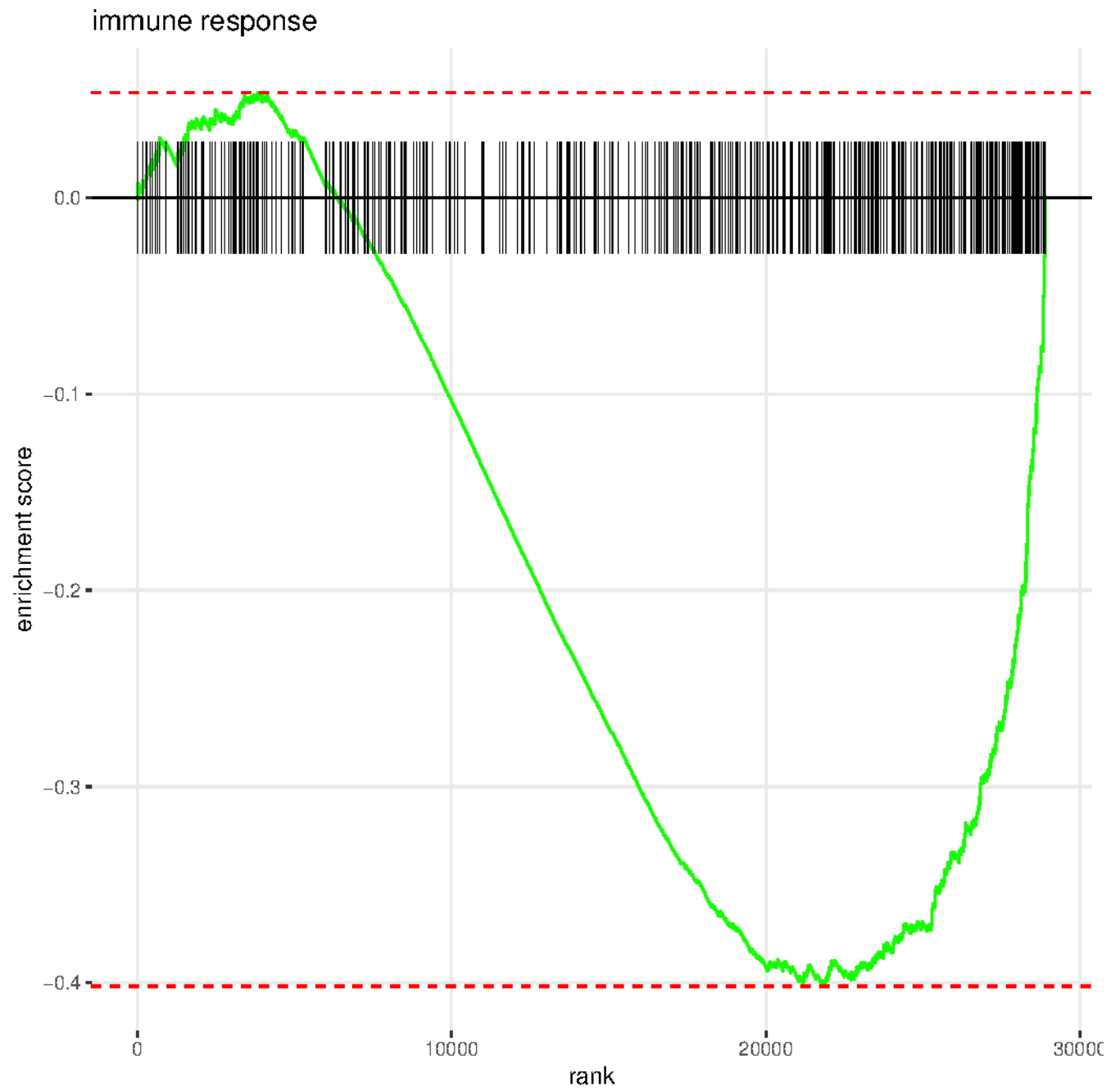
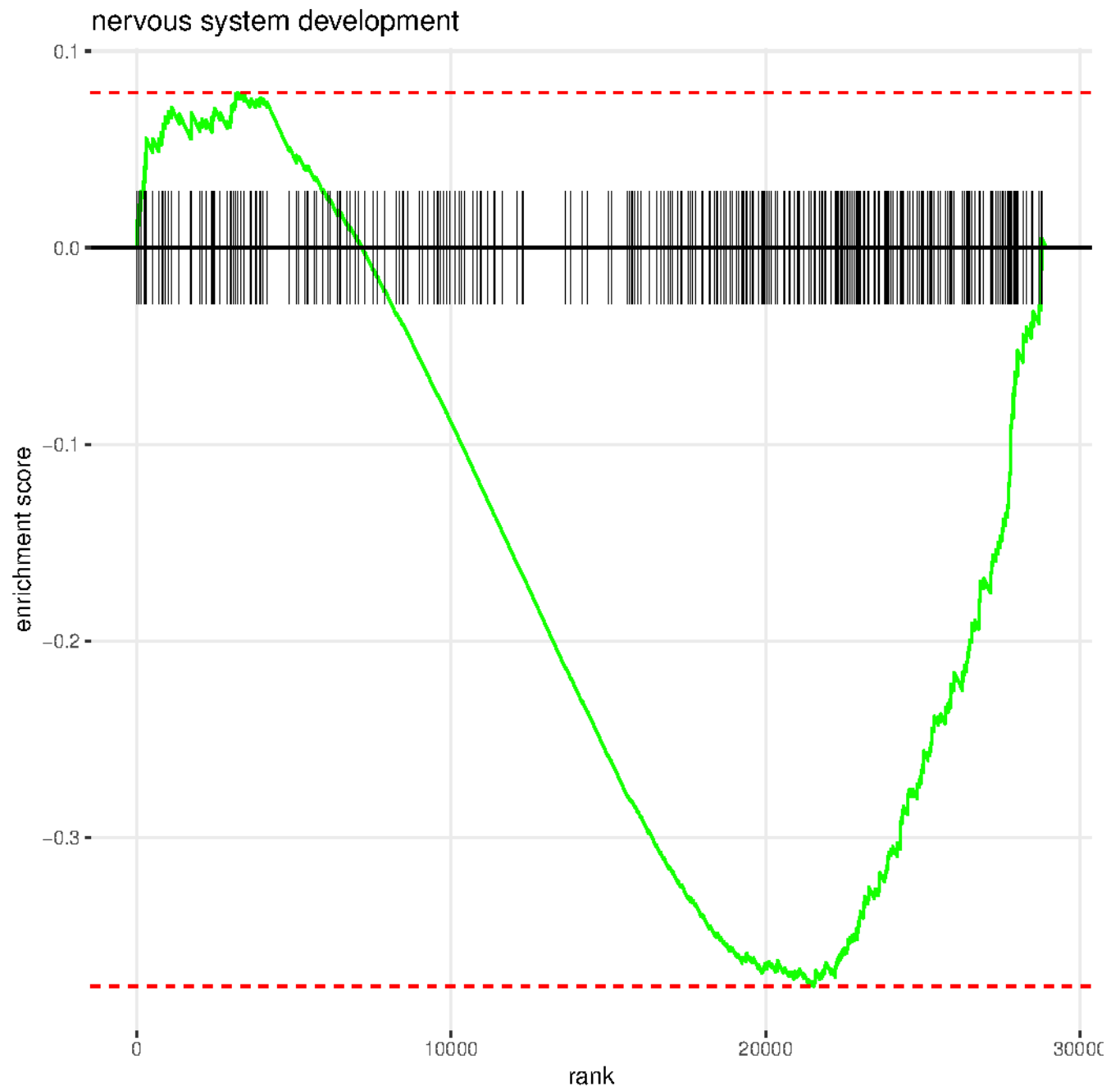


