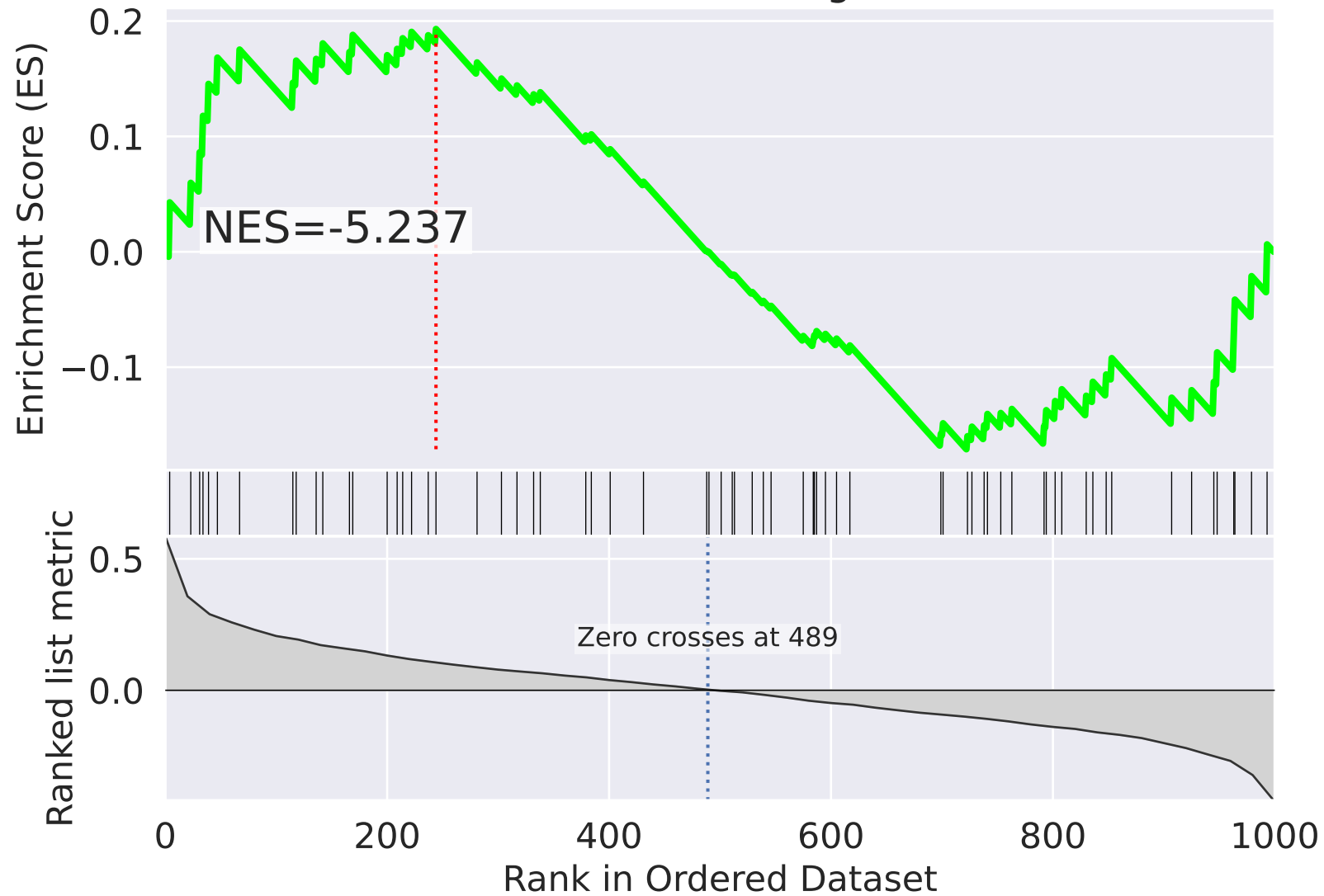
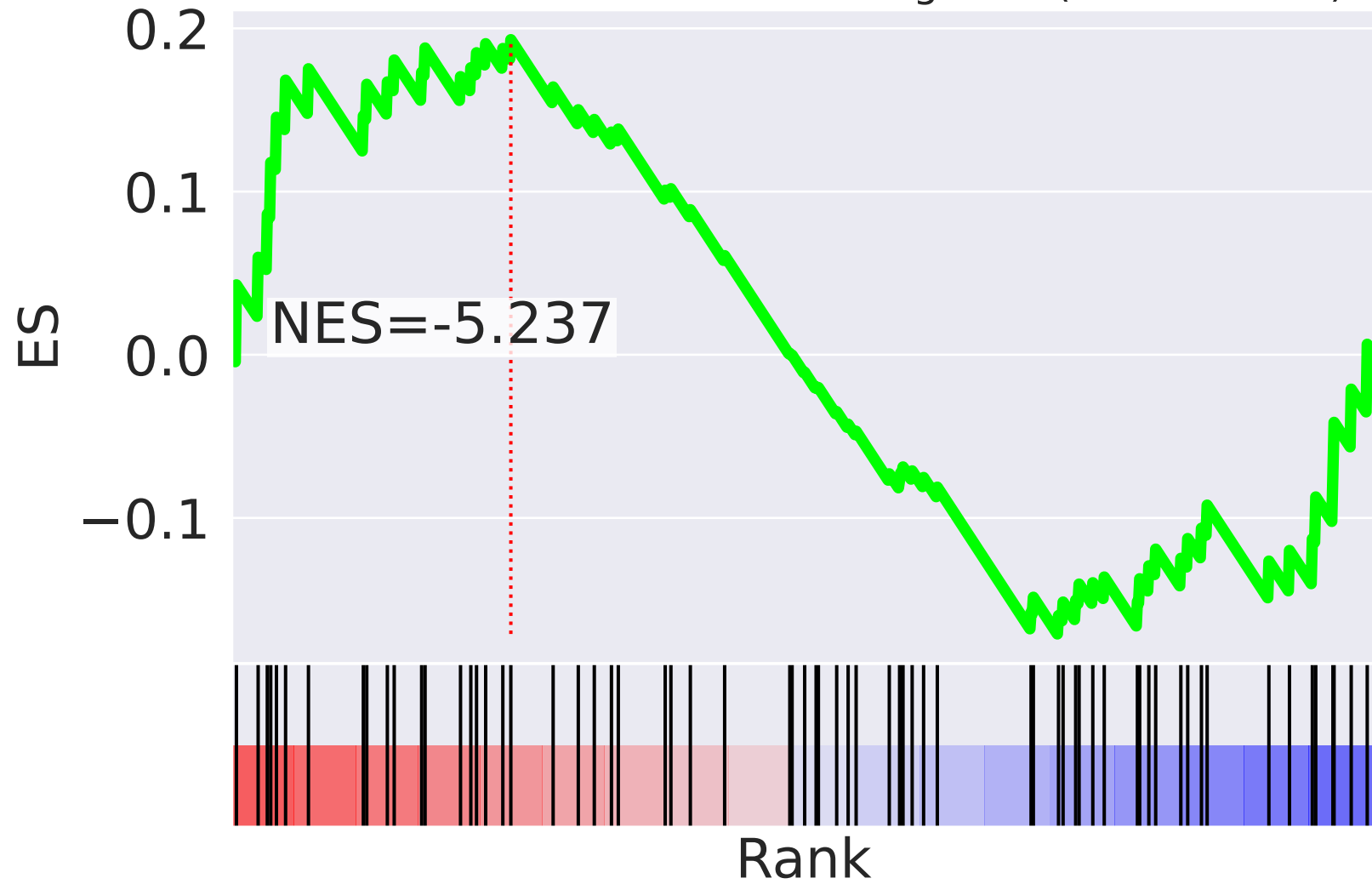


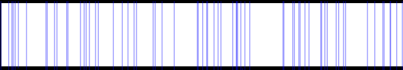
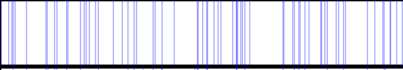
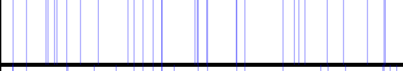

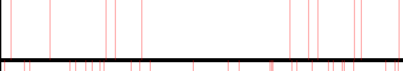
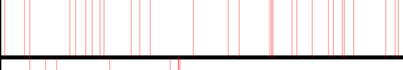
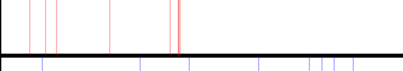

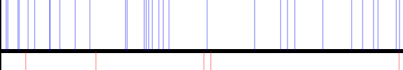
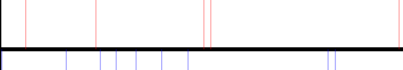

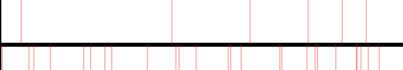
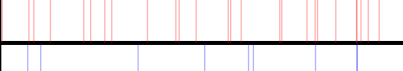
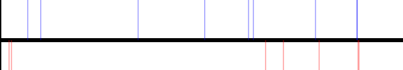
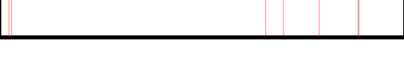
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=1$

mitochondrial translational elongation (GO:0070125)



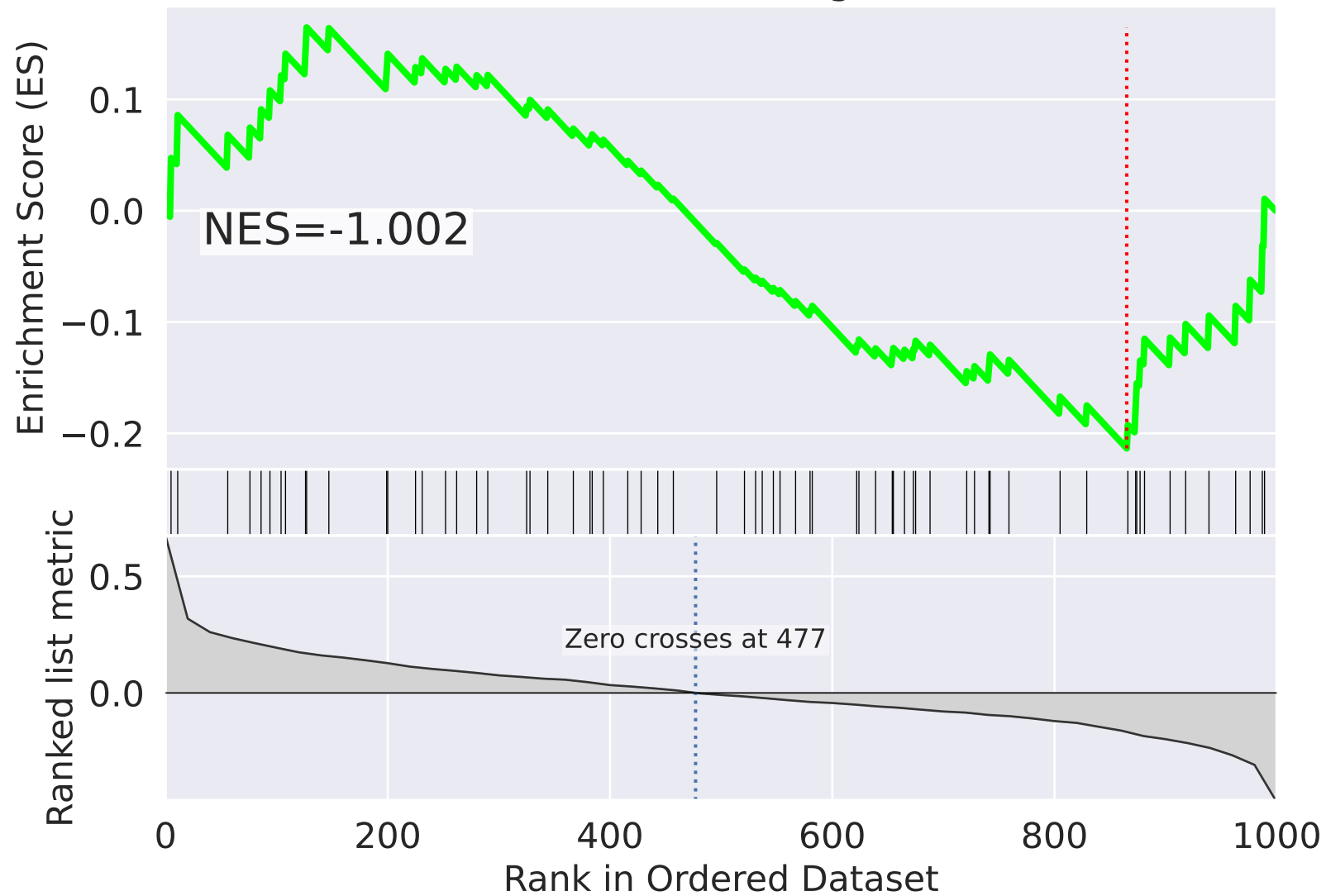
mitochondrial translational elongation (GO:0070125)



