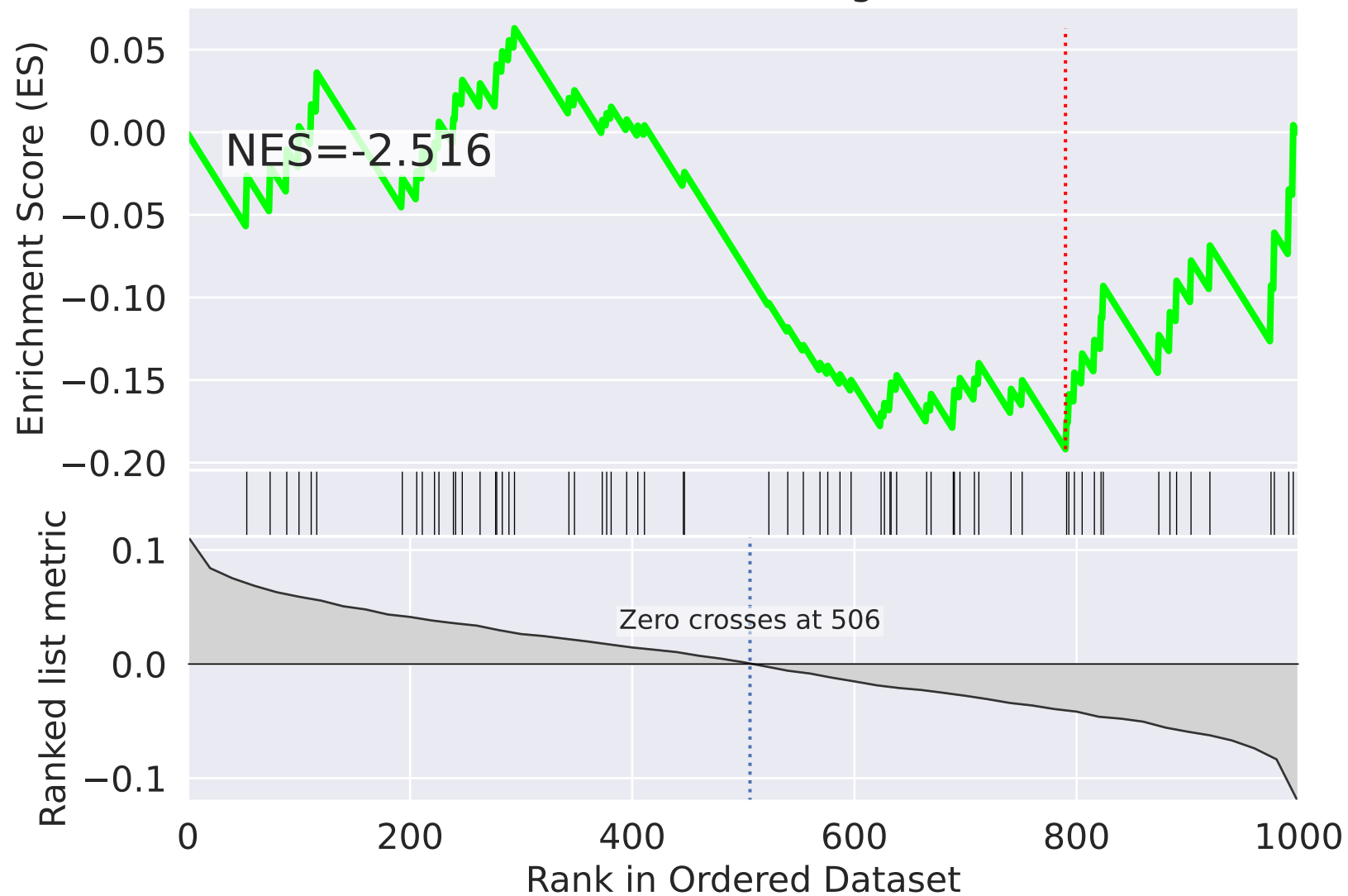
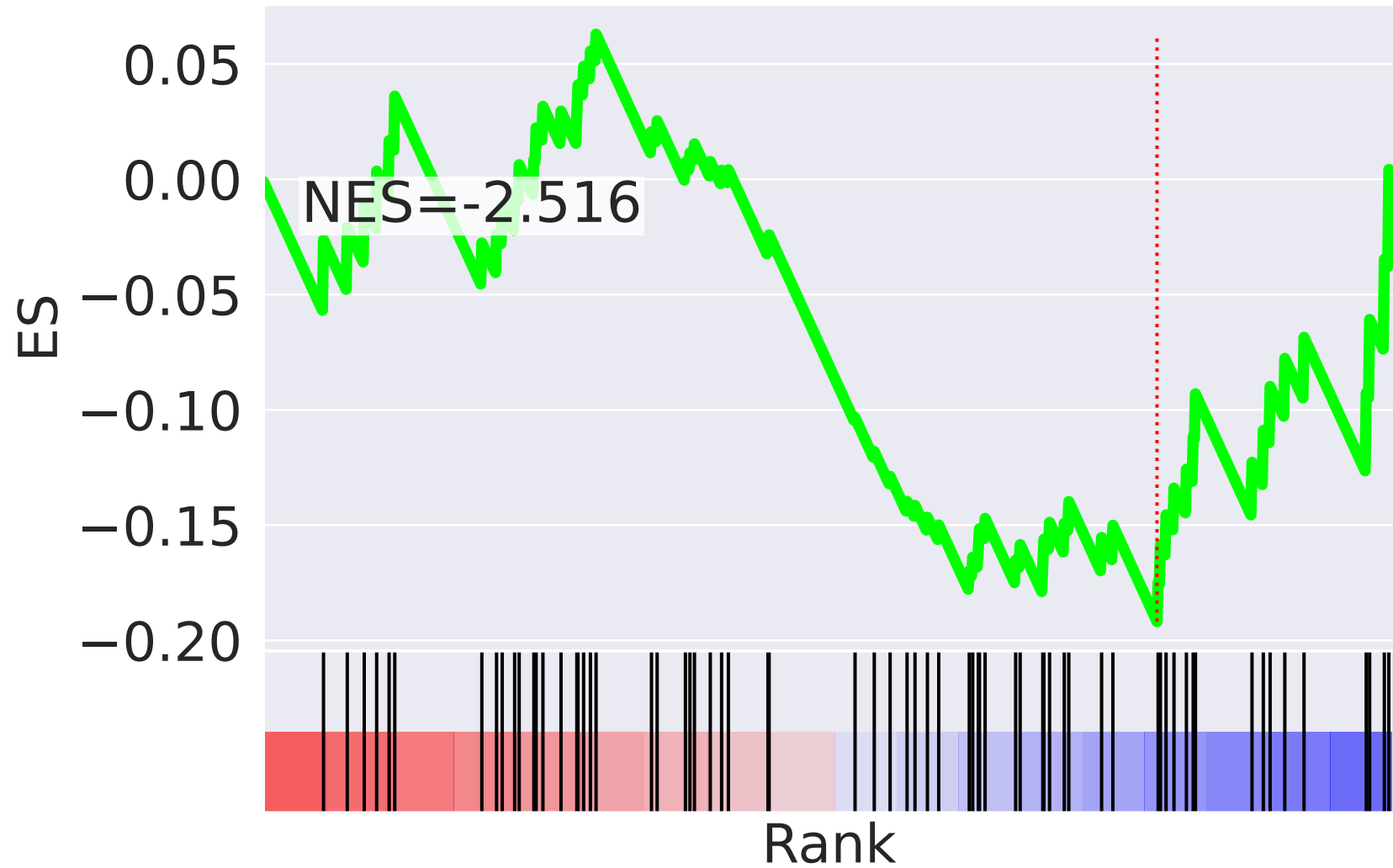






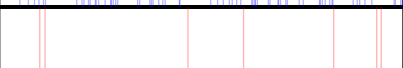


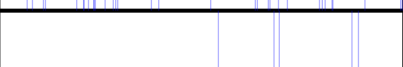
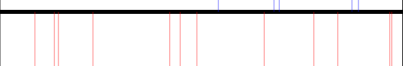



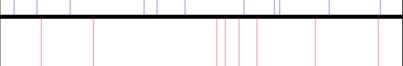
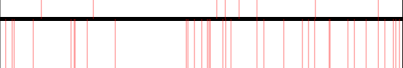
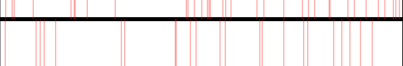
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=1$

mitochondrial translational elongation (GO:0070125)



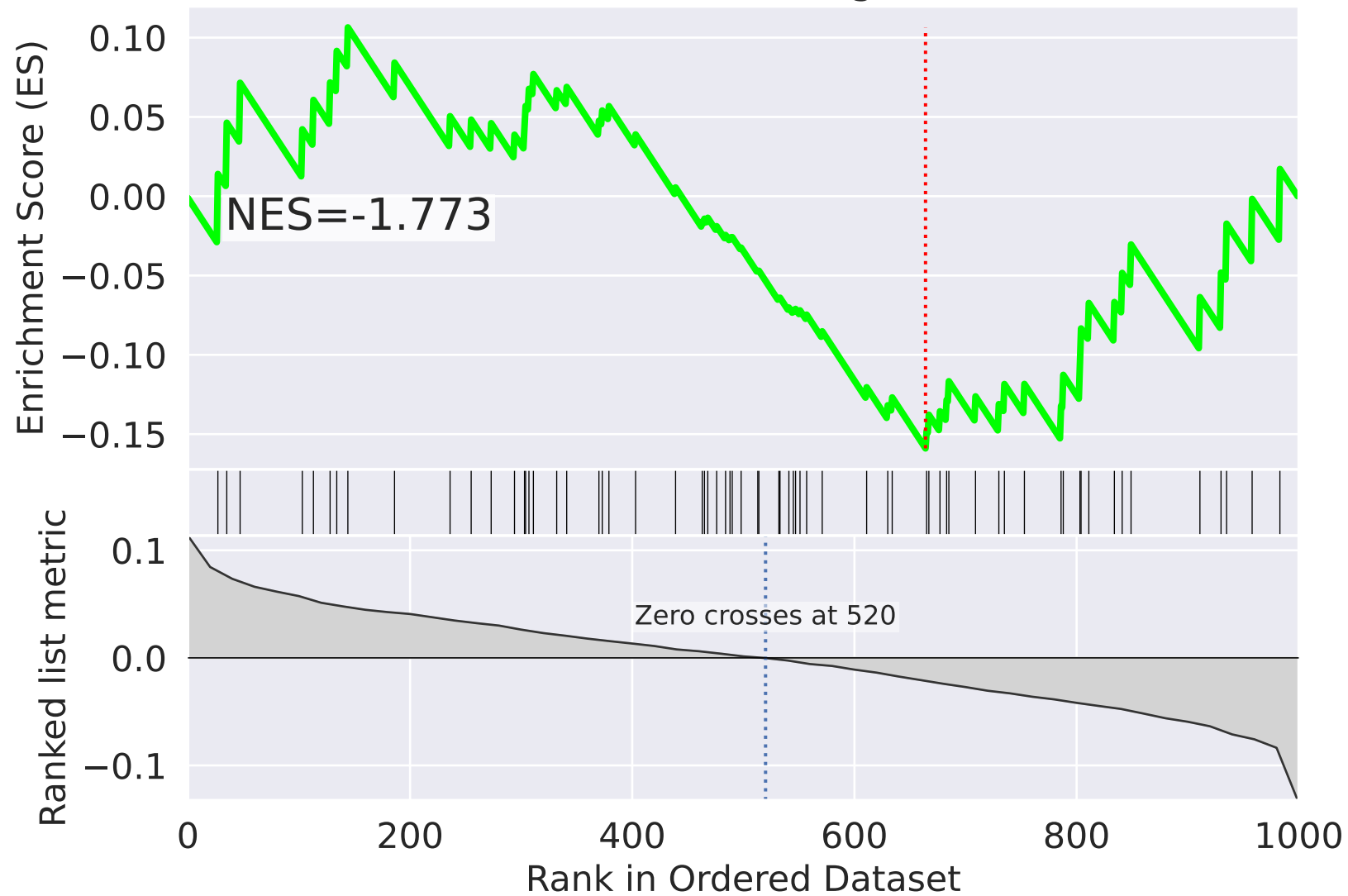
mitochondrial translational elongation (GO:0070125)



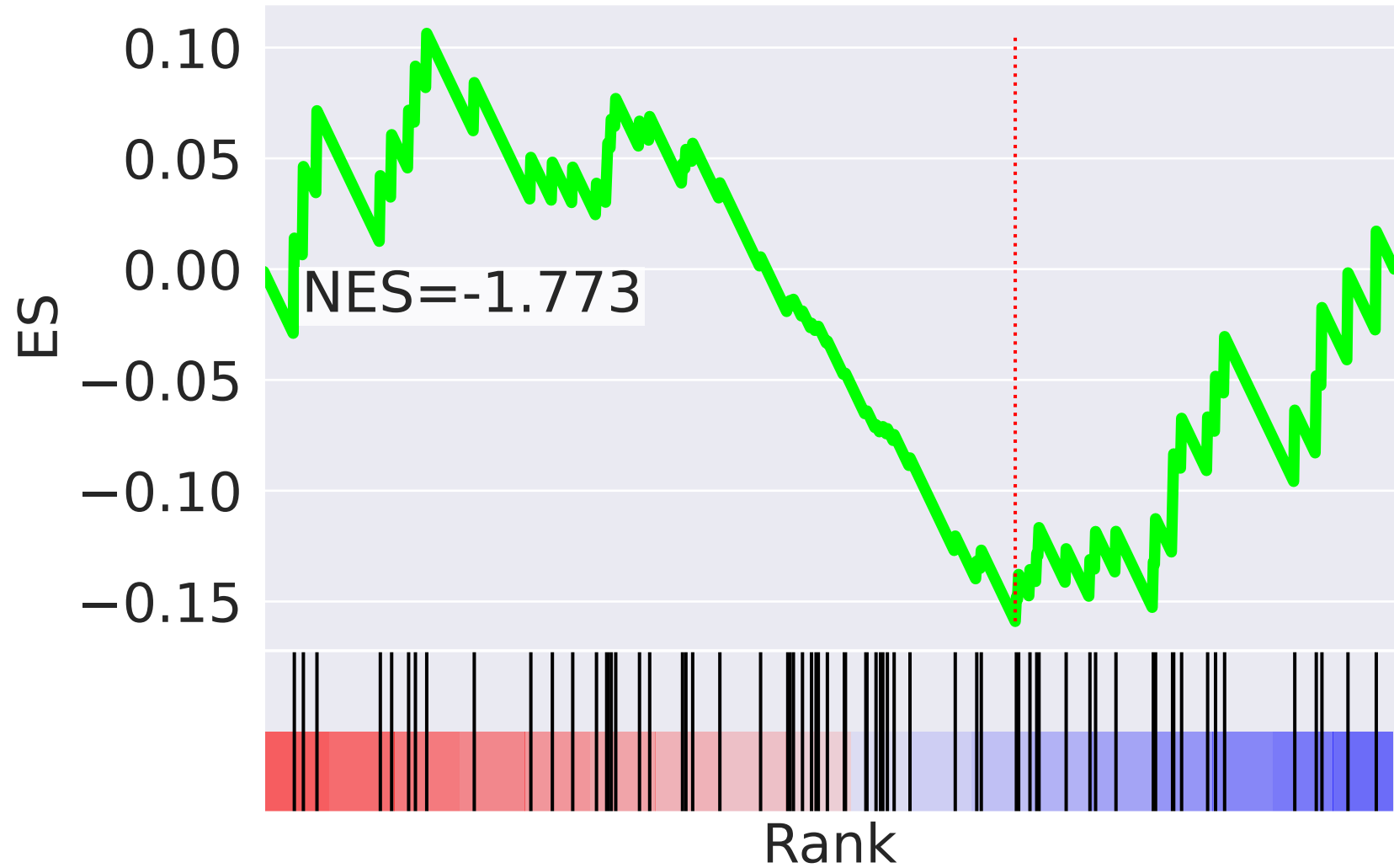
NES		SET
2.854		movement of cell or subcellular component (GO:0006928)
-2.686		mitochondrial translational termination (GO:0070126)
2.628		inflammatory response (GO:0006954)
-2.516		mitochondrial translational elongation (GO:0070125)
2.349		response to virus (GO:0009615)
2.317		protein autophosphorylation (GO:0046777)
-2.207		translation (GO:0006412)
-2.142		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
2.127		RNA splicing (GO:0008380)
2.070		positive regulation of cell migration (GO:0030335)
2.059		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
-2.035		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
2.017		regulation of cell proliferation (GO:0042127)
2.017		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.009		positive regulation of apoptotic process (GO:0043065)

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)



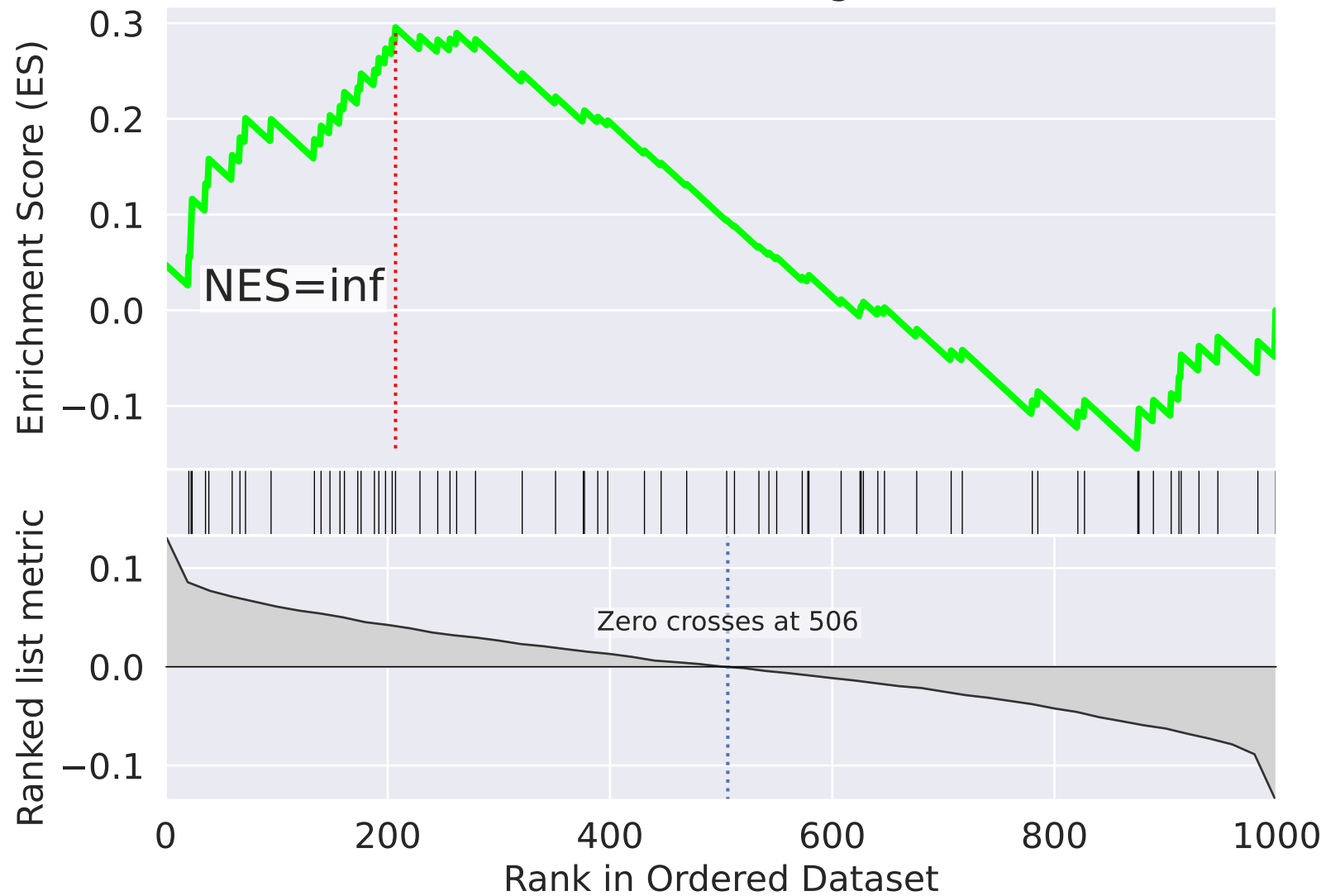
mitochondrial translational elongation (GO:0070125)



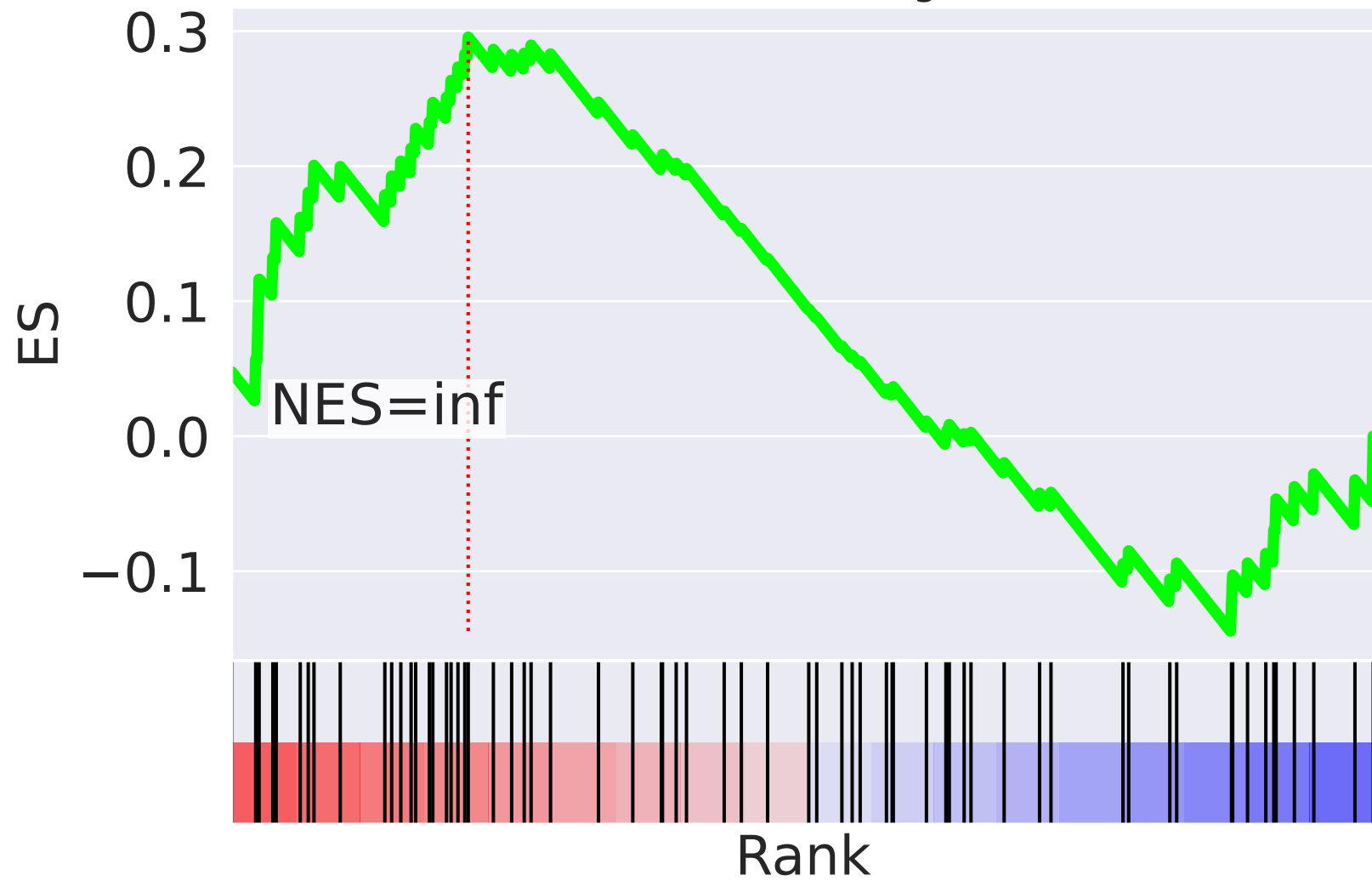
NES		SET
-2.610		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.372		positive regulation of TOR signaling (GO:0032008)
-2.371		regulation of signal transduction by p53 class mediator (GO:1901796)
2.345		protein K63-linked ubiquitination (GO:0070534)
-2.315		histone H3 acetylation (GO:0043966)
2.263		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.239		regulation of DNA replication (GO:0006275)
-2.175		negative regulation of cell proliferation (GO:0008285)
2.155		regulation of apoptotic process (GO:0042981)
-2.153		protein stabilization (GO:0050821)
2.150		MAPK cascade (GO:0000165)
2.147		axon guidance (GO:0007411)
-2.131		tricarboxylic acid cycle (GO:0006099)
-2.083		ER to Golgi vesicle-mediated transport (GO:0006888)
1.987		Wnt signaling pathway (GO:0016055)

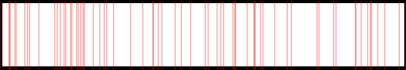
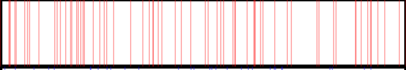
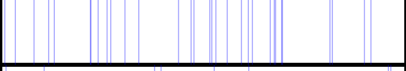
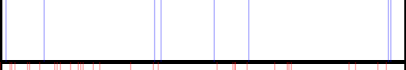
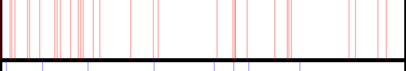
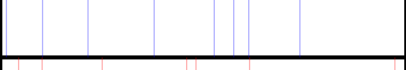

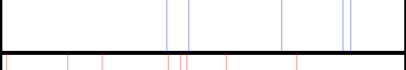


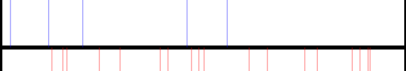
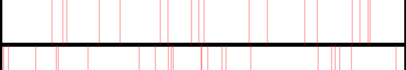
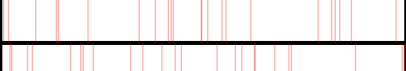

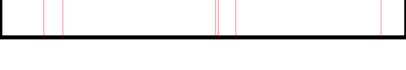
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=3$

mitochondrial translational elongation (GO:0070125)



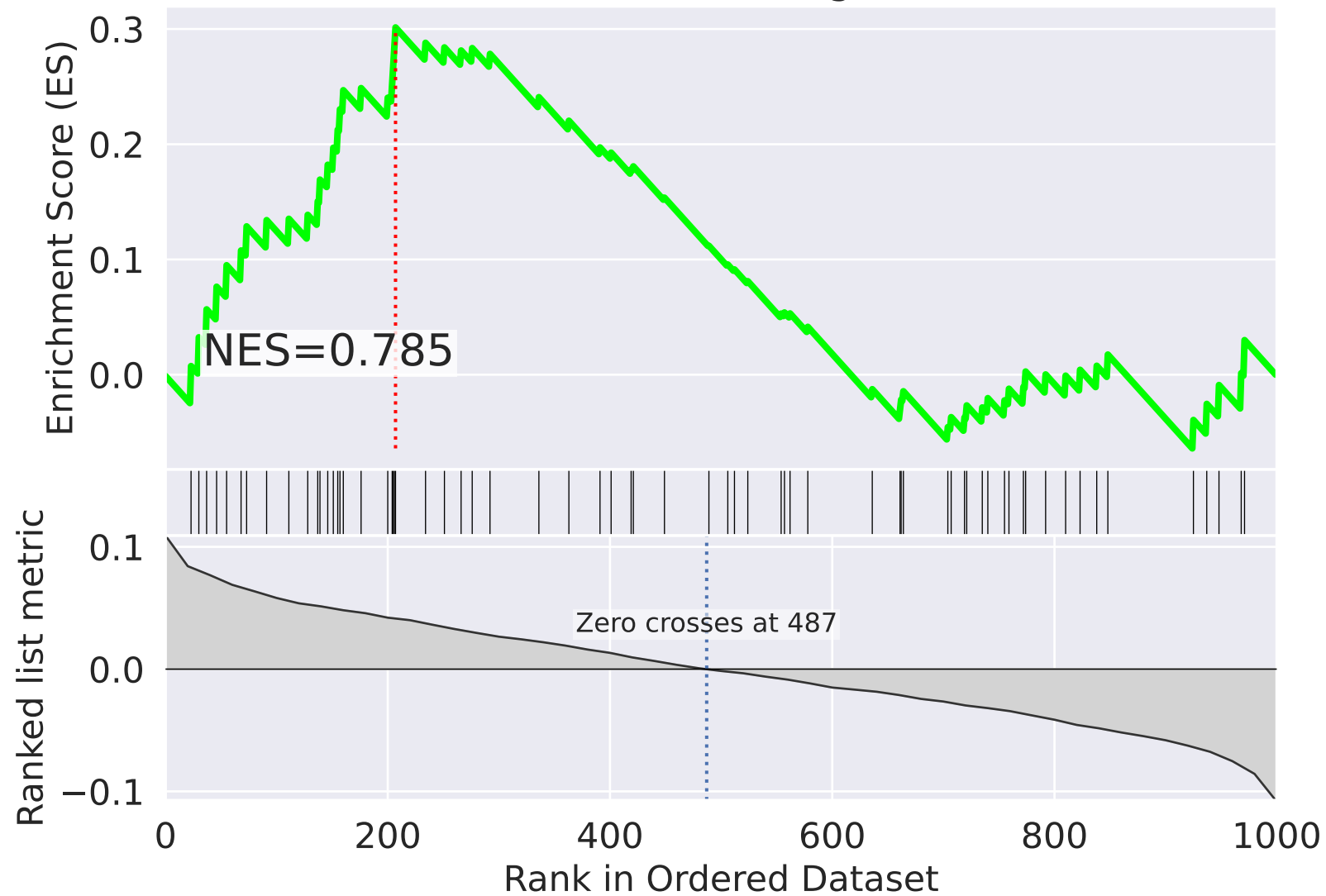
mitochondrial translational elongation (GO:0070125)



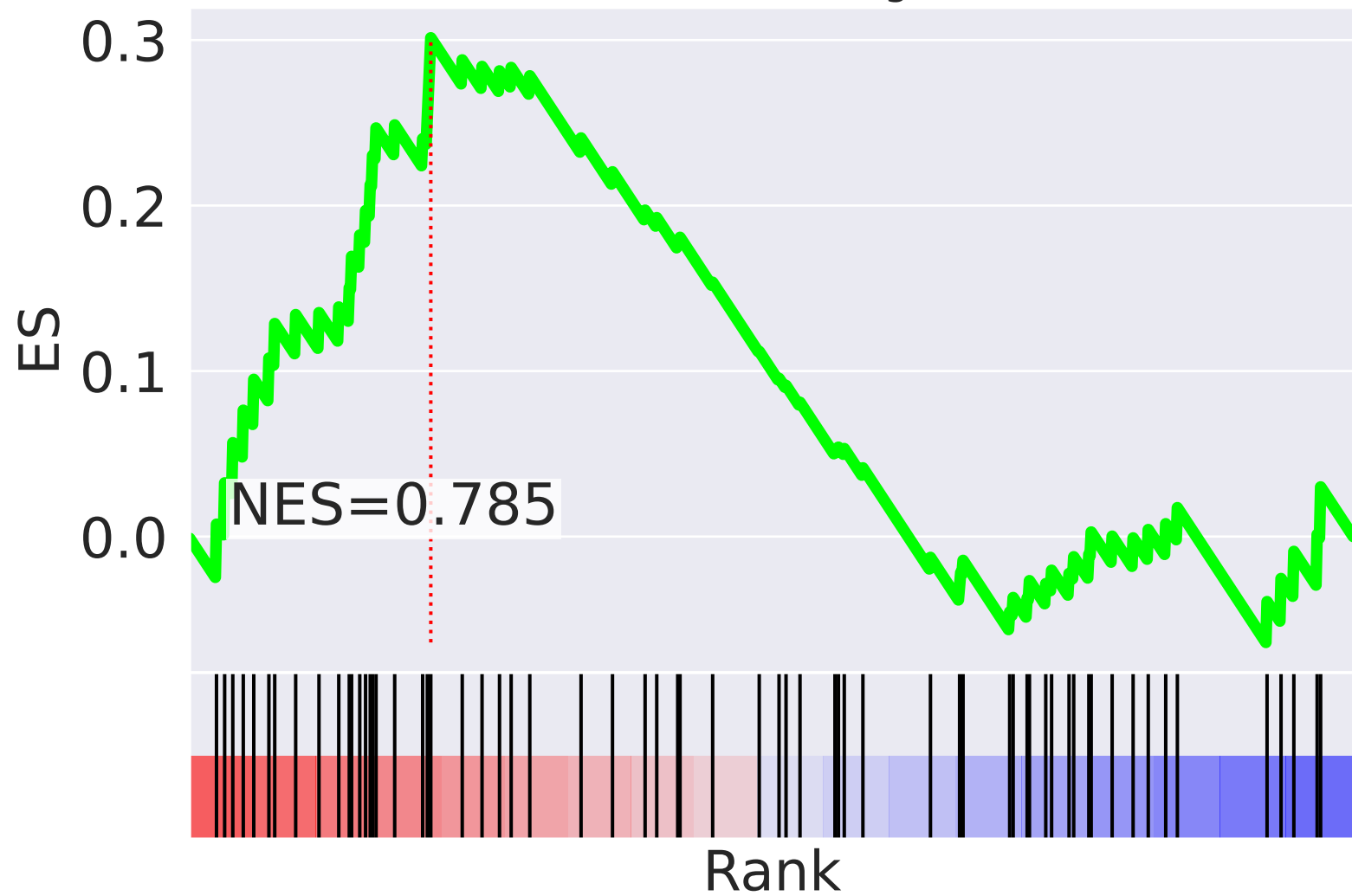
NES		SET
inf		mitochondrial translational elongation (GO:0070125)
inf		mitochondrial translational termination (GO:0070126)
-2.967		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.425		regulation of apoptotic process (GO:0042981)
2.384		translation (GO:0006412)
-2.334		regulation of cell proliferation (GO:0042127)
2.268		platelet aggregation (GO:0070527)
-2.249		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.225		integrin-mediated signaling pathway (GO:0007229)
2.209		protein polyubiquitination (GO:0000209)
-2.130		cellular respiration (GO:0045333)
2.033		DNA repair (GO:0006281)
2.019		positive regulation of apoptotic process (GO:0043065)
1.934		mitochondrial translation (GO:0032543)
1.851		DNA duplex unwinding (GO:0032508)

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)



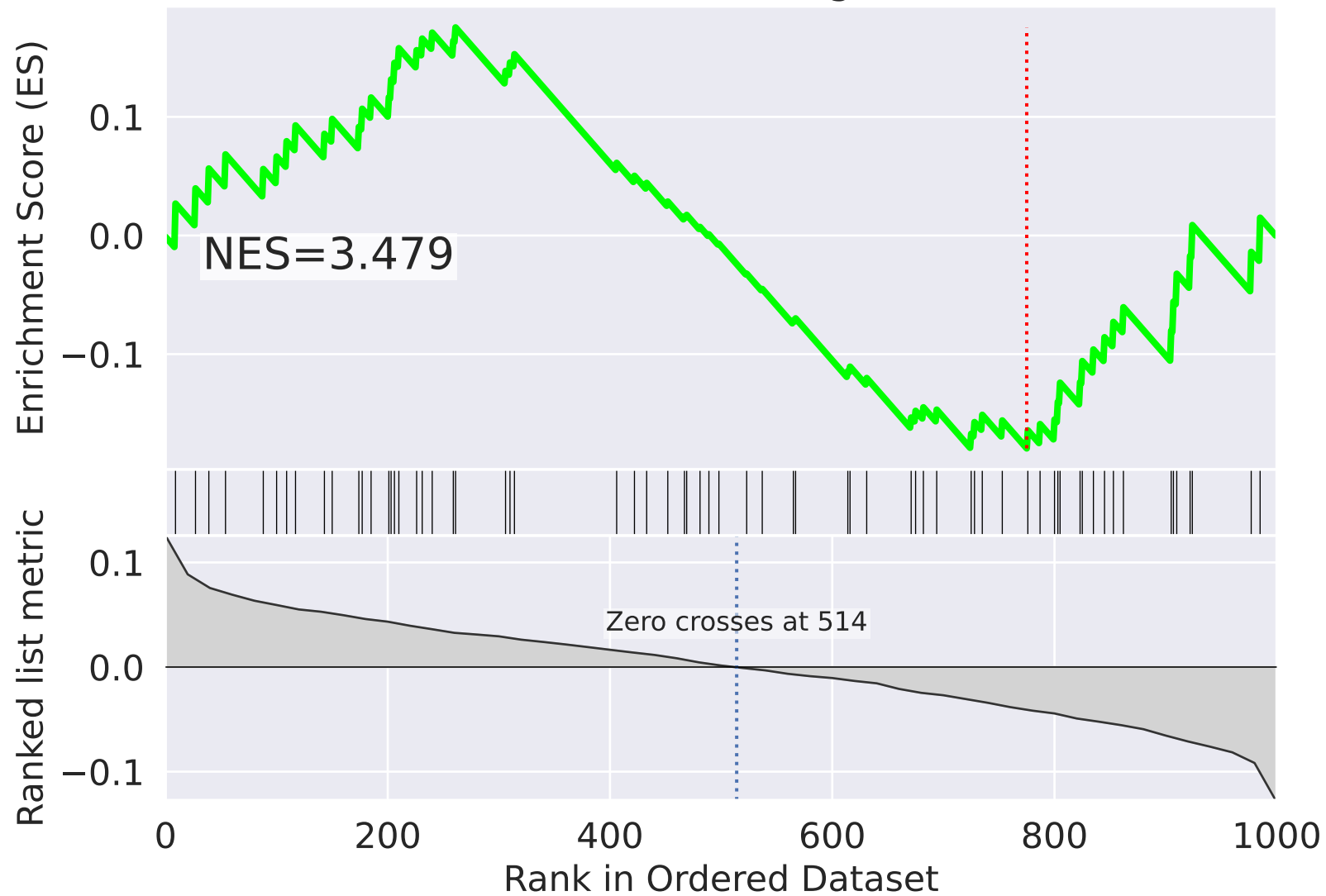
mitochondrial translational elongation (GO:0070125)



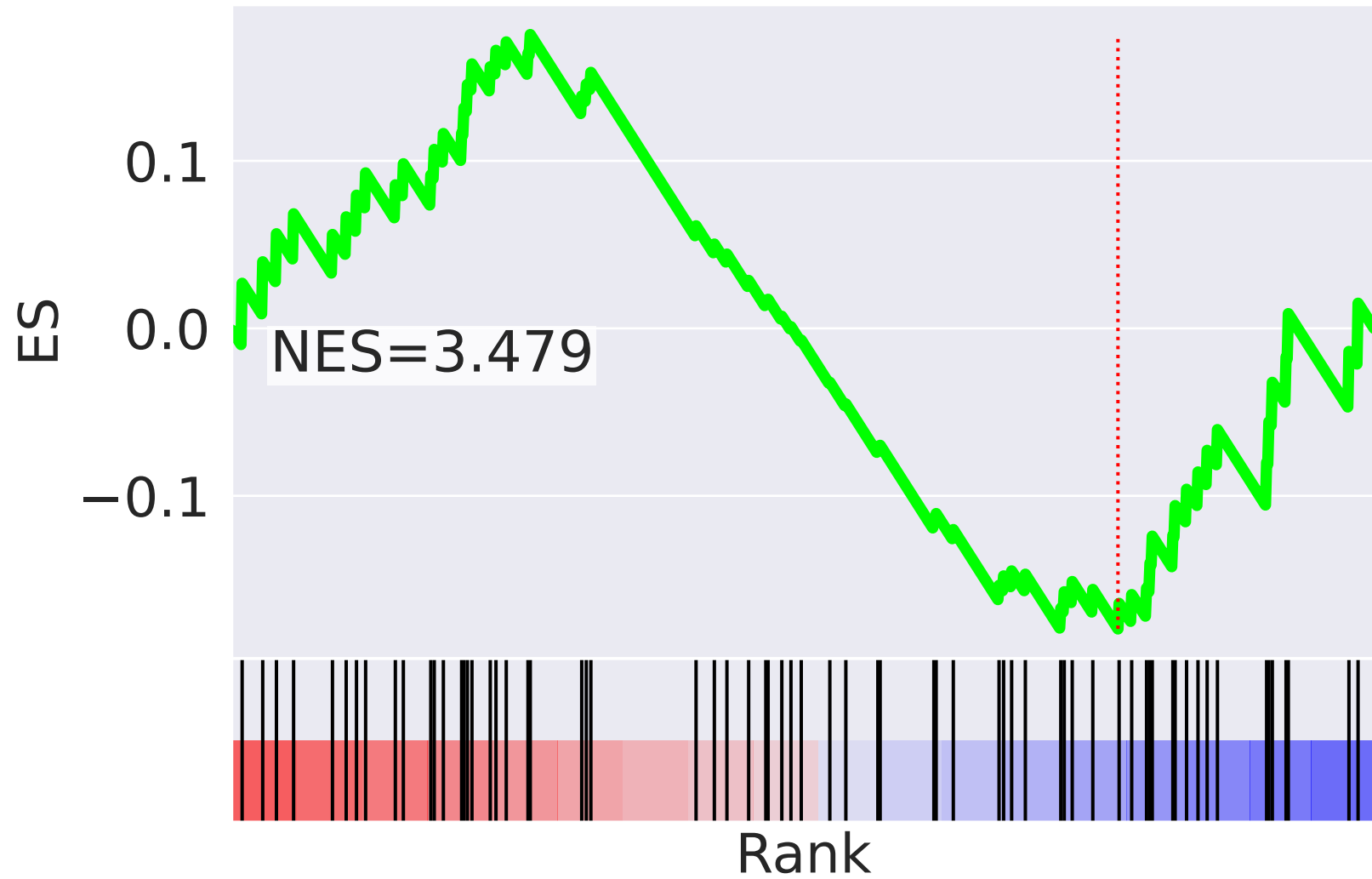
NES		SET
-2.571		transcription, DNA-templated (GO:0006351)
-2.540		innate immune response (GO:0045087)
2.526		tricarboxylic acid cycle (GO:0006099)
-2.318		RNA secondary structure unwinding (GO:0010501)
-2.234		positive regulation of apoptotic process (GO:0043065)
2.224		post-Golgi vesicle-mediated transport (GO:0006892)
2.202		iron-sulfur cluster assembly (GO:0016226)
2.169		CENP-A containing nucleosome assembly (GO:0034080)
2.118		translation (GO:0006412)
-2.085		DNA replication (GO:0006260)
-2.081		regulation of protein stability (GO:0031647)
2.066		Ras protein signal transduction (GO:0007265)
2.029		mitochondrial translation (GO:0032543)
-1.954		positive regulation of cytokinesis (GO:0032467)
-1.949		anaphase-promoting complex-dependent catabolic process (GO:0031145)

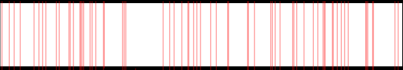
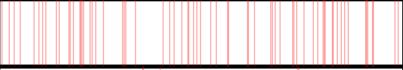