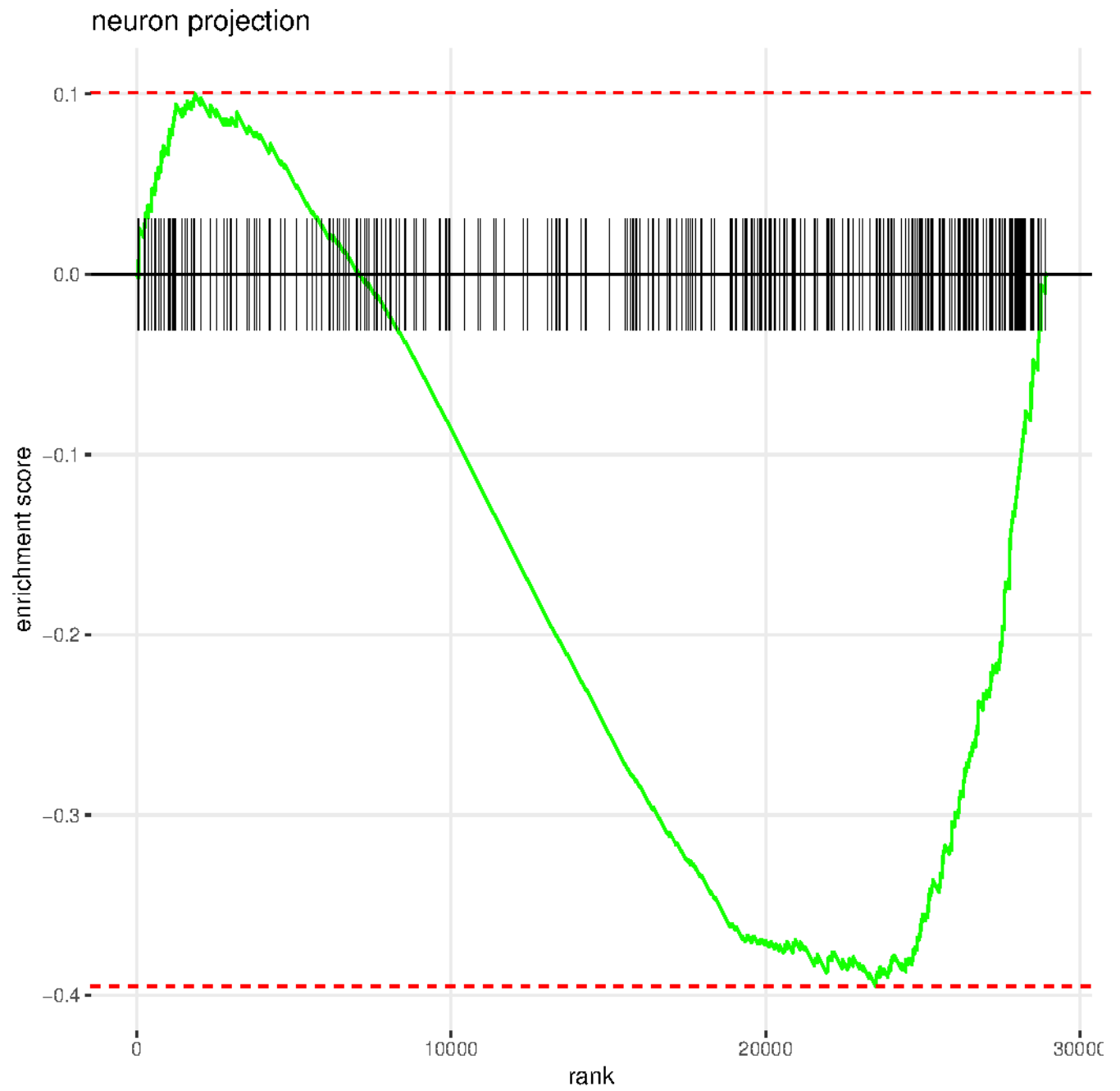
Figure 1 RUG plots of significant functional categories of GSEA analysis (Pathways).