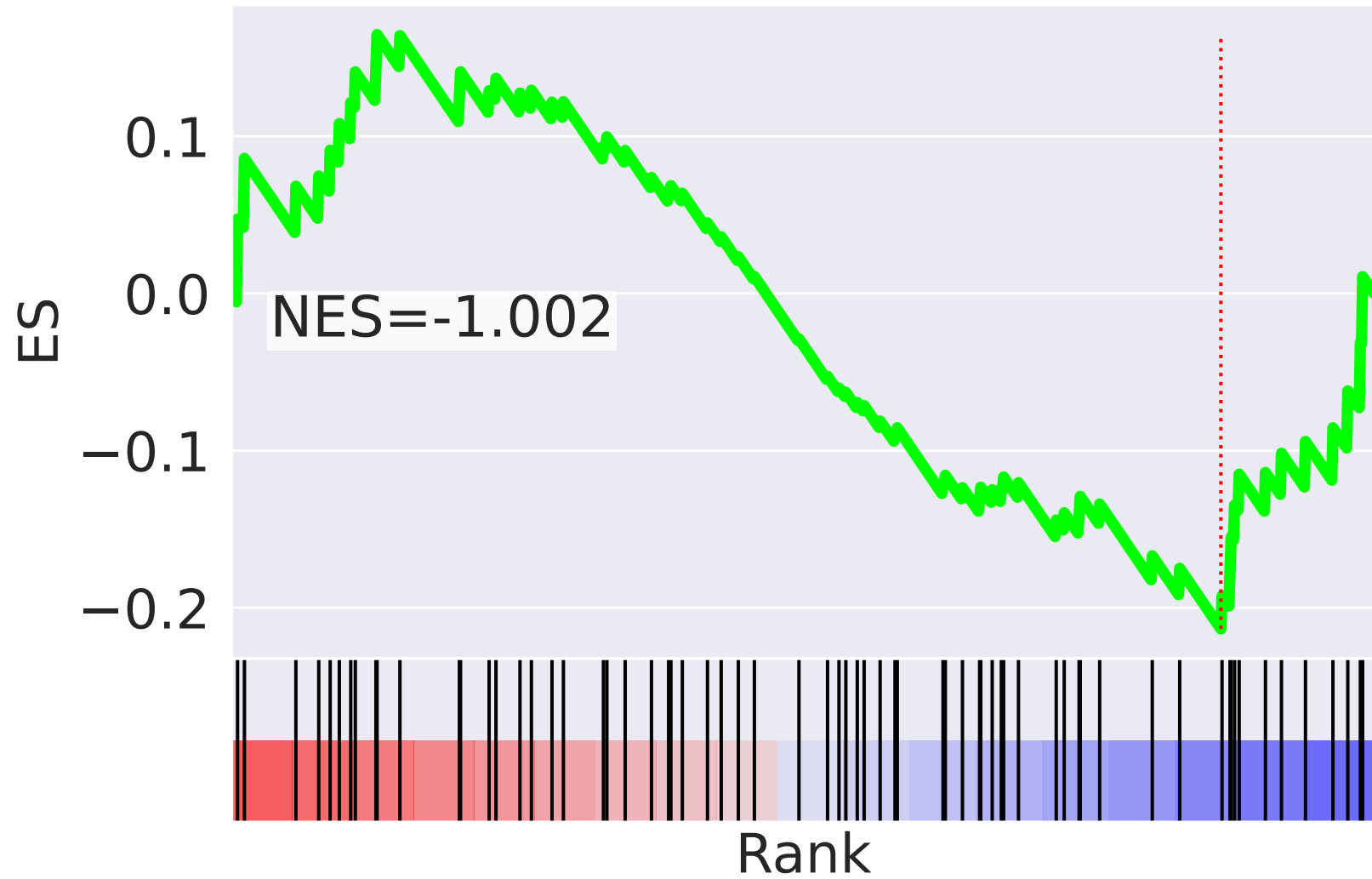
NES		SET
-5.237		mitochondrial translational elongation (GO:0070125)
-5.039		mitochondrial translational termination (GO:0070126)
-3.291		translation (GO:0006412)
-2.972		mitochondrial translation (GO:0032543)
2.677		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.676		neutrophil degranulation (GO:0043312)
2.646		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
-2.374		protein homooligomerization (GO:0051260)
-2.368		negative regulation of transcription, DNA-templated (GO:0045892)
2.263		mitotic spindle organization (GO:0007052)
-2.253		tRNA aminoacylation for protein translation (GO:0006418)
2.227		transcription-coupled nucleotide-excision repair (GO:0006283)
2.196		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.181		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.128		negative regulation of telomere maintenance via telomerase (GO:0032211)









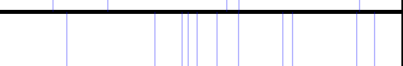



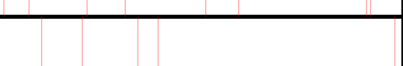
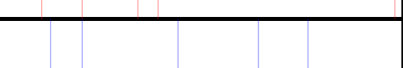
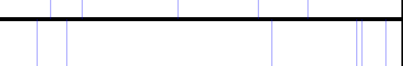
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=2$

mitochondrial translational elongation (GO:0070125)



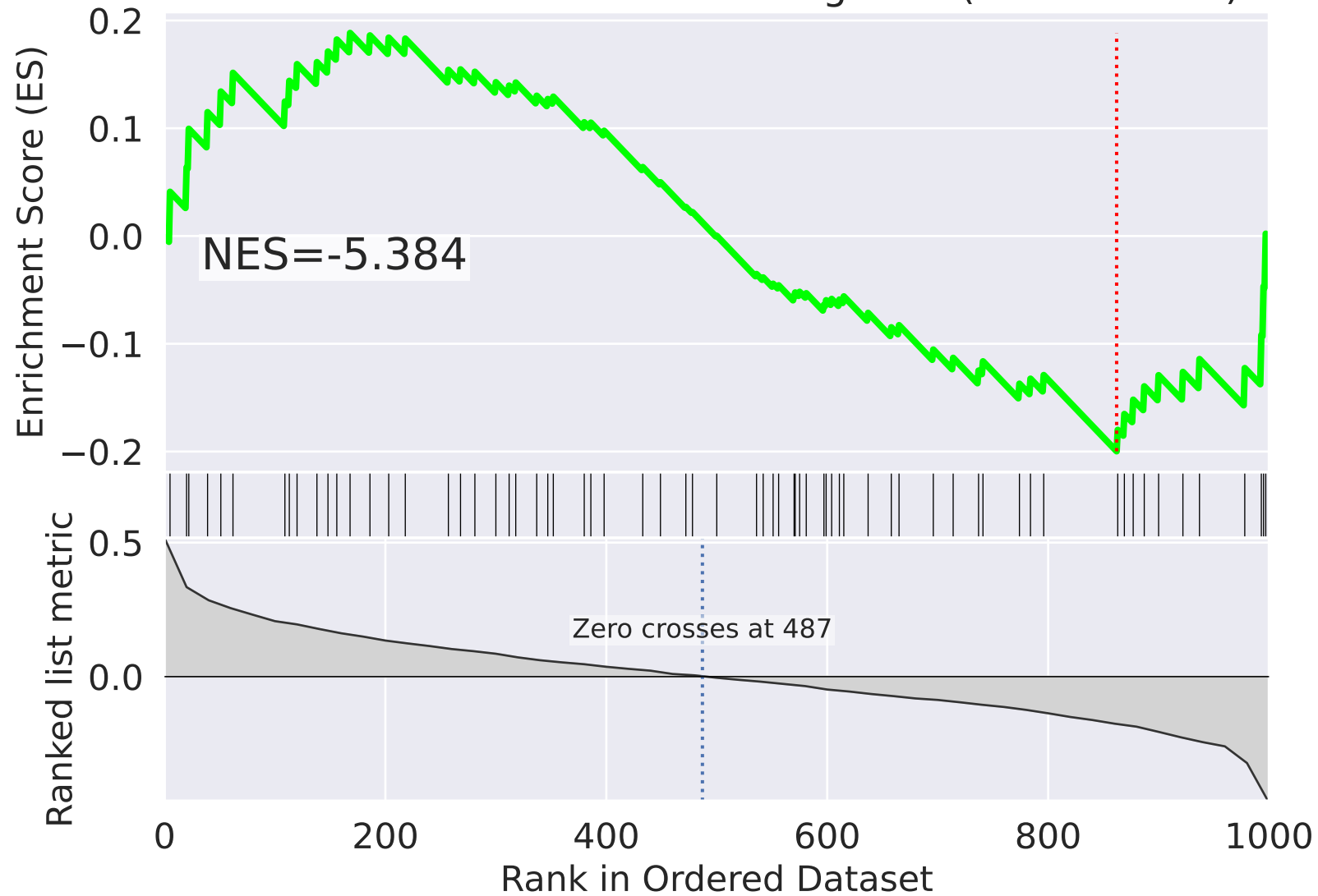
mitochondrial translational elongation (GO:0070125)



