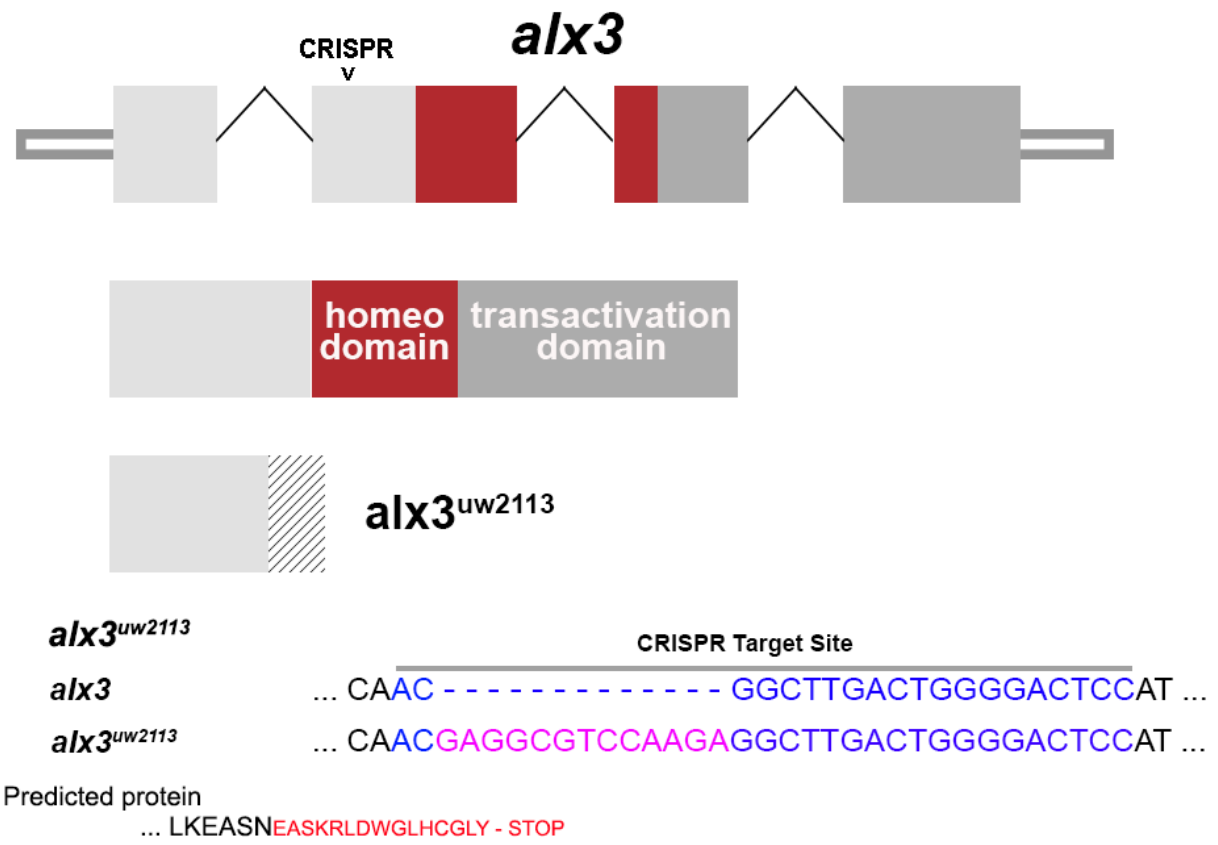


Fig. S1. Generation of mutant alleles at the zebrafish *alx3* locus. *alx3* mutations were induced by CRISPR/Cas9 mutagenesis targeted to the second exon of the alx3 locus. *alx3*^{uw2113} allele contains a net insertion of 13 nt (magenta letters) which is predicted to cause a frameshift and a premature stop (red letters).

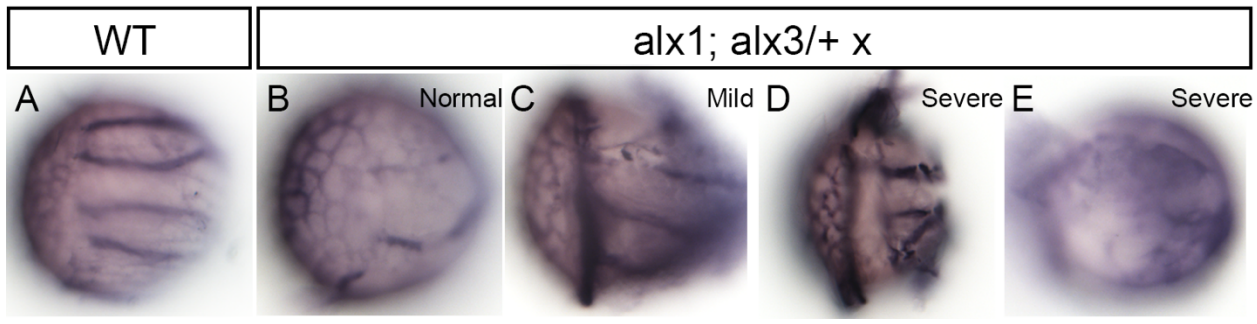


Fig. S2. *alx1* and *alx3* are required for hyaloid vascular patterning. Embryos derived from WT (A) or *alx1; alx3/+* (B – E) parents were first scored for the presence of misshapen eyes and stained for alkaline phosphatase to visualize hyaloid vasculature that surrounds the lens at 5 dpf. A: Normal hyaloid pattern in WT (6/6), B: Reduced hyaloid network formation in embryo with normally shaped eyes (5/6), C: Embryos with mildly misshapen eyes and disorganized hyaloid pattern (5/6). D-E: Embryos with severely misshapen eyes and disorganized (D; 2/5) or no hyaloid vasculature (E; 2/5 lens).

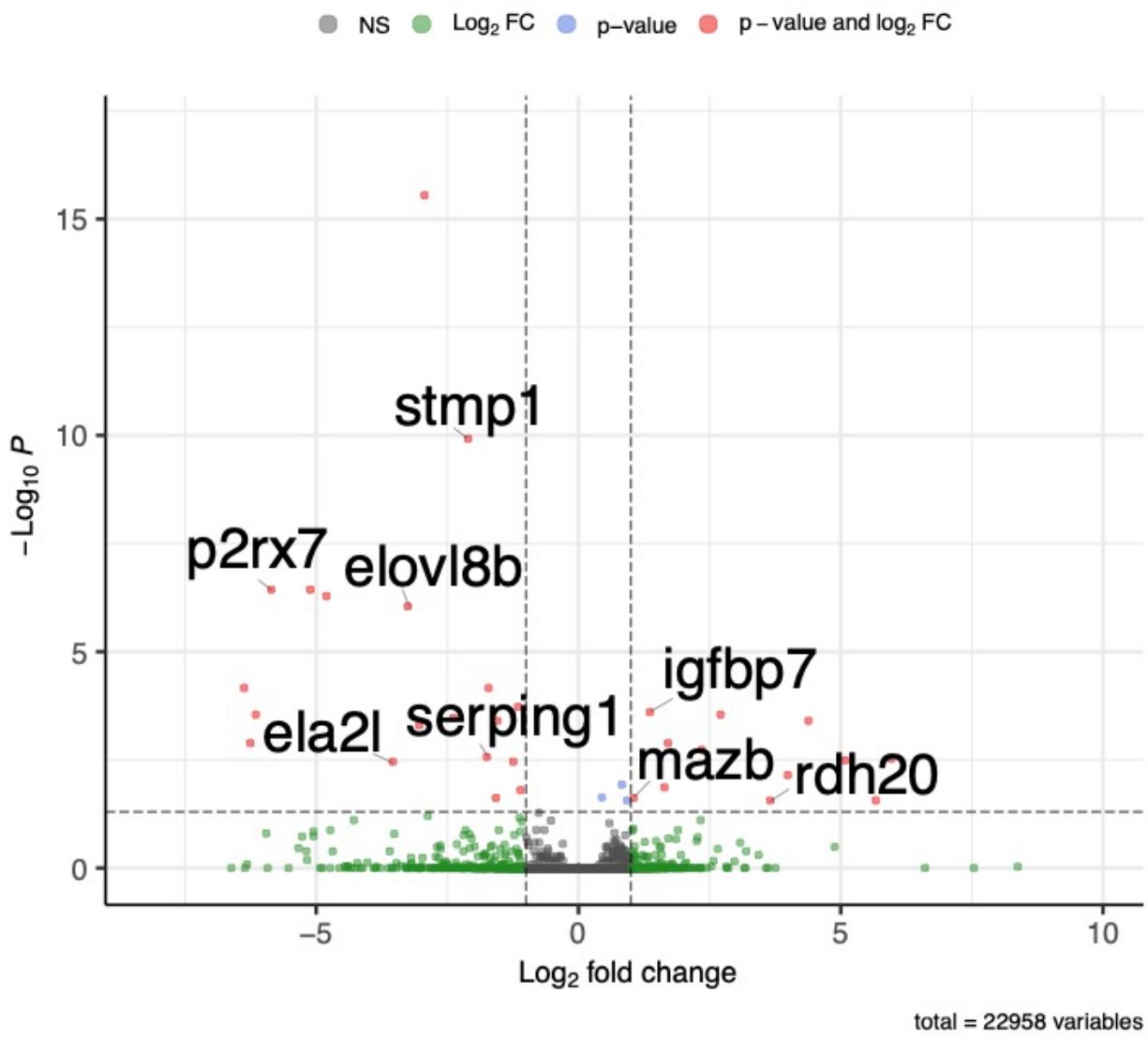
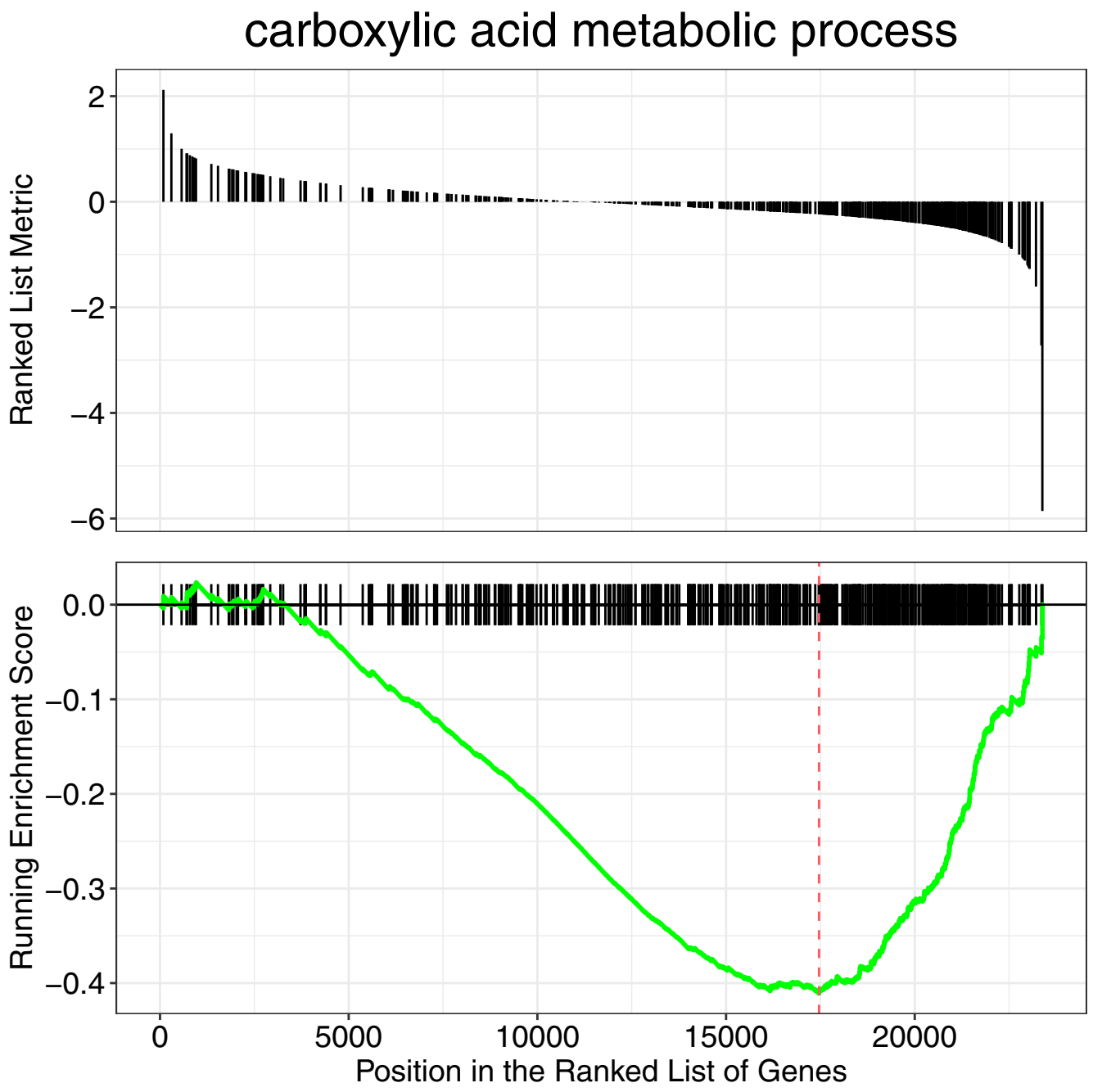
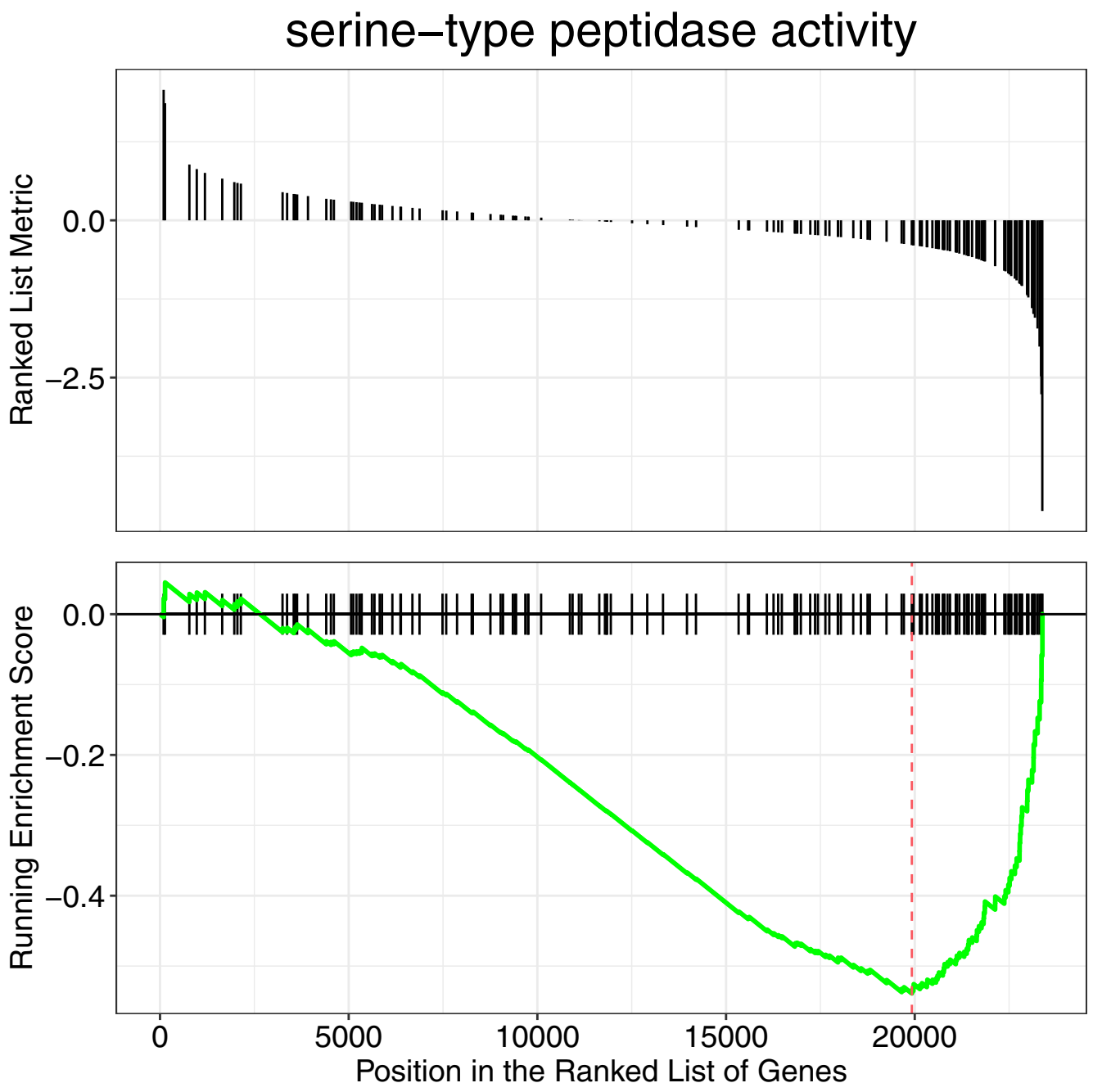
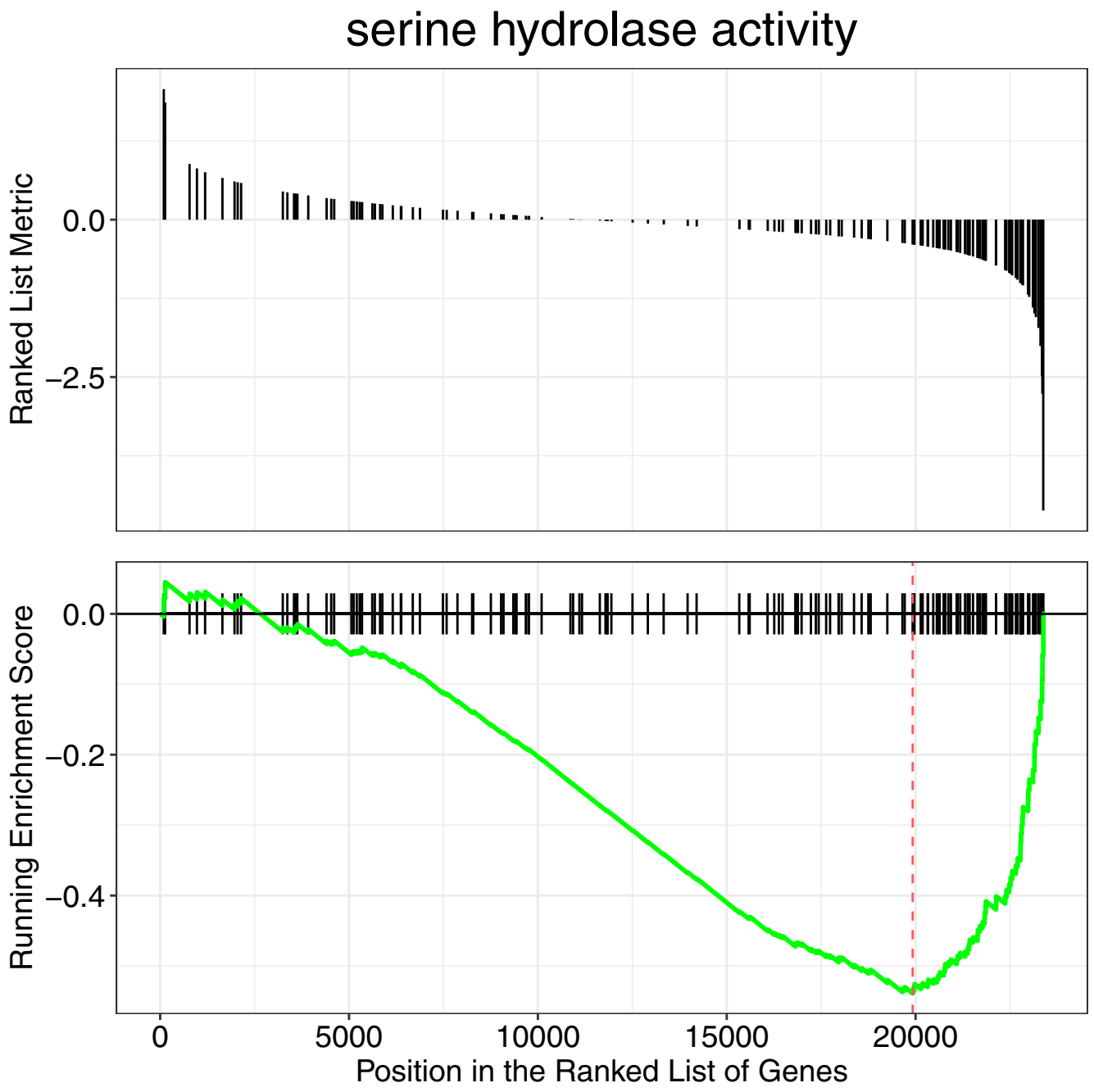
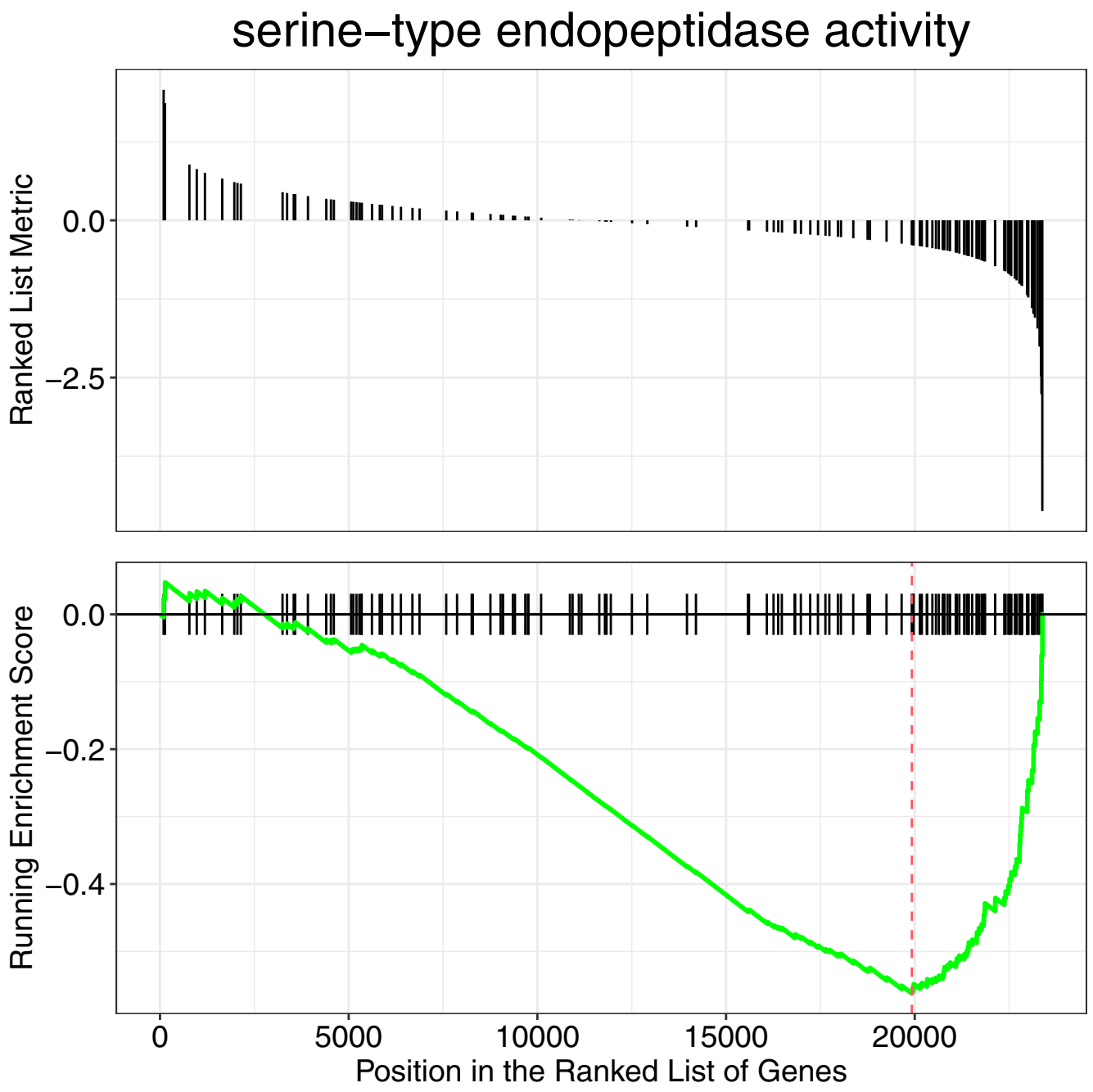


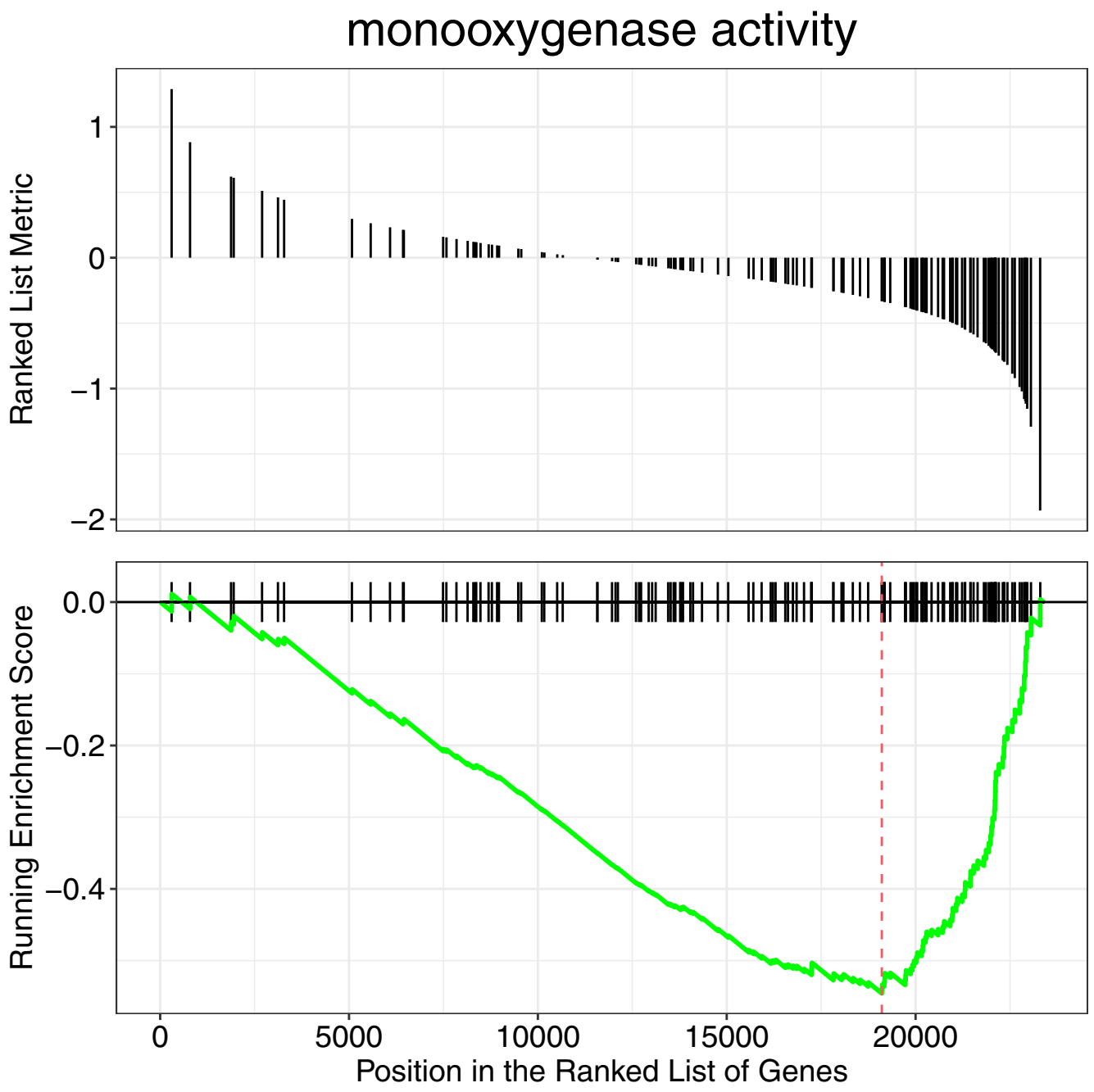
Fig. S3. Differentially expressed genes in alx1;alx3/+ mutants relative to wildtype siblings. A heat map (A) and volcano plot diagram (B) of differentially expressed genes in *alx1;alx3/+* mutants relative to wildtype siblings (see Figure 6 for details).

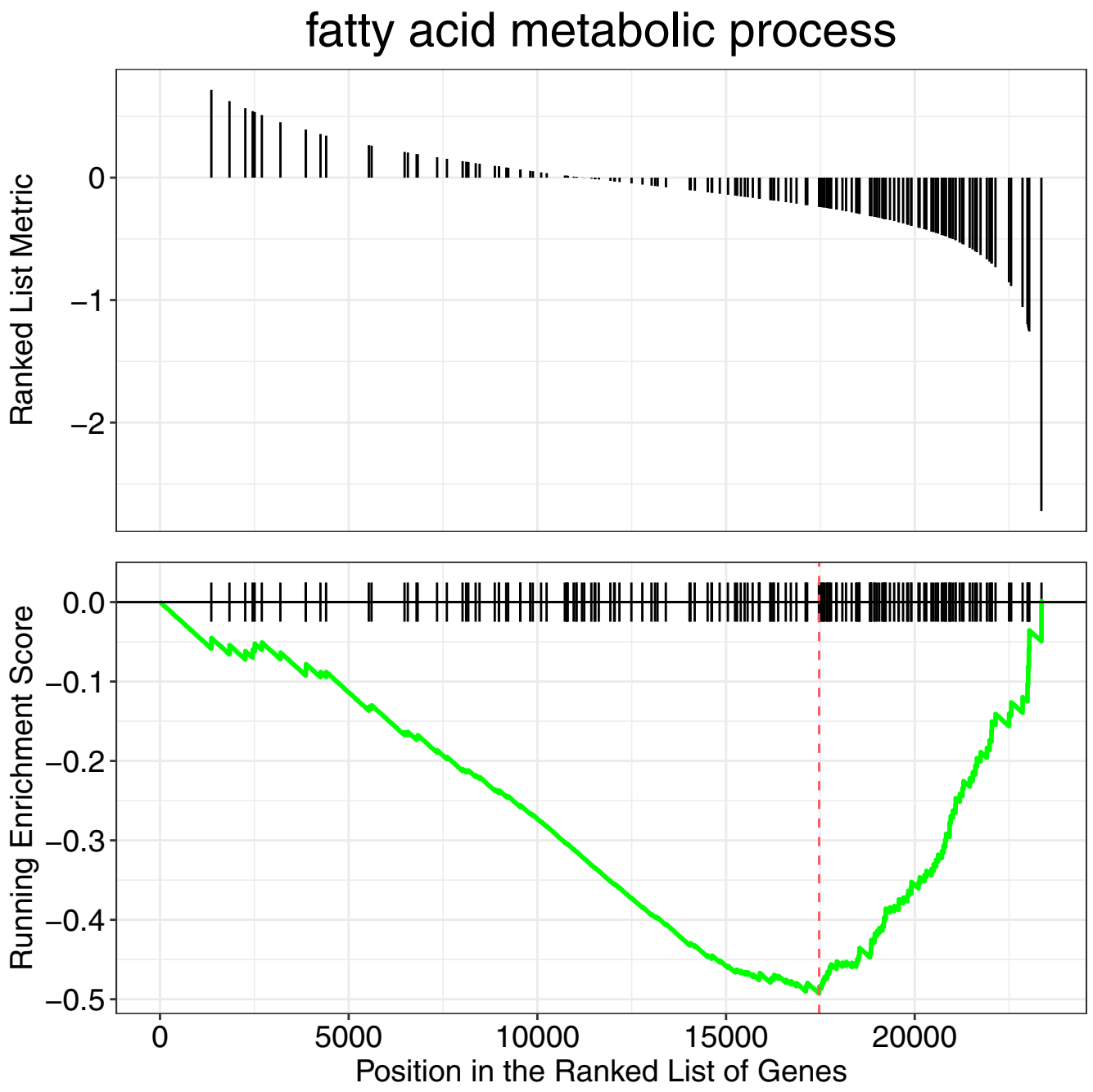

carboxylic acid metabolic process
Ranked List Metric
2
0
−2
−4
−6
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

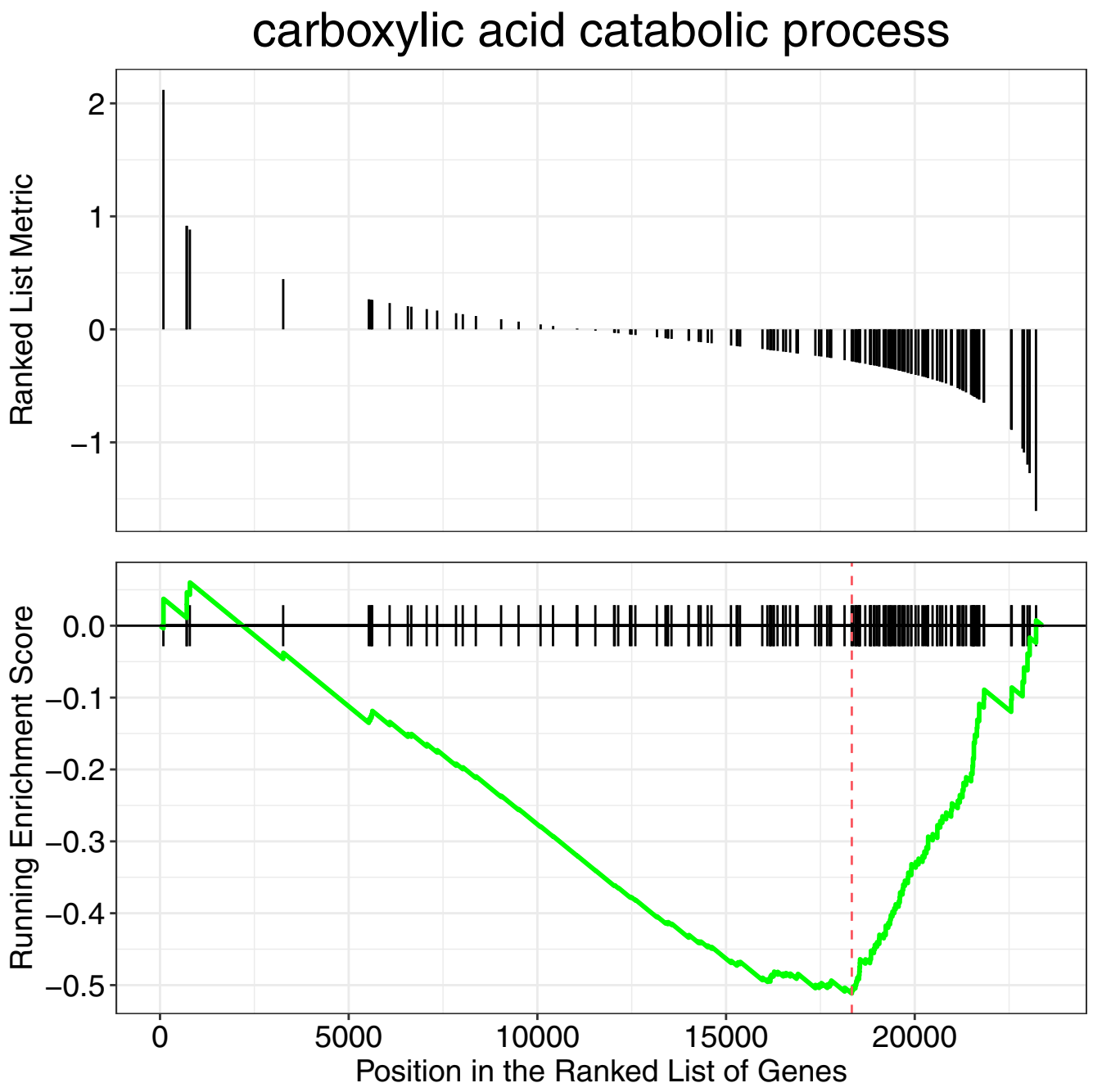

serine−type peptidase activity
Ranked List Metric
0.0
−2.5
Running Enrichment Score
0.0
−0.2
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

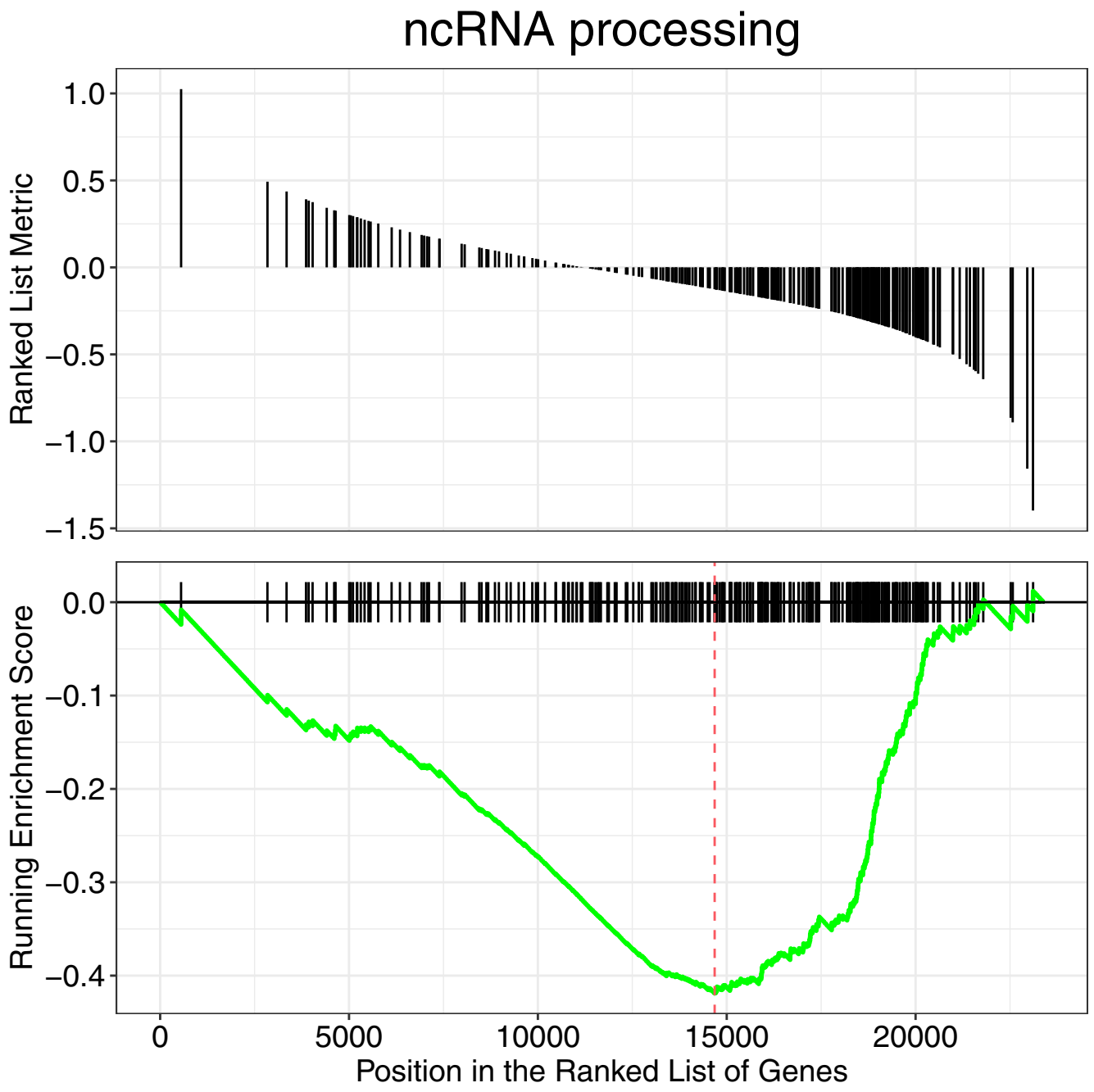

serine hydrolase activity
Ranked List Metric
0.0
−2.5
Running Enrichment Score
0.0
−0.2
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

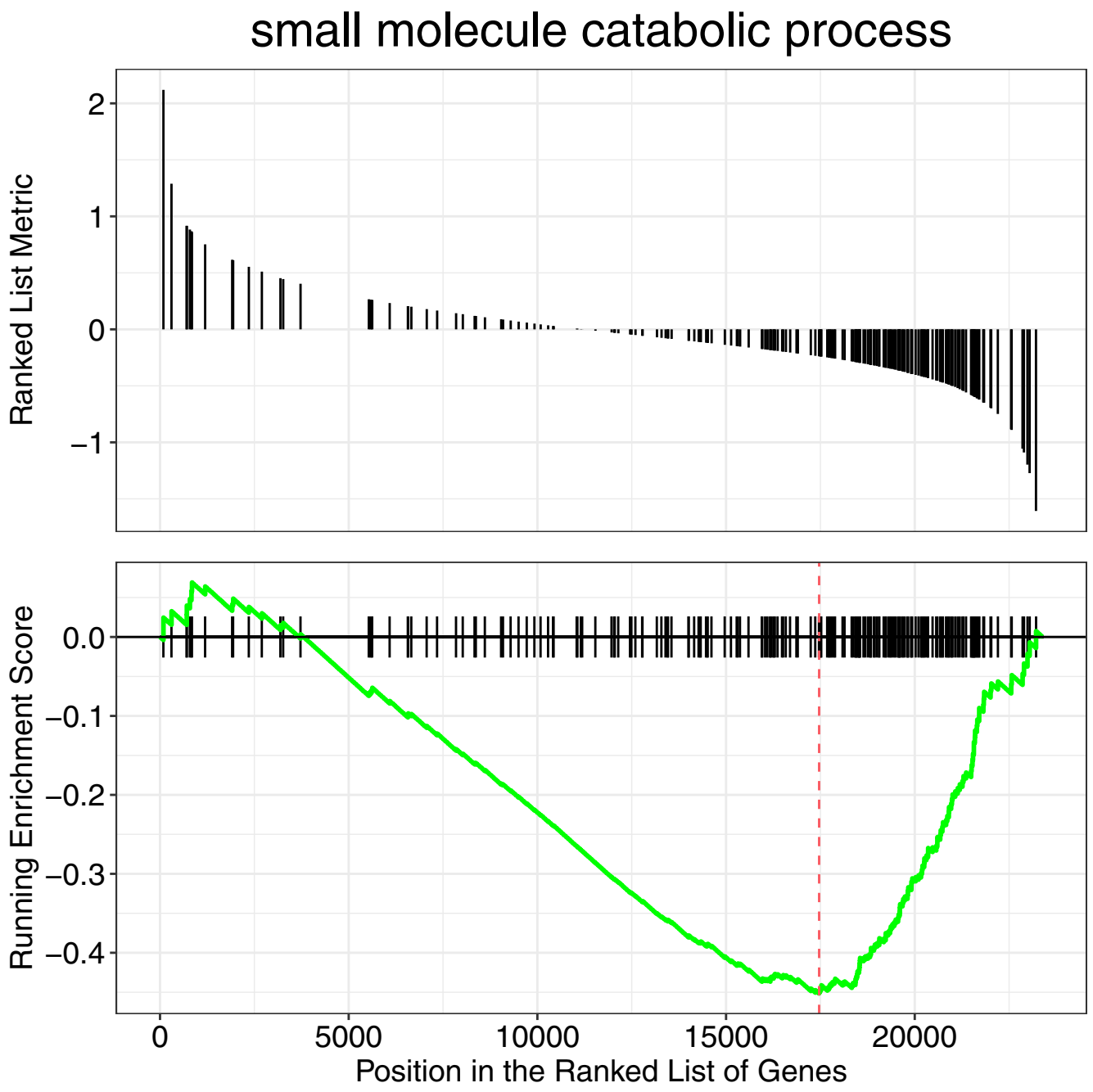

serine−type endopeptidase activity
Ranked List Metric
0.0
−2.5
Running Enrichment Score
0.0
−0.2
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