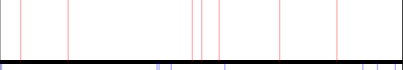




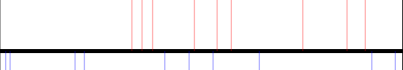
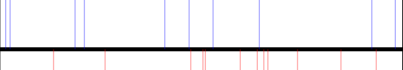
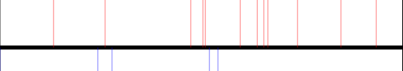


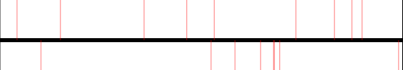
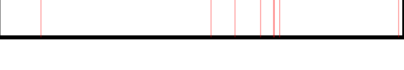
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=5$

mitochondrial translational elongation (GO:0070125)



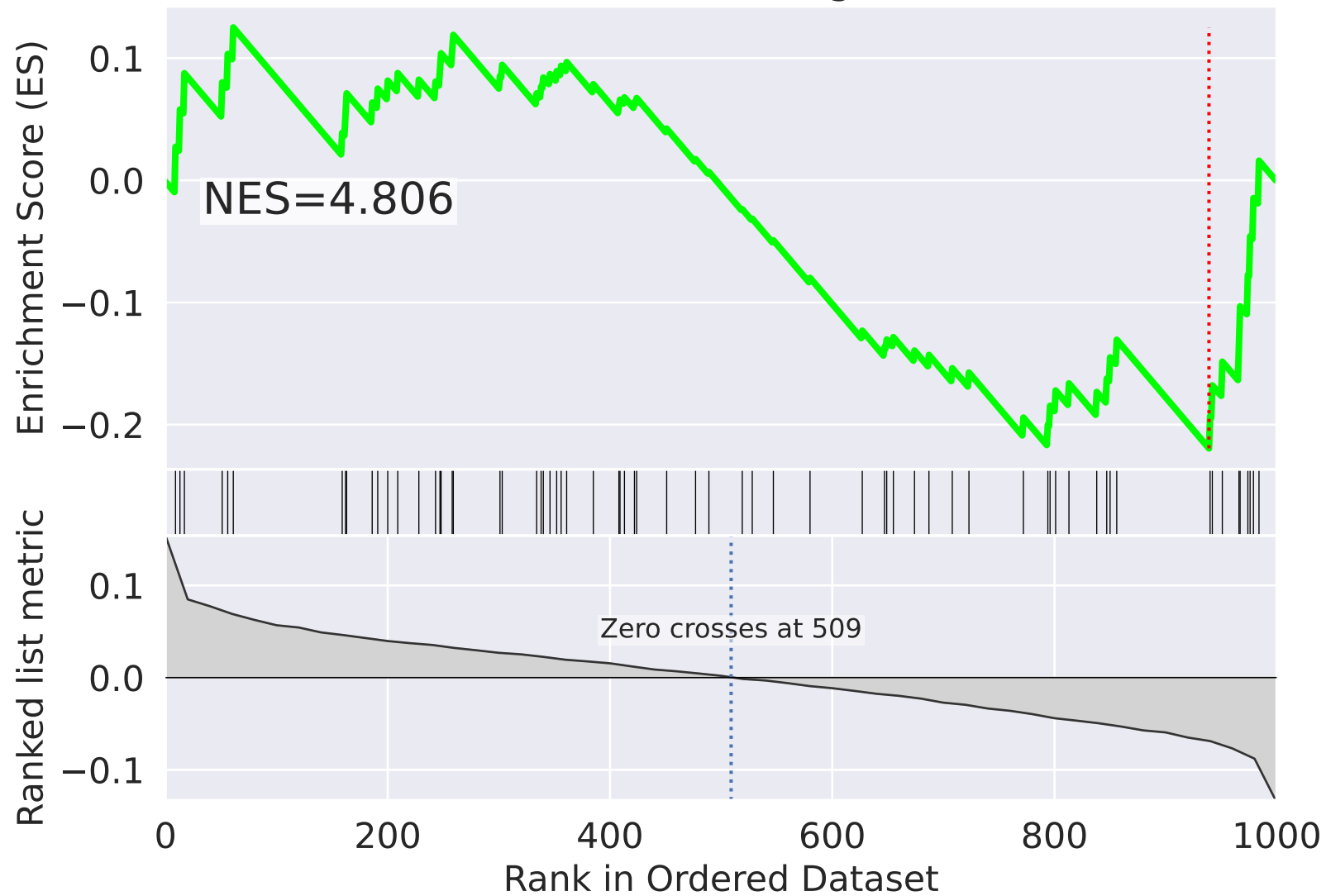
mitochondrial translational elongation (GO:0070125)



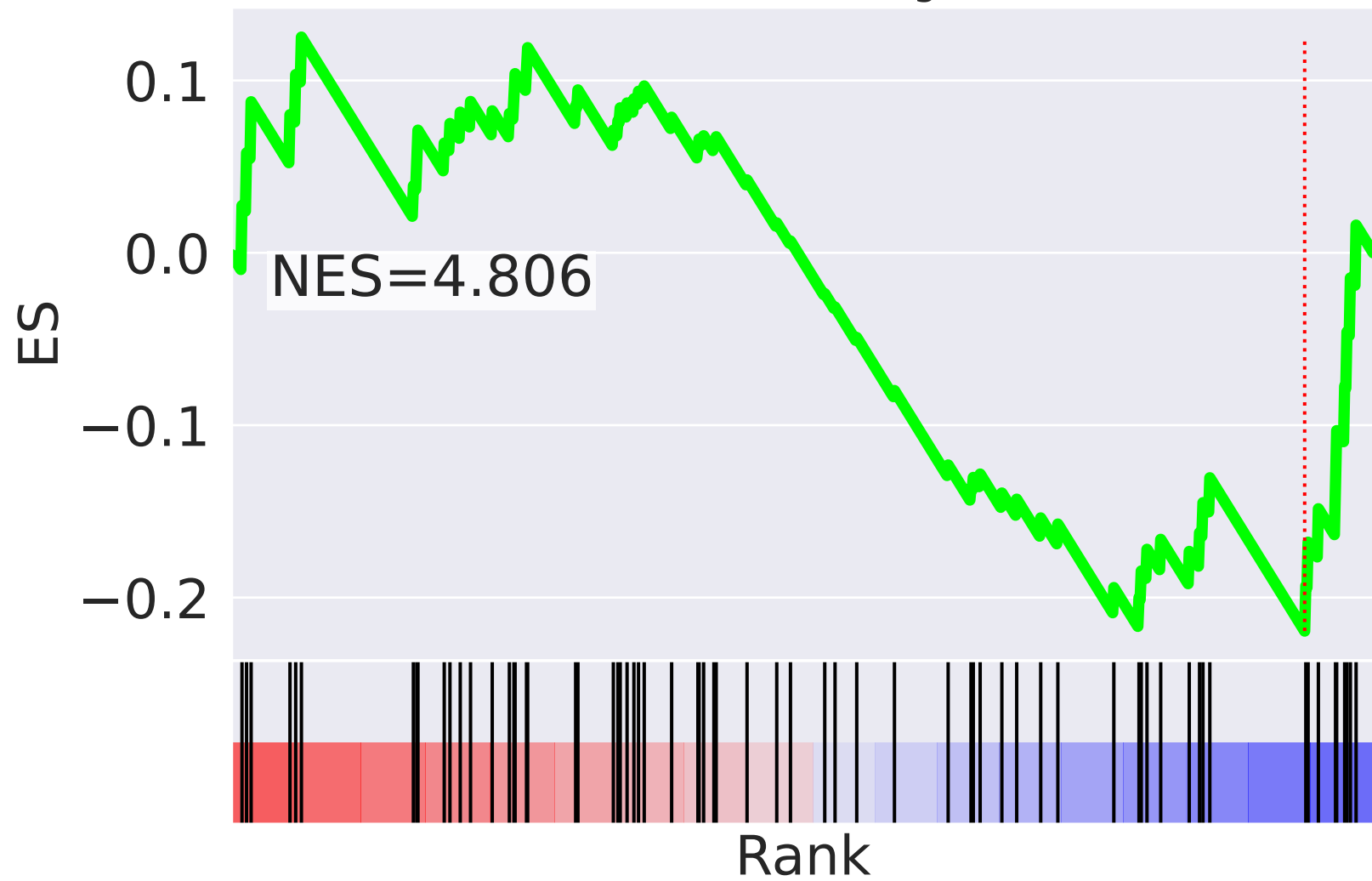
NES		SET
3.479		mitochondrial translational elongation (GO:0070125)
3.425		mitochondrial translational termination (GO:0070126)
2.355		positive regulation of GTPase activity (GO:0043547)
2.340		negative regulation of telomere maintenance via telomerase (GO:0032211)
-2.322		androgen receptor signaling pathway (GO:0030521)
-2.280		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.204		protein autophosphorylation (GO:0046777)
-2.072		platelet degranulation (GO:0002576)
1.951		response to endoplasmic reticulum stress (GO:0034976)
-1.914		strand displacement (GO:0000732)
1.873		leukocyte migration (GO:0050900)
-1.870		cellular response to hypoxia (GO:0071456)
1.863		DNA replication initiation (GO:0006270)
1.861		intracellular signal transduction (GO:0035556)
1.837		rRNA processing (GO:0006364)

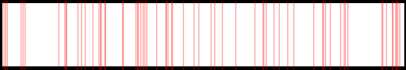
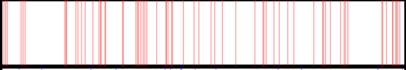
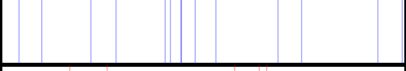


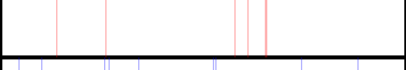
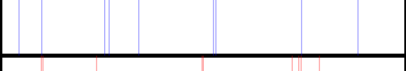

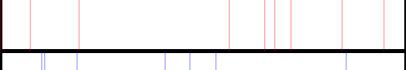
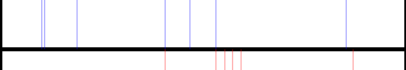
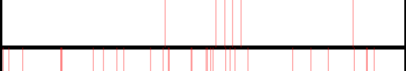
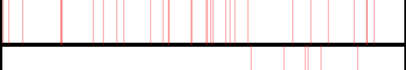
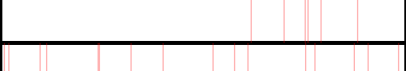
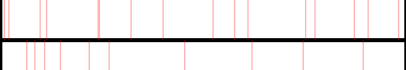
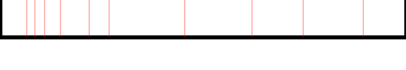
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=6$

mitochondrial translational elongation (GO:0070125)



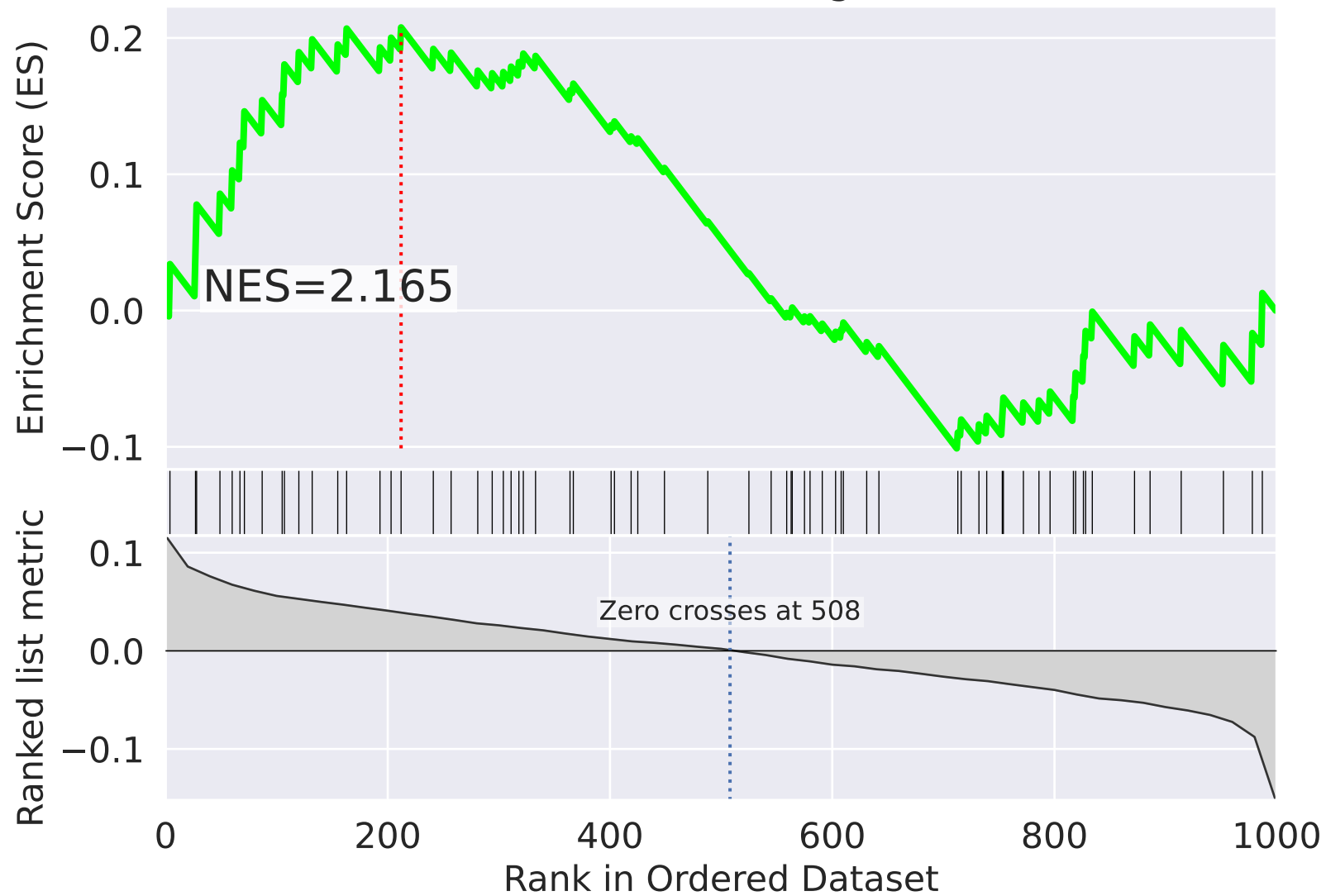
mitochondrial translational elongation (GO:0070125)



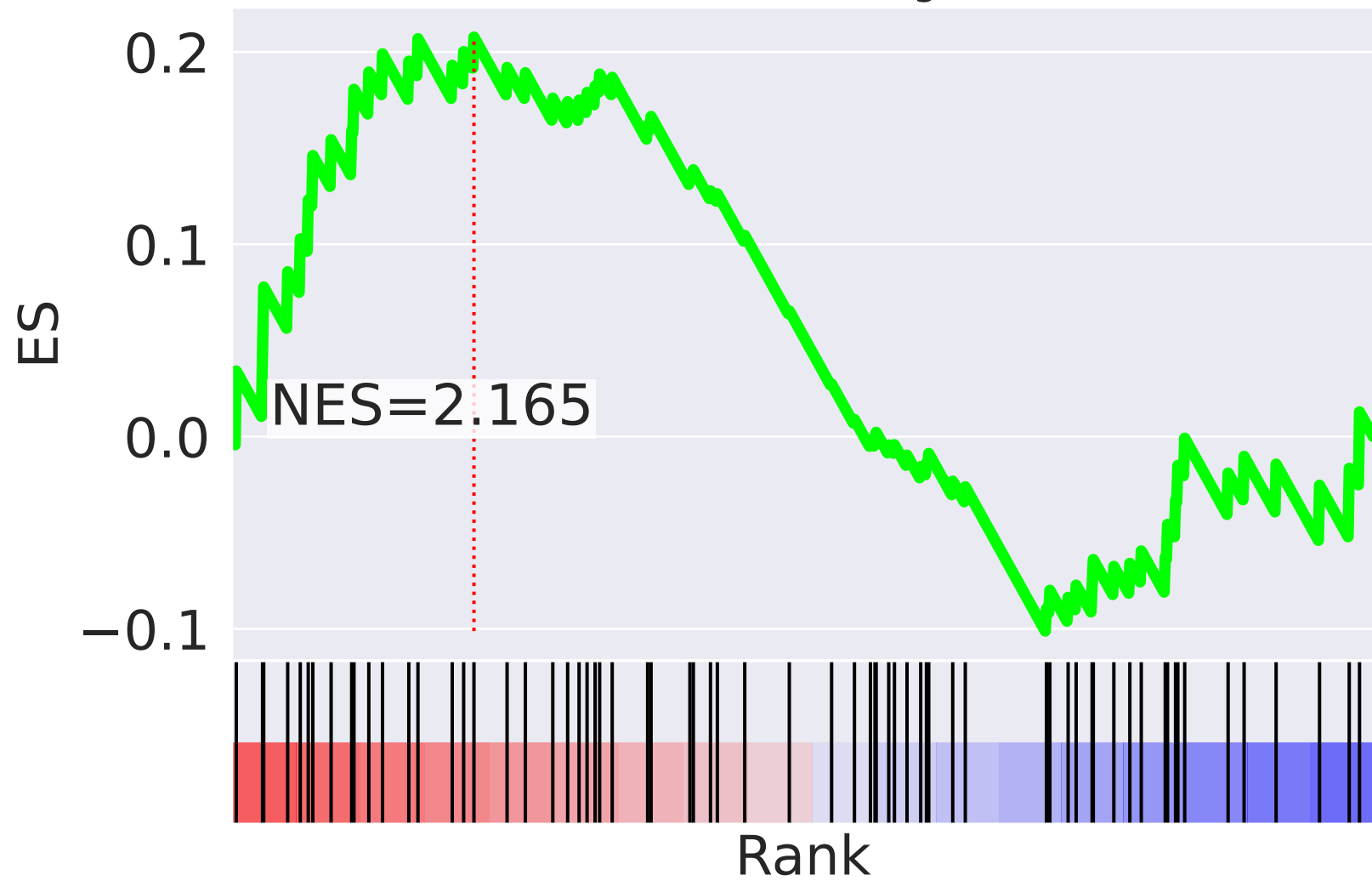
NES		SET
4.825		mitochondrial translational termination (GO:0070126)
4.806		mitochondrial translational elongation (GO:0070125)
-3.058		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.536		nucleotide-excision repair (GO:0006289)
2.528		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.381		transcription-coupled nucleotide-excision repair (GO:0006283)
-2.195		Golgi organization (GO:0007030)
2.163		intracellular signal transduction (GO:0035556)
2.149		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.098		intracellular protein transport (GO:0006886)
2.064		COPII vesicle coating (GO:0048208)
2.060		protein deubiquitination (GO:0016579)
2.002		RNA metabolic process (GO:0016070)
1.968		regulation of signal transduction by p53 class mediator (GO:1901796)
1.957		retrograde transport, endosome to Golgi (GO:0042147)

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)




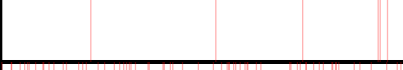
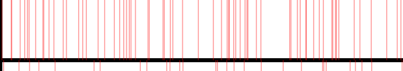
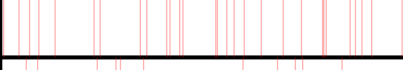
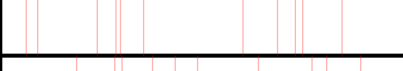
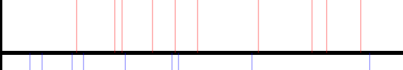

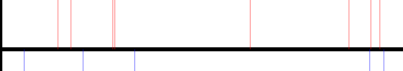

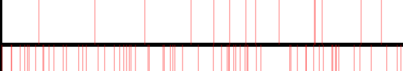
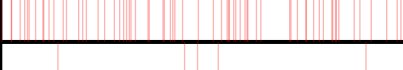

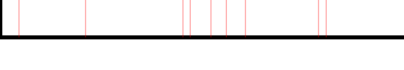


mitochondrial translational elongation (GO:0070125)



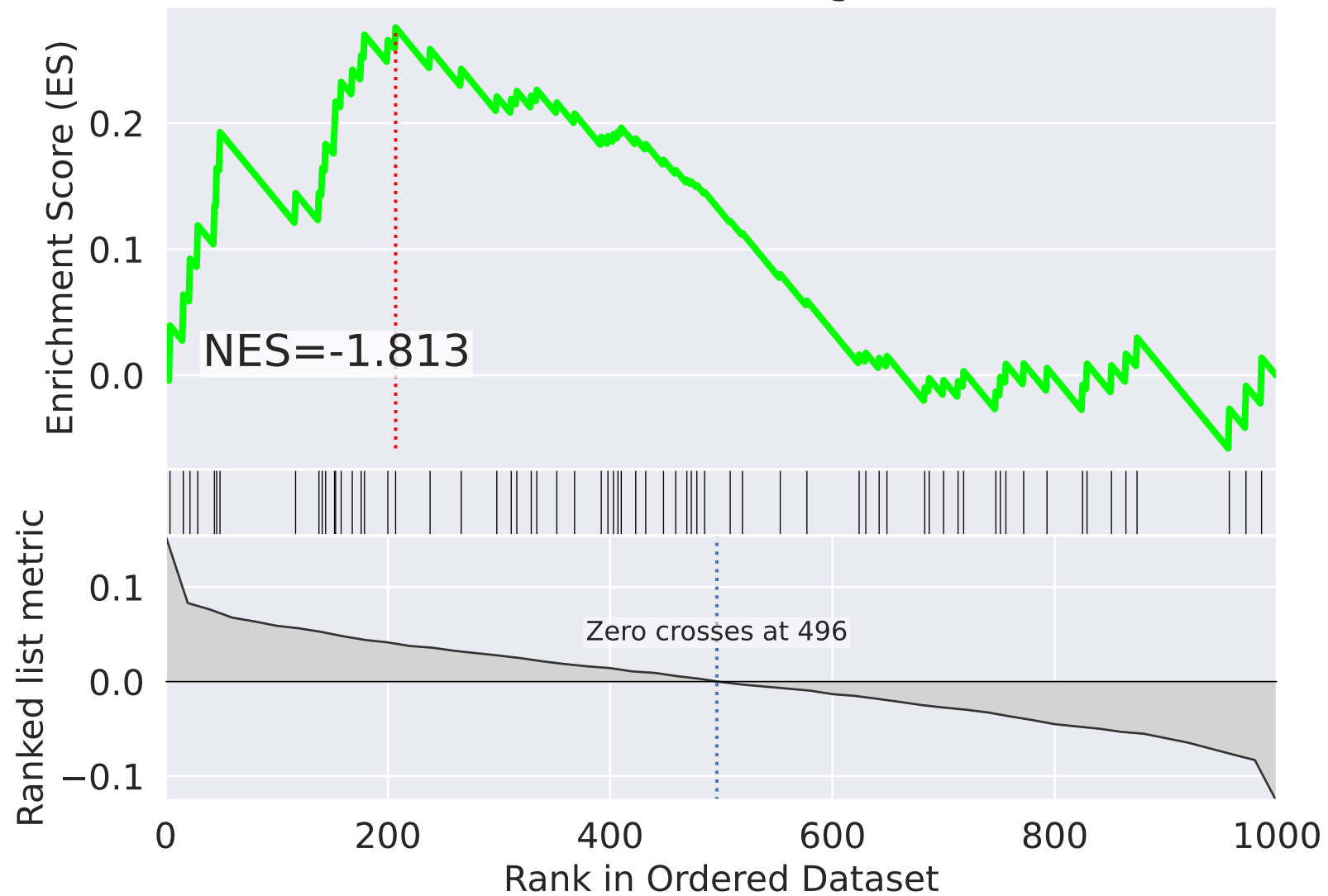
NES

SET

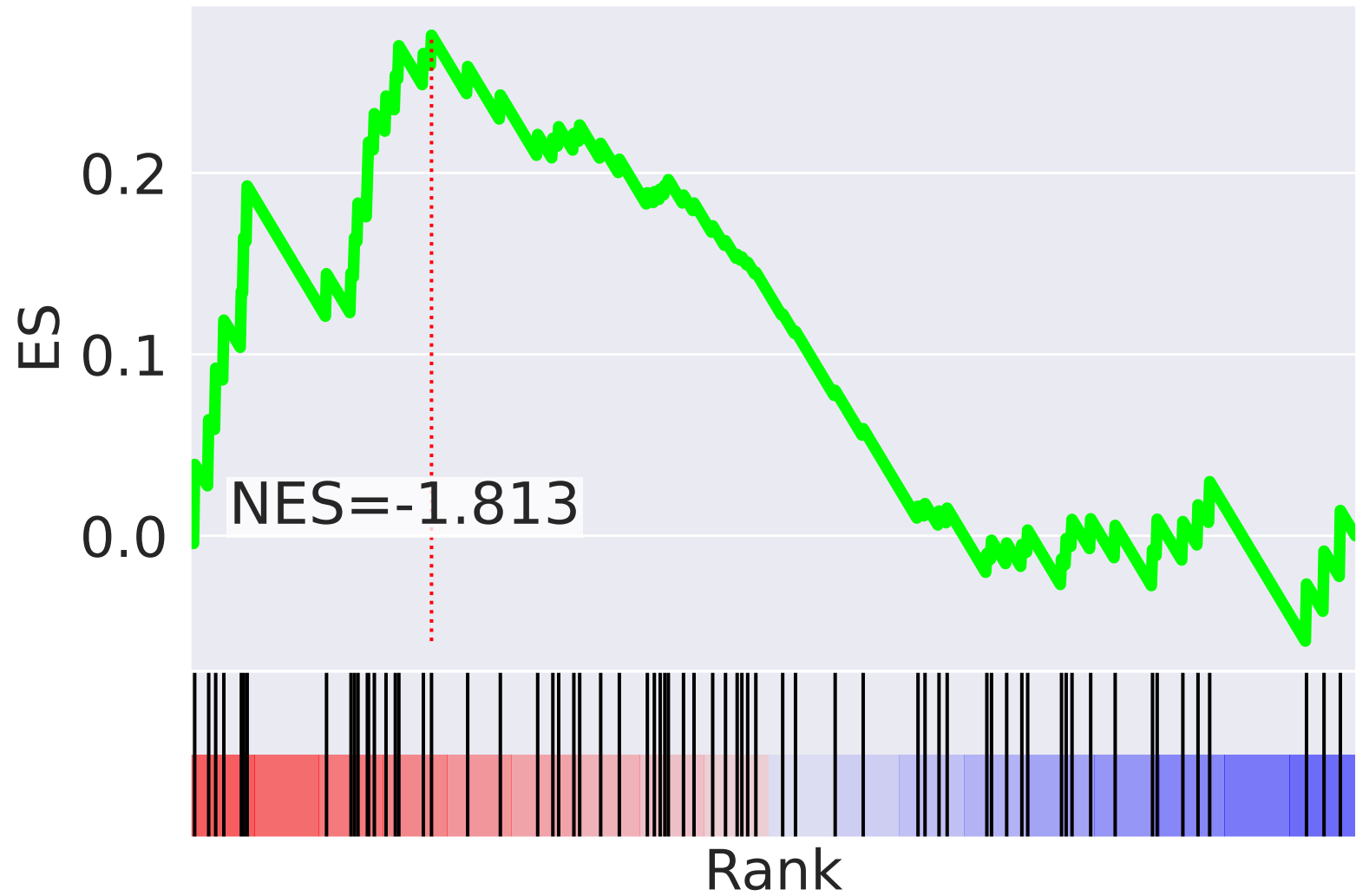
-2.792		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.417		ERBB2 signaling pathway (GO:0038128)
2.200		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.199		positive regulation of cell growth (GO:0030307)
2.165		mitochondrial translational elongation (GO:0070125)
2.136		neutrophil degranulation (GO:0043312)
2.126		epidermal growth factor receptor signaling pathway (GO:0007173)
2.111		double-strand break repair via homologous recombination (GO:0000724)
-2.101		transcription, DNA-templated (GO:0006351)
2.090		interstrand cross-link repair (GO:0036297)
-2.083		iron-sulfur cluster assembly (GO:0016226)
2.043		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.038		mitochondrial translational termination (GO:0070126)
2.025		DNA damage checkpoint (GO:0000077)
2.003		movement of cell or subcellular component (GO:0006928)

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)



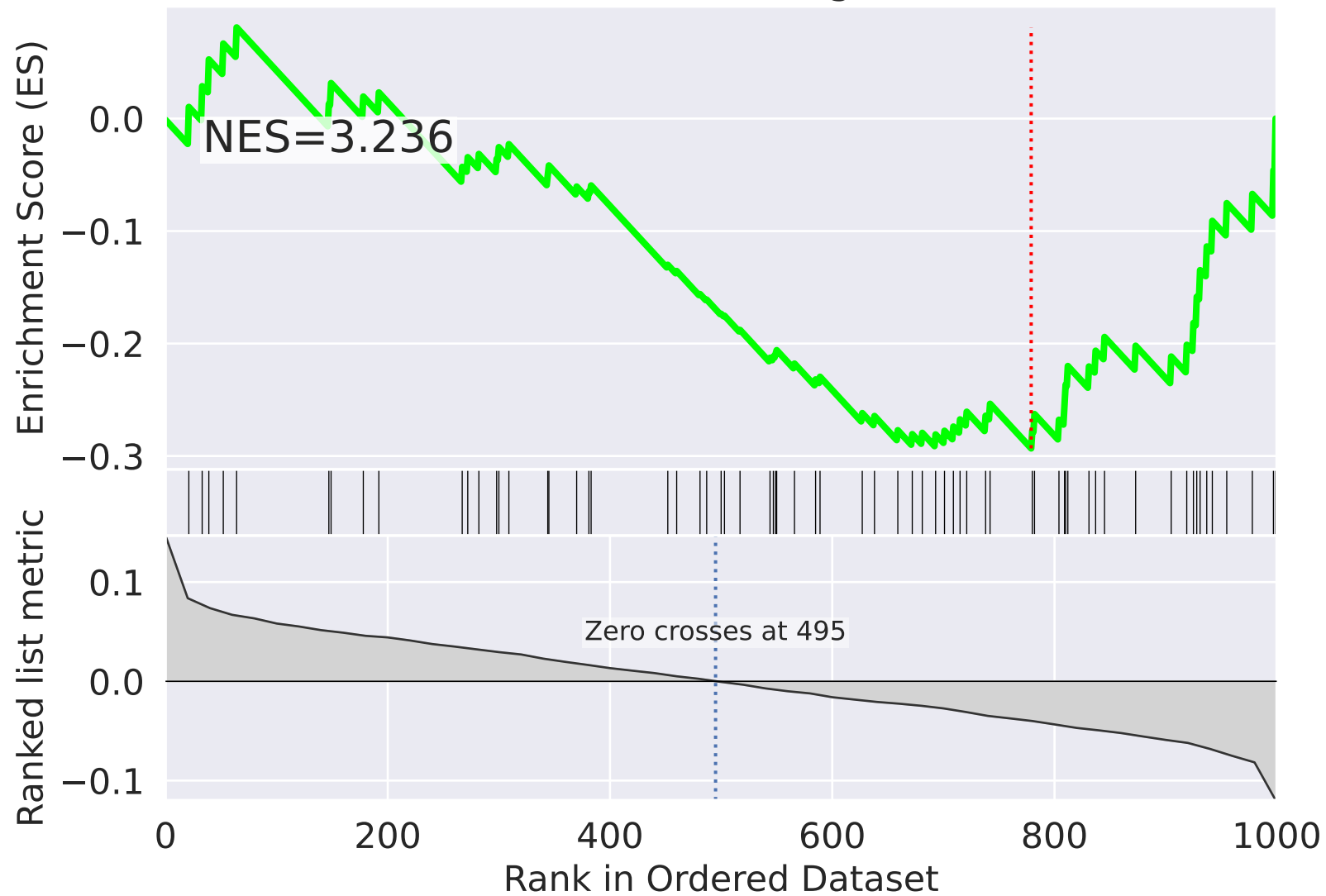
mitochondrial translational elongation (GO:0070125)



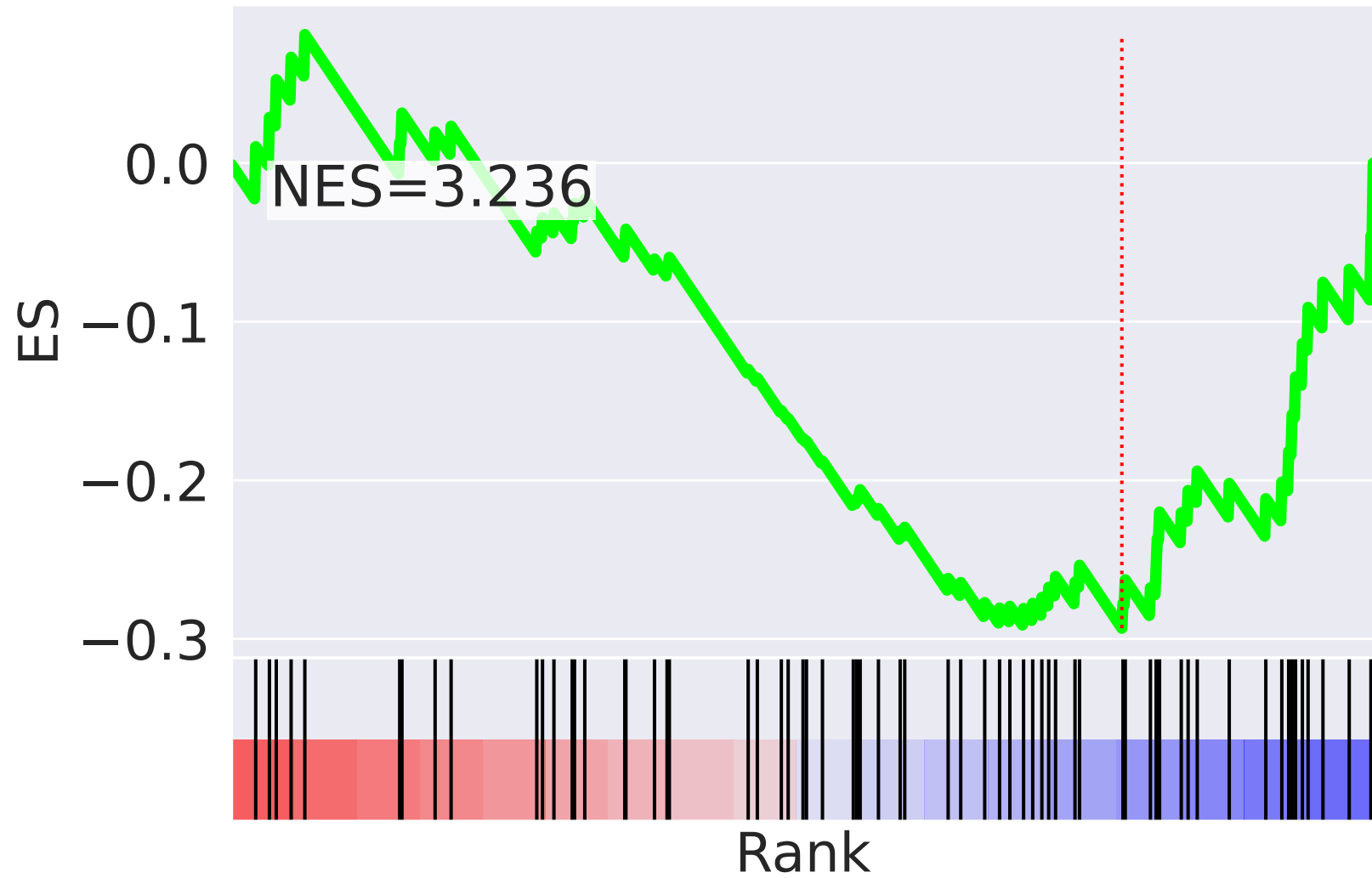
NES		SET
-3.336		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.831		signal transduction (GO:0007165)
2.702		cellular nitrogen compound metabolic process (GO:0034641)
2.663		vesicle-mediated transport (GO:0016192)
2.521		protein complex assembly (GO:0006461)
2.414		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.396		negative regulation of transcription, DNA-templated (GO:0045892)
-2.332		strand displacement (GO:0000732)
-2.259		regulation of cellular response to heat (GO:1900034)
2.245		tricarboxylic acid cycle (GO:0006099)
-2.222		DNA synthesis involved in DNA repair (GO:0000731)
2.150		regulation of apoptotic process (GO:0042981)
2.093		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
2.067		negative regulation of cell growth (GO:0030308)
-2.044		viral transcription (GO:0019083)

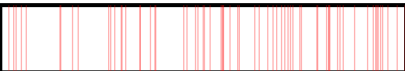




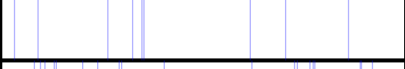




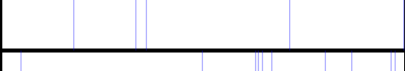




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=9$

mitochondrial translational elongation (GO:0070125)



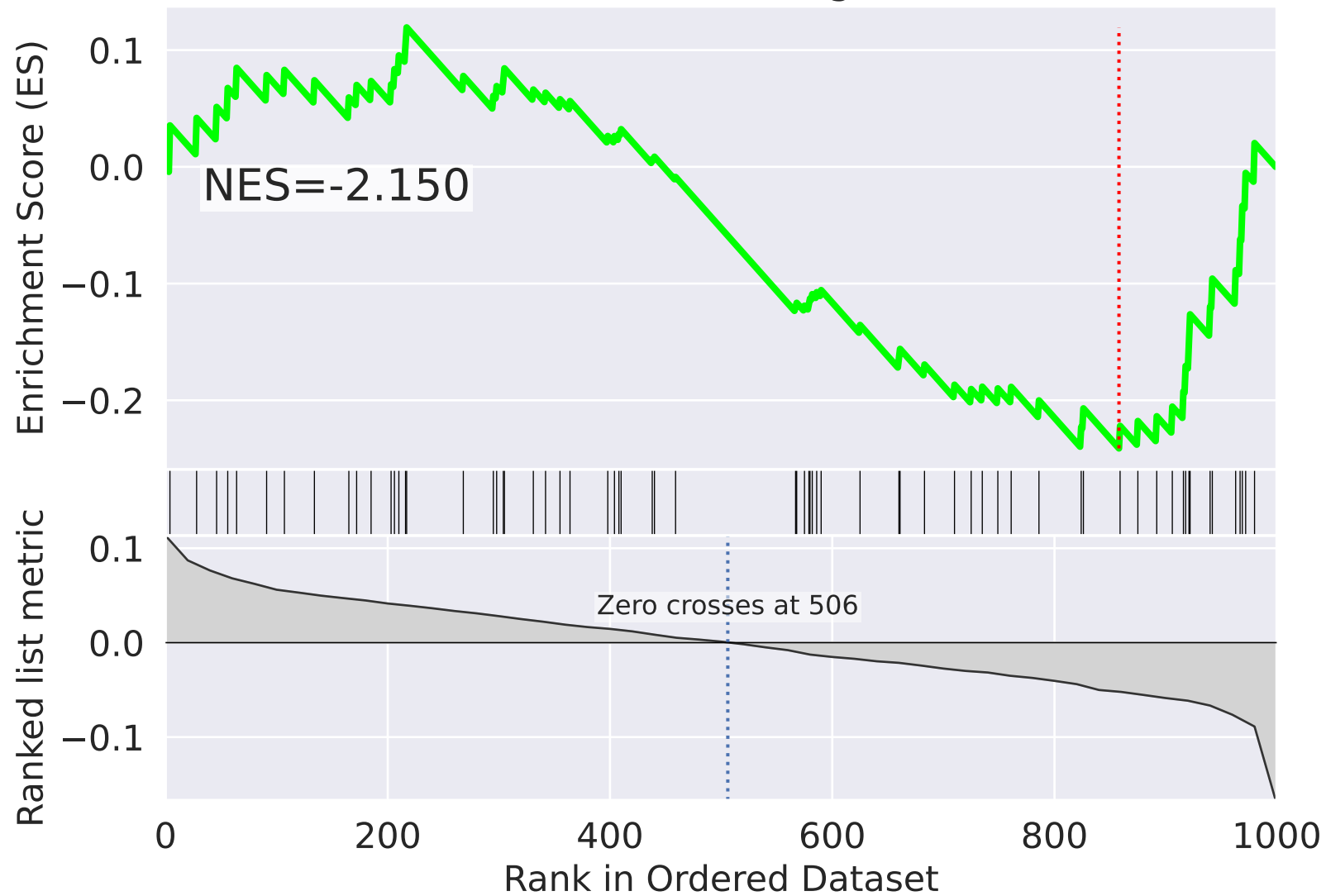
mitochondrial translational elongation (GO:0070125)



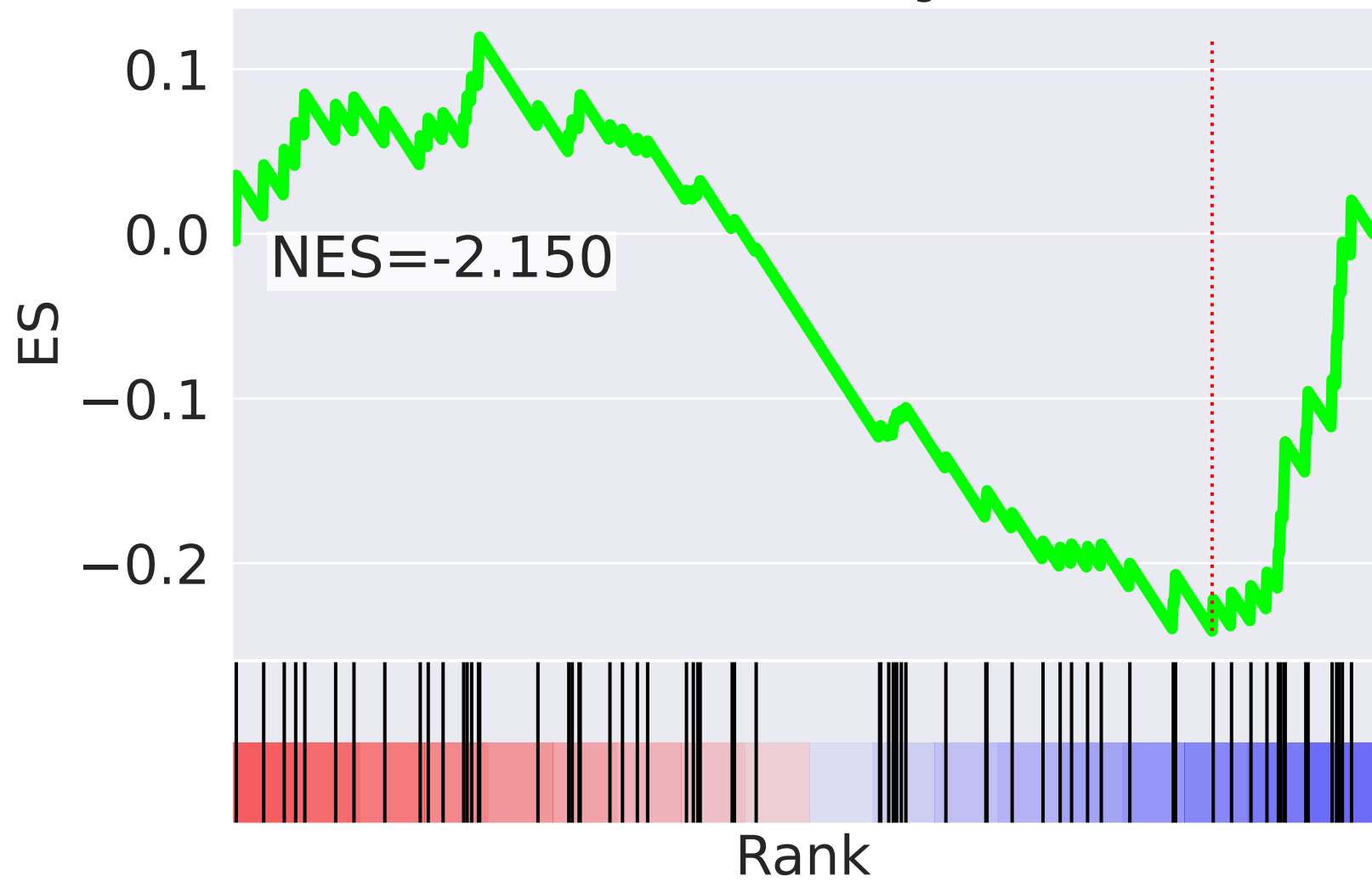
NES		SET
3.236		mitochondrial translational elongation (GO:0070125)
3.058		mitochondrial translational termination (GO:0070126)
-2.935		response to endoplasmic reticulum stress (GO:0034976)
-2.577		protein phosphorylation (GO:0006468)
-2.529		mRNA 3'-end processing (GO:0031124)
-2.380		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
-2.378		mRNA export from nucleus (GO:0006406)
-2.360		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.310		platelet aggregation (GO:0070527)
-2.207		mitotic spindle organization (GO:0007052)
-2.192		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.159		strand displacement (GO:0000732)
-2.152		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
-2.128		positive regulation of protein catabolic process (GO:0045732)
-2.025		DNA-dependent DNA replication (GO:0006261)