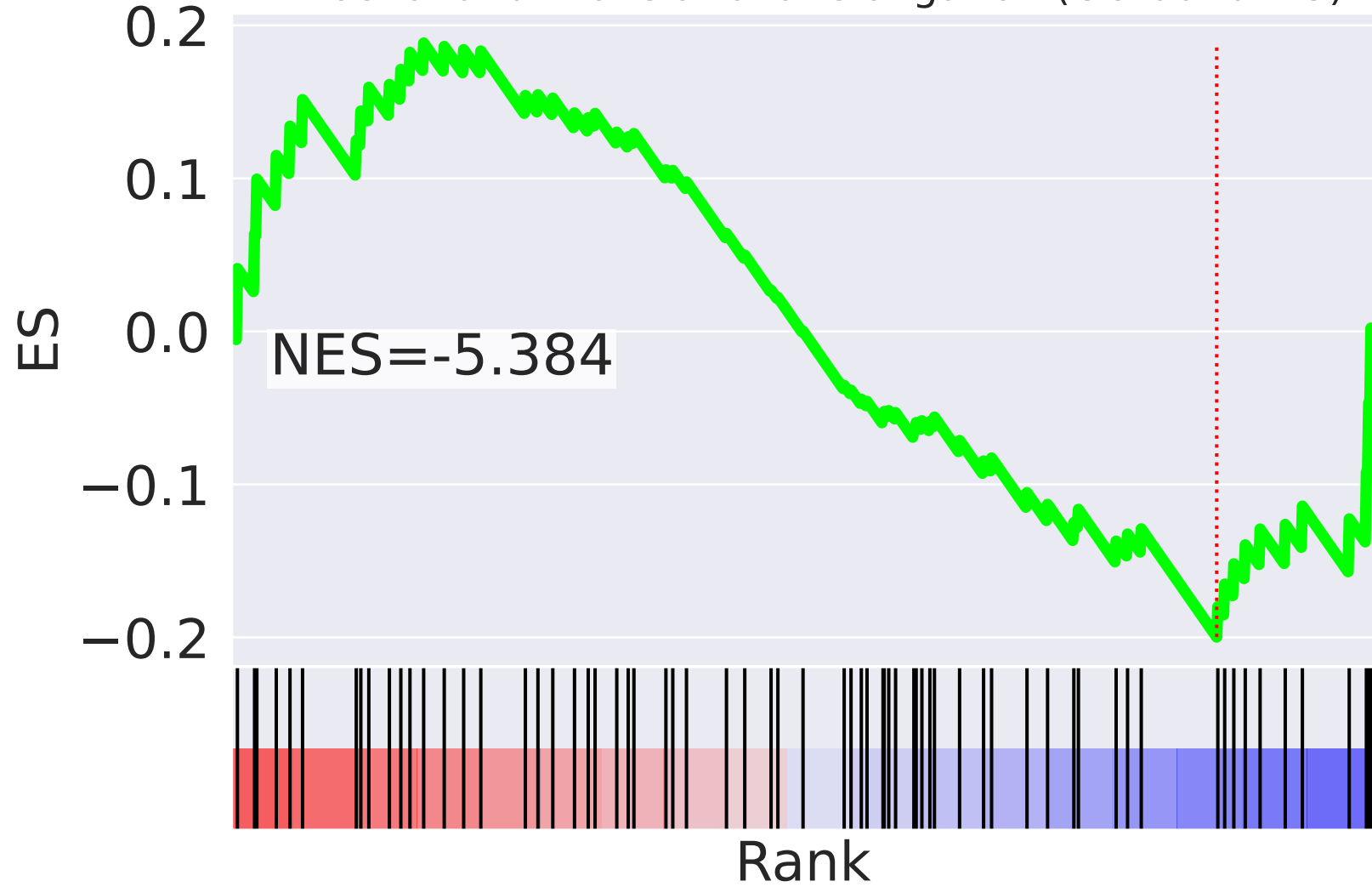
NES		SET
-3.279		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
-2.843		insulin receptor signaling pathway (GO:0008286)
-2.767		Ras protein signal transduction (GO:0007265)
2.710		regulation of mRNA stability (GO:0043488)
-2.486		regulation of cholesterol biosynthetic process (GO:0045540)
-2.464		axon guidance (GO:0007411)
-2.454		ERBB2 signaling pathway (GO:0038128)
-2.312		cholesterol biosynthetic process (GO:0006695)
-2.309		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.300		leukocyte migration (GO:0050900)
-2.293		response to endoplasmic reticulum stress (GO:0034976)
2.213		regulation of apoptotic process (GO:0042981)
2.188		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
-2.160		positive regulation of mitotic cell cycle (GO:0045931)
-2.135		fibroblast growth factor receptor signaling pathway (GO:0008543)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=3$

mitochondrial translational elongation (GO:0070125)

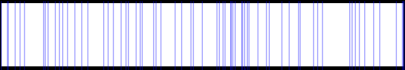
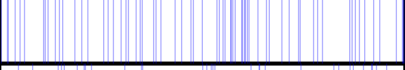

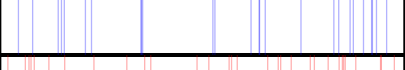
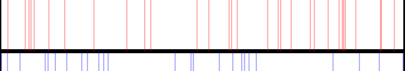
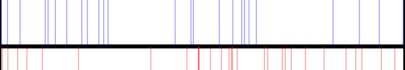
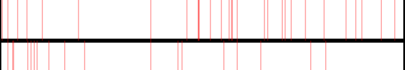

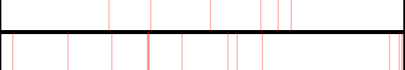
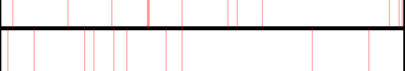
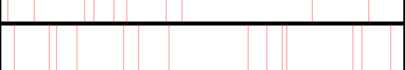

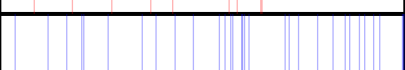




mitochondrial translational elongation (GO:0070125)



