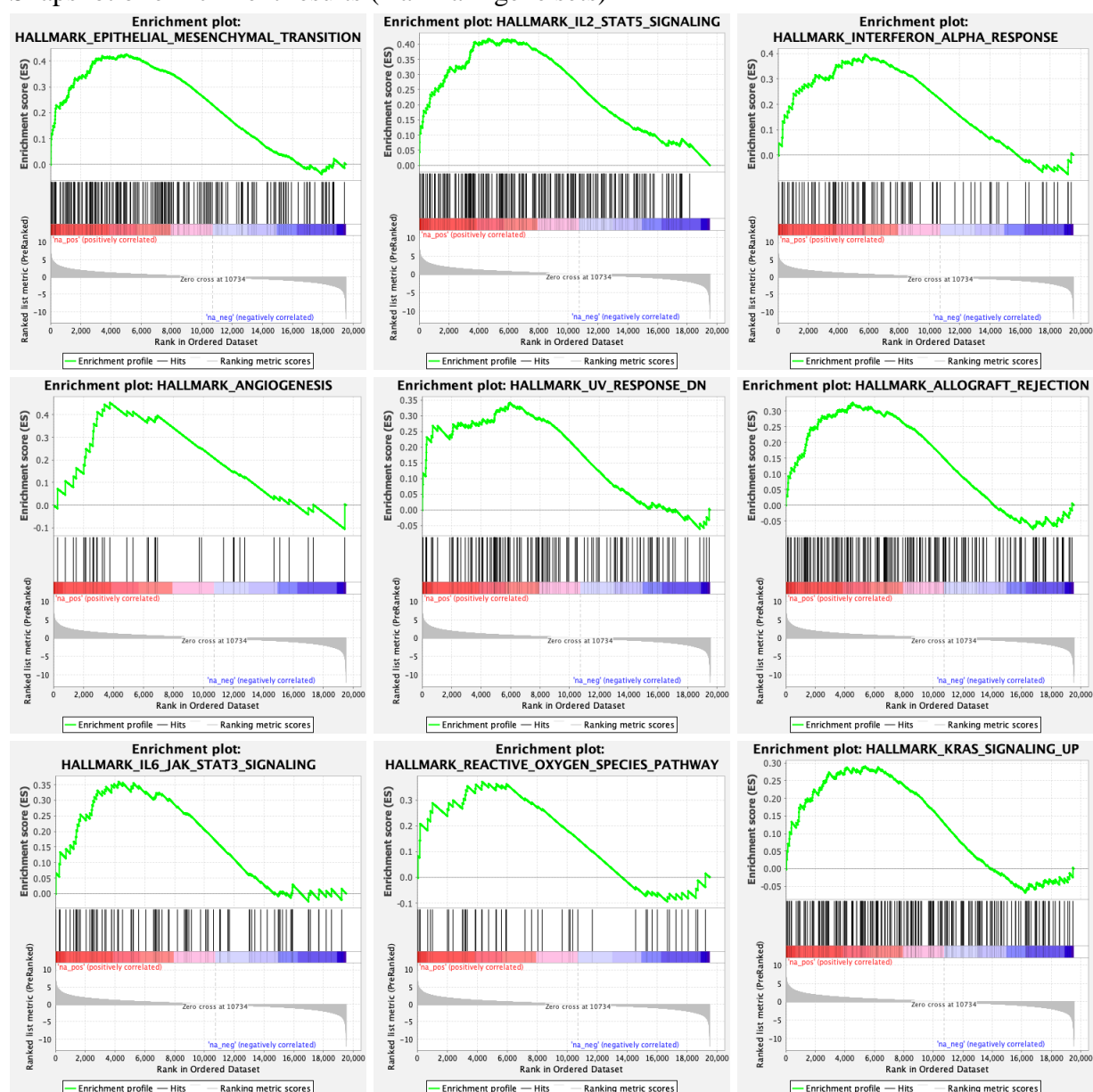


Supplementary Materials: Gene Expression Profiling of Olfactory Neuroblastoma Helps Identify Prognostic Pathways and Define Potentially Therapeutic Targets