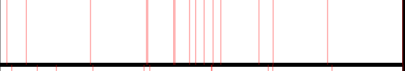
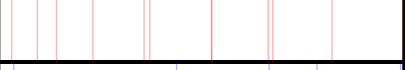




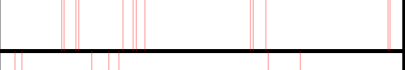
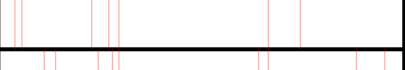
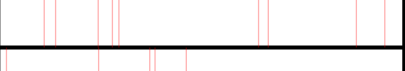
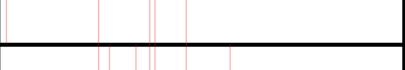

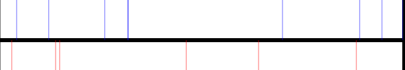
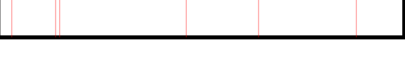
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=10$

mitochondrial translational elongation (GO:0070125)



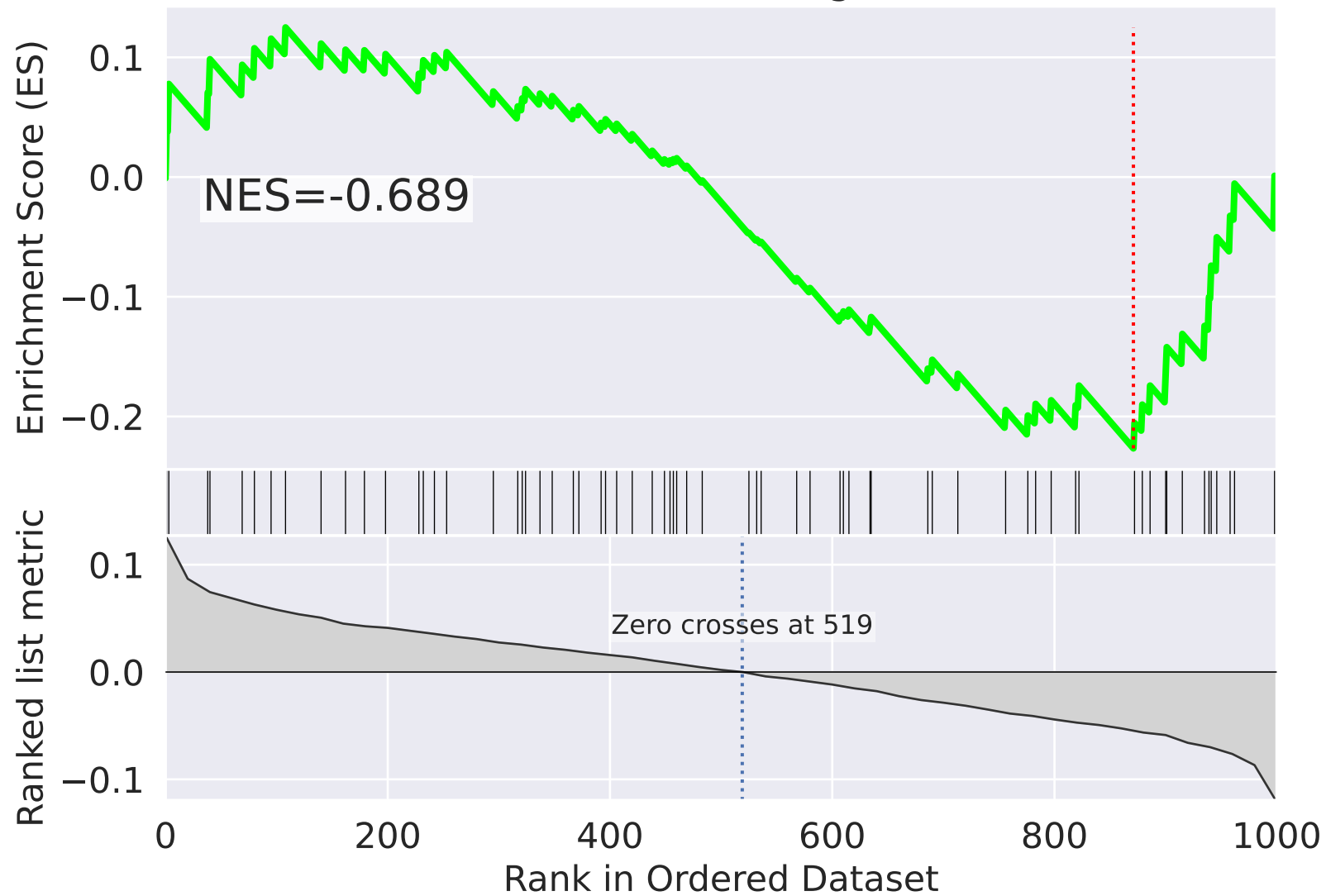
mitochondrial translational elongation (GO:0070125)



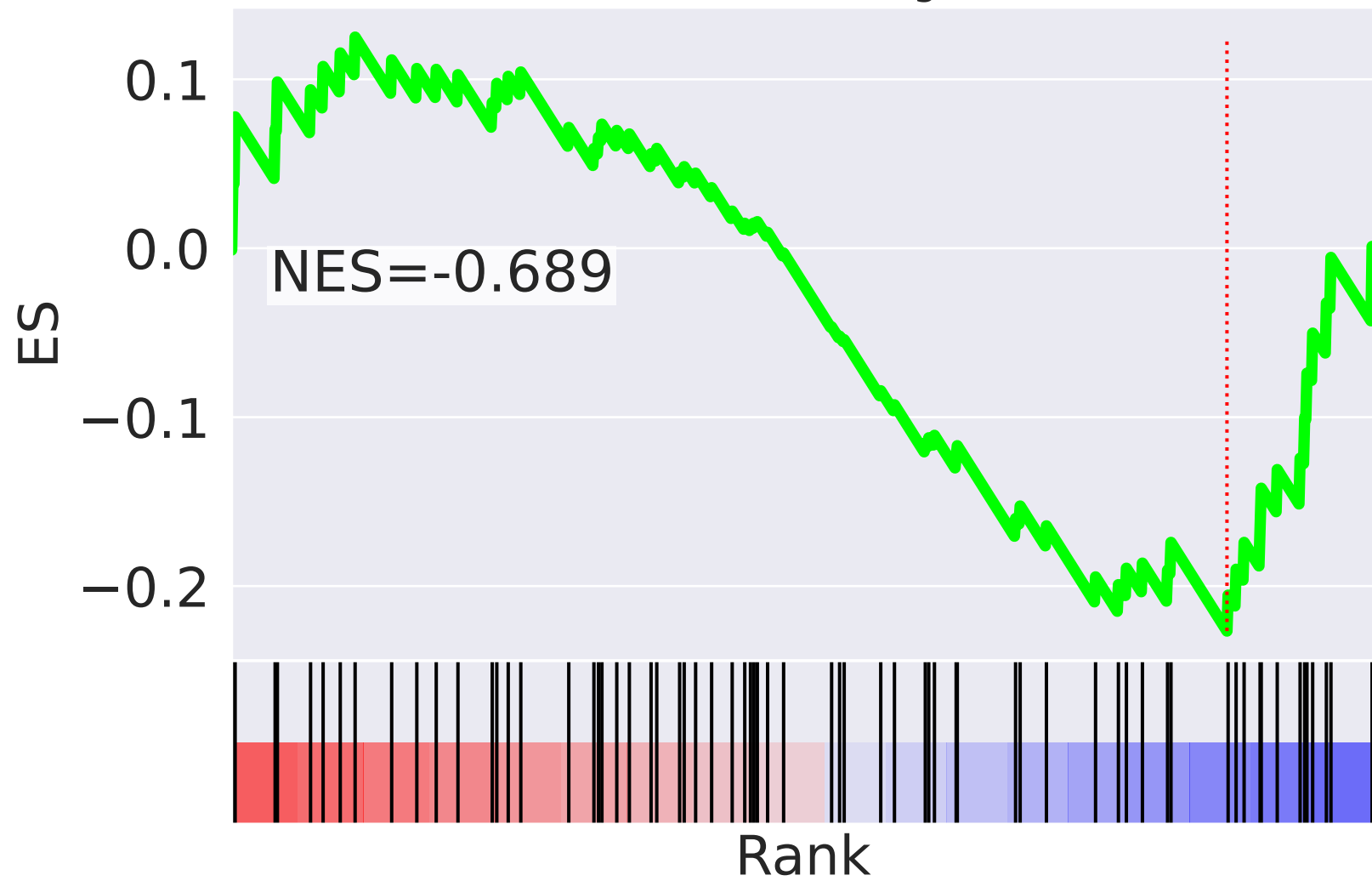
NES		SET
2.686		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.676		epidermal growth factor receptor signaling pathway (GO:0007173)
2.632		protein complex assembly (GO:0006461)
2.559		protein phosphorylation (GO:0006468)
-2.555		cellular iron ion homeostasis (GO:0006879)
2.524		G2/M transition of mitotic cell cycle (GO:0000086)
2.499		MAPK cascade (GO:0000165)
2.475		ciliary basal body docking (GO:0097711)
2.457		ER to Golgi vesicle-mediated transport (GO:0006888)
2.415		regulation of protein stability (GO:0031647)
2.359		axon guidance (GO:0007411)
2.332		substrate adhesion-dependent cell spreading (GO:0034446)
2.258		cell-matrix adhesion (GO:0007160)
-2.251		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
2.248		T cell costimulation (GO:0031295)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=11$

mitochondrial translational elongation (GO:0070125)



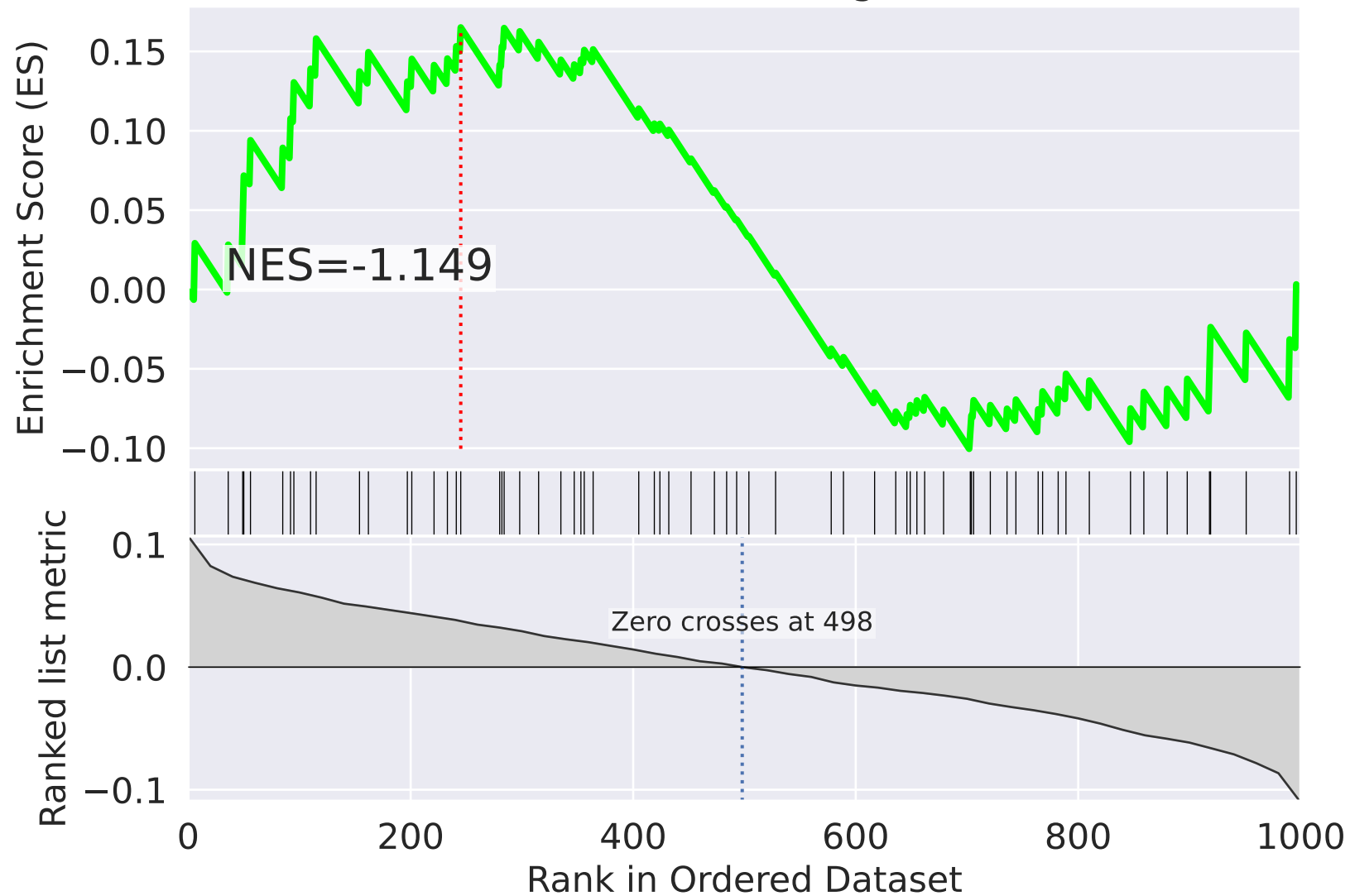
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.533		protein complex assembly (GO:0006461)
2.527		protein homooligomerization (GO:0051260)
2.451		epidermal growth factor receptor signaling pathway (GO:0007173)
2.329		sister chromatid cohesion (GO:0007062)
2.198		cellular response to epidermal growth factor stimulus (GO:0071364)
2.179		regulation of centrosome duplication (GO:0010824)
2.177		regulation of lipid metabolic process (GO:0019216)
-2.091		cell-matrix adhesion (GO:0007160)
2.013		substantia nigra development (GO:0021762)
1.993		positive regulation by host of viral transcription (GO:0043923)
1.886		Wnt signaling pathway (GO:0016055)
1.861		post-translational protein modification (GO:0043687)
-1.857		intracellular signal transduction (GO:0035556)
1.853		telomere maintenance via recombination (GO:0000722)
1.829		mitotic metaphase plate congression (GO:0007080)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=12$

mitochondrial translational elongation (GO:0070125)



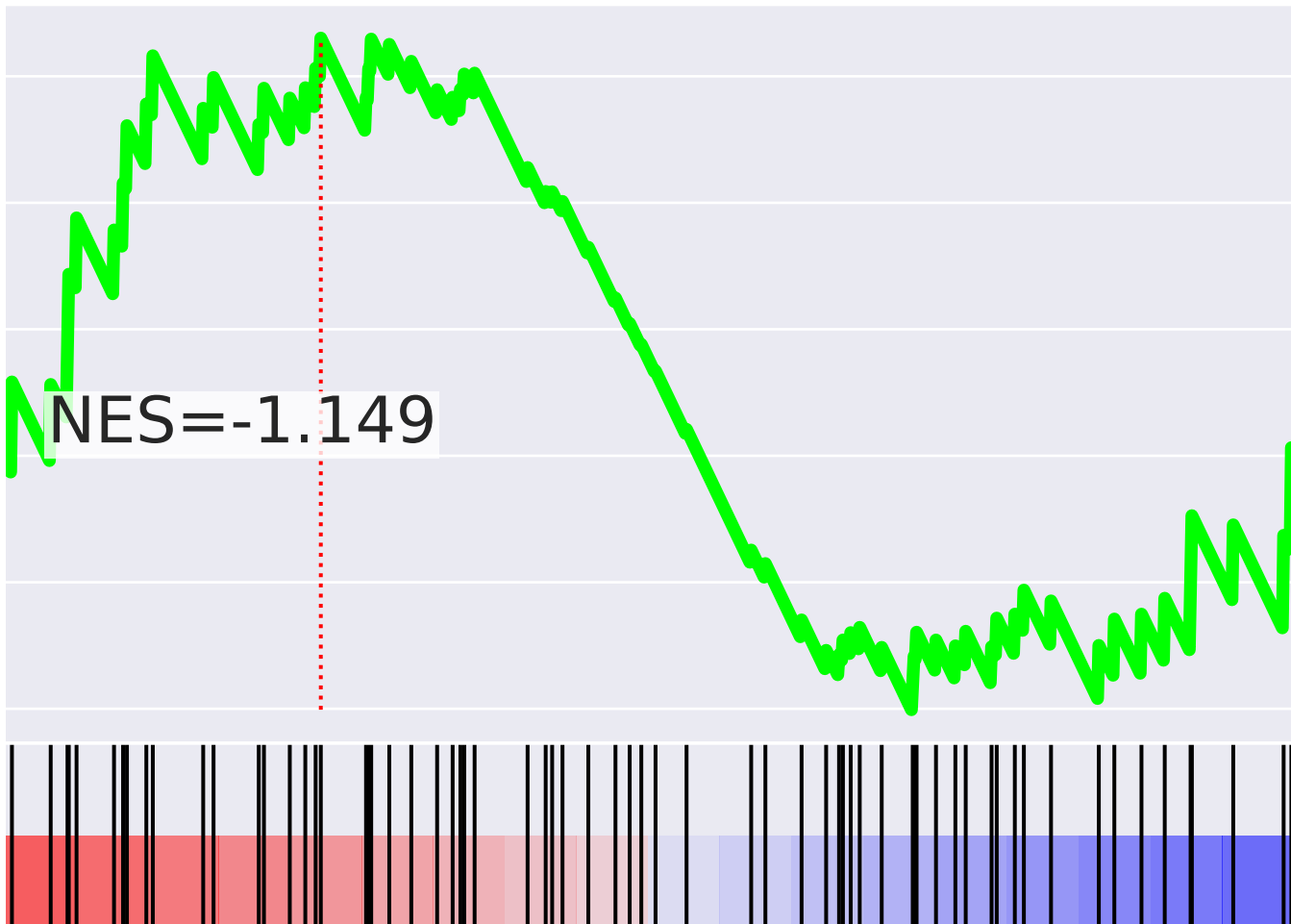
mitochondrial translational elongation (GO:0070125)

ES

0.15
0.10
0.05
0.00
-0.05
-0.10




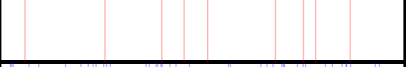
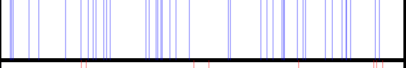
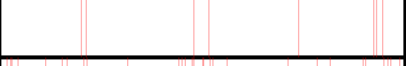
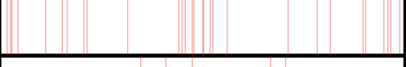





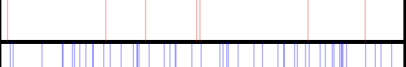
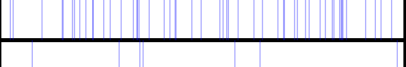
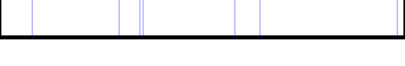
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Rank



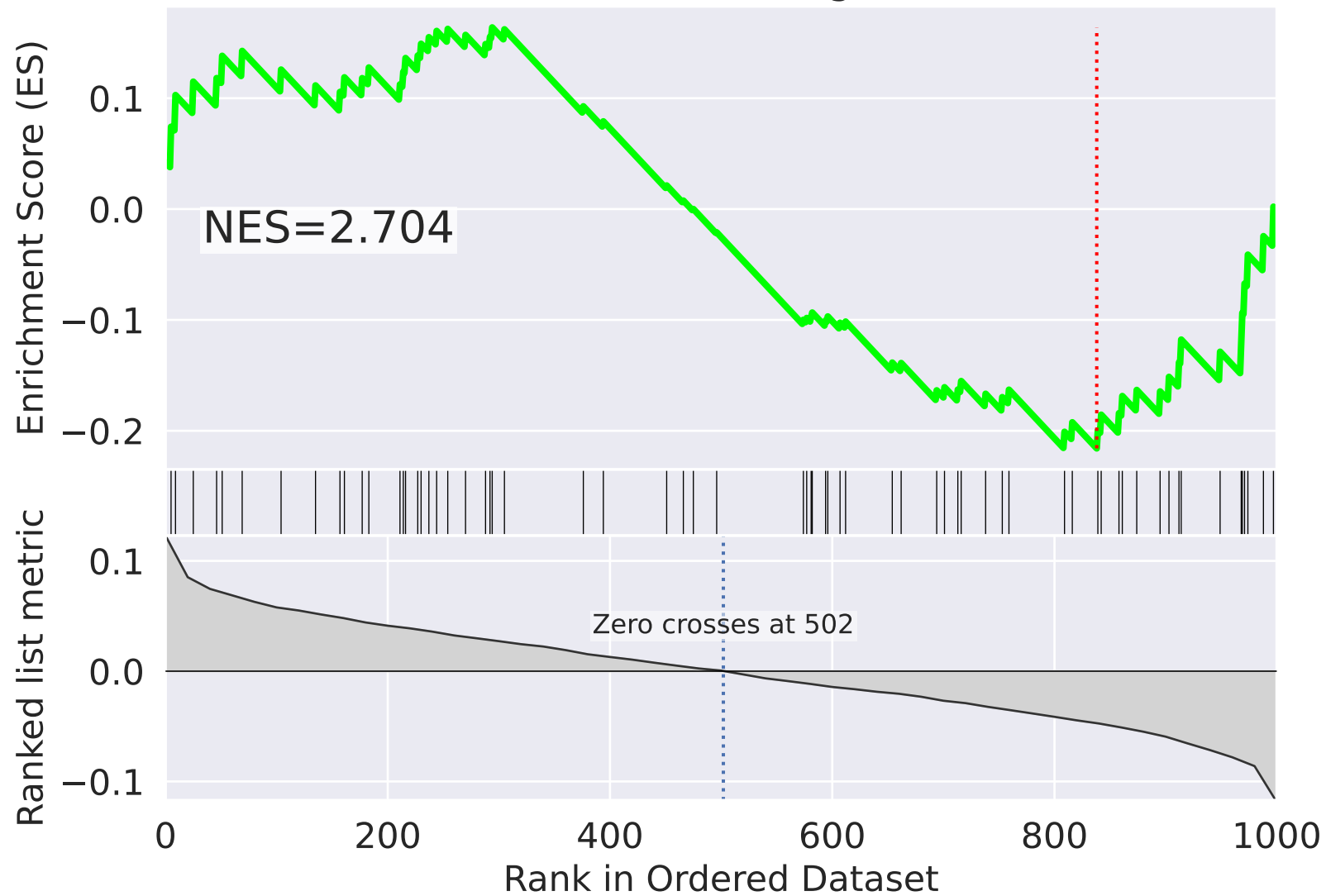
NES

SET

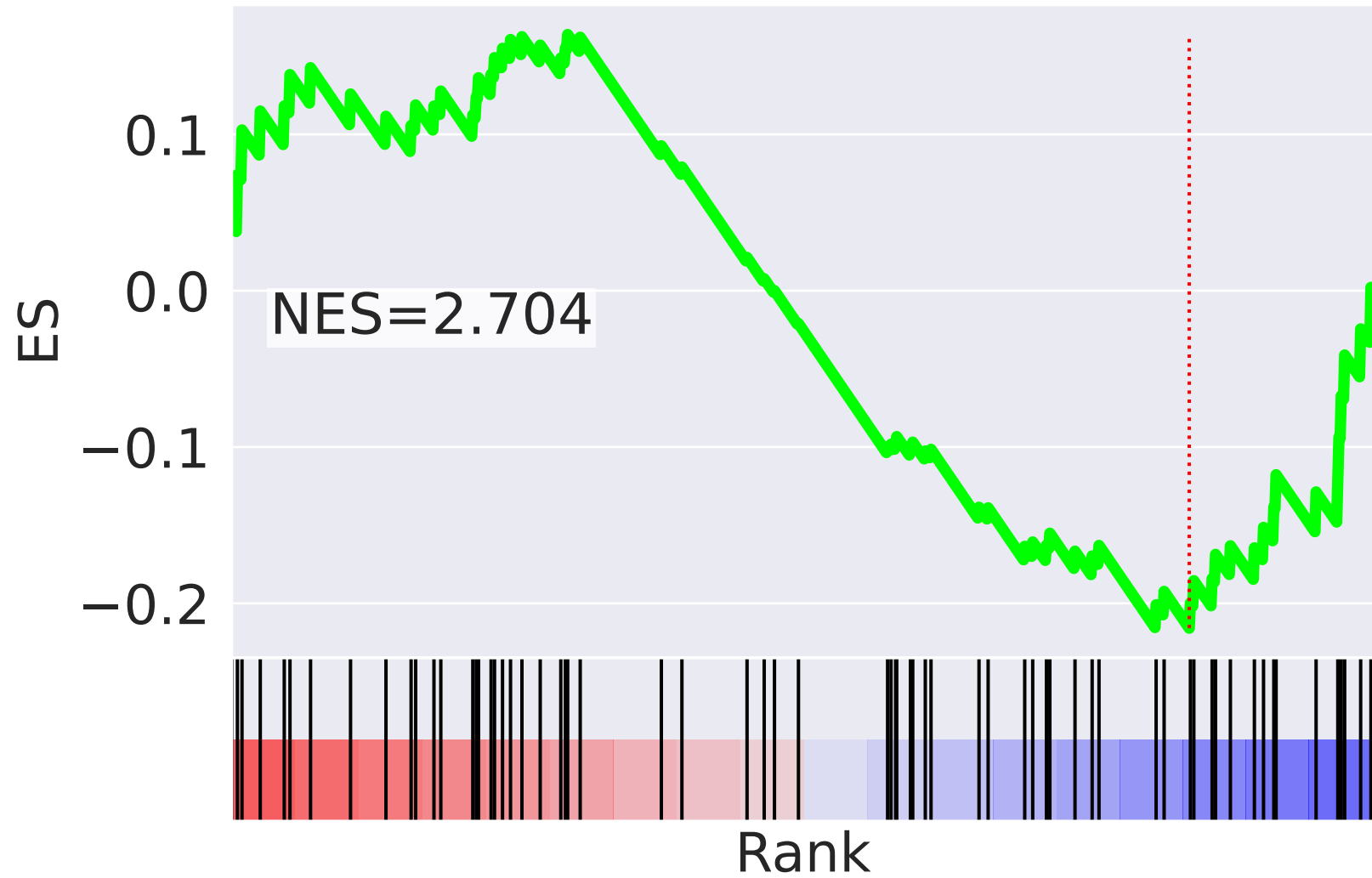
-2.514		phosphatidylinositol biosynthetic process (GO:0006661)
-2.378		telomere capping (GO:0016233)
2.162		protein K11-linked ubiquitination (GO:0070979)
2.151		mitotic cytokinesis (GO:0000281)
-2.087		positive regulation of transcription, DNA-templated (GO:0045893)
2.078		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.000		neutrophil degranulation (GO:0043312)
1.952		cellular iron ion homeostasis (GO:0006879)
1.914		viral life cycle (GO:0019058)
-1.899		telomere maintenance (GO:0000723)
1.899		mRNA 3'-end processing (GO:0031124)
1.895		platelet aggregation (GO:0070527)
1.892		termination of RNA polymerase II transcription (GO:0006369)
-1.891		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-1.834		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 $z=13$

mitochondrial translational elongation (GO:0070125)





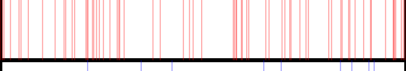
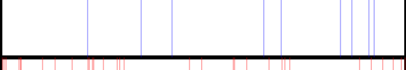


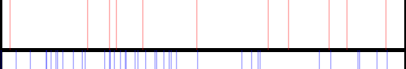
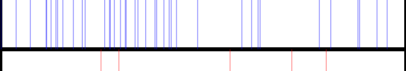
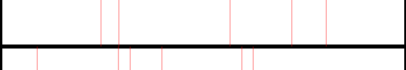

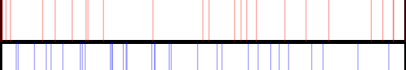
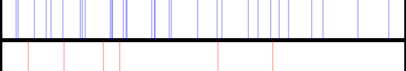



mitochondrial translational elongation (GO:0070125)



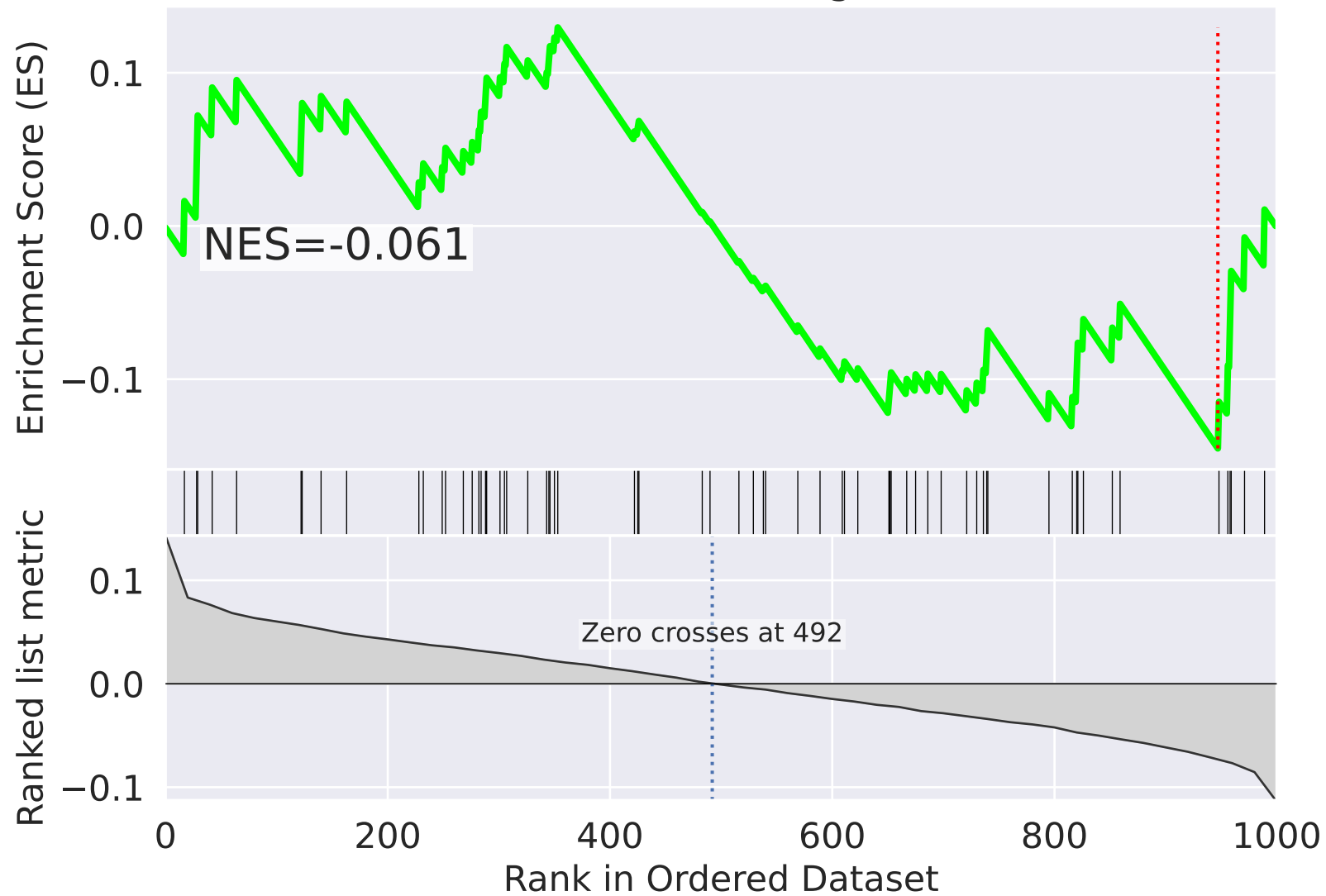
NES

SET

3.255		retrograde transport, endosome to Golgi (GO:0042147)
2.778		positive regulation of GTPase activity (GO:0043547)
2.766		cell migration (GO:0016477)
2.704		mitochondrial translational elongation (GO:0070125)
2.688		mitochondrial translational termination (GO:0070126)
-2.329		regulation of macroautophagy (GO:0016241)
2.293		translation (GO:0006412)
2.235		double-strand break repair (GO:0006302)
2.217		positive regulation of gene expression (GO:0010628)
-2.202		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.152		transcription from mitochondrial promoter (GO:0006390)
2.101		mRNA processing (GO:0006397)
2.078		mitochondrial translation (GO:0032543)
-2.066		negative regulation of transcription, DNA-templated (GO:0045892)
2.046		DNA damage response, detection of DNA damage (GO:0042769)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=14$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

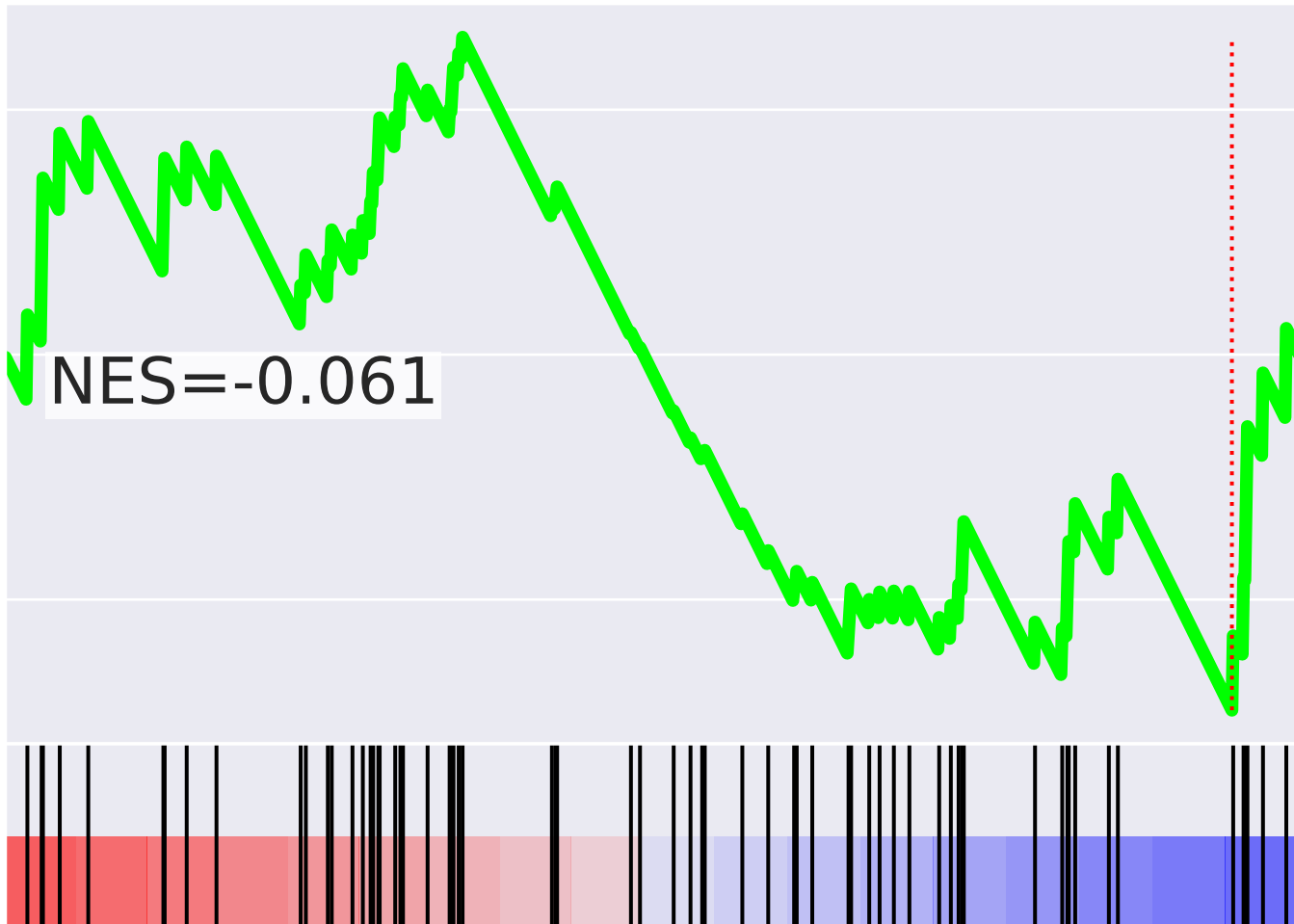
0.1

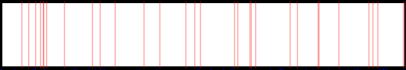



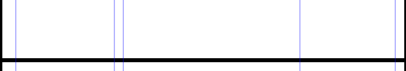



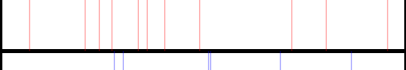




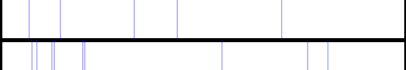

0.0

-0.1

NES=-0.061

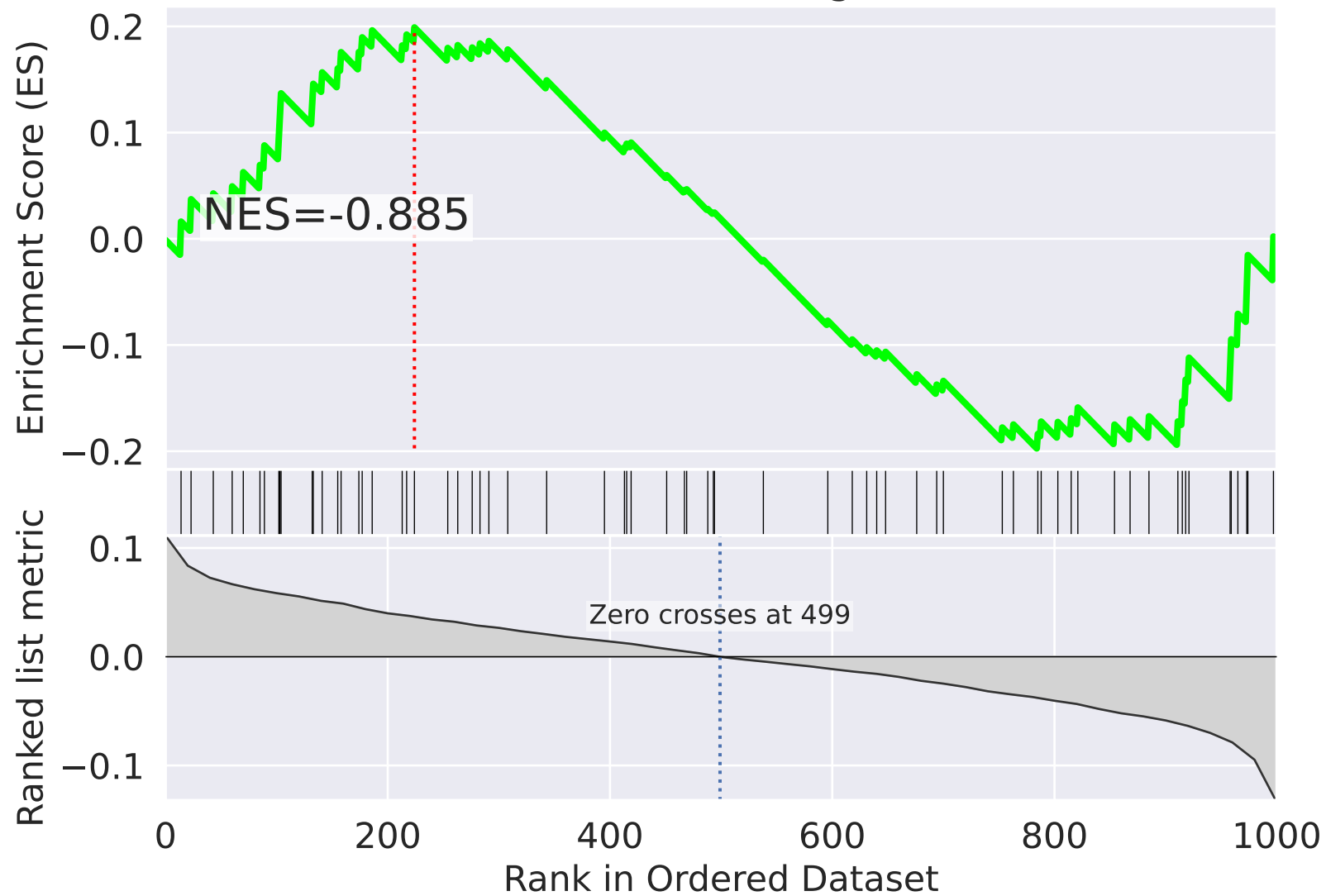
Rank



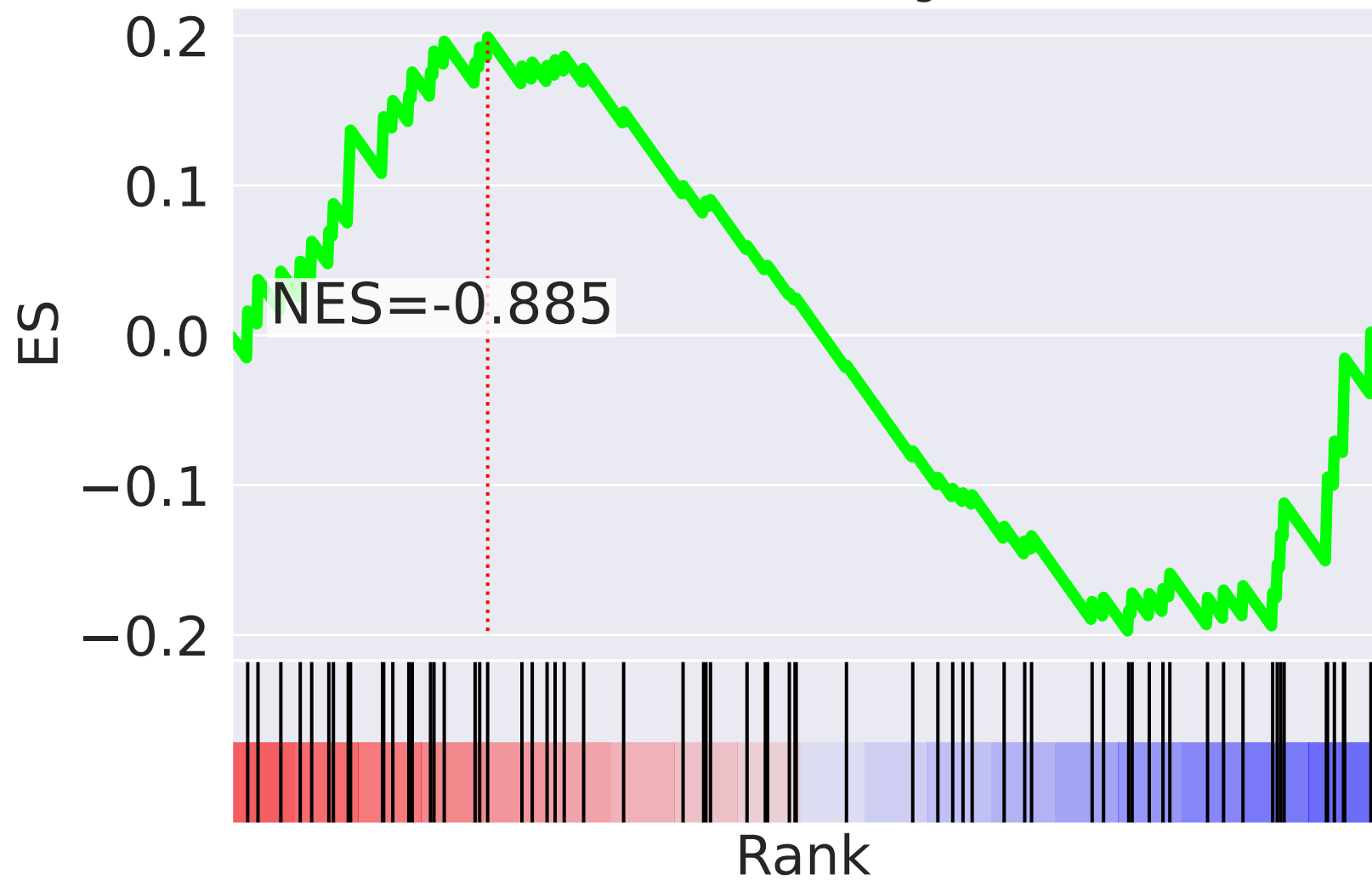
NES		SET
2.649		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.453		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.401		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.221		termination of RNA polymerase I transcription (GO:0006363)
-2.221		transcription elongation from RNA polymerase I promoter (GO:0006362)
-2.221		transcription initiation from RNA polymerase I promoter (GO:0006361)
-2.114		transforming growth factor beta receptor signaling pathway (GO:0007179)
-2.102		apoptotic process (GO:0006915)
2.033		regulation of mRNA stability (GO:0043488)
-1.991		transcription-coupled nucleotide-excision repair (GO:0006283)
1.953		cell differentiation (GO:0030154)
1.949		tricarboxylic acid cycle (GO:0006099)
1.920		protein polyubiquitination (GO:0000209)
-1.874		regulation of defense response to virus by virus (GO:0050690)
-1.866		Golgi organization (GO:0007030)