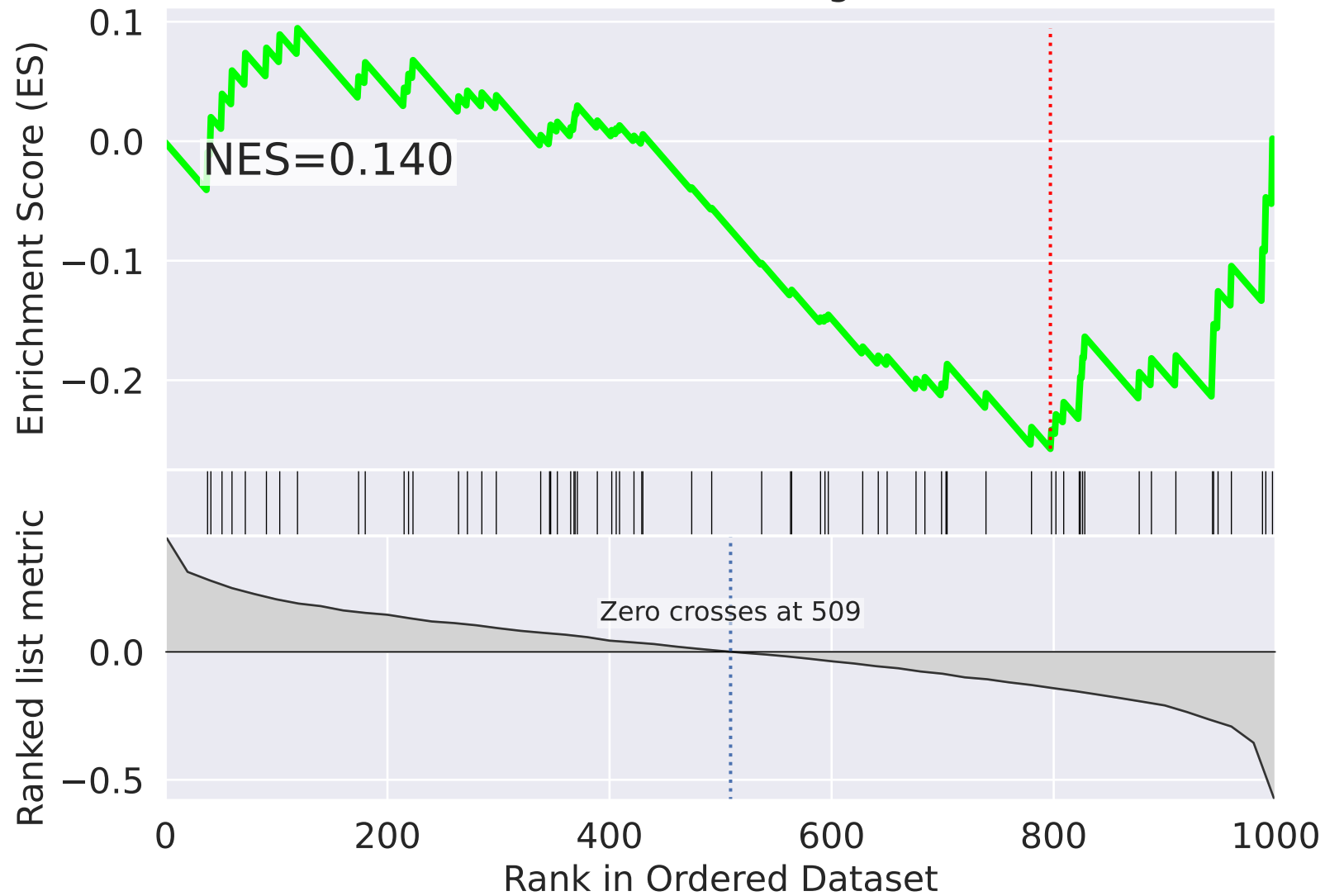
NES

SET

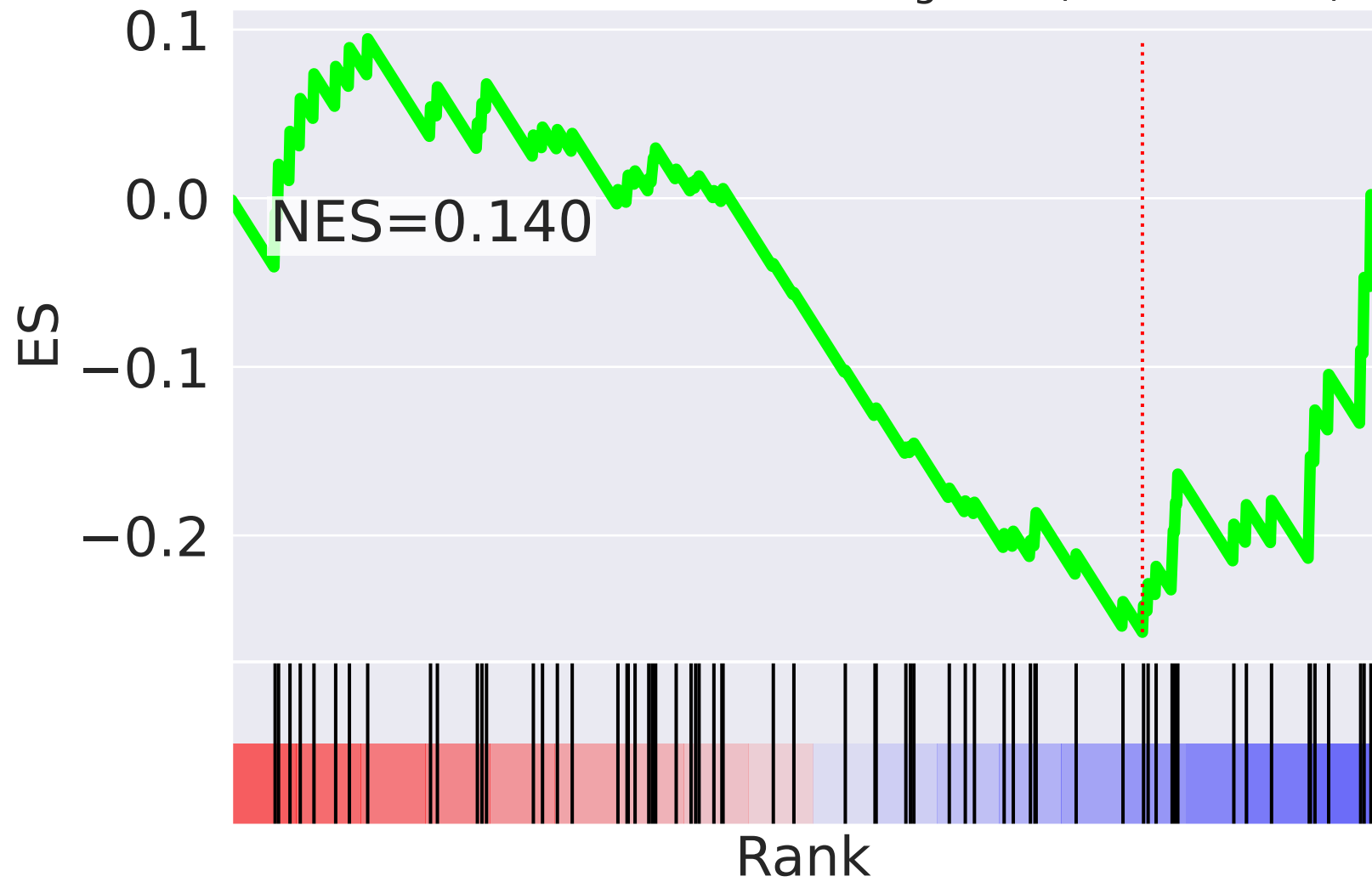
-5.384		mitochondrial translational elongation (GO:0070125)
-5.241		mitochondrial translational termination (GO:0070126)
-4.313		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.127		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.475		positive regulation of cell proliferation (GO:0008284)
-3.259		mitochondrial translation (GO:0032543)
3.103		negative regulation of apoptotic process (GO:0043066)
3.033		MAPK cascade (GO:0000165)
2.968		positive regulation of cell growth (GO:0030307)
2.896		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.860		Ras protein signal transduction (GO:0007265)
2.834		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.782		positive regulation of protein phosphorylation (GO:0001934)
-2.780		translation (GO:0006412)
2.760		endosomal transport (GO:0016197)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=4$

mitochondrial translational elongation (GO:0070125)



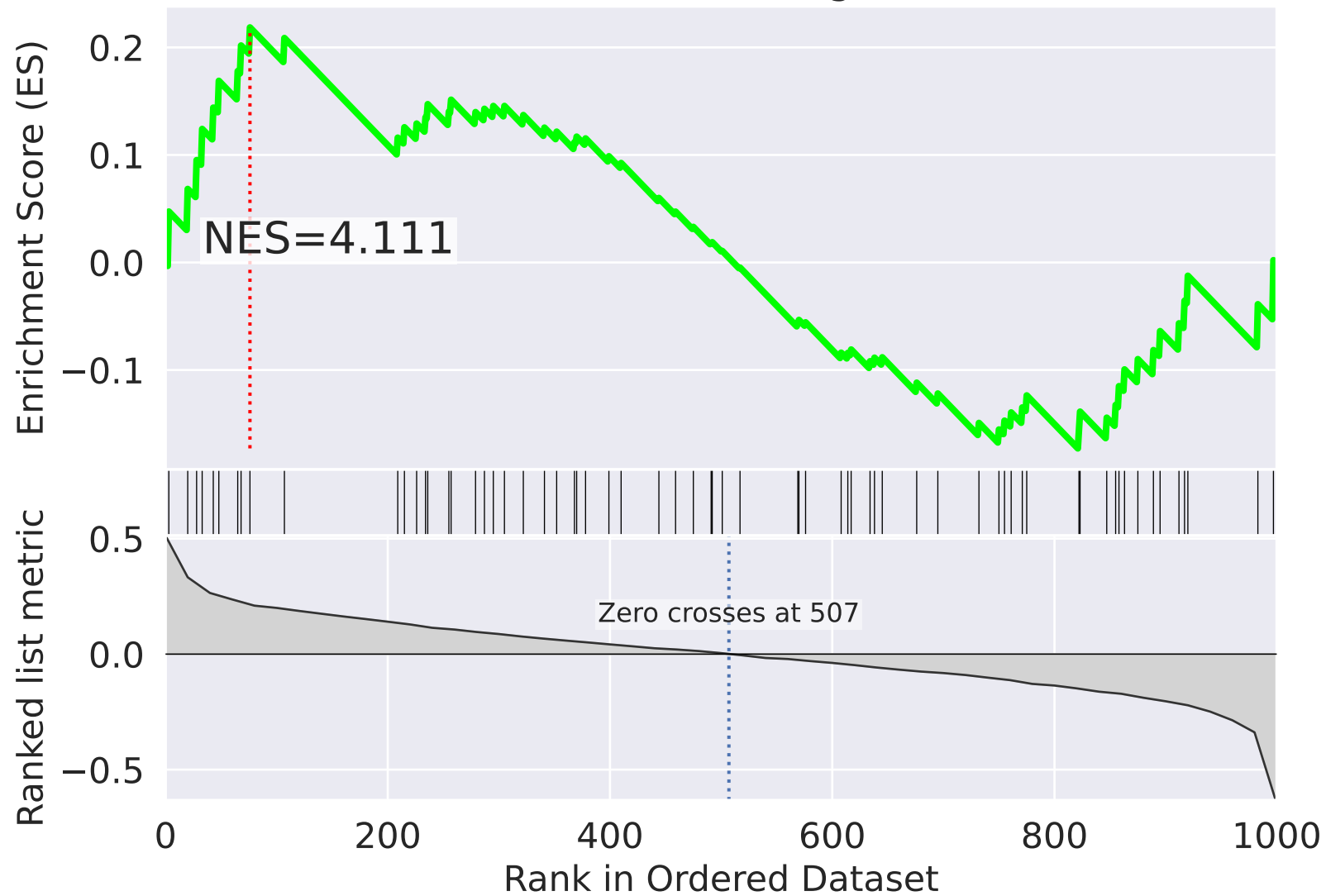
mitochondrial translational elongation (GO:0070125)



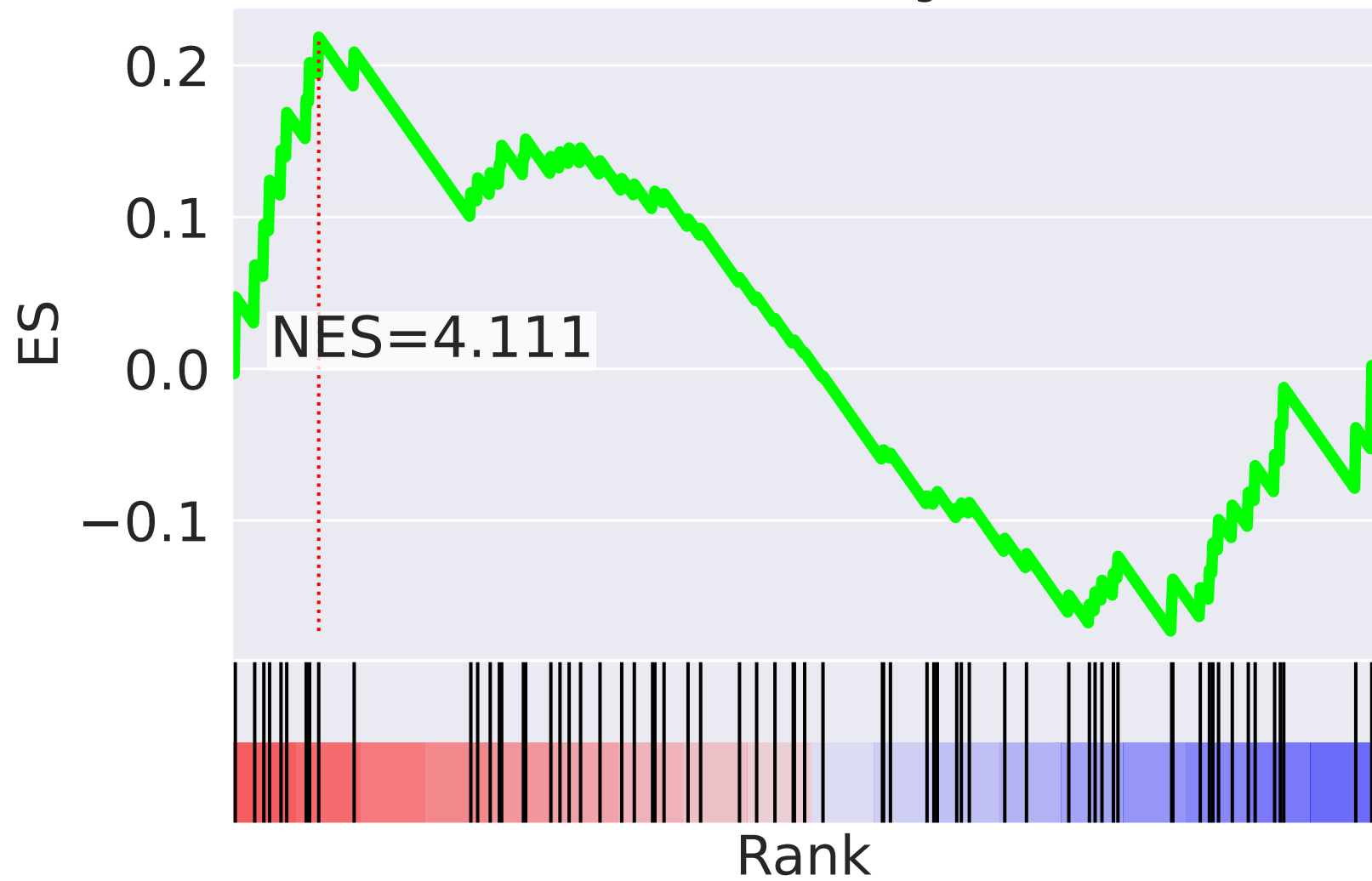
NES		SET
-3.332		membrane organization (GO:0061024)
2.962		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.839		mitotic cell cycle (GO:0000278)
2.735		mitotic cytokinesis (GO:0000281)
2.721		mitotic metaphase plate congression (GO:0007080)
-2.661		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.620		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-2.429		regulation of cholesterol biosynthetic process (GO:0045540)
-2.388		protein autophosphorylation (GO:0046777)
2.366		mRNA splicing, via spliceosome (GO:0000398)
2.303		chromosome segregation (GO:0007059)
2.251		DNA replication (GO:0006260)
2.238		intrinsic apoptotic signaling pathway (GO:0097193)
2.209		tRNA modification (GO:0006400)
2.196		sister chromatid cohesion (GO:0007062)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=5$

mitochondrial translational elongation (GO:0070125)