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Snapshot of enrichment results (Hallmark gene sets)



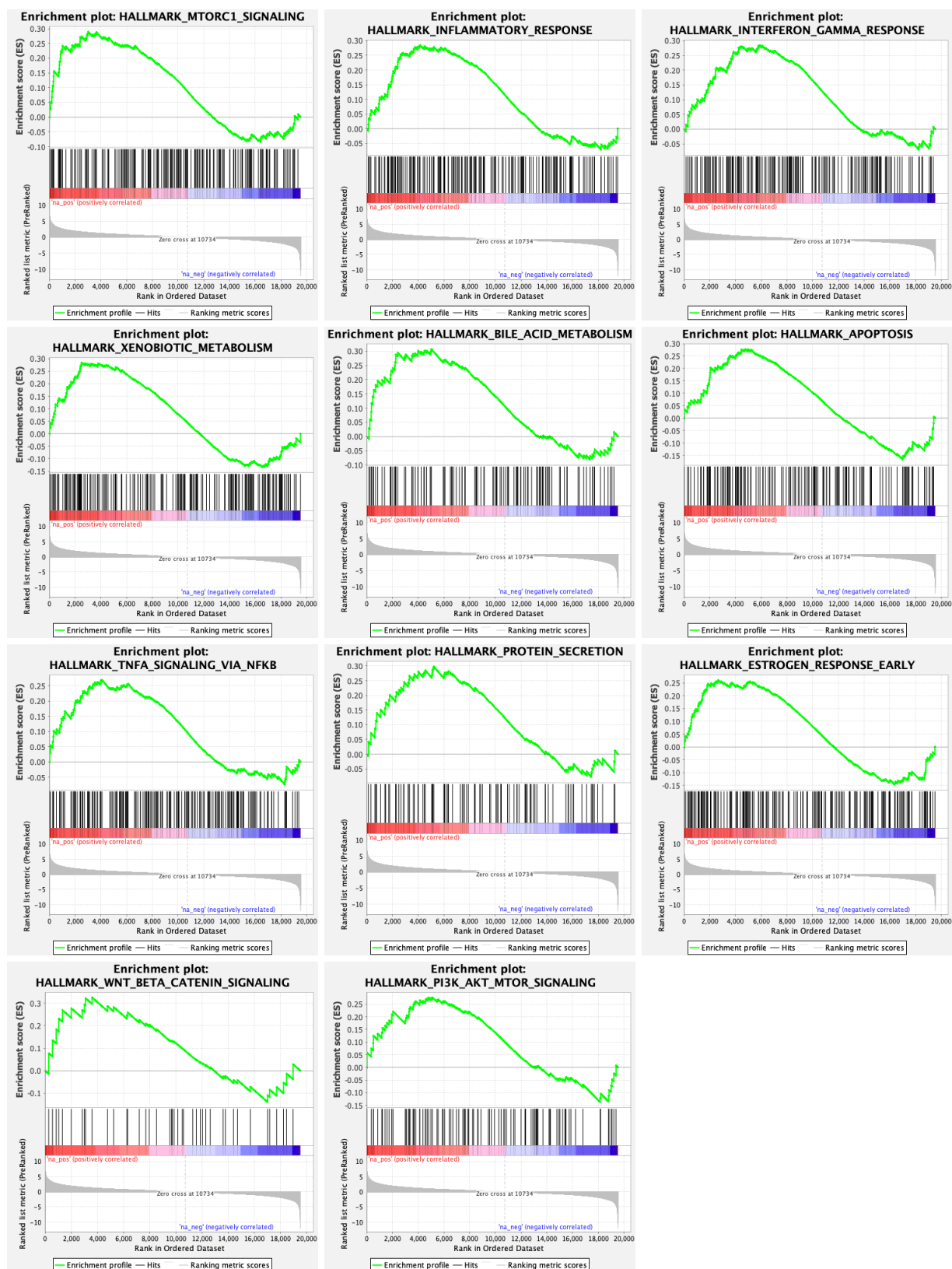