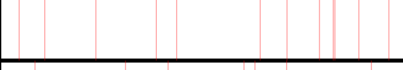

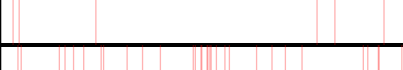
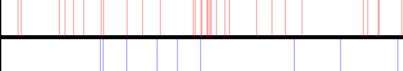

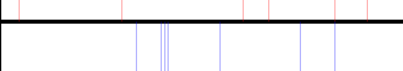



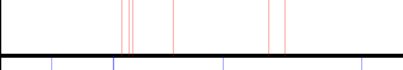
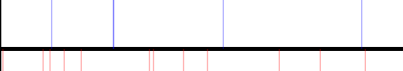
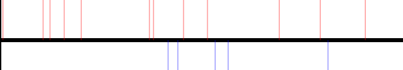


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=15$

mitochondrial translational elongation (GO:0070125)



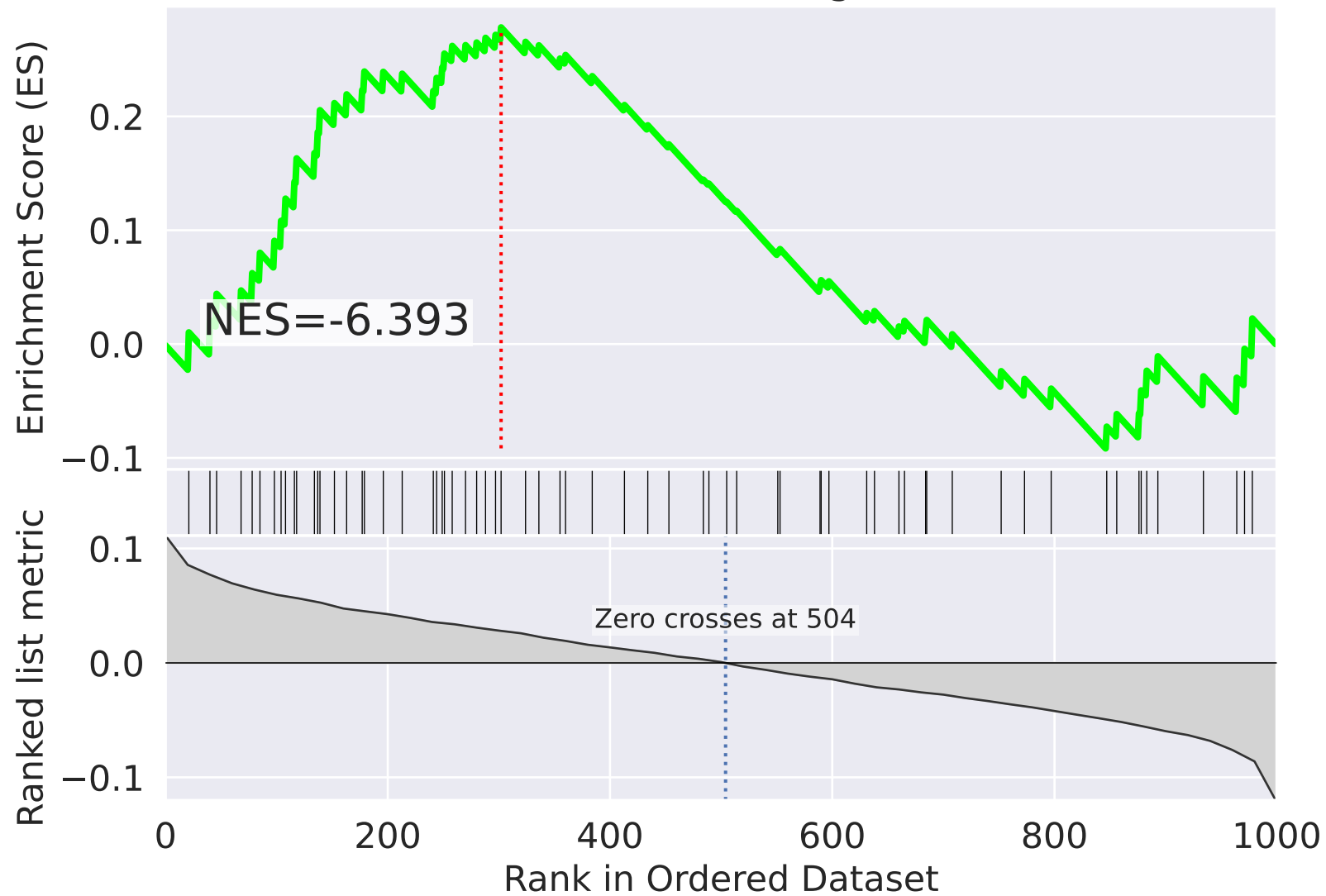
mitochondrial translational elongation (GO:0070125)



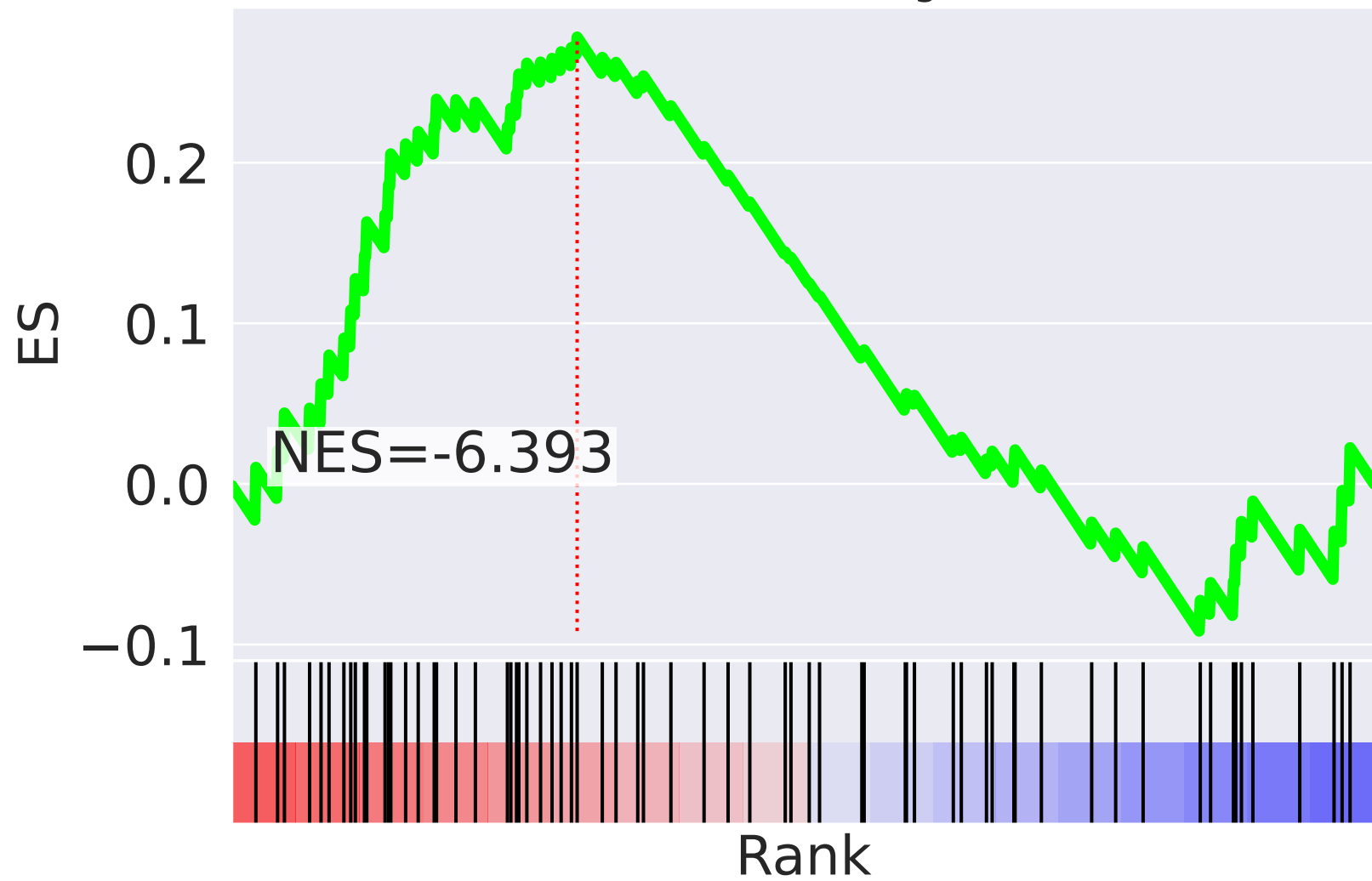
NES		SET
3.277		epidermal growth factor receptor signaling pathway (GO:0007173)
2.911		leukocyte migration (GO:0050900)
2.643		negative regulation of translation (GO:0017148)
2.553		T cell costimulation (GO:0031295)
2.538		protein deubiquitination (GO:0016579)
-2.437		tRNA aminoacylation for protein translation (GO:0006418)
2.379		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.312		innate immune response (GO:0045087)
-2.237		iron-sulfur cluster assembly (GO:0016226)
-2.233		chromatin remodeling (GO:0006338)
-2.154		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.140		RNA metabolic process (GO:0016070)
-2.122		cellular respiration (GO:0045333)
2.116		regulation of cholesterol biosynthetic process (GO:0045540)
-2.115		RNA secondary structure unwinding (GO:0010501)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=16$

mitochondrial translational elongation (GO:0070125)



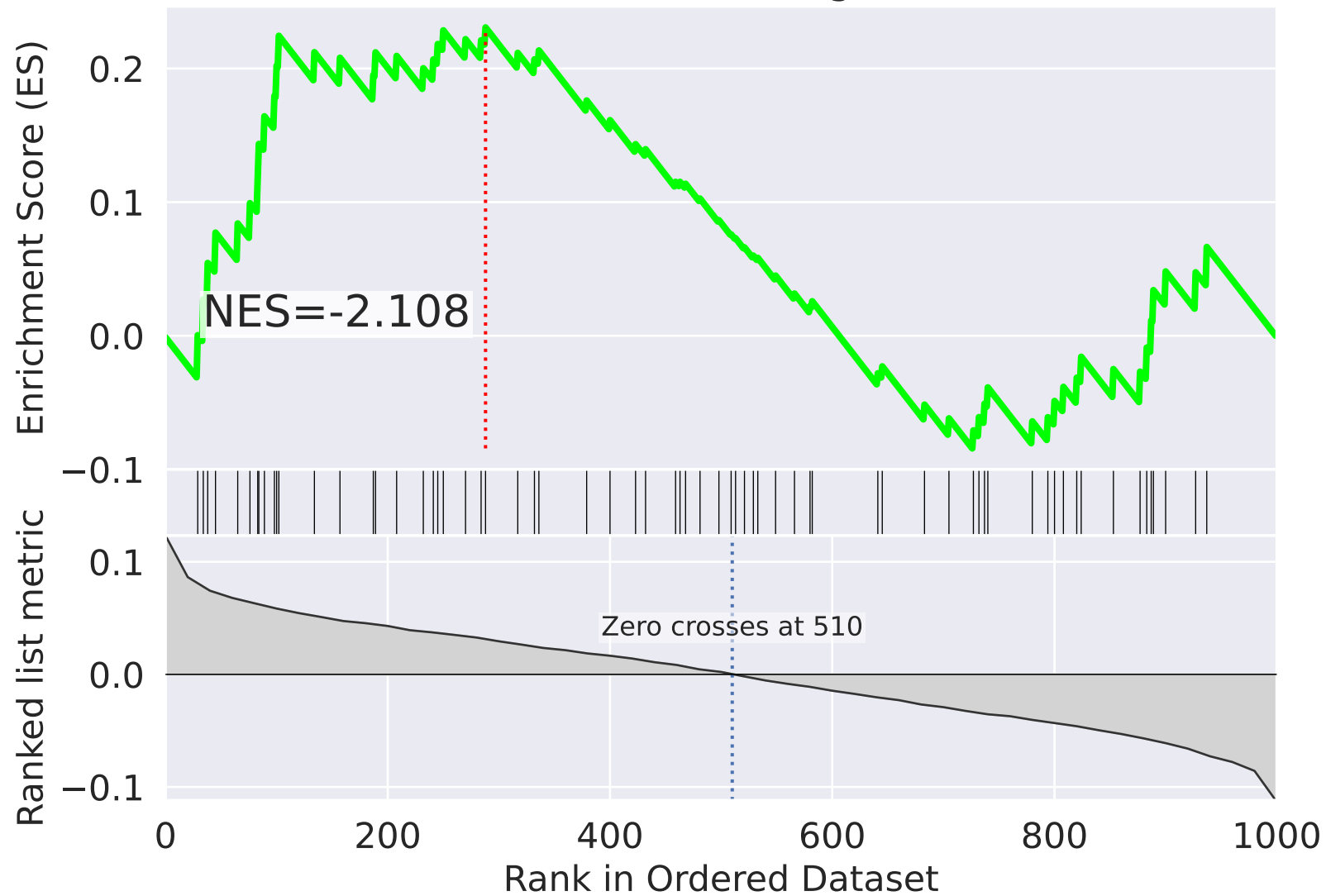
mitochondrial translational elongation (GO:0070125)



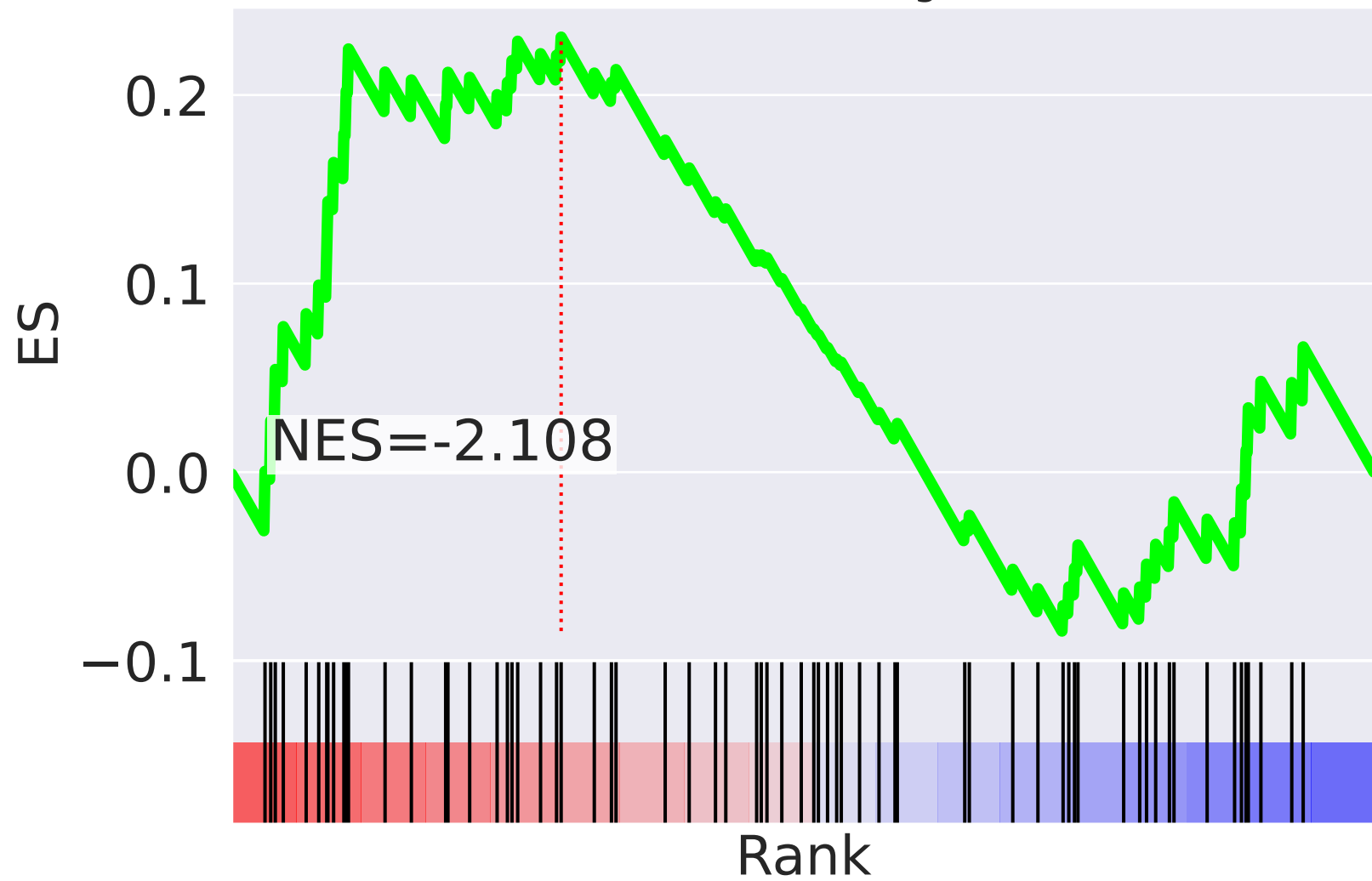
NES		SET
-6.393		mitochondrial translational elongation (GO:0070125)
-6.277		mitochondrial translational termination (GO:0070126)
2.766		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.495		negative regulation of cell proliferation (GO:0008285)
2.486		androgen receptor signaling pathway (GO:0030521)
-2.452		G1/S transition of mitotic cell cycle (GO:0000082)
2.436		positive regulation of transcription, DNA-templated (GO:0045893)
-2.310		cellular response to hypoxia (GO:0071456)
2.161		neutrophil degranulation (GO:0043312)
2.146		regulation of cell cycle (GO:0051726)
2.066		protein K63-linked ubiquitination (GO:0070534)
2.042		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
2.033		histone H4 acetylation (GO:0043967)
2.022		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.009		protein dephosphorylation (GO:0006470)


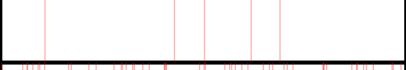
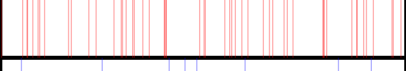
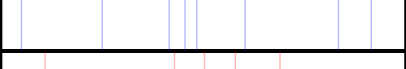

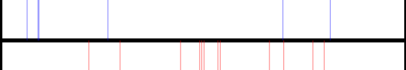
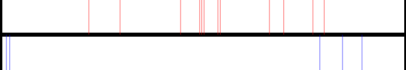

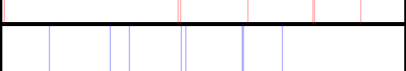

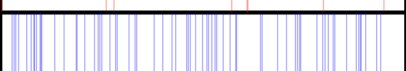


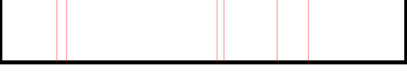

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=17$

mitochondrial translational elongation (GO:0070125)



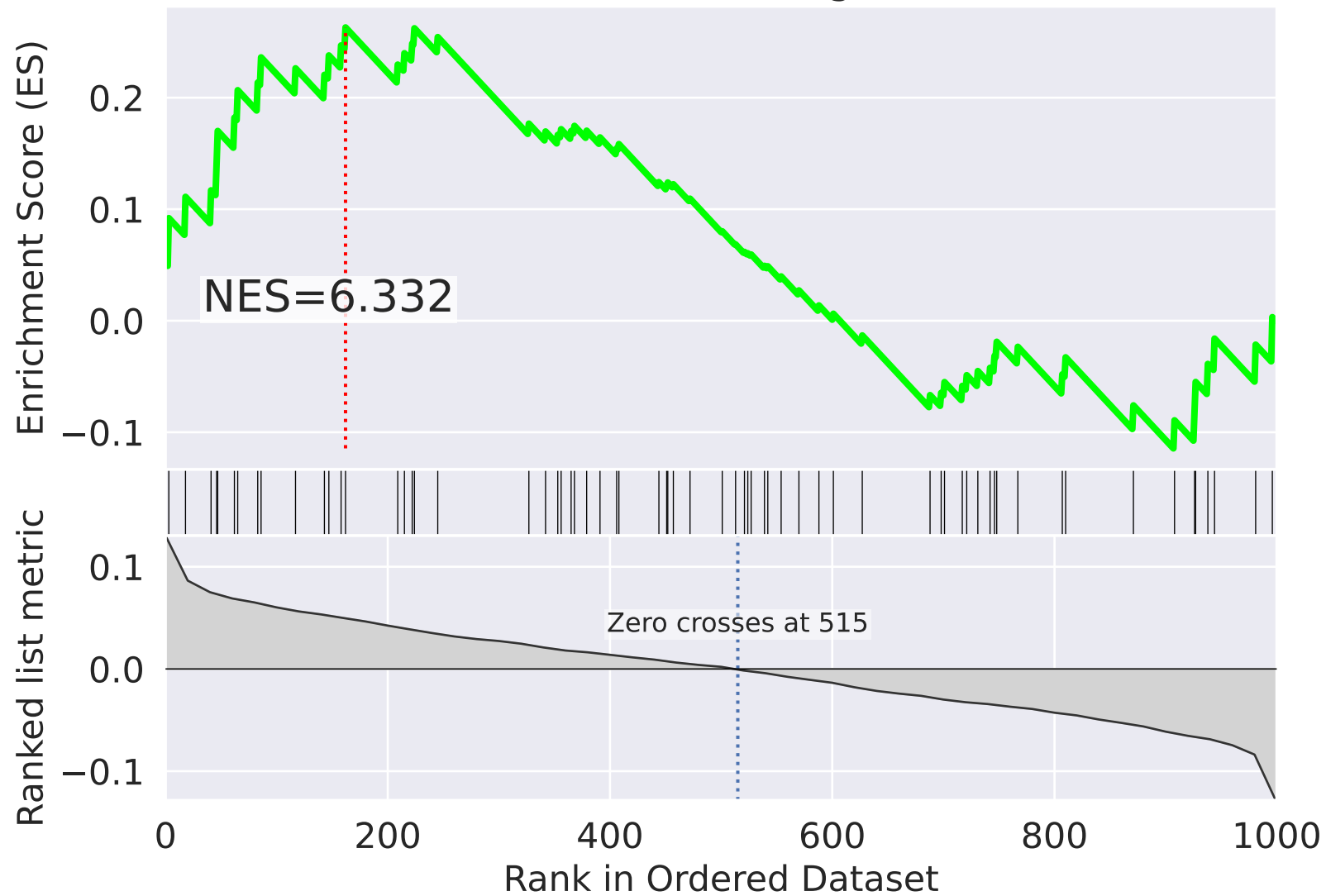
mitochondrial translational elongation (GO:0070125)



NES		SET
2.983		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.766		canonical glycolysis (GO:0061621)
2.423		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.391		tricarboxylic acid cycle (GO:0006099)
2.388		gluconeogenesis (GO:0006094)
-2.344		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
2.321		chromatin remodeling (GO:0006338)
-2.245		cellular respiration (GO:0045333)
2.153		positive regulation of gene expression, epigenetic (GO:0045815)
-2.116		rRNA processing (GO:0006364)
2.115		regulation of cell cycle (GO:0051726)
-2.108		mitochondrial translational elongation (GO:0070125)
-2.108		telomere maintenance (GO:0000723)
-2.040		intrinsic apoptotic signaling pathway (GO:0097193)
2.030		fibroblast growth factor receptor signaling pathway (GO:0008543)

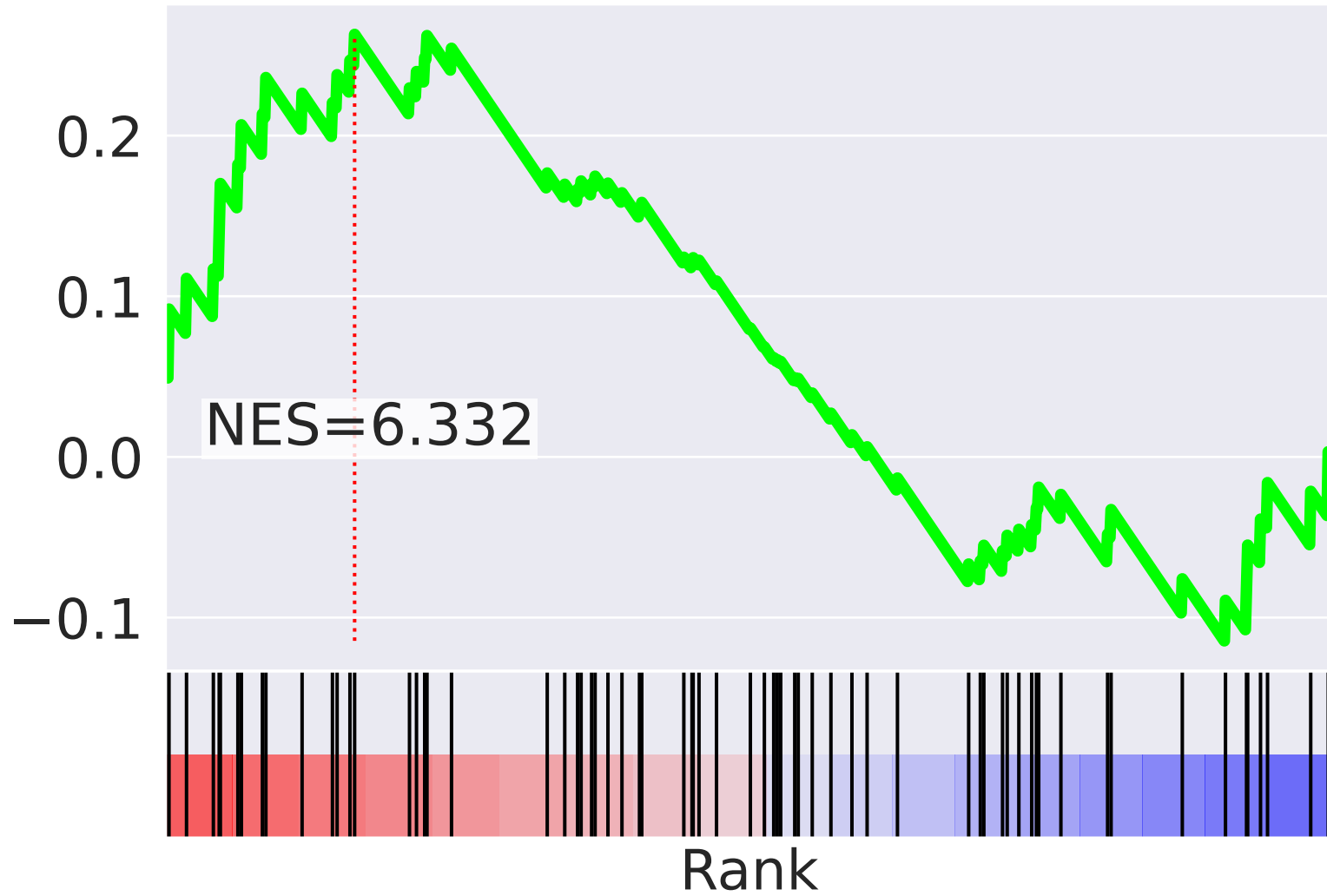
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=18$

mitochondrial translational elongation (GO:0070125)



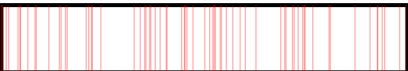
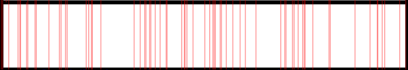



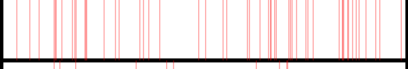
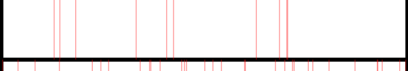
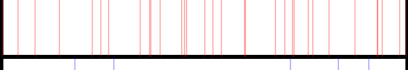


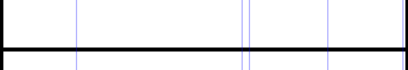
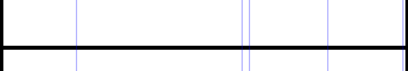


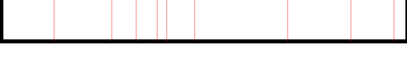
mitochondrial translational elongation (GO:0070125)

ES



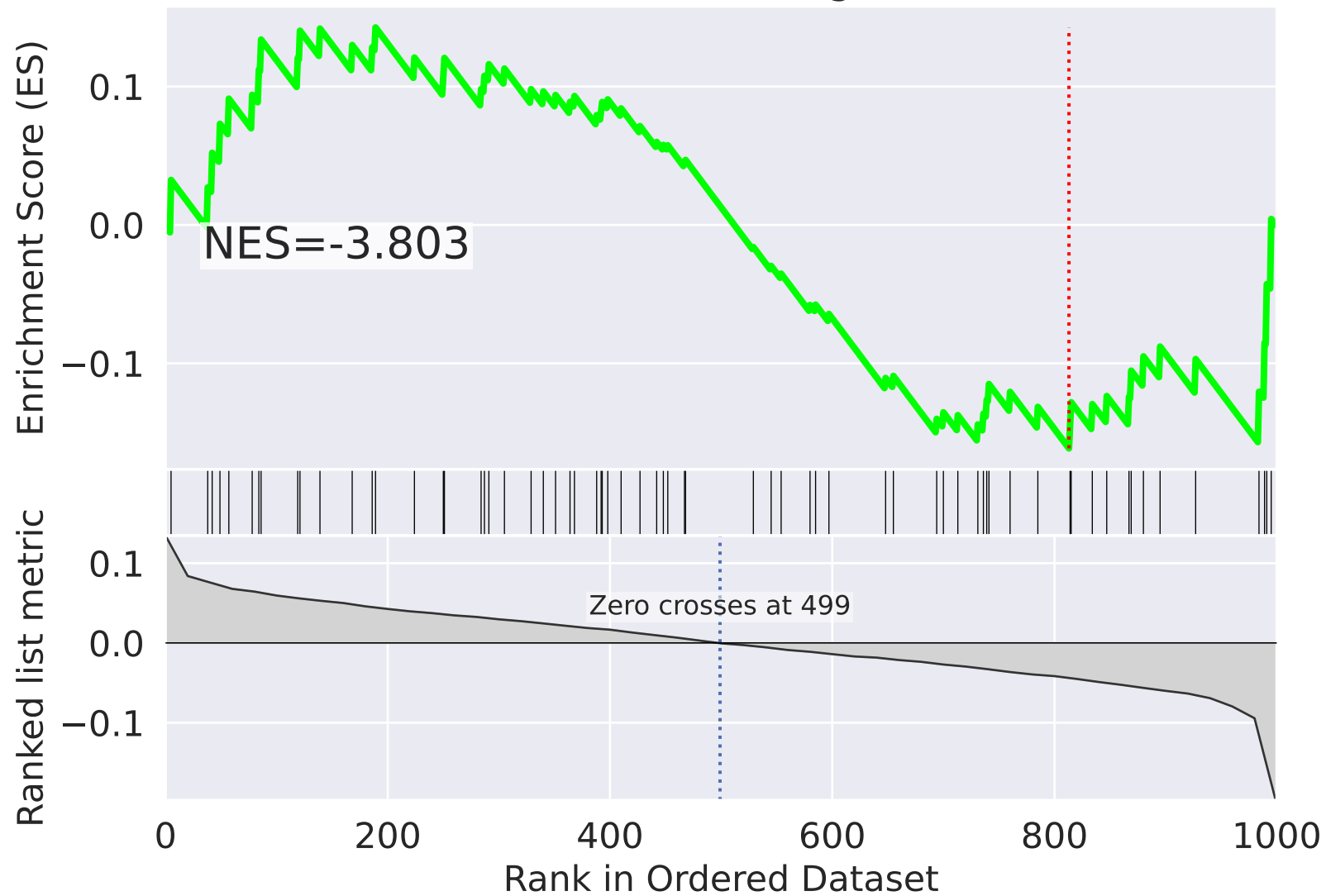
NES

SET

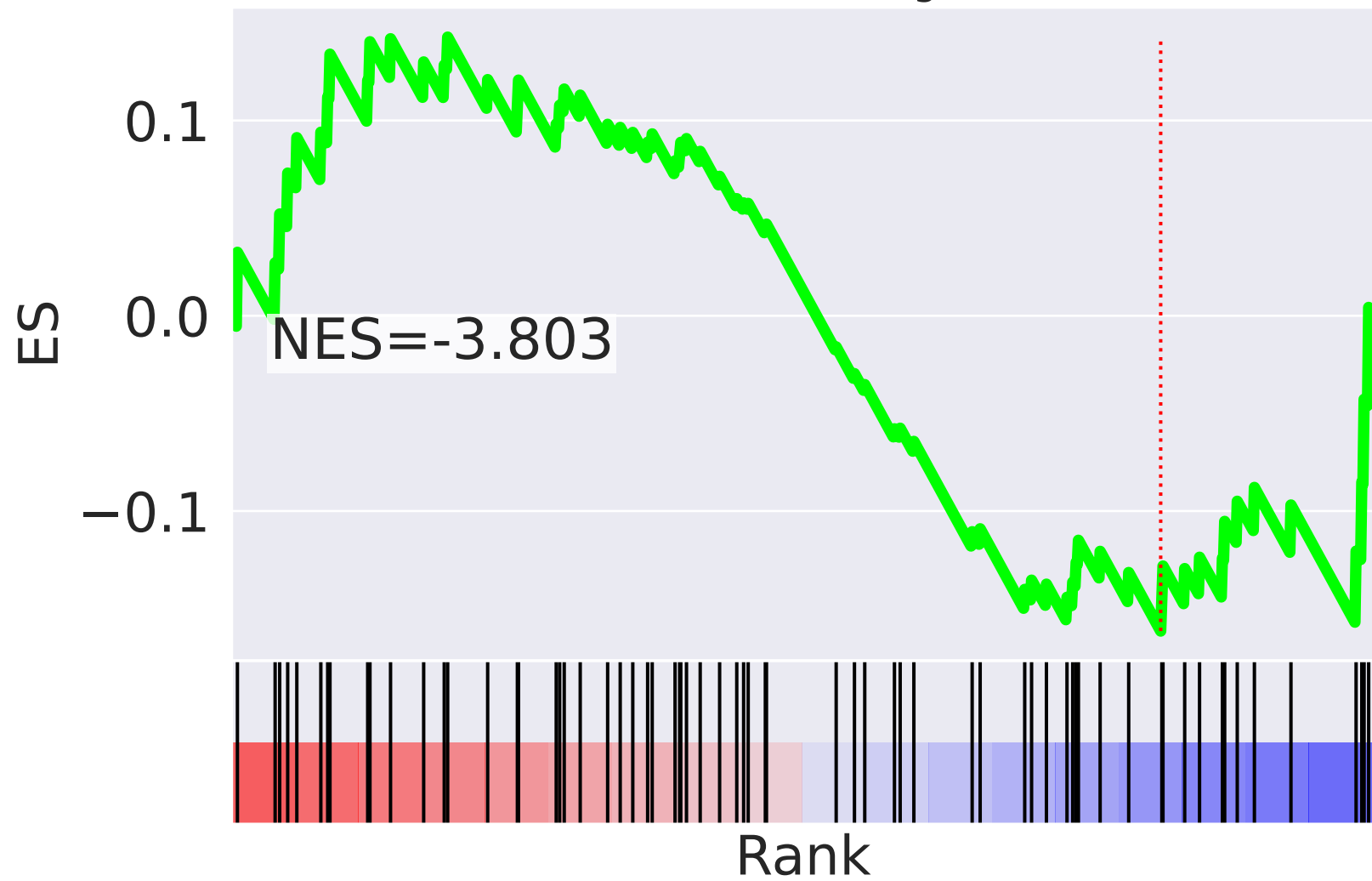
6.488		mitochondrial translational termination (GO:0070126)
6.332		mitochondrial translational elongation (GO:0070125)
-2.728		Fc-epsilon receptor signaling pathway (GO:0038095)
2.469		ciliary basal body docking (GO:0097711)
-2.423		T cell receptor signaling pathway (GO:0050852)
2.324		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.261		double-strand break repair via homologous recombination (GO:0000724)
2.187		translation (GO:0006412)
-2.167		regulation of lipid metabolic process (GO:0019216)
-2.157		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-2.088		termination of RNA polymerase I transcription (GO:0006363)
-2.088		transcription elongation from RNA polymerase I promoter (GO:0006362)
-2.088		transcription initiation from RNA polymerase I promoter (GO:0006361)
-2.073		DNA replication initiation (GO:0006270)
2.068		double-strand break repair (GO:0006302)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=19$

mitochondrial translational elongation (GO:0070125)



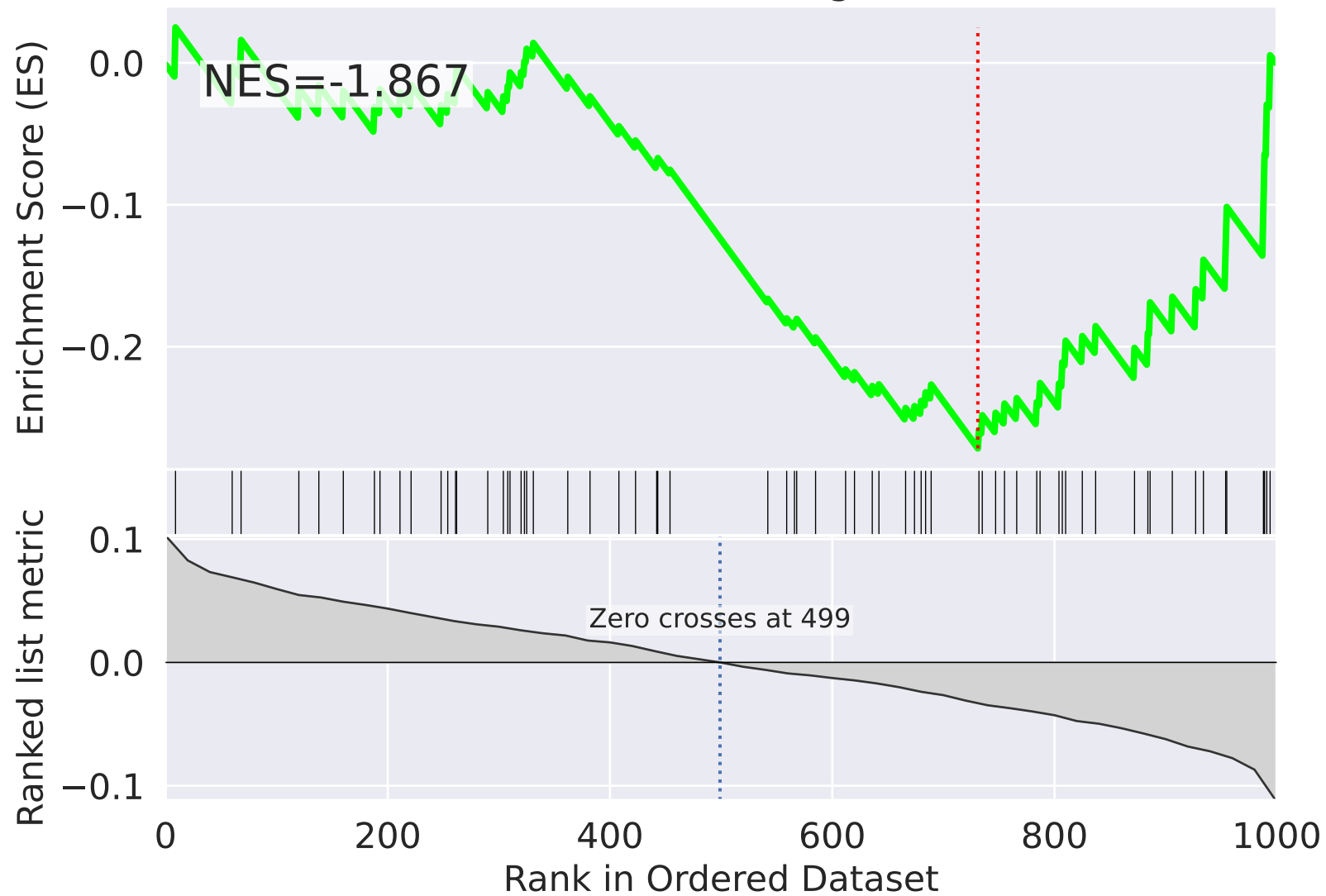
mitochondrial translational elongation (GO:0070125)