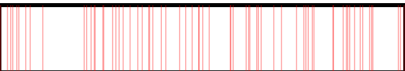



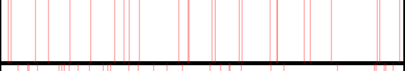
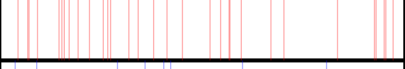






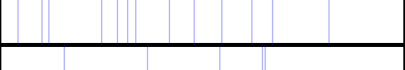




mitochondrial translational elongation (GO:0070125)



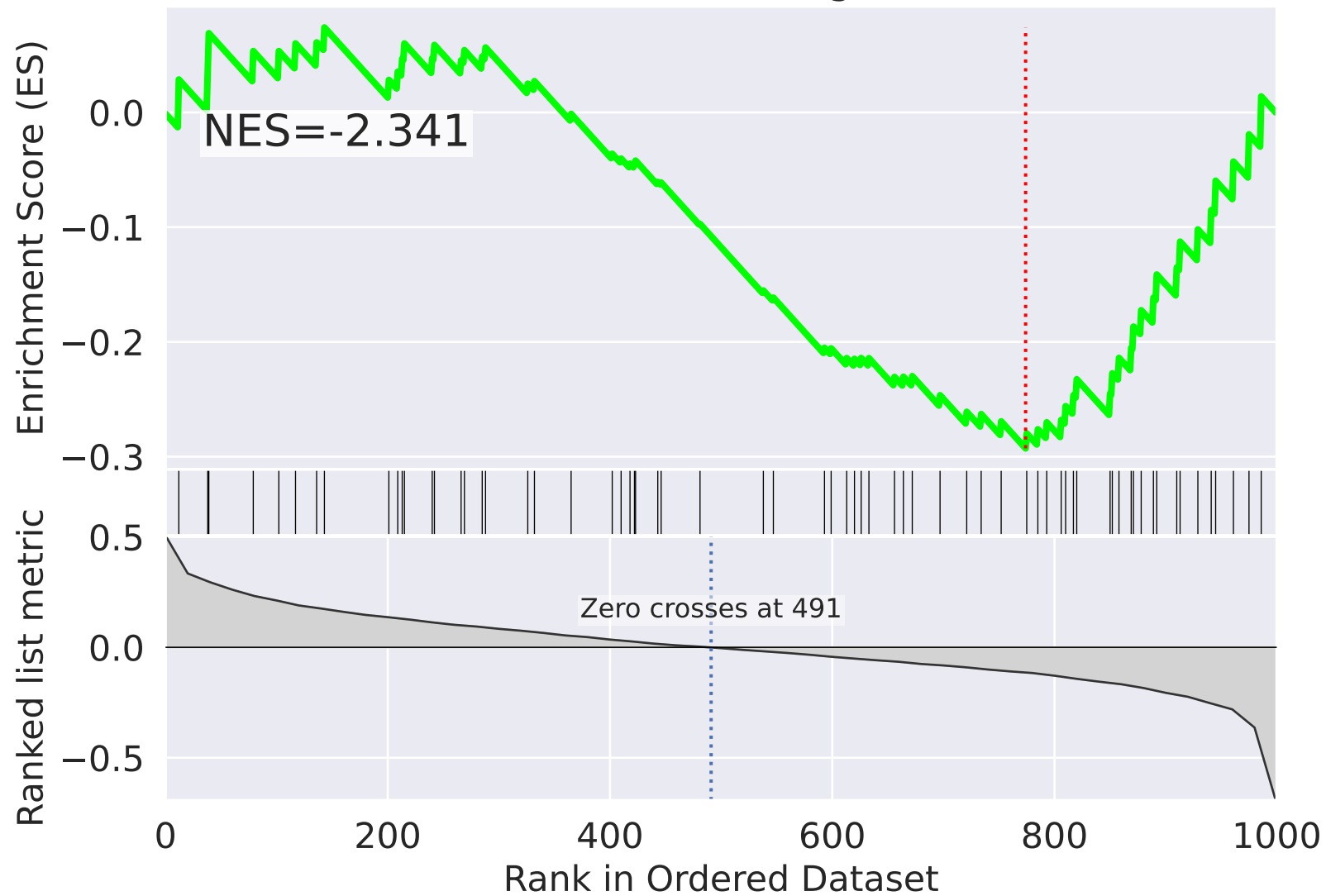
NES

SET

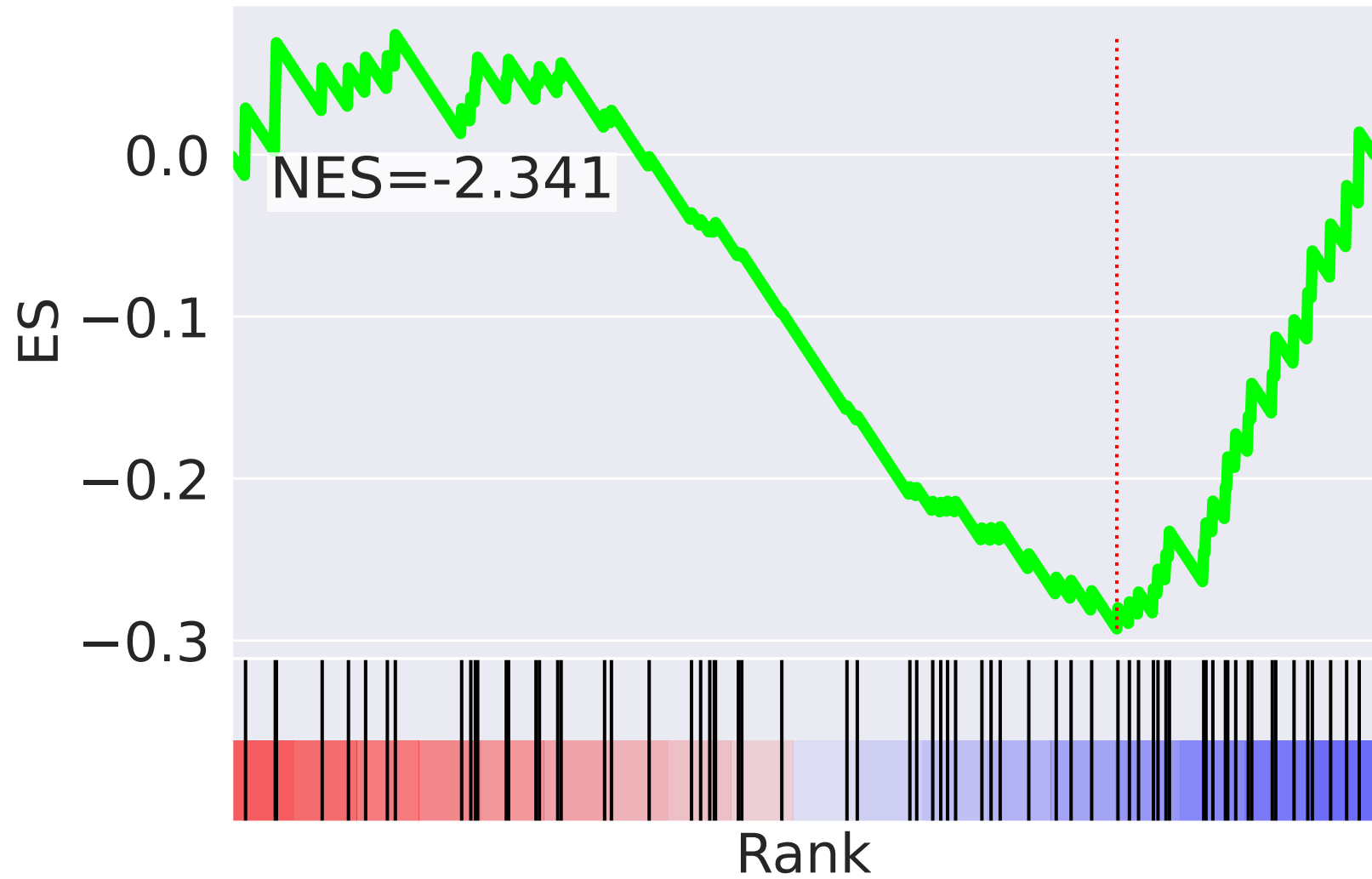
4.189		mitochondrial translational termination (GO:0070126)
4.111		mitochondrial translational elongation (GO:0070125)
-3.523		positive regulation of cell proliferation (GO:0008284)
3.130		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.068		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.897		protein deubiquitination (GO:0016579)
-2.759		protein autophosphorylation (GO:0046777)
-2.749		signal transduction (GO:0007165)
-2.698		positive regulation of cell migration (GO:0030335)
-2.617		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.578		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.557		movement of cell or subcellular component (GO:0006928)
-2.556		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.493		protein K63-linked ubiquitination (GO:0070534)
-2.465		vascular endothelial growth factor receptor signaling pathway (GO:0048010)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=6$

mitochondrial translational elongation (GO:0070125)