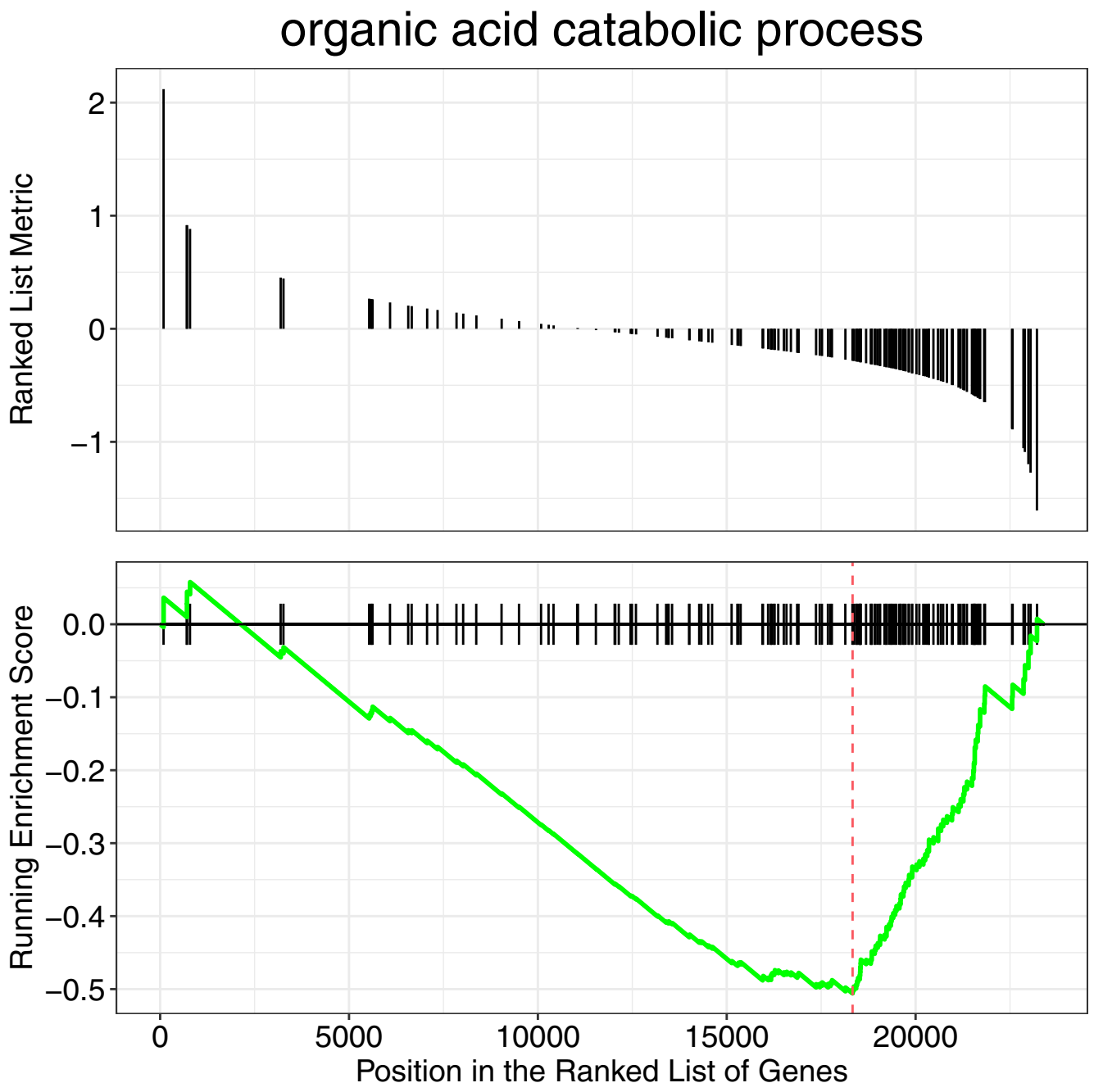

monooxygenase activity
Ranked List Metric
1
0
−1
−2
Running Enrichment Score
0.0
−0.2
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

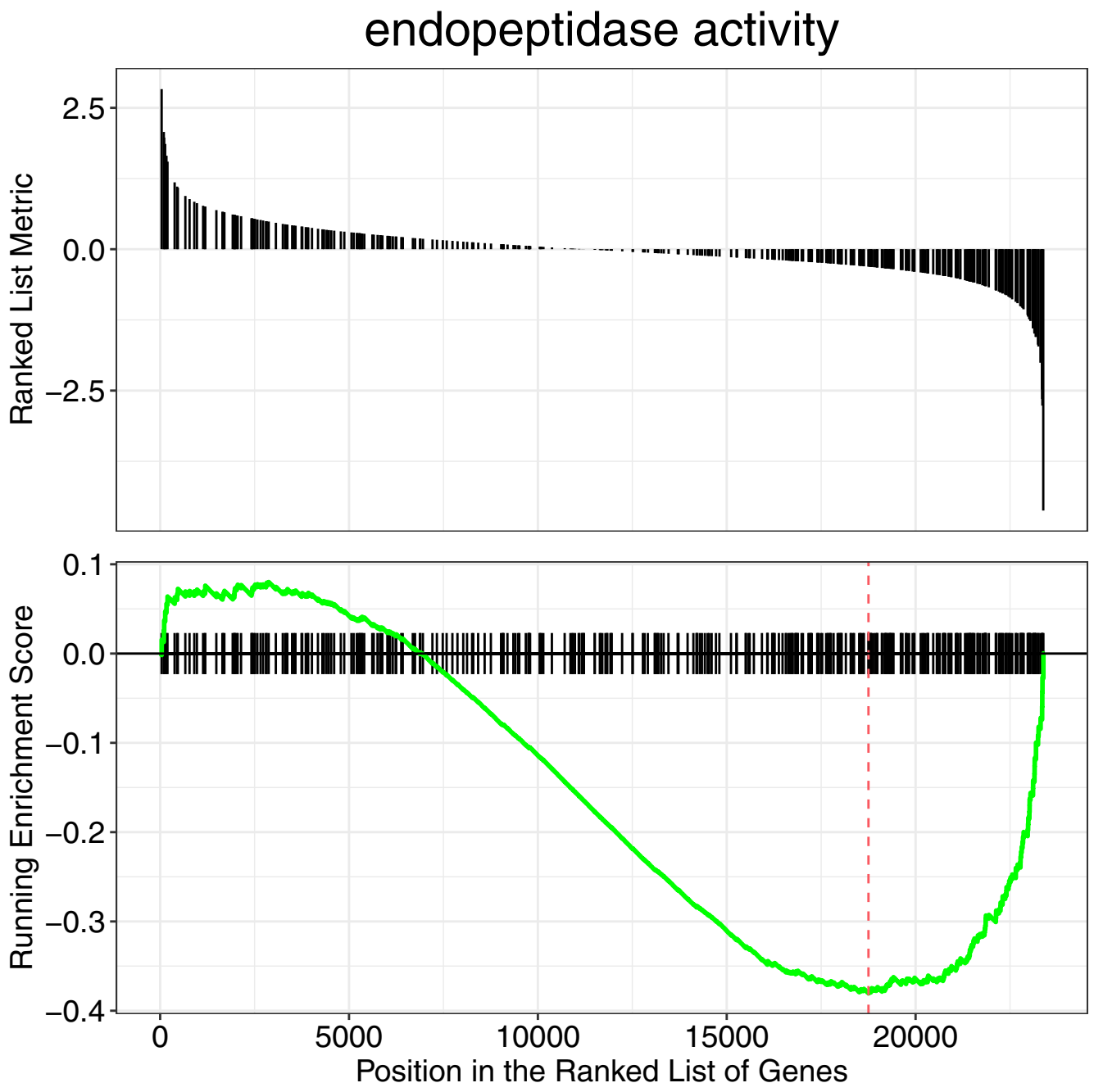

fatty acid metabolic process
Ranked List Metric
0
−1
−2
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
5000
10000
15000
20000
Position in the Ranked List of Genes

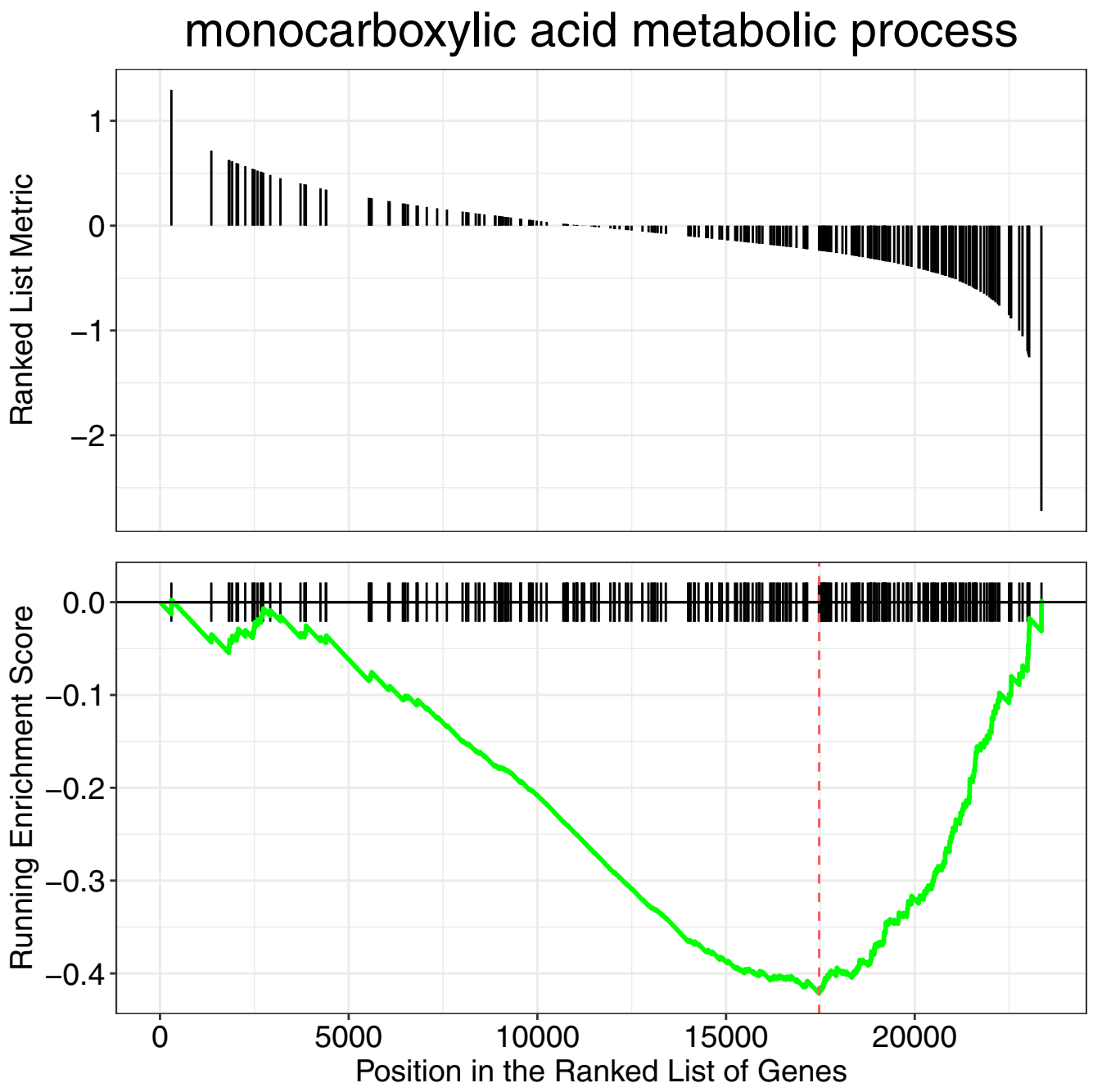

carboxylic acid catabolic process
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
5000
10000
15000
20000
Position in the Ranked List of Genes

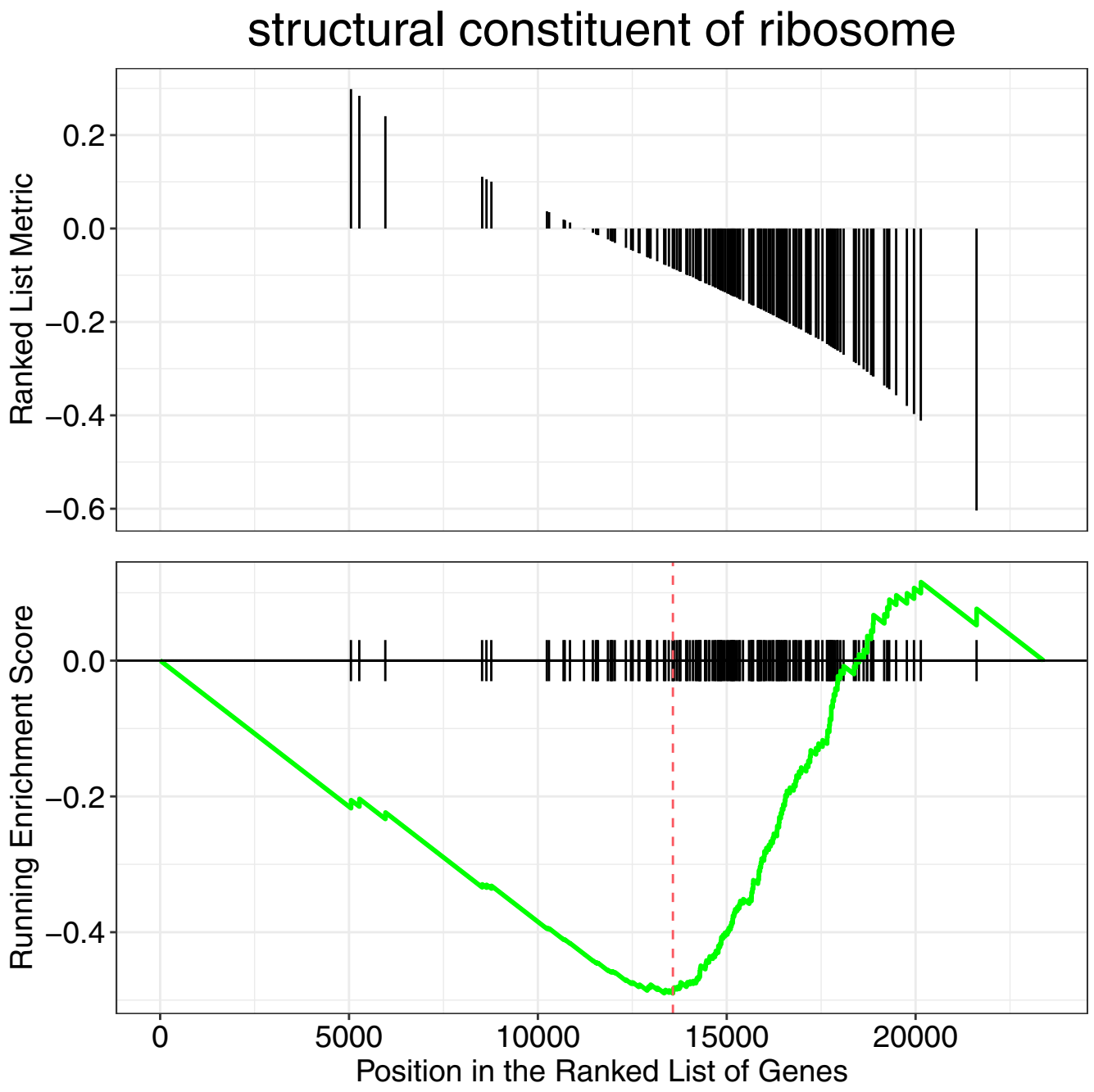

ncRNA processing
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

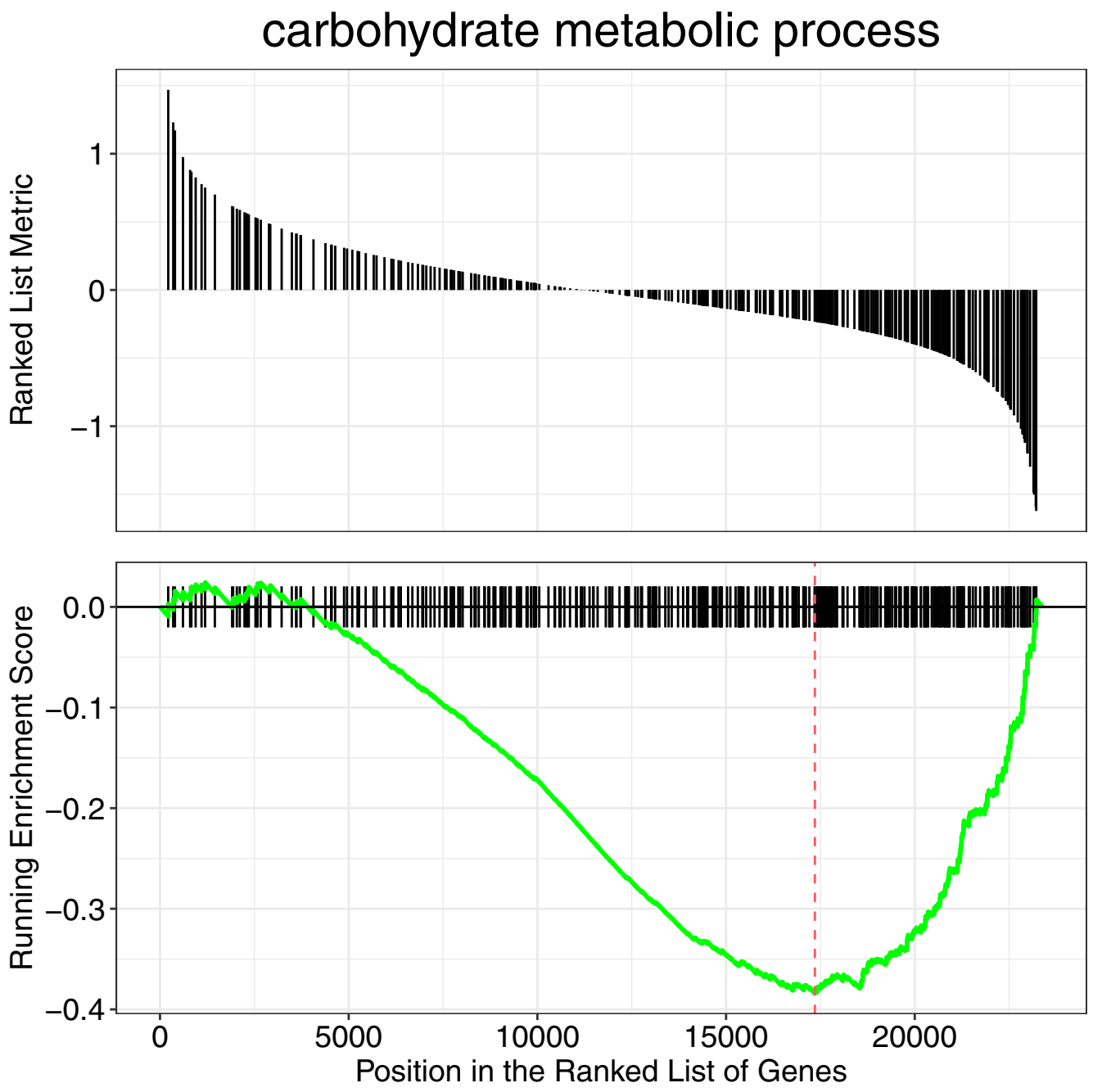


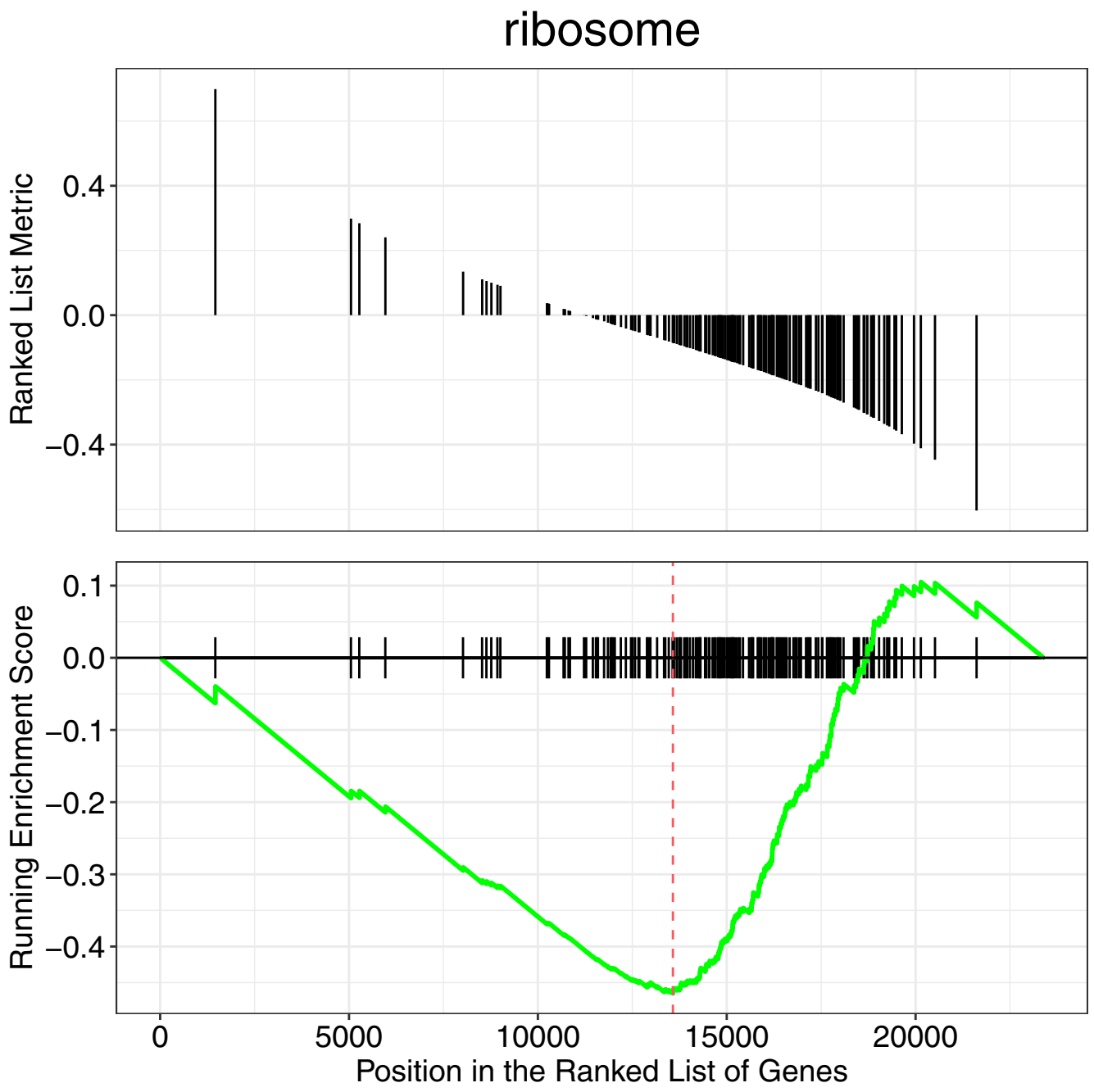

organic acid catabolic process
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
5000
10000
15000
20000
Position in the Ranked List of Genes

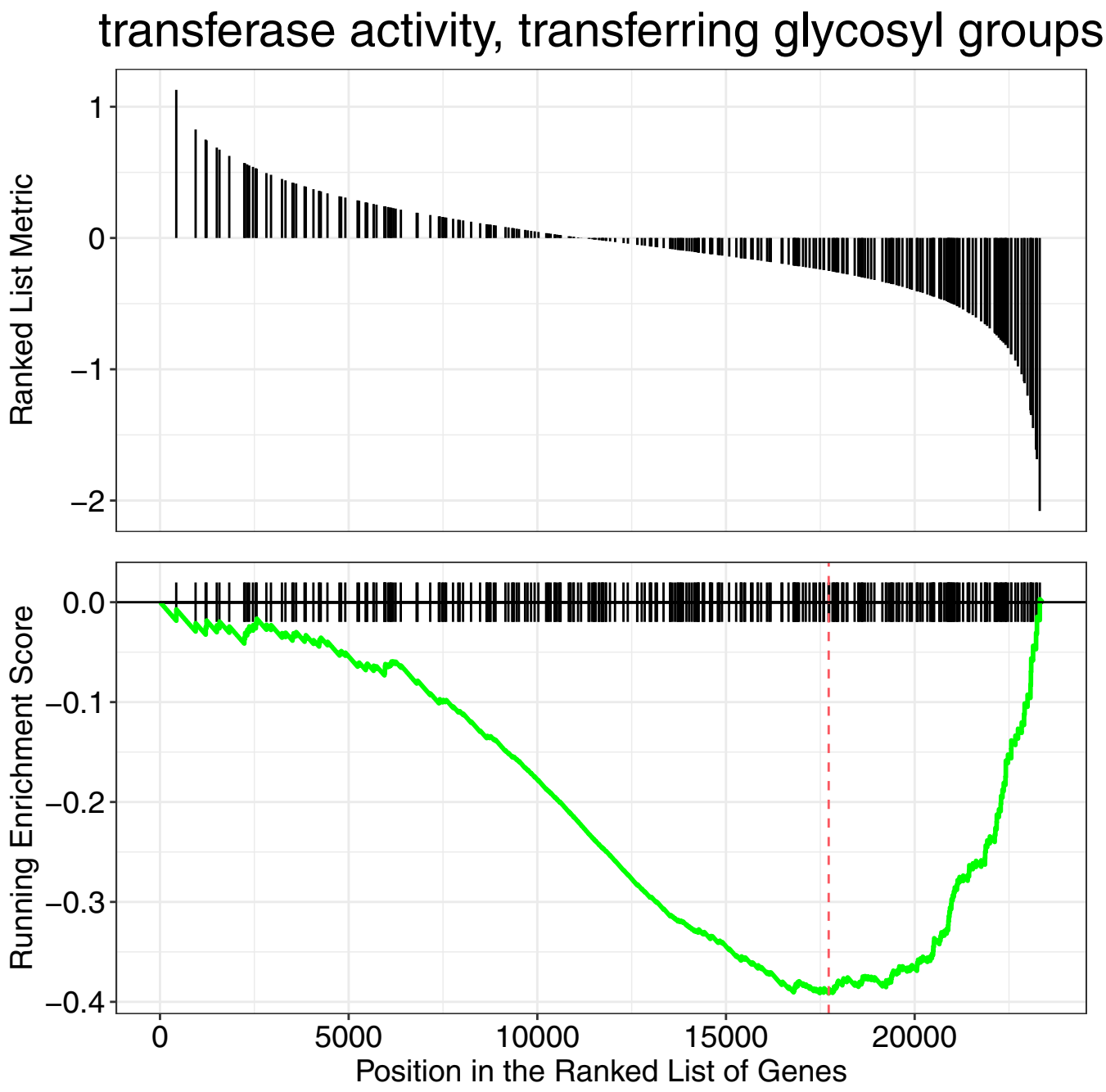

endopeptidase activity
Ranked List Metric
2.5
0.0
−2.5
0.1
0.0
−0.1
−0.2
−0.3
−0.4
Running Enrichment Score
0
5000
10000
15000
20000
Position in the Ranked List of Genes

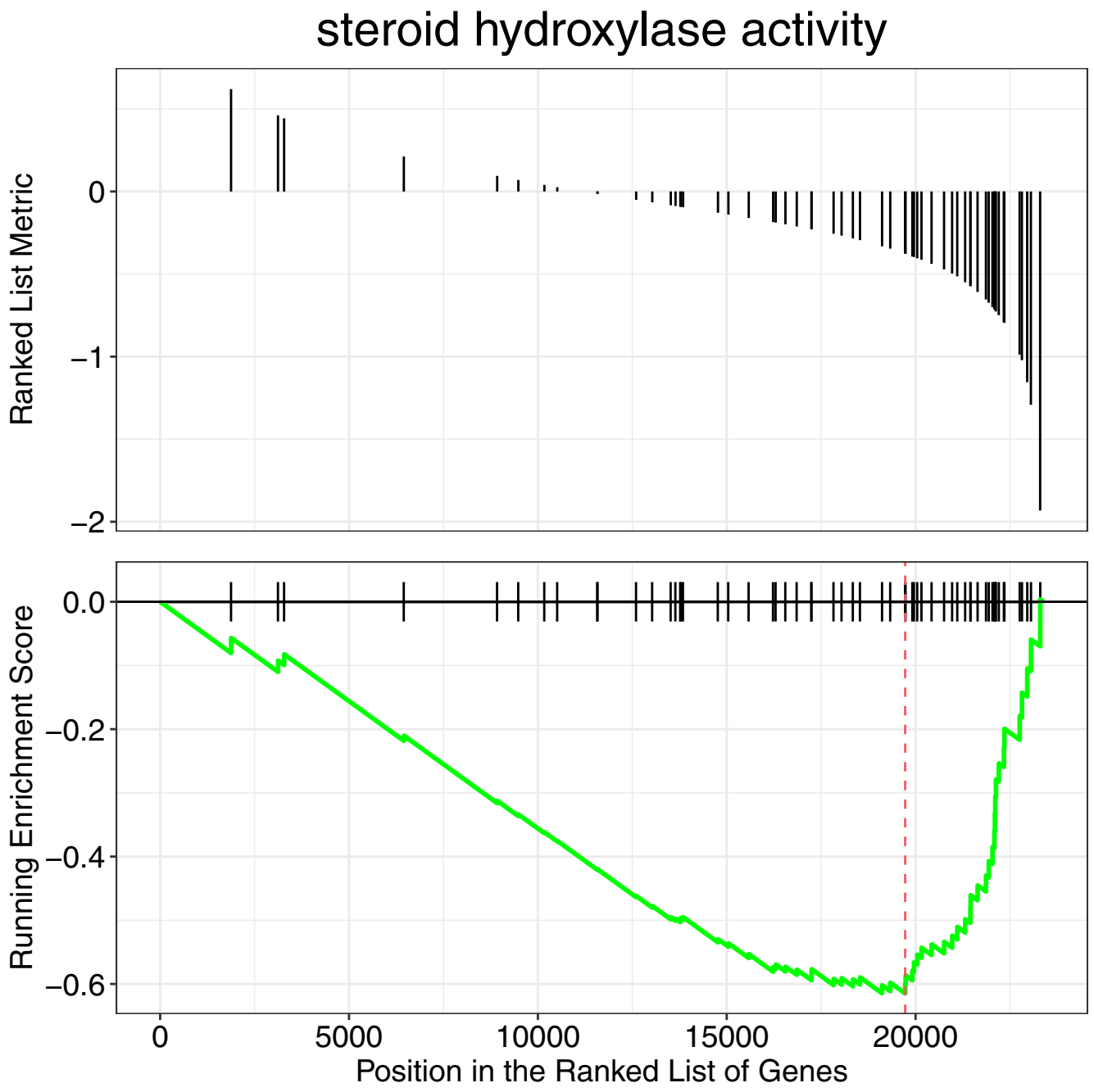

monocarboxylic acid metabolic process
Ranked List Metric
1
0
−1
−2
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

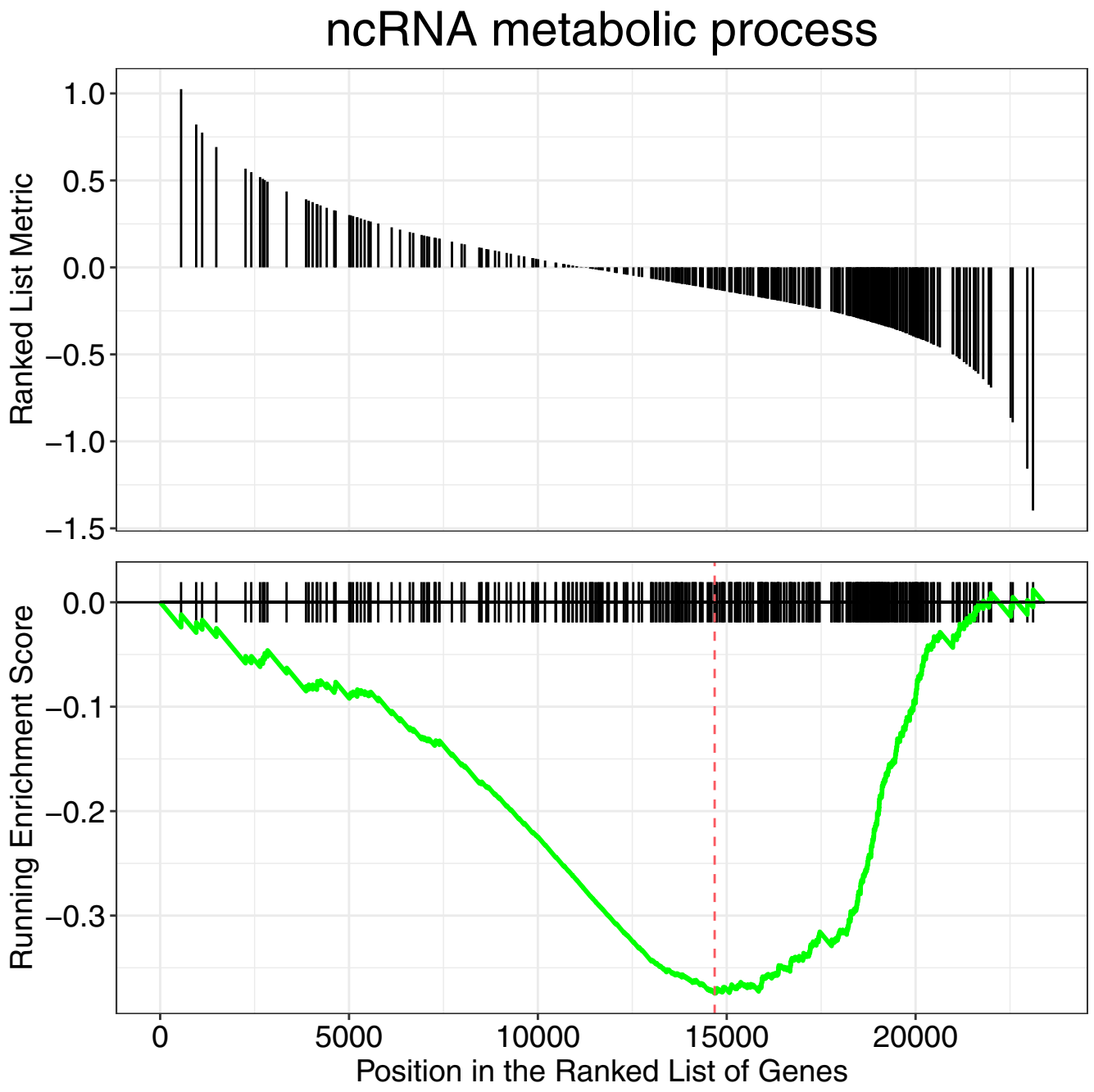

structural constituent of ribosome
Ranked List Metric
0.2
0.0
−0.2
−0.4
−0.6
Running Enrichment Score
0.0
−0.2
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

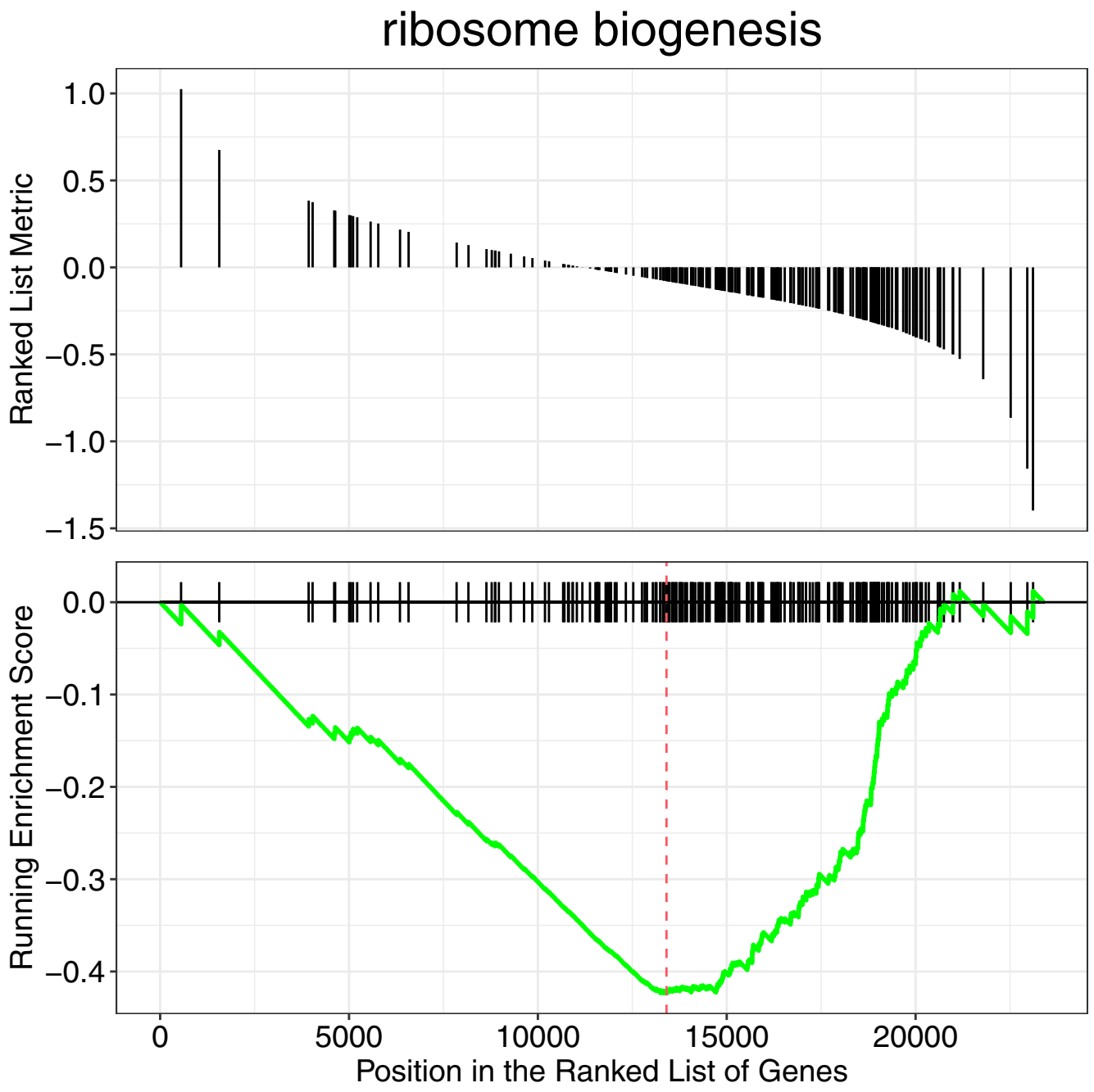

carbohydrate metabolic process
Ranked List Metric
1
0
−1
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes


ribosome
Ranked List Metric
0.4
0.0
−0.4
Running Enrichment Score
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes


transferase activity, transferring glycosyl groups
Ranked List Metric
1
0
−1
−2
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes


steroid hydroxylase activity
Ranked List Metric
0
−1
−2
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
5000
10000
15000
20000
Position in the Ranked List of Genes


ncRNA metabolic process
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
0
5000
10000
15000
20000
Position in the Ranked List of Genes


ribosome biogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
5000
10000
15000
20000
Position in the Ranked List of Genes