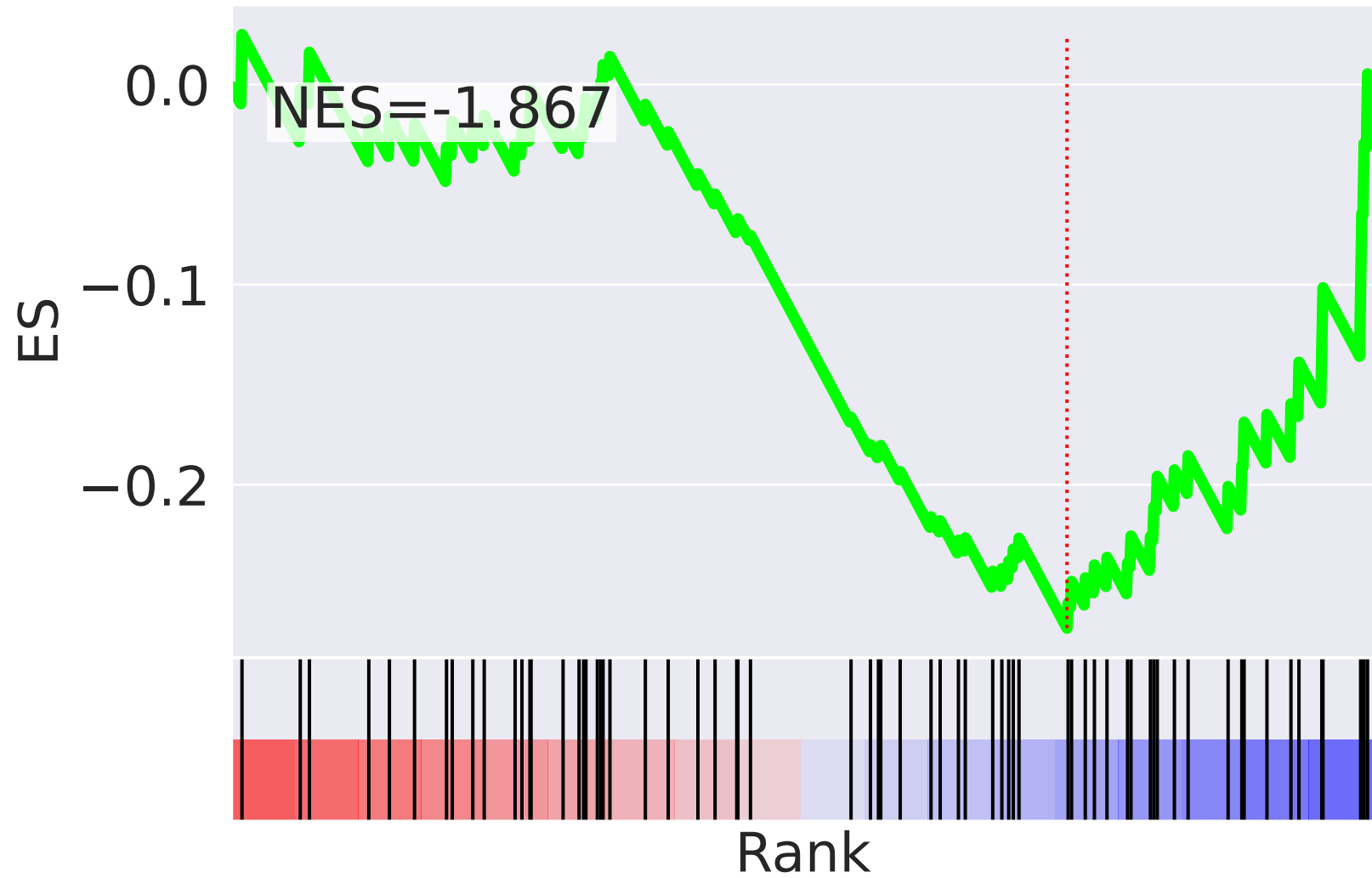
NES		SET
-3.930		mitochondrial translational termination (GO:0070126)
-3.803		mitochondrial translational elongation (GO:0070125)
-2.736		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.715		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.683		mRNA 3'-end processing (GO:0031124)
-2.630		cellular respiration (GO:0045333)
-2.621		DNA damage response, detection of DNA damage (GO:0042769)
2.548		chromatin remodeling (GO:0006338)
-2.501		DNA-dependent DNA replication (GO:0006261)
-2.468		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.437		rRNA processing (GO:0006364)
2.382		cell cycle arrest (GO:0007050)
2.373		vesicle-mediated transport (GO:0016192)
2.202		peptidyl-serine phosphorylation (GO:0018105)
2.185		telomere capping (GO:0016233)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=20$

mitochondrial translational elongation (GO:0070125)



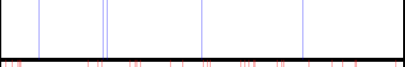
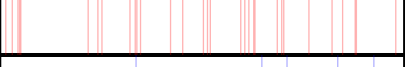

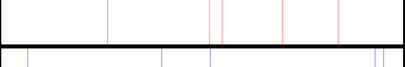
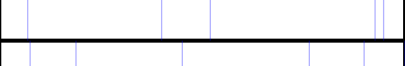
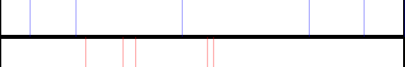

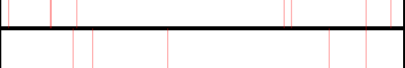

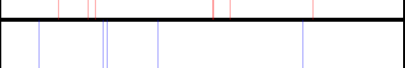


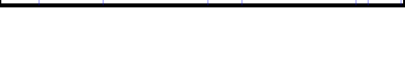


mitochondrial translational elongation (GO:0070125)



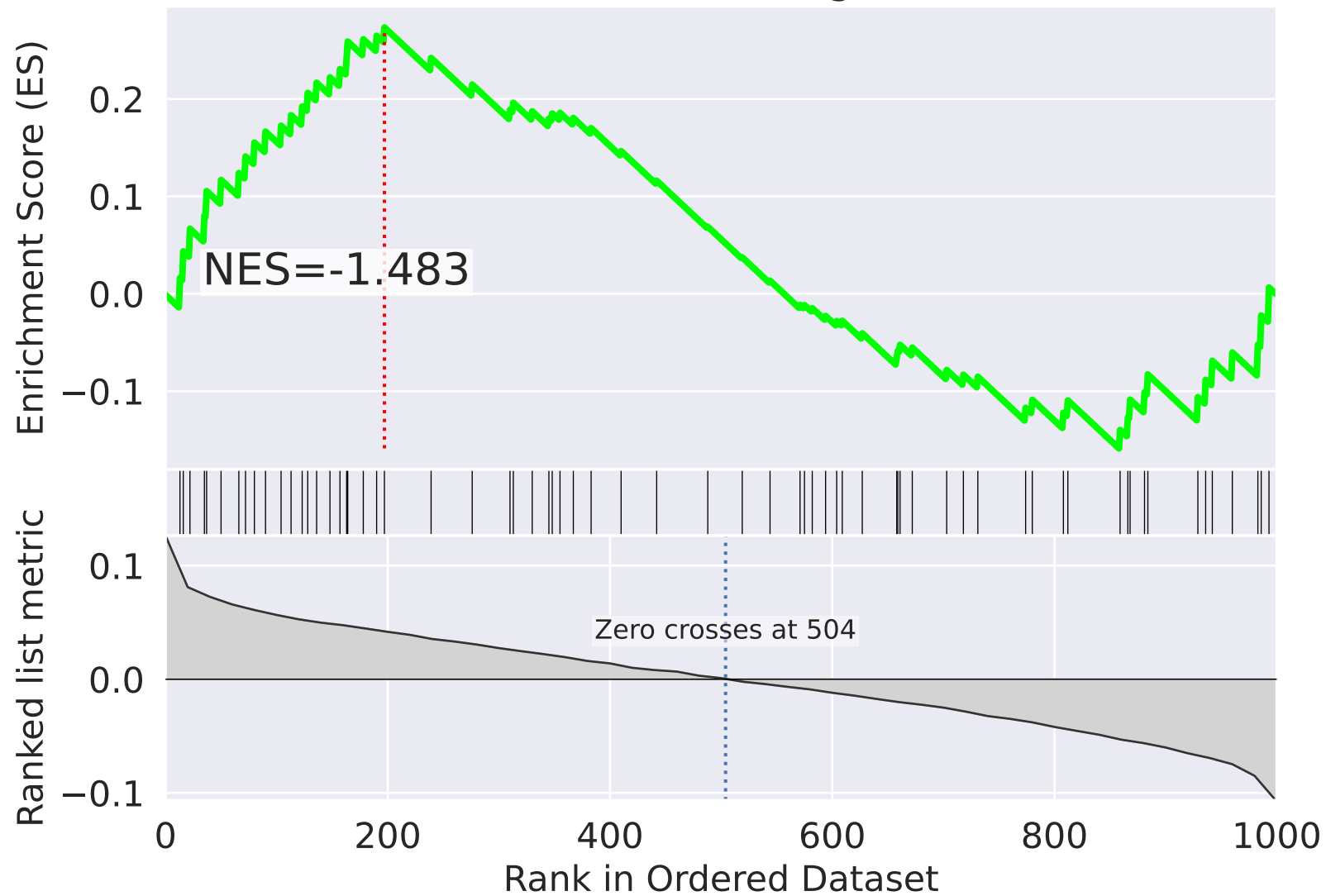
NES

SET

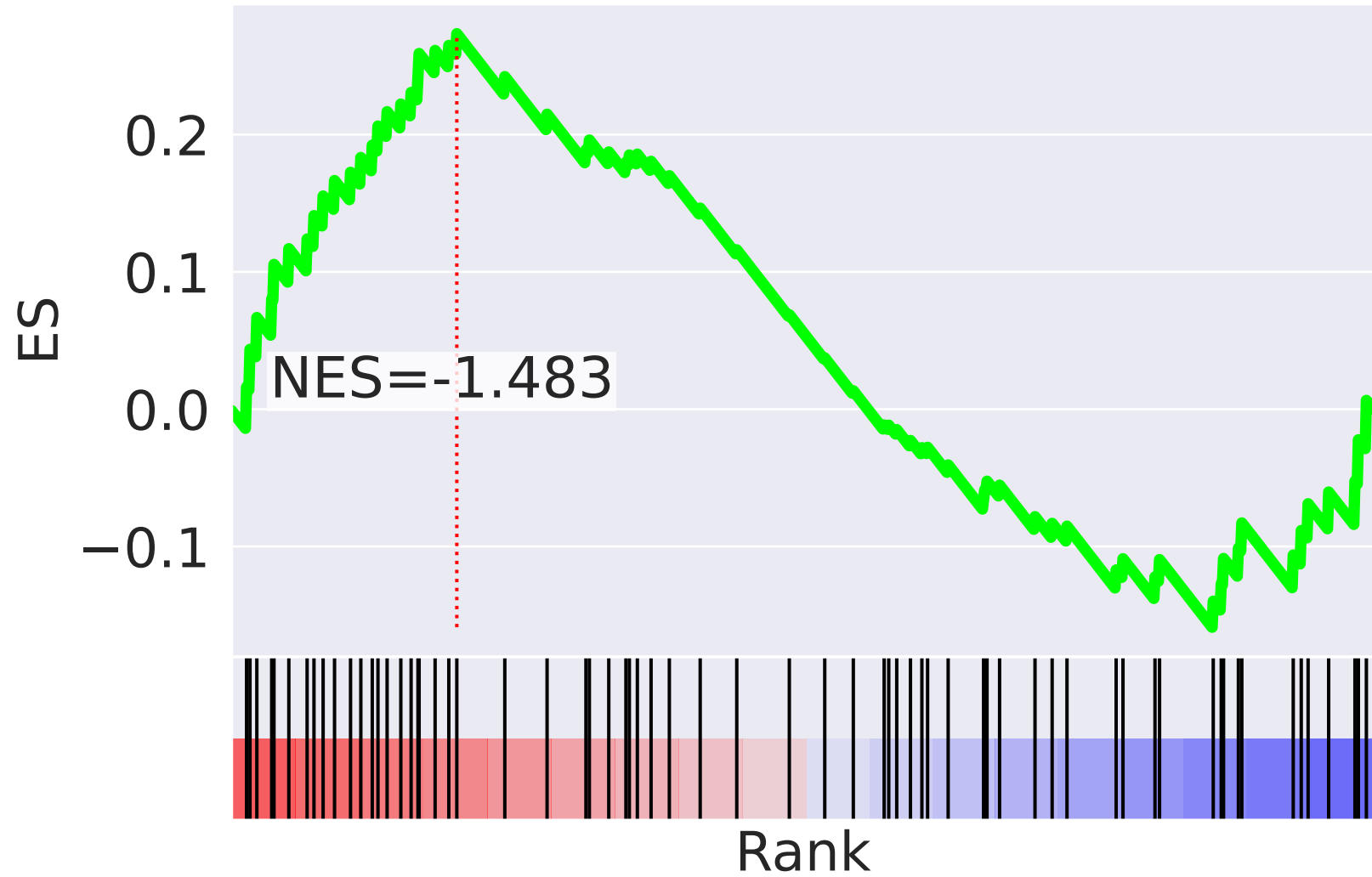
-2.764		positive regulation of TOR signaling (GO:0032008)
2.544		positive regulation of GTPase activity (GO:0043547)
-2.511		cellular protein localization (GO:0034613)
2.446		positive regulation of cell proliferation (GO:0008284)
-2.331		DNA replication initiation (GO:0006270)
2.330		regulation of DNA replication (GO:0006275)
-2.312		cellular response to hypoxia (GO:0071456)
-2.284		positive regulation by host of viral transcription (GO:0043923)
2.245		inflammatory response (GO:0006954)
2.239		androgen receptor signaling pathway (GO:0030521)
2.234		protein K63-linked ubiquitination (GO:0070534)
2.216		cell-matrix adhesion (GO:0007160)
-2.207		cellular response to amino acid stimulus (GO:0071230)
-2.169		positive regulation of telomere maintenance via telomerase (GO:0032212)
-2.160		cellular response to amino acid starvation (GO:0034198)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=21$

mitochondrial translational elongation (GO:0070125)



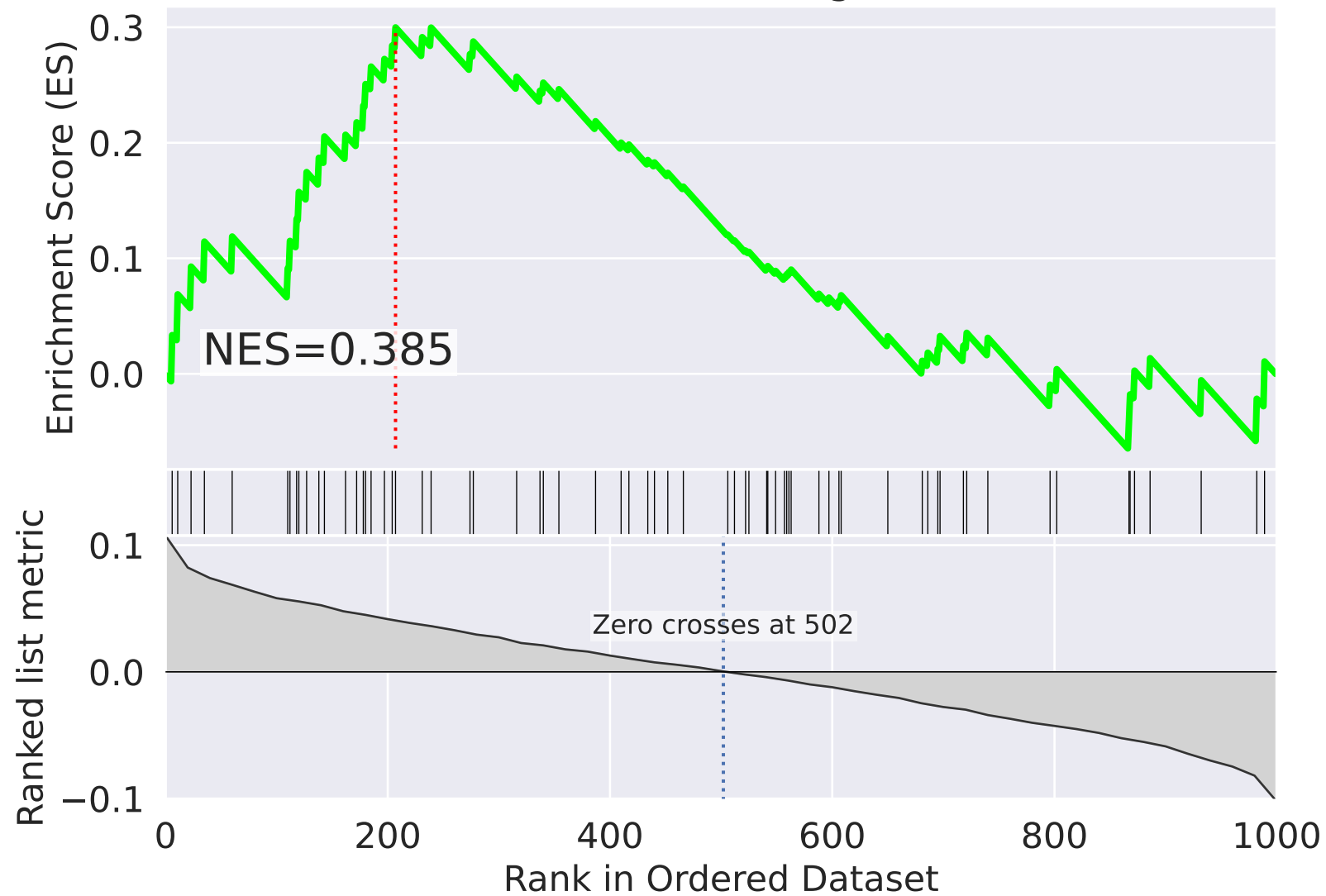
mitochondrial translational elongation (GO:0070125)



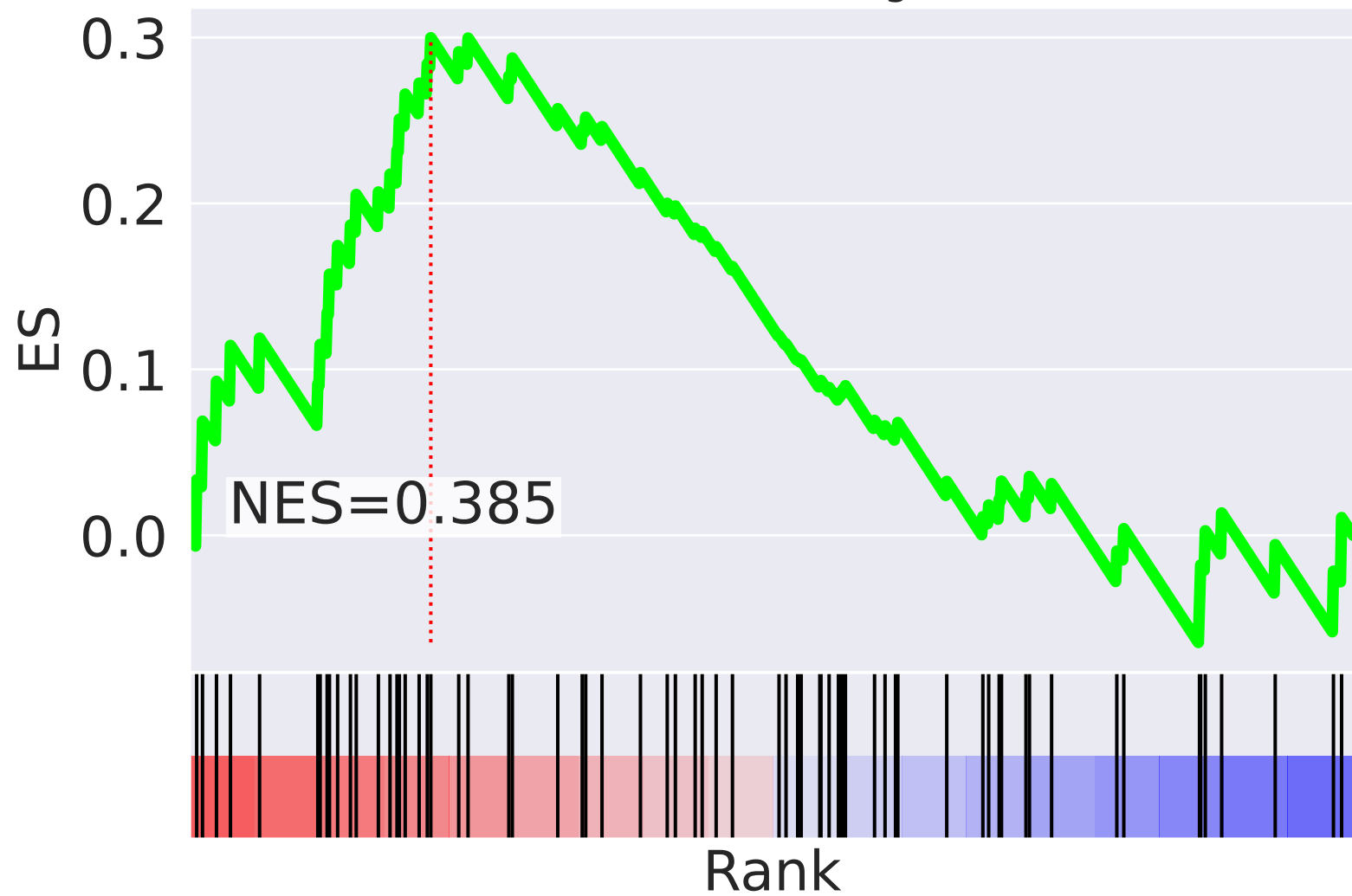
NES		SET
-2.187		tRNA modification (GO:0006400)
2.154		regulation of cell cycle (GO:0051726)
2.108		Wnt signaling pathway (GO:0016055)
-2.099		ER to Golgi vesicle-mediated transport (GO:0006888)
2.074		histone H4 acetylation (GO:0043967)
-2.012		regulation of apoptotic process (GO:0042981)
2.004		viral transcription (GO:0019083)
1.968		cellular response to hypoxia (GO:0071456)
1.928		positive regulation of type I interferon production (GO:0032481)
-1.908		apoptotic process (GO:0006915)
1.873		ERK1 and ERK2 cascade (GO:0070371)
-1.867		positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900740)
-1.846		cell cycle arrest (GO:0007050)
1.830		peptidyl-serine phosphorylation (GO:0018105)
-1.826		transcription elongation from RNA polymerase II promoter (GO:0006368)

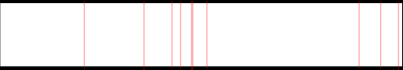

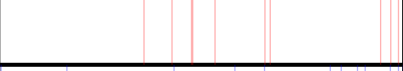





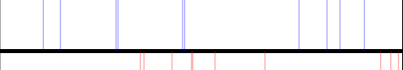

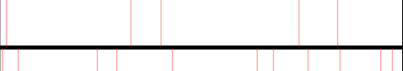


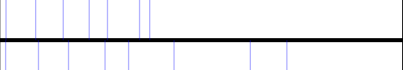
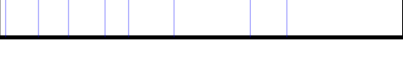
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=22$

mitochondrial translational elongation (GO:0070125)



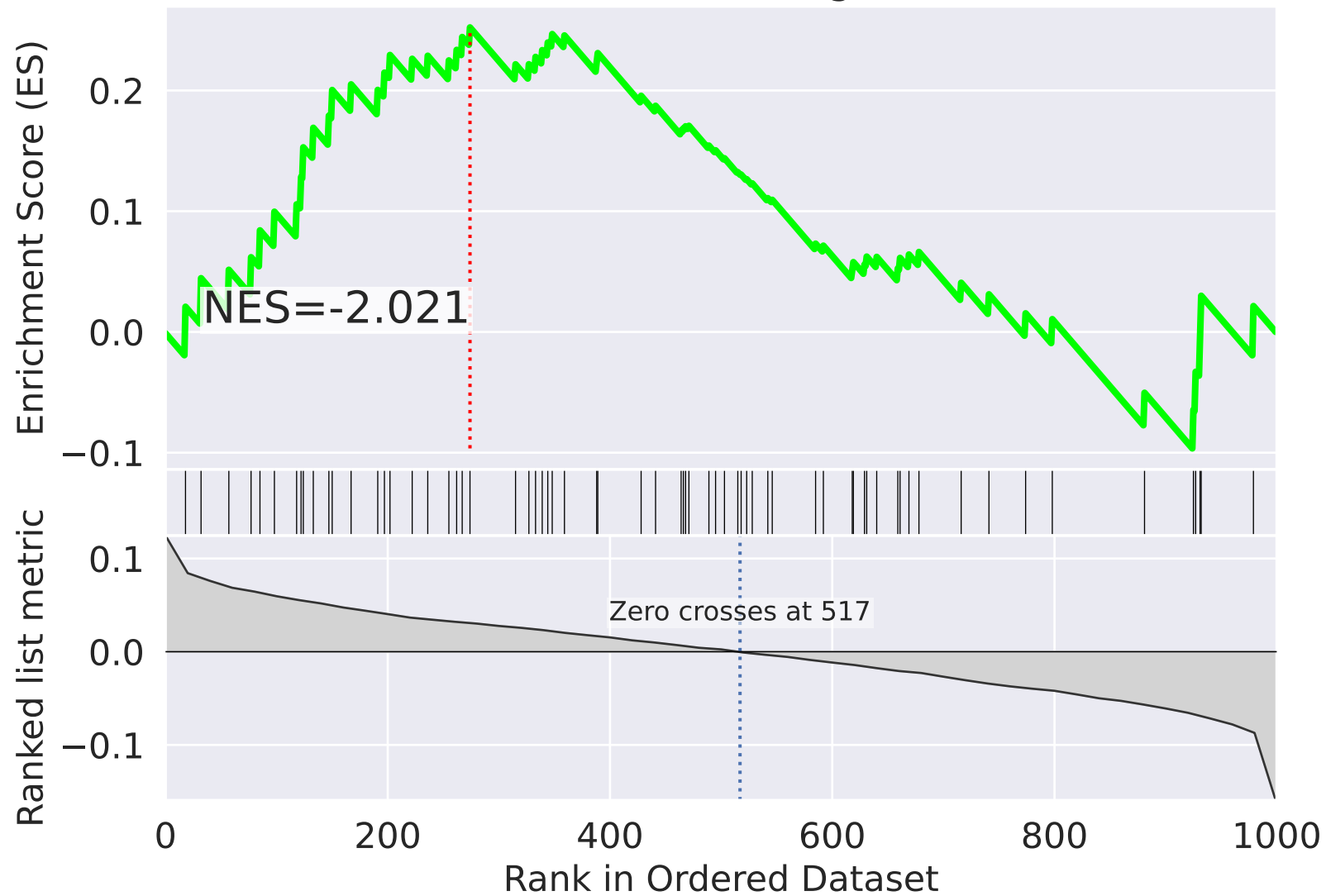
mitochondrial translational elongation (GO:0070125)



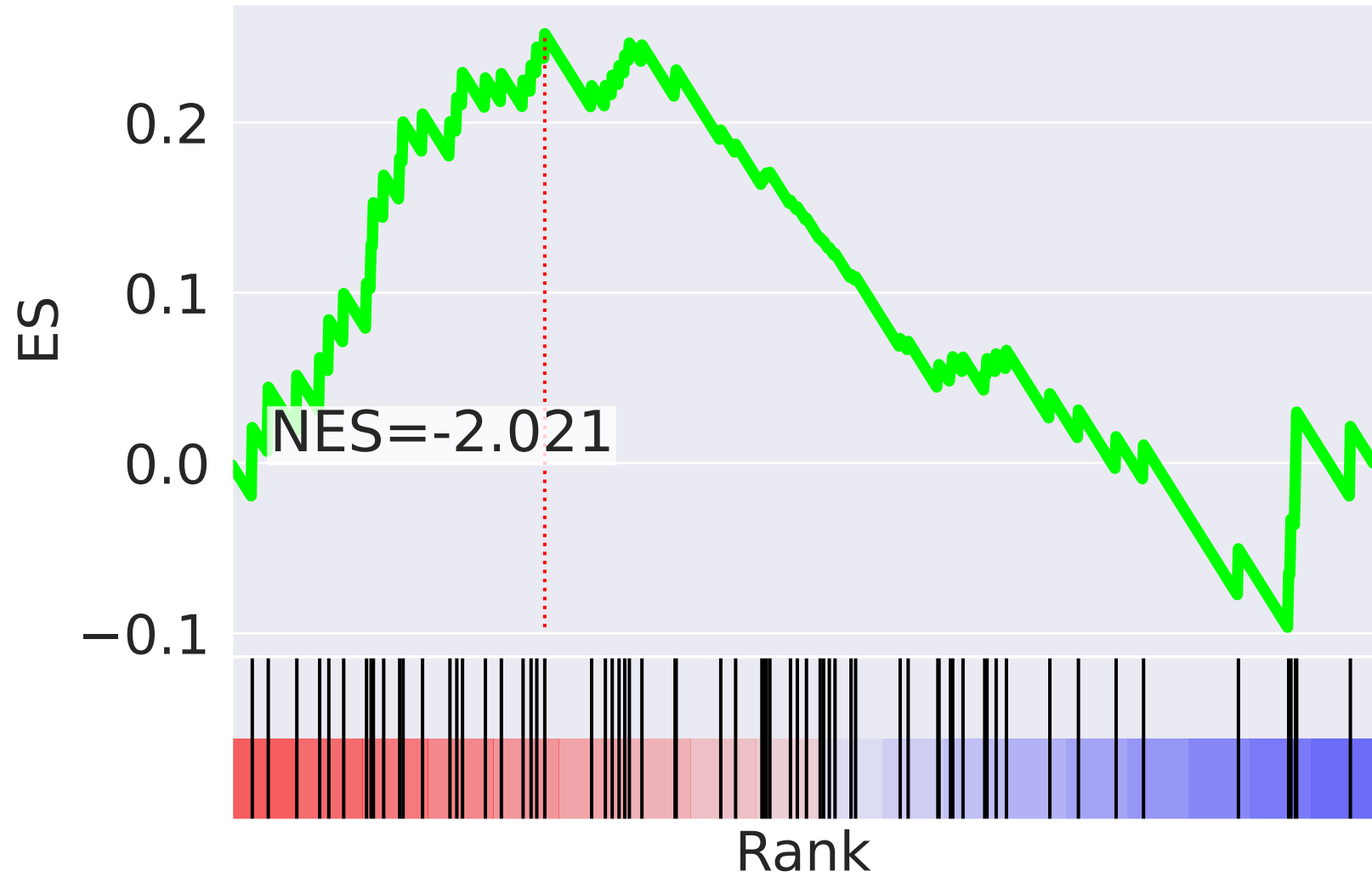
NES		SET
3.046		double-strand break repair via homologous recombination (GO:0000724)
2.780		reciprocal meiotic recombination (GO:0007131)
2.630		strand displacement (GO:0000732)
-2.573		mitotic cell cycle (GO:0000278)
2.379		CENP-A containing nucleosome assembly (GO:0034080)
2.332		RNA secondary structure unwinding (GO:0010501)
-2.327		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.327		response to virus (GO:0009615)
-2.294		protein polyubiquitination (GO:0000209)
2.242		DNA synthesis involved in DNA repair (GO:0000731)
2.189		proteolysis (GO:0006508)
2.145		positive regulation of gene expression (GO:0010628)
2.074		neutrophil degranulation (GO:0043312)
-2.066		intracellular protein transport (GO:0006886)
-2.043		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)

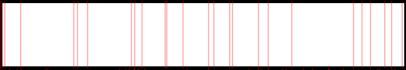

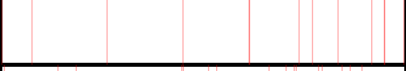
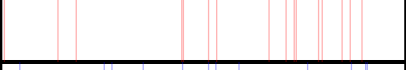
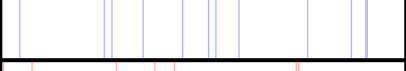
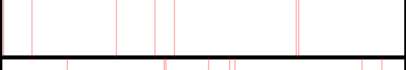

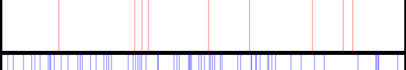
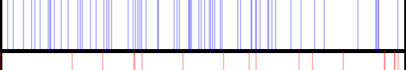






The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=23$

mitochondrial translational elongation (GO:0070125)



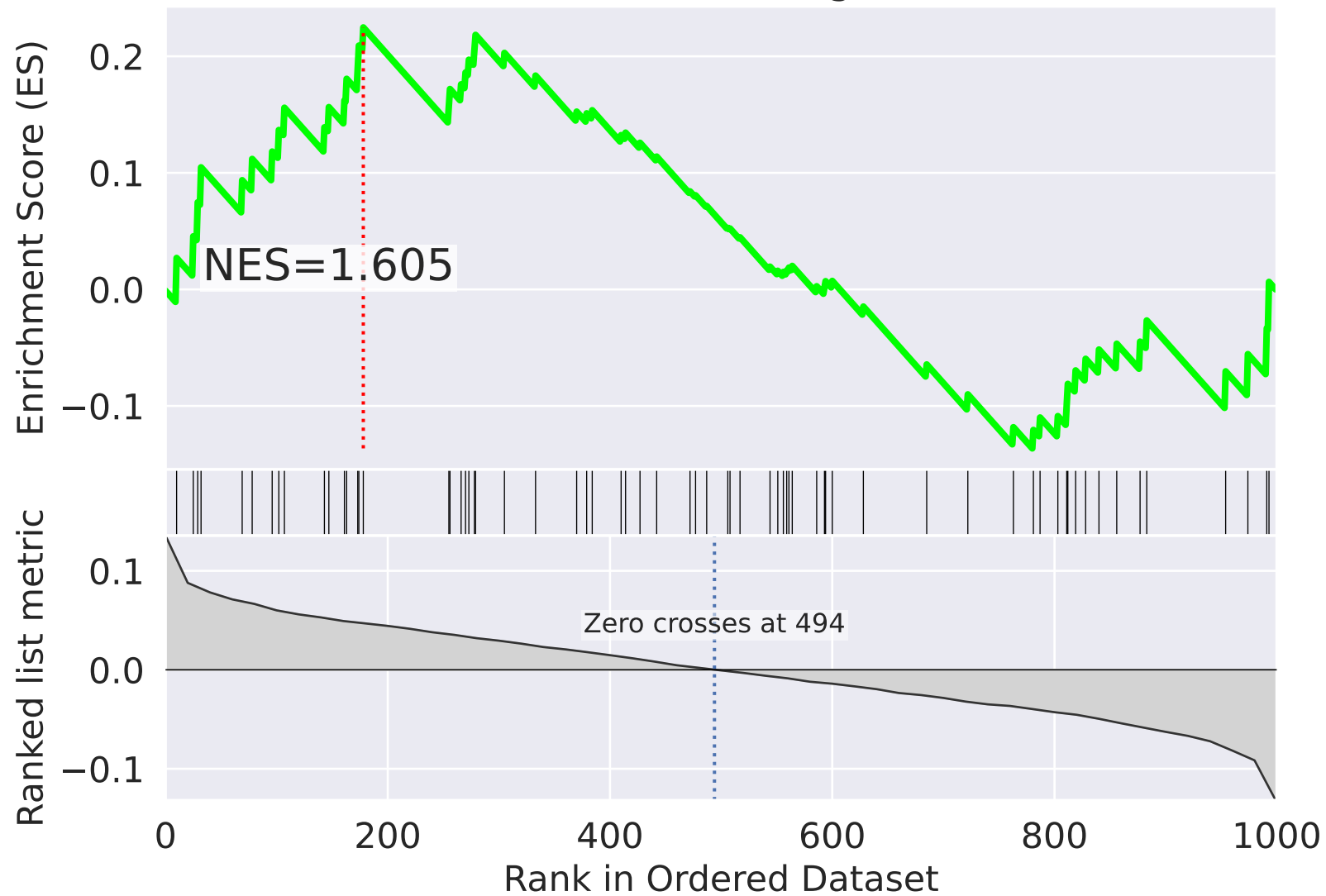
mitochondrial translational elongation (GO:0070125)



NES		SET
2.975		signal transduction (GO:0007165)
2.642		positive regulation of cell proliferation (GO:0008284)
2.627		Fc-epsilon receptor signaling pathway (GO:0038095)
2.566		protein complex assembly (GO:0006461)
-2.531		chromatin remodeling (GO:0006338)
2.491		Wnt signaling pathway (GO:0016055)
2.472		regulation of apoptotic process (GO:0042981)
2.467		positive regulation of protein phosphorylation (GO:0001934)
-2.403		mitochondrial translational termination (GO:0070126)
2.329		MAPK cascade (GO:0000165)
2.271		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-2.242		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.208		transcription from RNA polymerase II promoter (GO:0006366)
2.182		protein autophosphorylation (GO:0046777)
2.139		cellular response to DNA damage stimulus (GO:0006974)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=24$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1

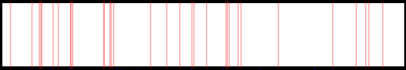






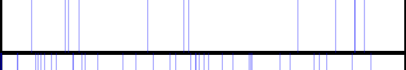
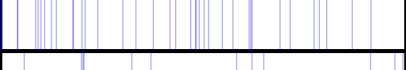
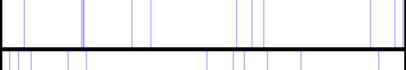

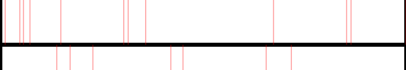



0.0

-0.1

NES=1.605

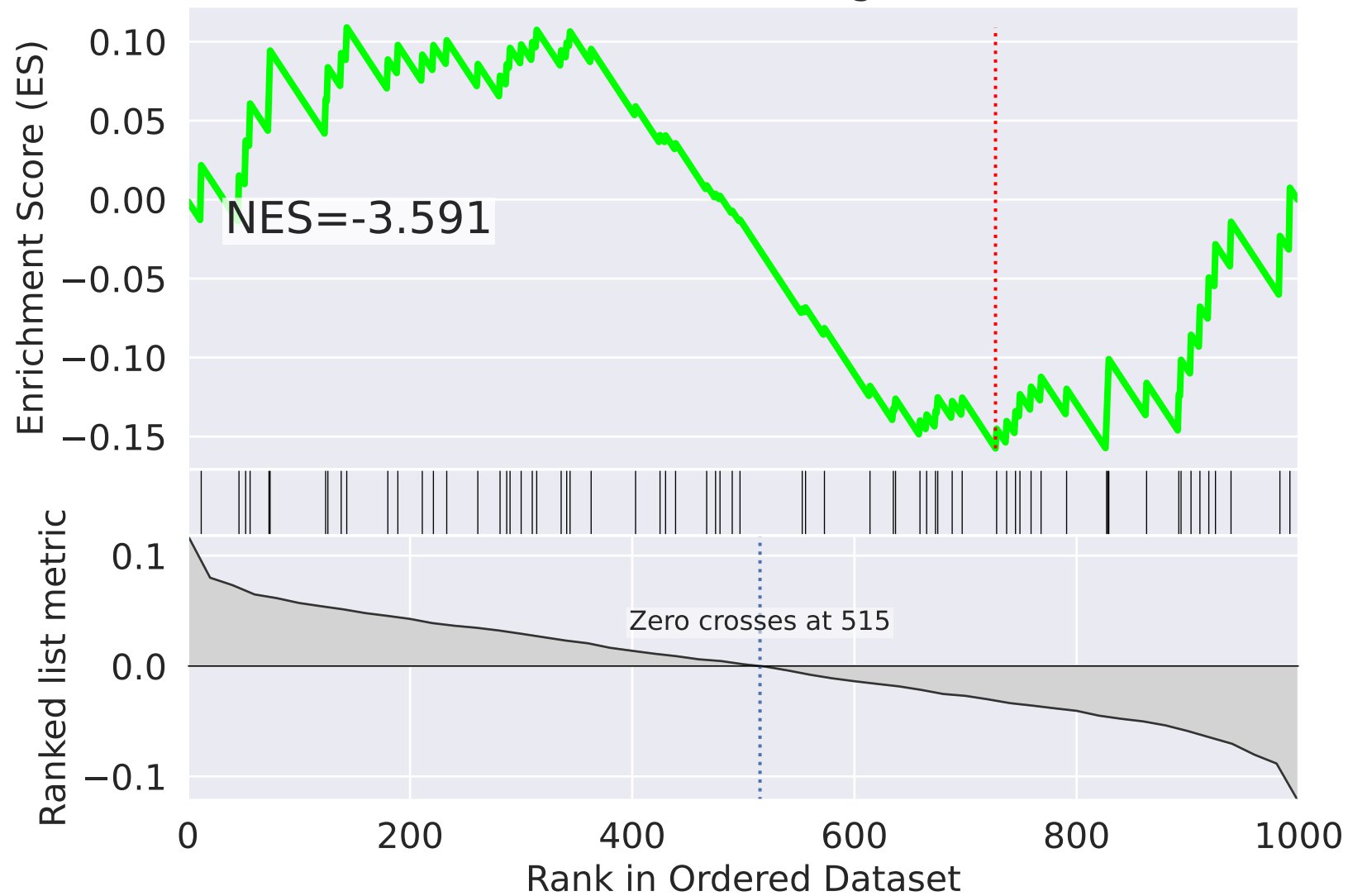
Rank



NES		SET
3.201		translation (GO:0006412)
-3.073		generation of precursor metabolites and energy (GO:0006091)
-2.613		cholesterol biosynthetic process (GO:0006695)
-2.546		positive regulation of TOR signaling (GO:0032008)
2.458		telomere maintenance (GO:0000723)
-2.346		nucleotide-excision repair (GO:0006289)
-2.293		nervous system development (GO:0007399)
-2.186		regulation of cholesterol biosynthetic process (GO:0045540)
-2.073		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-1.969		transcription elongation from RNA polymerase II promoter (GO:0006368)
-1.934		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
1.925		mitotic metaphase plate congression (GO:0007080)
1.900		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-1.863		double-strand break repair via homologous recombination (GO:0000724)
1.821		positive regulation of GTPase activity (GO:0043547)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=25$

mitochondrial translational elongation (GO:0070125)