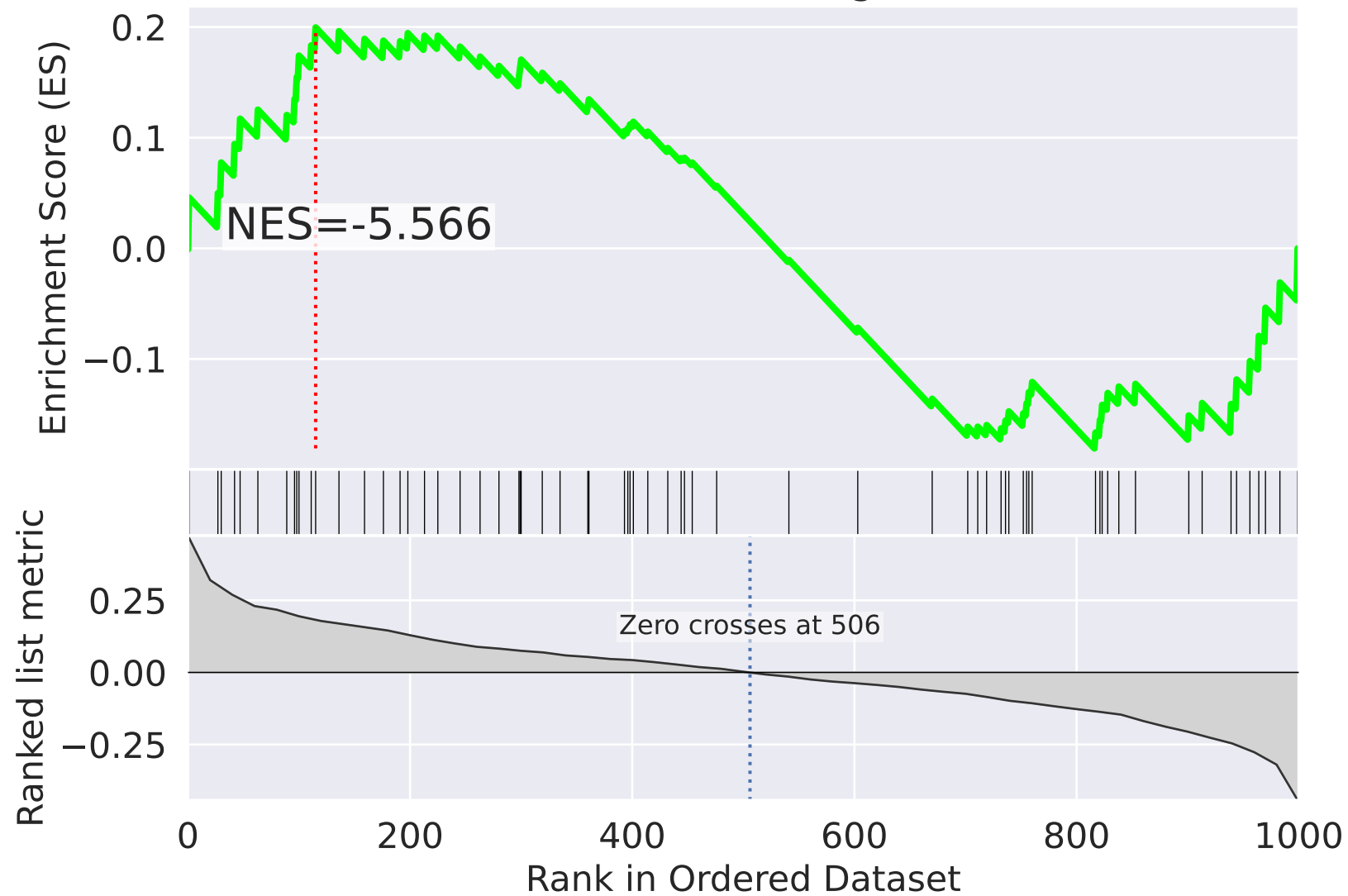
mitochondrial translational elongation (GO:0070125)



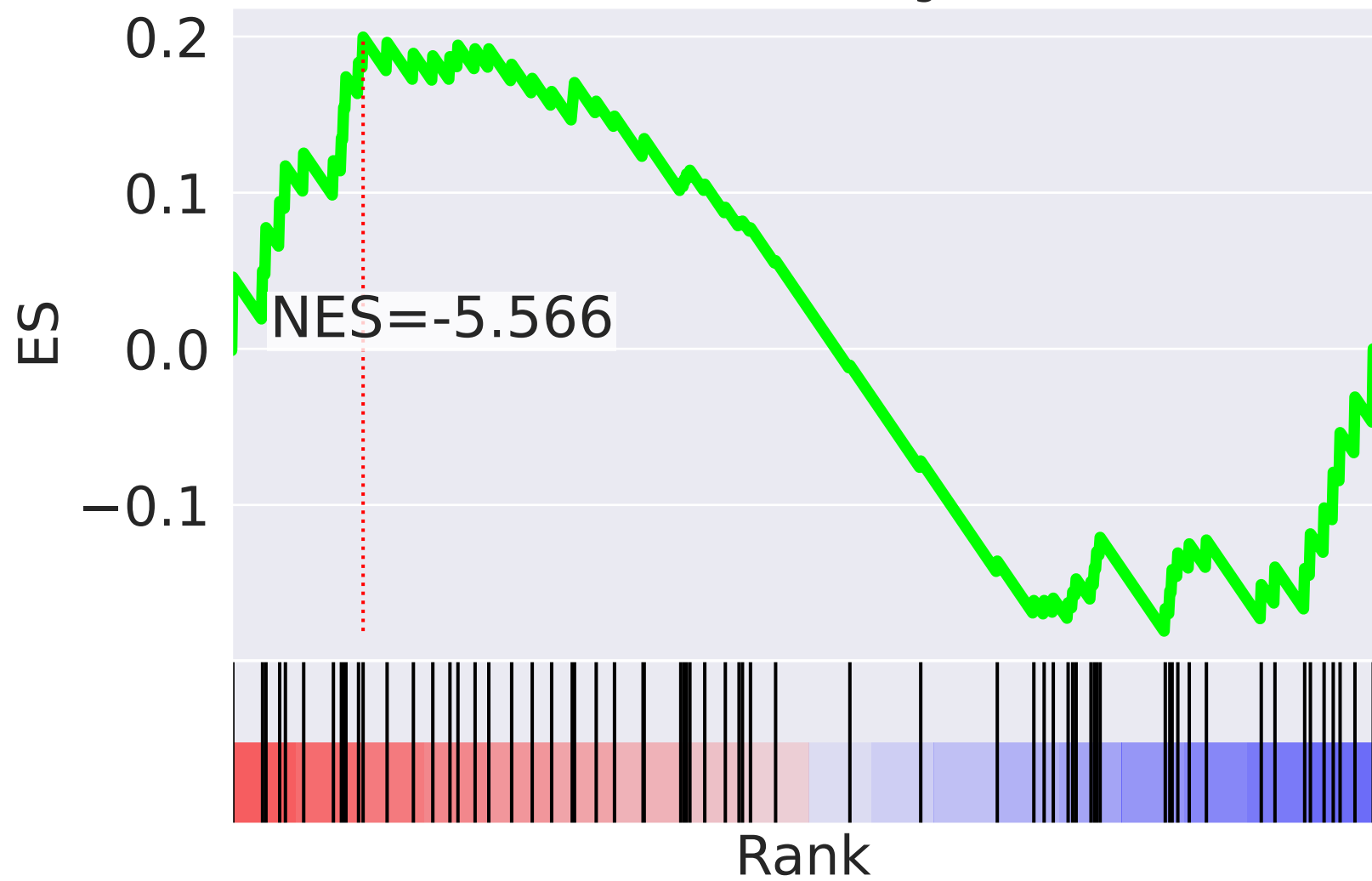
NES		SET
-3.442		tricarboxylic acid cycle (GO:0006099)
-3.180		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.613		DNA repair (GO:0006281)
2.601		integrin-mediated signaling pathway (GO:0007229)
2.466		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.425		cellular nitrogen compound metabolic process (GO:0034641)
-2.346		membrane organization (GO:0061024)
-2.341		mitochondrial translational elongation (GO:0070125)
-2.310		androgen receptor signaling pathway (GO:0030521)
-2.284		retrograde transport, endosome to Golgi (GO:0042147)
-2.204		tRNA aminoacylation for protein translation (GO:0006418)
2.185		protein K63-linked ubiquitination (GO:0070534)
2.167		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.152		transforming growth factor beta receptor signaling pathway (GO:0007179)
2.151		protein autoubiquitination (GO:0051865)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=7$

mitochondrial translational elongation (GO:0070125)

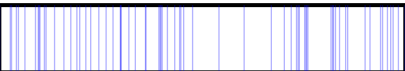
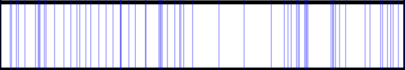
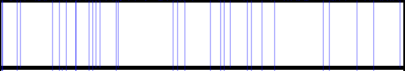
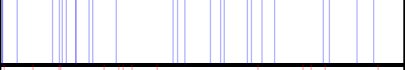


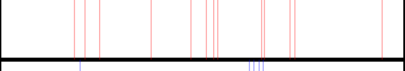
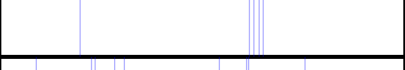

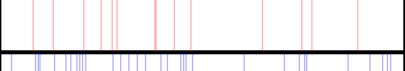
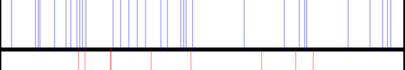
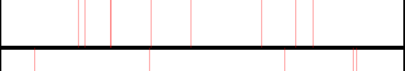
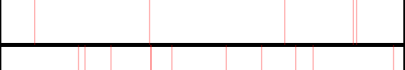




mitochondrial translational elongation (GO:0070125)