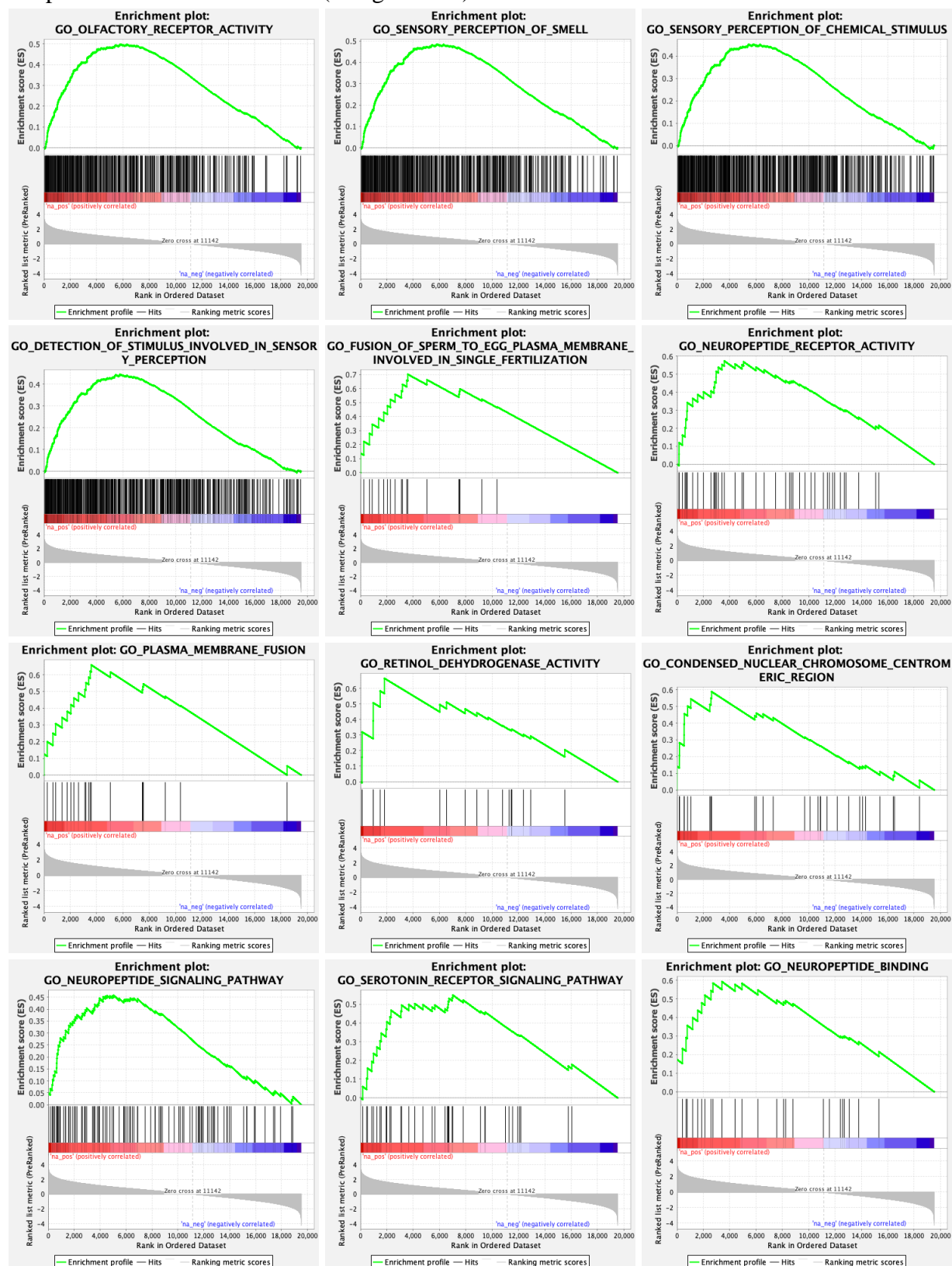
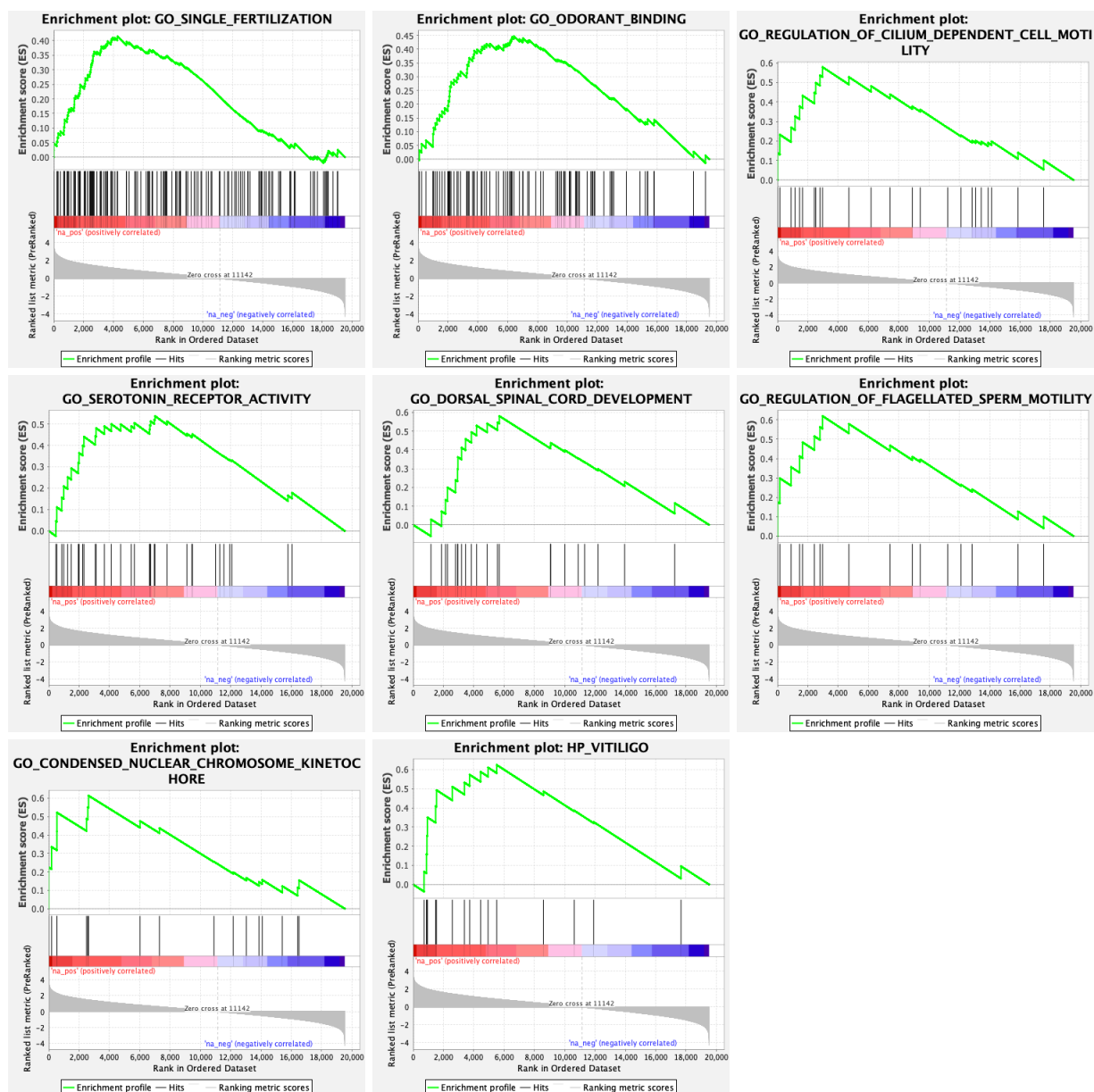


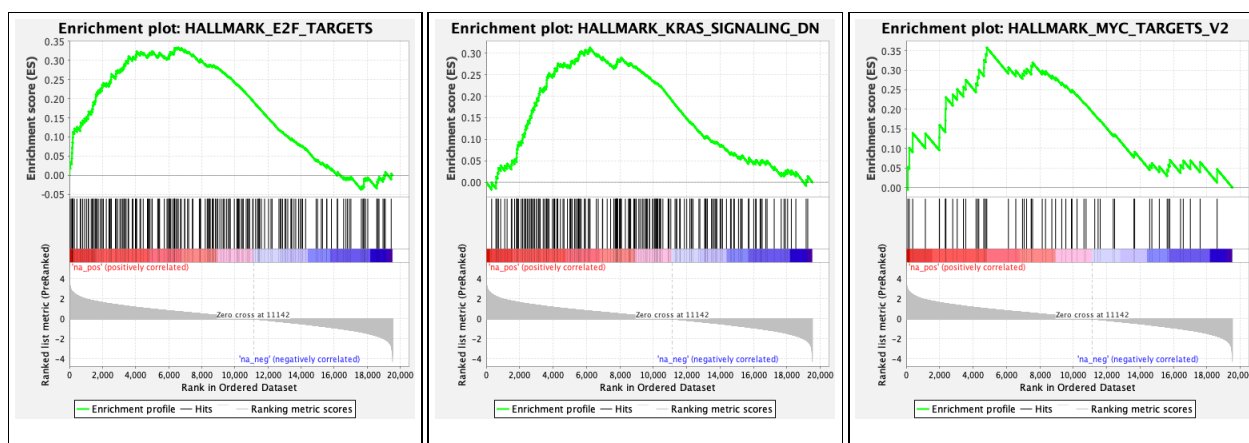
Figure S1. GSEA enrichment plots showing pathways associated with prognosis