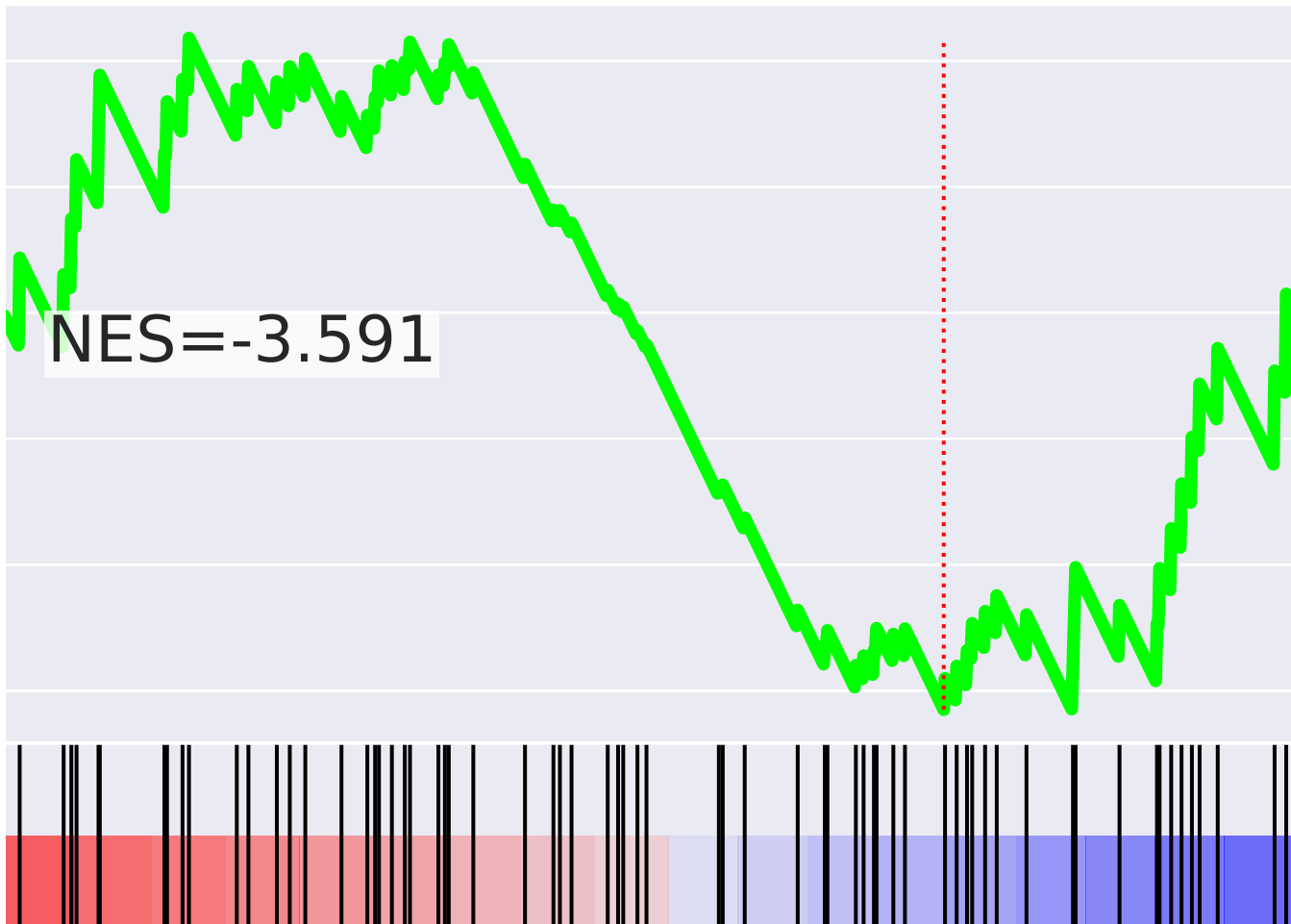
mitochondrial translational elongation (GO:0070125)

ES

0.10
0.05
0.00
-0.05
-0.10
-0.15

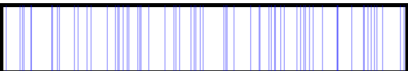

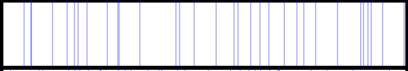

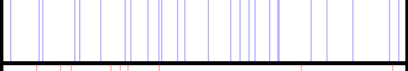

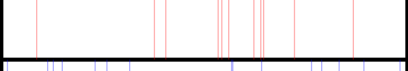



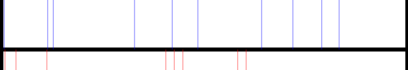

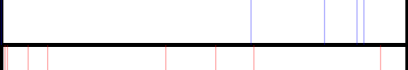
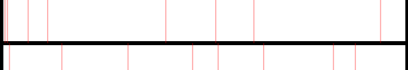

NES=-3.591

Rank



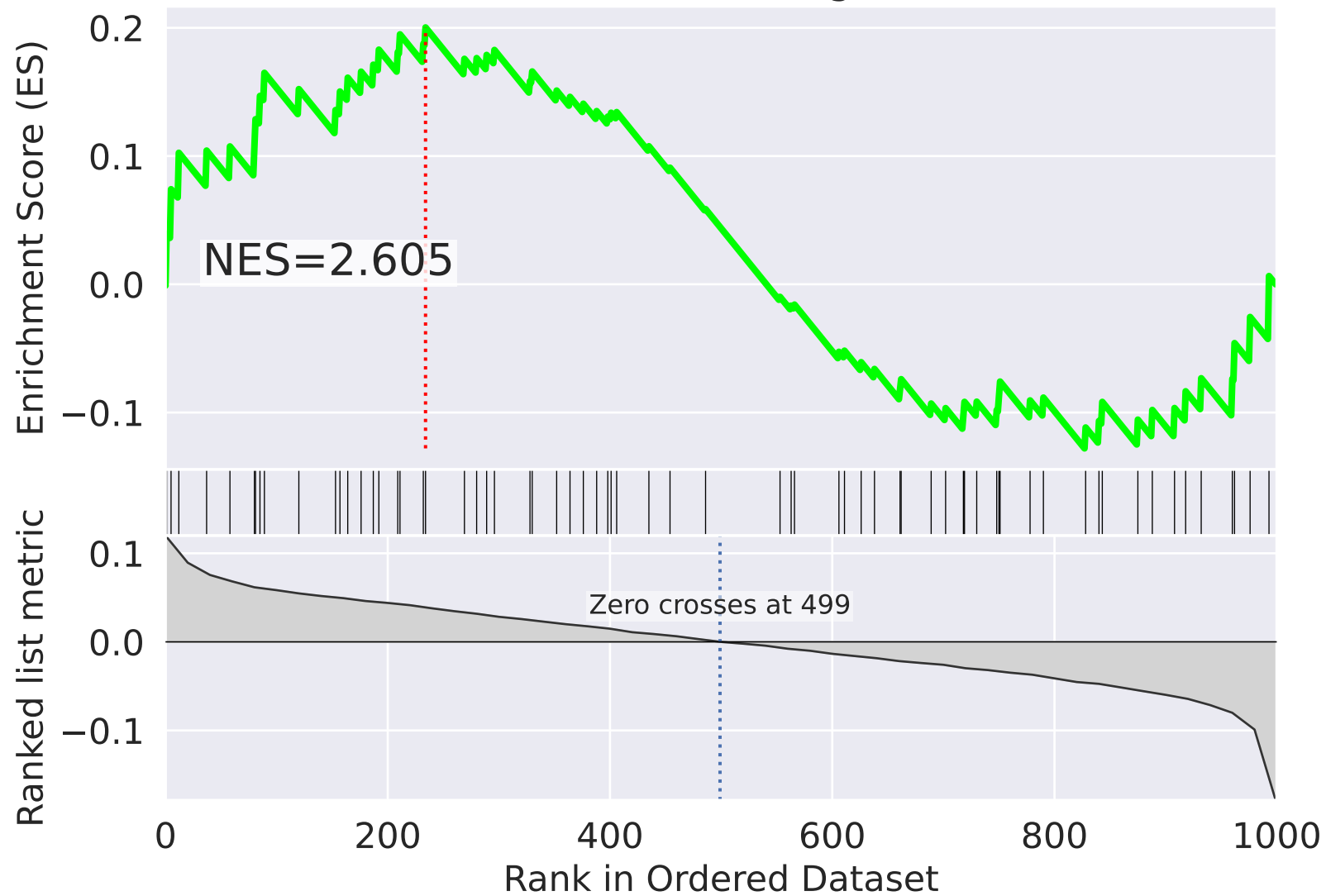
NES

SET

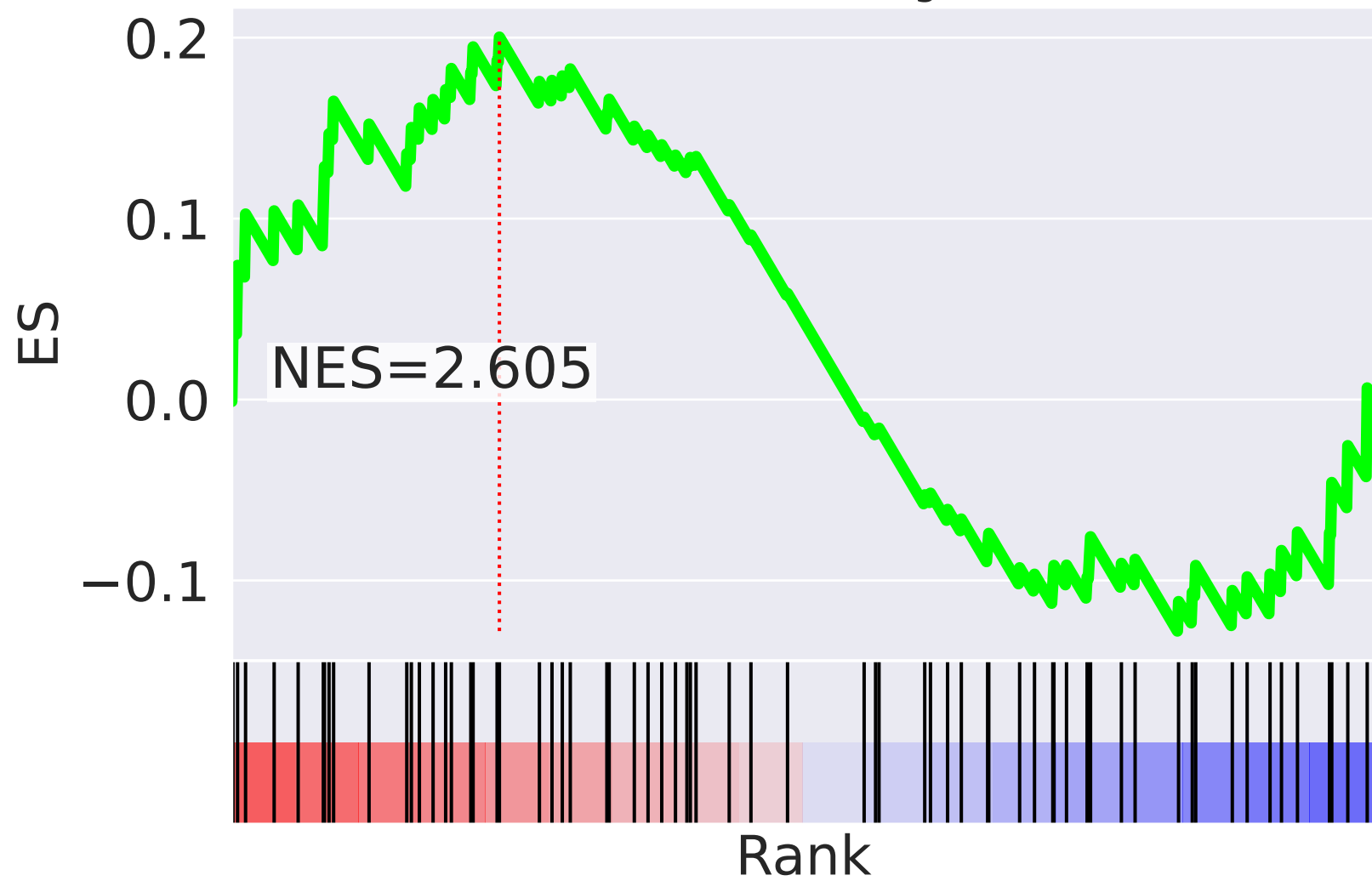
-3.655		mitochondrial translational termination (GO:0070126)
-3.591		mitochondrial translational elongation (GO:0070125)
-3.344		translation (GO:0006412)
-3.273		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.083		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.626		intracellular signal transduction (GO:0035556)
2.553		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.510		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
2.422		protein phosphorylation (GO:0006468)
-2.241		protein autoubiquitination (GO:0051865)
-2.132		protein polyubiquitination (GO:0000209)
2.088		cell growth (GO:0016049)
-2.063		regulation of cell adhesion (GO:0030155)
1.986		cell migration (GO:0016477)
1.971		protein autophosphorylation (GO:0046777)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=26$

mitochondrial translational elongation (GO:0070125)



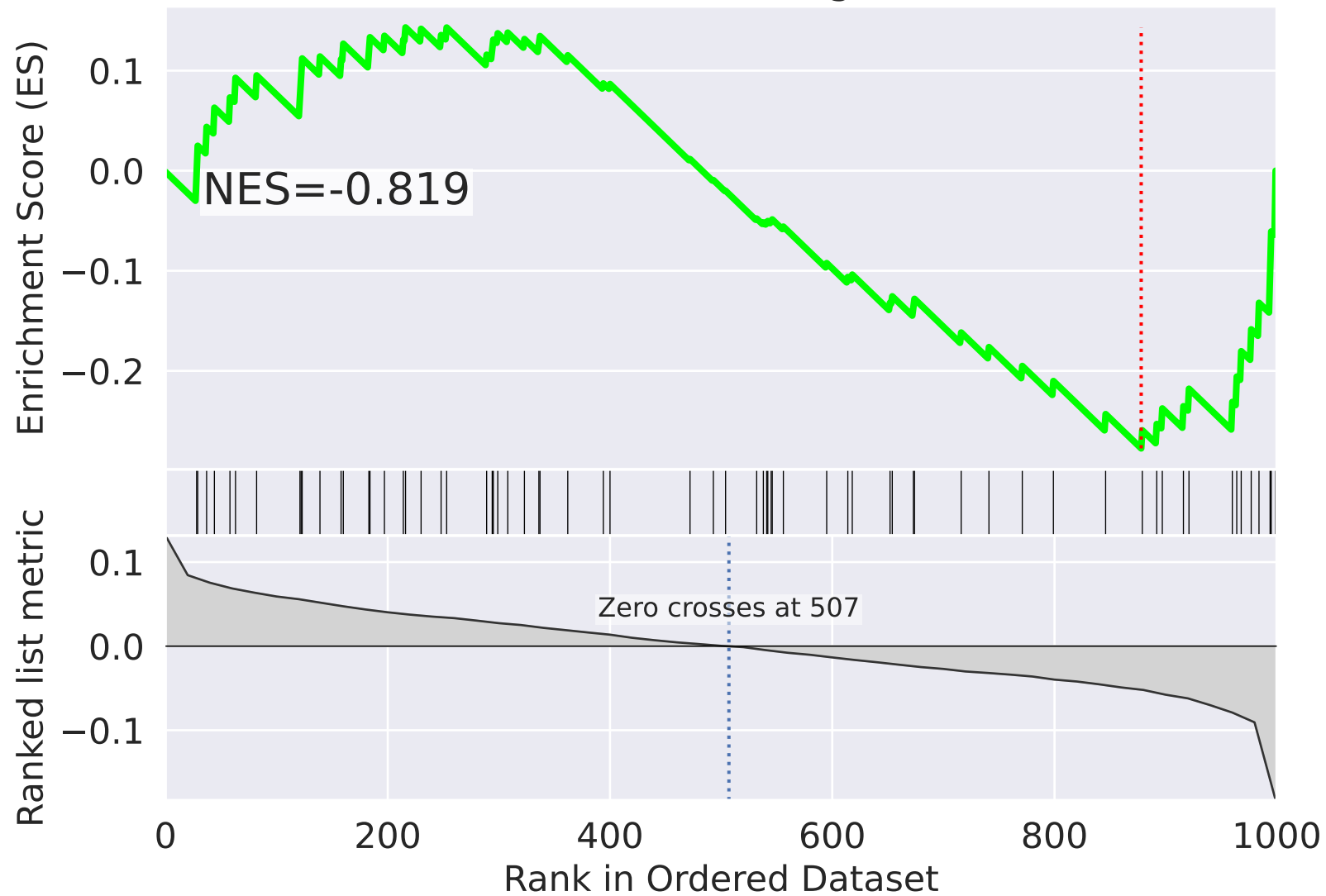
mitochondrial translational elongation (GO:0070125)



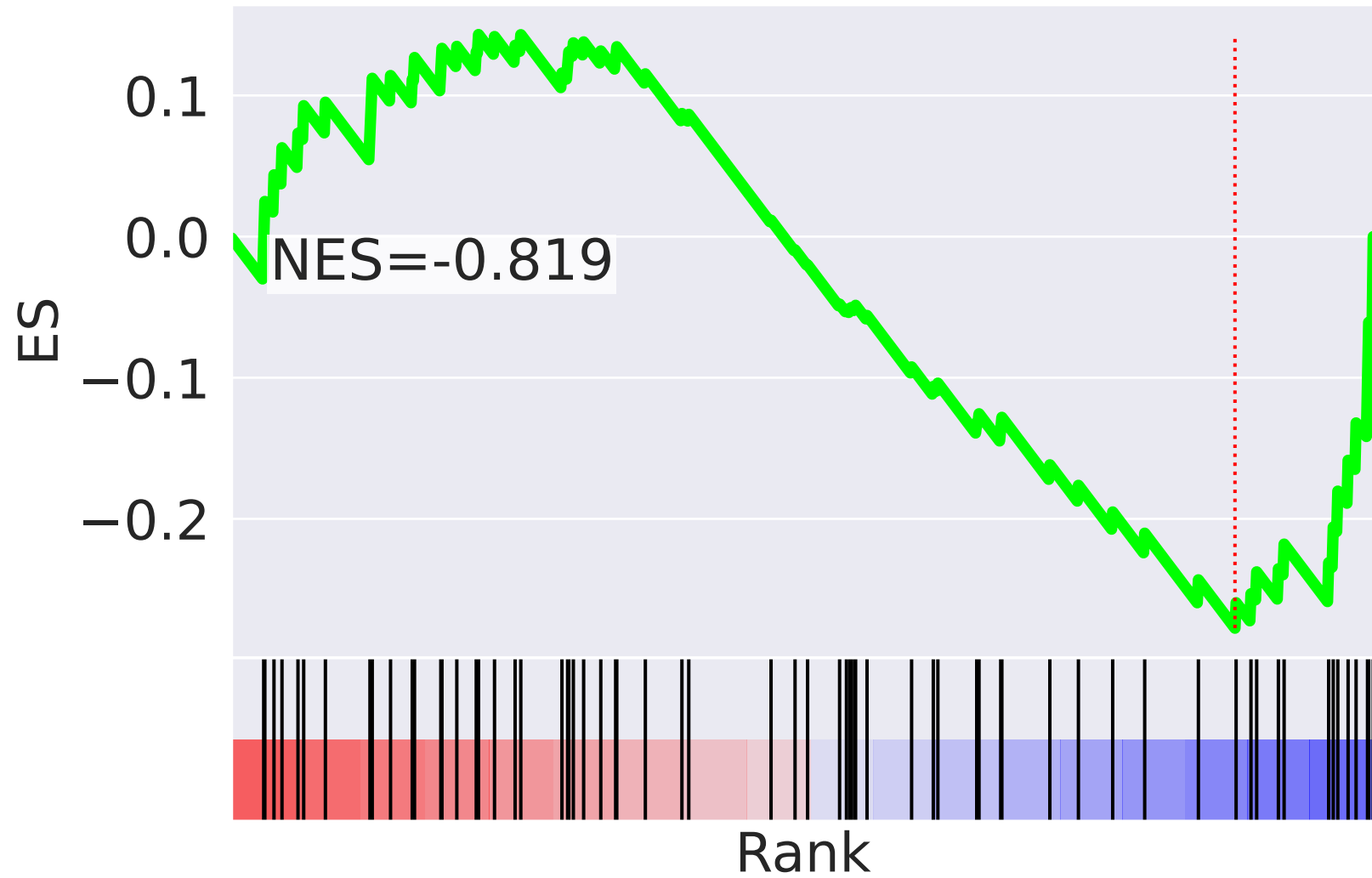
NES		SET
2.901		positive regulation of apoptotic process (GO:0043065)
2.605		mitochondrial translational elongation (GO:0070125)
-2.559		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
2.547		negative regulation of cell proliferation (GO:0008285)
-2.306		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.294		mitochondrial translational termination (GO:0070126)
2.288		translation (GO:0006412)
2.251		positive regulation of GTPase activity (GO:0043547)
2.154		protein dephosphorylation (GO:0006470)
-2.114		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-2.031		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.007		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-1.988		platelet degranulation (GO:0002576)
-1.931		cellular respiration (GO:0045333)
-1.900		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=27$

mitochondrial translational elongation (GO:0070125)


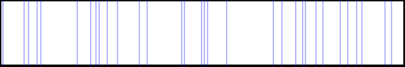
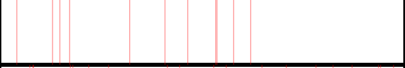
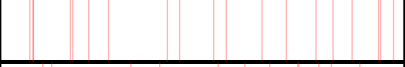



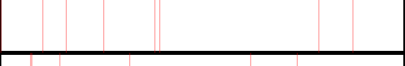


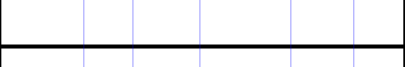


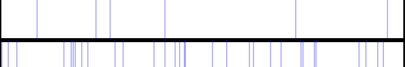



mitochondrial translational elongation (GO:0070125)



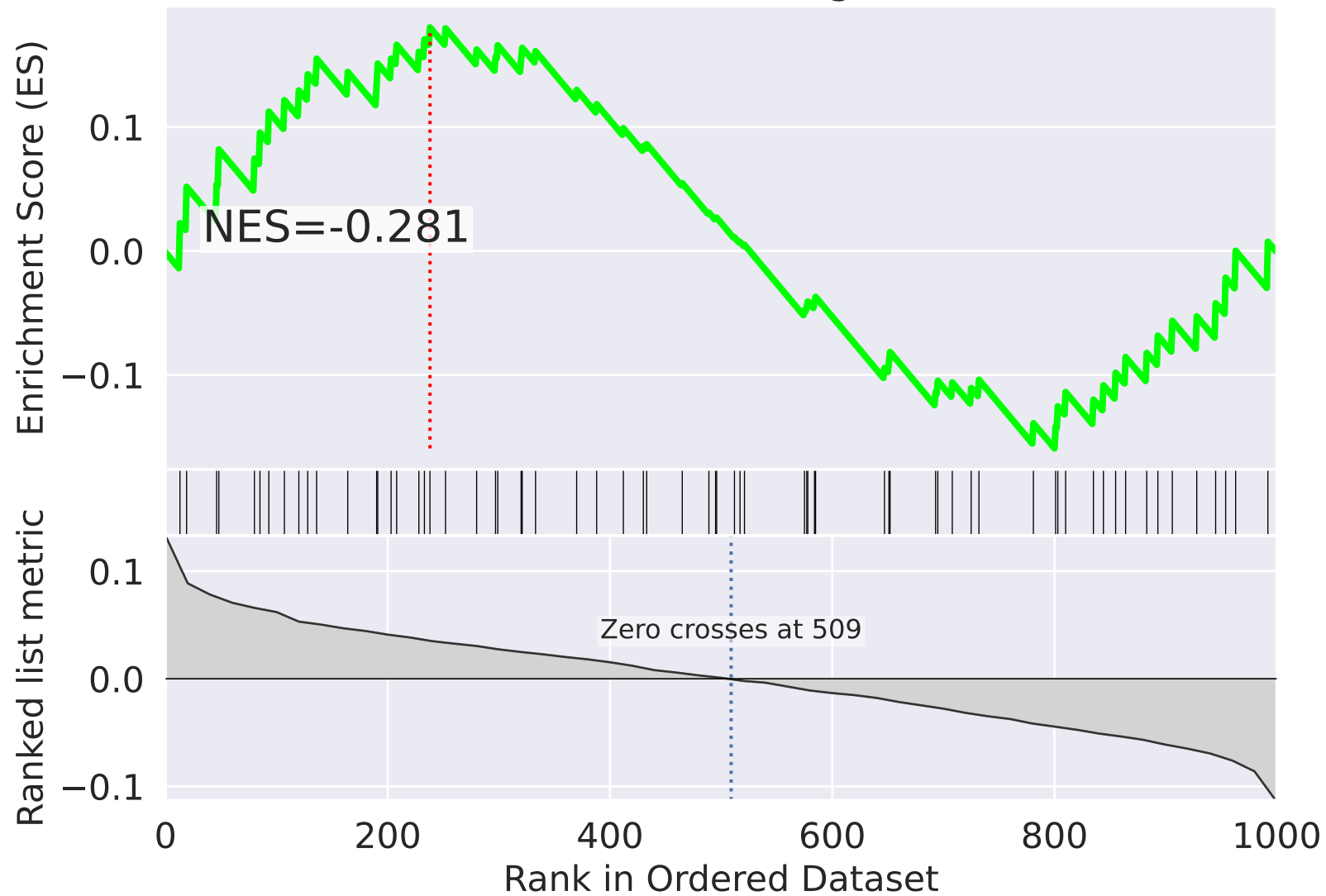
NES

SET

2.921		regulation of defense response to virus by virus (GO:0050690)
-2.861		negative regulation of transcription, DNA-templated (GO:0045892)
2.553		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.267		DNA replication (GO:0006260)
2.224		mitotic metaphase plate congression (GO:0007080)
2.085		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.031		DNA-dependent DNA replication (GO:0006261)
1.982		microtubule-based movement (GO:0007018)
1.978		T cell costimulation (GO:0031295)
-1.971		chromatin remodeling (GO:0006338)
-1.907		ubiquitin-dependent ERAD pathway (GO:0030433)
-1.907		retrograde protein transport, ER to cytosol (GO:0030970)
-1.899		transcription-coupled nucleotide-excision repair (GO:0006283)
-1.855		ATP-dependent chromatin remodeling (GO:0043044)
-1.849		protein deubiquitination (GO:0016579)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=28$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

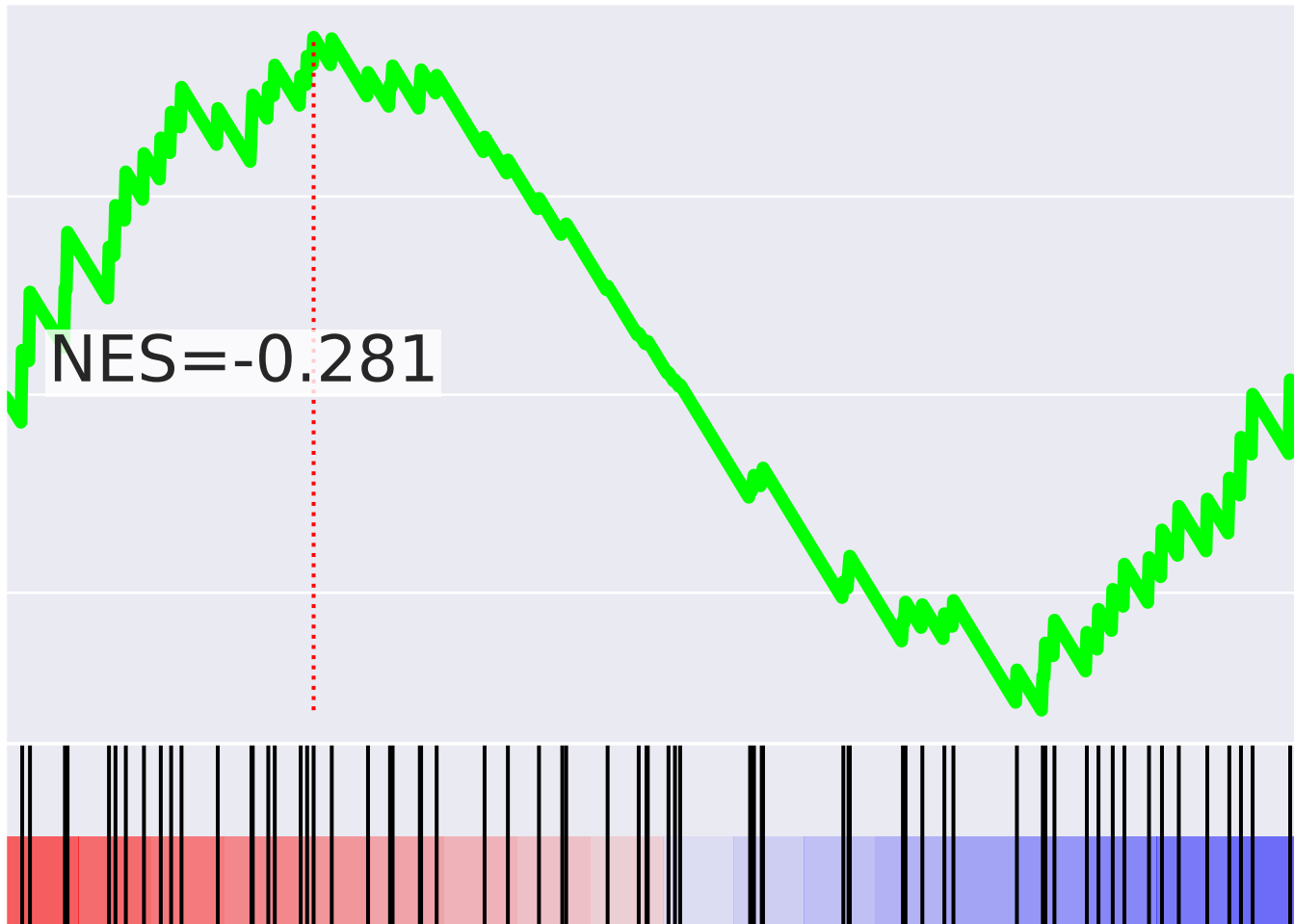
0.1

0.0

-0.1

NES=-0.281

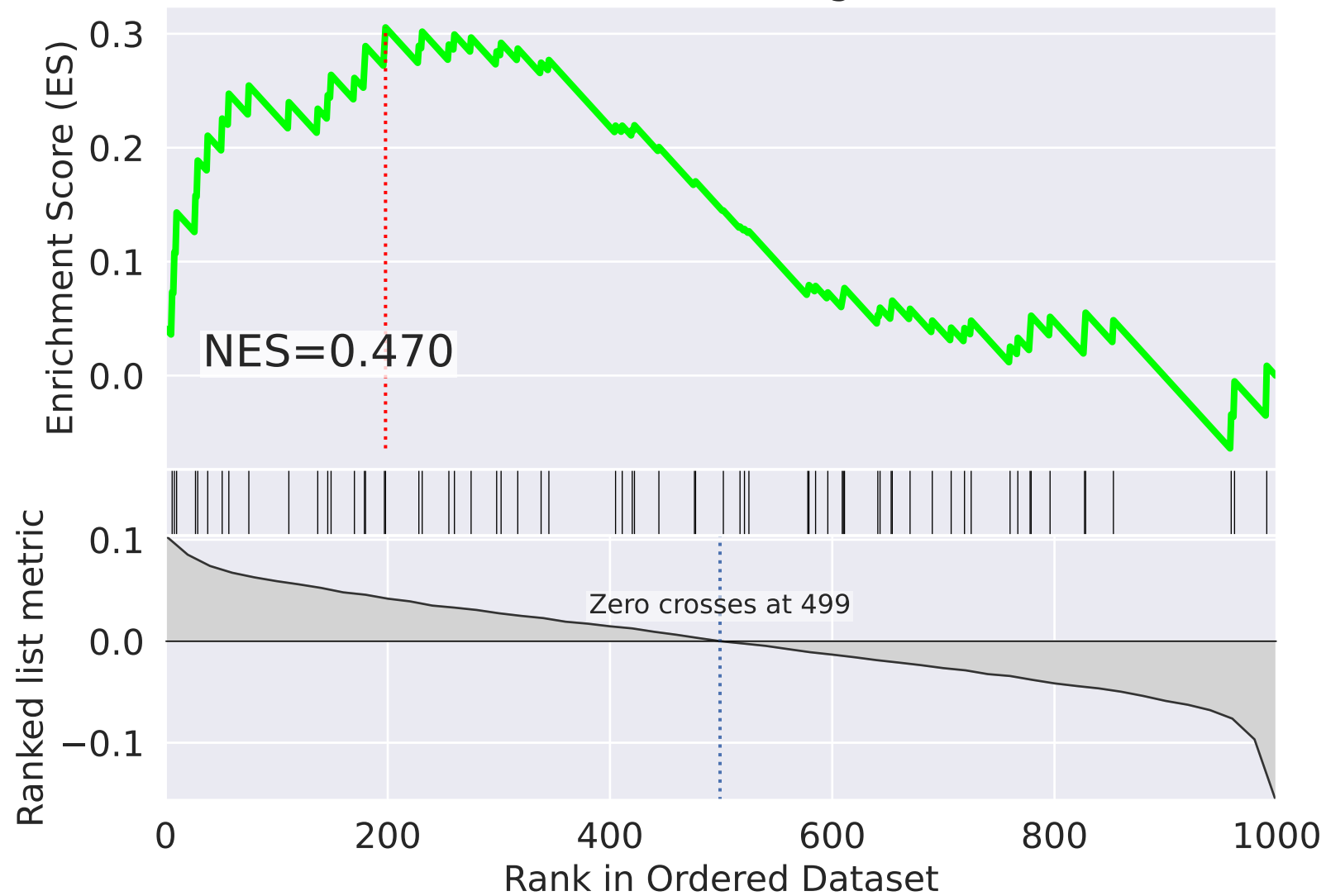
Rank



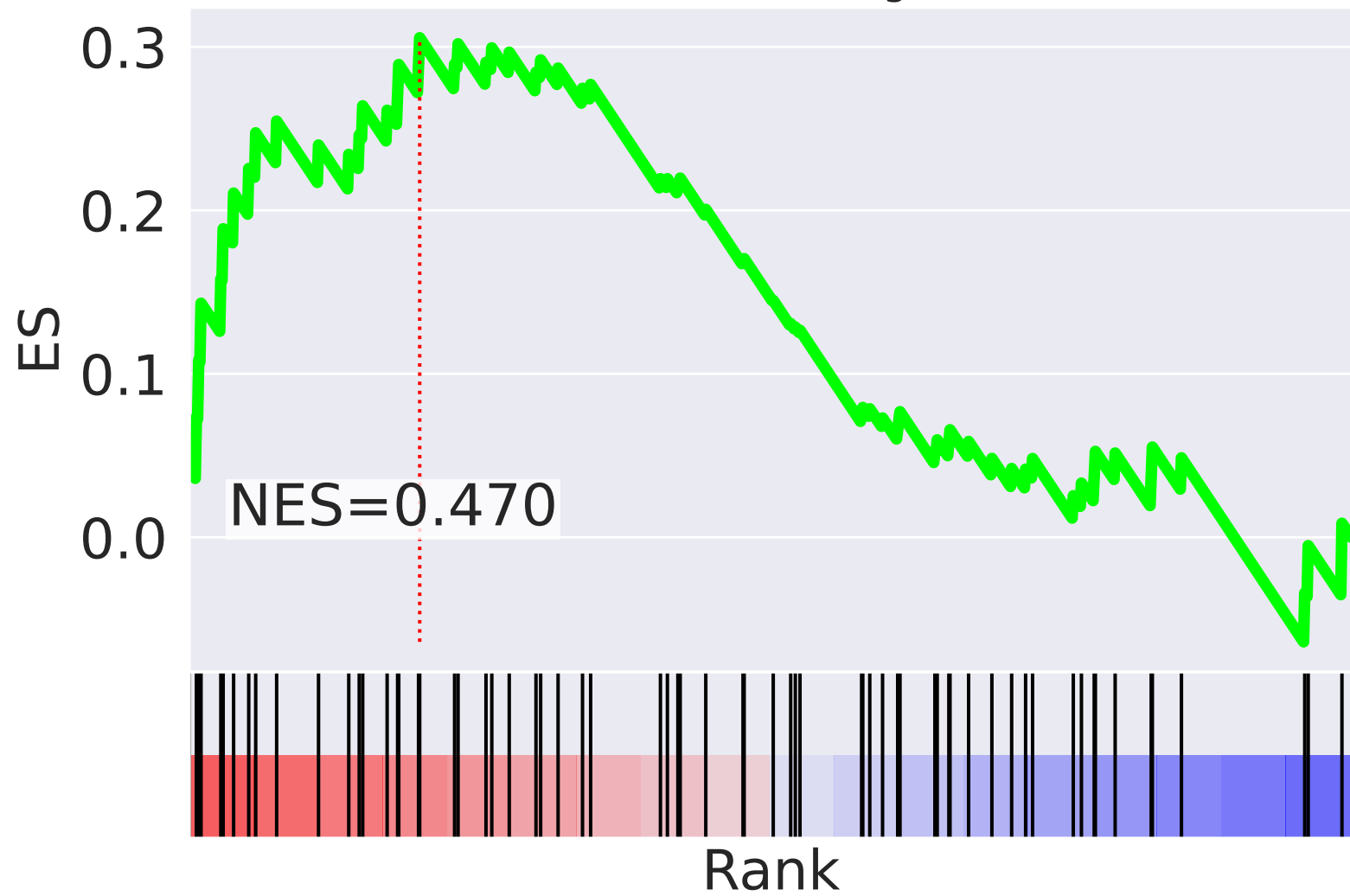
NES		SET
2.701		macroautophagy (GO:0016236)
-2.672		positive regulation of transcription, DNA-templated (GO:0045893)
-2.551		regulation of transcription, DNA-templated (GO:0006355)
2.328		protein polyubiquitination (GO:0000209)
-2.191		transcription from RNA polymerase II promoter (GO:0006366)
2.081		viral budding via host ESCRT complex (GO:0039702)
2.070		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.055		regulation of cell proliferation (GO:0042127)
2.037		neutrophil degranulation (GO:0043312)
2.030		ubiquitin-dependent protein catabolic process (GO:0006511)
2.017		mitotic metaphase plate congression (GO:0007080)
2.015		multivesicular body assembly (GO:0036258)
-2.002		spermatogenesis (GO:0007283)
-1.996		mRNA splicing, via spliceosome (GO:0000398)
1.958		apoptotic process (GO:0006915)

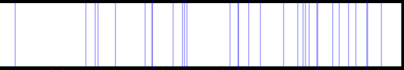


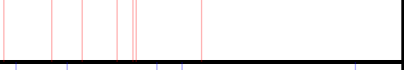

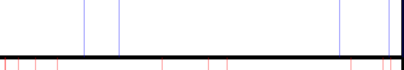

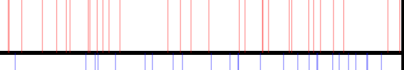


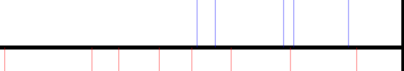

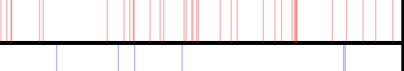

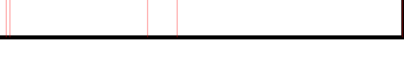
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=29$

mitochondrial translational elongation (GO:0070125)



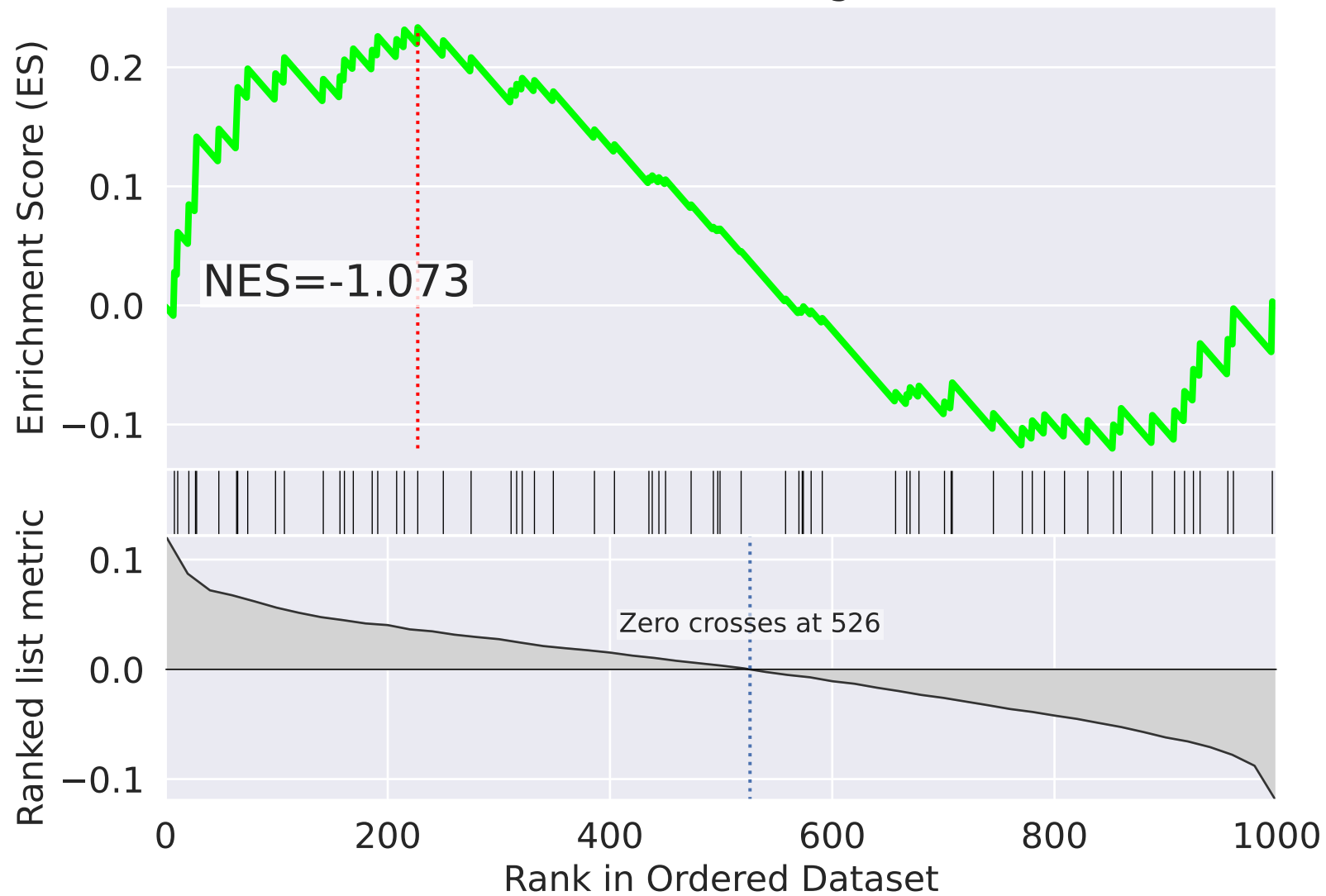
mitochondrial translational elongation (GO:0070125)