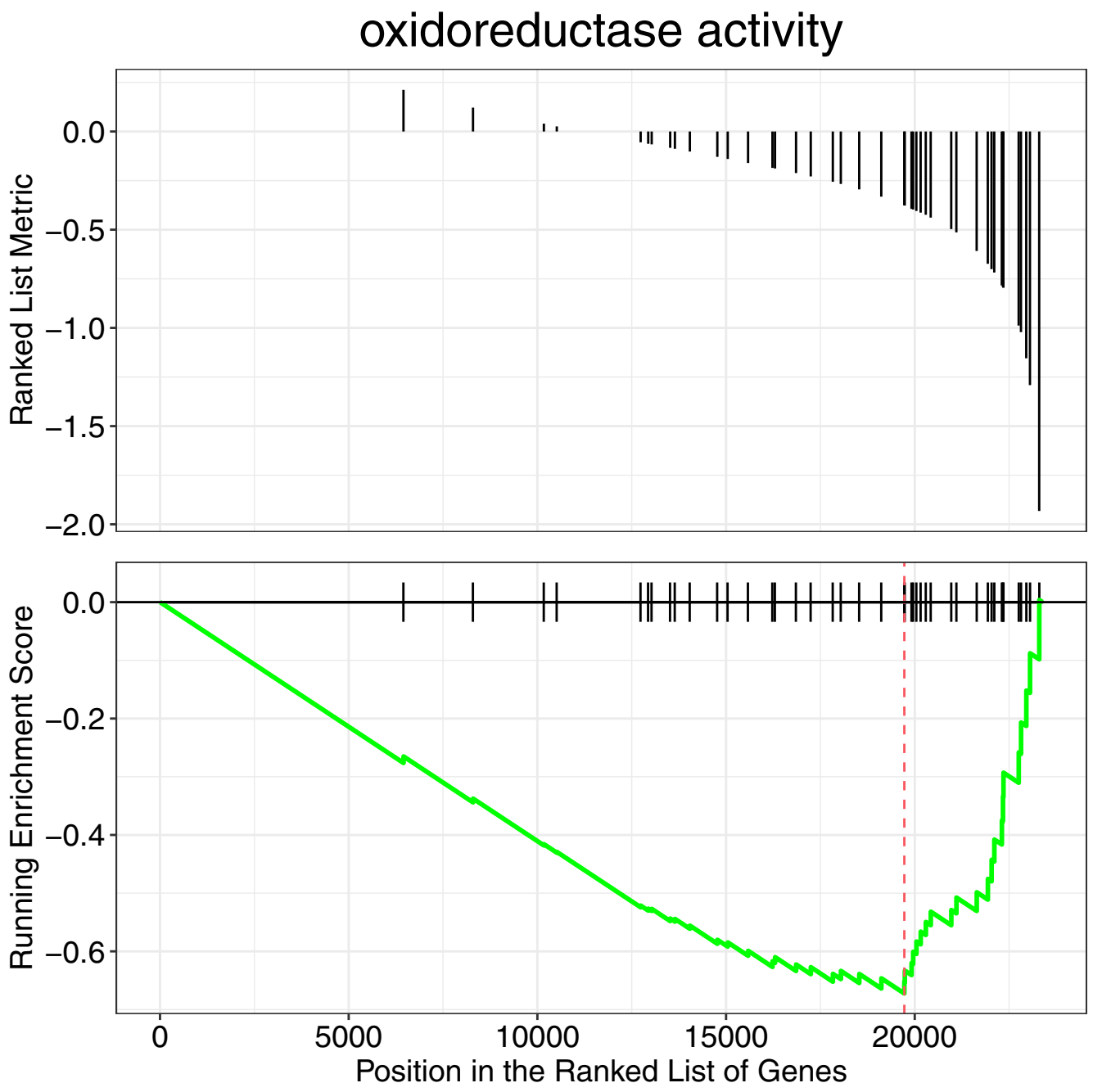
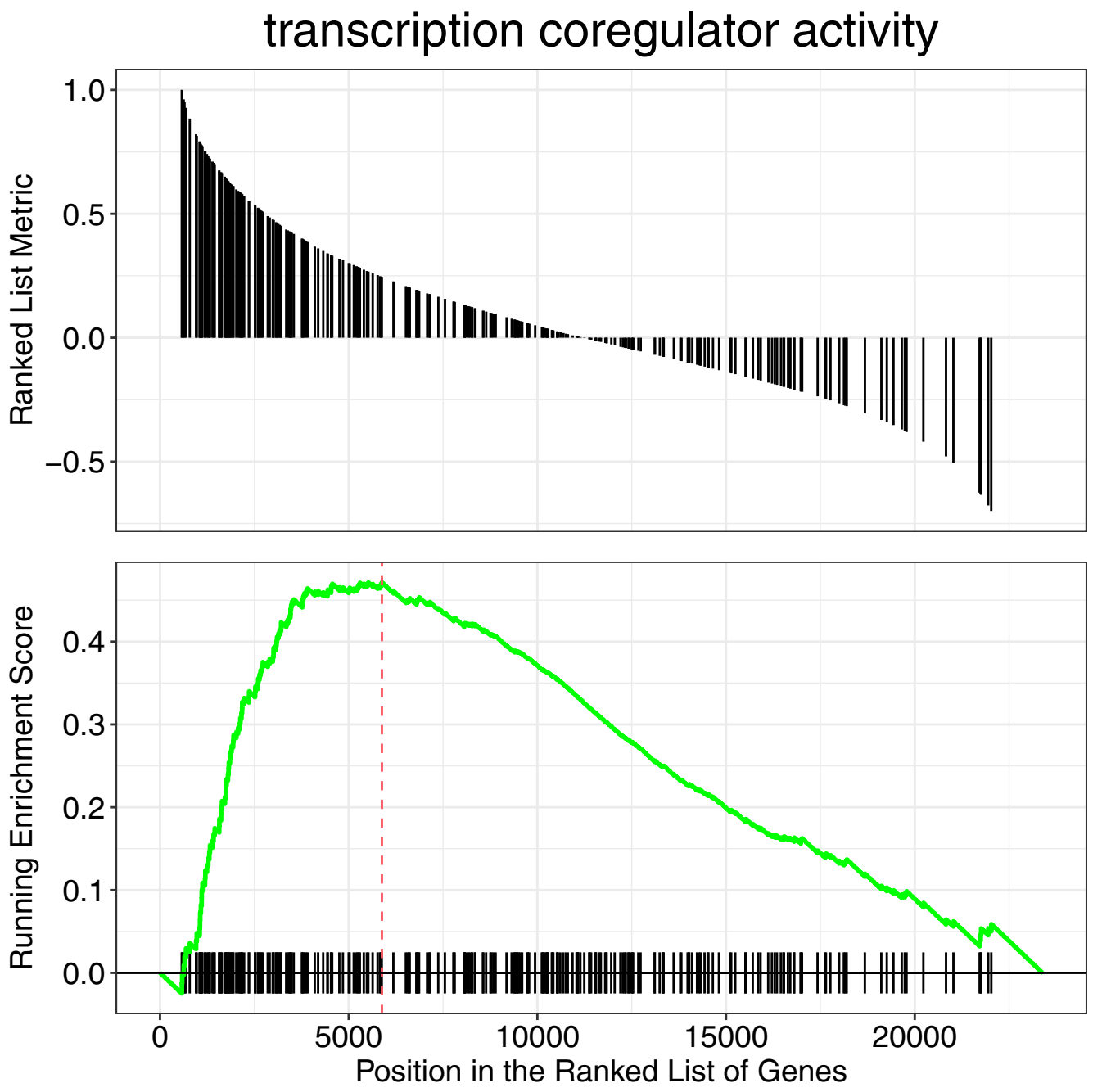
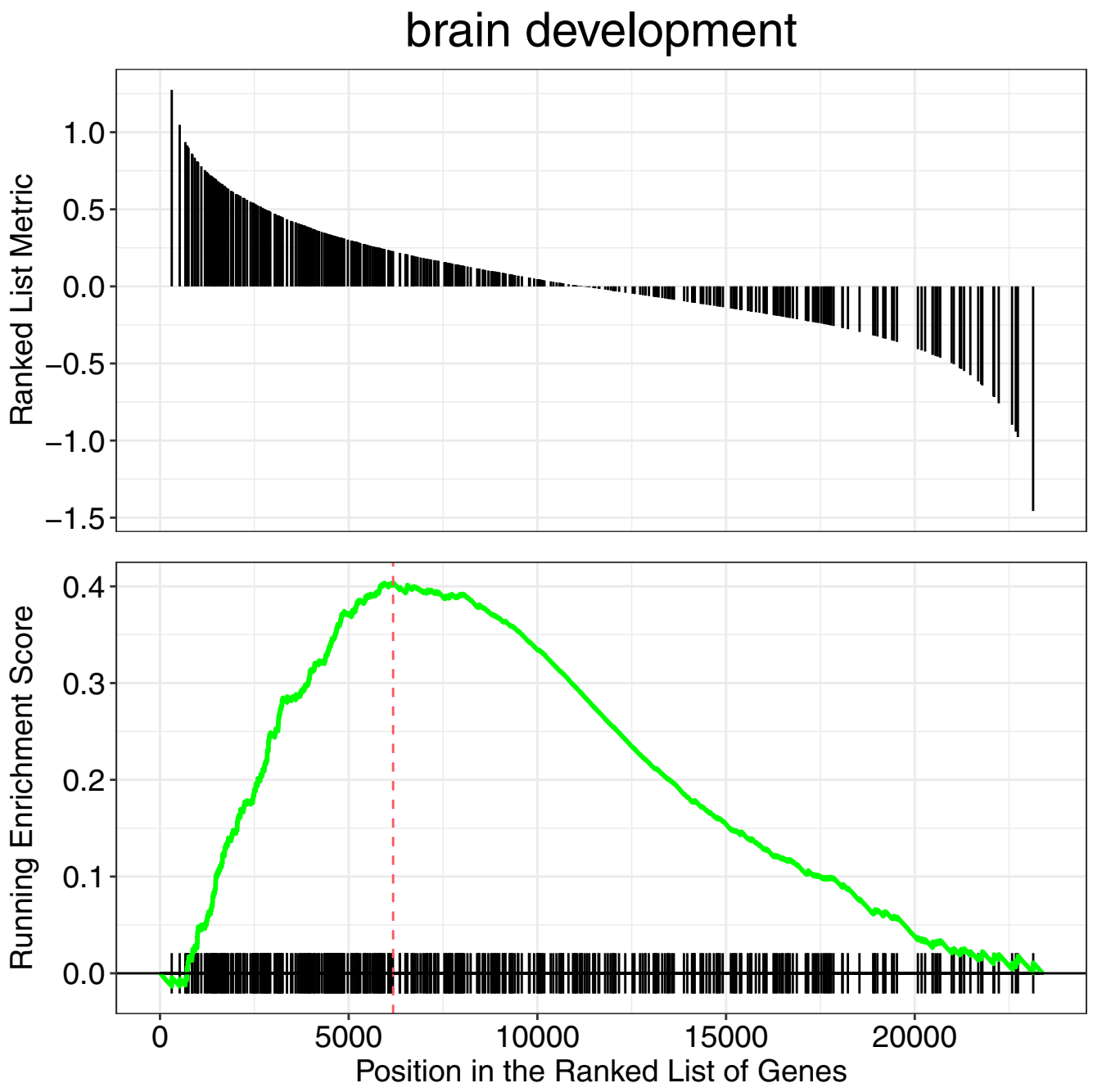
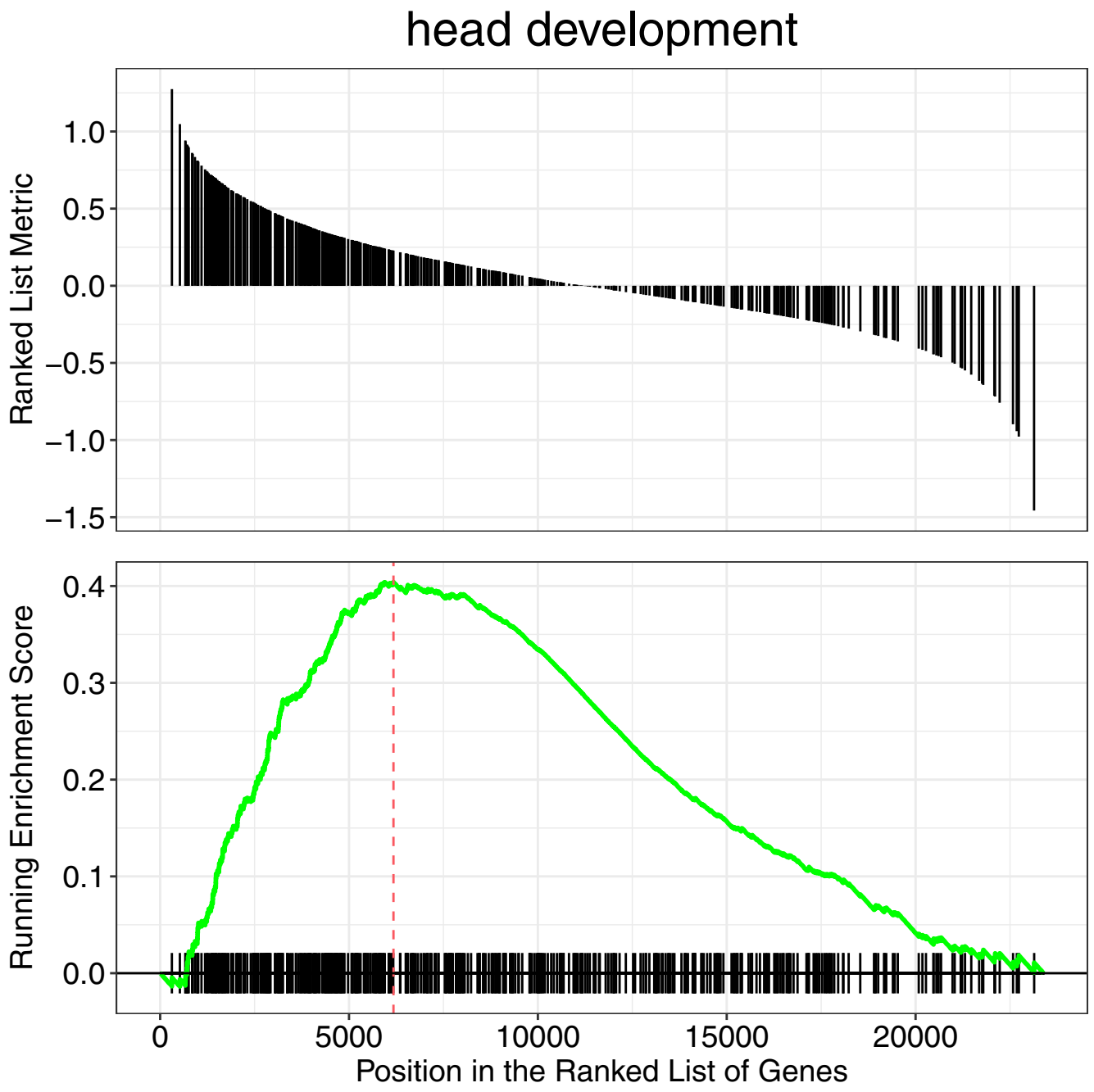
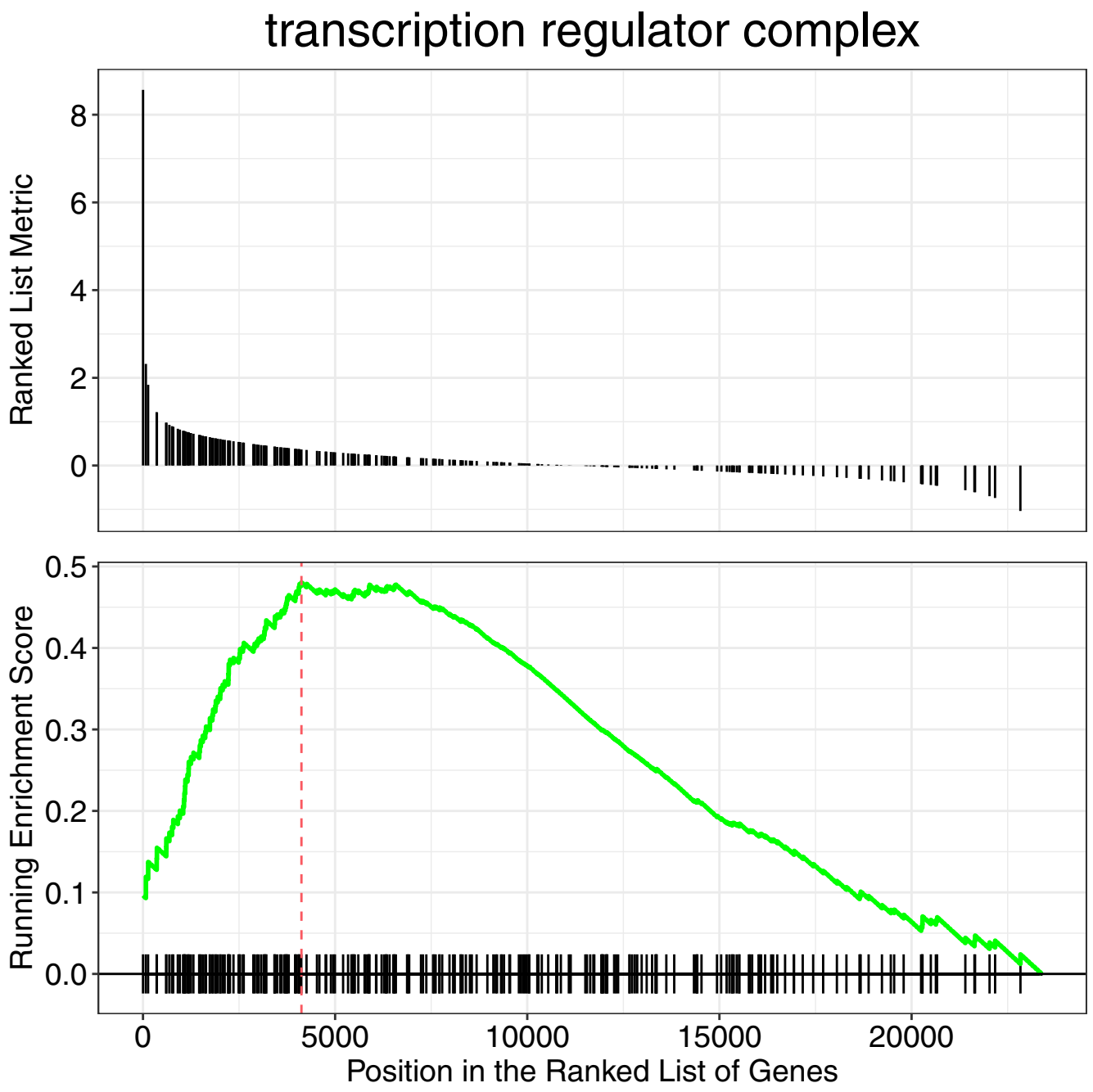


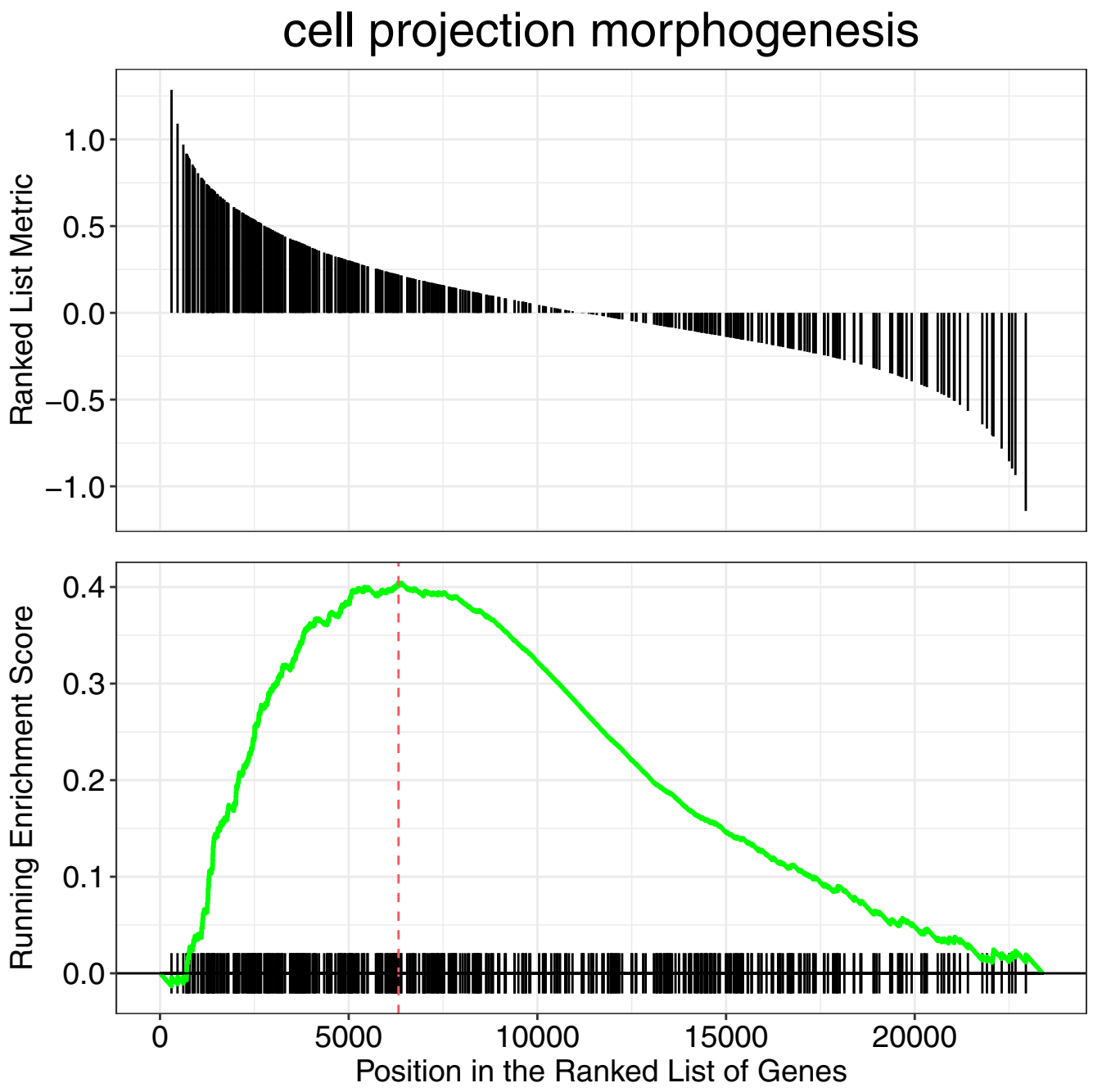
Fig. S4. Enrichment plots of Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 mutants. Running score plot and pre-ranked list of top 25 suppressed GSEA terms shown in Figure 5C.

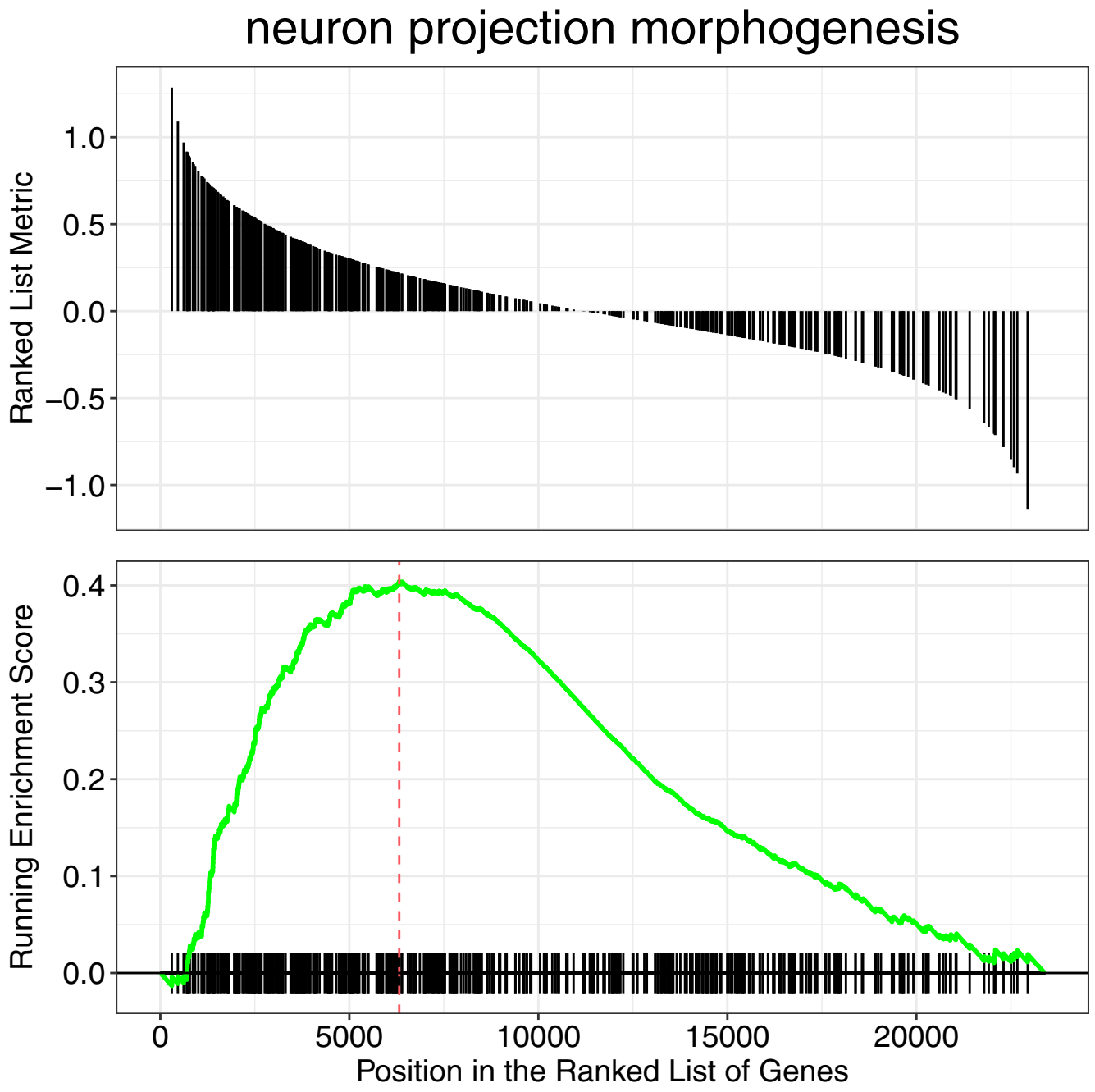

transcription coregulator activity
Ranked List Metric
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

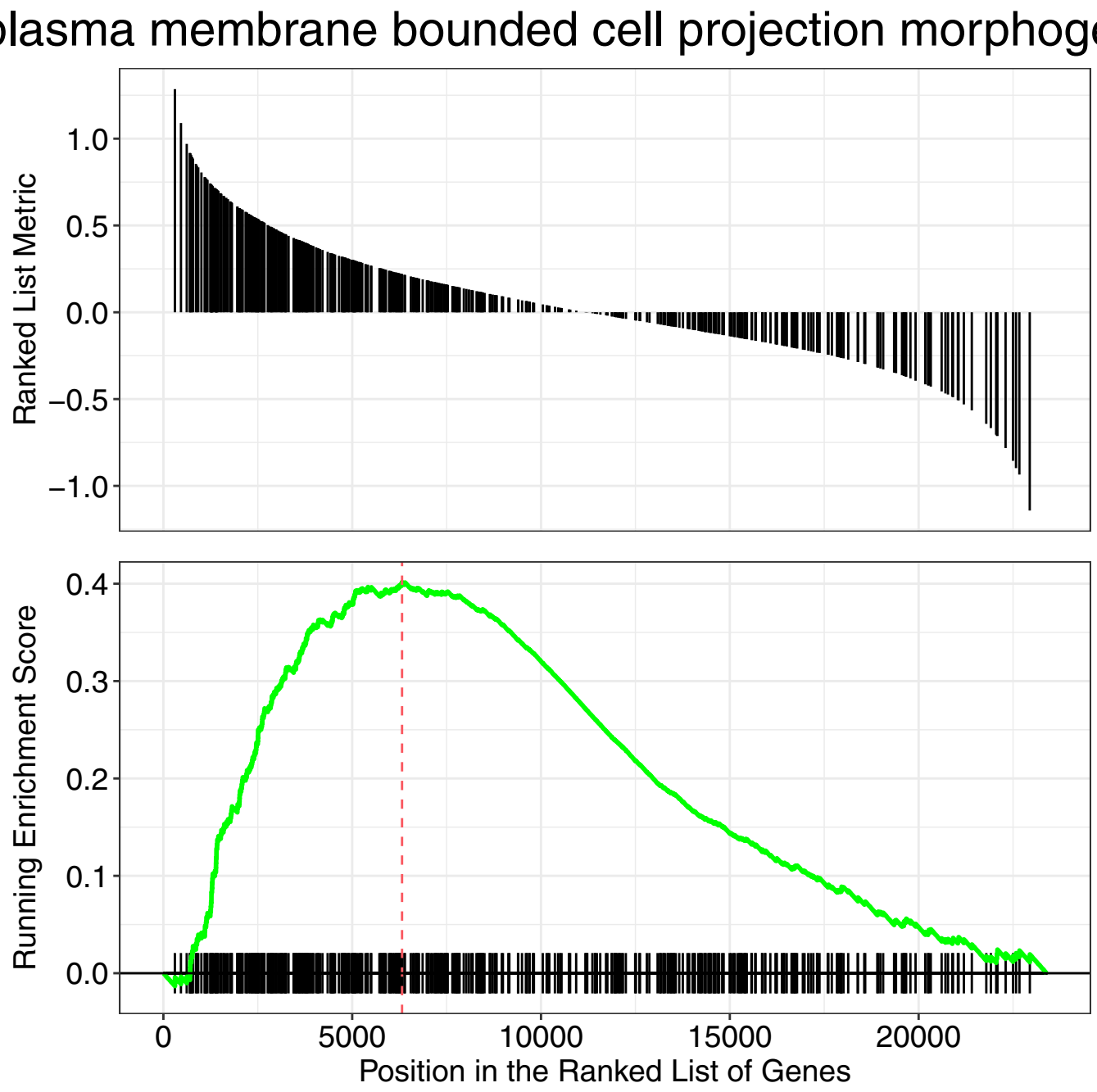

brain development
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

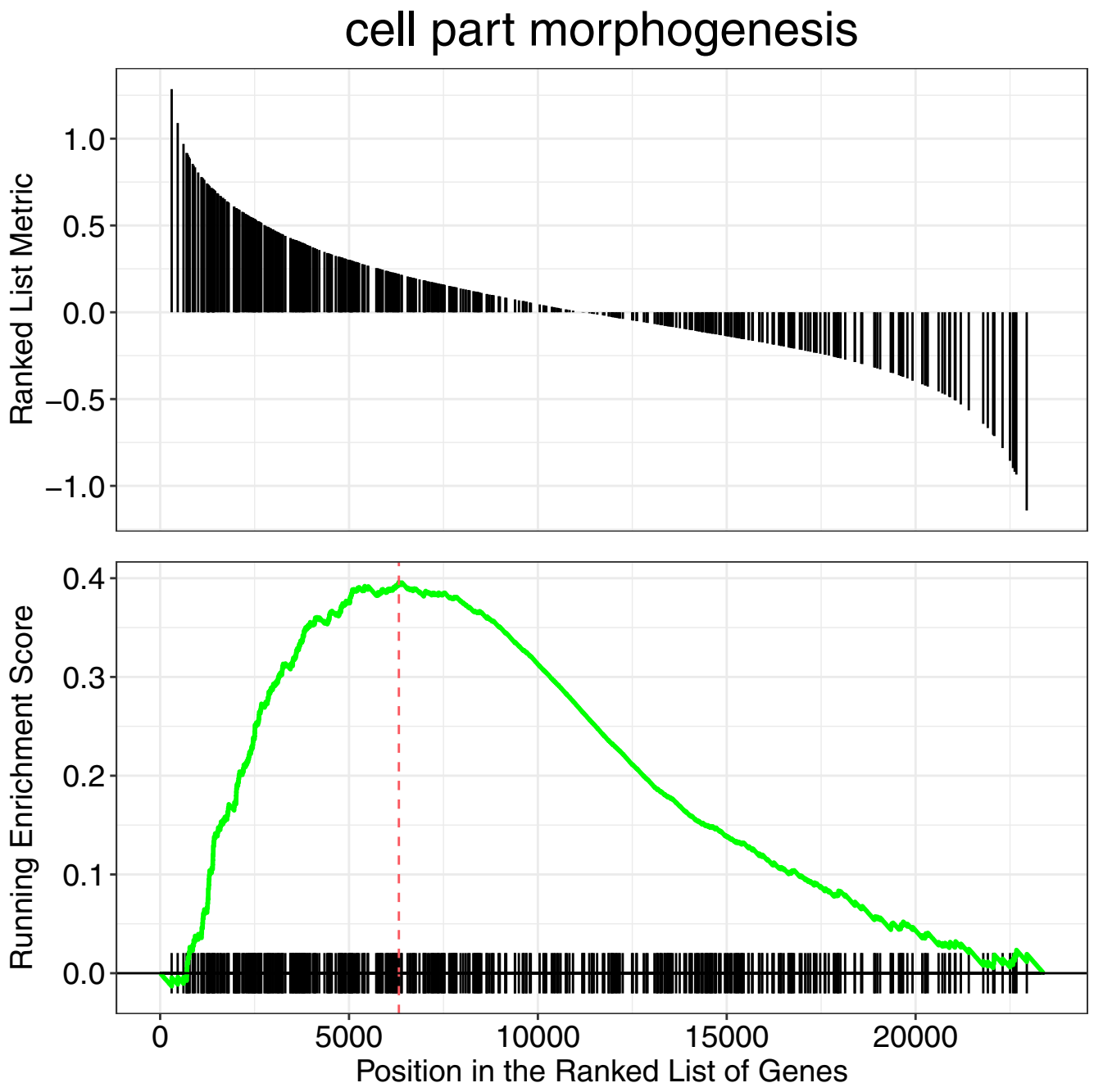

head development
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

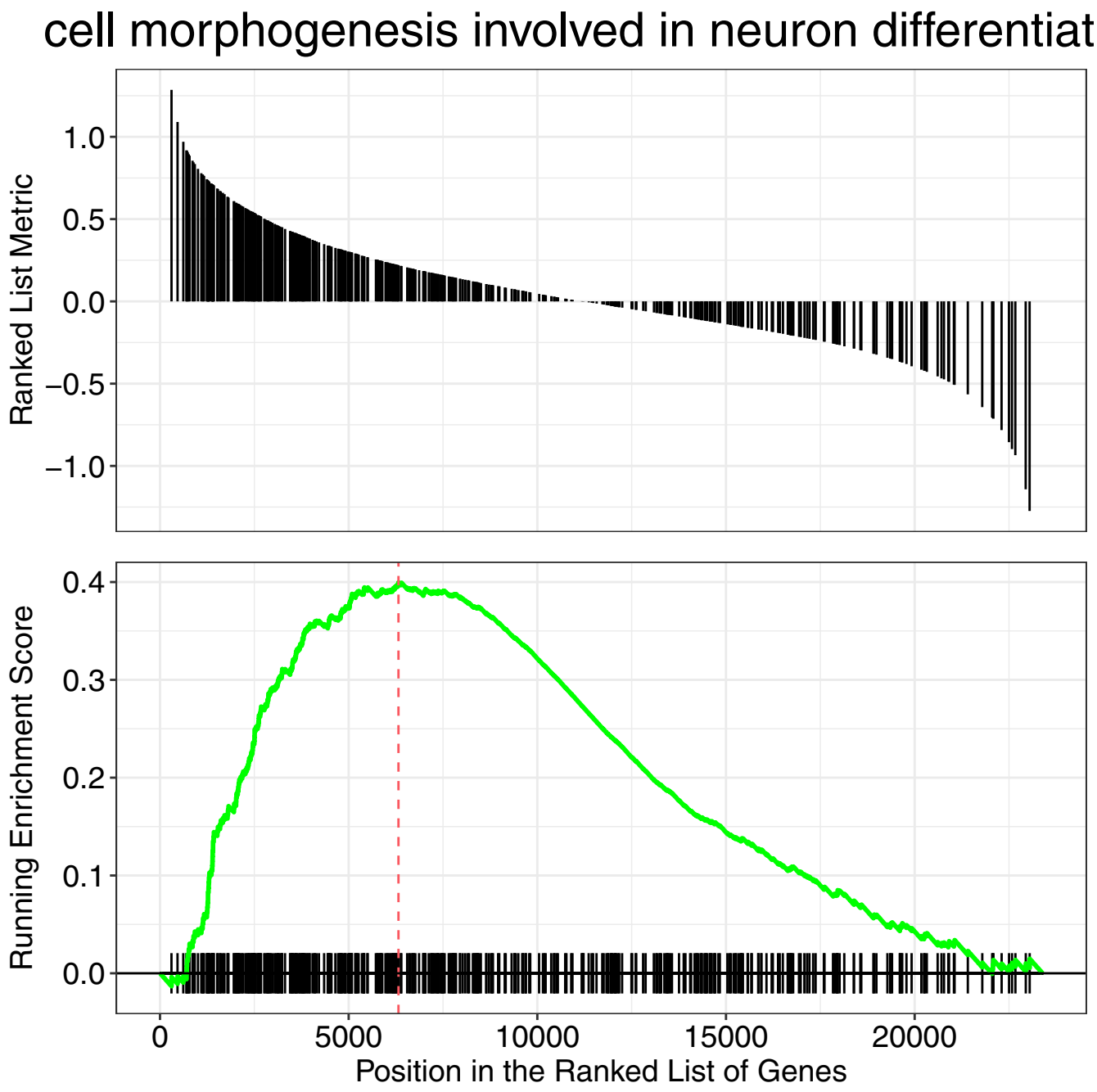

transcription regulator complex
Ranked List Metric
8
6
4
2
0
0.5
0.4
0.3
0.2
0.1
0.0
Running Enrichment Score
0
5000
10000
15000
20000
Position in the Ranked List of Genes

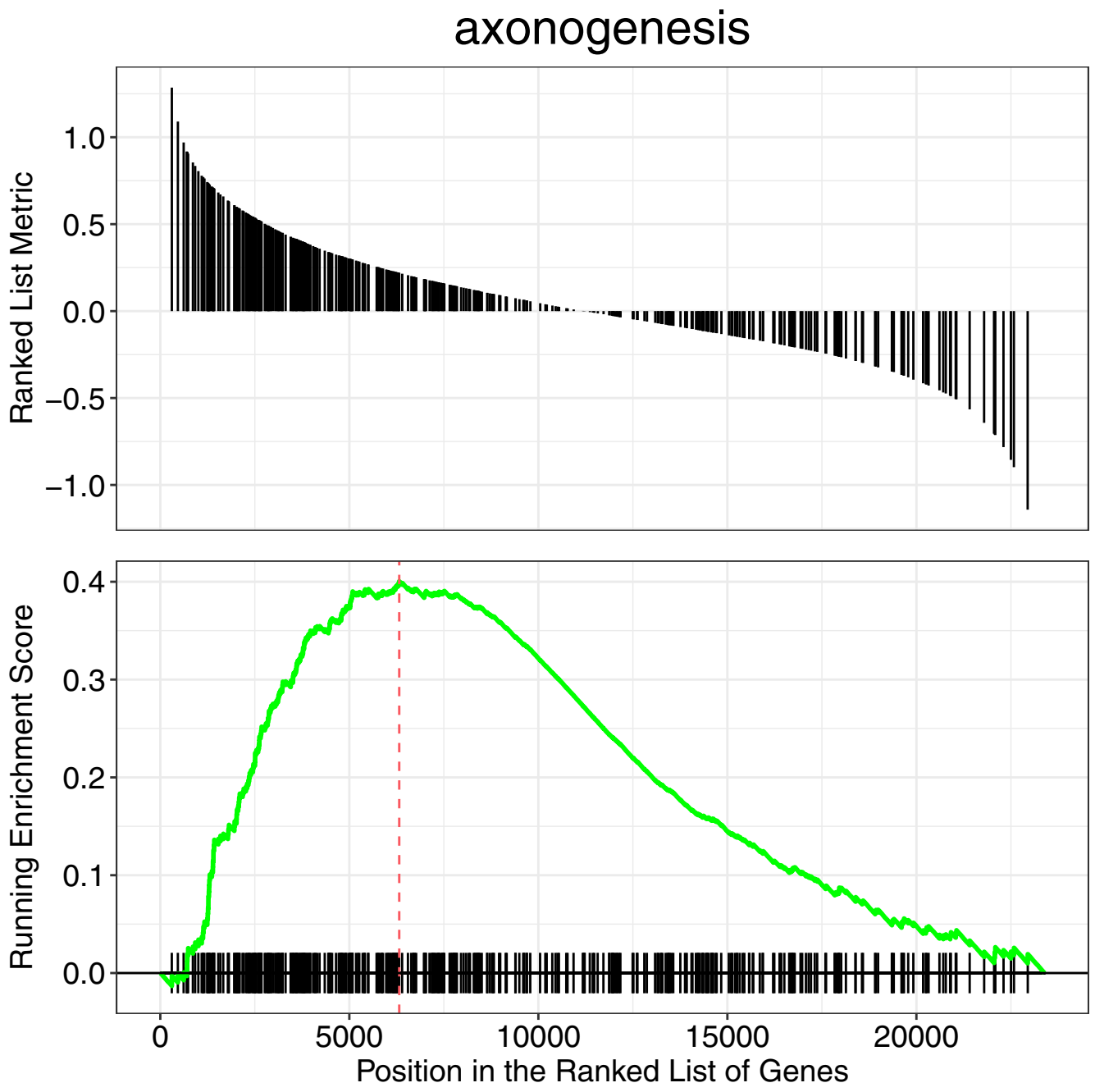

cell projection morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

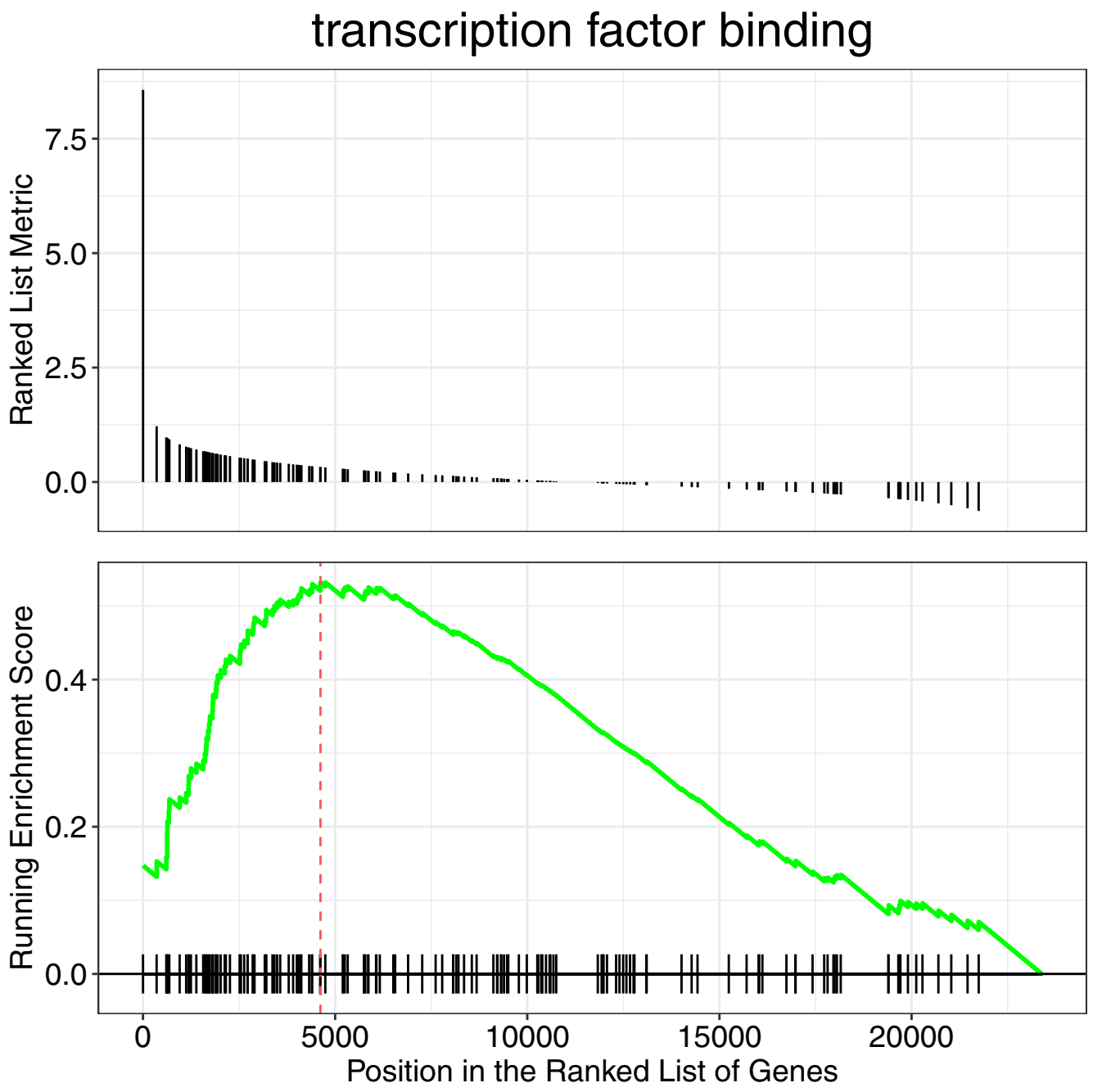

neuron projection morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

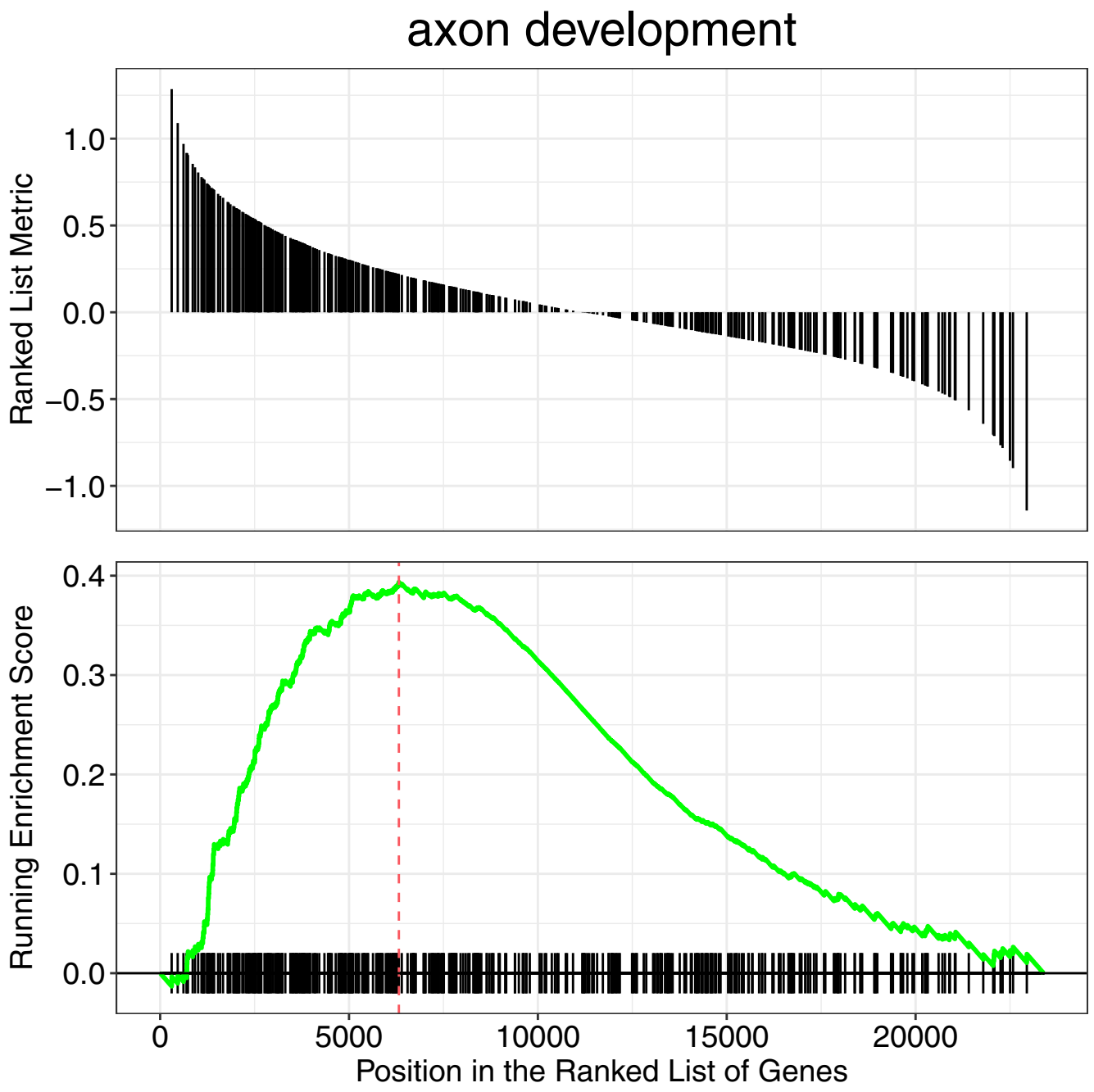

plasma membrane bounded cell projection morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