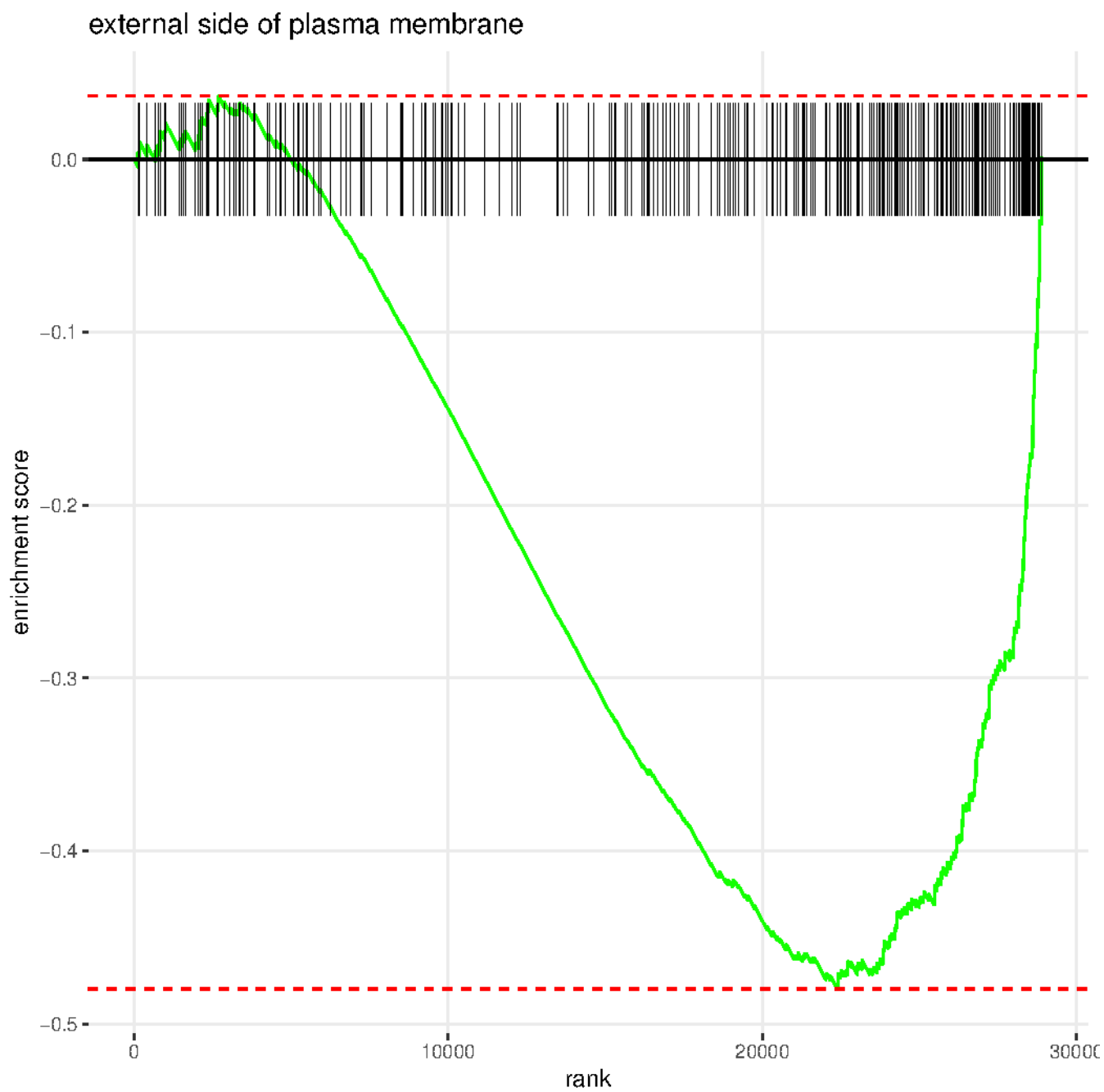
GO RUG plots

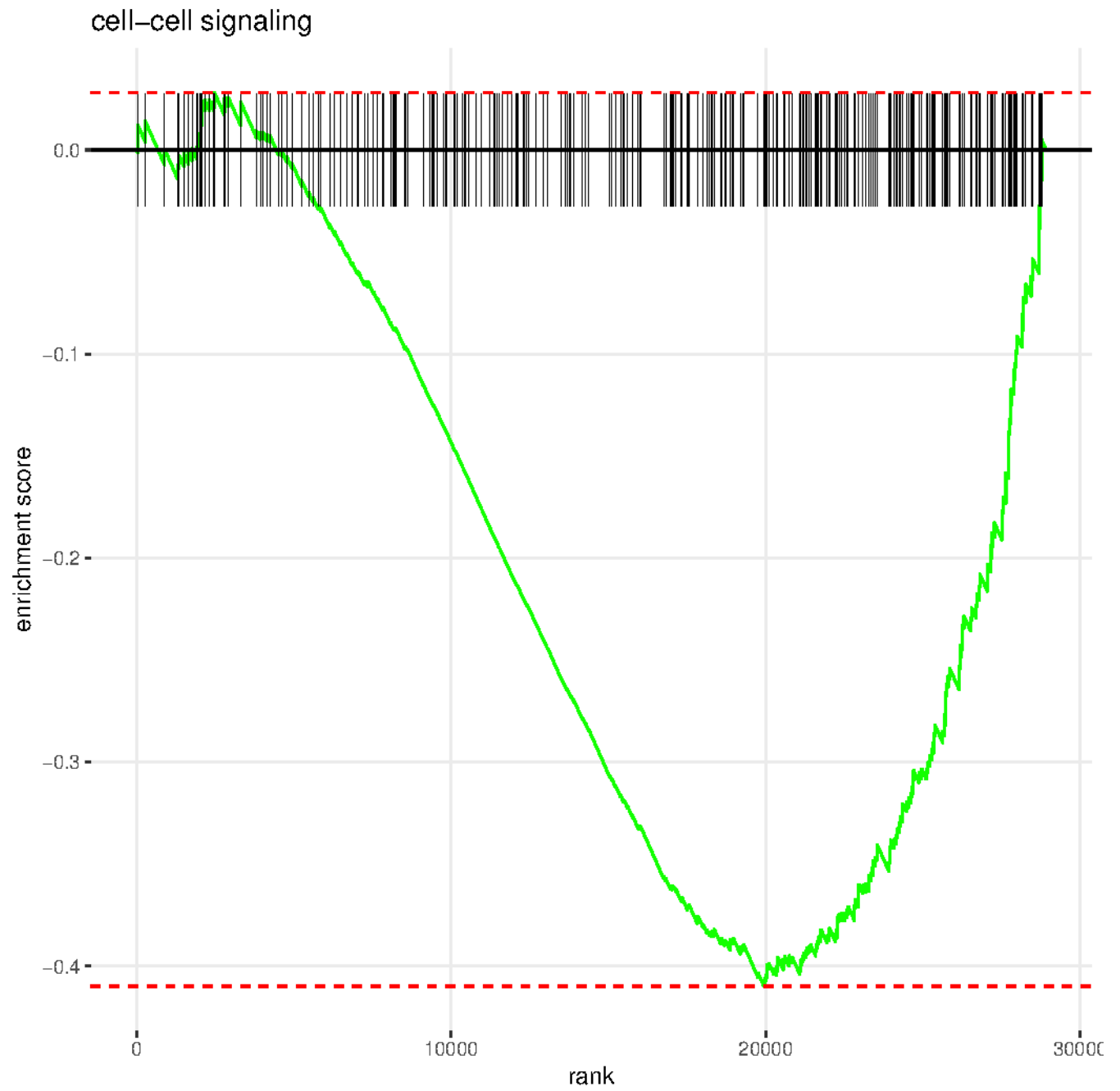


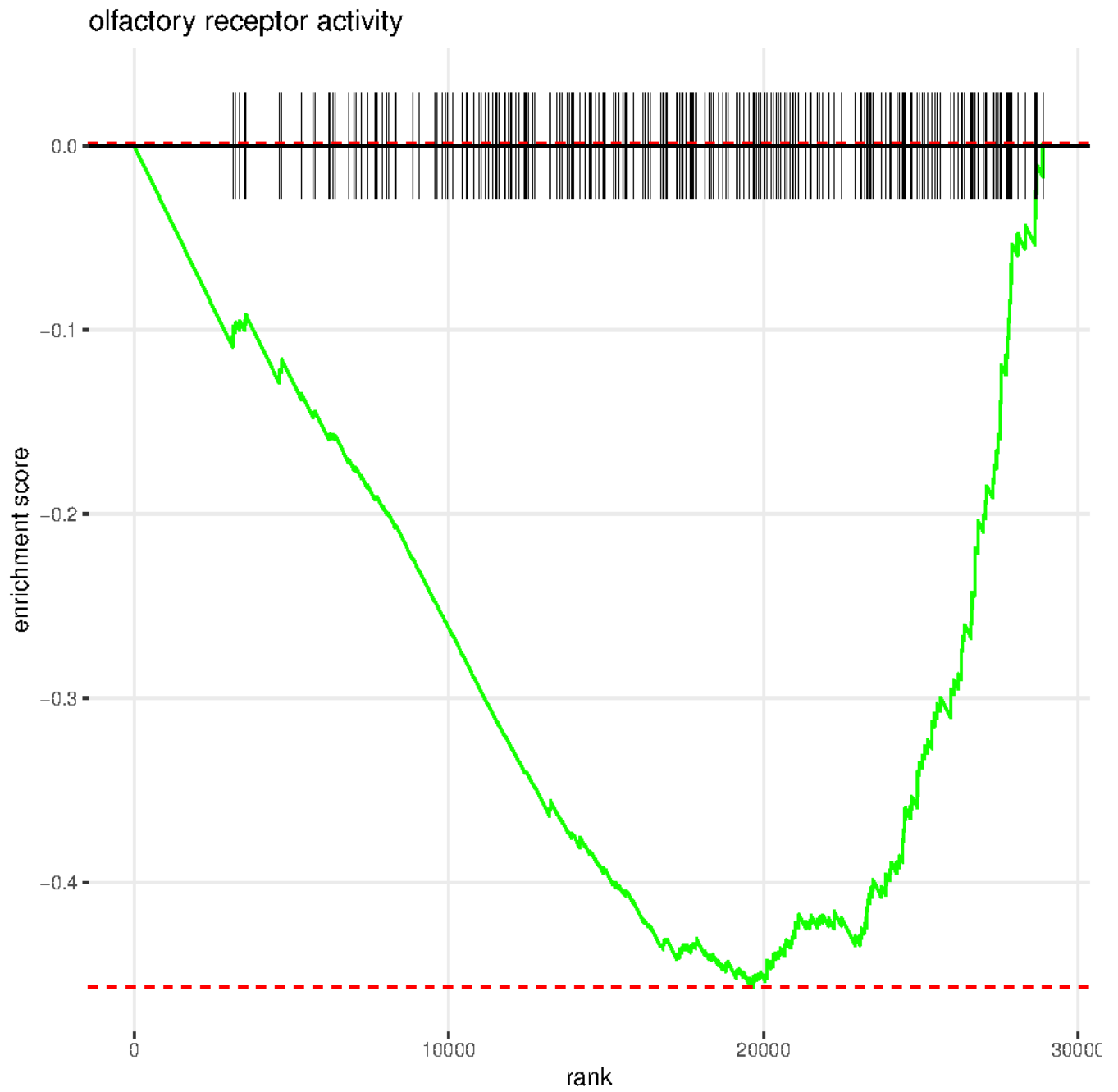