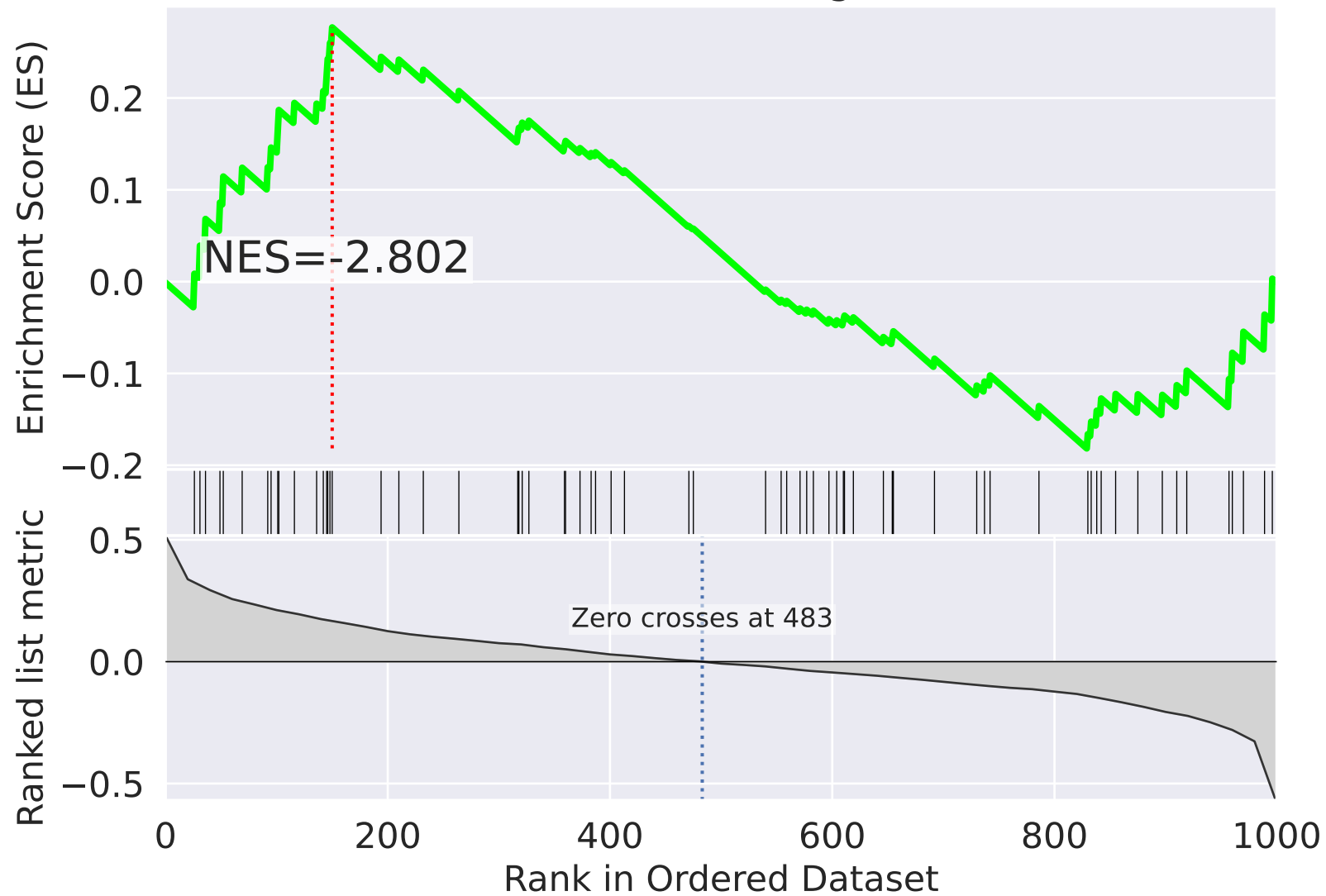
NES

SET

-5.744		mitochondrial translational termination (GO:0070126)
-5.566		mitochondrial translational elongation (GO:0070125)
-4.183		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.861		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.765		sister chromatid cohesion (GO:0007062)
2.562		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.486		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.421		nucleosome disassembly (GO:0006337)
-2.420		regulation of macroautophagy (GO:0016241)
2.382		regulation of cellular response to heat (GO:1900034)
-2.353		translation (GO:0006412)
2.327		axon guidance (GO:0007411)
2.325		cytokinesis (GO:0000910)
2.252		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.235		endosomal transport (GO:0016197)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=8$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1

0.0

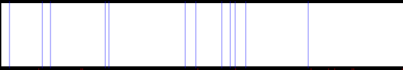



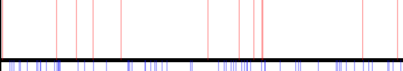
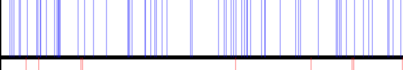

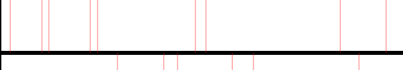


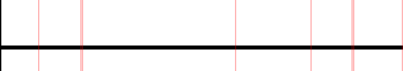

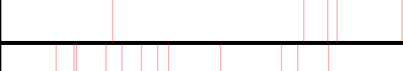
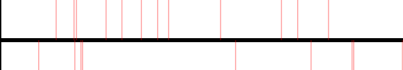

-0.1

-0.2

NES=-2.802

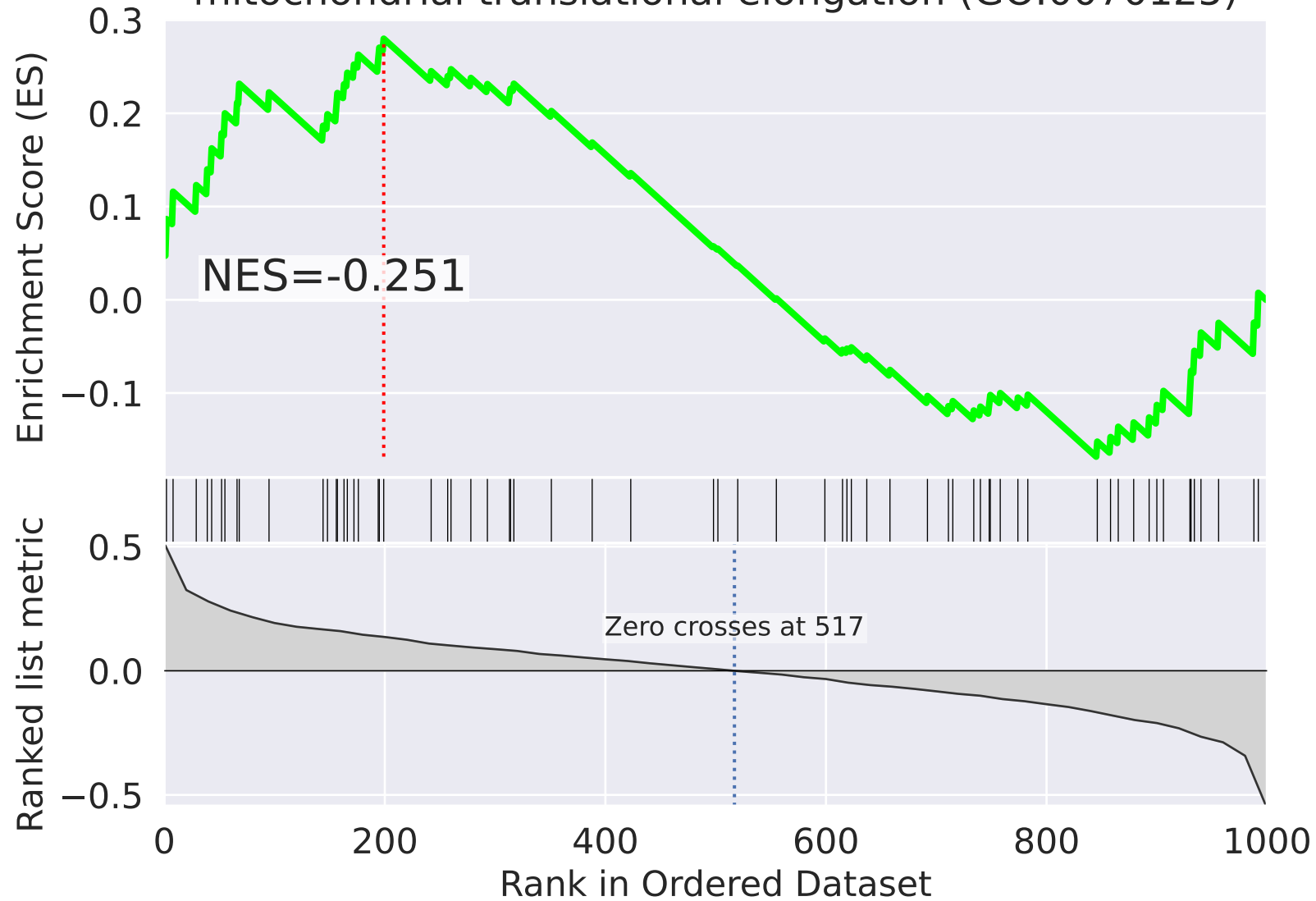
Rank



NES		SET
-3.194		regulation of cholesterol biosynthetic process (GO:0045540)
3.068		mitotic nuclear envelope disassembly (GO:0007077)
3.010		rRNA processing (GO:0006364)
-2.955		histone H3 acetylation (GO:0043966)
2.876		mitotic cell cycle (GO:0000278)
-2.802		mitochondrial translational elongation (GO:0070125)
2.703		protein sumoylation (GO:0016925)
2.687		double-strand break repair (GO:0006302)
2.648		platelet aggregation (GO:0070527)
2.645		tRNA export from nucleus (GO:0006409)
2.645		regulation of glucose transport (GO:0010827)
2.645		regulation of gene silencing by miRNA (GO:0060964)
2.628		telomere capping (GO:0016233)
2.611		mitotic metaphase plate congression (GO:0007080)
2.602		intracellular transport of virus (GO:0075733)

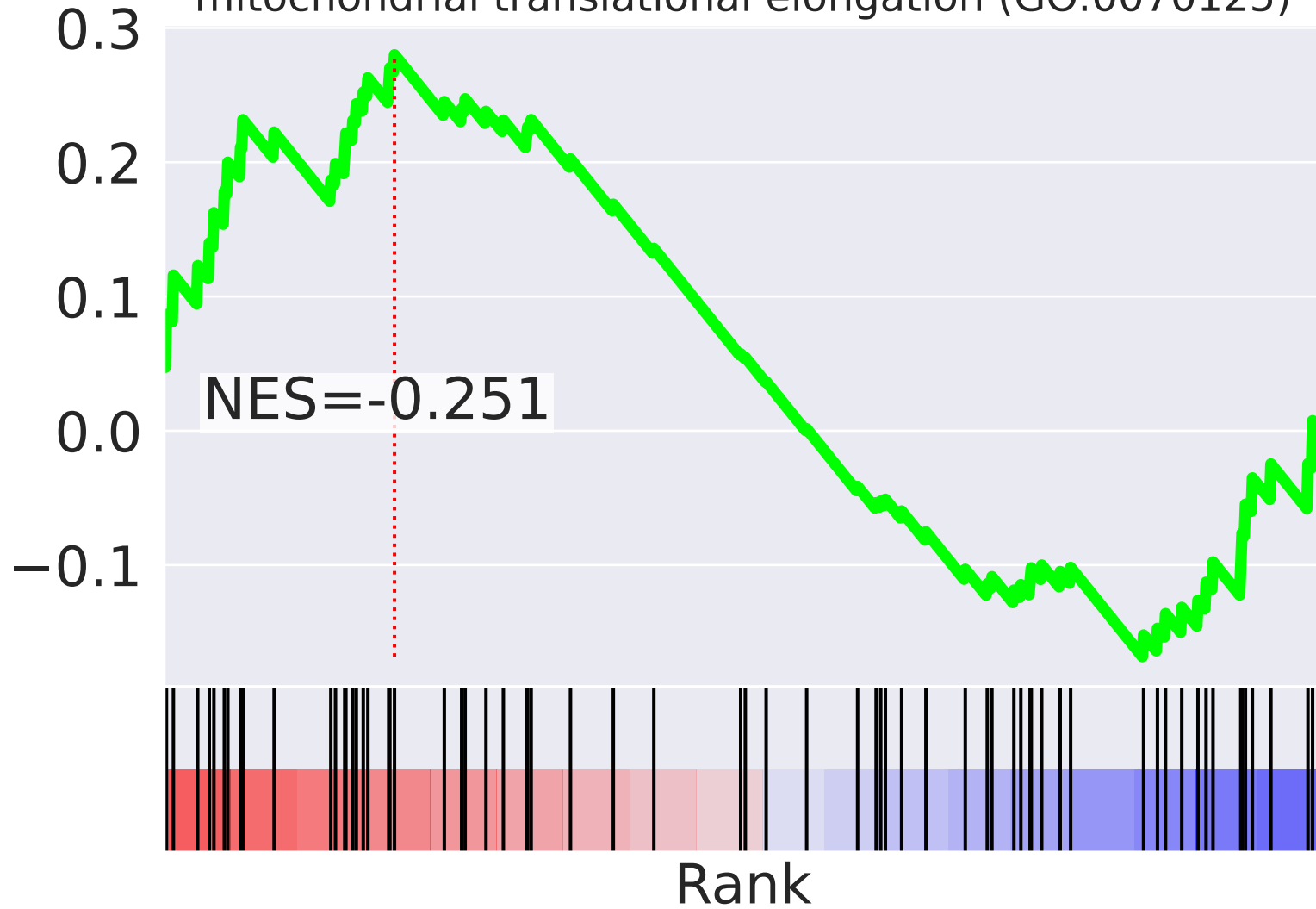
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=9$