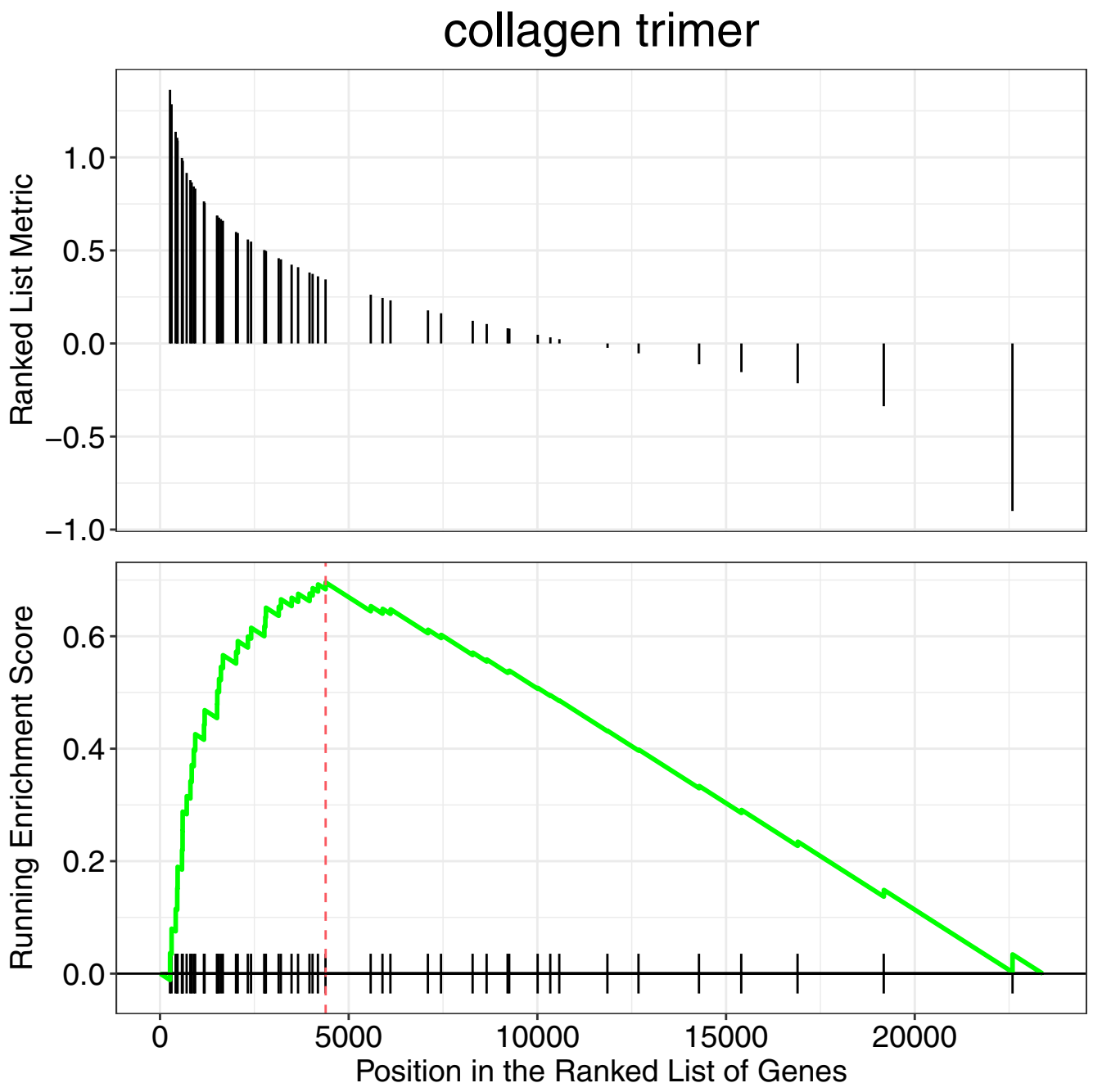

cell part morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

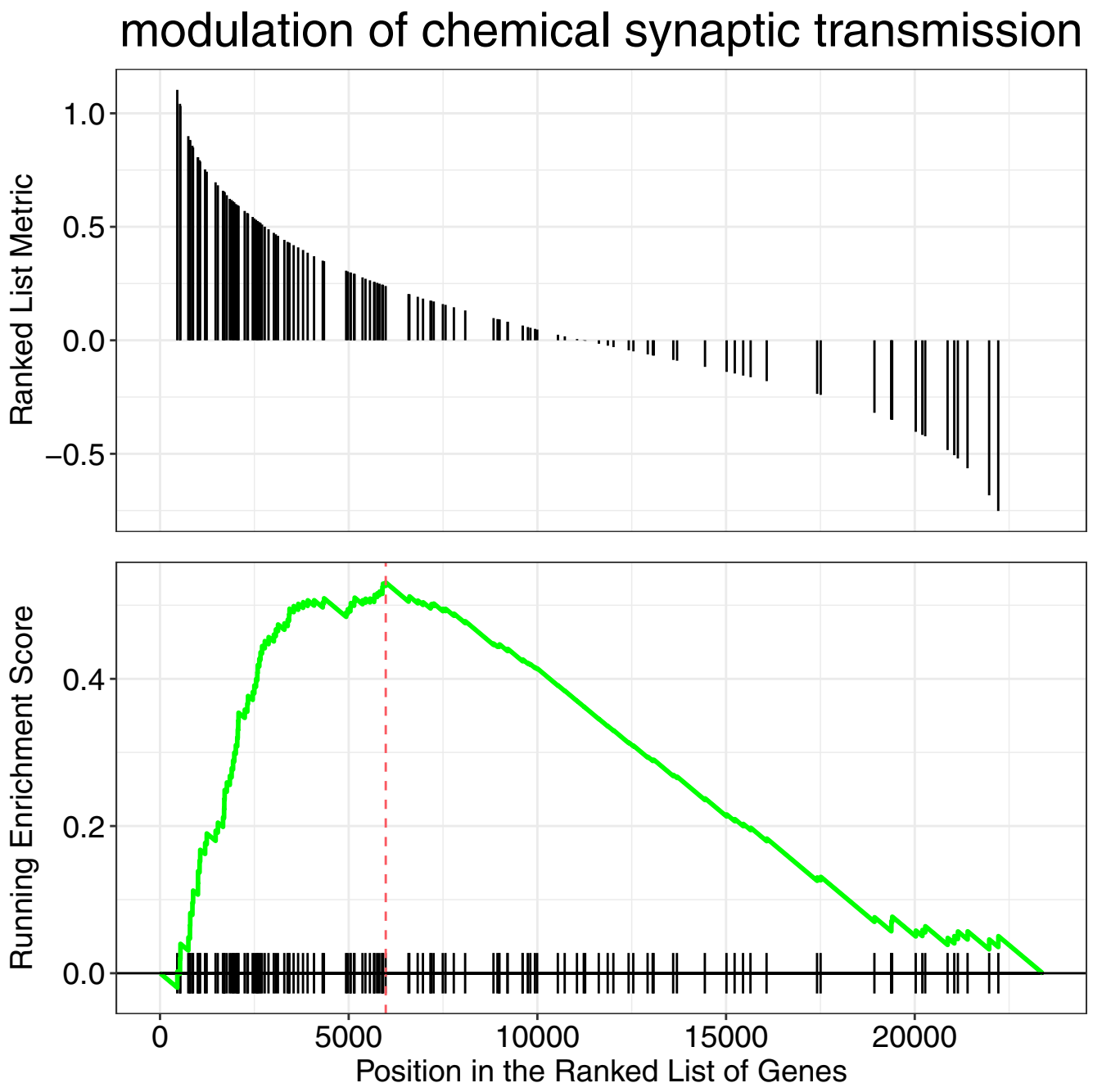

cell morphogenesis involved in neuron differentiation
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

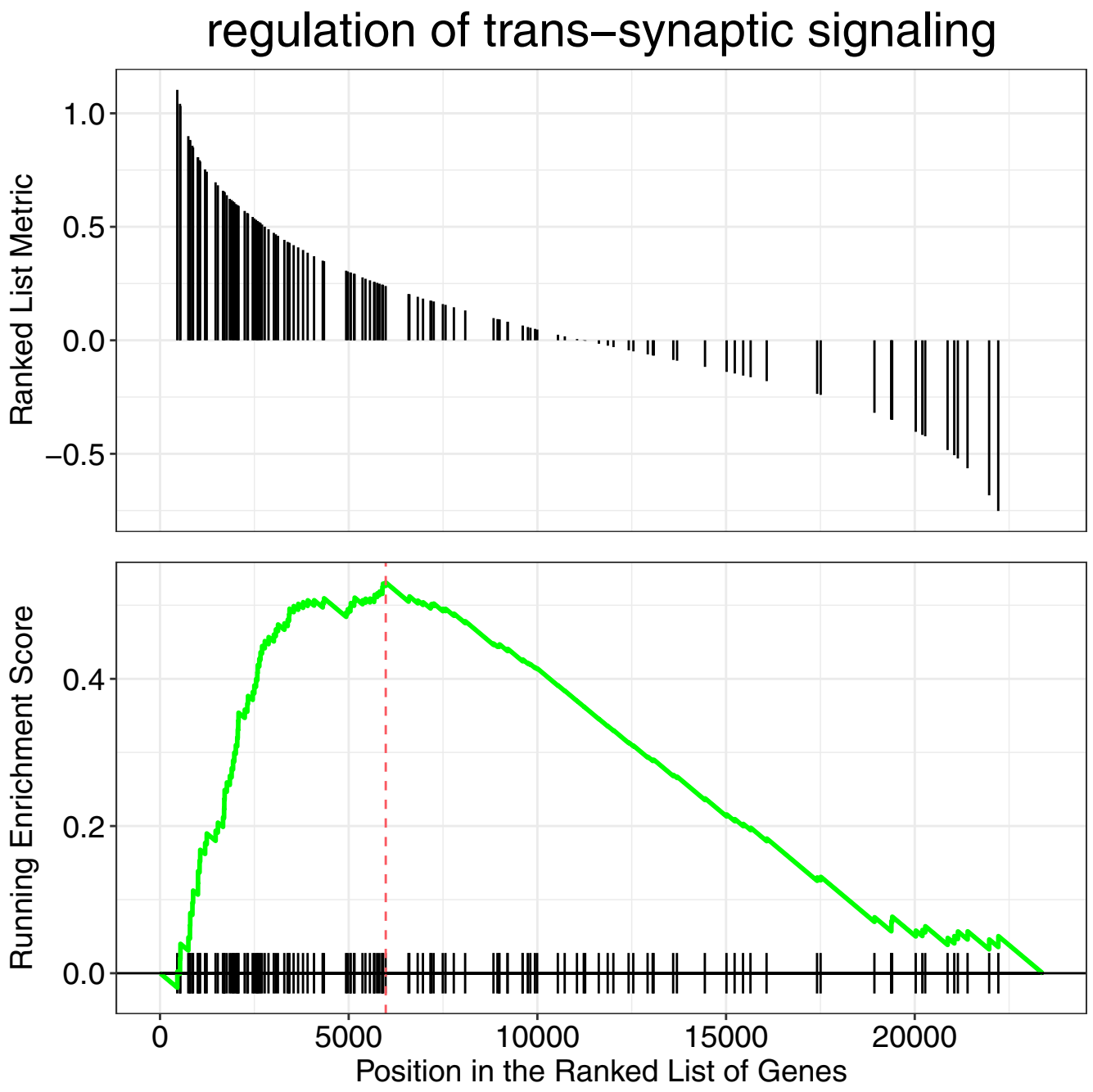

axonogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

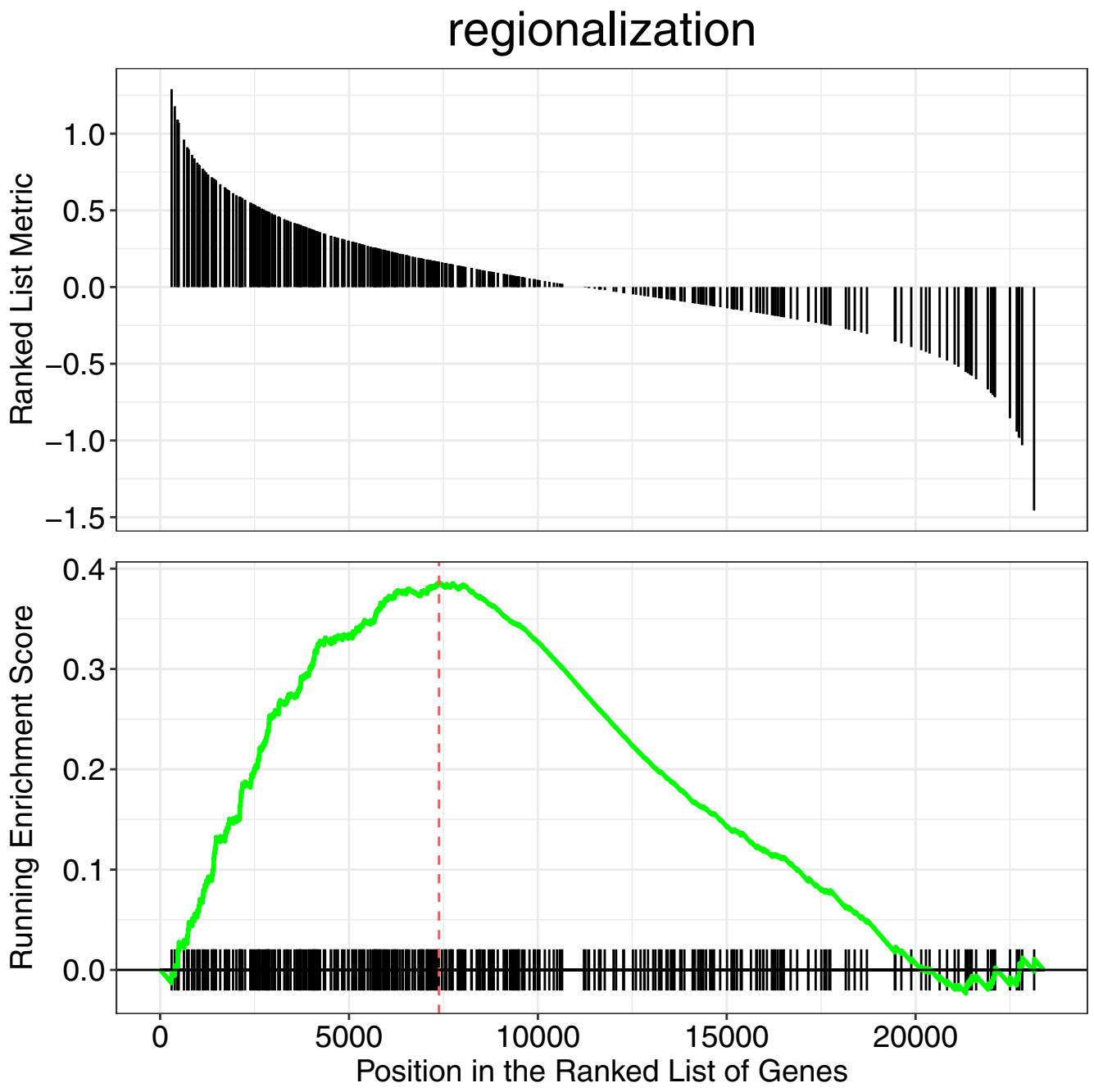


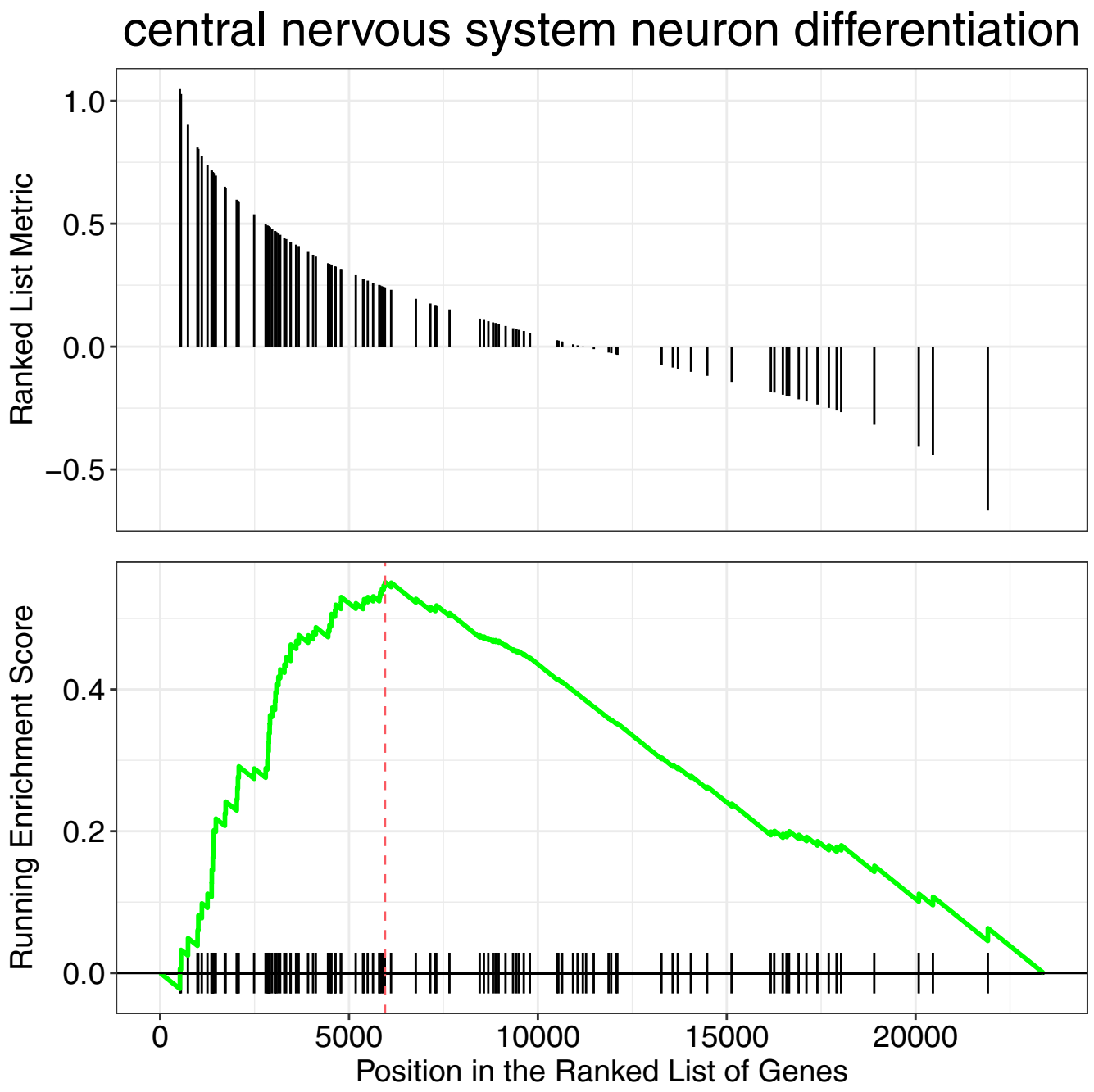

axon development
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

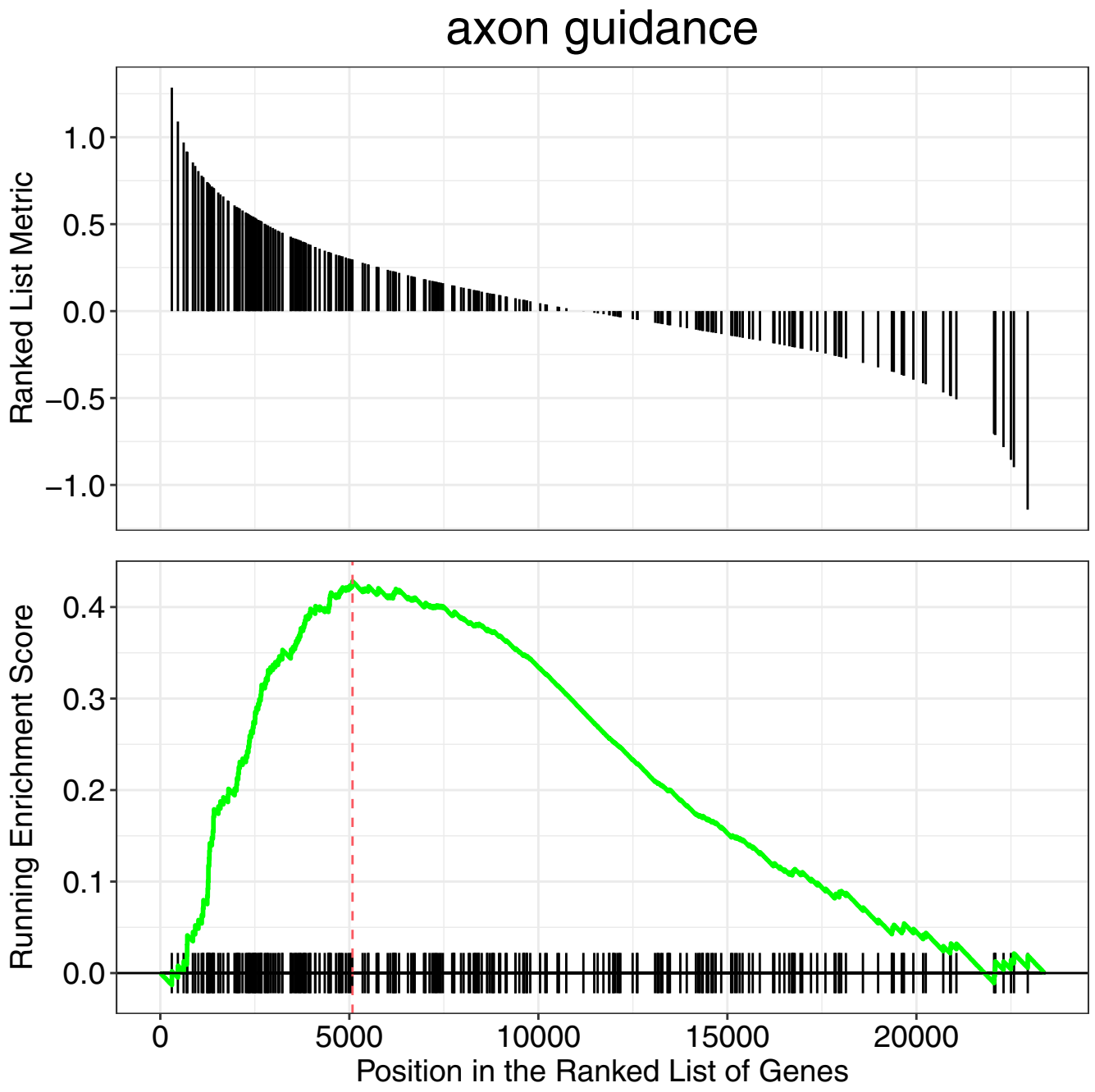

collagen trimer
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.6
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

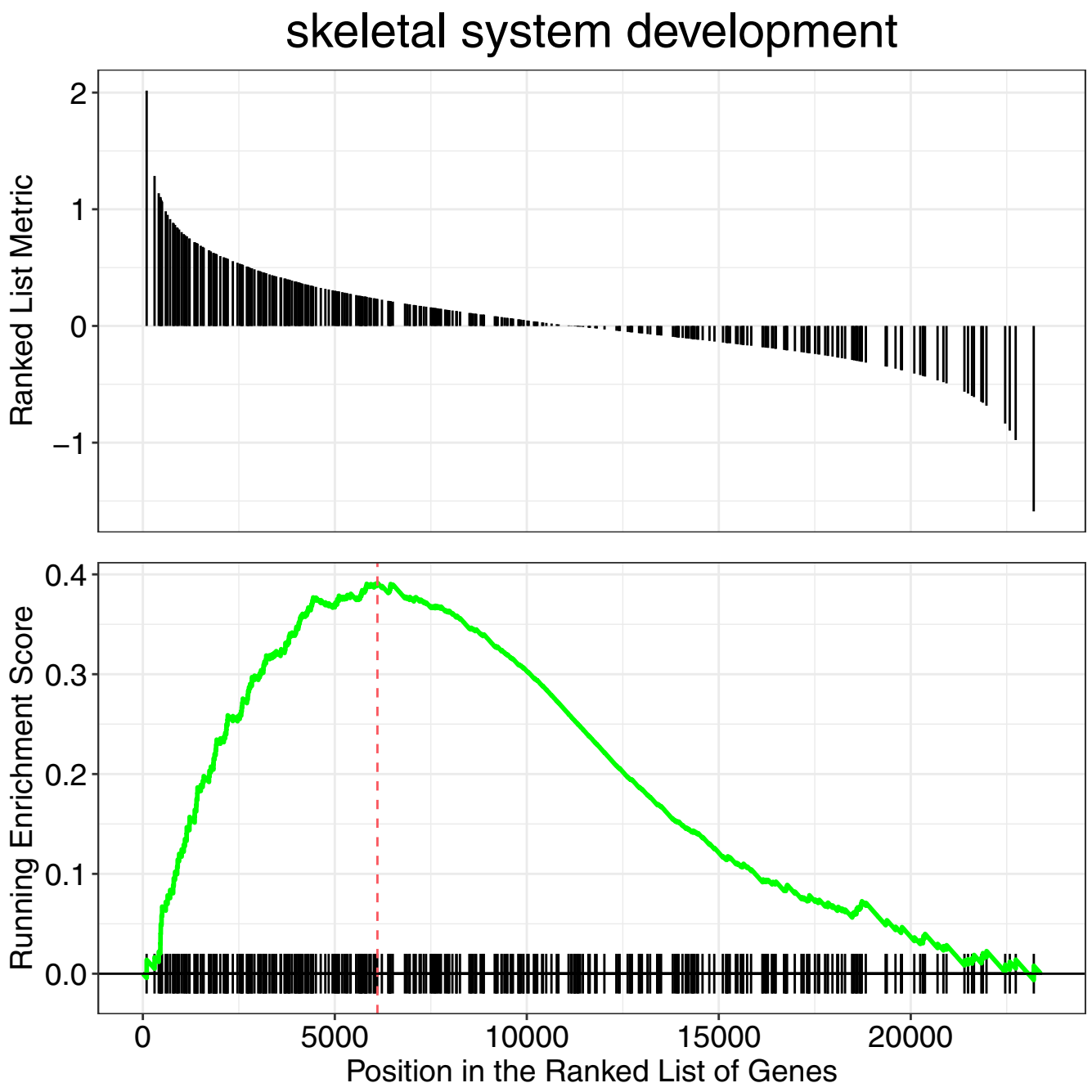

modulation of chemical synaptic transmission
Ranked List Metric
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

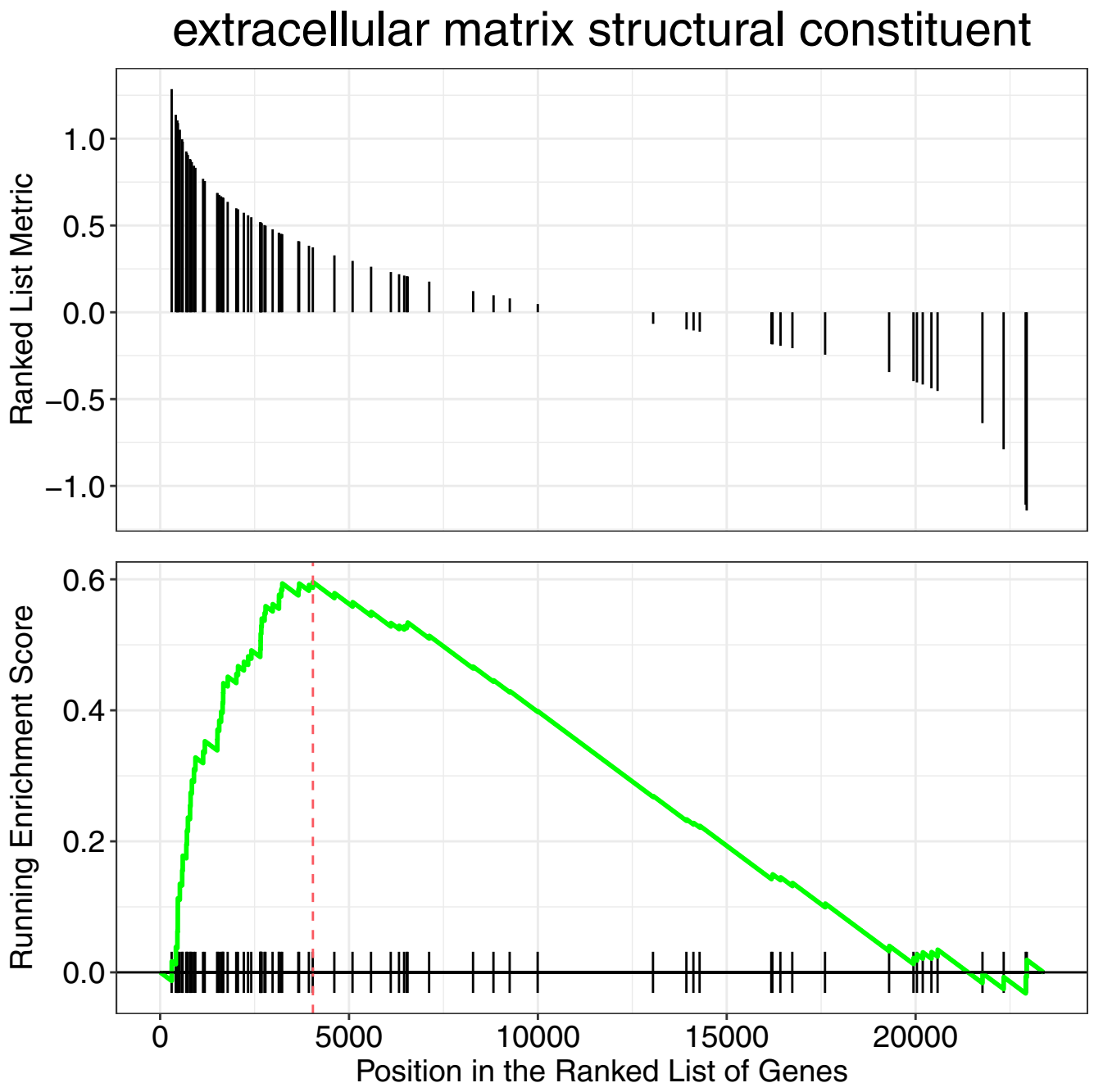

regulation of trans−synaptic signaling
Ranked List Metric
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

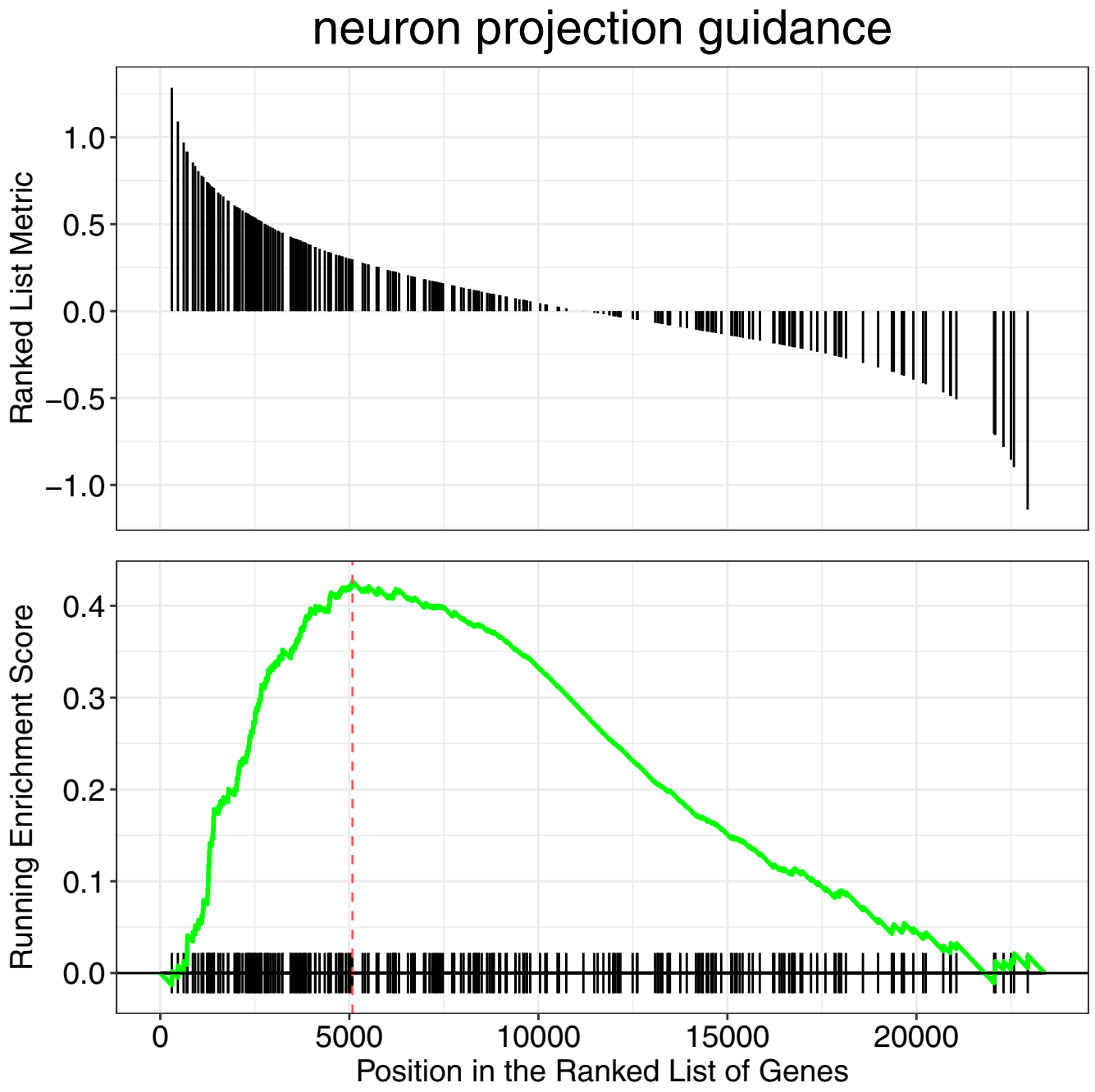

regionalization
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

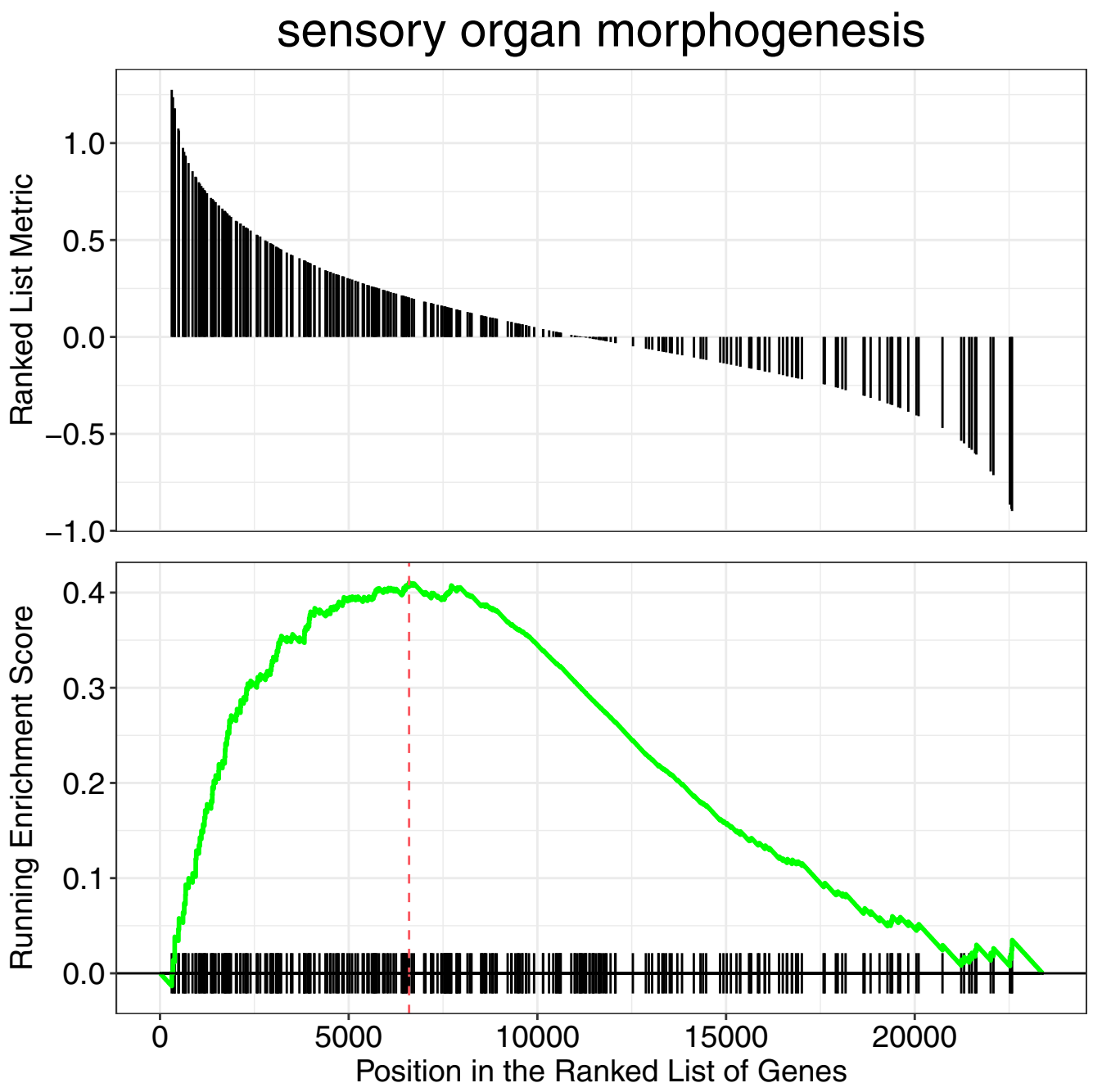

central nervous system neuron differentiation
Ranked List Metric
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

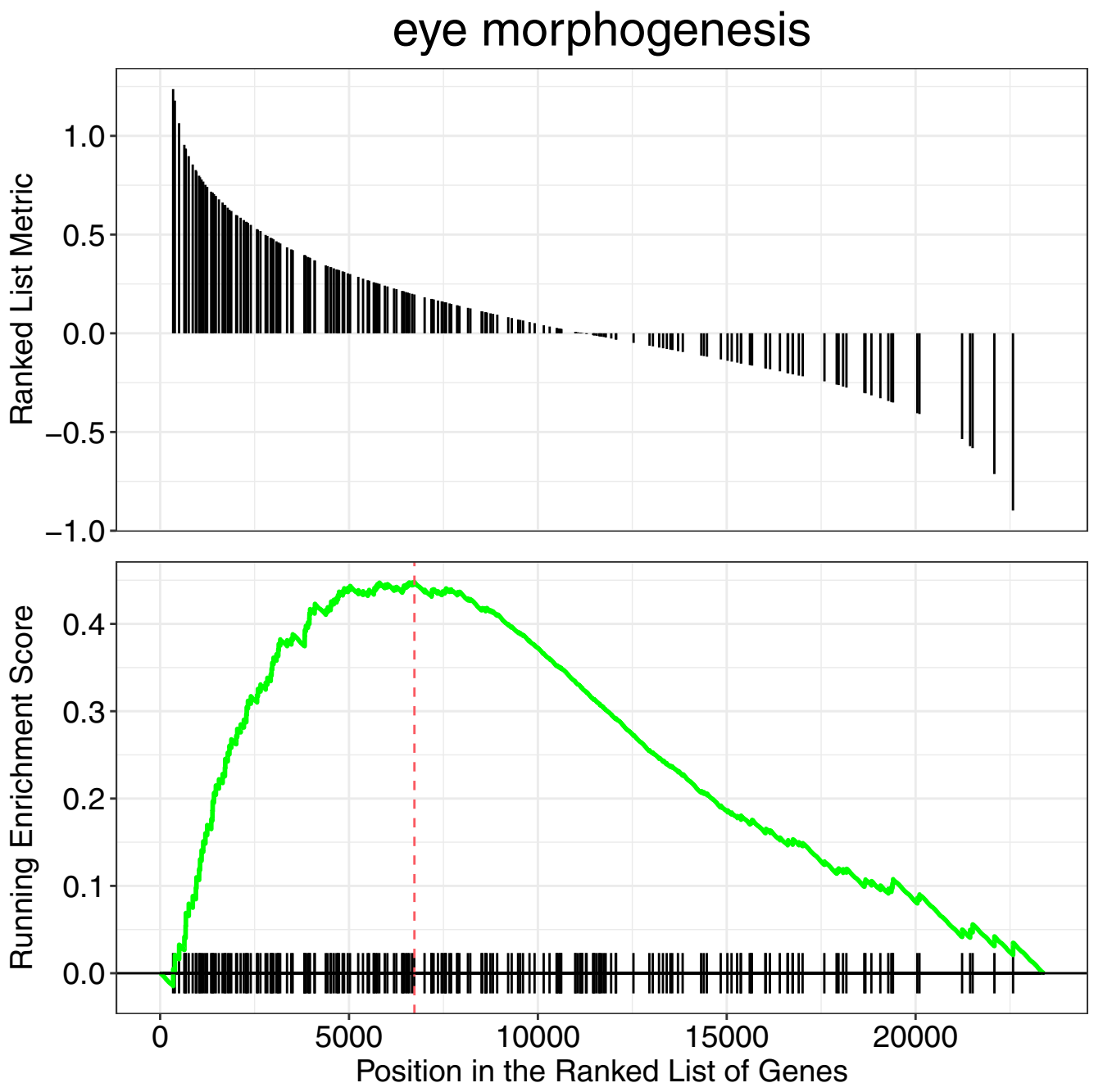

axon guidance
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

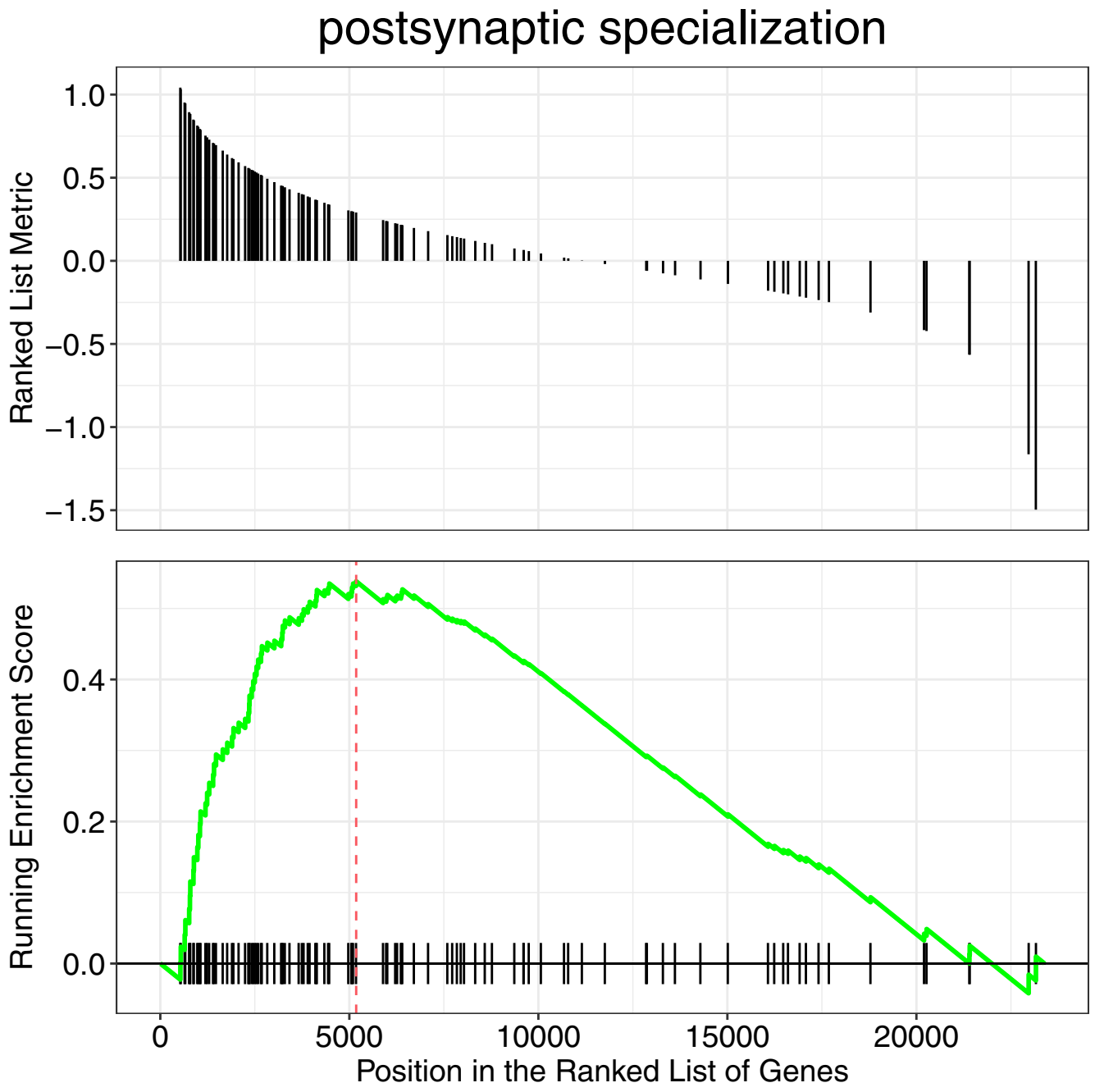



extracellular matrix structural constituent
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.6
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes


neuron projection guidance
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes


sensory organ morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes


eye morphogenesis
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes


postsynaptic specialization
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
−1.5
Running Enrichment Score
0.4
0.2
0.0
0
5000
10000
15000
20000
Position in the Ranked List of Genes

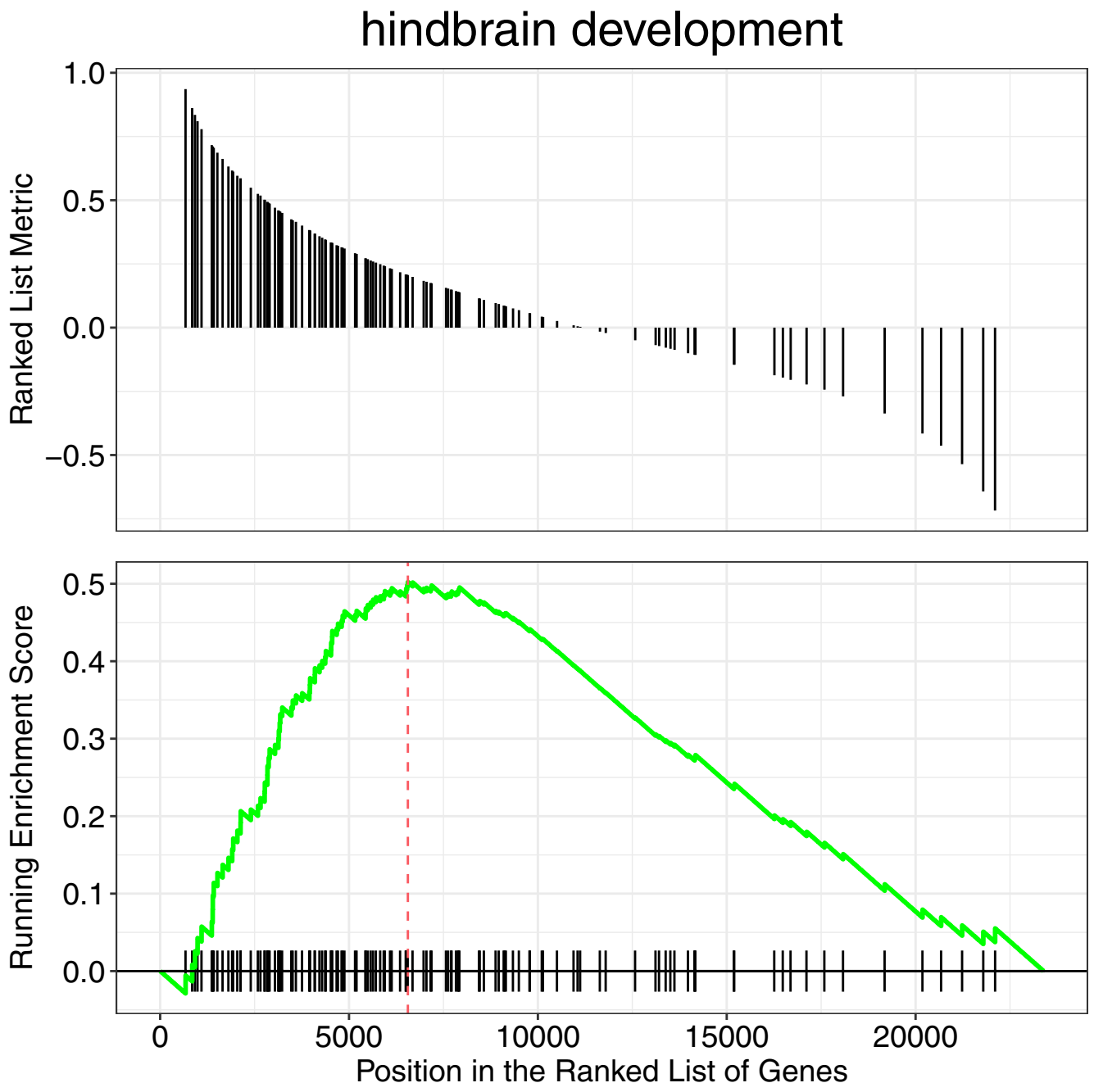


Fig. S5. Enrichment plots of Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 mutants. Running score plot and pre-ranked list of top 25 activated GSEA terms shown in Figure 5D.