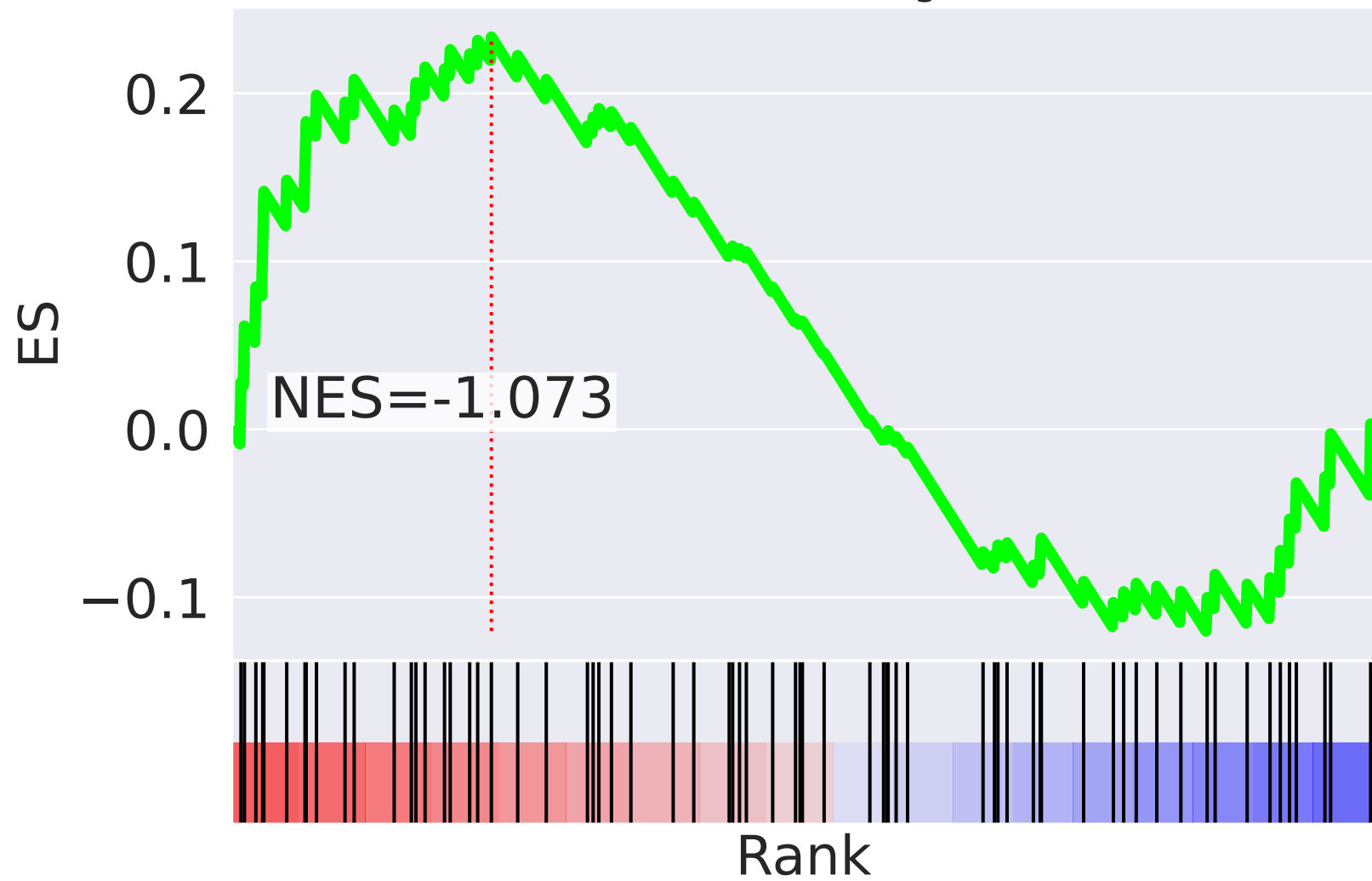
NES		SET
-3.096		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.306		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.126		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.101		platelet aggregation (GO:0070527)
-2.083		positive regulation of telomere maintenance via telomerase (GO:0032212)
-2.080		protein targeting to mitochondrion (GO:0006626)
1.991		generation of precursor metabolites and energy (GO:0006091)
1.986		translation (GO:0006412)
-1.969		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-1.956		regulation of defense response to virus by virus (GO:0050690)
-1.924		cellular respiration (GO:0045333)
1.907		androgen receptor signaling pathway (GO:0030521)
1.863		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-1.851		DNA damage response, detection of DNA damage (GO:0042769)
1.840		heart development (GO:0007507)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=30$

mitochondrial translational elongation (GO:0070125)



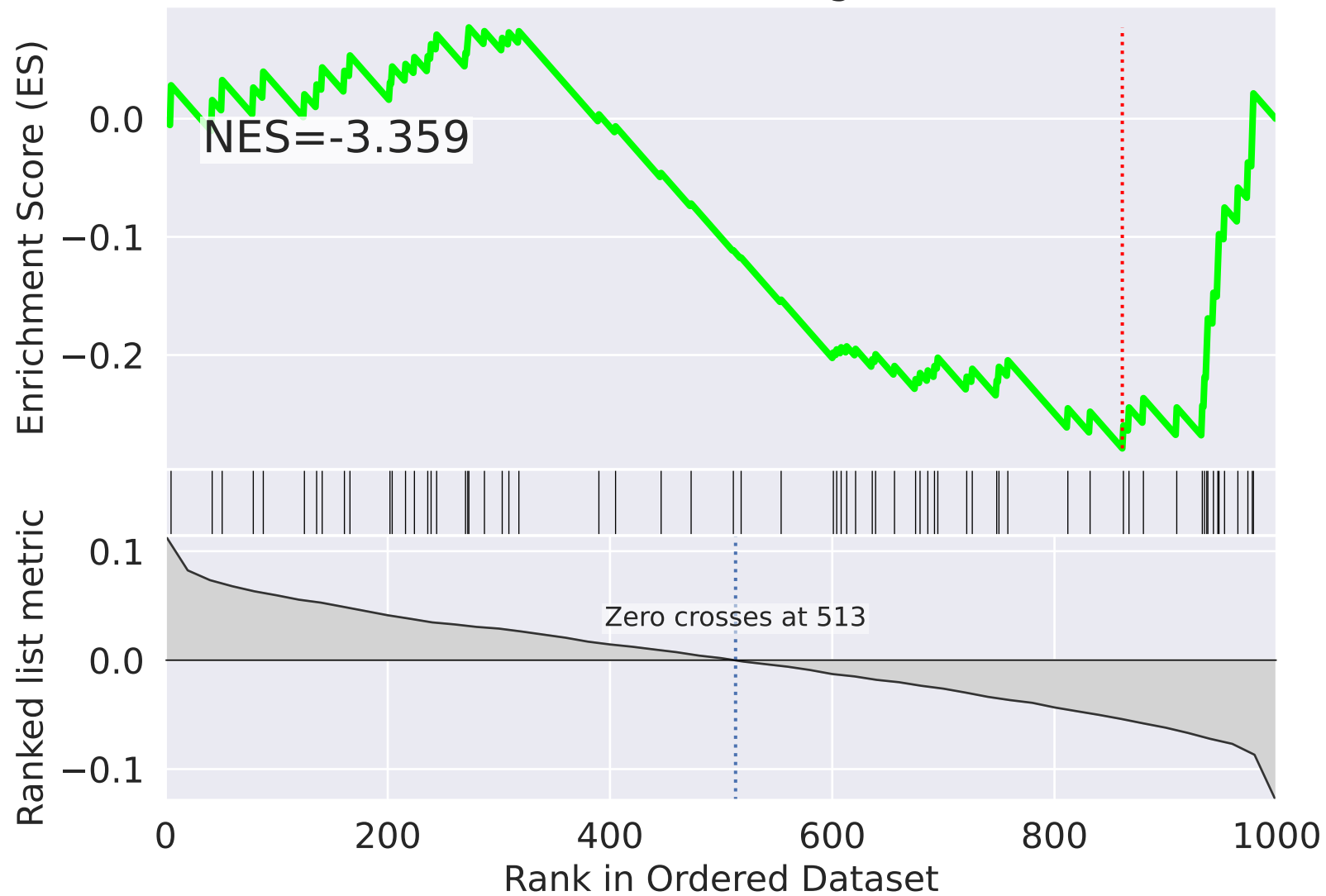
mitochondrial translational elongation (GO:0070125)



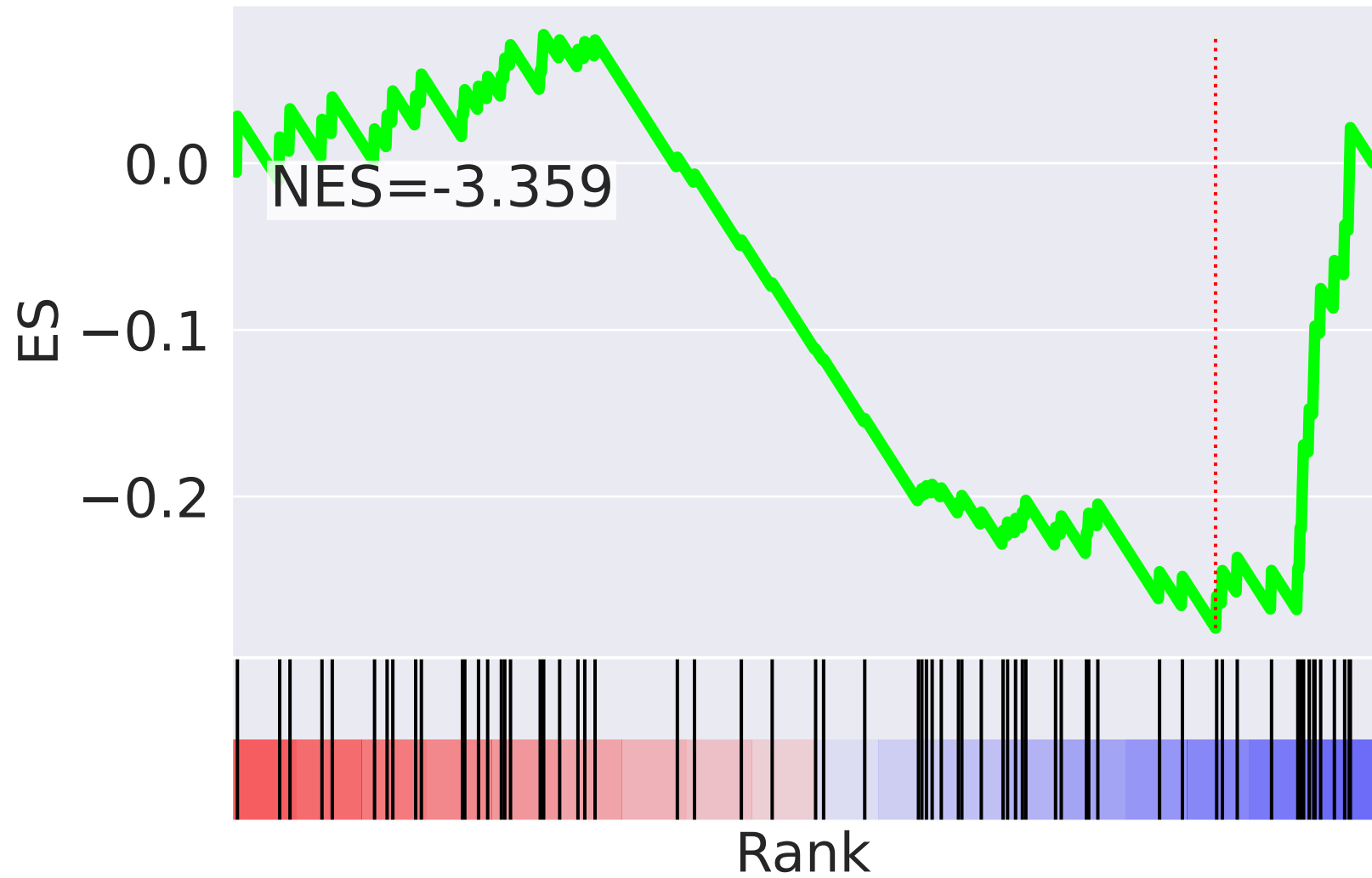
NES		SET
-2.751		DNA replication (GO:0006260)
-2.708		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.693		regulation of lipid metabolic process (GO:0019216)
2.551		positive regulation of gene expression, epigenetic (GO:0045815)
-2.534		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.495		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
2.442		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-2.407		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.404		protein K63-linked ubiquitination (GO:0070534)
2.364		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.298		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
2.128		lysosomal transport (GO:0007041)
-2.078		blood coagulation (GO:0007596)
-2.034		G1/S transition of mitotic cell cycle (GO:0000082)
-1.931		DNA replication initiation (GO:0006270)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=31$

mitochondrial translational elongation (GO:0070125)



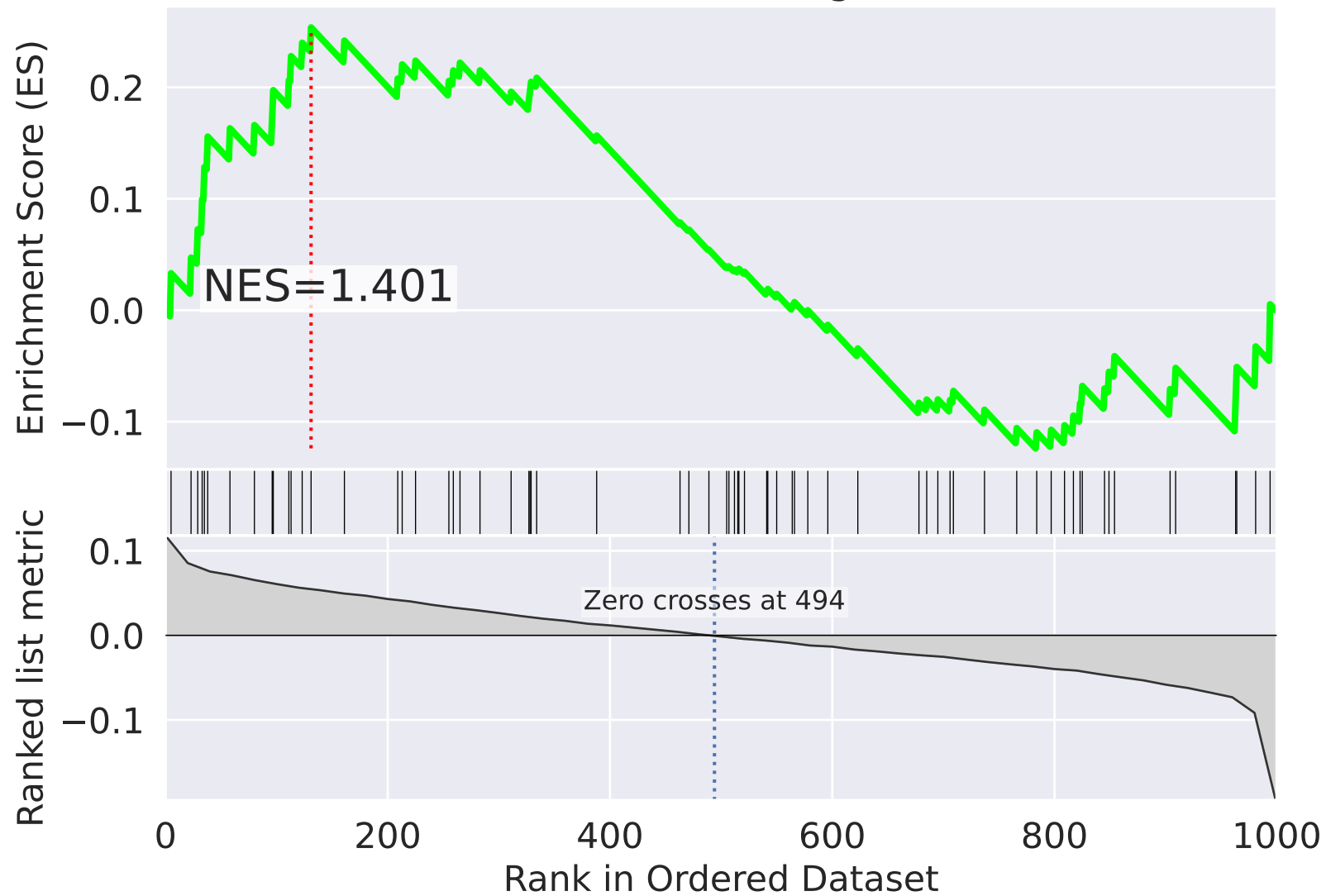
mitochondrial translational elongation (GO:0070125)



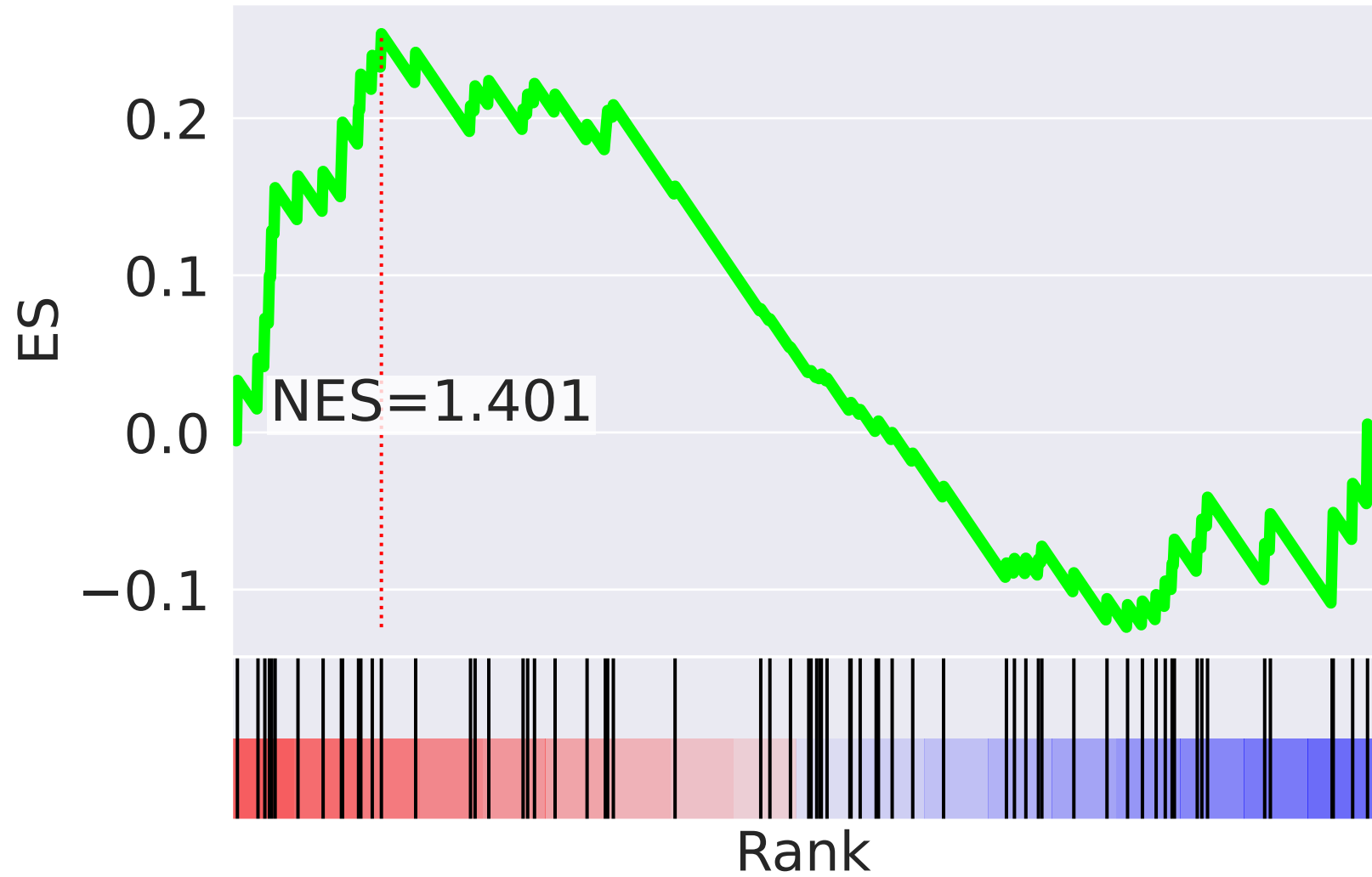
NES		SET
-3.559		mitochondrial translational termination (GO:0070126)
-3.359		mitochondrial translational elongation (GO:0070125)
3.058		transcription, DNA-templated (GO:0006351)
2.820		protein deubiquitination (GO:0016579)
2.757		proteolysis (GO:0006508)
-2.673		translation (GO:0006412)
2.603		tRNA modification (GO:0006400)
2.570		T cell receptor signaling pathway (GO:0050852)
2.523		ERBB2 signaling pathway (GO:0038128)
2.498		Fc-epsilon receptor signaling pathway (GO:0038095)
2.462		double-strand break repair (GO:0006302)
2.285		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
2.261		Ras protein signal transduction (GO:0007265)
2.239		regulation of apoptotic process (GO:0042981)
-2.237		viral budding via host ESCRT complex (GO:0039702)


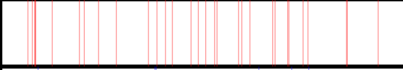


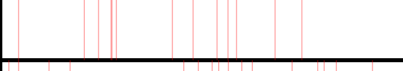
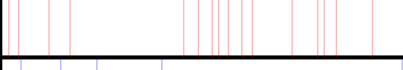
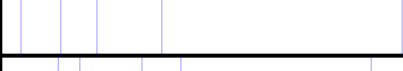

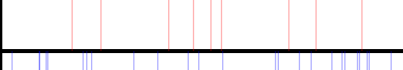
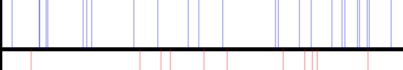


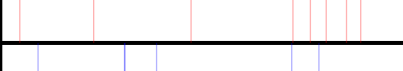


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=32$

mitochondrial translational elongation (GO:0070125)



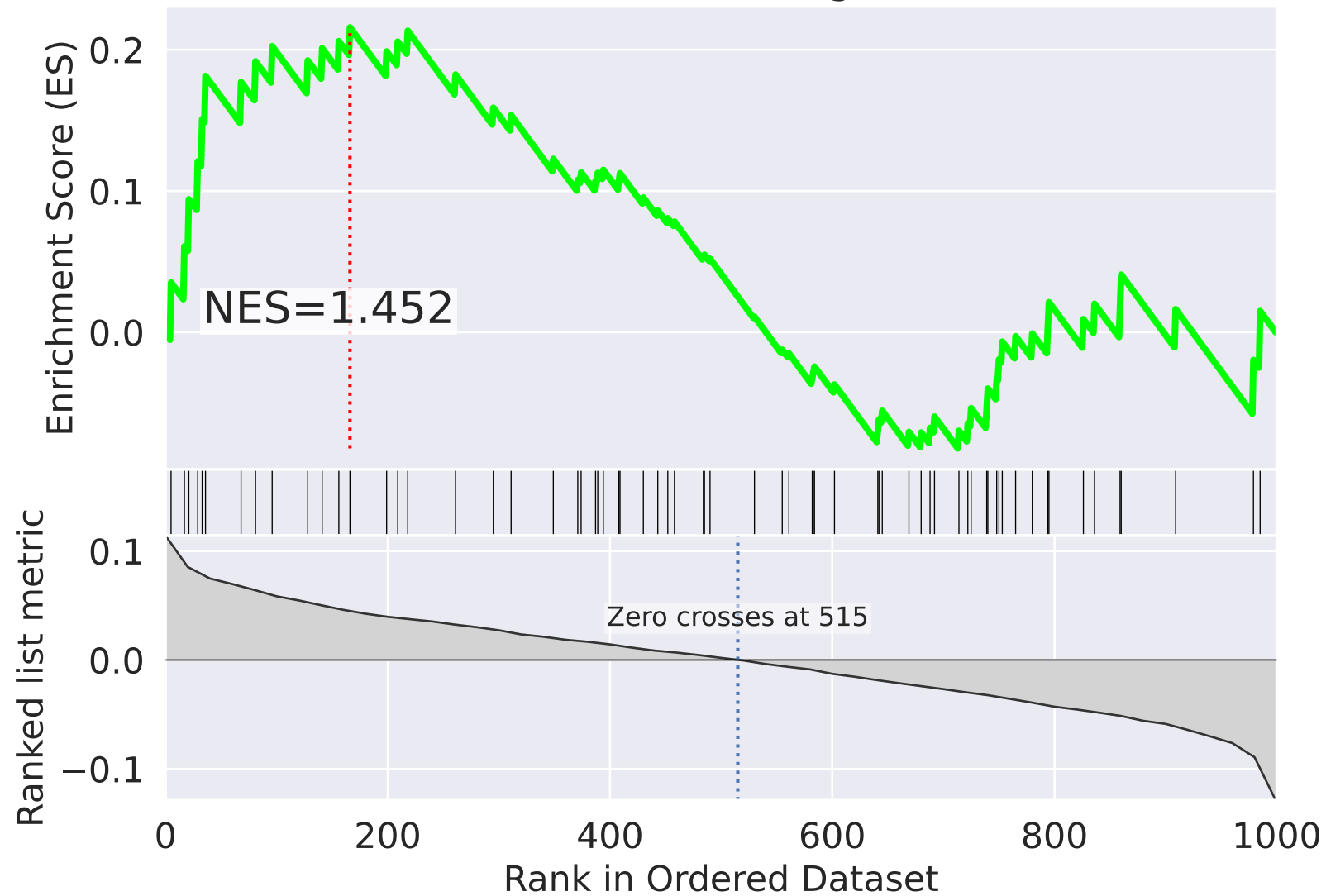
mitochondrial translational elongation (GO:0070125)



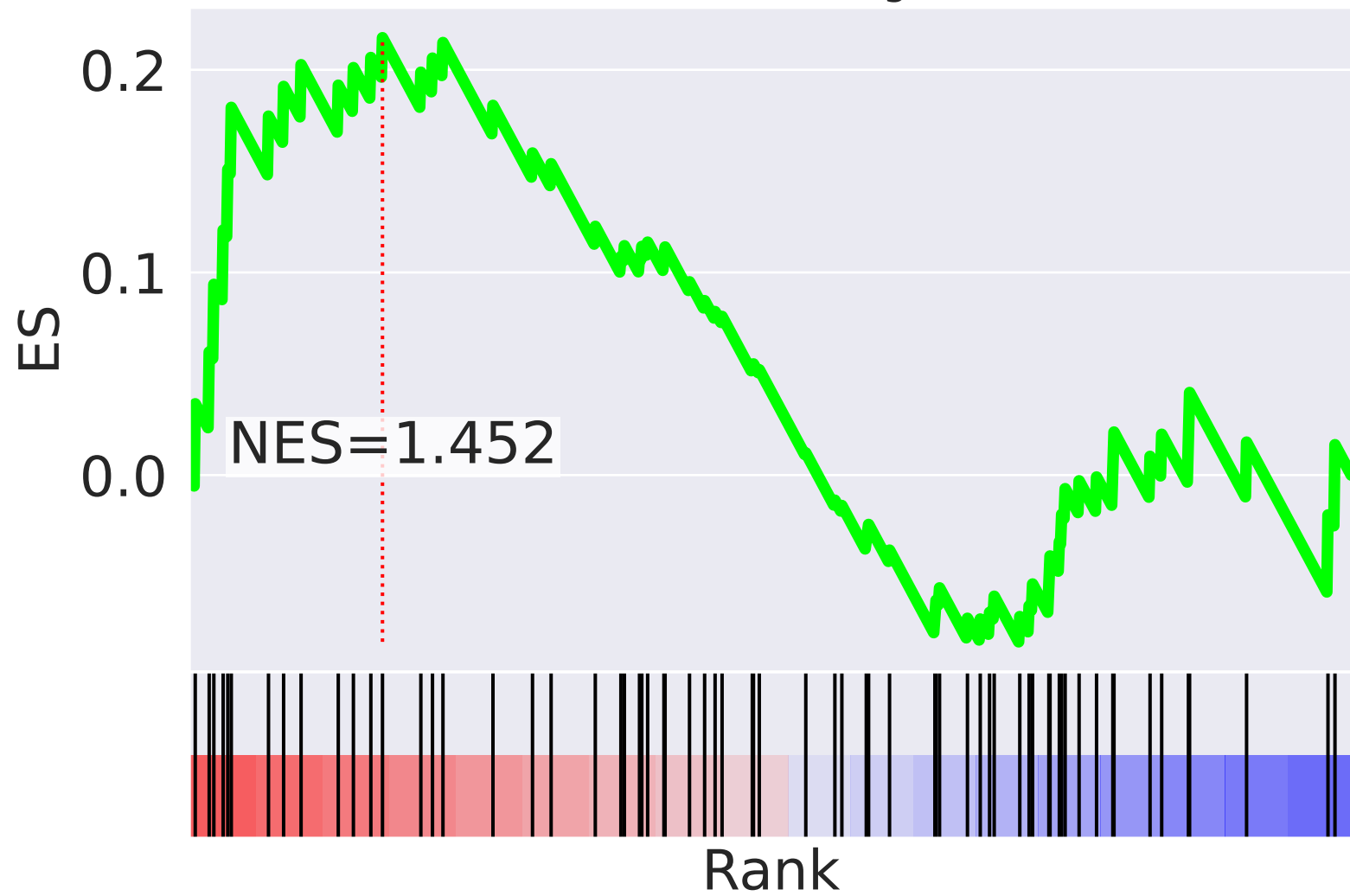
NES		SET
2.455		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.321		positive regulation of cell proliferation (GO:0008284)
-2.247		mRNA processing (GO:0006397)
2.146		platelet aggregation (GO:0070527)
2.111		positive regulation of cell migration (GO:0030335)
2.039		protein complex assembly (GO:0006461)
-2.031		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.955		DNA-dependent DNA replication (GO:0006261)
1.946		intracellular signal transduction (GO:0035556)
-1.843		mitochondrial translation (GO:0032543)
1.837		generation of precursor metabolites and energy (GO:0006091)
1.805		cell-matrix adhesion (GO:0007160)
1.781		multicellular organism development (GO:0007275)
-1.762		fibroblast growth factor receptor signaling pathway (GO:0008543)
1.729		movement of cell or subcellular component (GO:0006928)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=33$

mitochondrial translational elongation (GO:0070125)

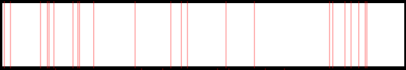



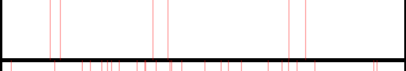
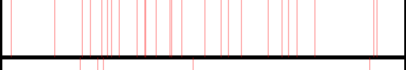



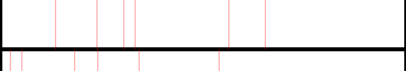

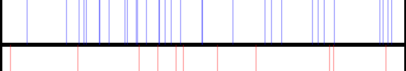

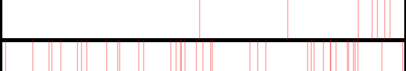



mitochondrial translational elongation (GO:0070125)



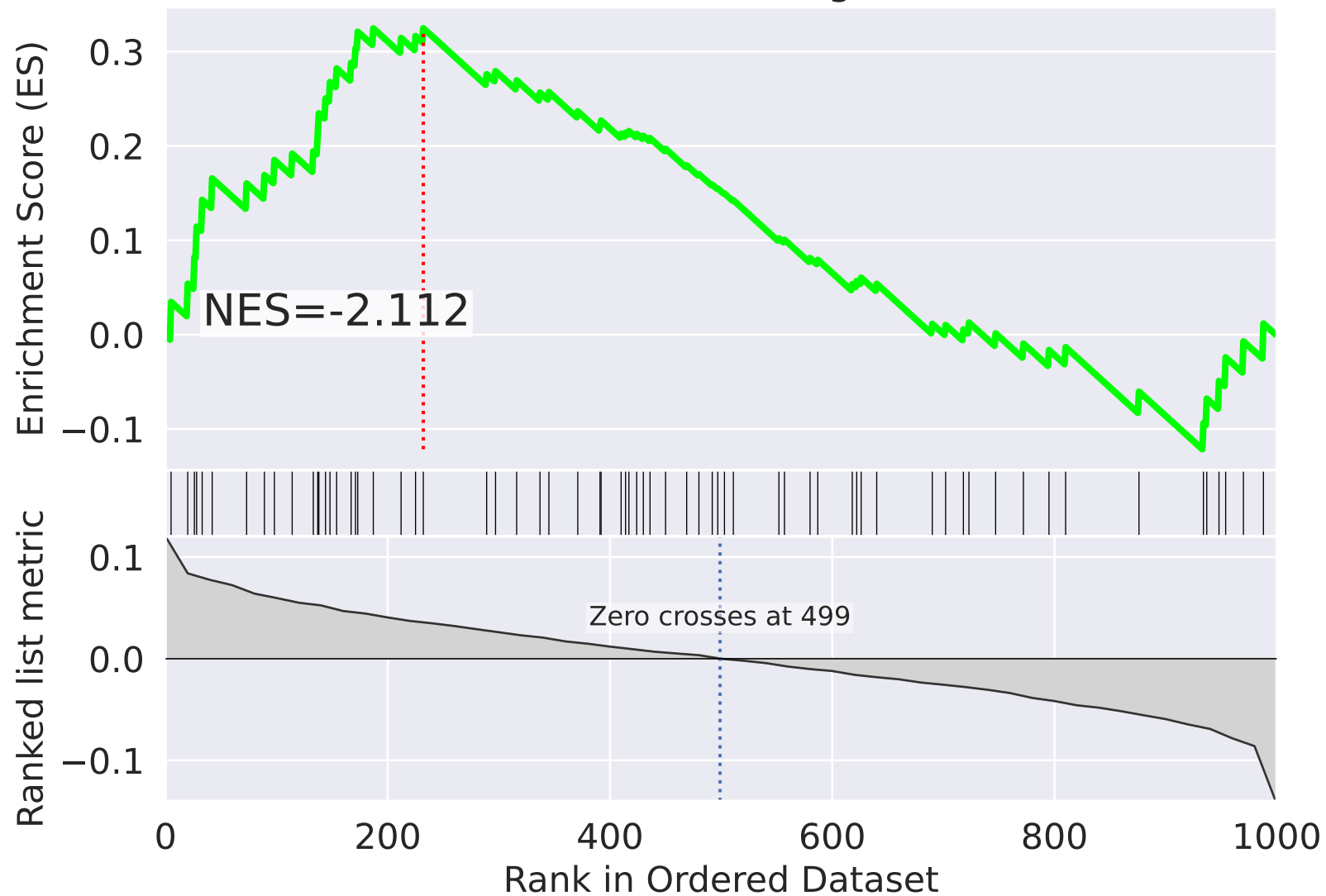
NES

SET

2.581		positive regulation of apoptotic process (GO:0043065)
2.491		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.394		viral budding via host ESCRT complex (GO:0039702)
2.359		positive regulation of GTPase activity (GO:0043547)
2.308		aerobic respiration (GO:0009060)
2.127		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.116		iron-sulfur cluster assembly (GO:0016226)
-2.078		tRNA aminoacylation for protein translation (GO:0006418)
2.065		positive regulation of mitotic cell cycle (GO:0045931)
2.056		T cell costimulation (GO:0031295)
2.045		chromosome segregation (GO:0007059)
-2.012		mRNA splicing, via spliceosome (GO:0000398)
2.009		positive regulation of gene expression (GO:0010628)
2.008		intracellular protein transport (GO:0006886)
1.999		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=34$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)



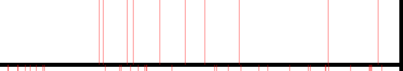
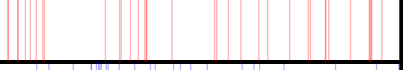
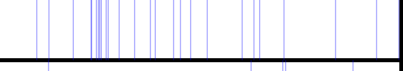

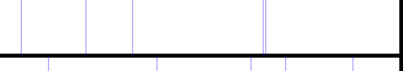
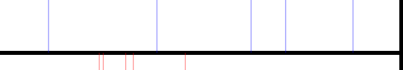
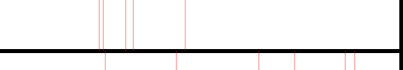

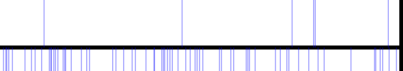
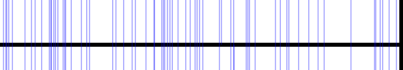
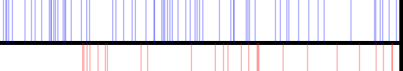

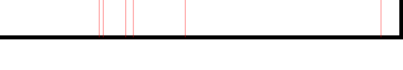
ES

0.3
0.2
0.1
0.0
-0.1

NES=-2.112

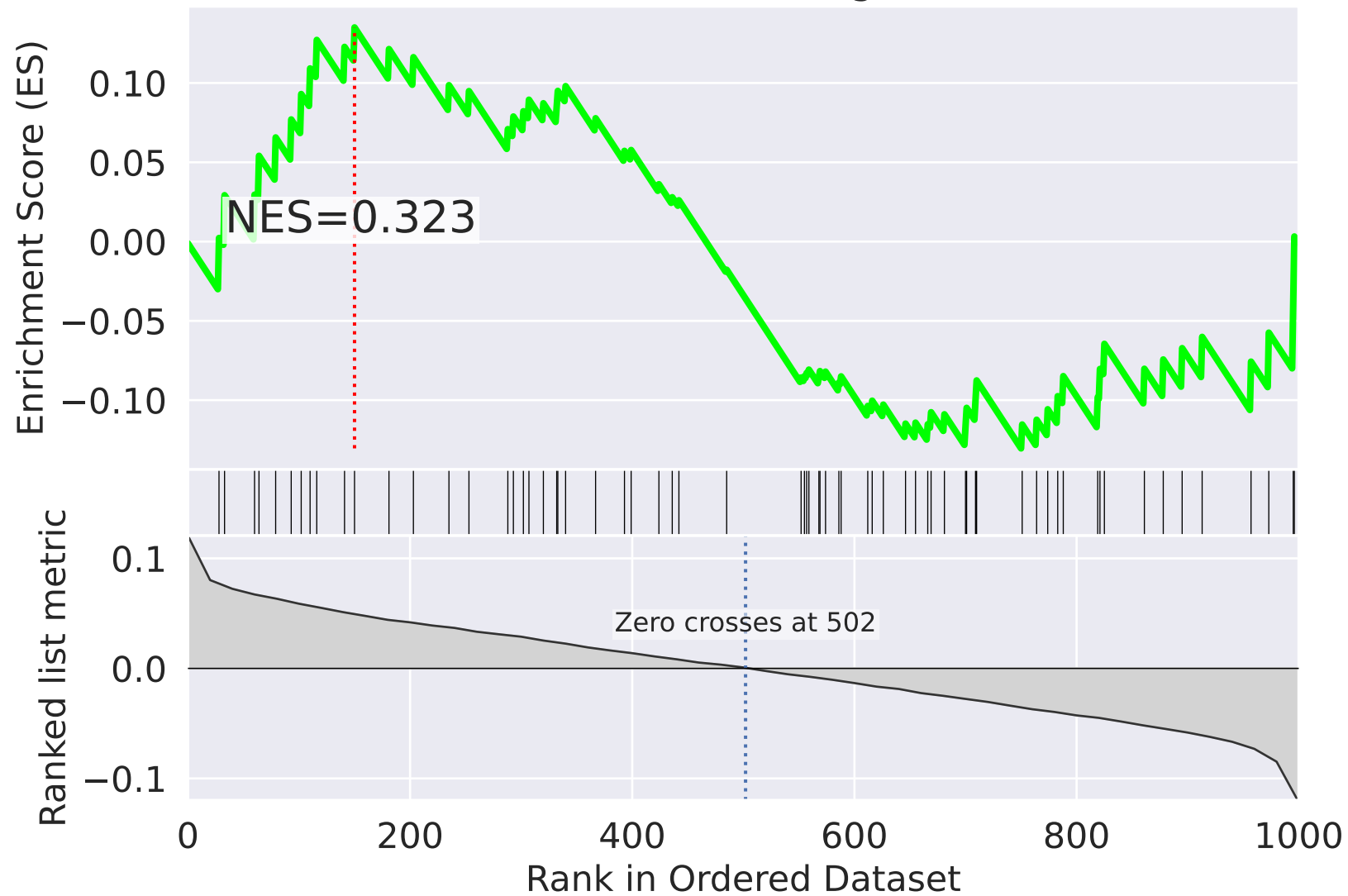
Rank



NES		SET
2.643		positive regulation of cell proliferation (GO:0008284)
2.578		ERBB2 signaling pathway (GO:0038128)
2.558		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.467		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-2.450		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.352		canonical glycolysis (GO:0061621)
-2.231		substrate adhesion-dependent cell spreading (GO:0034446)
-2.228		gluconeogenesis (GO:0006094)
2.176		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
2.160		positive regulation of cell growth (GO:0030307)
-2.136		aerobic respiration (GO:0009060)
-2.112		mitochondrial translational elongation (GO:0070125)
-2.106		mitochondrial translational termination (GO:0070126)
2.073		signal transduction (GO:0007165)
2.042		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=35$

mitochondrial translational elongation (GO:0070125)