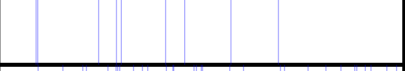
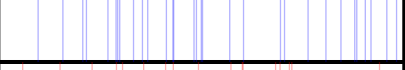


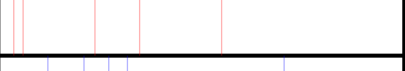

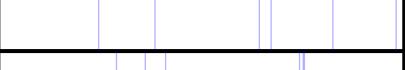
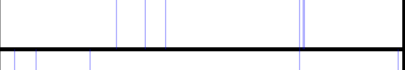


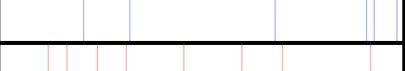
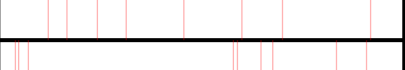

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

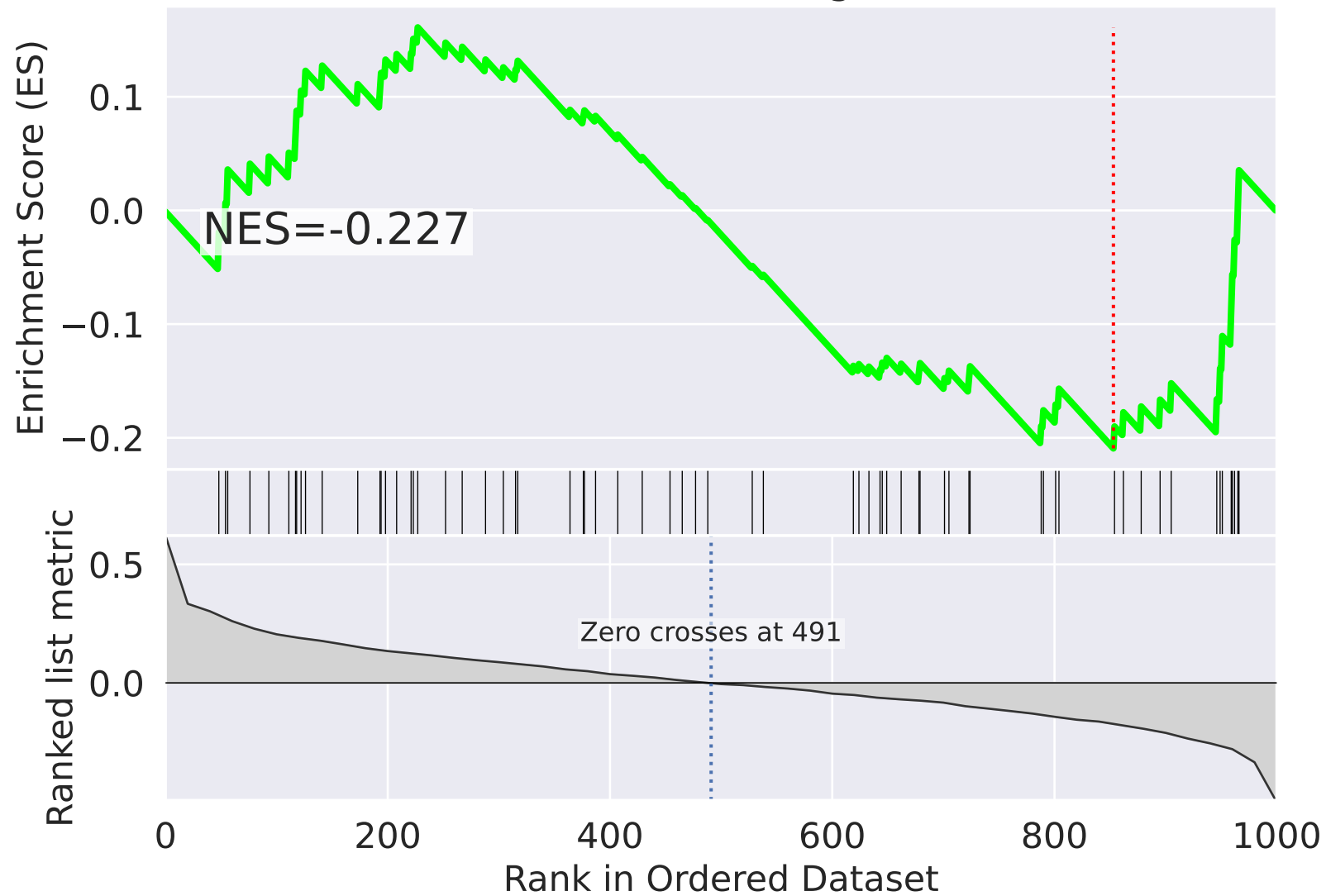
ES



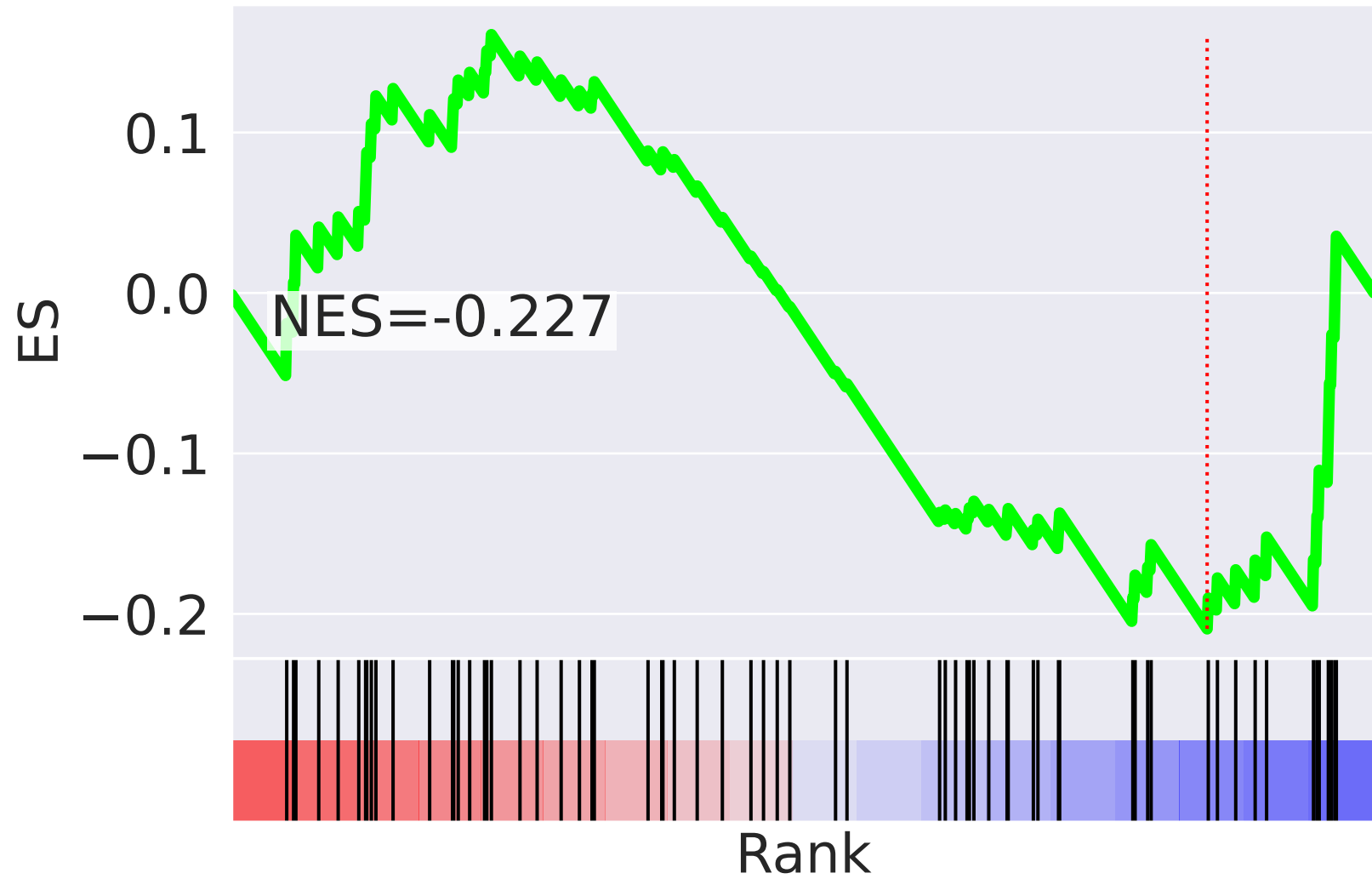
NES		SET
-2.512		double-strand break repair via nonhomologous end joining (GO:0006303)
2.439		cell differentiation (GO:0030154)
-2.395		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-2.356		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.342		post-translational protein modification (GO:0043687)
2.252		nucleus organization (GO:0006997)
2.251		cholesterol biosynthetic process (GO:0006695)
-2.205		telomere capping (GO:0016233)
-2.182		protein K48-linked ubiquitination (GO:0070936)
-2.182		negative regulation of canonical Wnt signaling pathway (GO:0090090)
-2.177		spermatogenesis (GO:0007283)
-2.173		protein K11-linked ubiquitination (GO:0070979)
-2.168		histone H4 acetylation (GO:0043967)
2.142		viral life cycle (GO:0019058)
2.100		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=10$

mitochondrial translational elongation (GO:0070125)





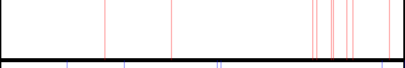
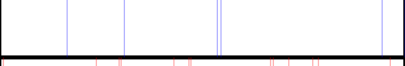
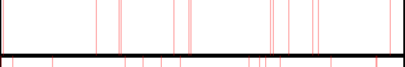


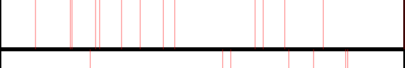
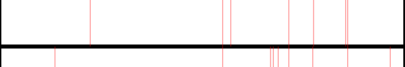
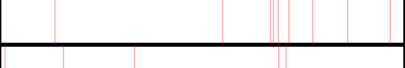
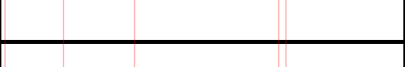




mitochondrial translational elongation (GO:0070125)



NES

SET

-3.213		regulation of cholesterol biosynthetic process (GO:0045540)
3.121		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
3.106		cell-matrix adhesion (GO:0007160)
2.990		integrin-mediated signaling pathway (GO:0007229)
2.944		intracellular signal transduction (GO:0035556)
-2.911		cellular nitrogen compound metabolic process (GO:0034641)
2.767		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.685		ubiquitin-dependent protein catabolic process (GO:0006511)
2.656		protein phosphorylation (GO:0006468)
2.647		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.596		platelet aggregation (GO:0070527)
2.506		movement of cell or subcellular component (GO:0006928)
2.440		ubiquitin-dependent ERAD pathway (GO:0030433)
2.440		retrograde protein transport, ER to cytosol (GO:0030970)
-2.435		tricarboxylic acid cycle (GO:0006099)