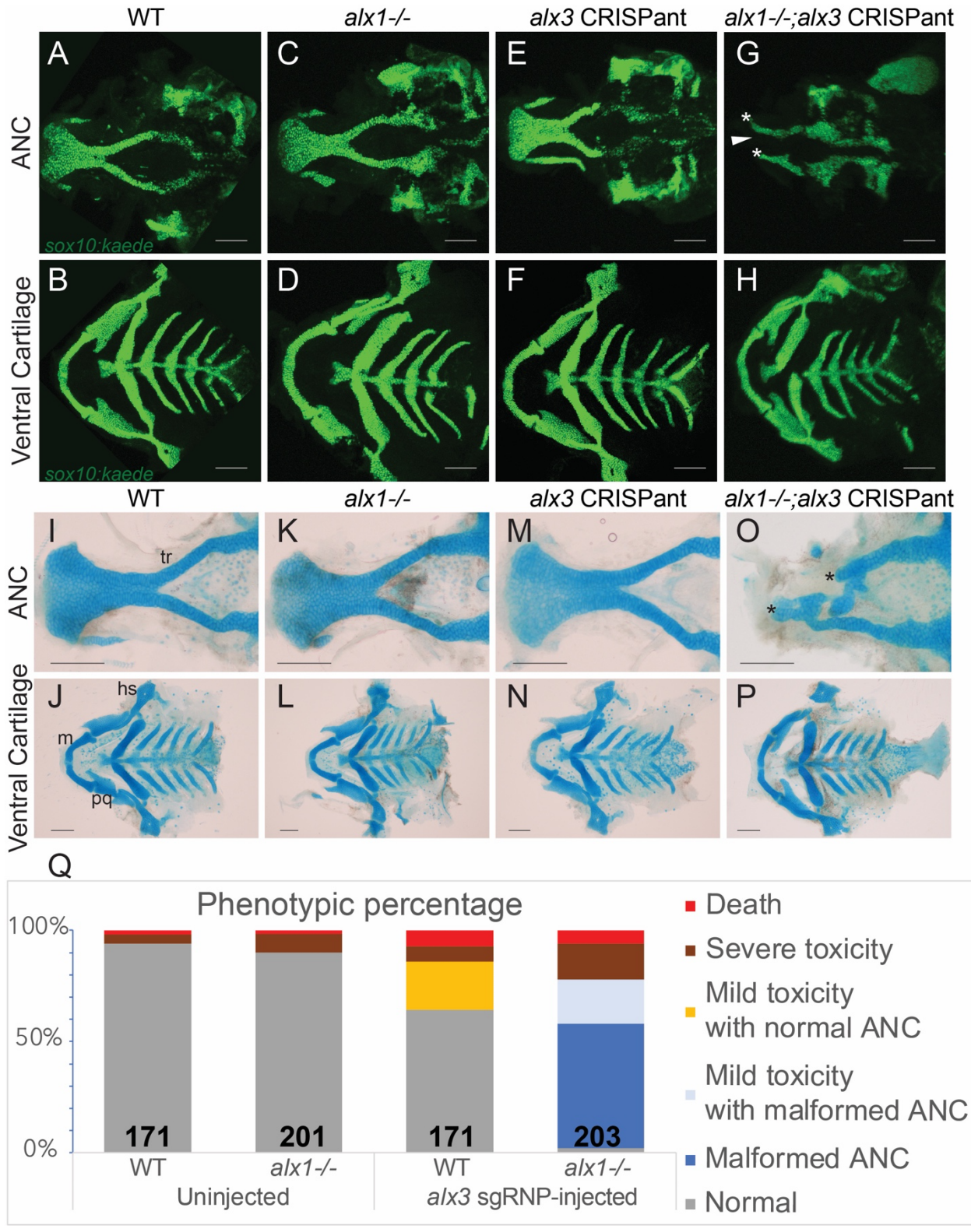
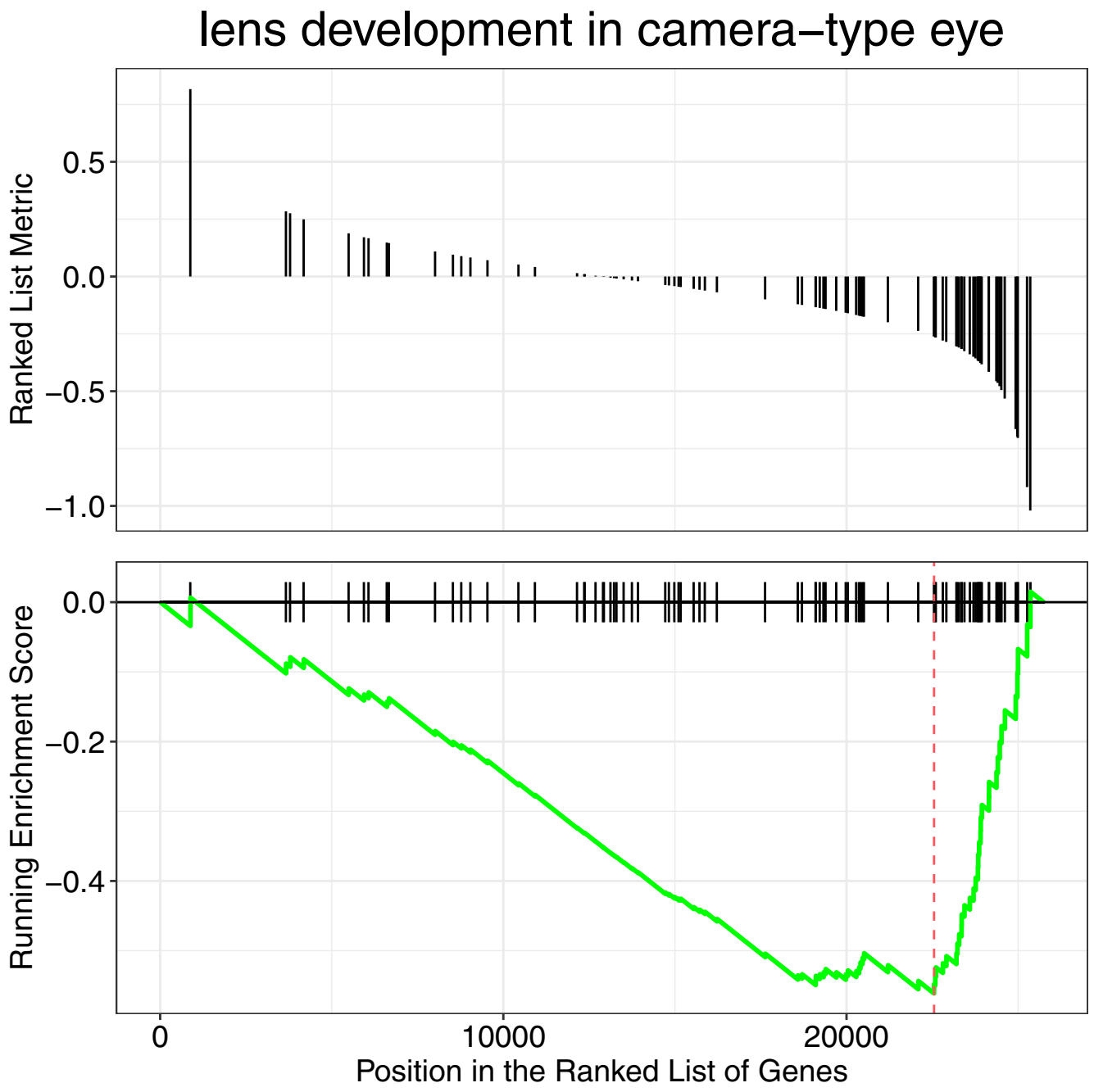
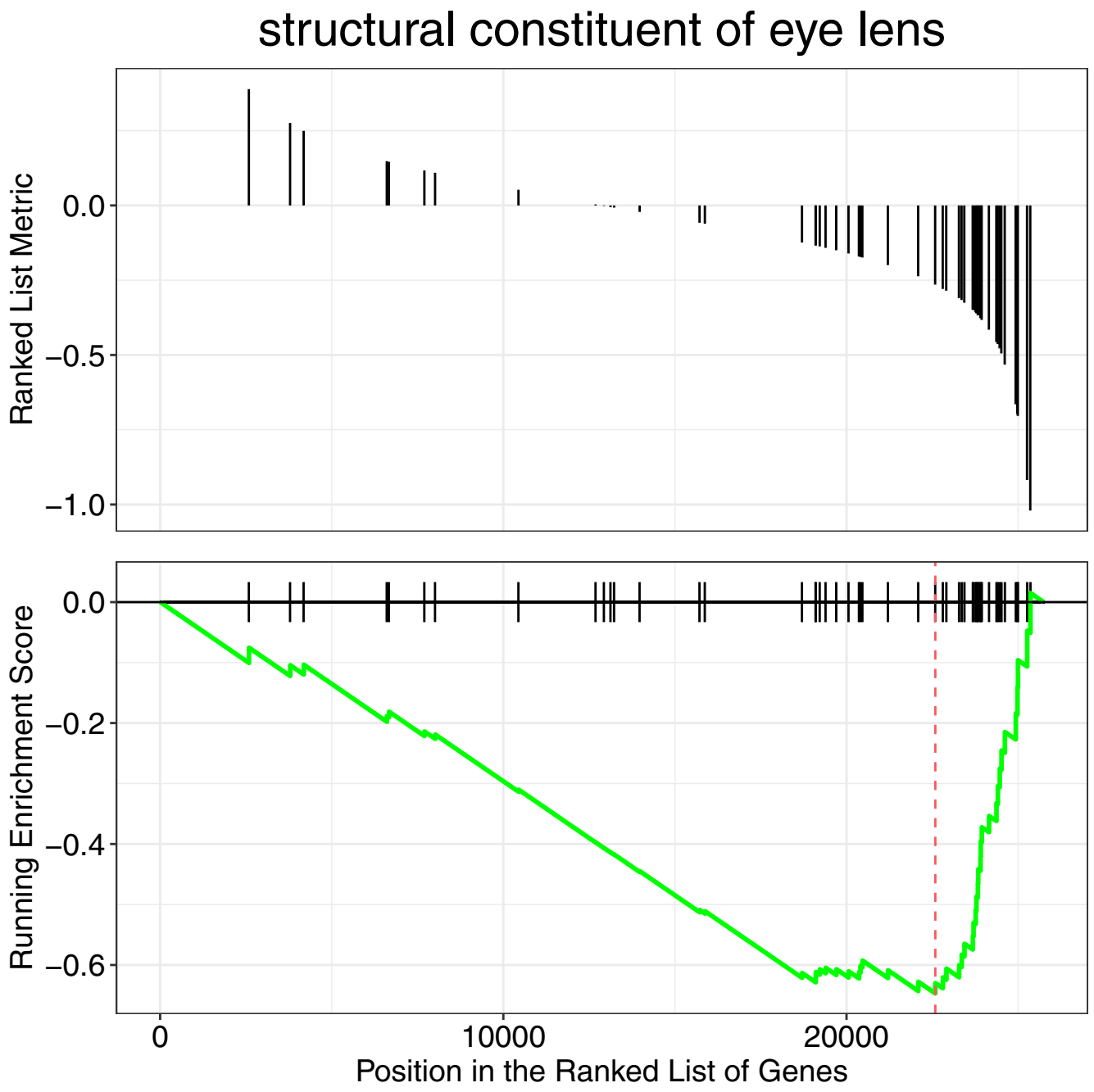
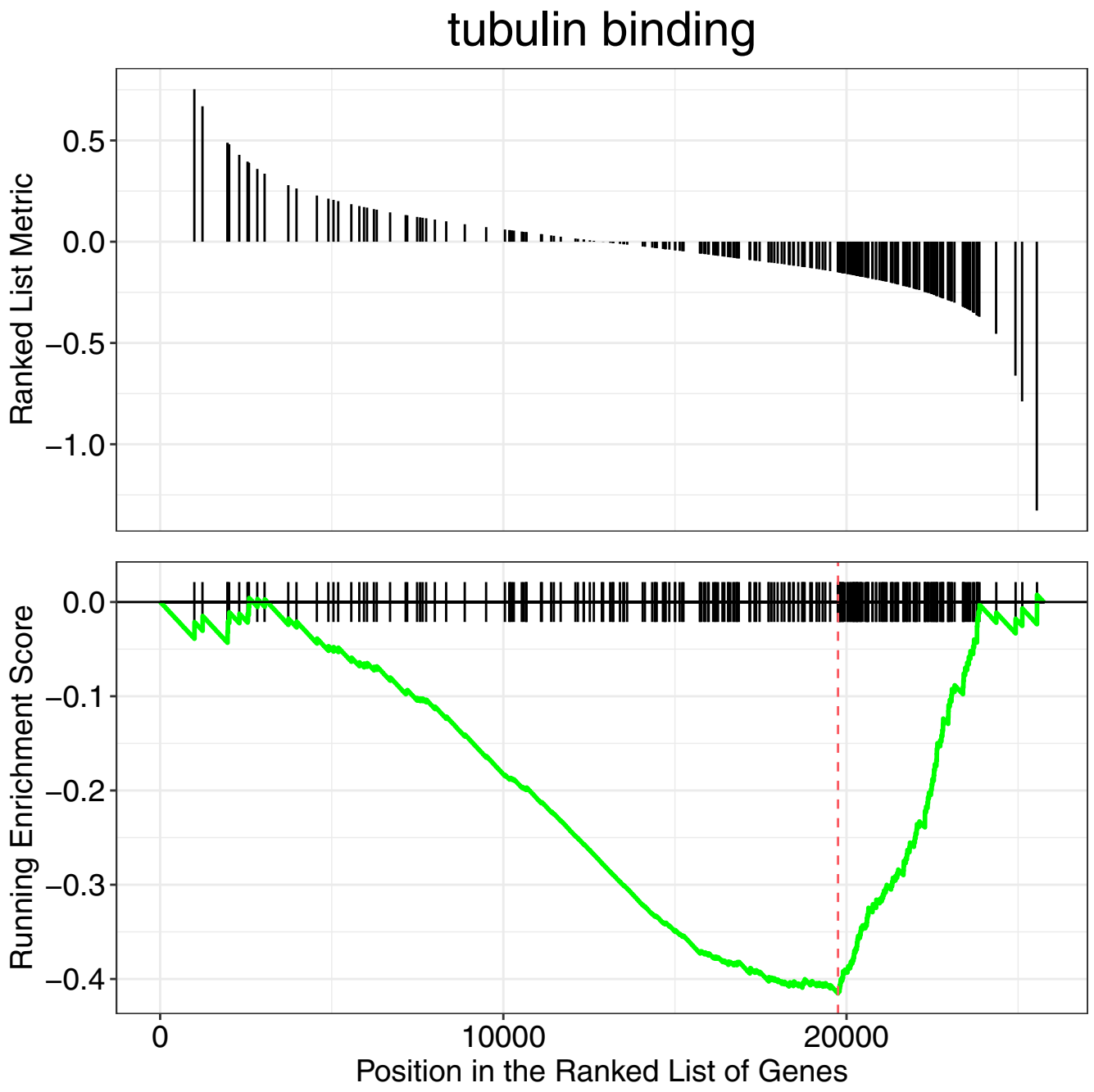
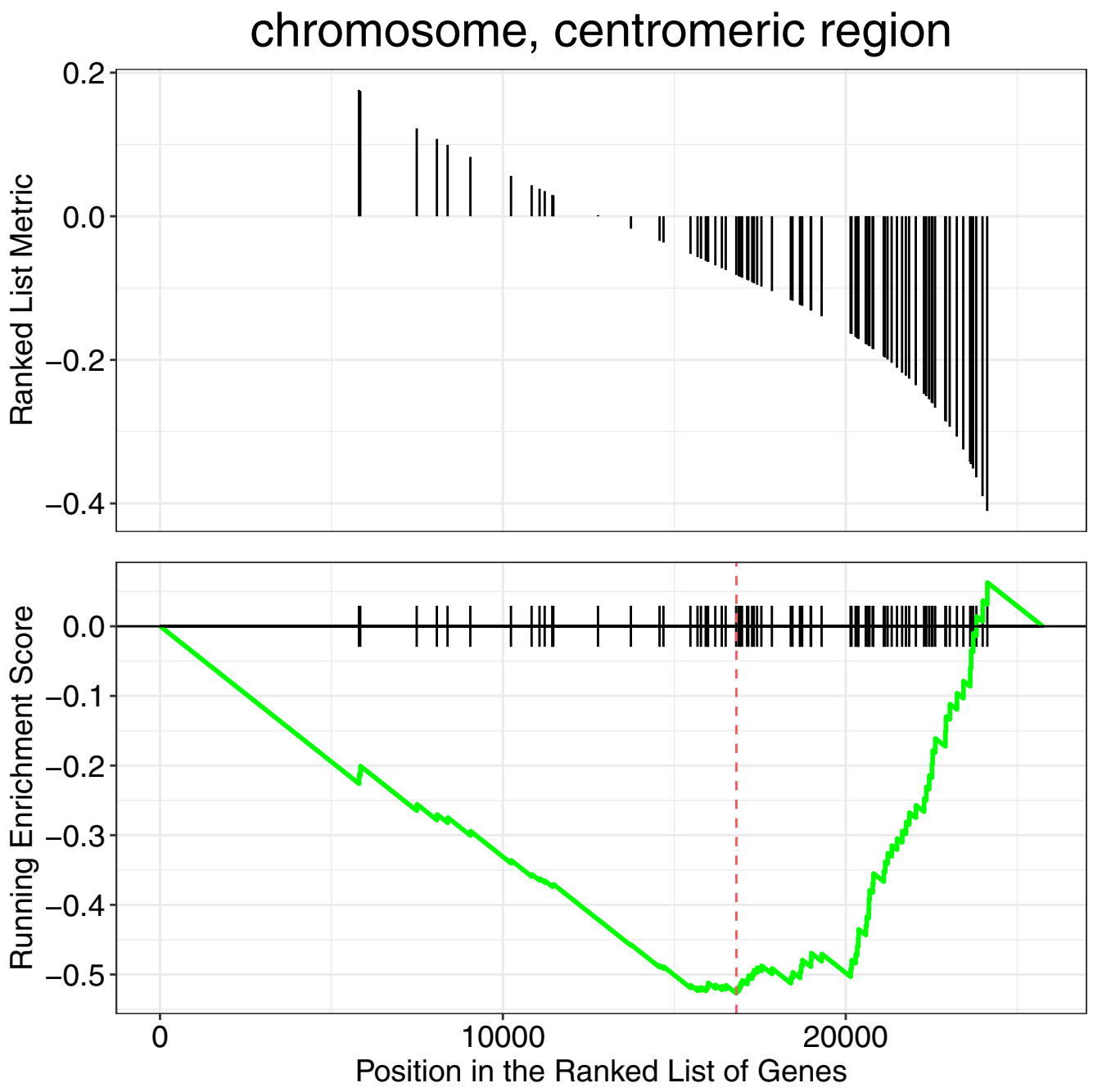


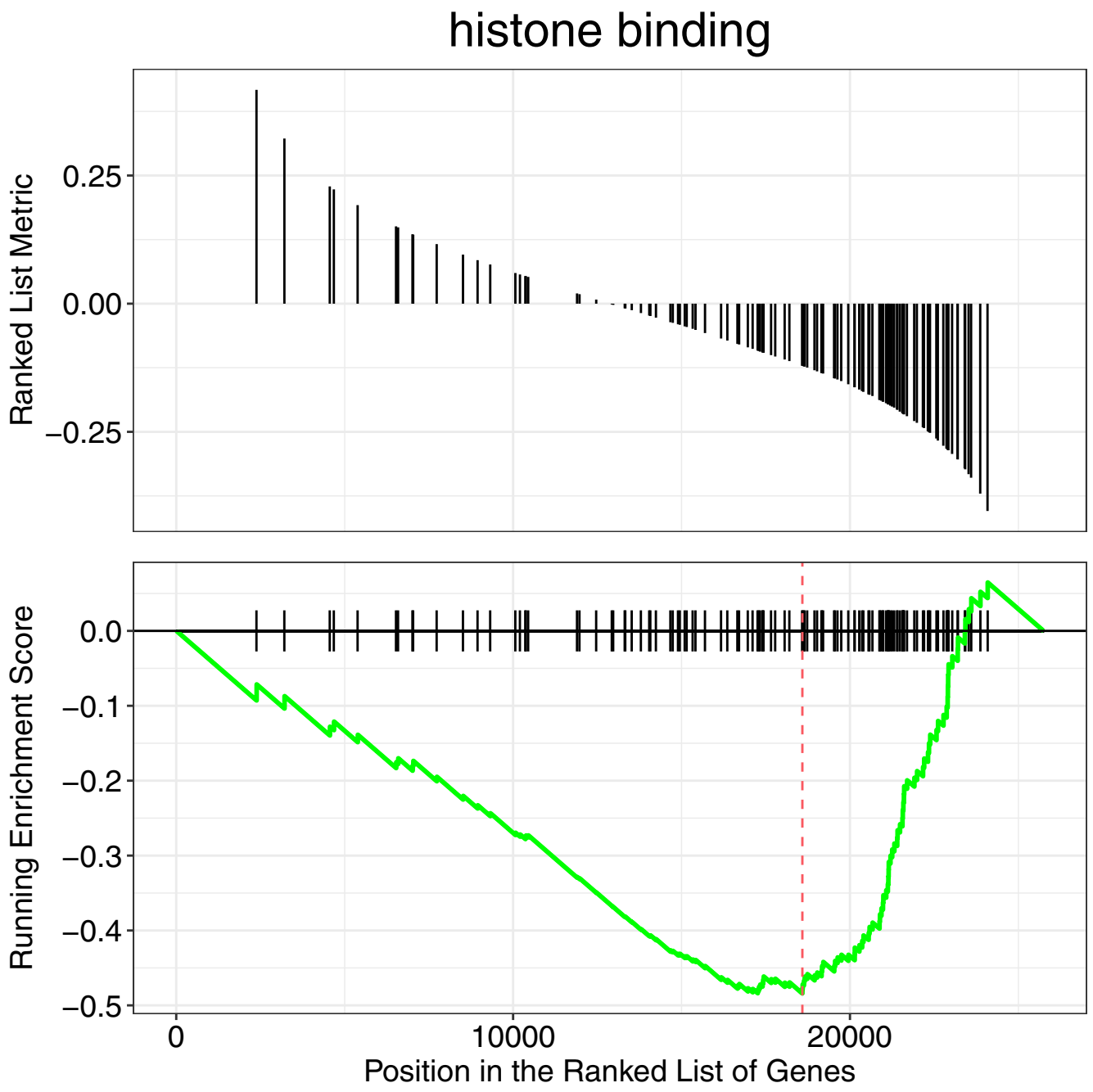
Fig. S6. alx1; alx3CR phenocopy alx1; alx3 double mutants. Embryos derived from Tg(sox10:kaede) embryos or alx1^{uw2016}; Tg(sox10:kaede) were injected with alx3 CRISPR/Cas9 and fixed at 4 dpf. Embryos were dissected, and flat-mounted in order to image the anterior neurocranium (ANC) and ventral pharyngeal cartilage. *alx1; alx3CR* developed with midline cleft (arrowhead in G), with the lateral elements (asterisks in G) separated due to the missing median element. I – P: Dissected flat-mount Alcian Blue-stained cartilage in larvae of different genotypes, anterior to the left. I: WT embryo with normal paired trabeculae (tr) and a normal ANC. O: *alx1; alx3CR* with defective trabeculae fusion (asterisks) and depleted ethmoid plate. Q: Percentage of embryos displaying malformed anterior neurocranium (ANC) phenotype in larvae of different genotypes. All embryos are shown with anterior to the left. Scale bar: 100μm.

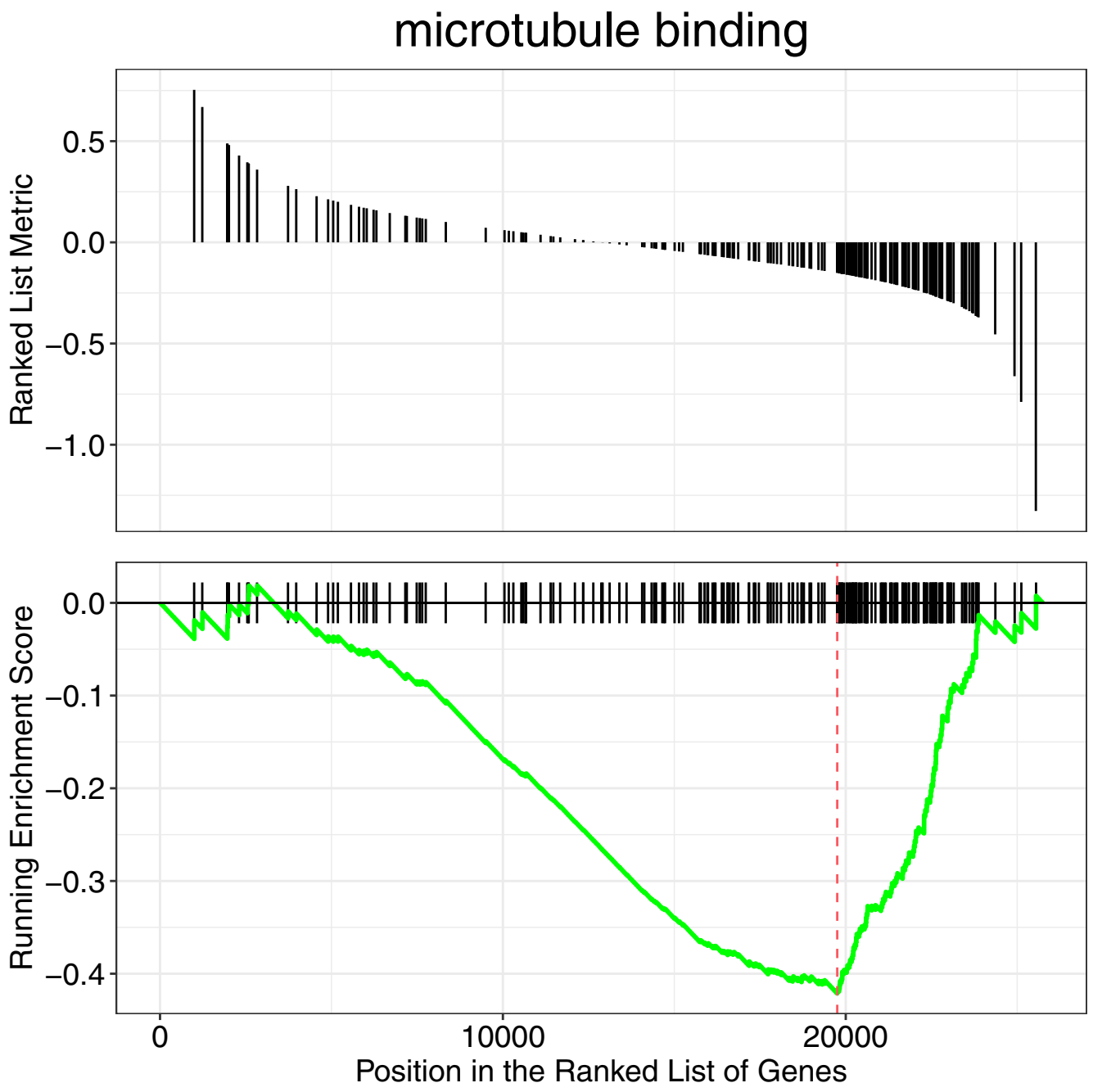

lens development in camera−type eye
Ranked List Metric
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.0
−0.2
−0.4
0
10000
20000
Position in the Ranked List of Genes

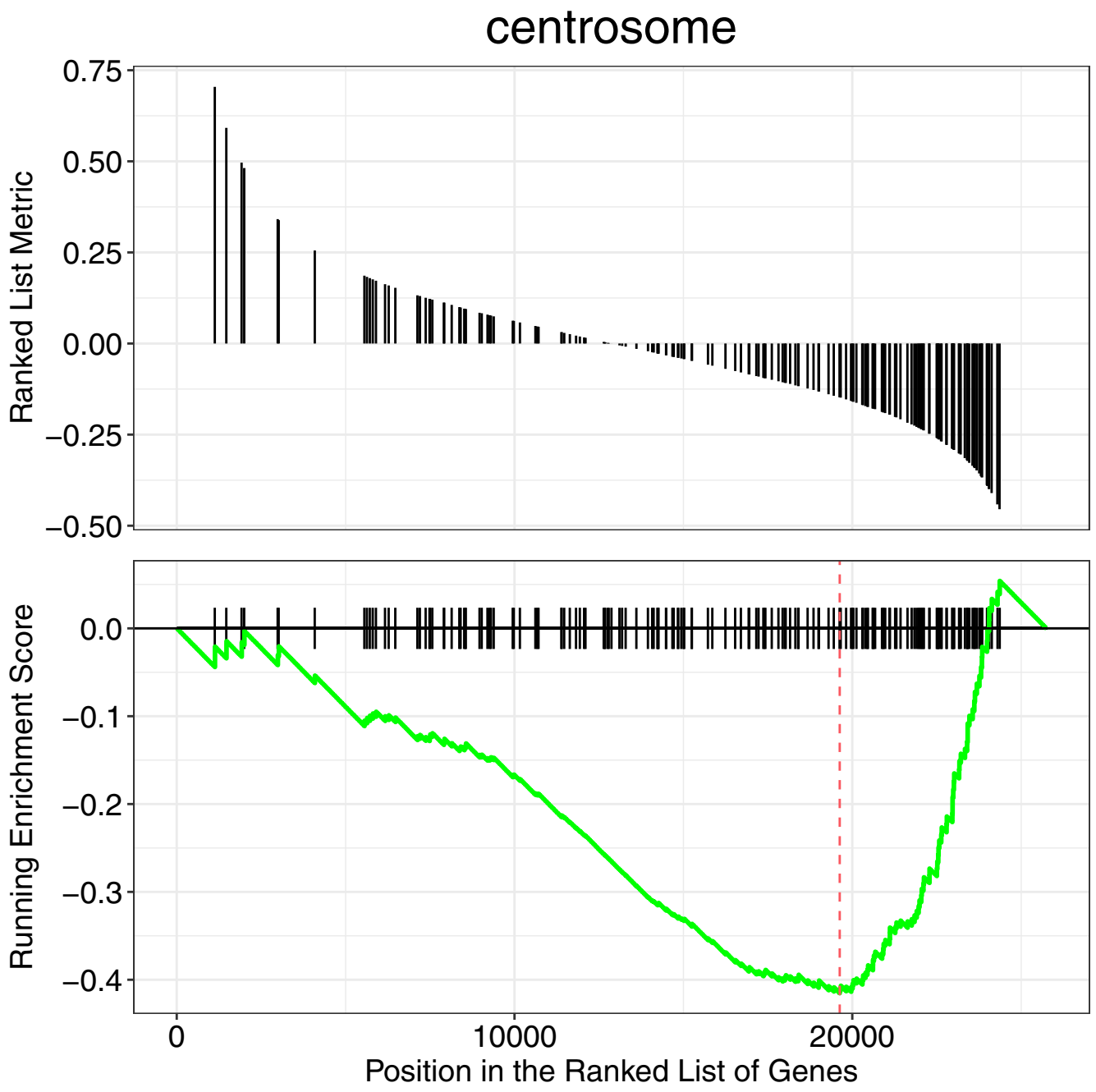

structural constituent of eye lens
Ranked List Metric
0.0
−0.5
−1.0
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
10000
20000
Position in the Ranked List of Genes

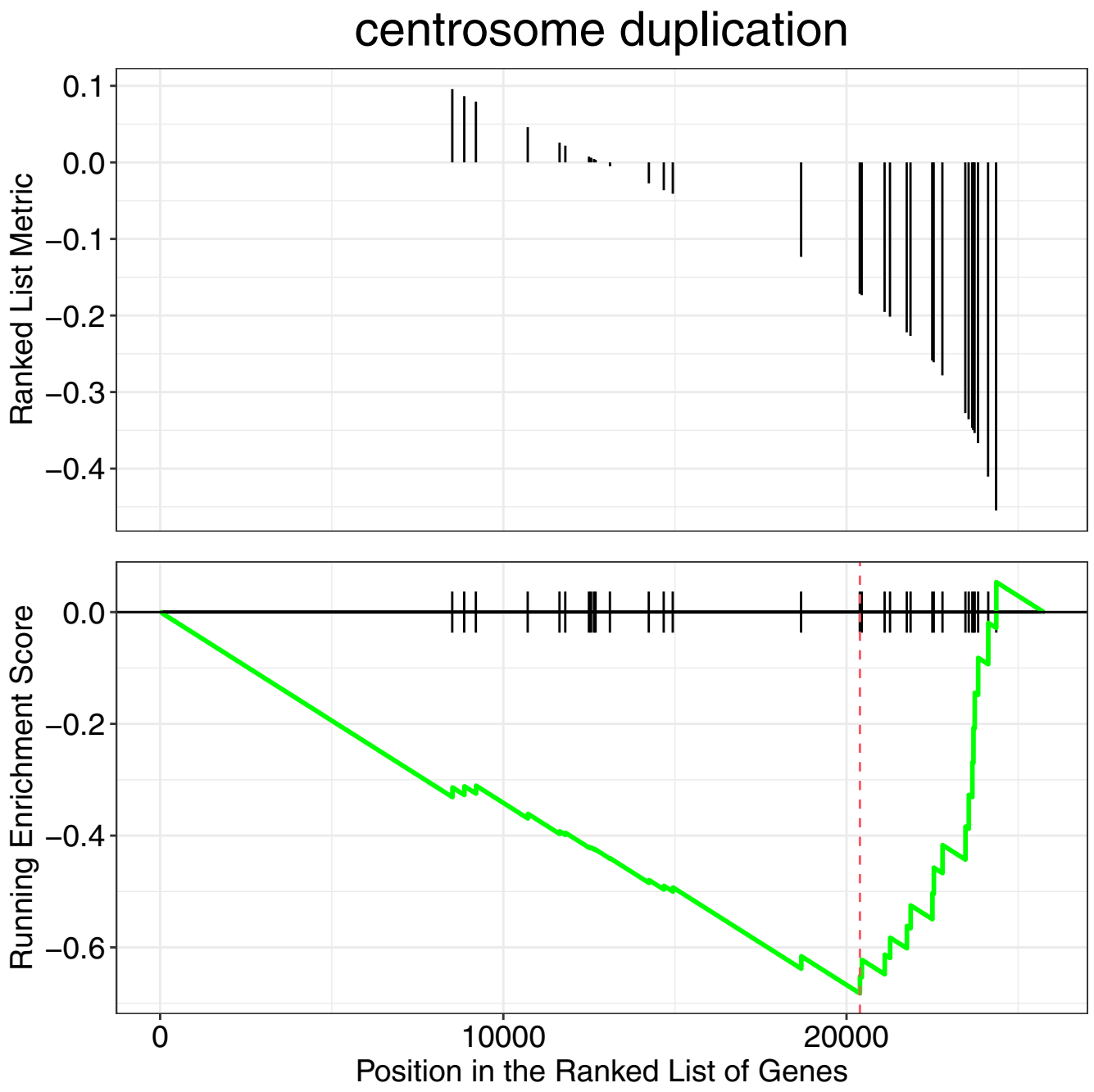

tubulin binding
Ranked List Metric
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
10000
20000
Position in the Ranked List of Genes

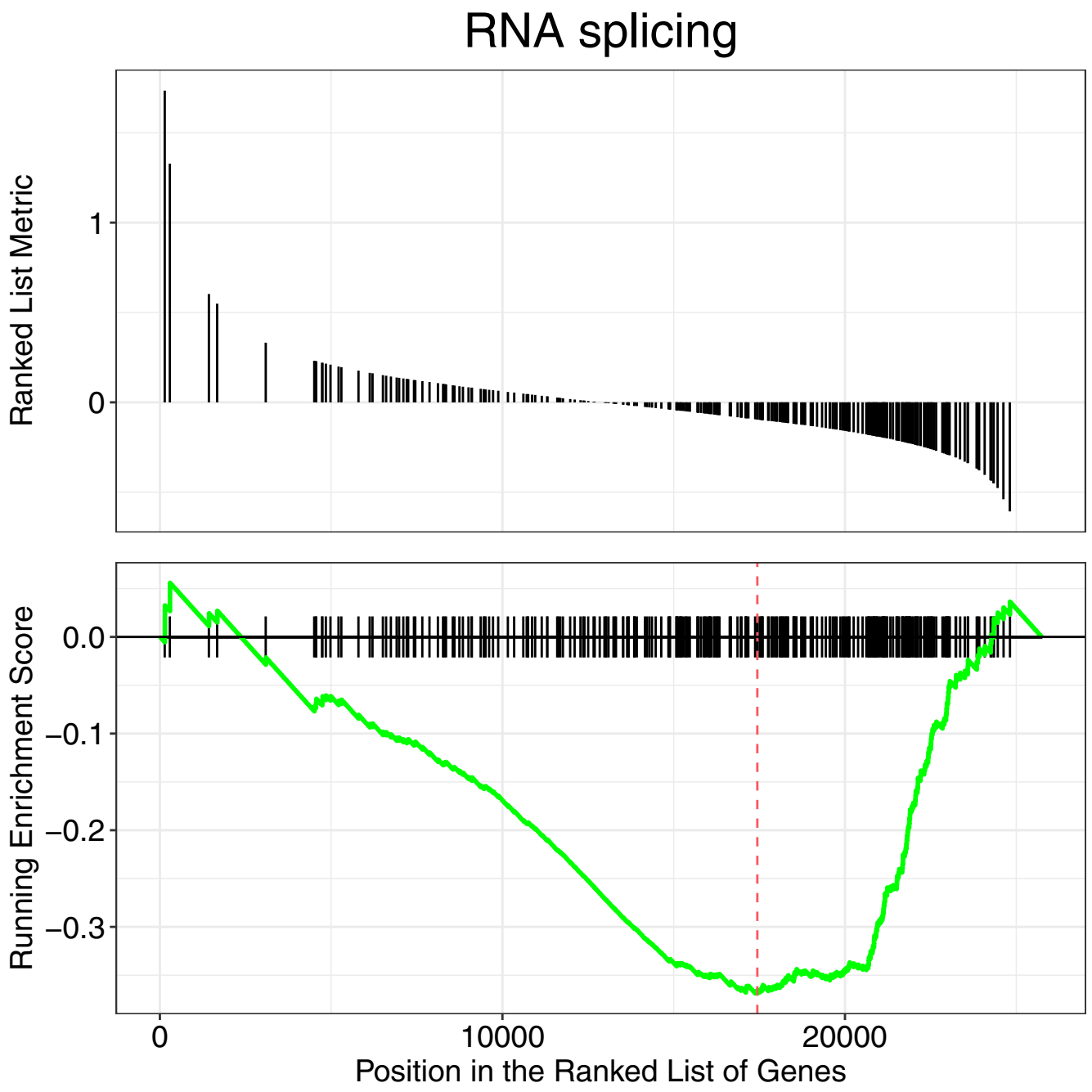

chromosome, centromeric region
Ranked List Metric
0.2
0.0
−0.2
−0.4
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
10000
20000
Position in the Ranked List of Genes

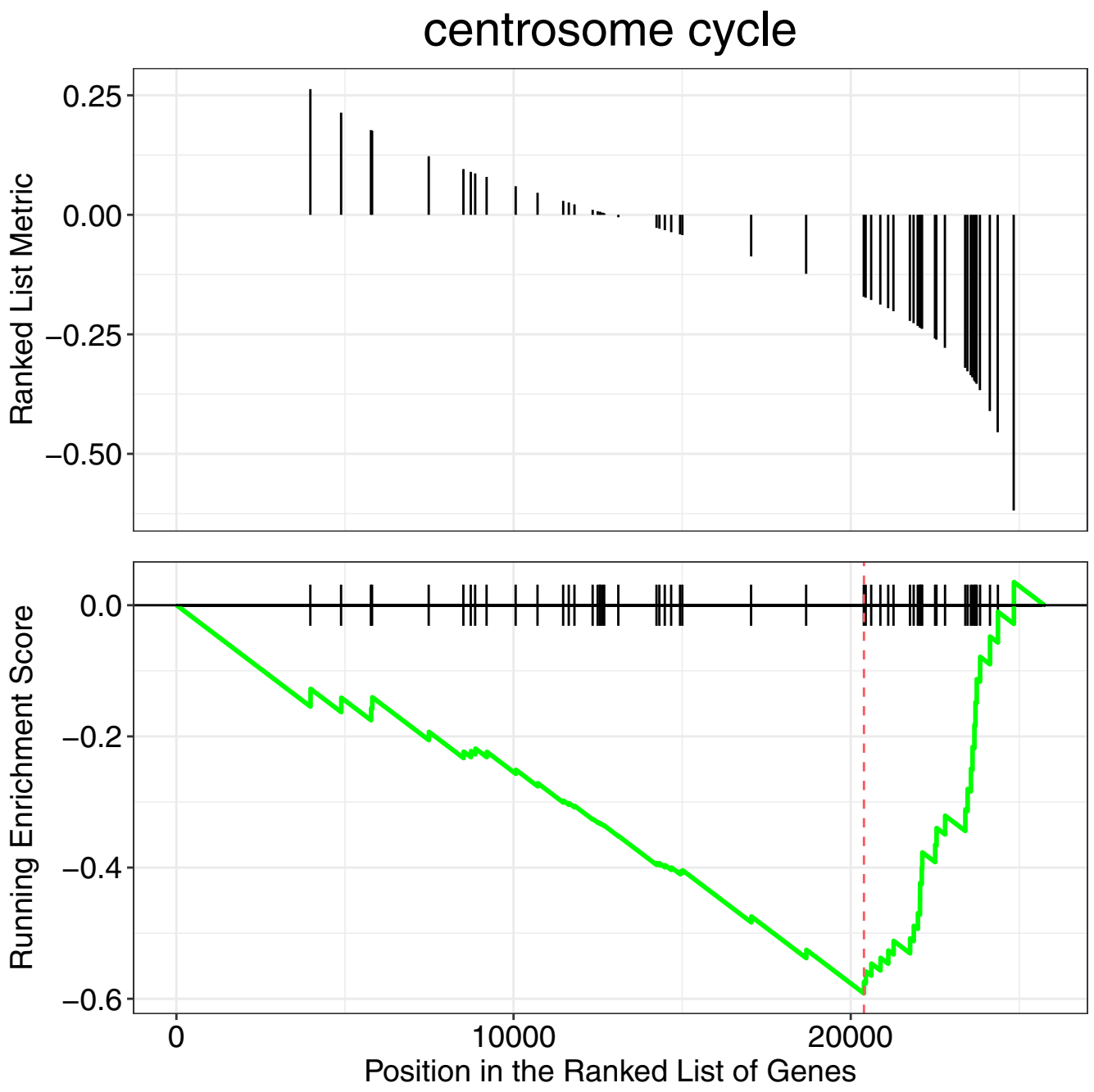

histone binding
Ranked List Metric
0.25
0.00
−0.25
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
10000
20000
Position in the Ranked List of Genes