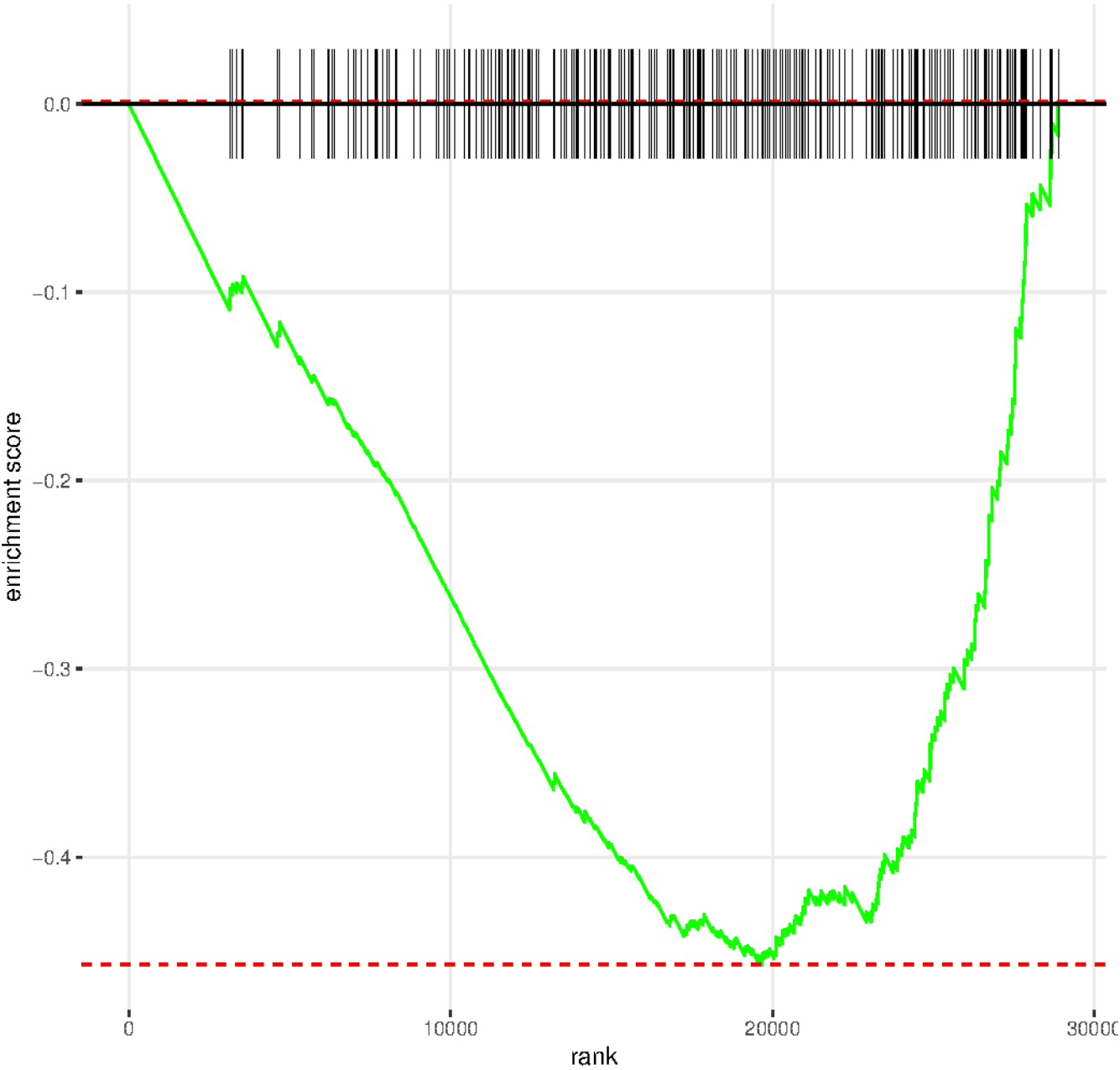


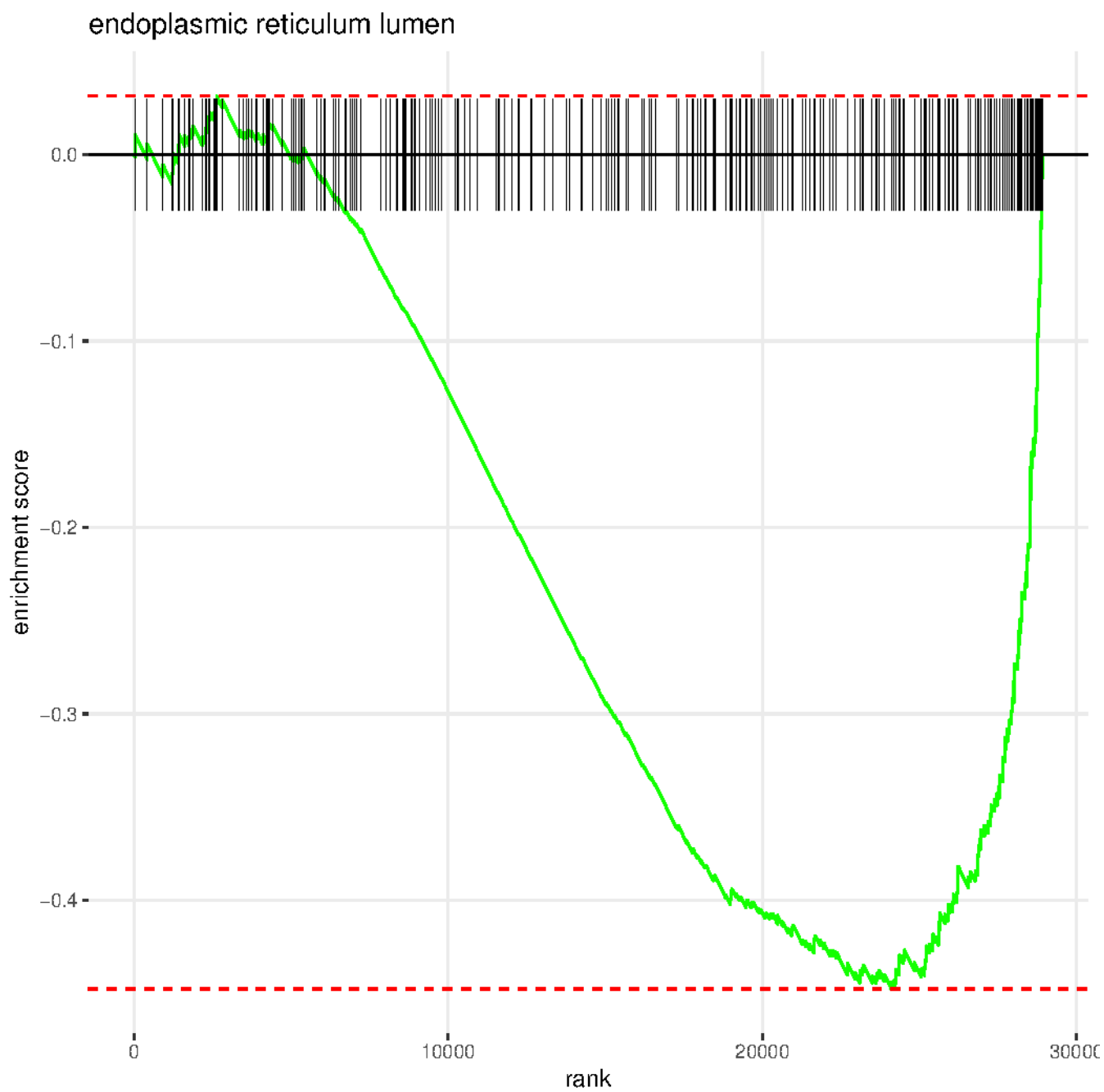


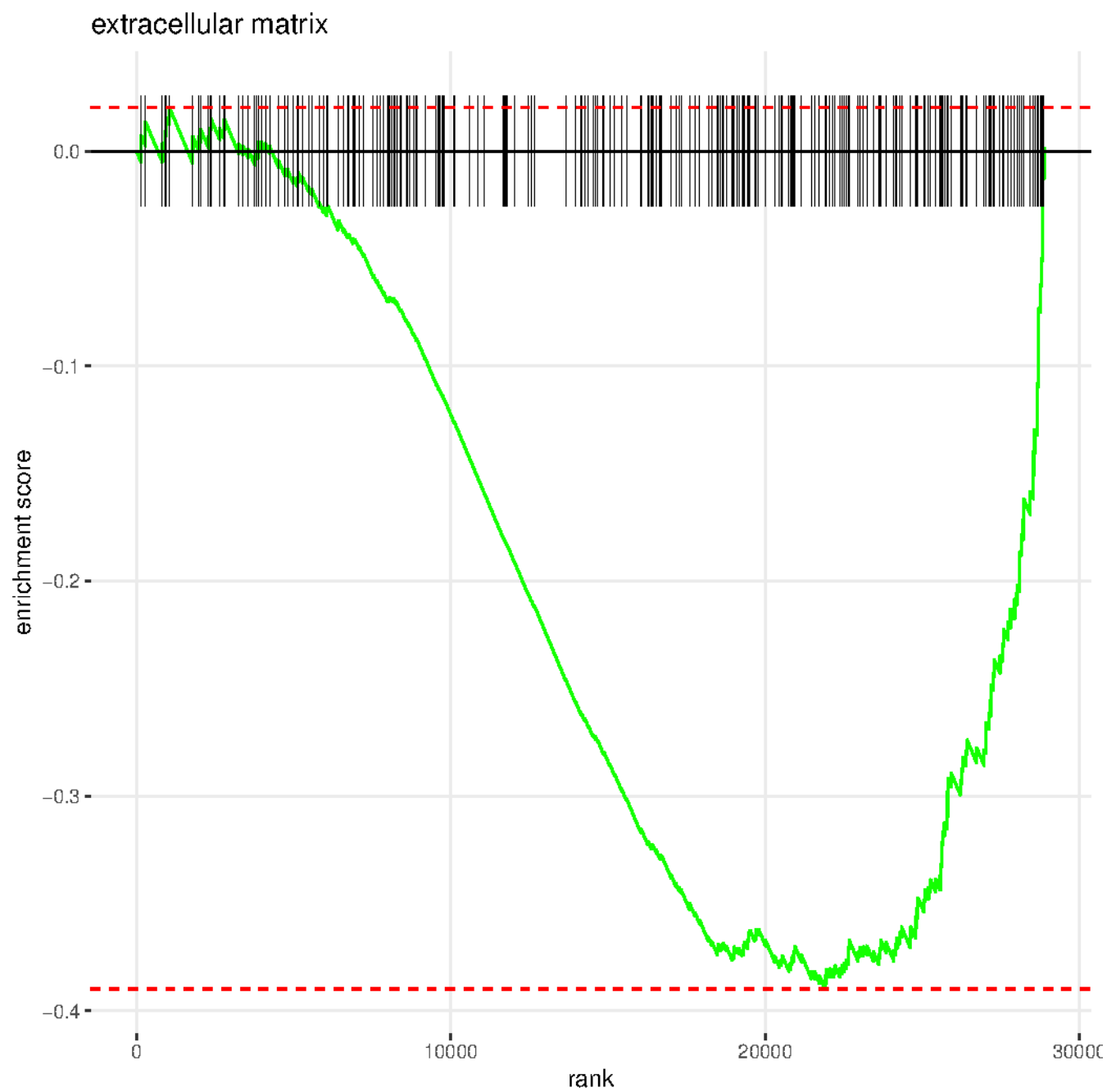