in ONB patients. The plots contain the profile of the running enrichment score (ES green line) and position of gene set members on the rank ordered list in GSEA (black strokes on the bottom).

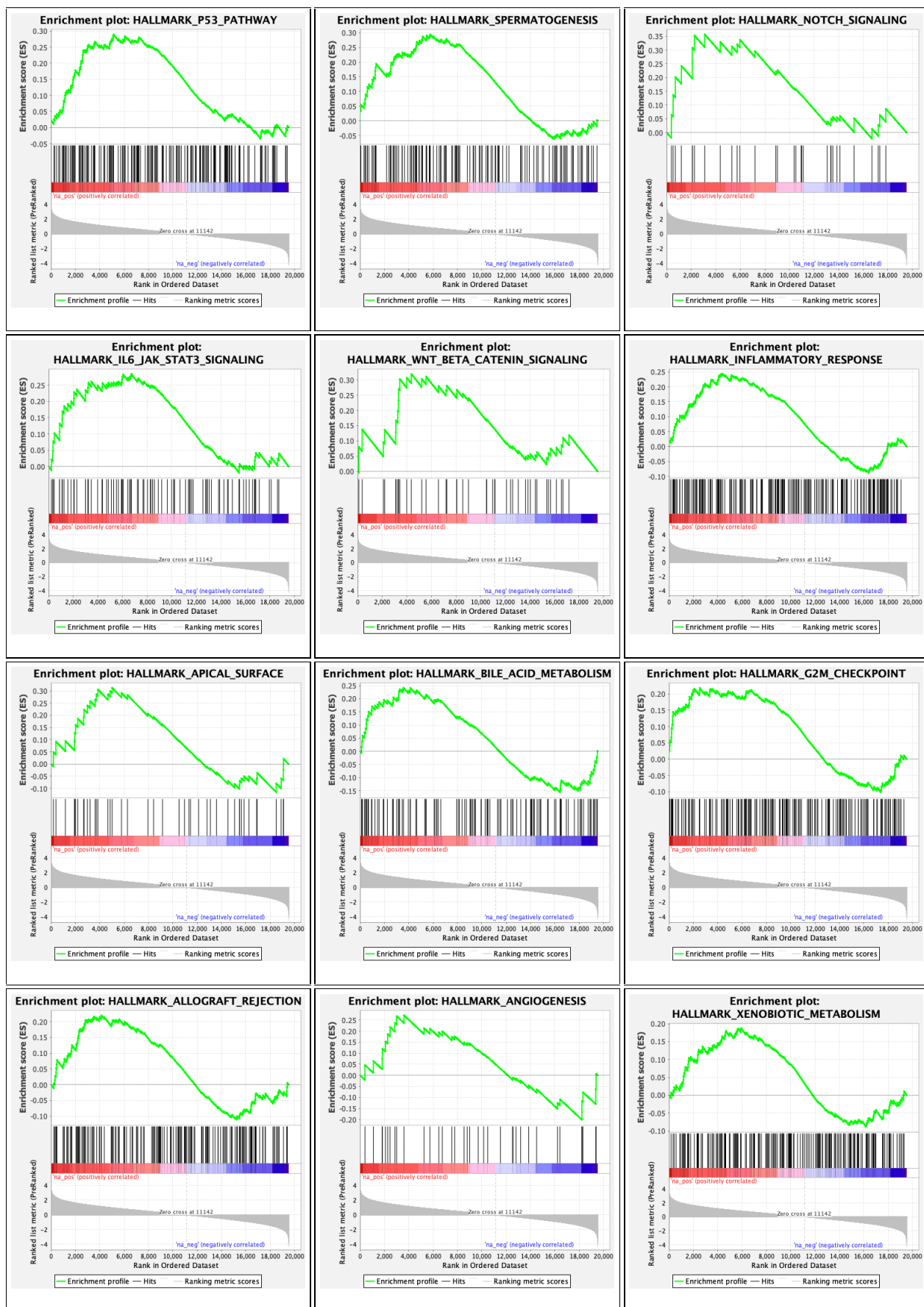
Snapshot of enrichment results (GO gene sets)

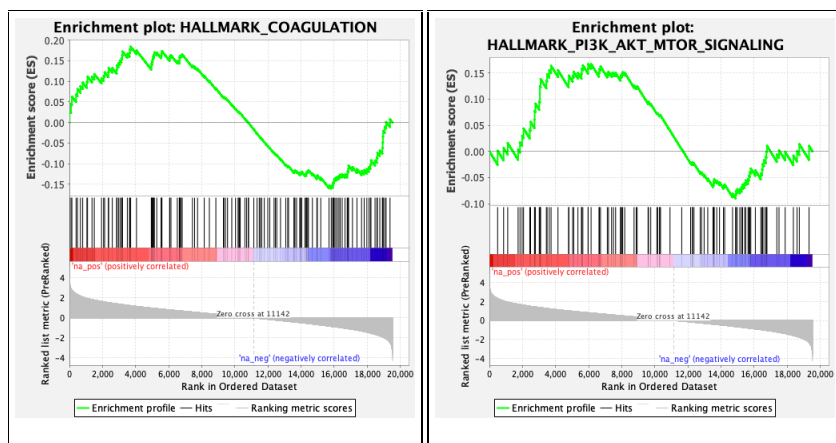




Snapshot of enrichment results (Hallmark gene sets)