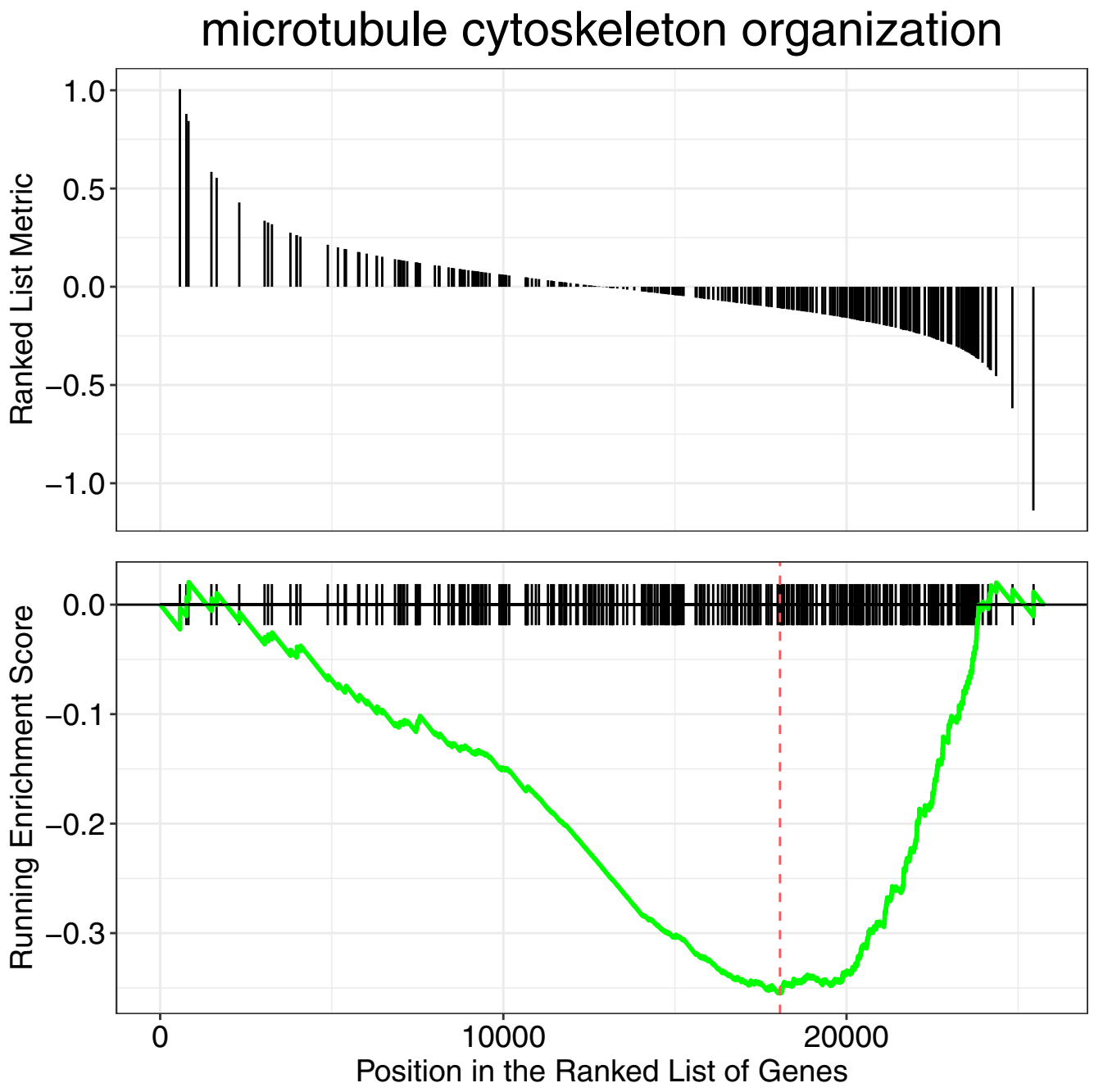

microtubule binding
Ranked List Metric
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
10000
20000
Position in the Ranked List of Genes

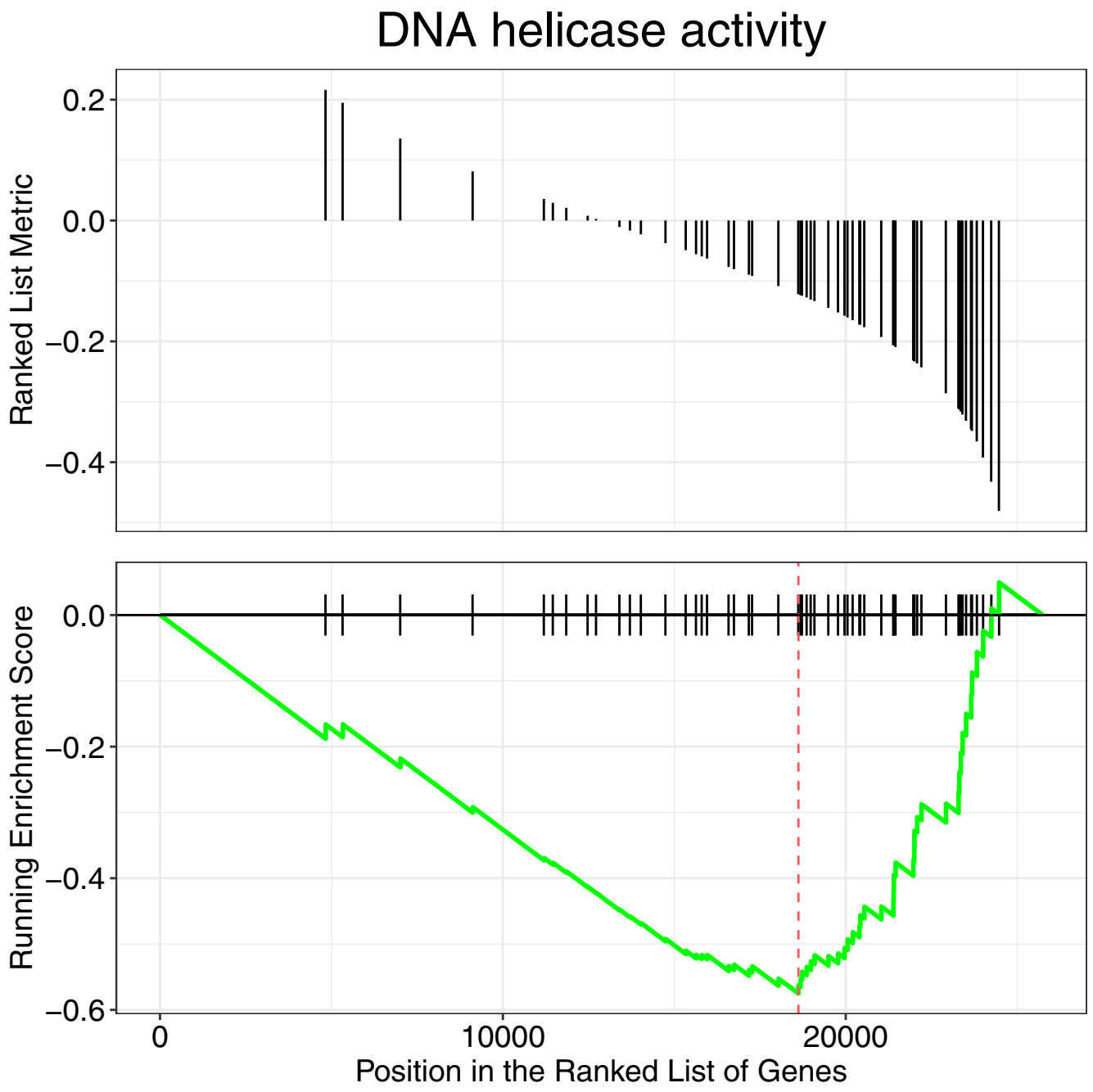

centrosome
Ranked List Metric
0.75
0.50
0.25
0.00
−0.25
−0.50
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
−0.4
0
10000
20000
Position in the Ranked List of Genes

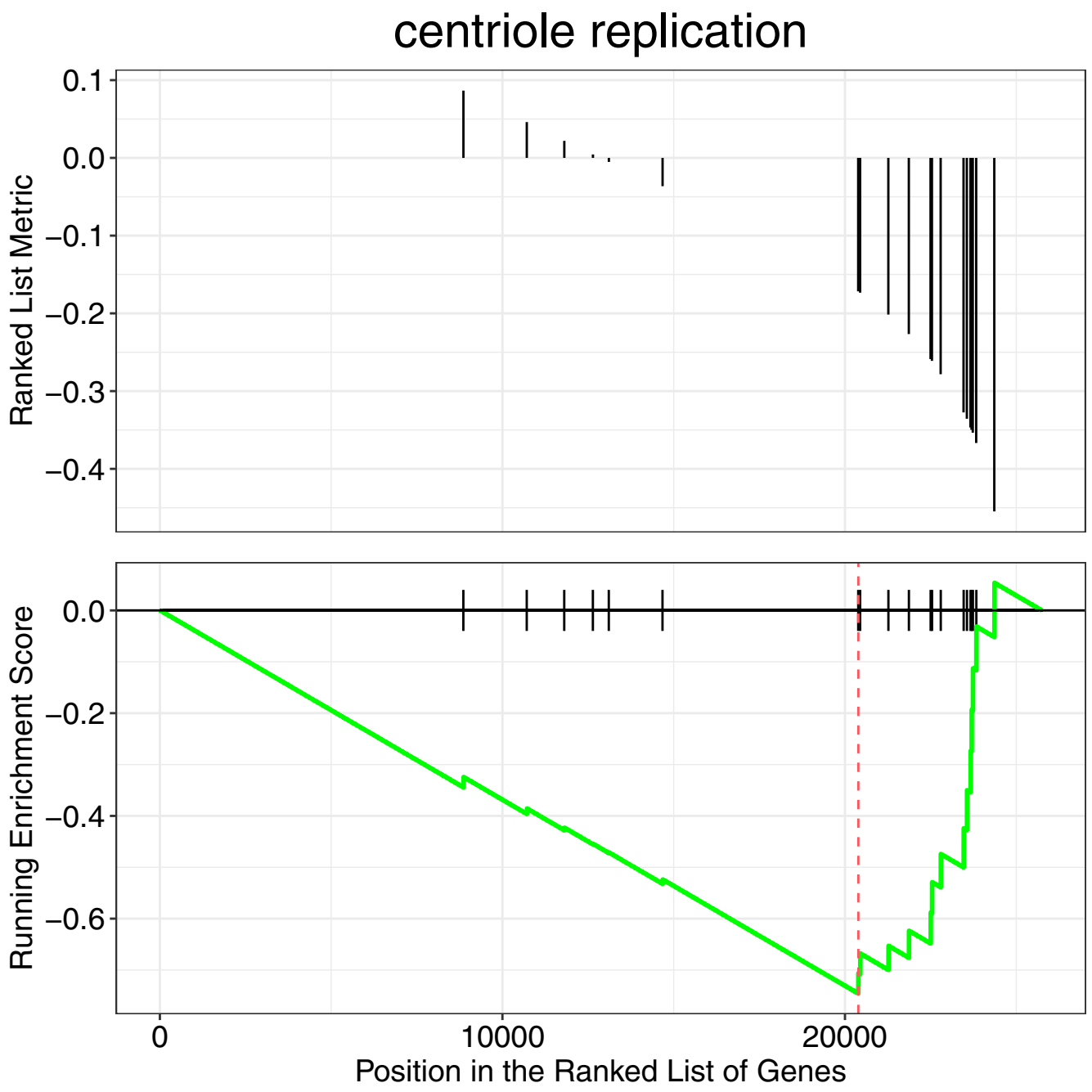

centrosome duplication
Ranked List Metric
0.1
0.0
−0.1
−0.2
−0.3
−0.4
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
10000
20000
Position in the Ranked List of Genes

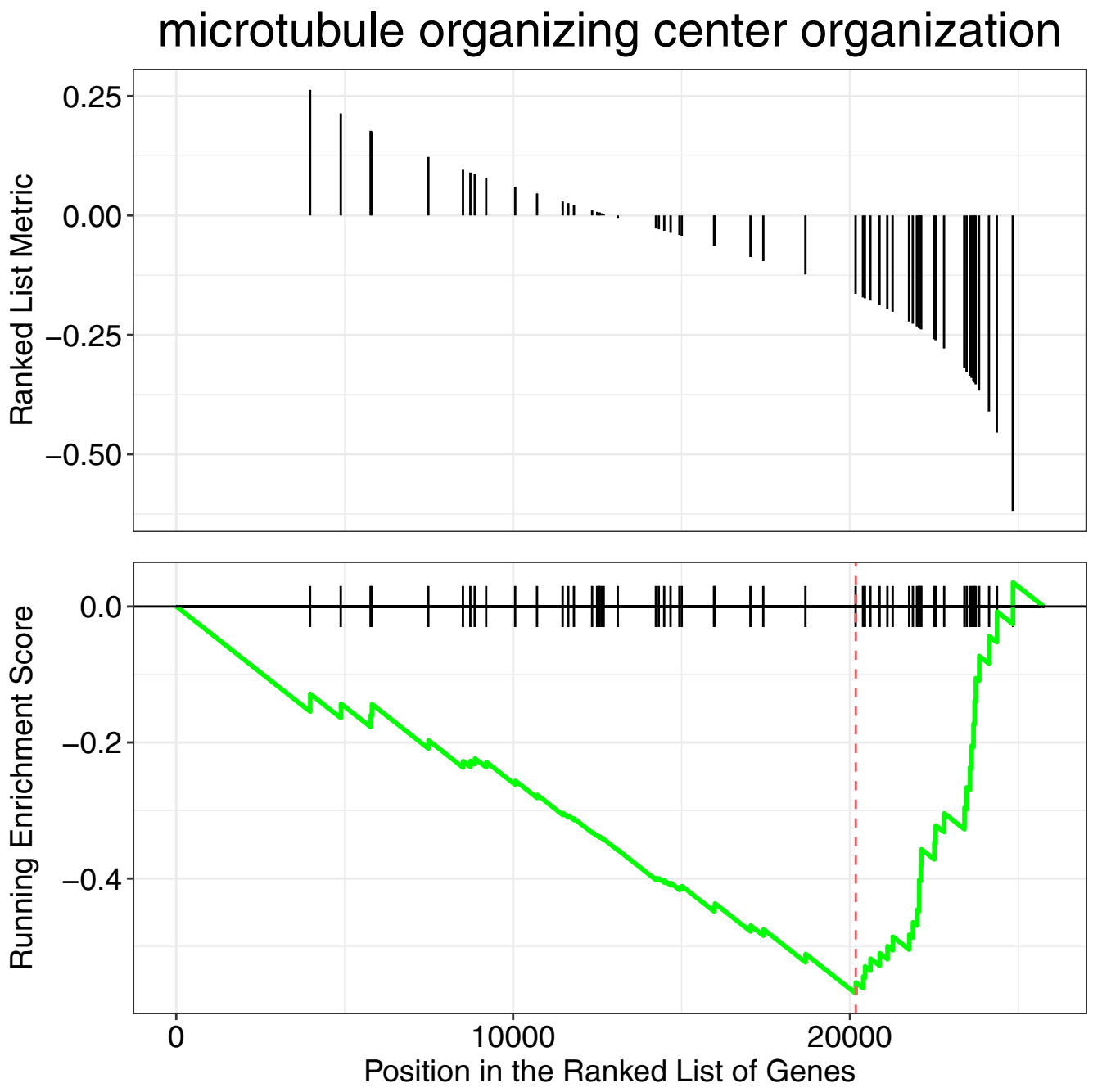

RNA splicing
Ranked List Metric
1
0
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
0
10000
20000
Position in the Ranked List of Genes

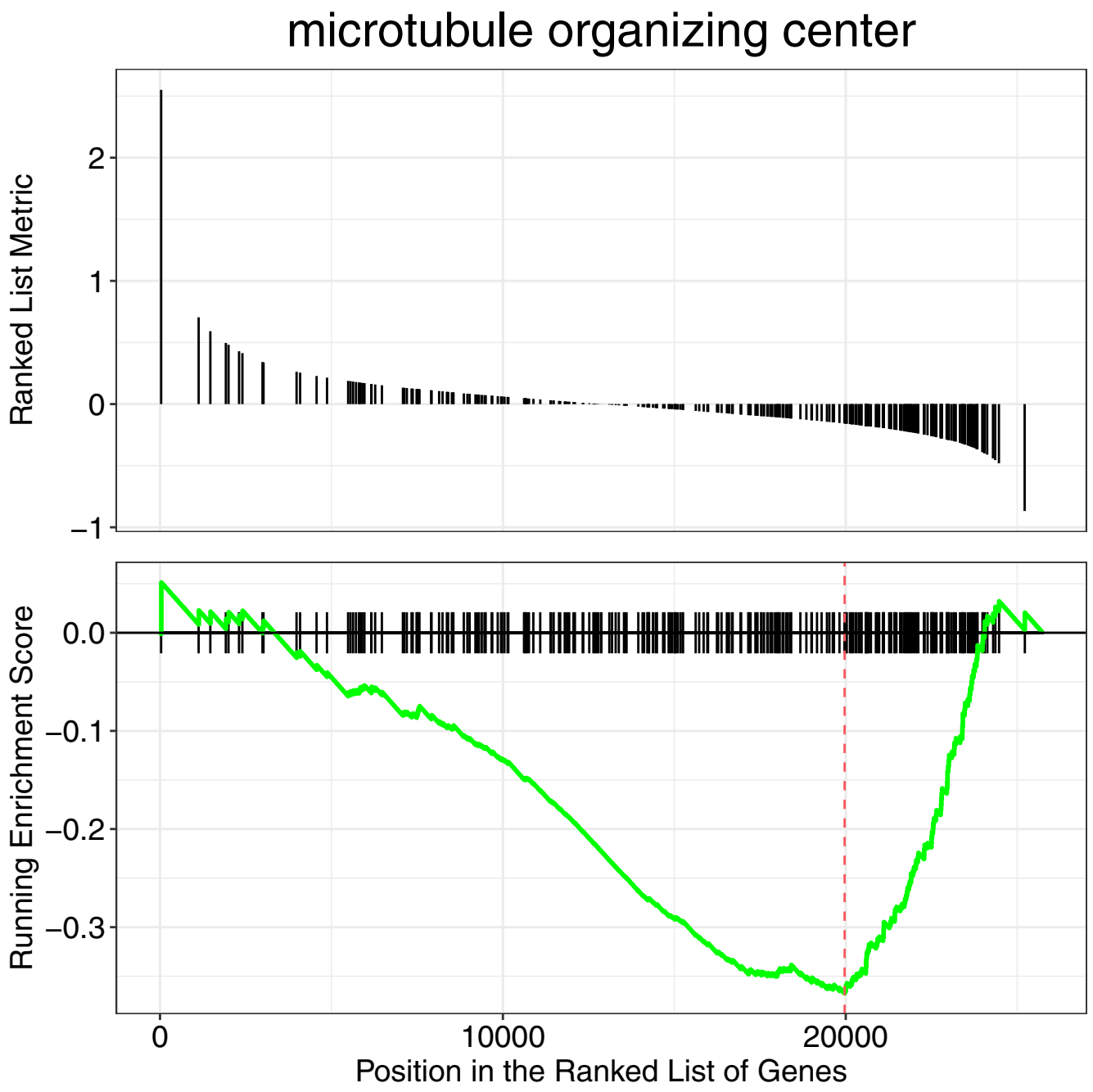

centrosome cycle
Ranked List Metric
0.25
0.00
−0.25
−0.50
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
10000
20000
Position in the Ranked List of Genes


microtubule cytoskeleton organization
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
0
10000
20000
Position in the Ranked List of Genes


DNA helicase activity
Ranked List Metric
0.2
0.0
−0.2
−0.4
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
10000
20000
Position in the Ranked List of Genes


centriole replication
Ranked List Metric
0.1
0.0
−0.1
−0.2
−0.3
−0.4
Running Enrichment Score
0.0
−0.2
−0.4
−0.6
0
10000
20000
Position in the Ranked List of Genes


microtubule organizing center organization
Ranked List Metric
0.25
0.00
−0.25
−0.50
Running Enrichment Score
0.0
−0.2
−0.4
0
10000
20000
Position in the Ranked List of Genes


microtubule organizing center
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.0
−0.1
−0.2
−0.3
0
10000
20000
Position in the Ranked List of Genes

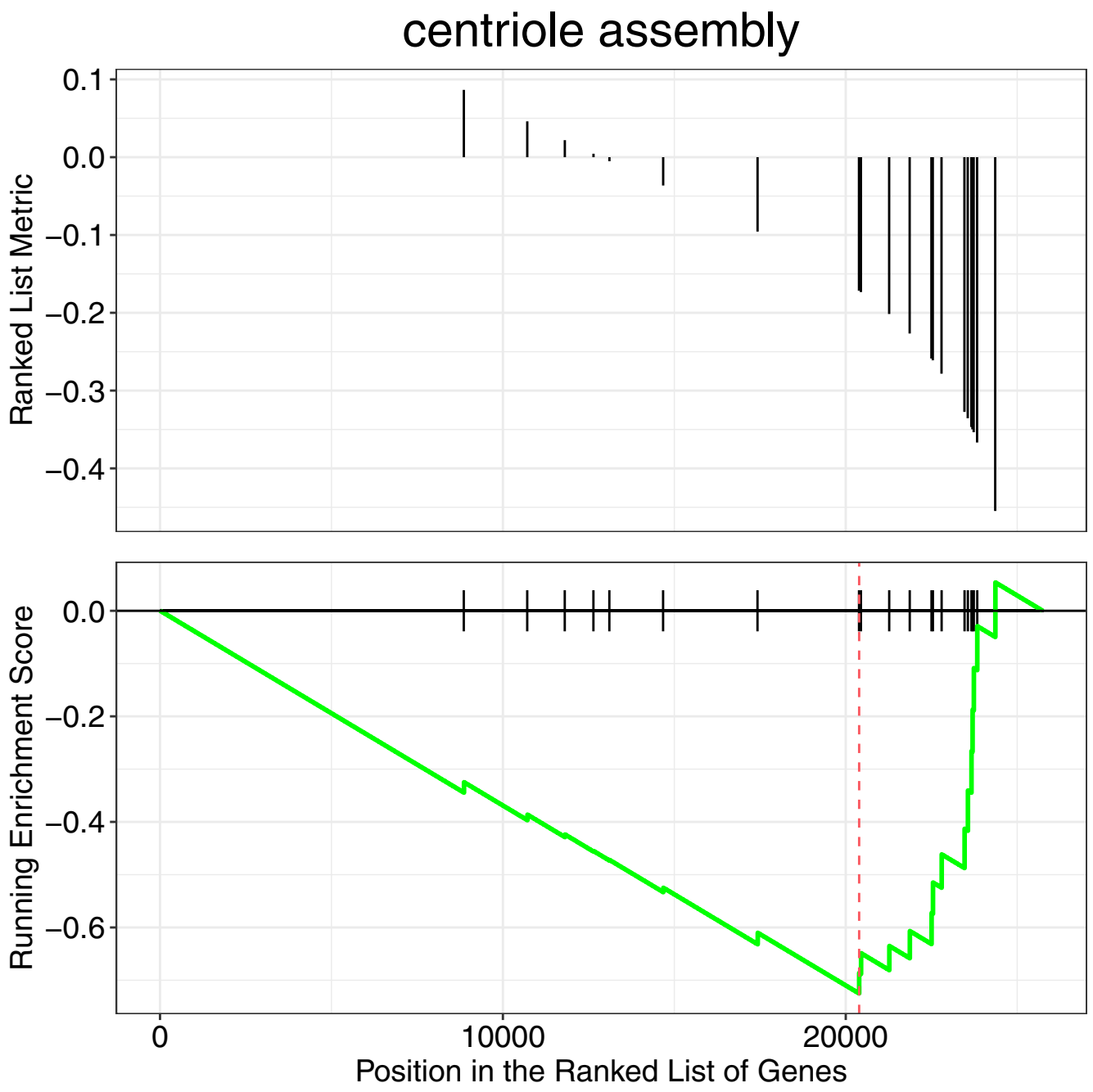
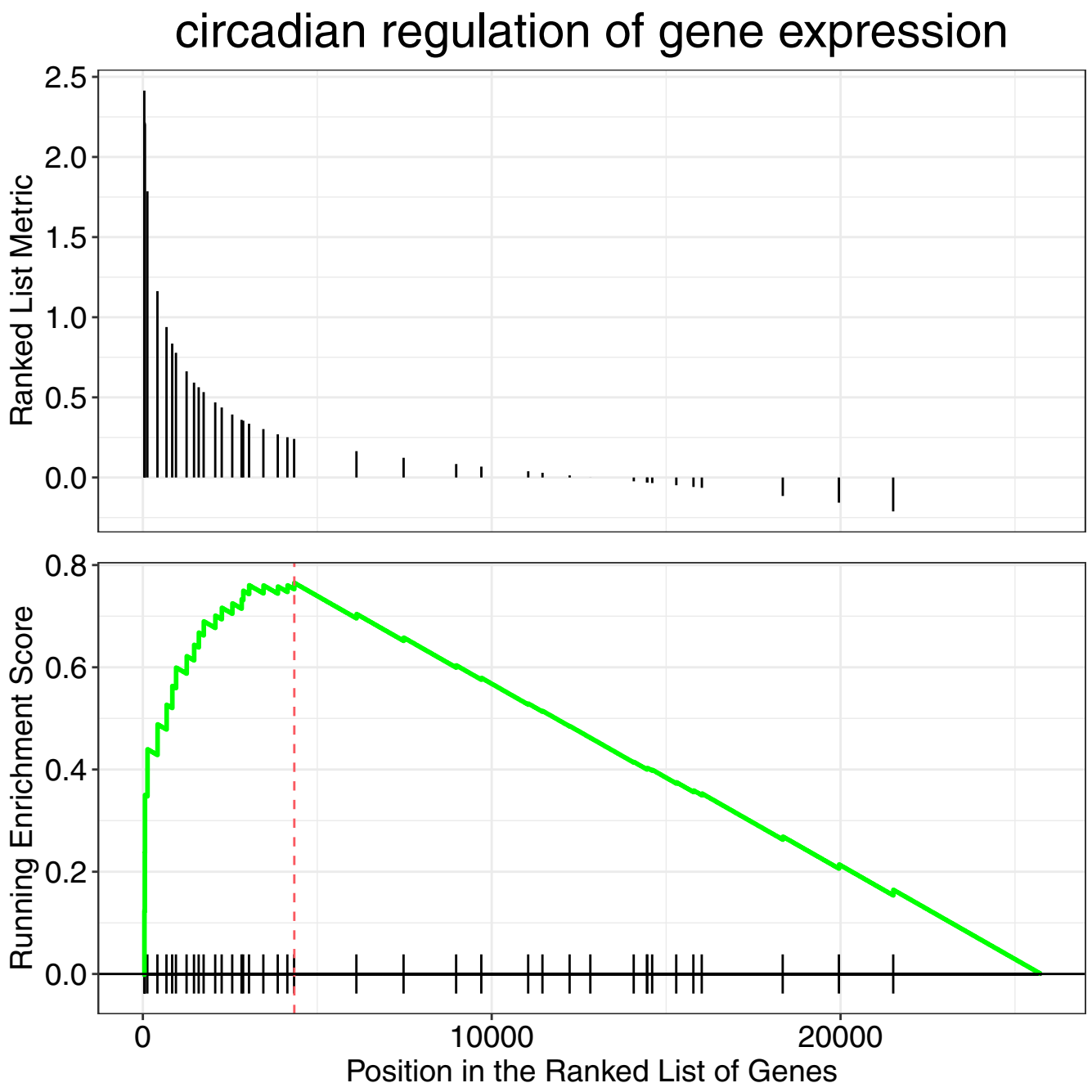
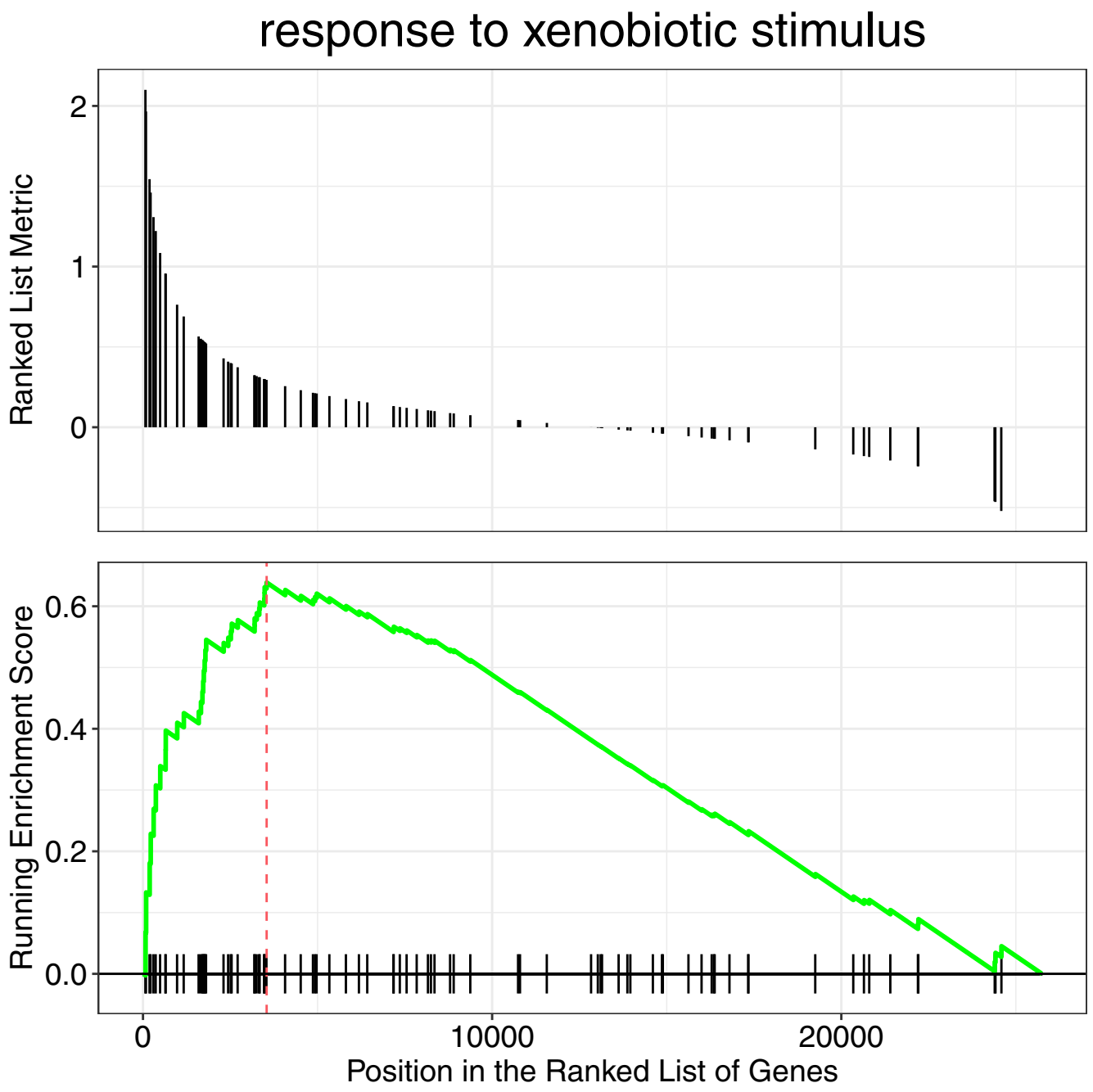
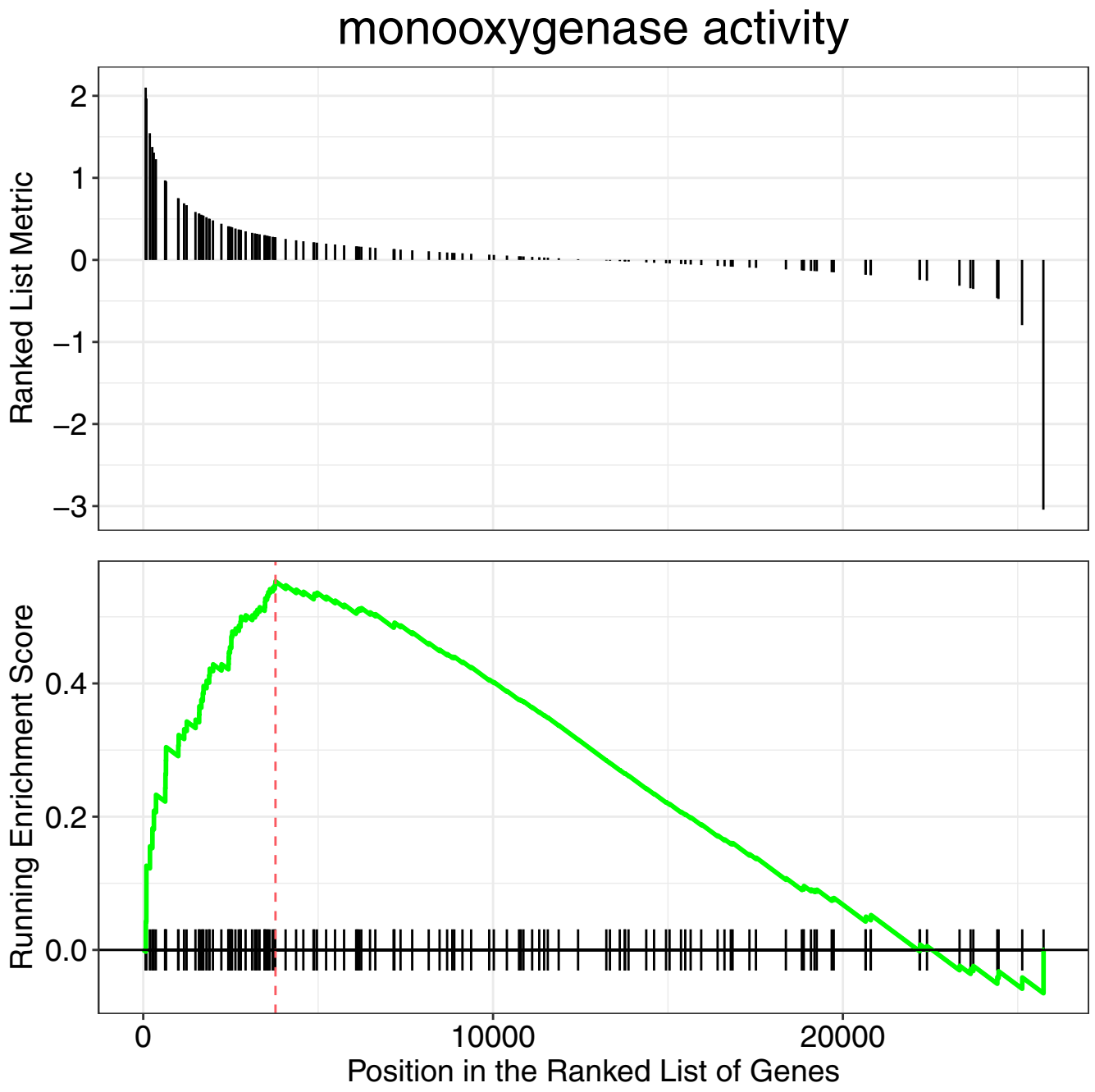
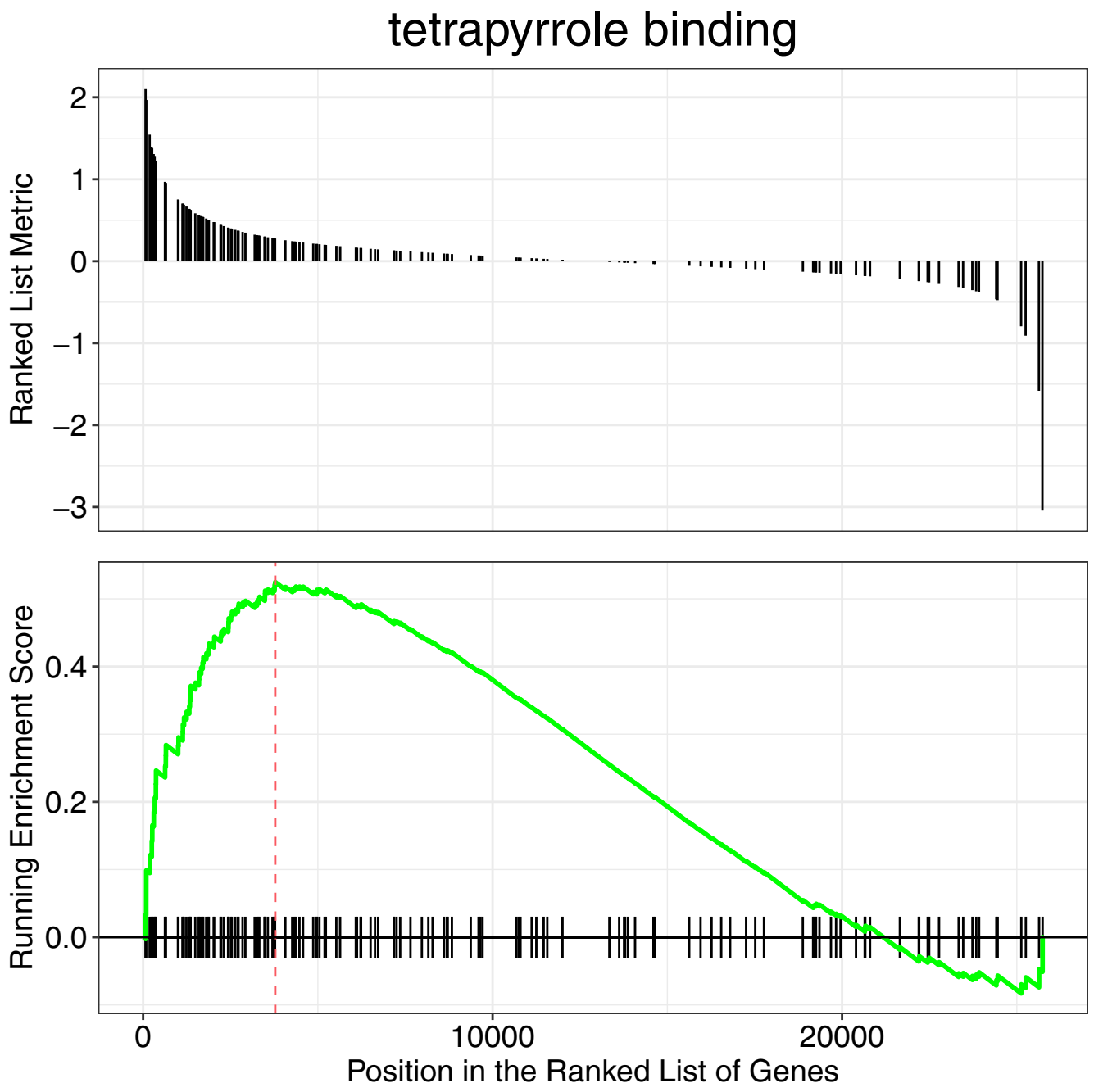


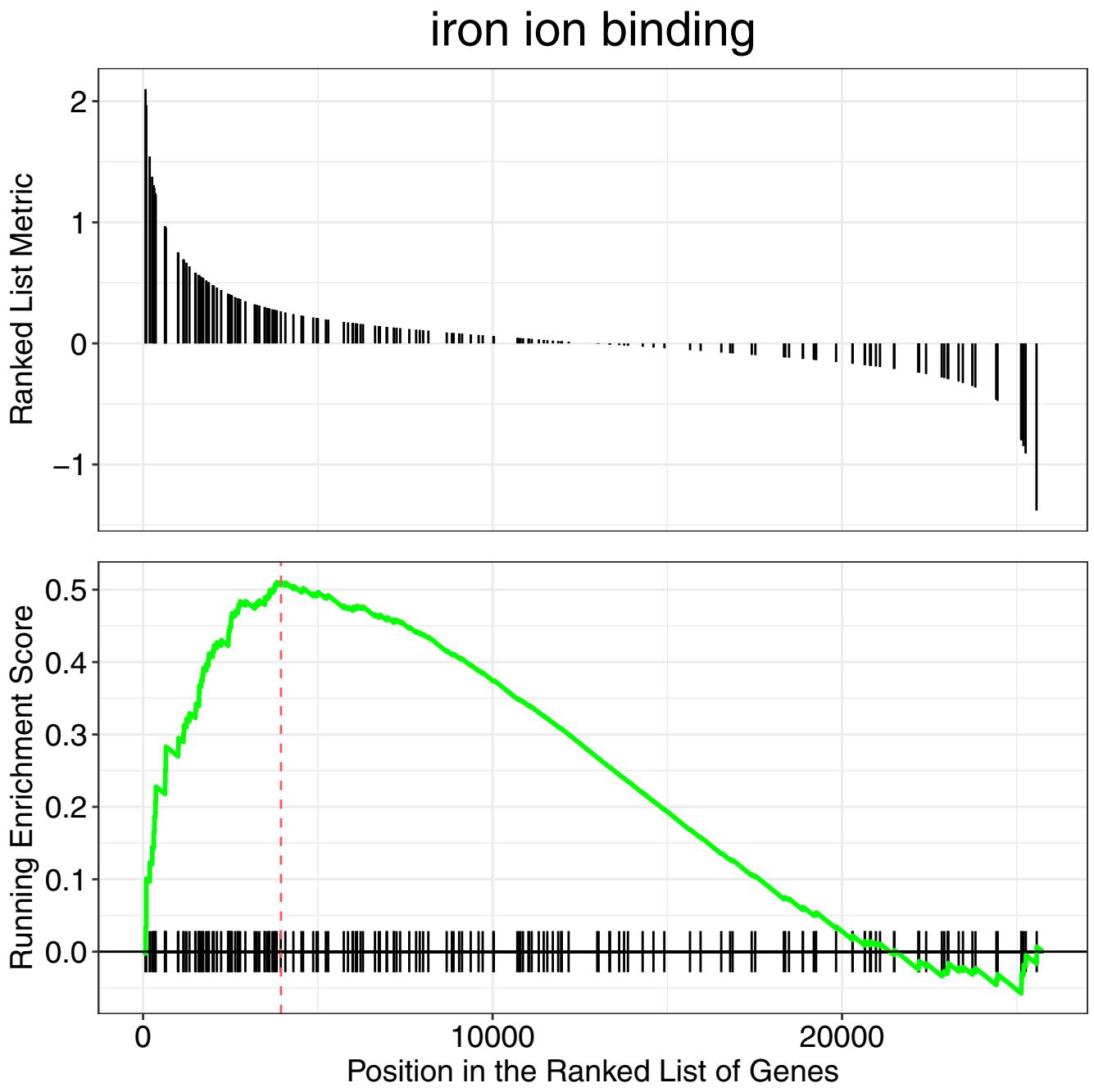
Fig. S7. Enrichment plots of Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 crispants. Running score plot and pre-ranked list of all suppressed GSEA terms shown in alx1;alx3 crispants.