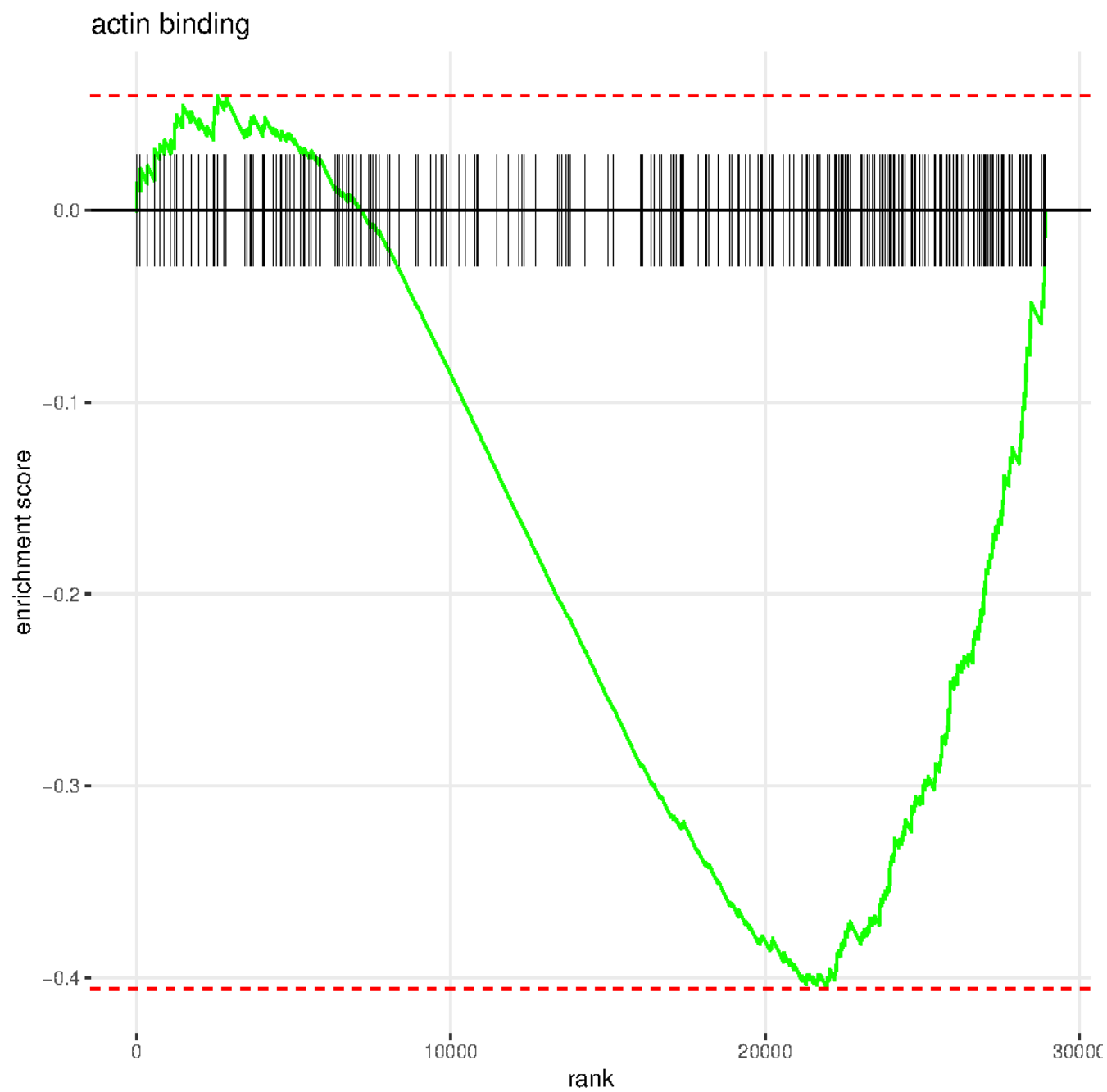


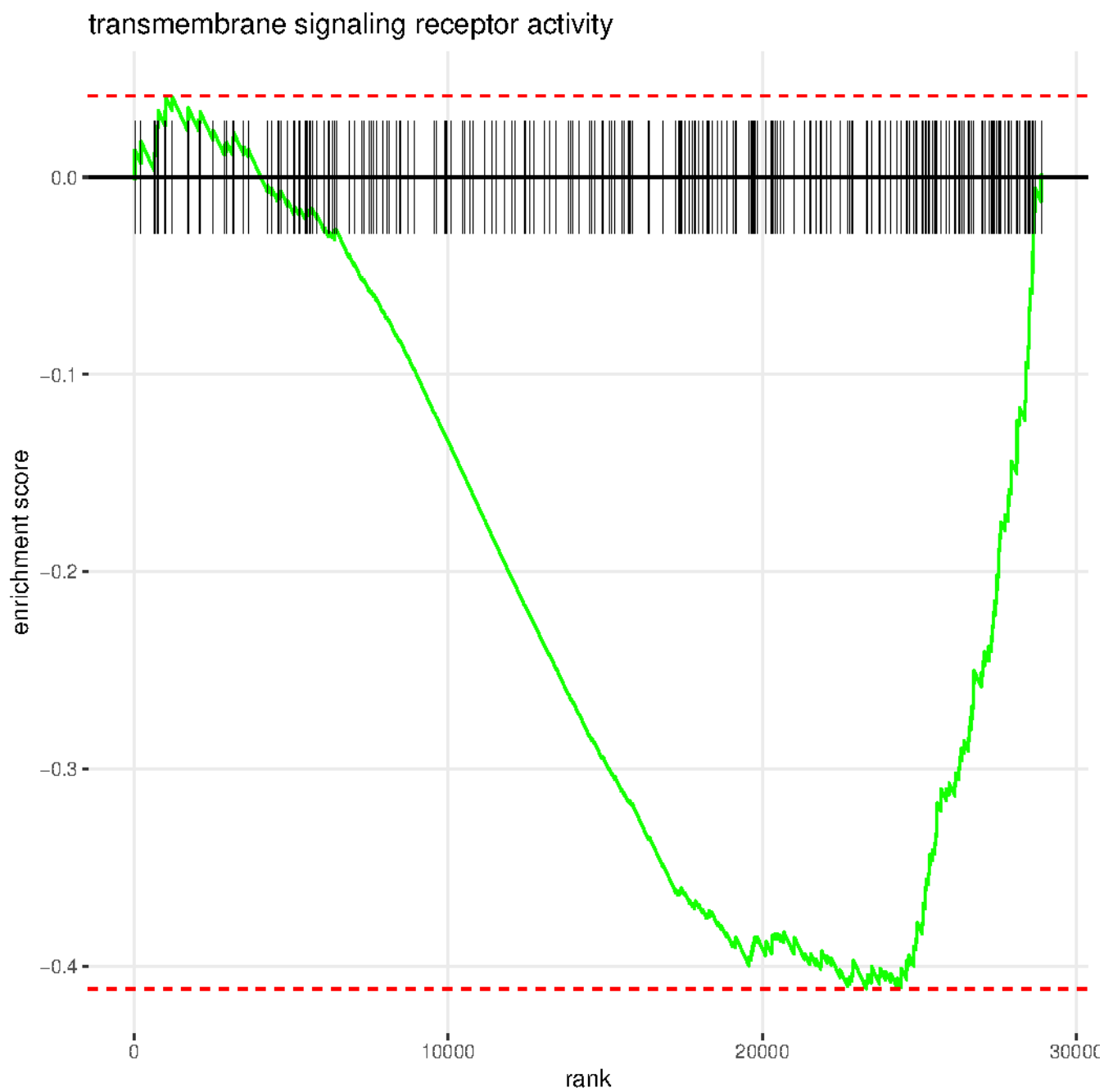
detection of chemical stimulus involved in sensory perception of smell