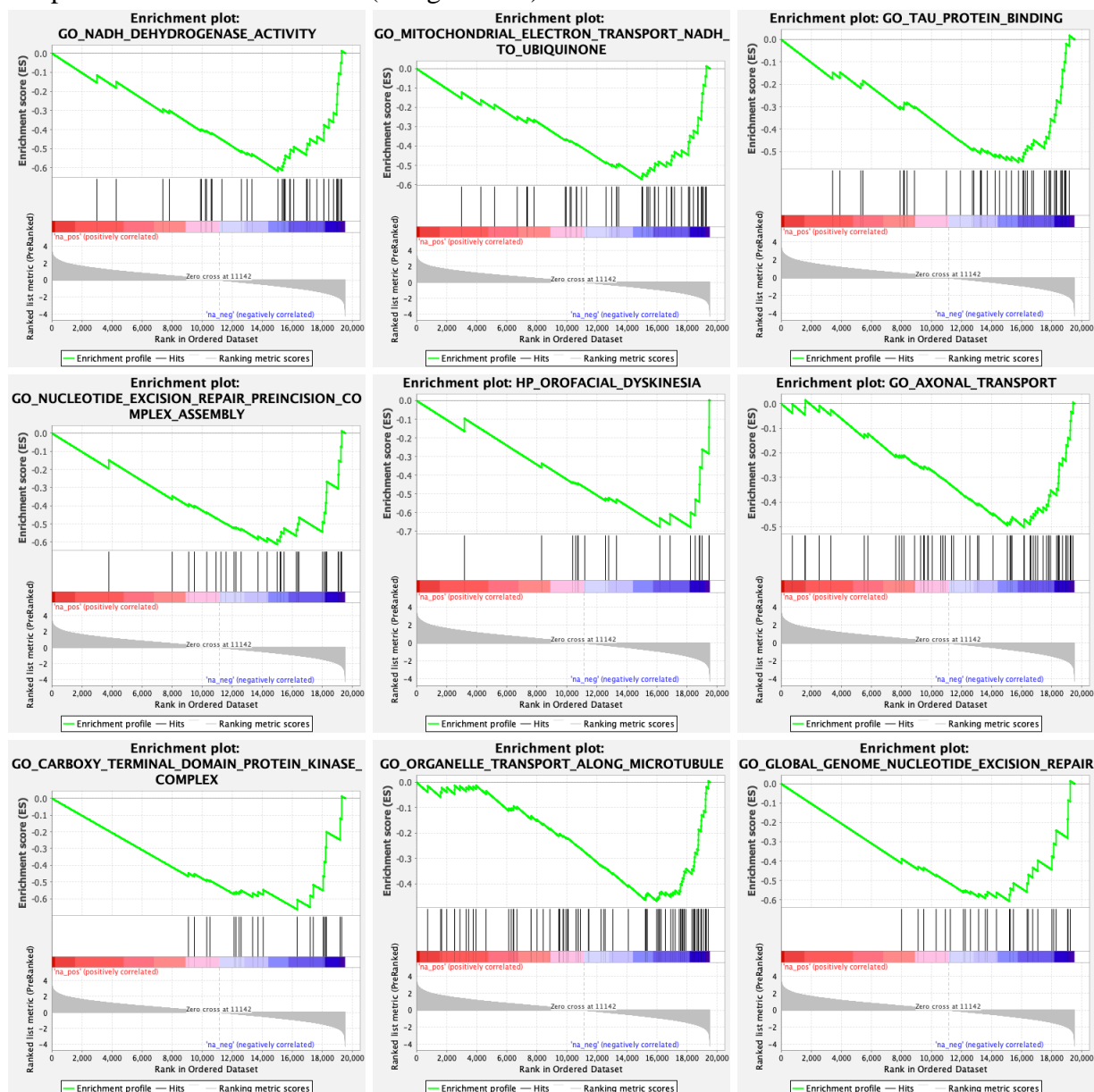


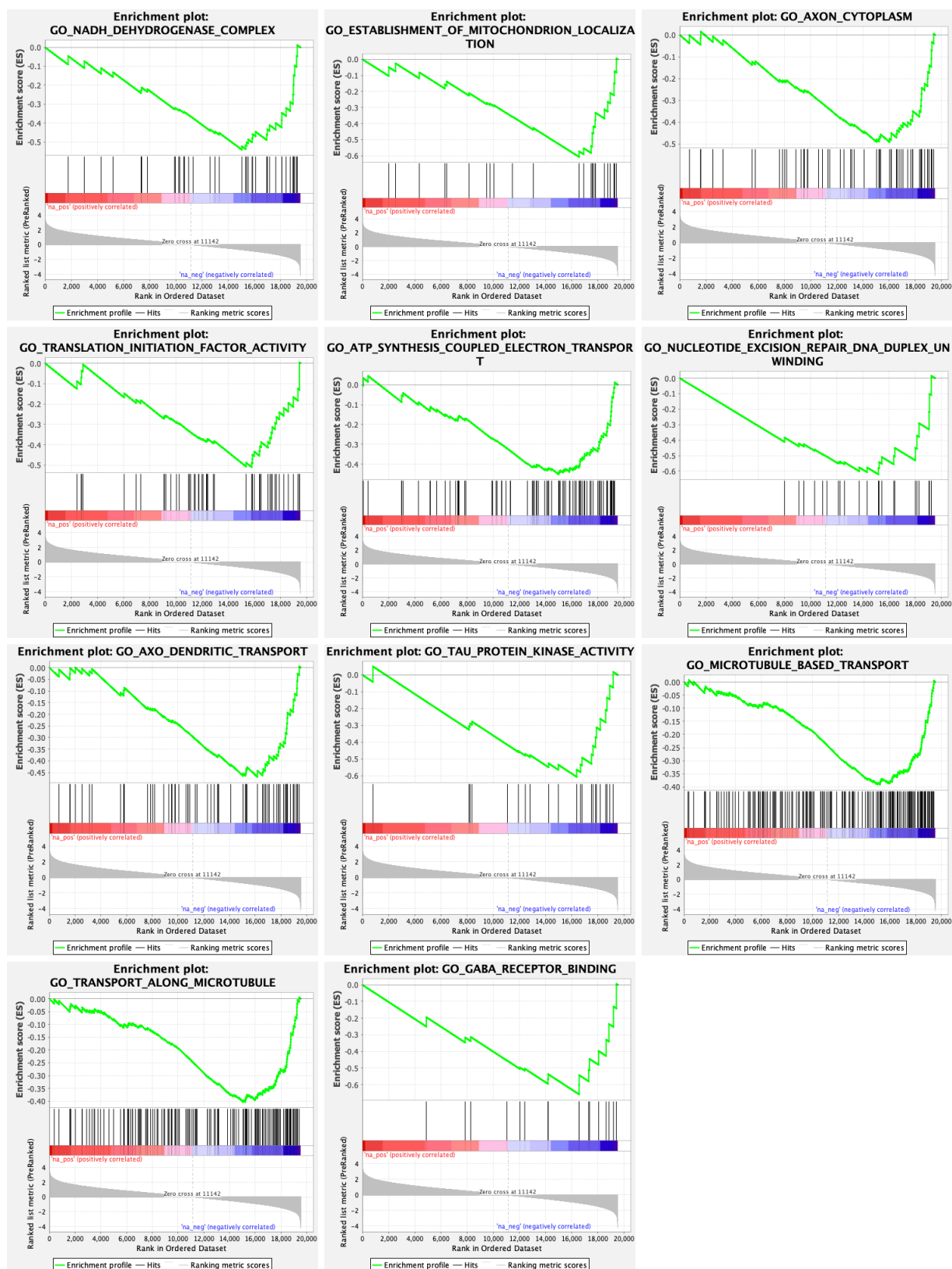




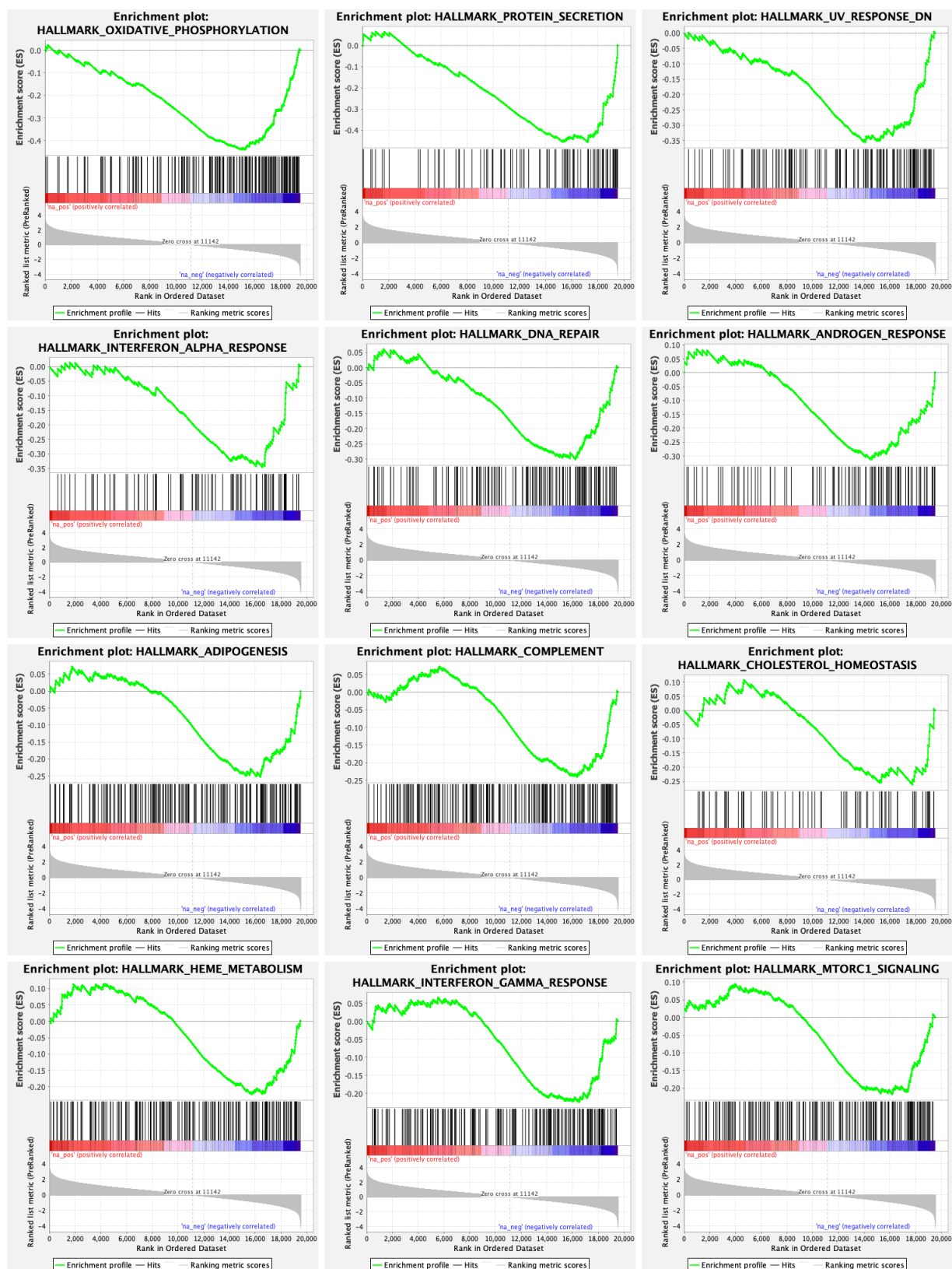
Positive enrichment in CK^{negative} patients group. The plots contain the profile of the running enrichment score (ES green line) and position of gene set members on the rank ordered list in GSEA (black strokes on the bottom).