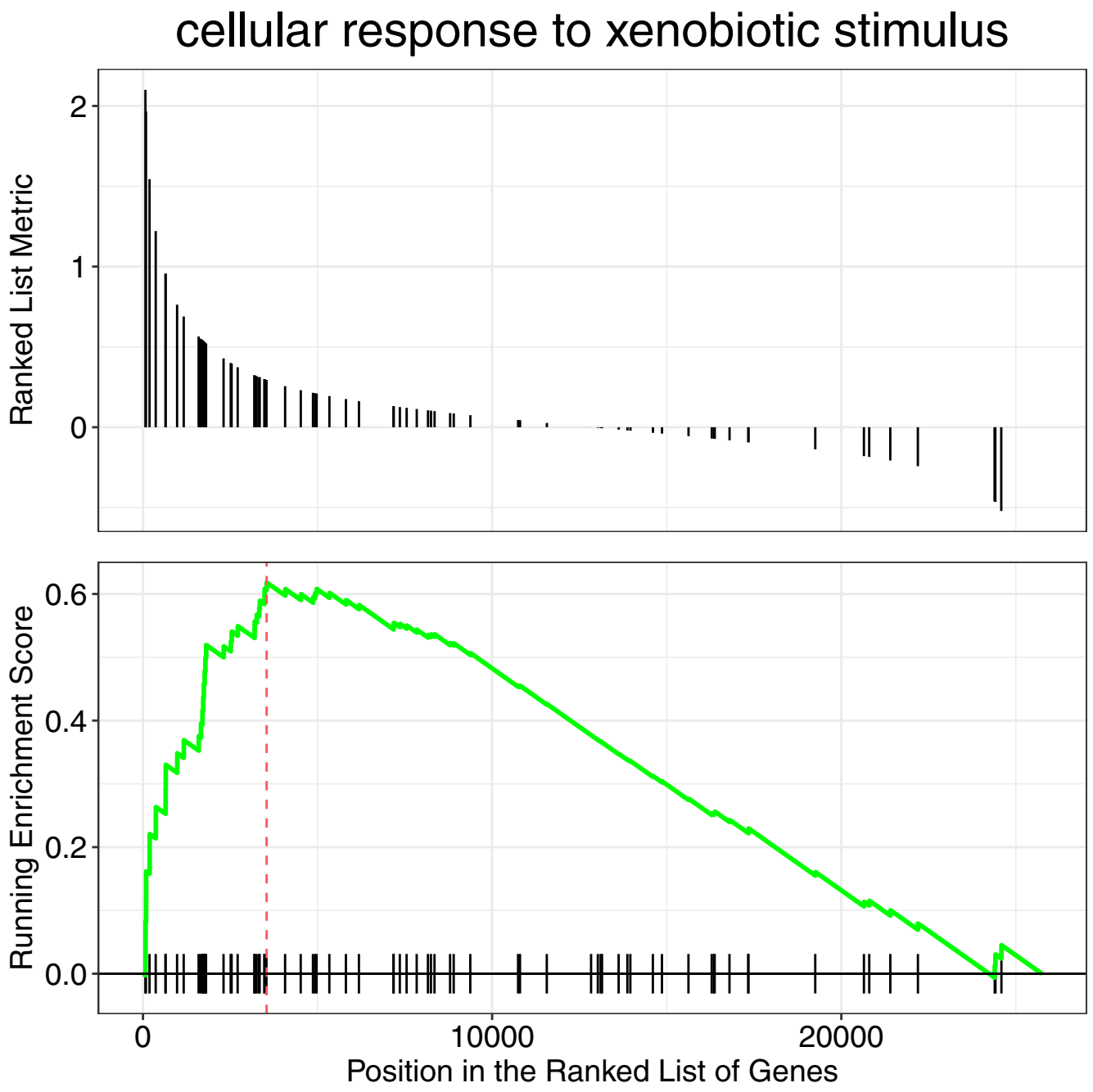

circadian regulation of gene expression
Ranked List Metric
2.5
2.0
1.5
1.0
0.5
0.0
Running Enrichment Score
0.8
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

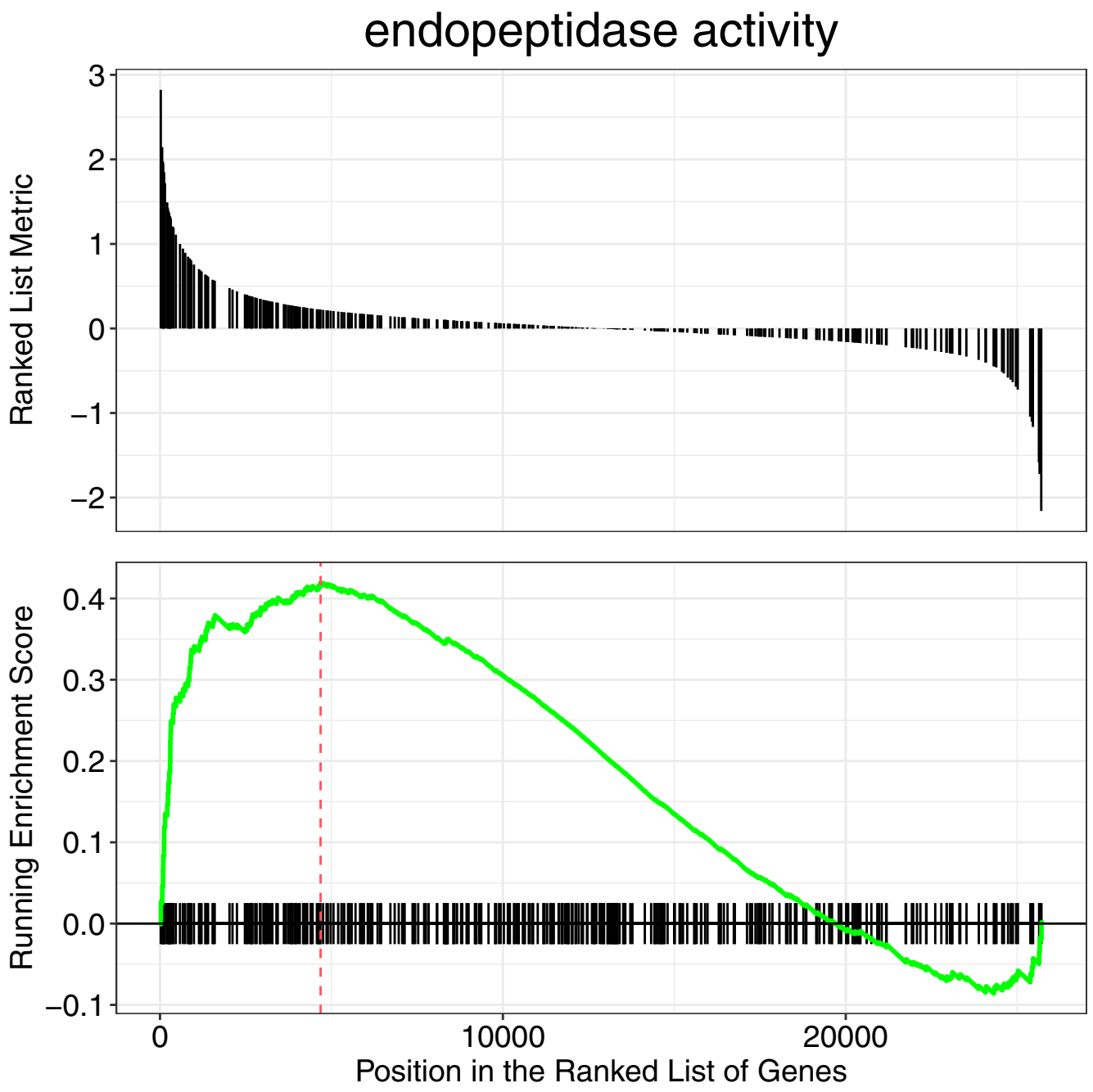

response to xenobiotic stimulus
Ranked List Metric
2
1
0
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

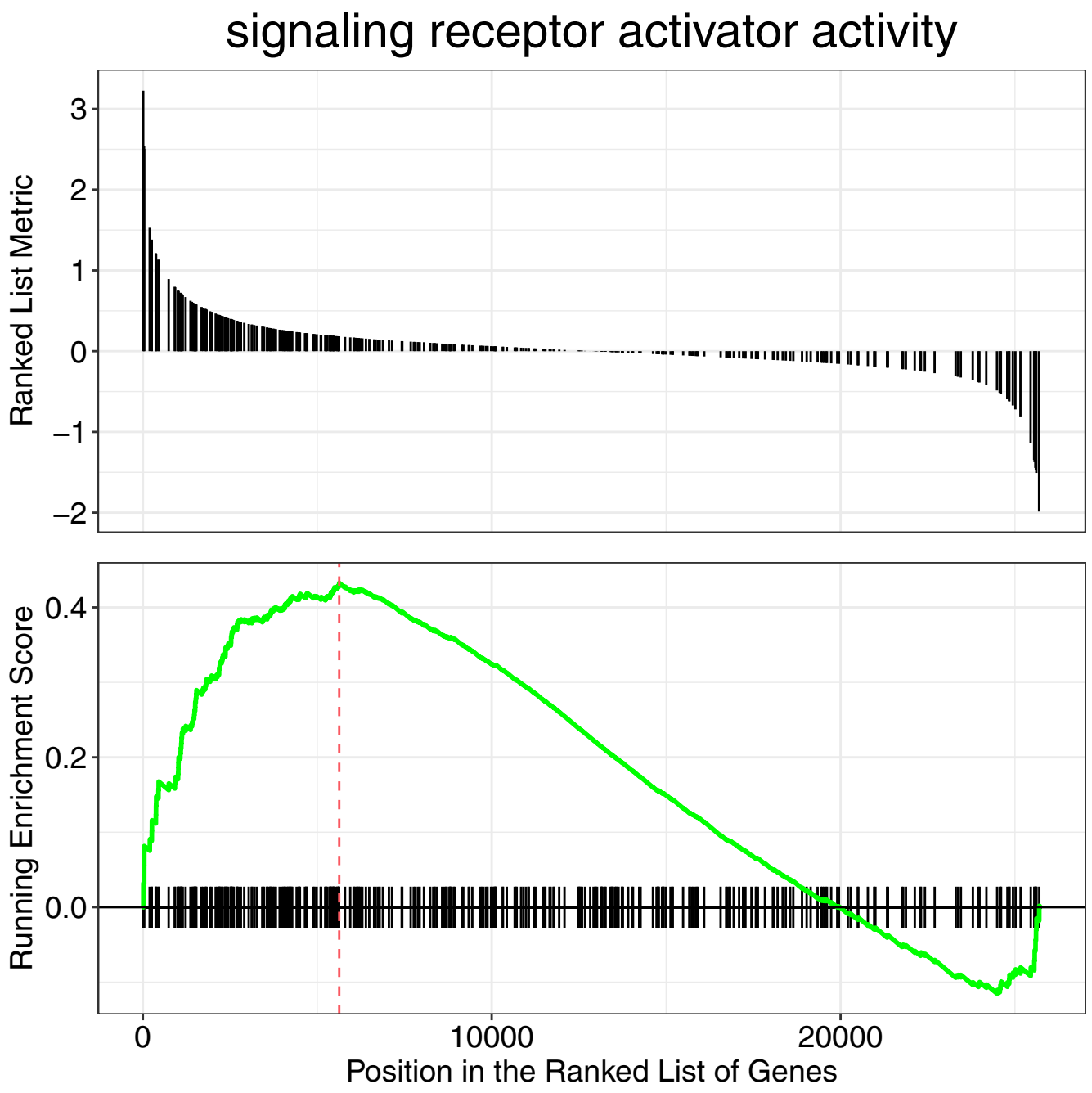

monooxygenase activity
Ranked List Metric
2
1
0
−1
−2
−3
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

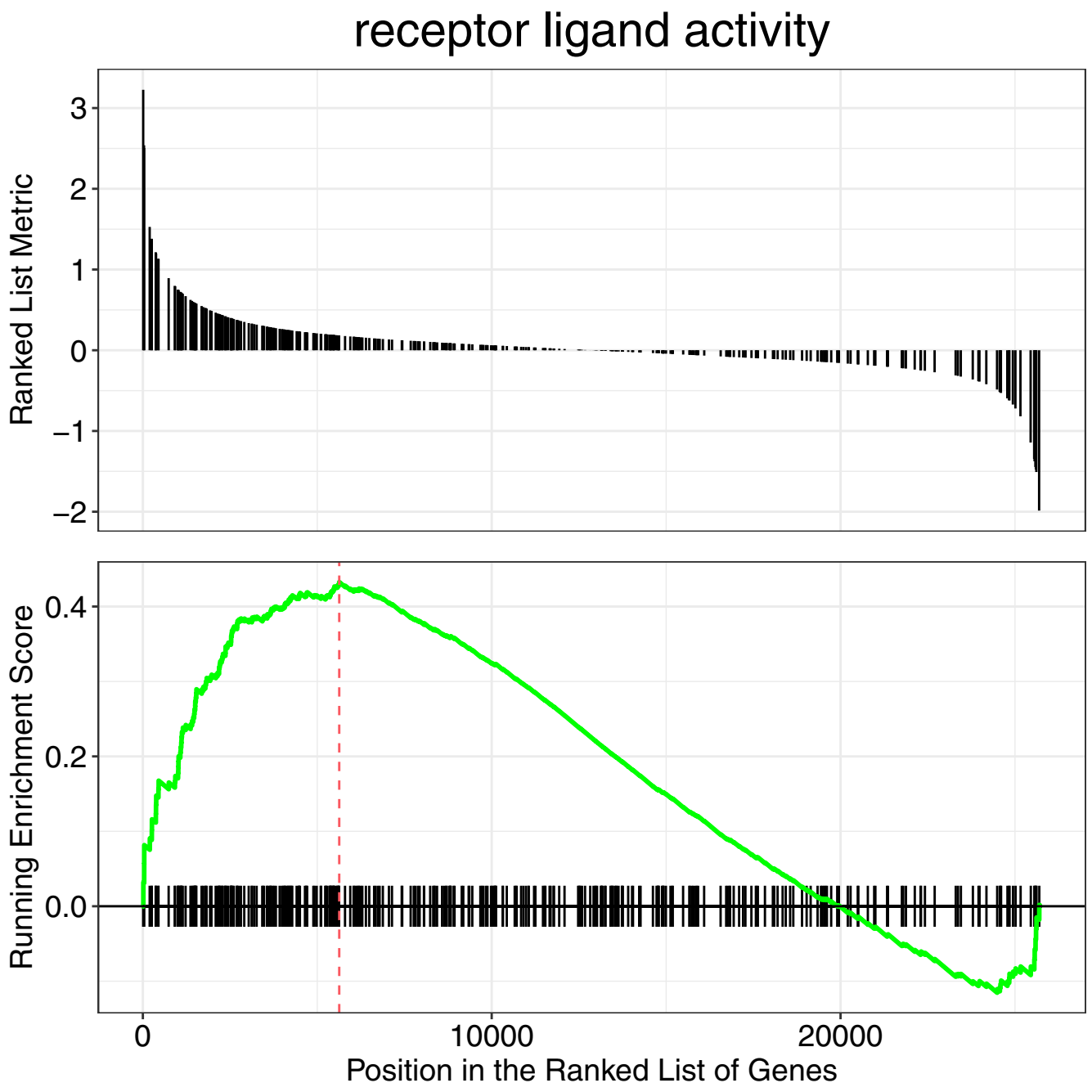

tetrapyrrole binding
Ranked List Metric
2
1
0
−1
−2
−3
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

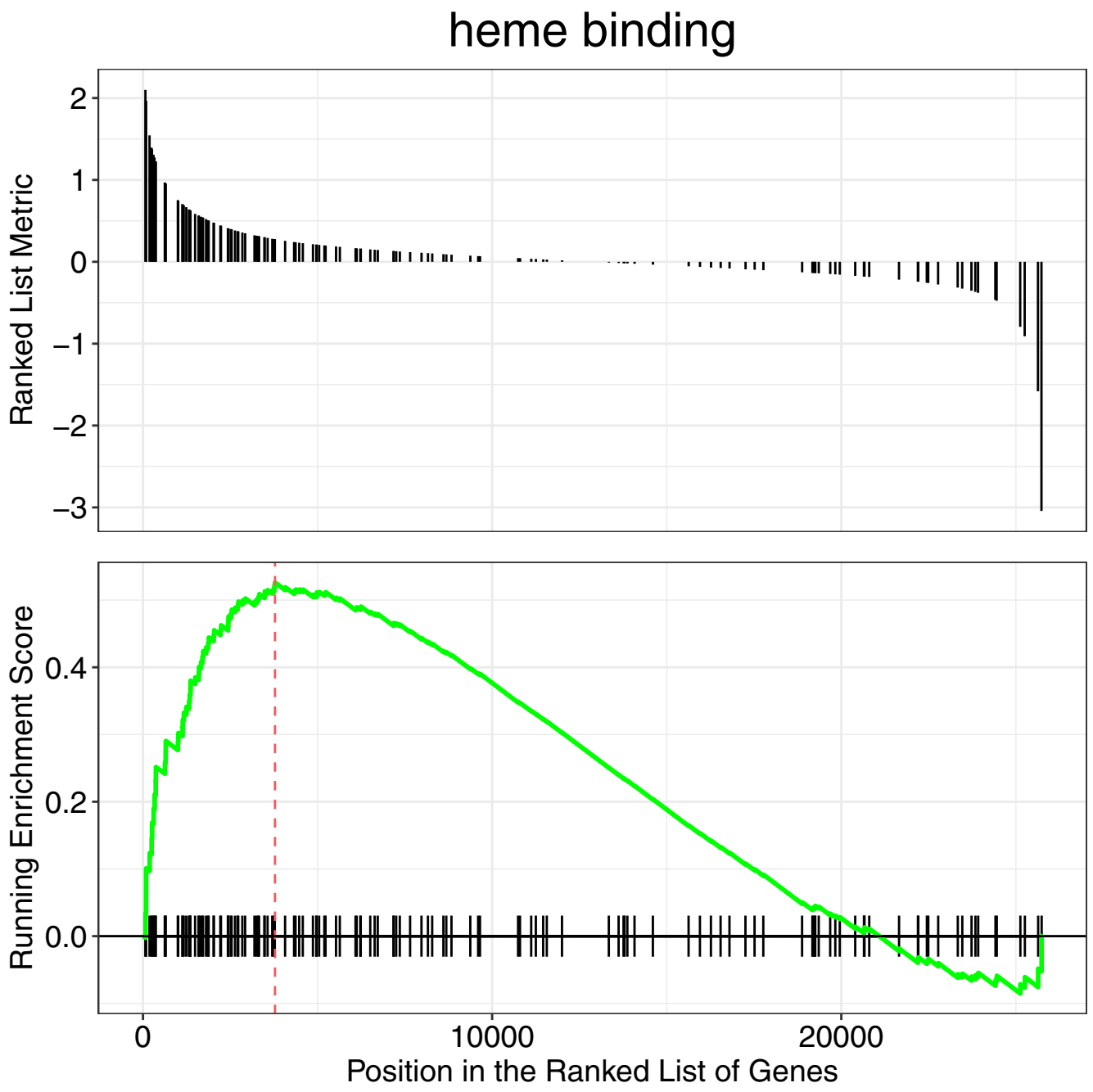

iron ion binding
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.5
0.4
0.3
0.2
0.1
0.0
0
10000
20000
Position in the Ranked List of Genes

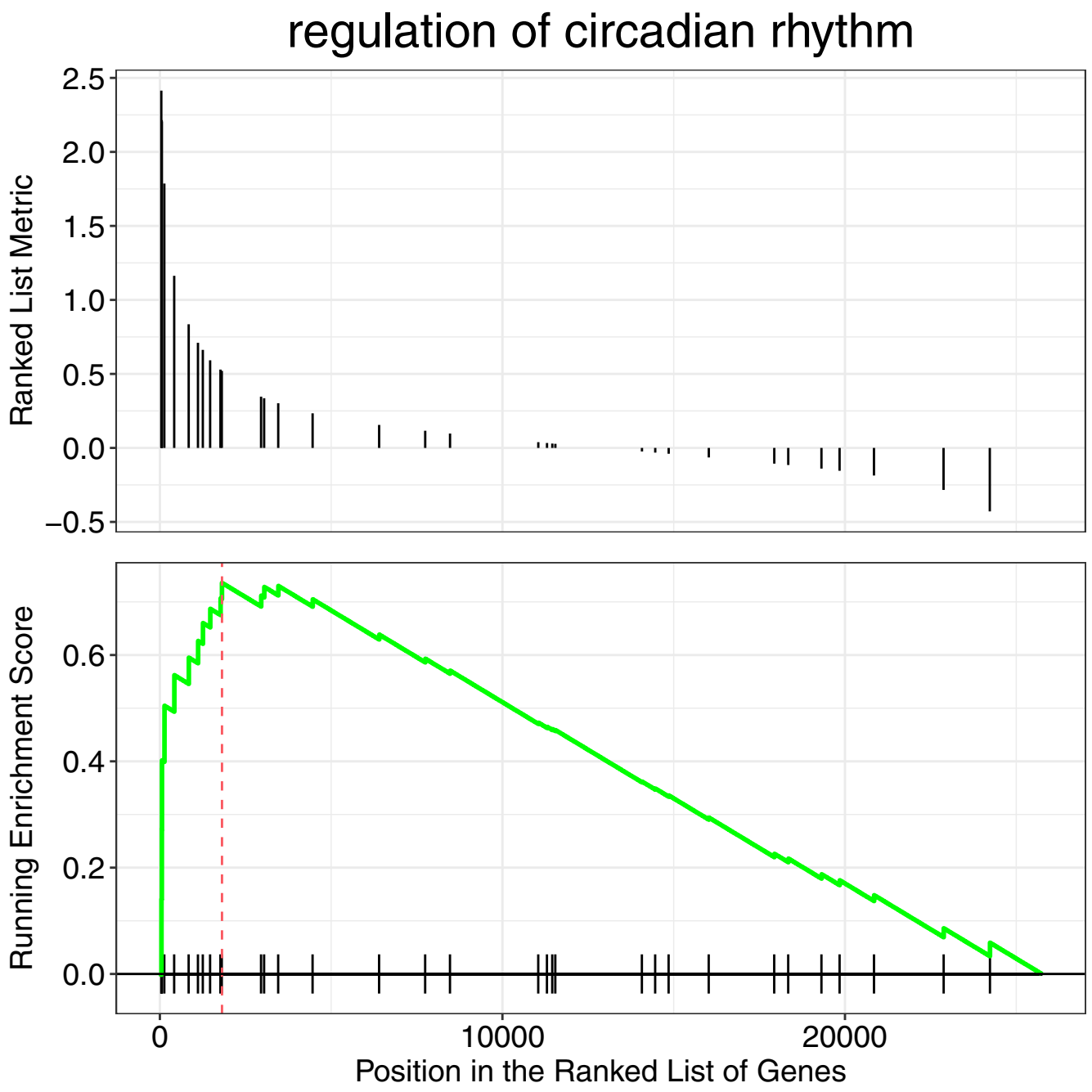

cellular response to xenobiotic stimulus
Ranked List Metric
2
1
0
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

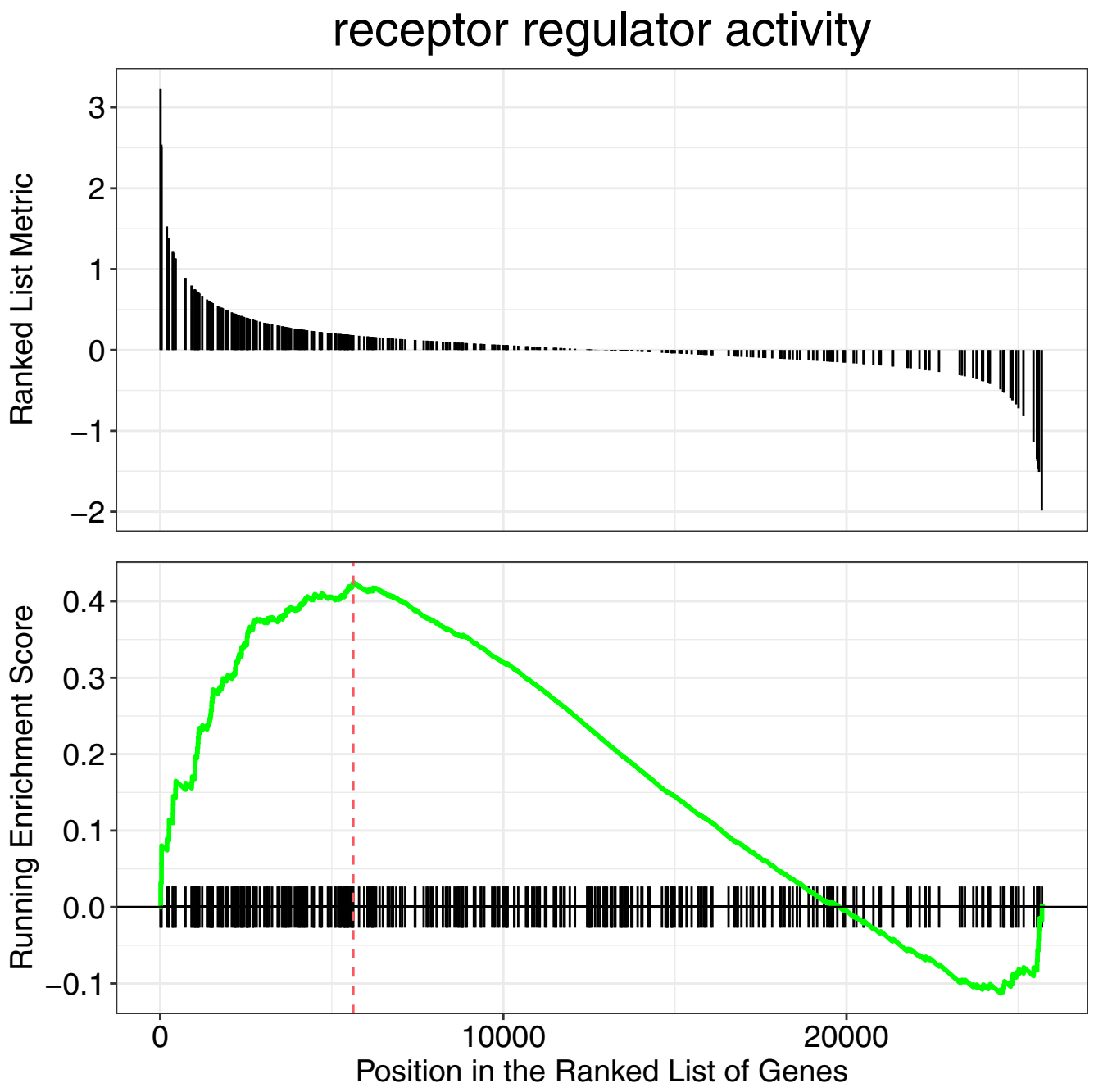

endopeptidase activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
−0.1
0
10000
20000
Position in the Ranked List of Genes

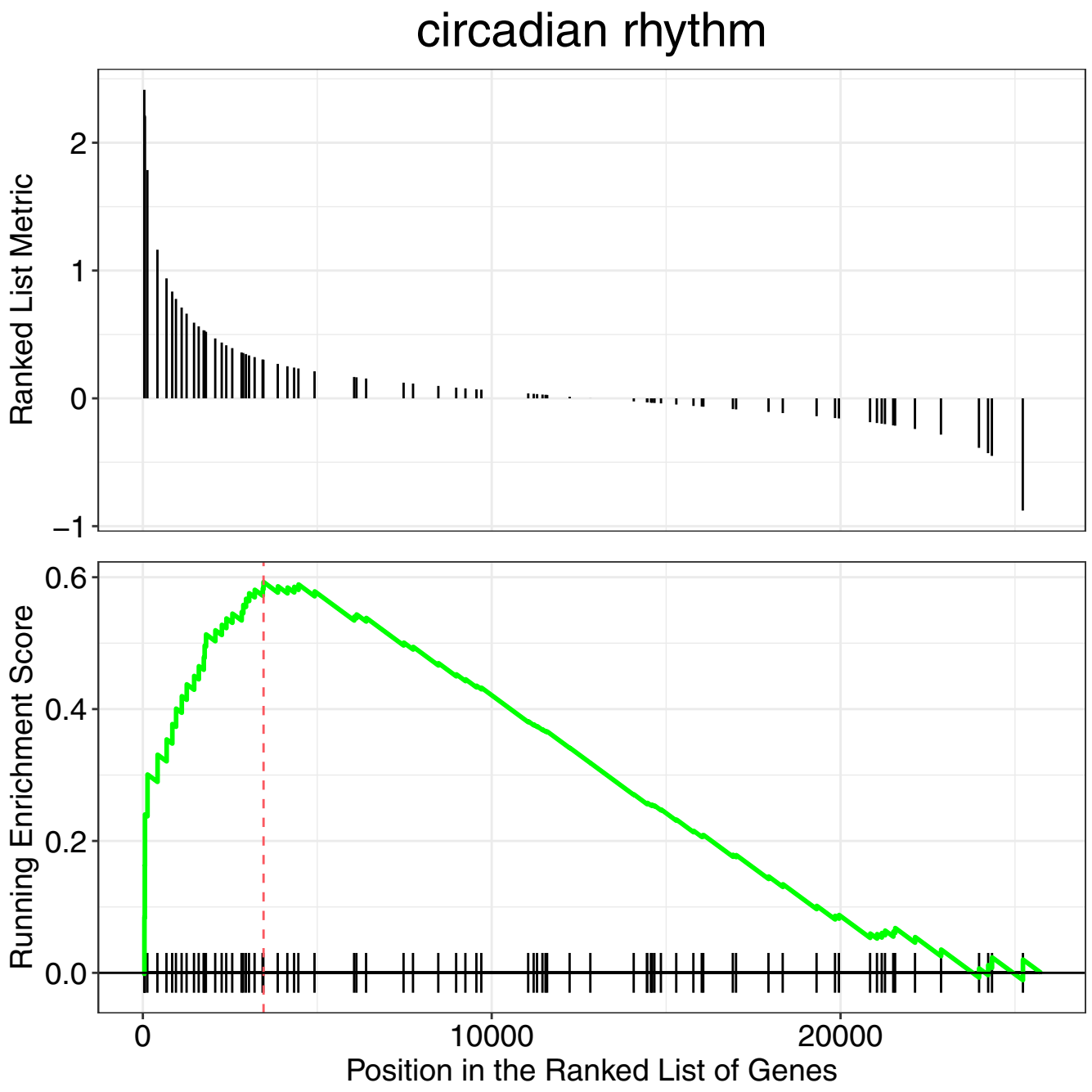

signaling receptor activator activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes


receptor ligand activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

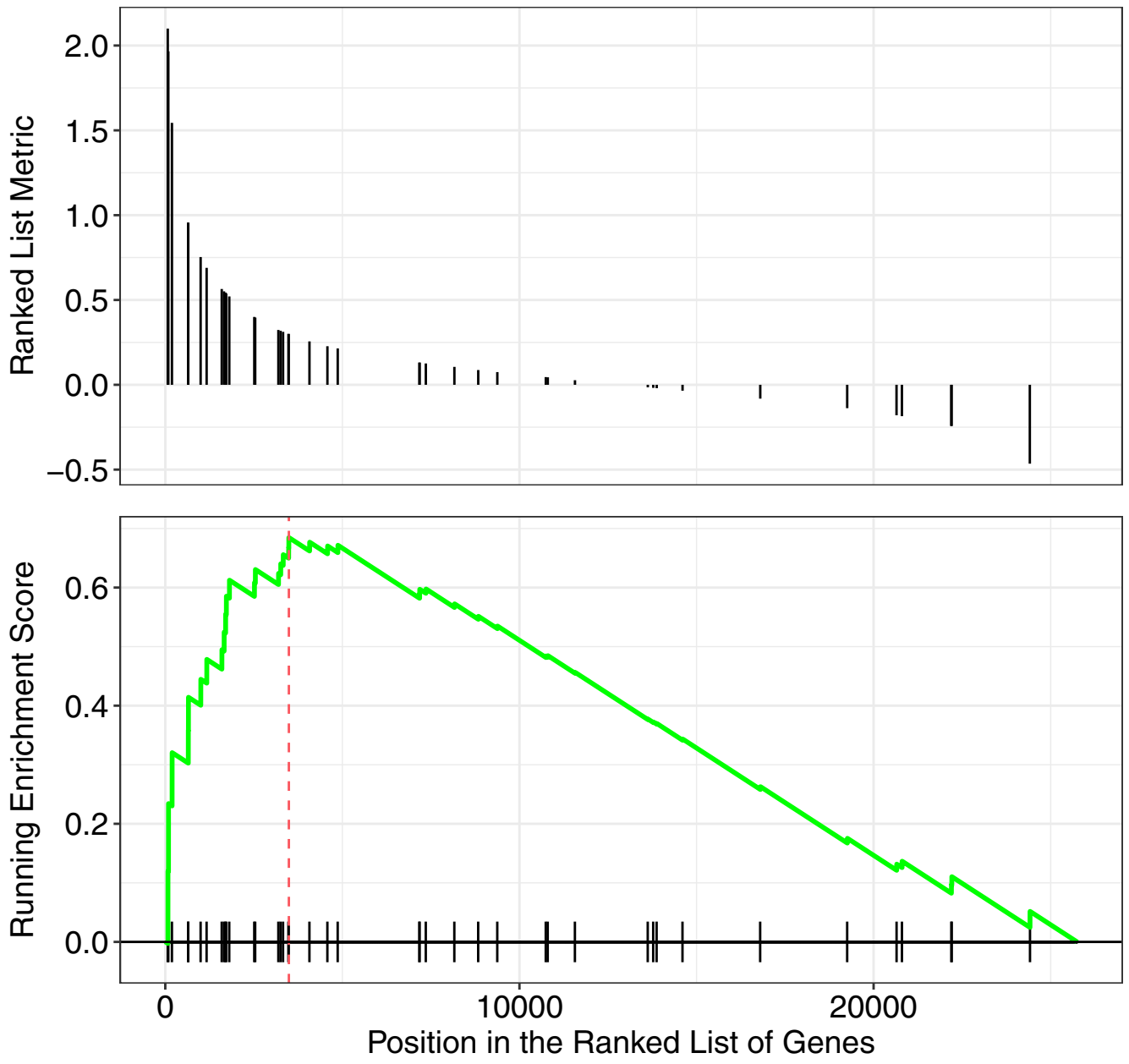

heme binding
Ranked List Metric
2
1
0
−1
−2
−3
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

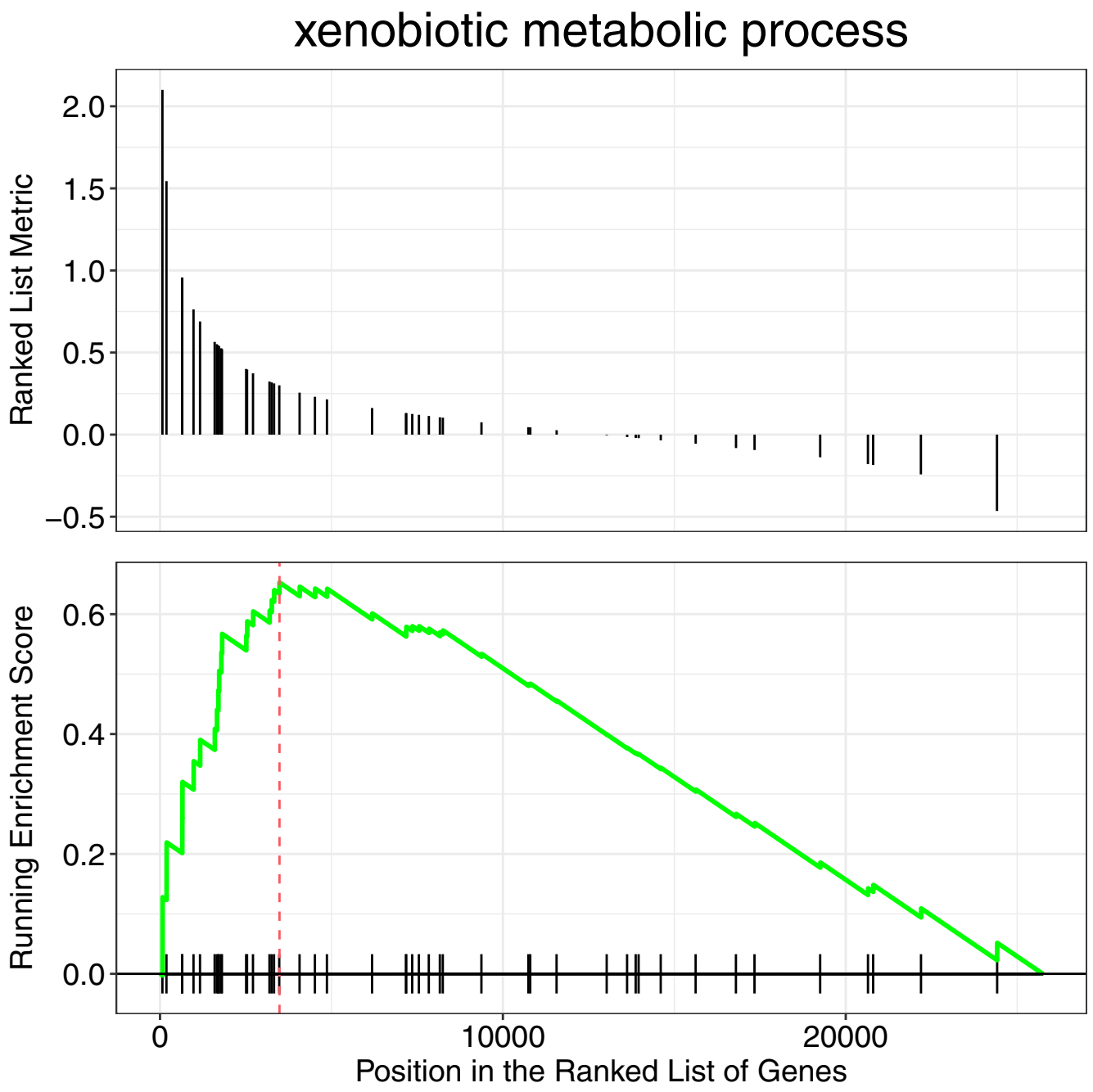

regulation of circadian rhythm
Ranked List Metric
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

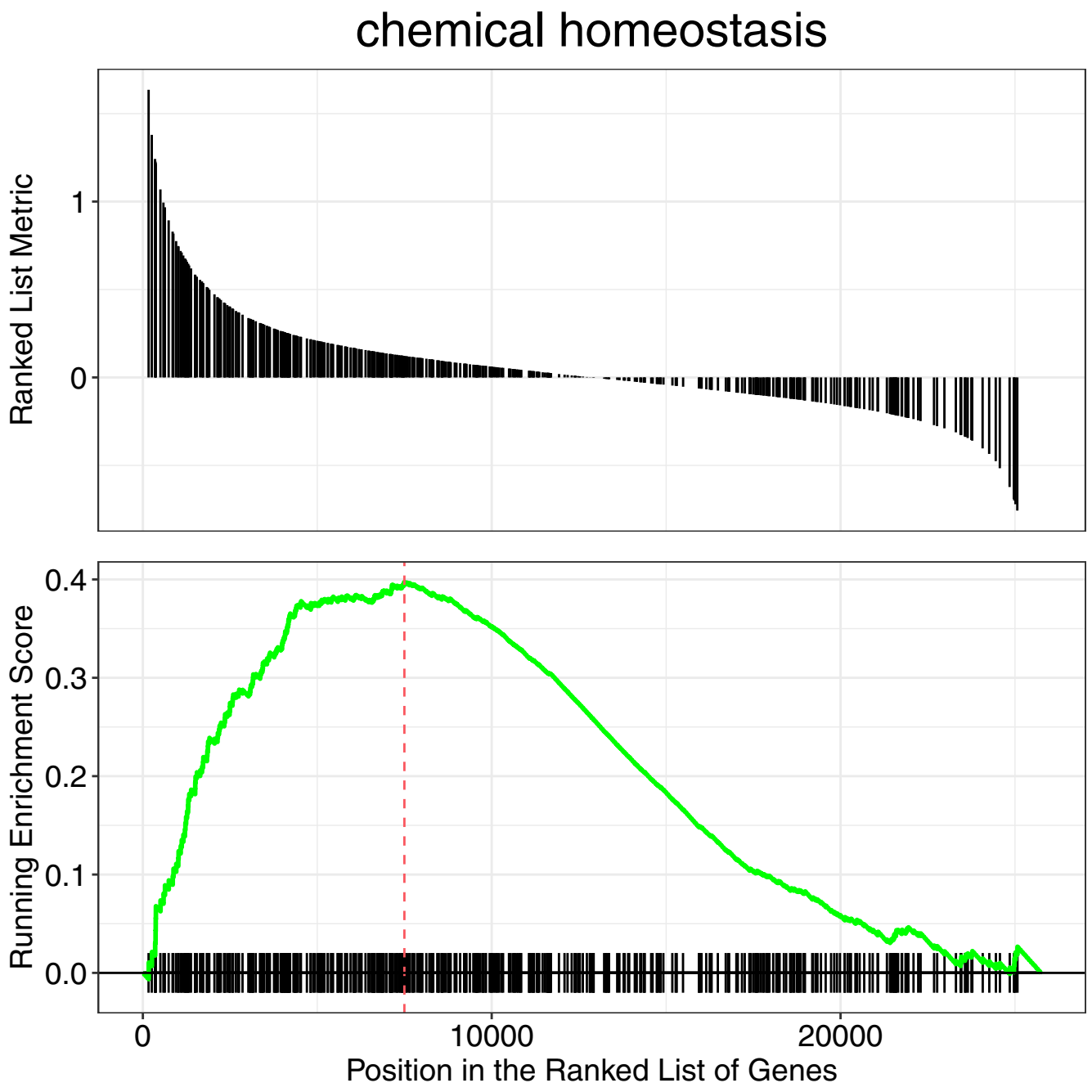

receptor regulator activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
−0.1
0
10000
20000
Position in the Ranked List of Genes

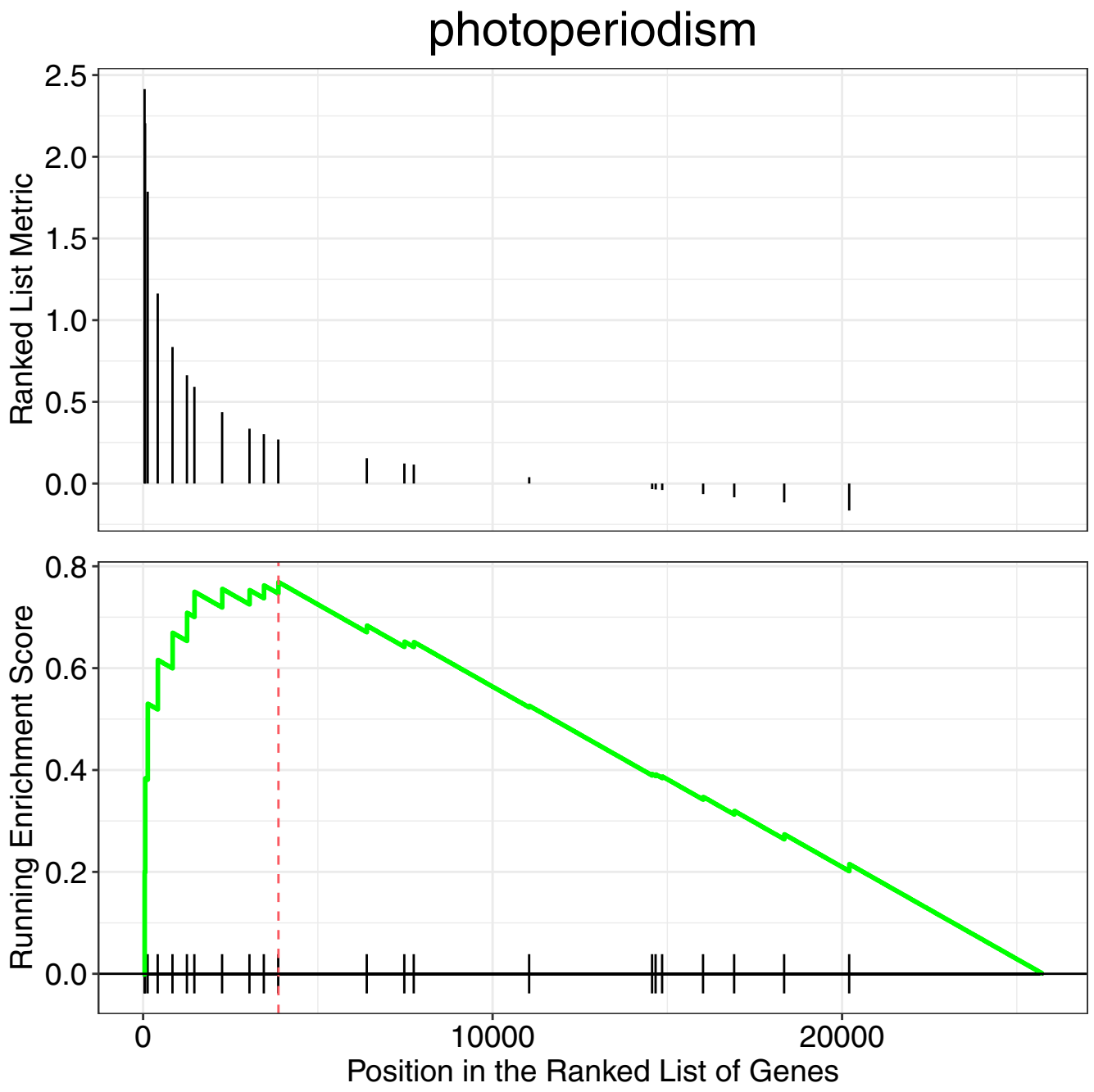

circadian rhythm
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

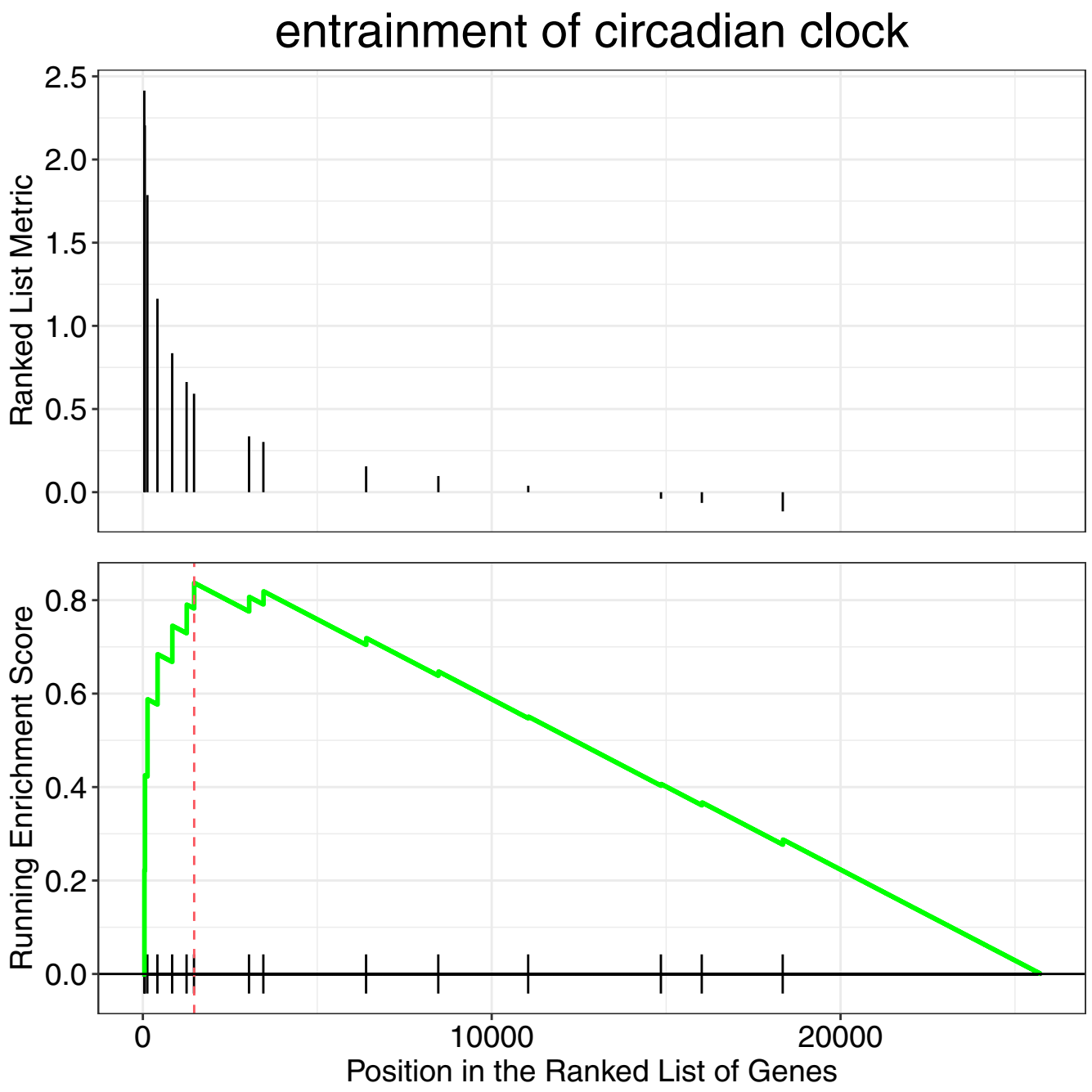
incorporation or reduction of molecular oxygen, reduced flavin or flavop e