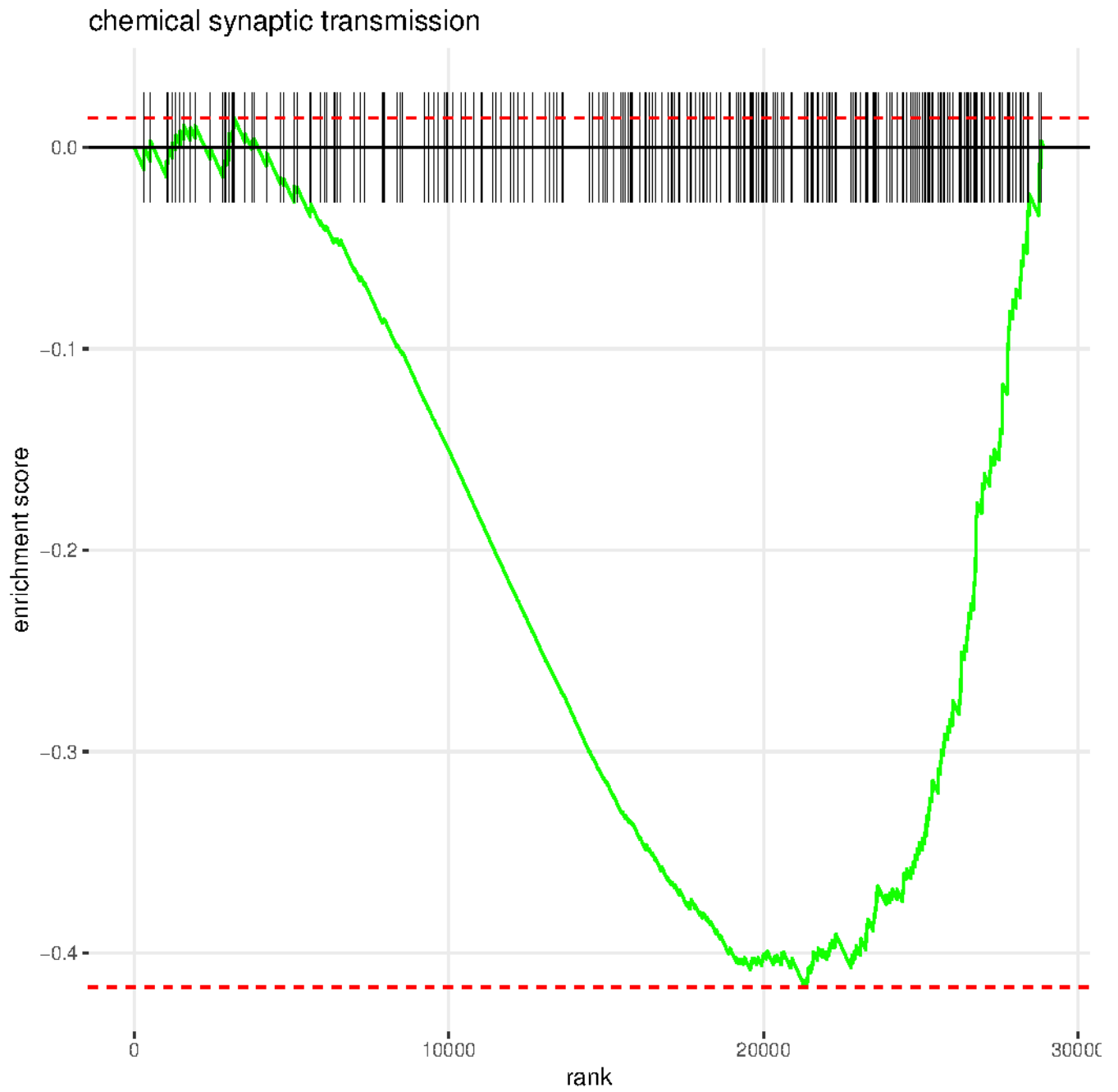


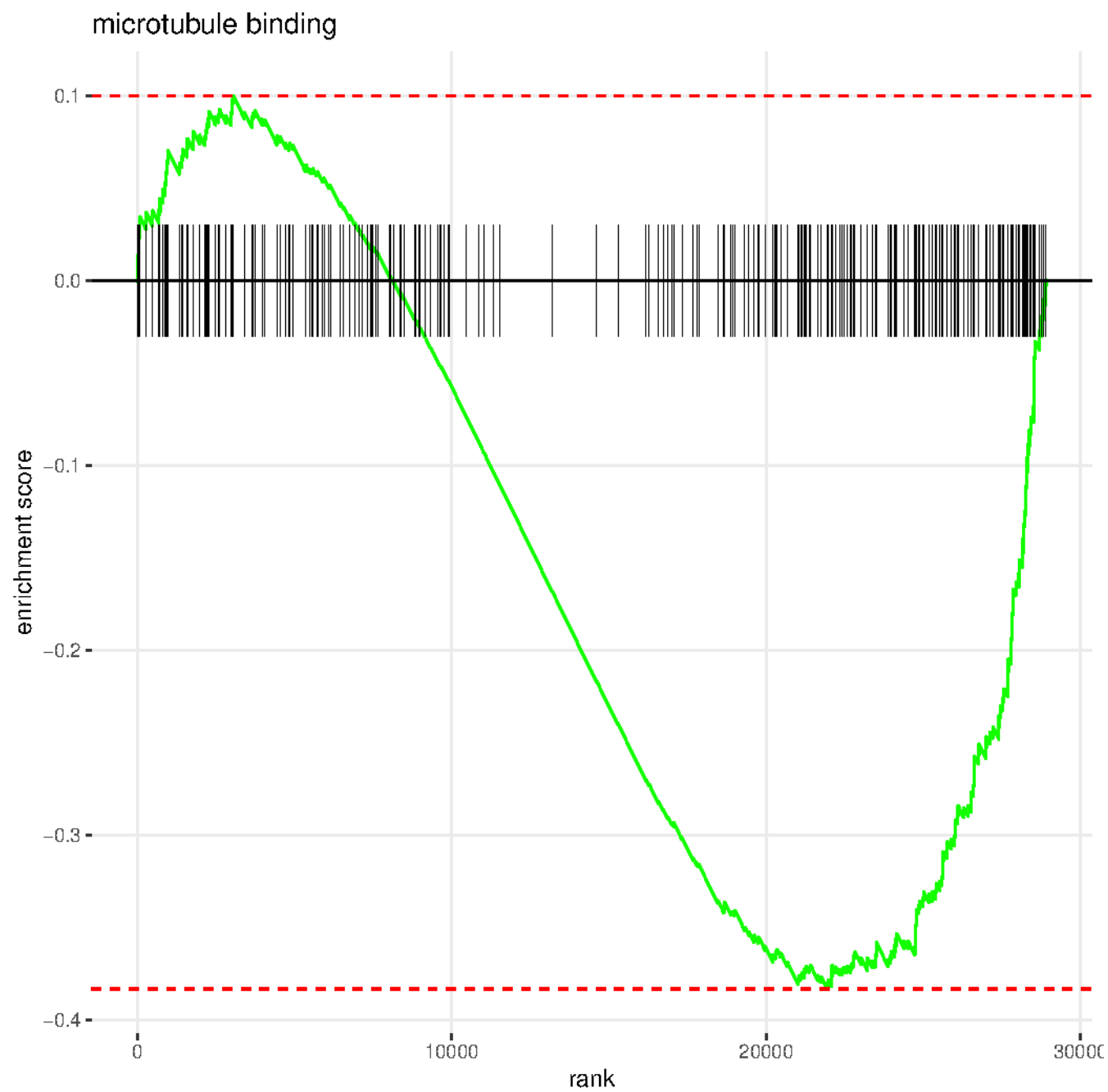


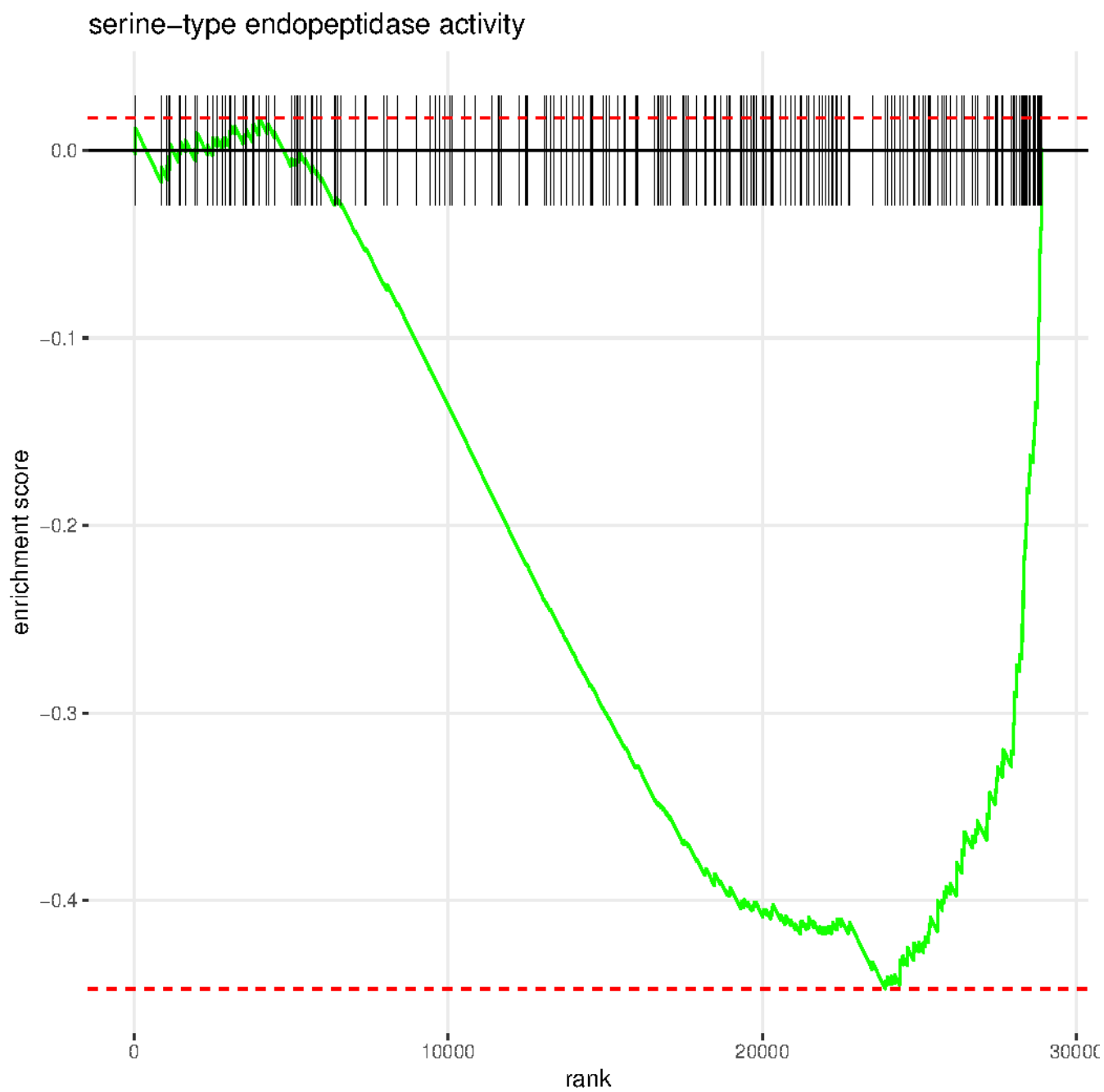


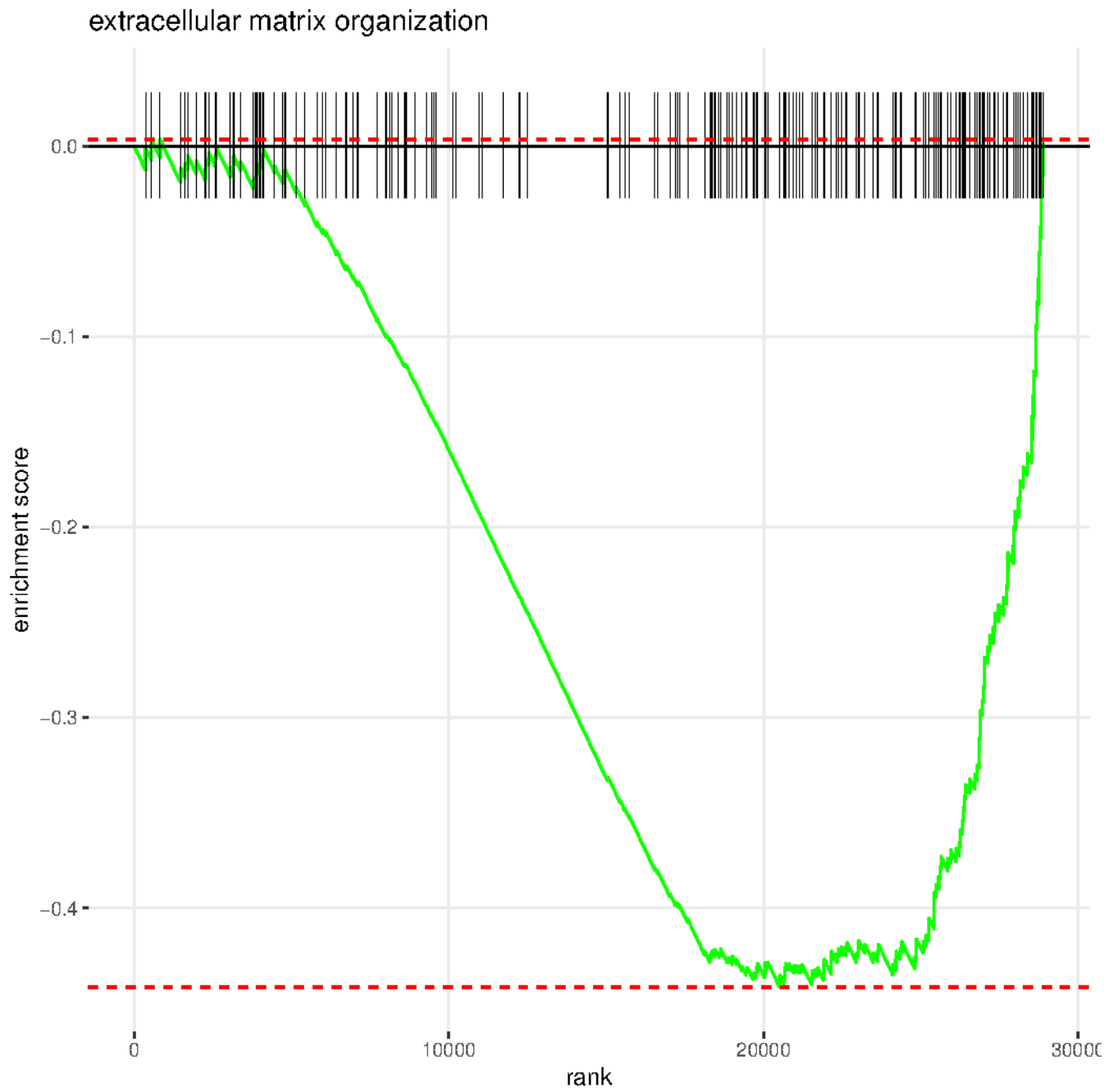


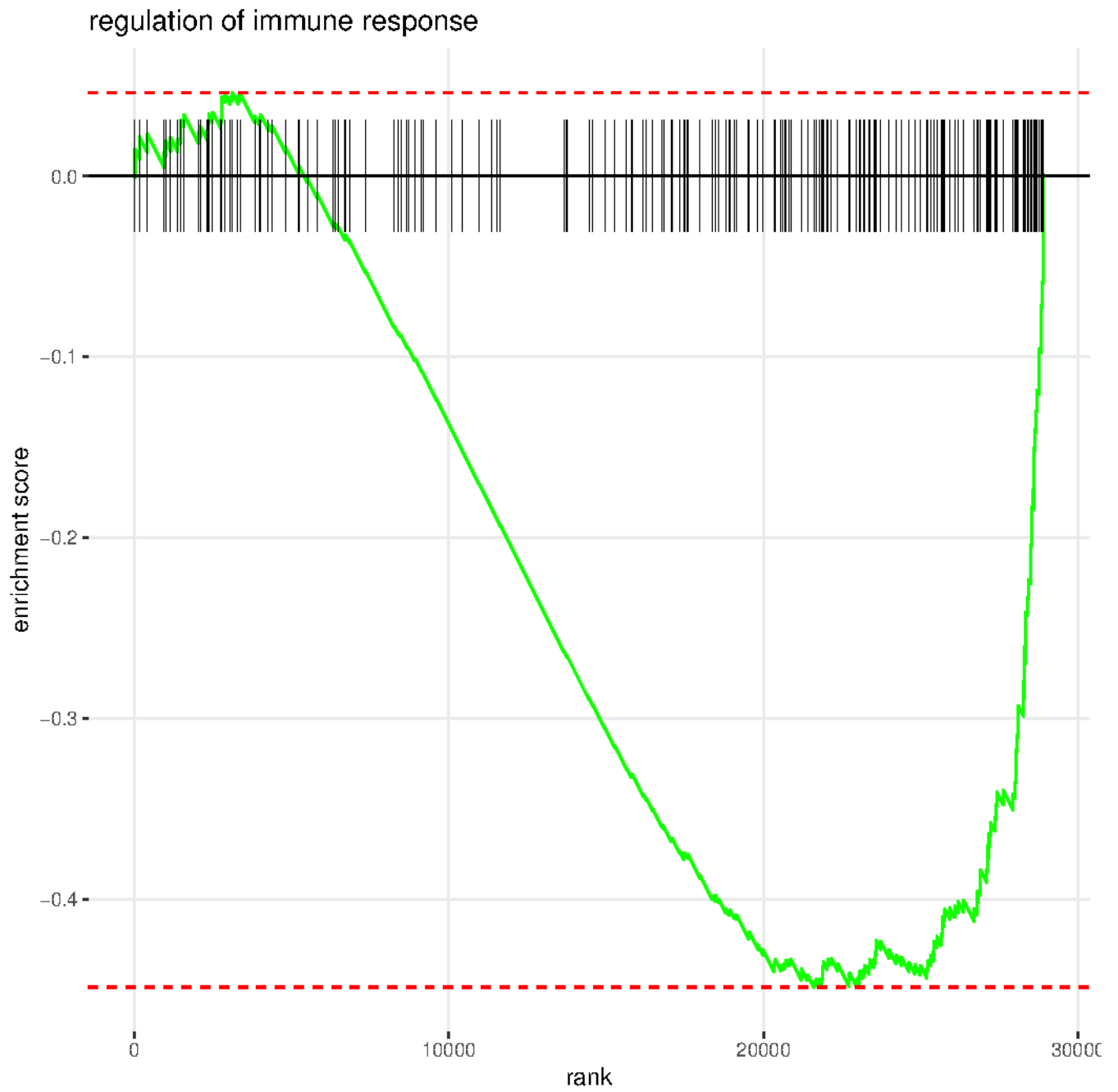