Snapshot of enrichment results (GO gene sets)





Snapshot of enrichment results (Hallmark gene sets)



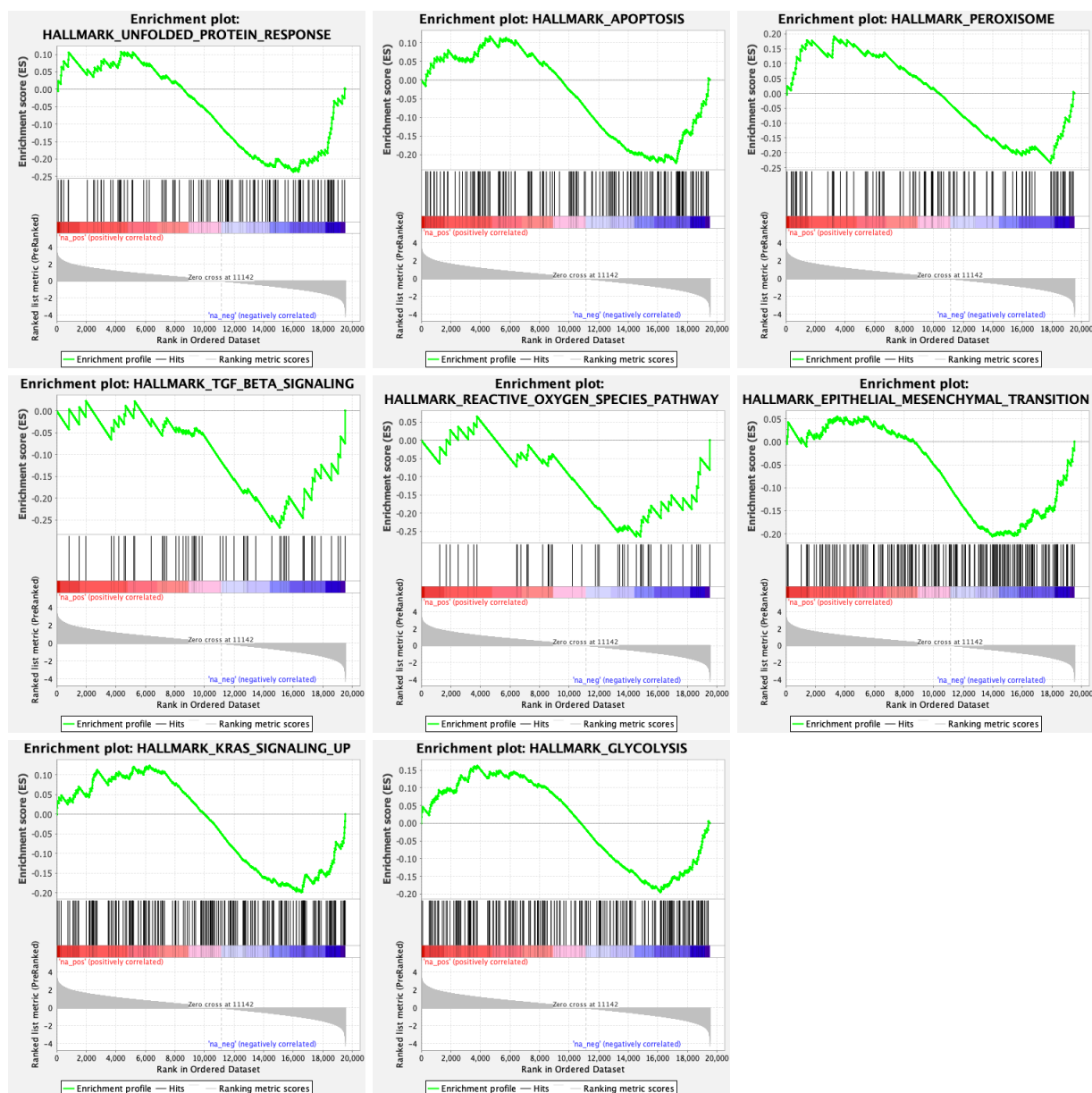


Figure S2. GSEA CK^{positive} vs CK^{negative} phenotype. Positive enrichment in CK^{positive} patients group. The plots contain the profile of the running enrichment score (ES green line) and position of gene set members on the rank ordered list in GSEA (black strokes on the bottom).