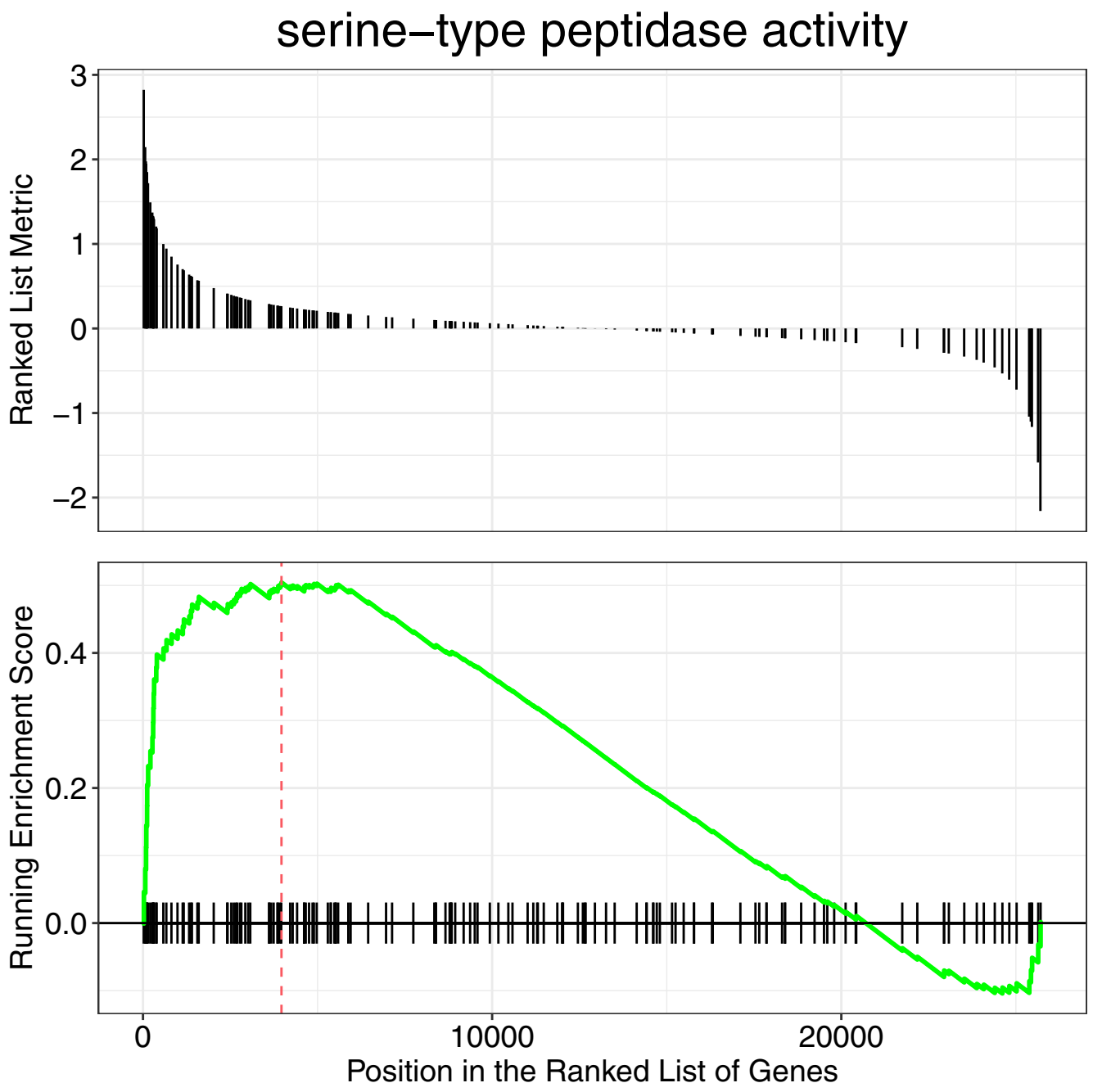


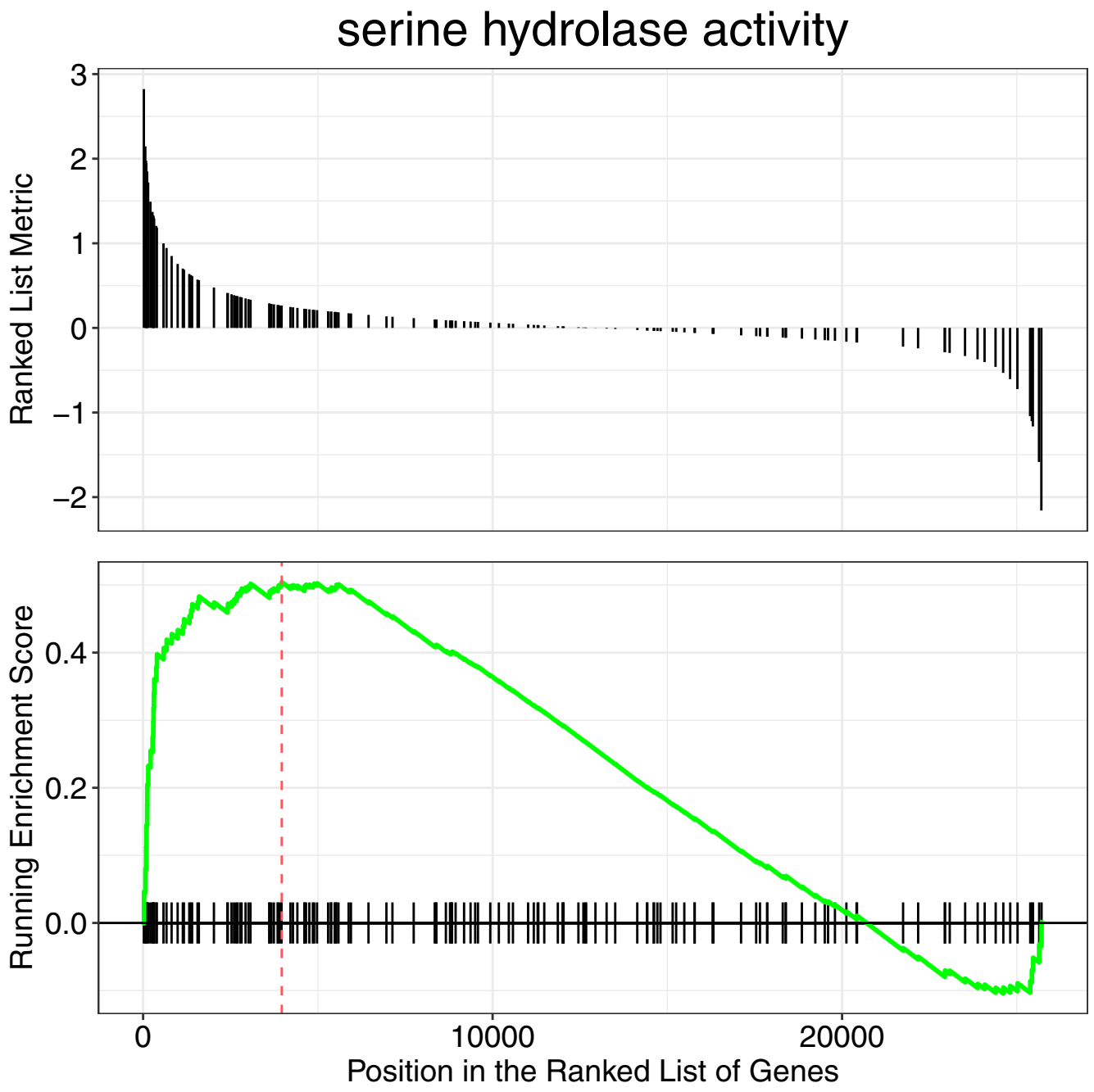

xenobiotic metabolic process
Ranked List Metric
2.0
1.5
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

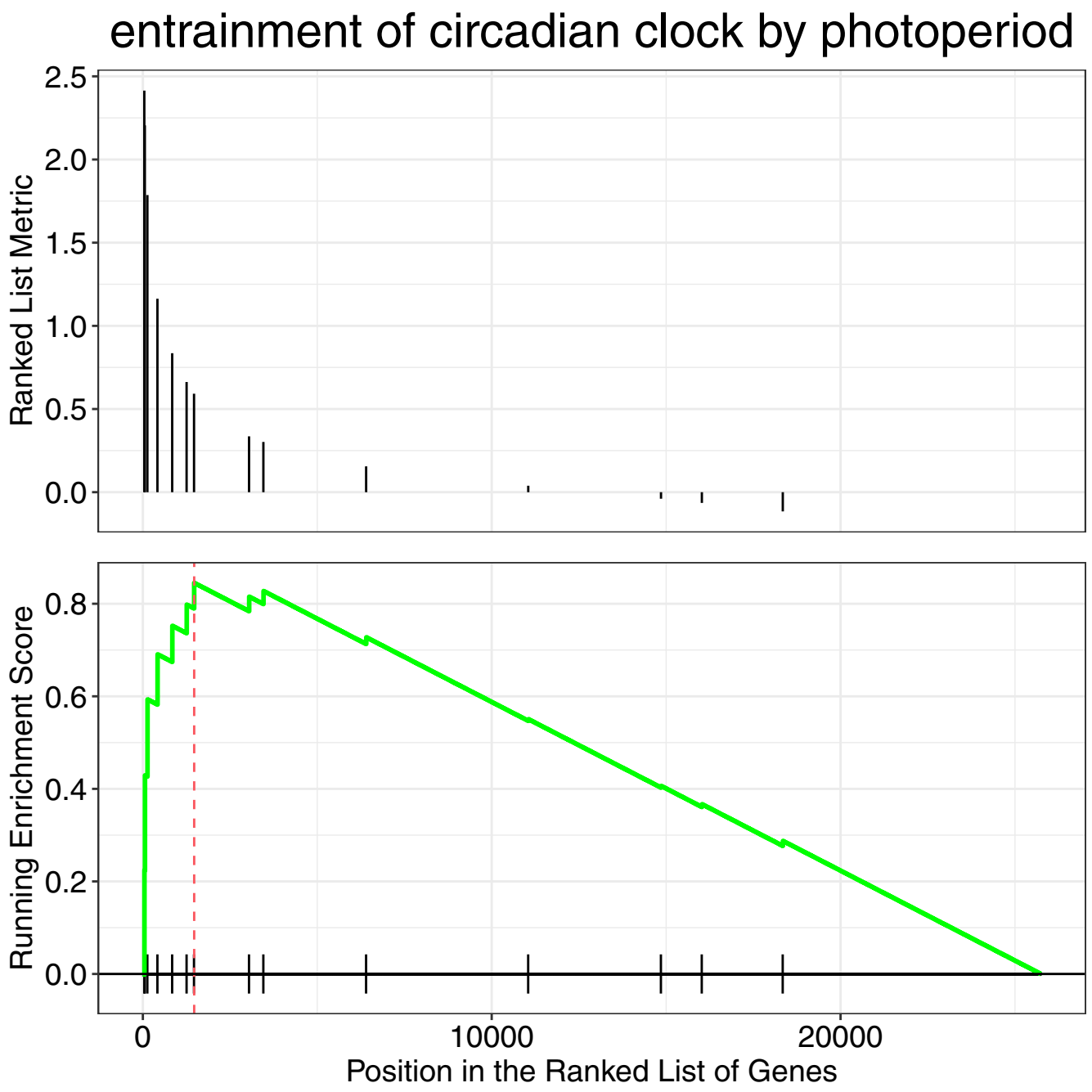

chemical homeostasis
Ranked List Metric
1
0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
10000
20000
Position in the Ranked List of Genes

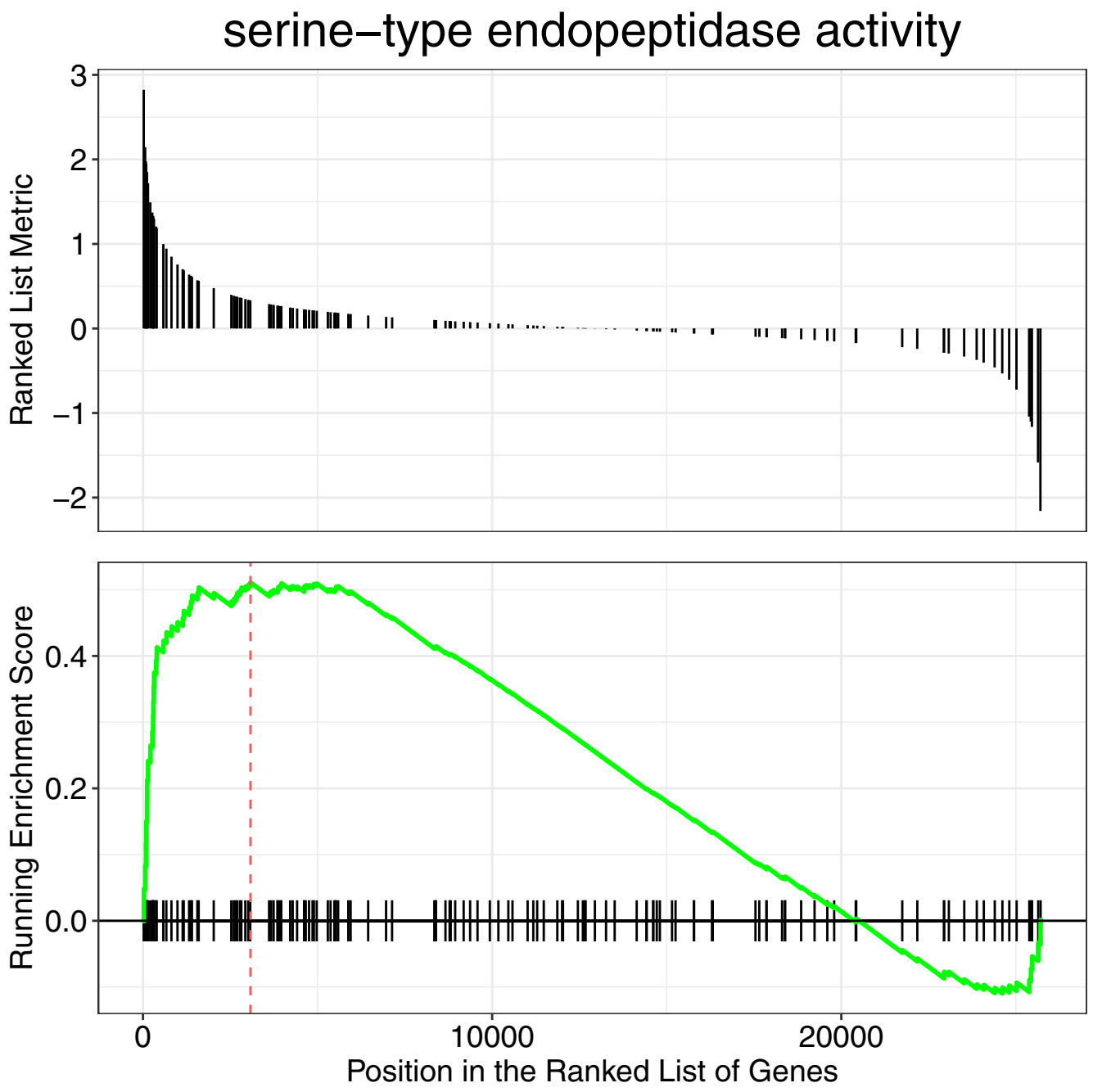

photoperiodism
Ranked List Metric
2.5
2.0
1.5
1.0
0.5
0.0
Running Enrichment Score
0.8
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

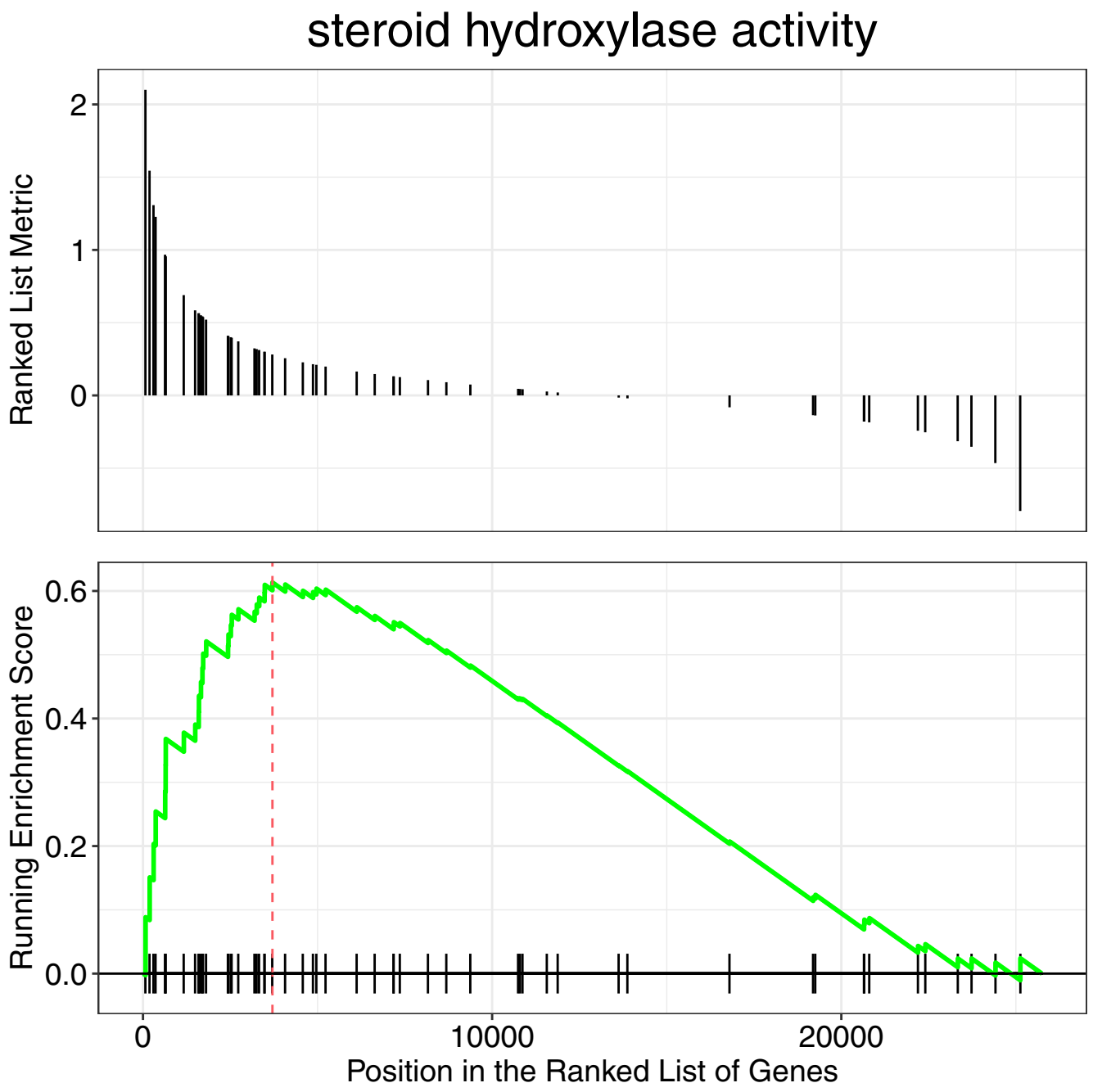

entrainment of circadian clock
Ranked List Metric
2.5
2.0
1.5
1.0
0.5
0.0
Running Enrichment Score
0.8
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

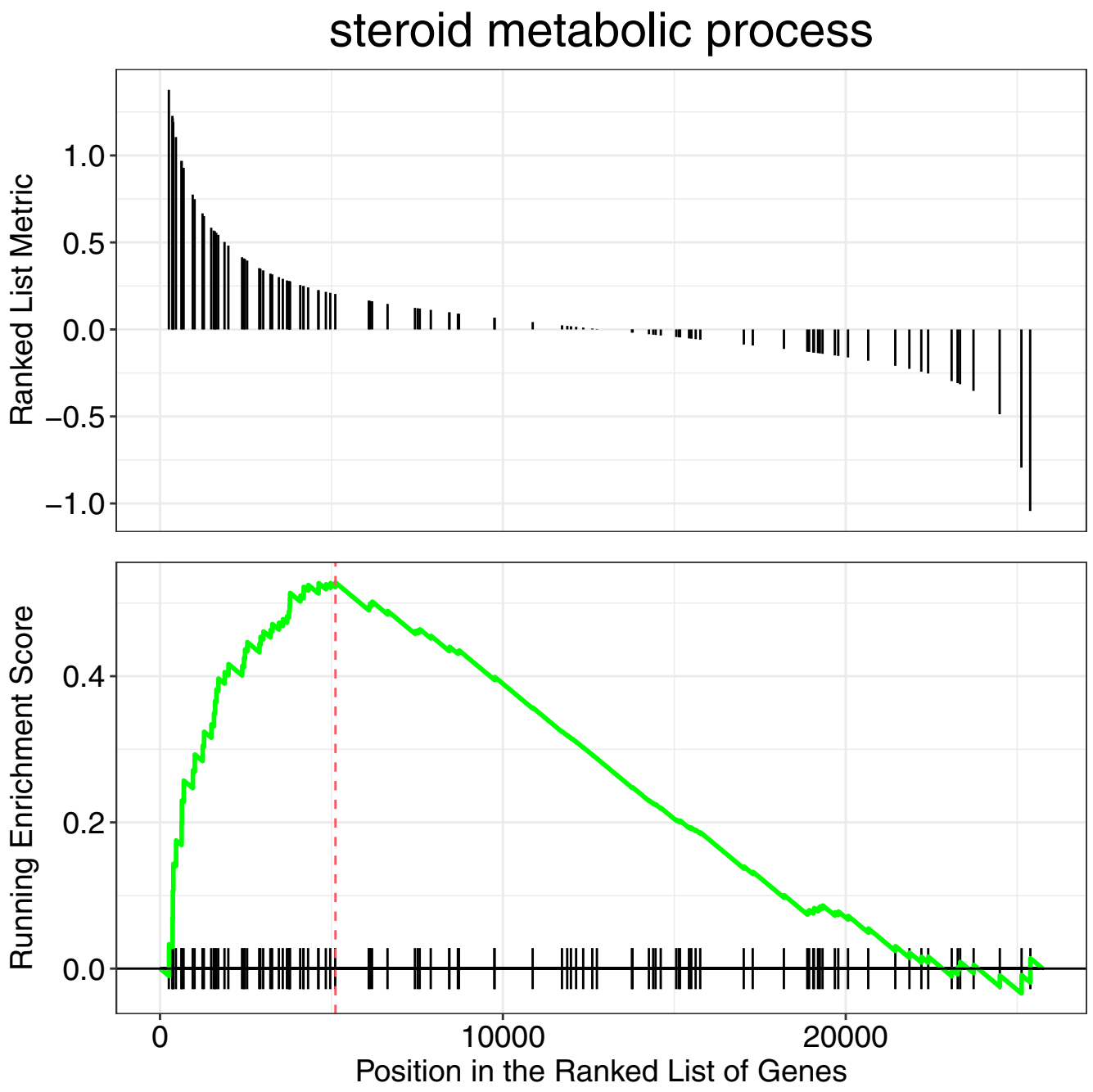

serine−type peptidase activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

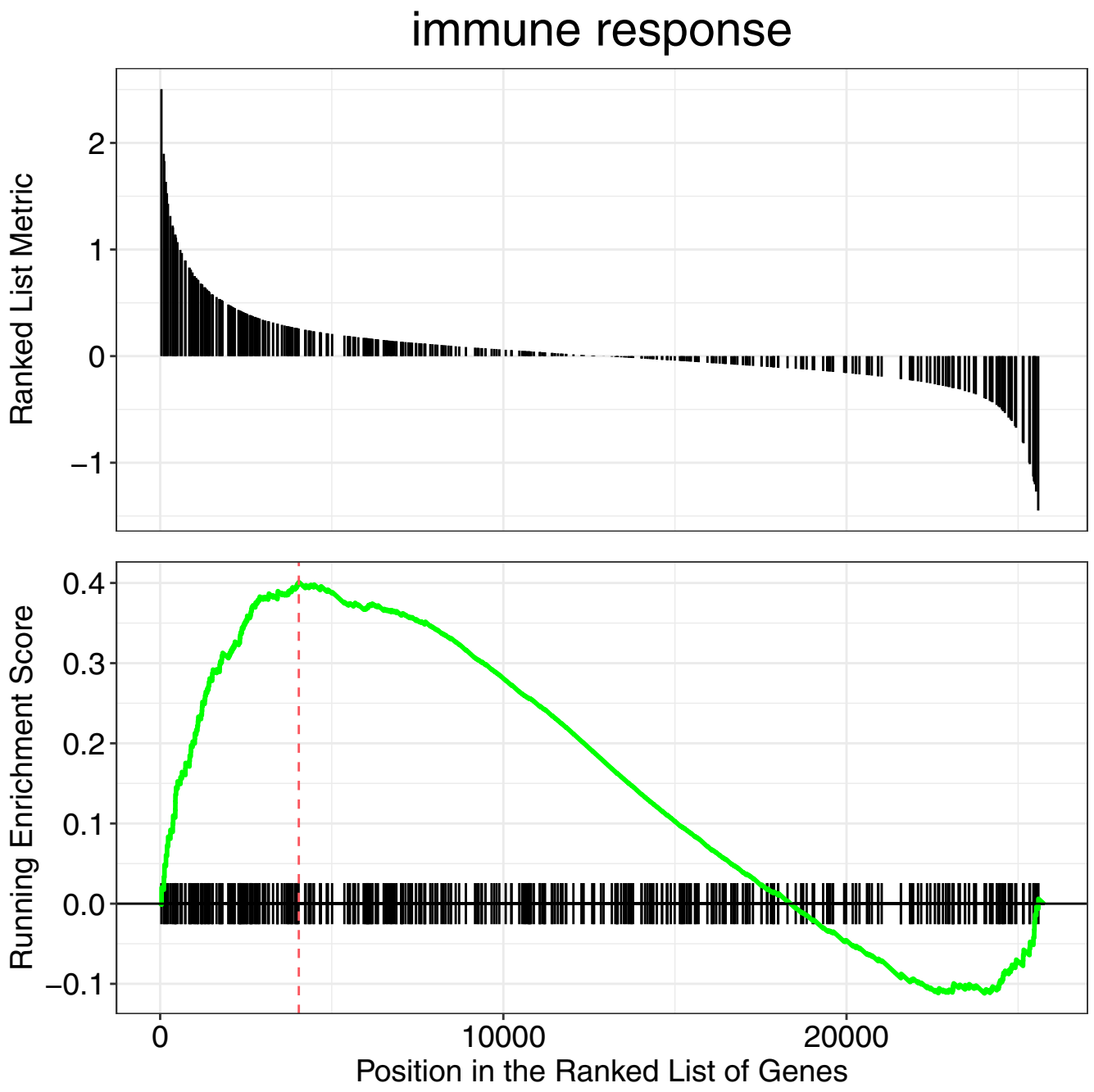

serine hydrolase activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

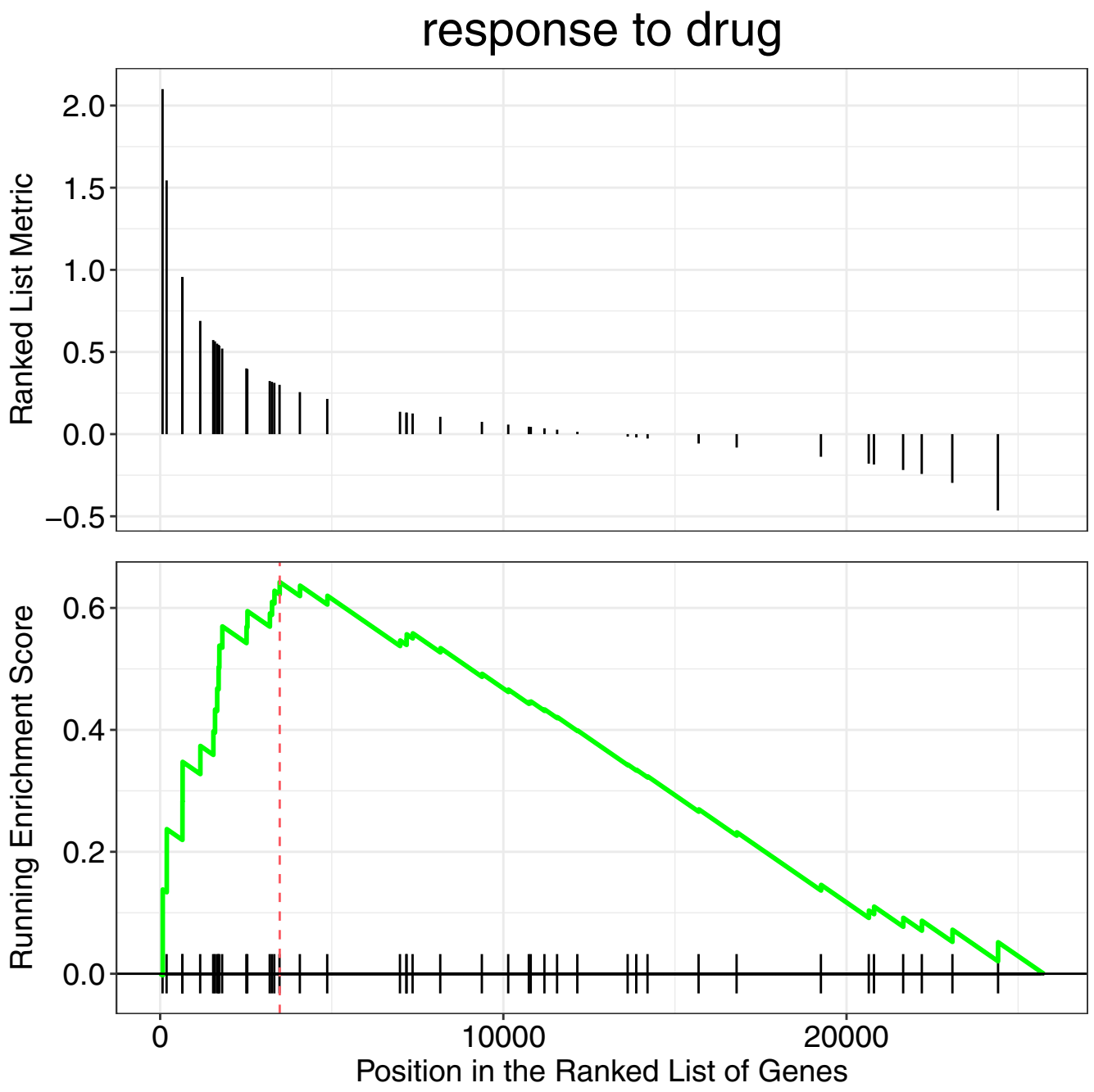

entrainment of circadian clock by photoperiod
Ranked List Metric
2.5
2.0
1.5
1.0
0.5
0.0
Running Enrichment Score
0.8
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

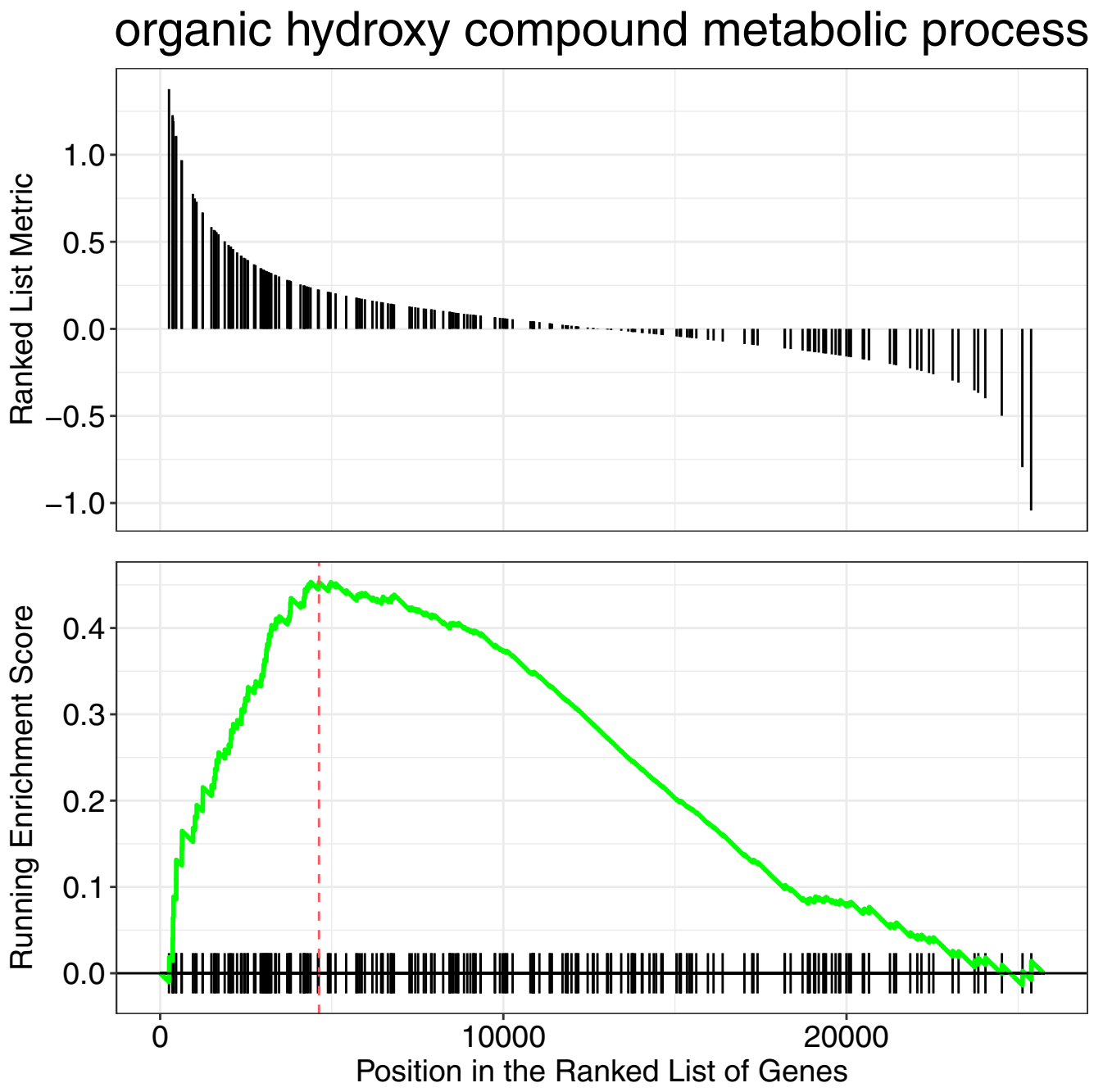

serine−type endopeptidase activity
Ranked List Metric
3
2
1
0
−1
−2
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes

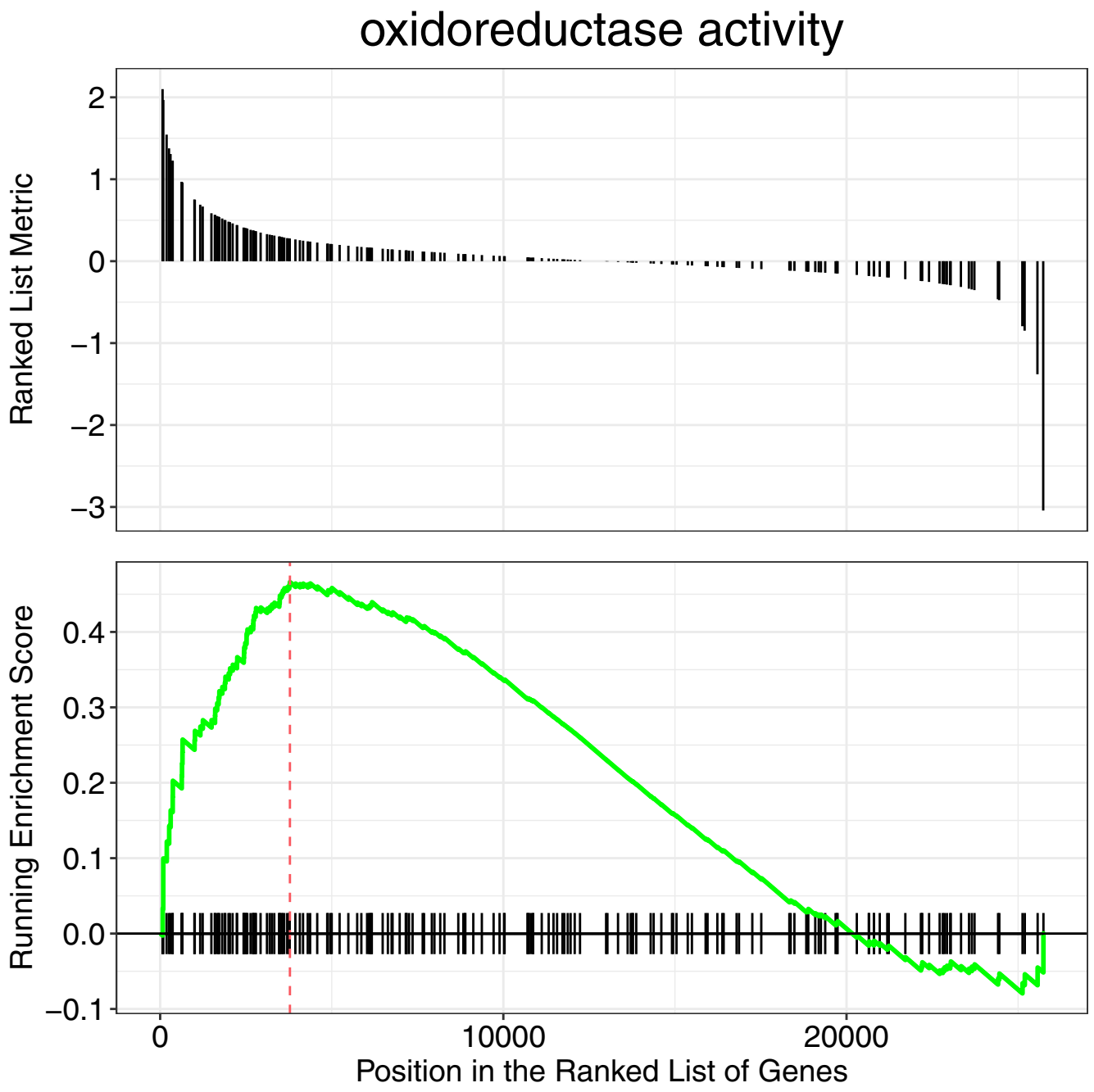

steroid hydroxylase activity
Ranked List Metric
2
1
0
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes


steroid metabolic process
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes


immune response
Ranked List Metric
2
1
0
−1
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
−0.1
0
10000
20000
Position in the Ranked List of Genes


response to drug
Ranked List Metric
2.0
1.5
1.0
0.5
0.0
−0.5
Running Enrichment Score
0.6
0.4
0.2
0.0
0
10000
20000
Position in the Ranked List of Genes


organic hydroxy compound metabolic process
Ranked List Metric
1.0
0.5
0.0
−0.5
−1.0
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
0
10000
20000
Position in the Ranked List of Genes


oxidoreductase activity
Ranked List Metric
2
1
0
−1
−2
−3
Running Enrichment Score
0.4
0.3
0.2
0.1
0.0
−0.1
0
10000
20000
Position in the Ranked List of Genes

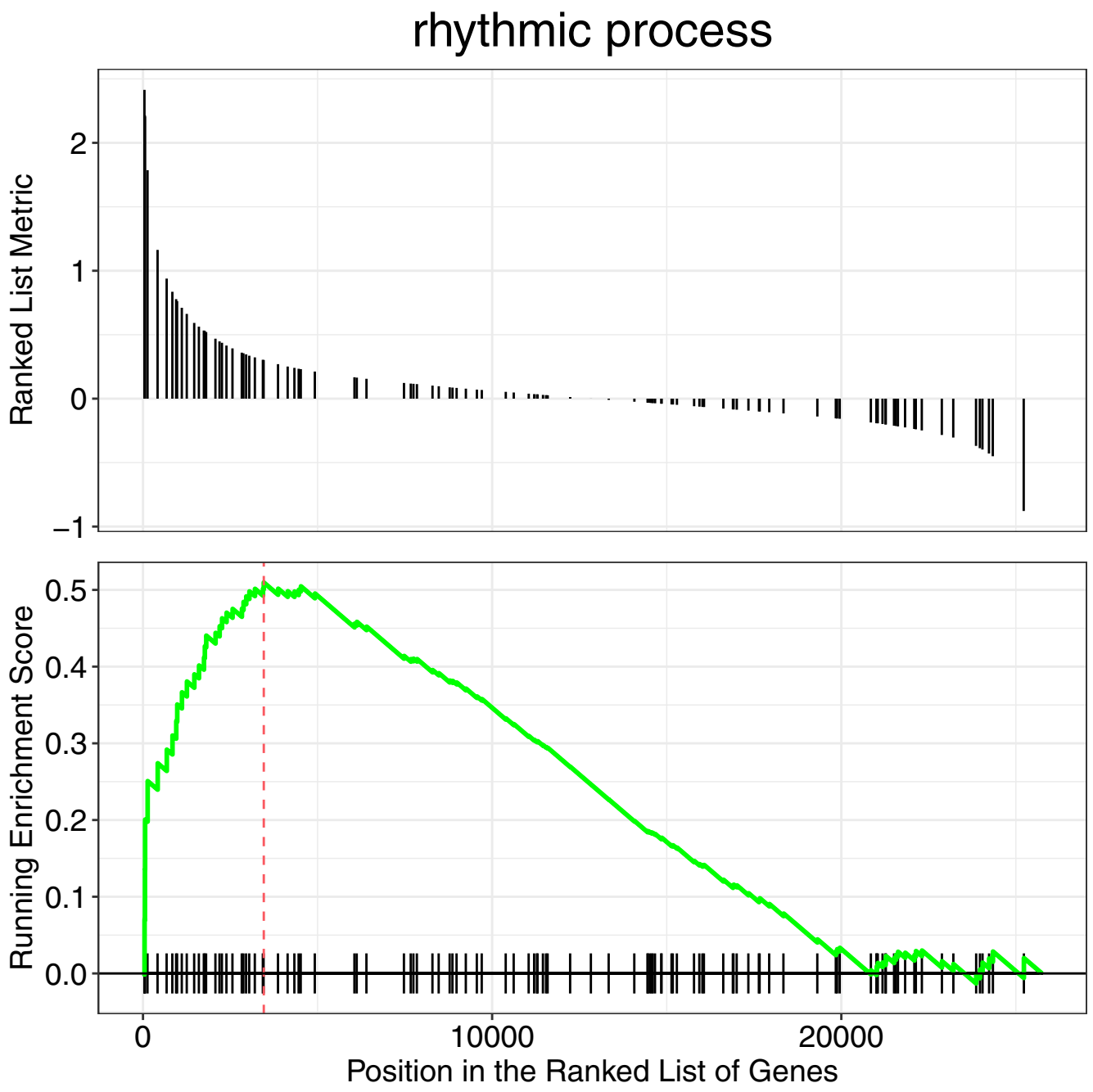


Fig. S8. Enrichment plots of Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 crispants. Running score plot and pre-ranked list of all activated GSEA terms.

Table S1. Differentially expressed genes in alx1;alx3 mutants.

All differentially expressed genes with multiple-testing adjusted p-value smaller than or equal to 0.05 in 5dpf alx1;alx3 mutants when compared to age-matched alx ^{uw2016} siblings.

Click here to download Table S1

Table S2. Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 mutants.

All enriched GO terms with multiple-testing adjusted p-value smaller than or equal to 0.05 from all differentially expressed genes in 5dpf alx1;alx3 mutants when compared to age-matched alx ^{uw2016} siblings.

Click here to download Table S2

Table S3. Differentially expressed genes in alx1;alx3 crispants. All differentially expressed genes with multiple-testing adjusted p-value smaller than or equal to 0.05 in 3dpf **alx1;alx3 crispants** when compared to age-matched wildtype embryos.

Click here to download Table S3

Table S4. Gene set enrichment analysis (GSEA) of differentially expressed genes in alx1;alx3 crispants.

All enriched GO terms with multiple-testing adjusted p-value smaller than or equal to 0.05 from all differentially expressed genes in alx1;alx3 crispants when compared to age-matched wildtype.

Click here to download Table S4