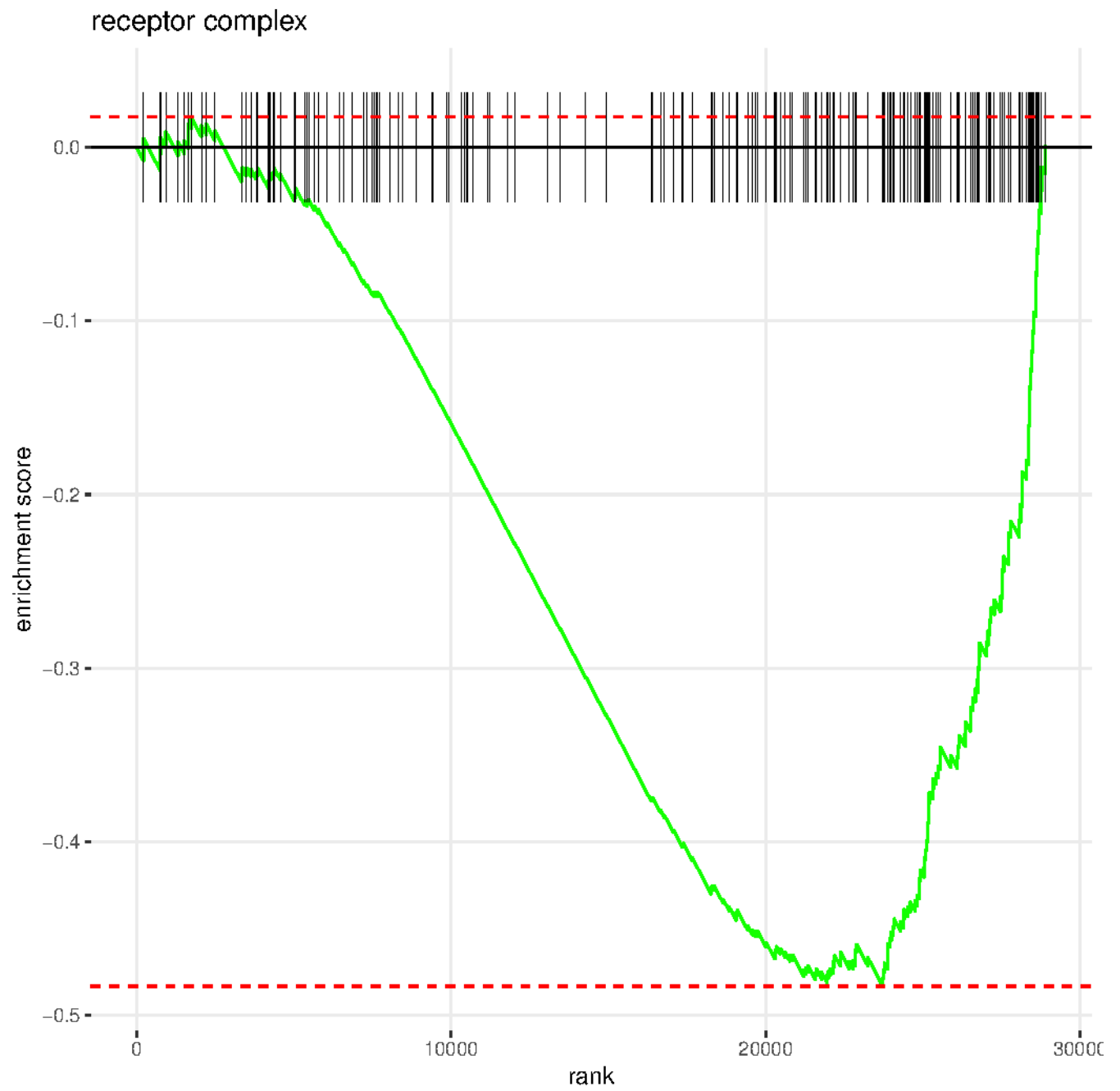












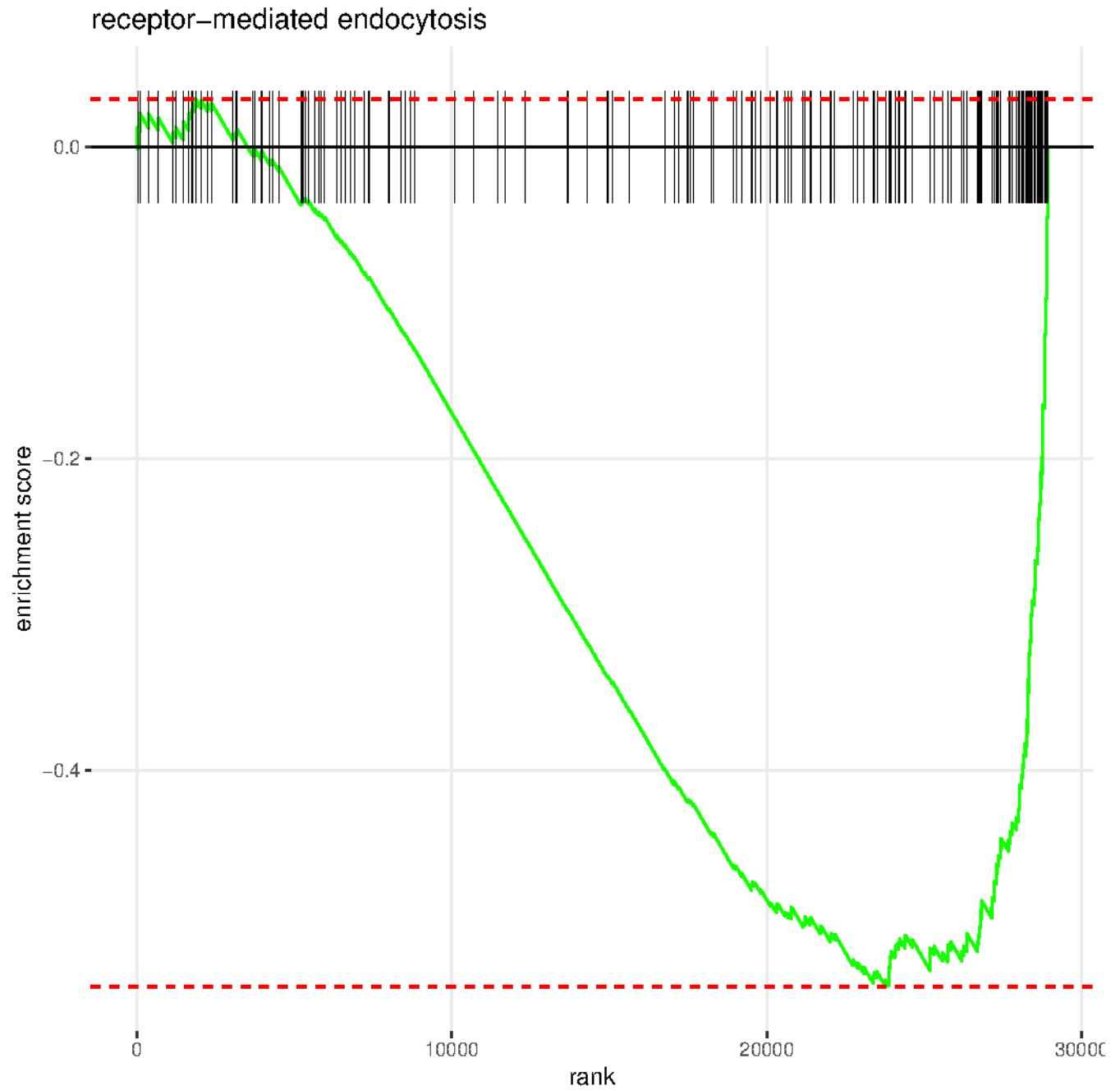


Figure 2 RUG plots of significant functional categories of GSEA analysis (GO).

References

Sergushichev, Alexey. 2016. "An algorithm for fast preranked gene set enrichment analysis using cumulative statistic calculation." *bioRxiv*, 060012. <https://doi.org/10.1101/060012>.