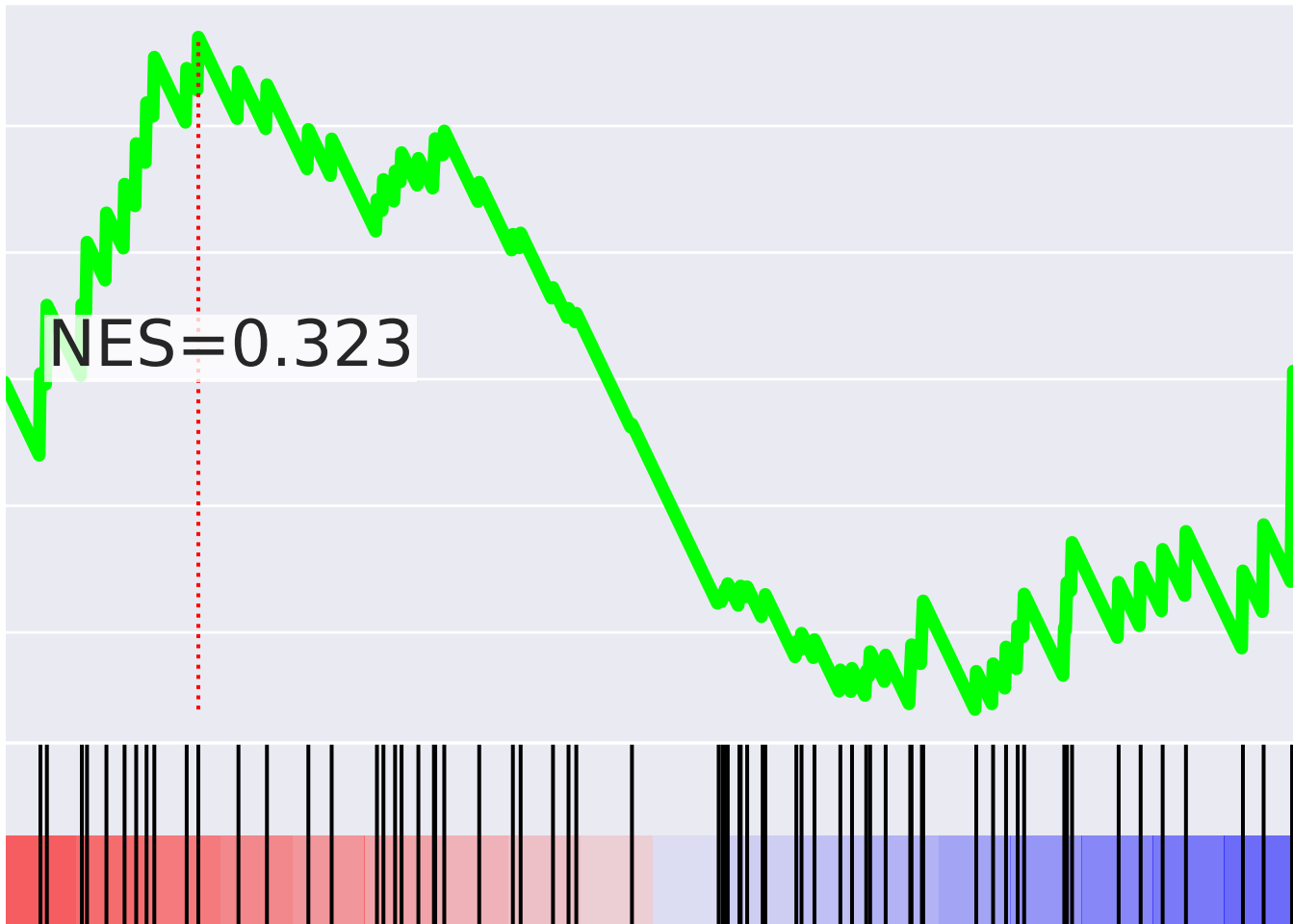
mitochondrial translational elongation (GO:0070125)

ES

0.10
0.05
0.00
-0.05
-0.10


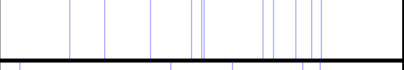


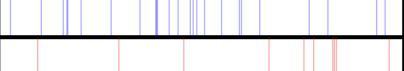
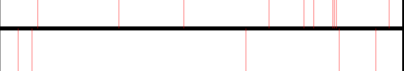
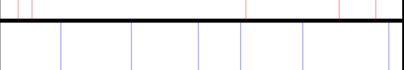

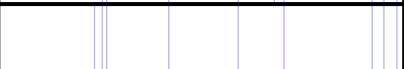

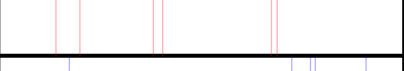

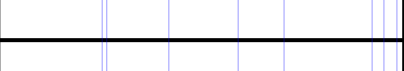
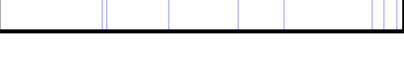

NES=0.323

Rank



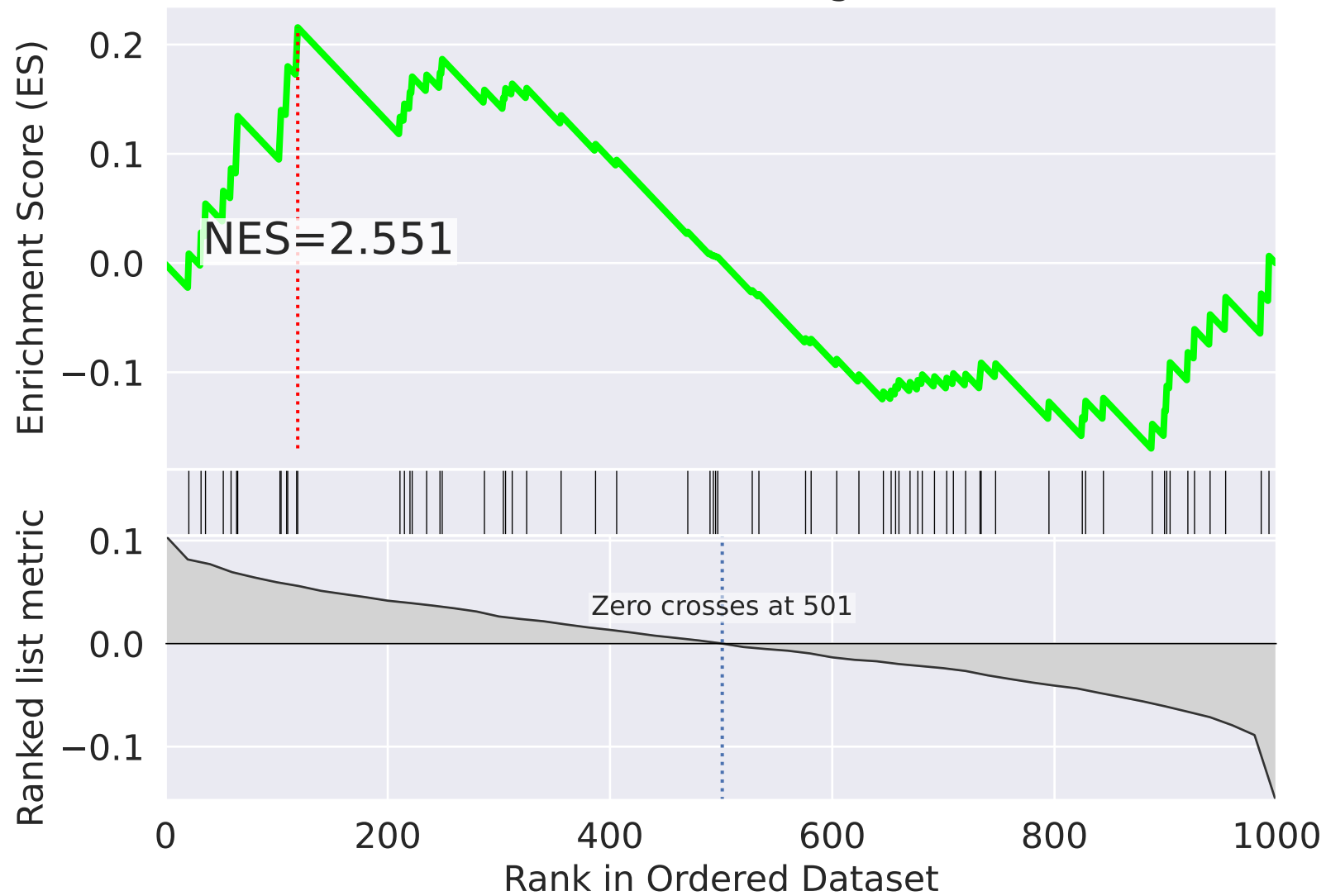
NES

SET

3.196		protein deubiquitination (GO:0016579)
-3.186		generation of precursor metabolites and energy (GO:0006091)
-2.355		positive regulation of cytokinesis (GO:0032467)
-2.338		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.138		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.053		double-strand break repair via homologous recombination (GO:0000724)
2.017		execution phase of apoptosis (GO:0097194)
-2.013		COPII vesicle coating (GO:0048208)
-1.988		protein sumoylation (GO:0016925)
-1.985		viral transcription (GO:0019083)
-1.922		positive regulation of viral genome replication (GO:0045070)
1.850		protein K48-linked ubiquitination (GO:0070936)
-1.788		mitotic spindle organization (GO:0007052)
-1.764		regulation of gene silencing by miRNA (GO:0060964)
-1.764		tRNA export from nucleus (GO:0006409)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=36$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1



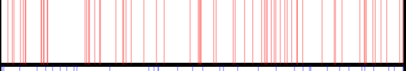
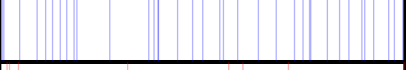


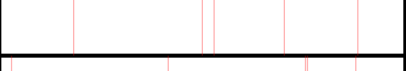


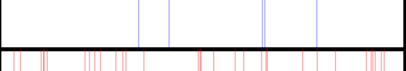
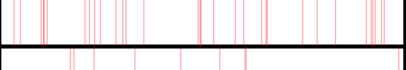
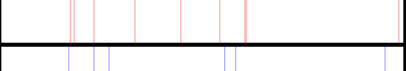
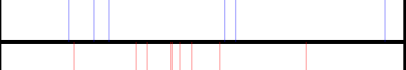


NES=2.551

Rank



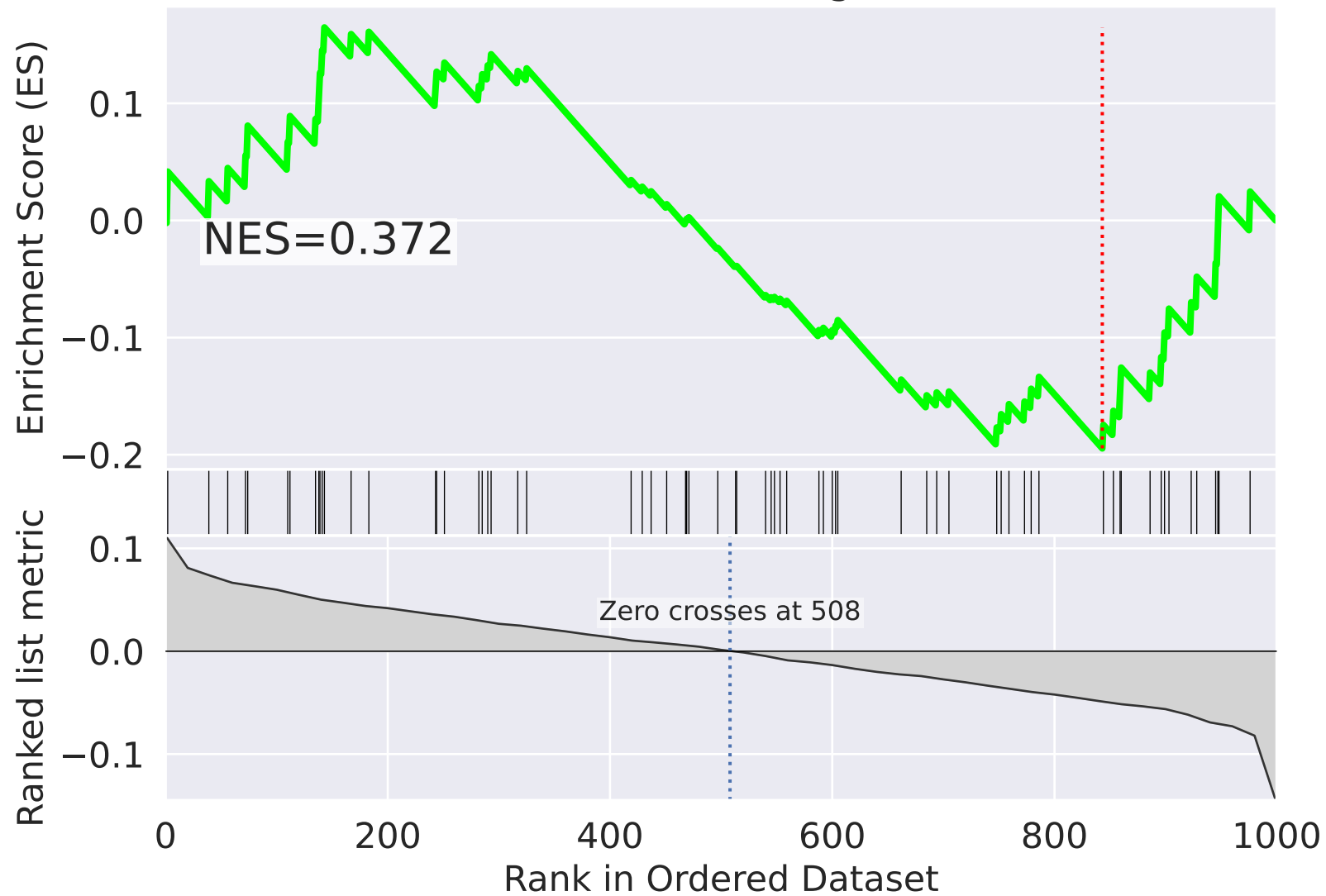
NES

SET

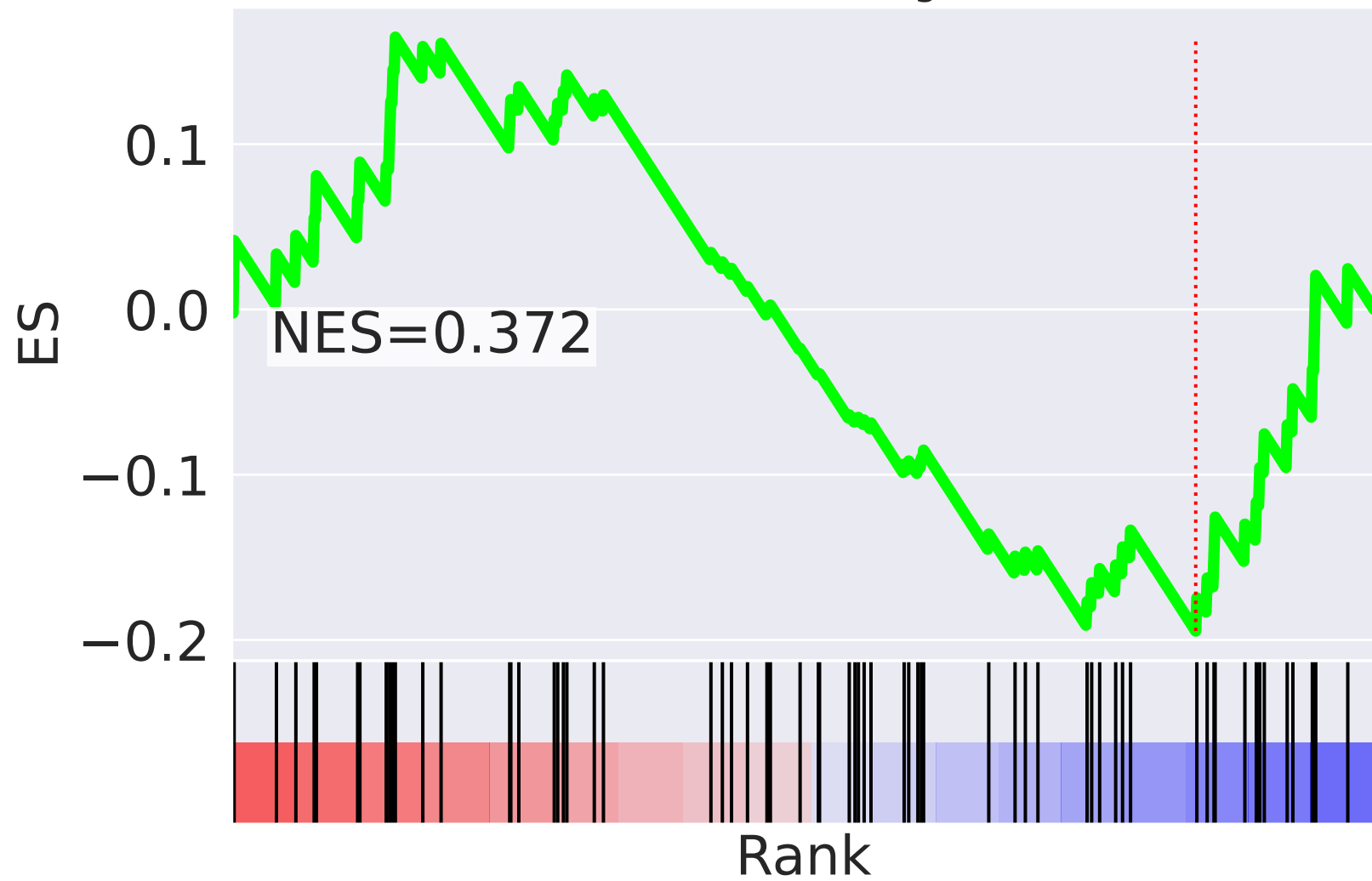
-2.721		chromatin remodeling (GO:0006338)
2.623		mitochondrial translational termination (GO:0070126)
2.551		mitochondrial translational elongation (GO:0070125)
-2.347		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.249		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.107		regulation of lipid metabolic process (GO:0019216)
1.987		gluconeogenesis (GO:0006094)
1.977		lysosomal transport (GO:0007041)
-1.916		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-1.915		mitochondrial respiratory chain complex IV assembly (GO:0033617)
1.913		translation (GO:0006412)
1.904		phosphatidylinositol-mediated signaling (GO:0048015)
-1.903		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
1.880		positive regulation of protein phosphorylation (GO:0001934)
1.879		canonical glycolysis (GO:0061621)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=37$

mitochondrial translational elongation (GO:0070125)



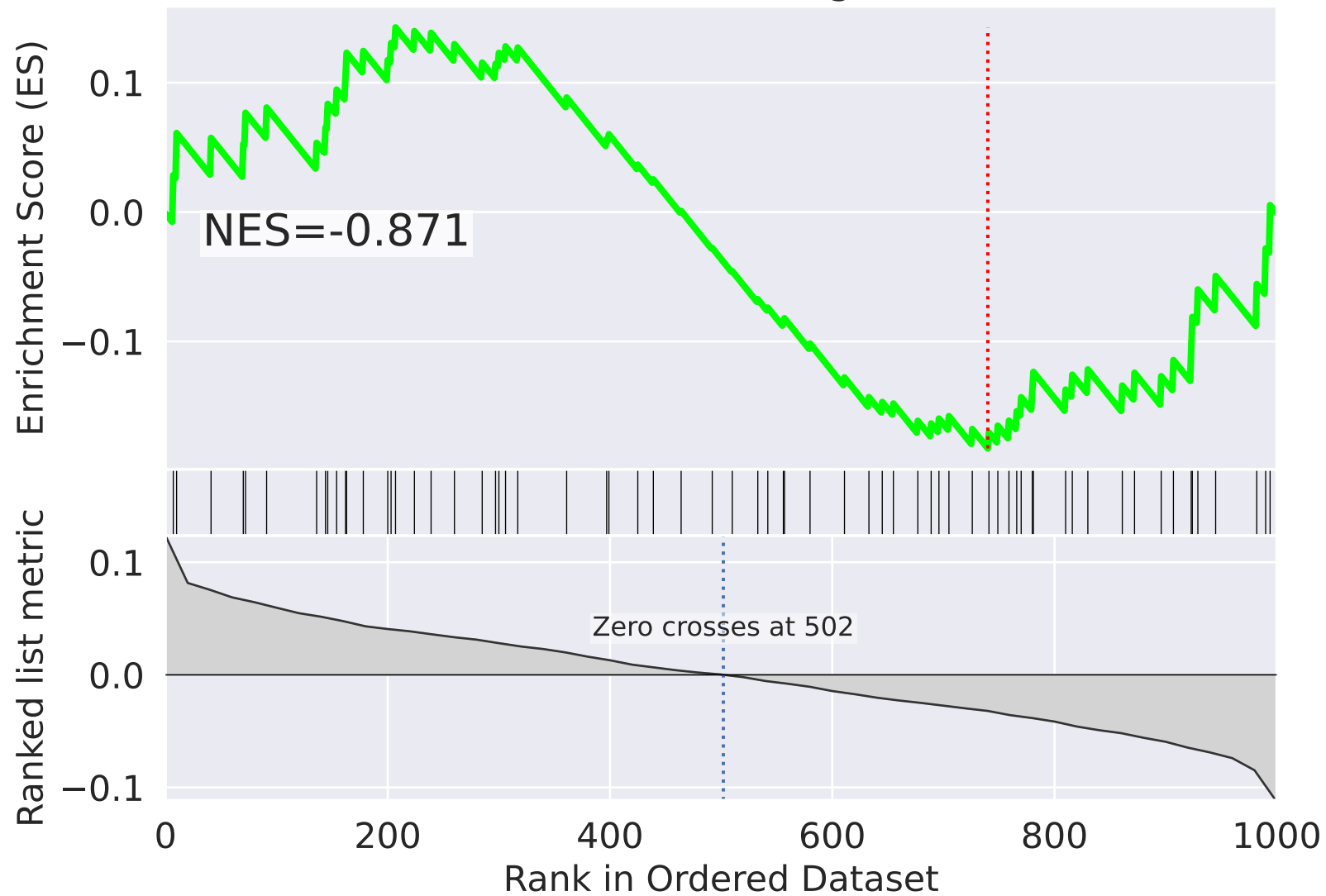
mitochondrial translational elongation (GO:0070125)



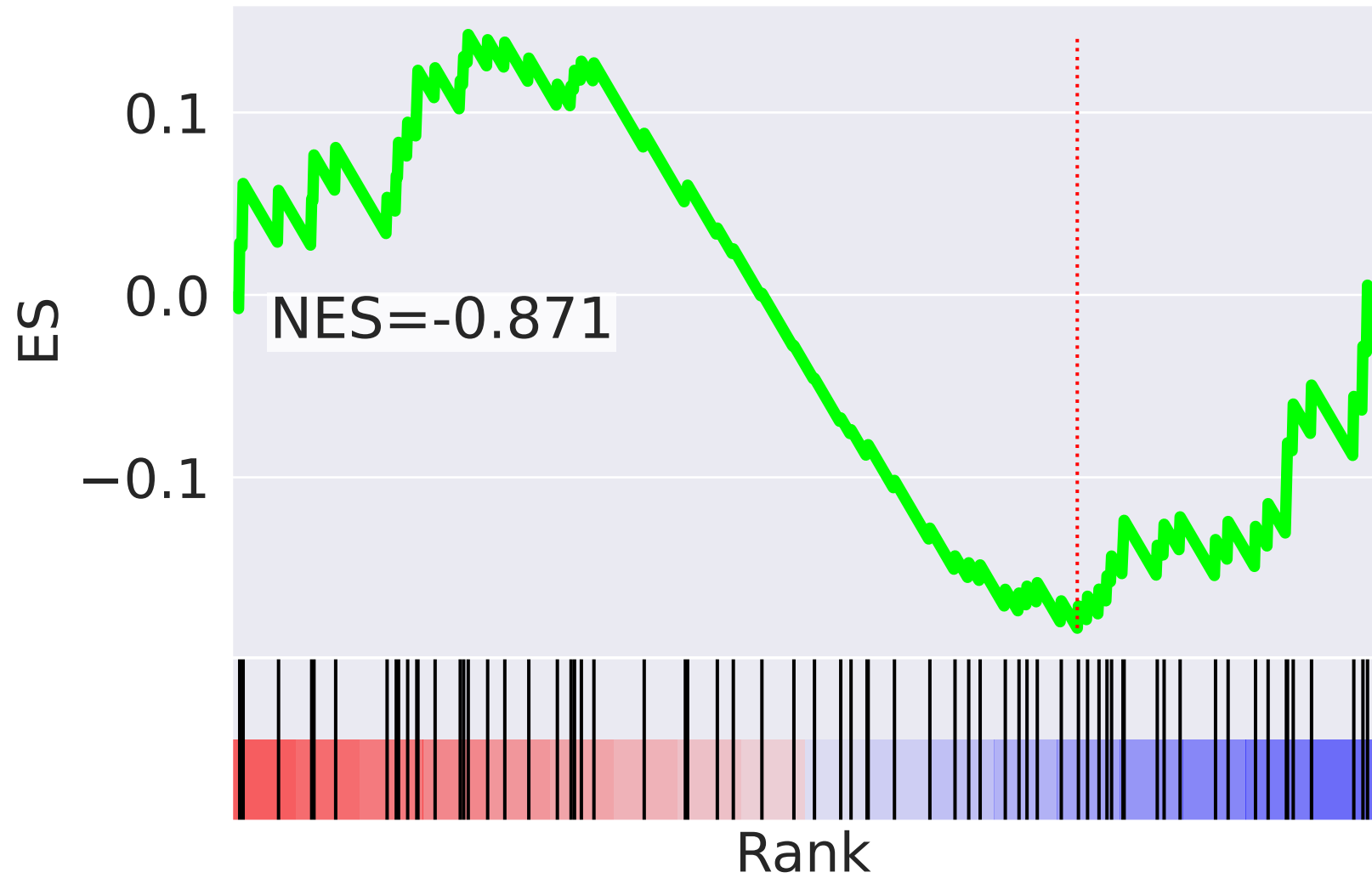
NES		SET
3.014		macroautophagy (GO:0016236)
-2.861		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.641		apoptotic process (GO:0006915)
-2.600		negative regulation of cell proliferation (GO:0008285)
2.493		mitotic metaphase plate congression (GO:0007080)
2.415		protein targeting to mitochondrion (GO:0006626)
-2.334		insulin receptor signaling pathway (GO:0008286)
2.323		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
-2.322		leukocyte migration (GO:0050900)
-2.224		cell cycle arrest (GO:0007050)
2.186		DNA damage checkpoint (GO:0000077)
-2.140		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
2.129		transcription initiation from RNA polymerase I promoter (GO:0006361)
2.129		transcription elongation from RNA polymerase I promoter (GO:0006362)
2.129		termination of RNA polymerase I transcription (GO:0006363)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=38$

mitochondrial translational elongation (GO:0070125)



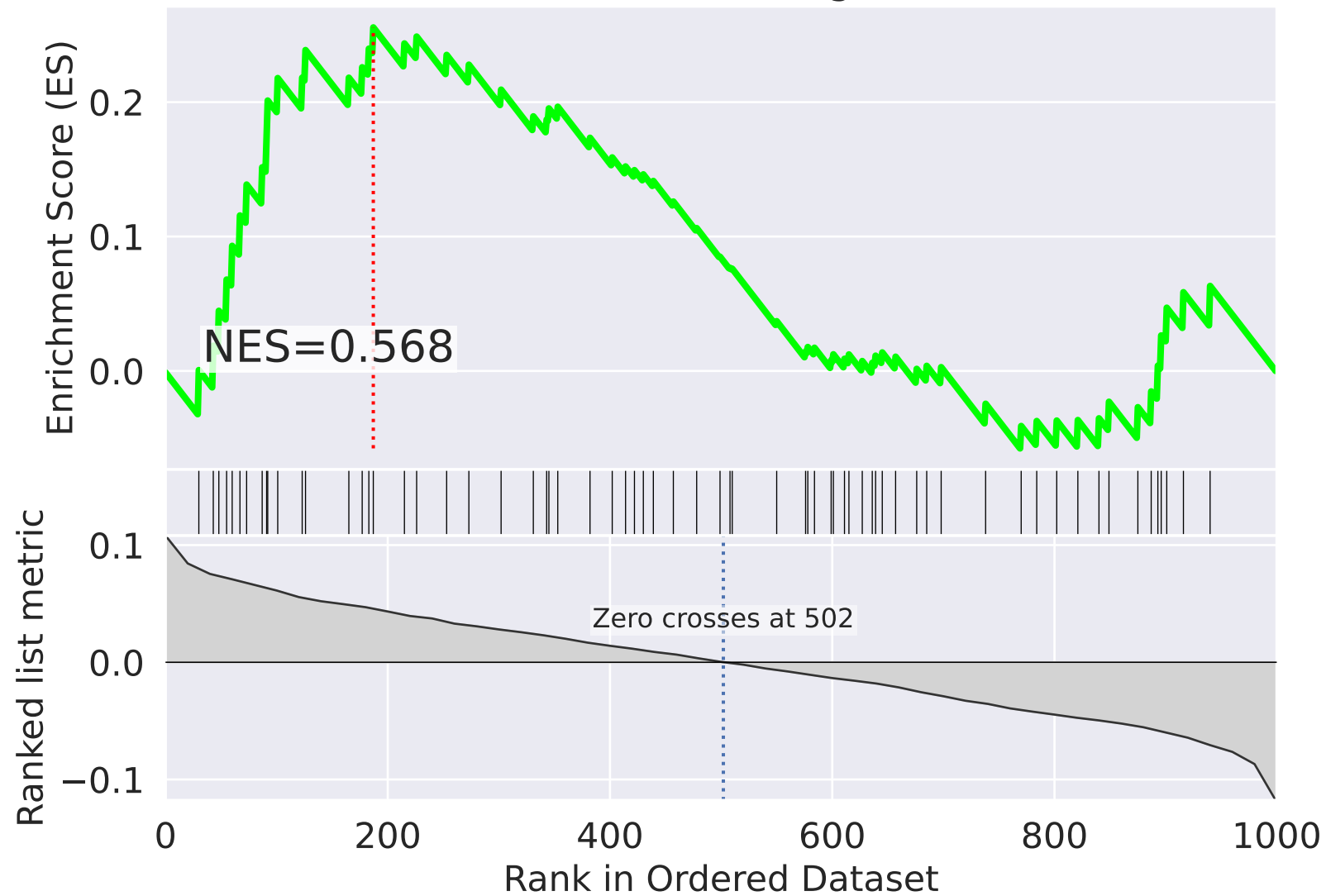
mitochondrial translational elongation (GO:0070125)



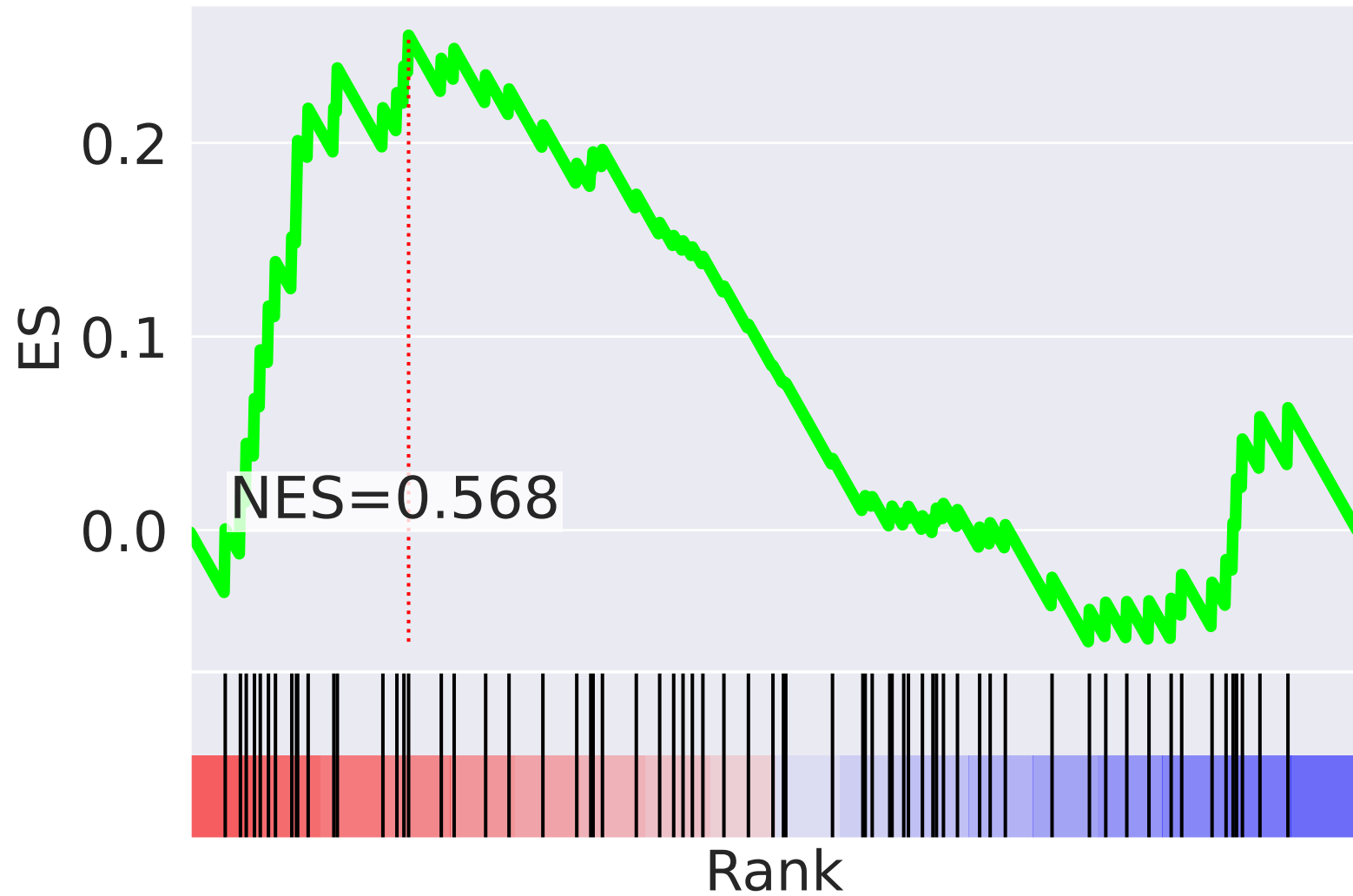
NES		SET
-2.709		DNA-dependent DNA replication (GO:0006261)
2.344		mRNA splicing, via spliceosome (GO:0000398)
2.217		RNA metabolic process (GO:0016070)
2.186		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.172		nucleosome disassembly (GO:0006337)
-2.167		protein import into nucleus (GO:0006606)
2.156		positive regulation of DNA replication (GO:0045740)
2.086		mRNA processing (GO:0006397)
2.084		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-1.964		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-1.941		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
1.919		response to virus (GO:0009615)
-1.918		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
1.907		nucleotide-excision repair (GO:0006289)
1.892		T cell costimulation (GO:0031295)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=39$

mitochondrial translational elongation (GO:0070125)



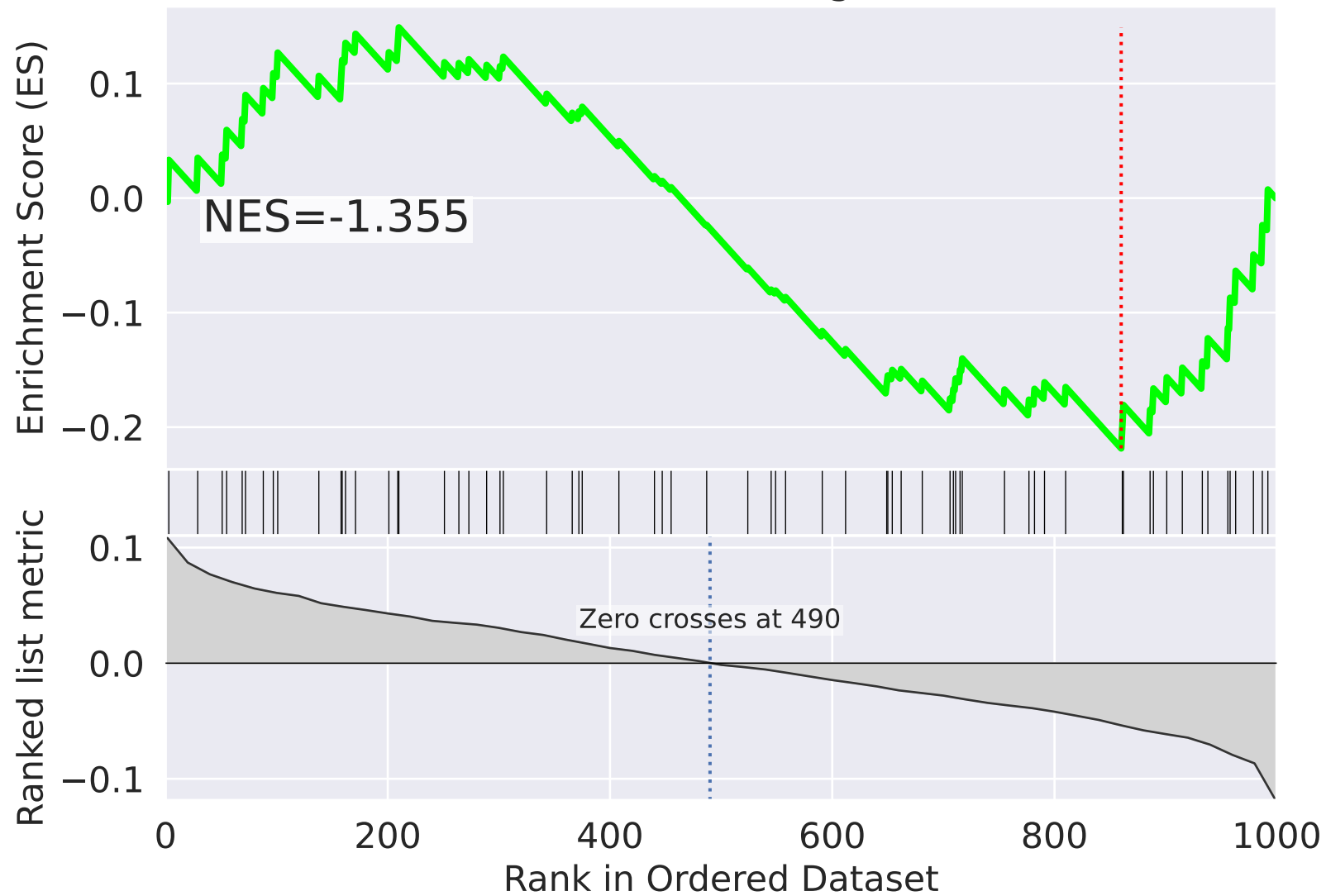
mitochondrial translational elongation (GO:0070125)



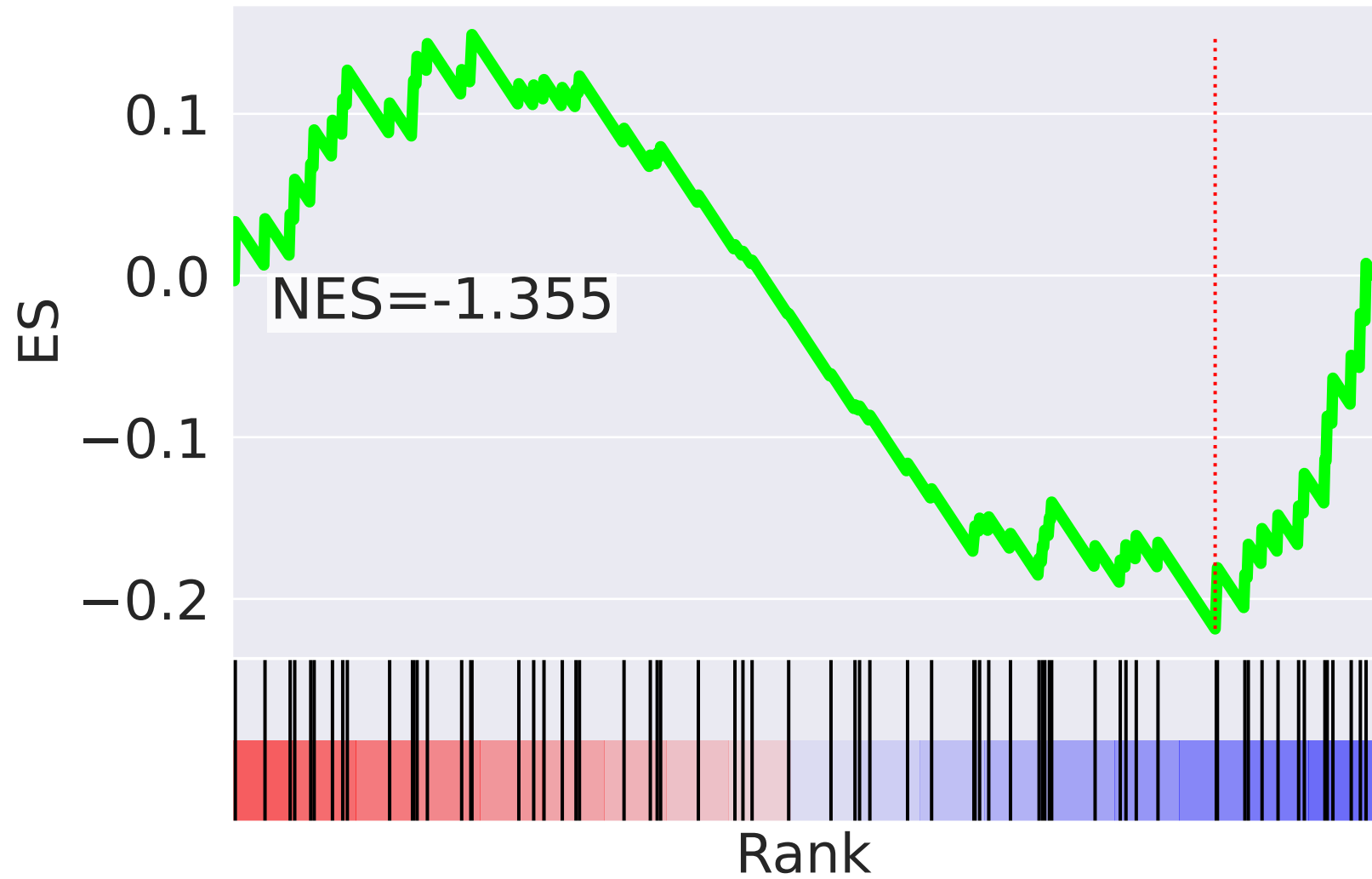
NES		SET
-2.845		membrane organization (GO:0061024)
2.420		Fc-epsilon receptor signaling pathway (GO:0038095)
2.286		axon guidance (GO:0007411)
2.284		cellular nitrogen compound metabolic process (GO:0034641)
2.283		generation of precursor metabolites and energy (GO:0006091)
2.229		Ras protein signal transduction (GO:0007265)
2.159		cholesterol biosynthetic process (GO:0006695)
2.156		interstrand cross-link repair (GO:0036297)
2.144		mitotic cell cycle (GO:0000278)
2.127		protein phosphorylation (GO:0006468)
2.098		platelet activation (GO:0030168)
2.091		positive regulation of gene expression (GO:0010628)
-2.072		telomere capping (GO:0016233)
2.063		T cell costimulation (GO:0031295)
-2.005		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)


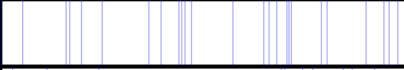

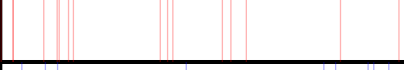

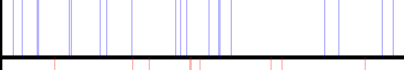
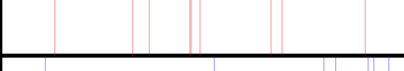


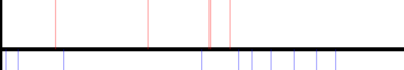

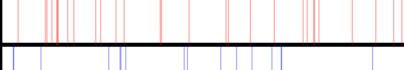
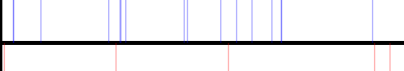
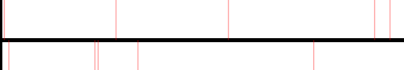
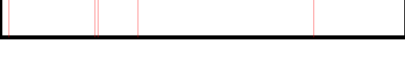
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=40$

mitochondrial translational elongation (GO:0070125)



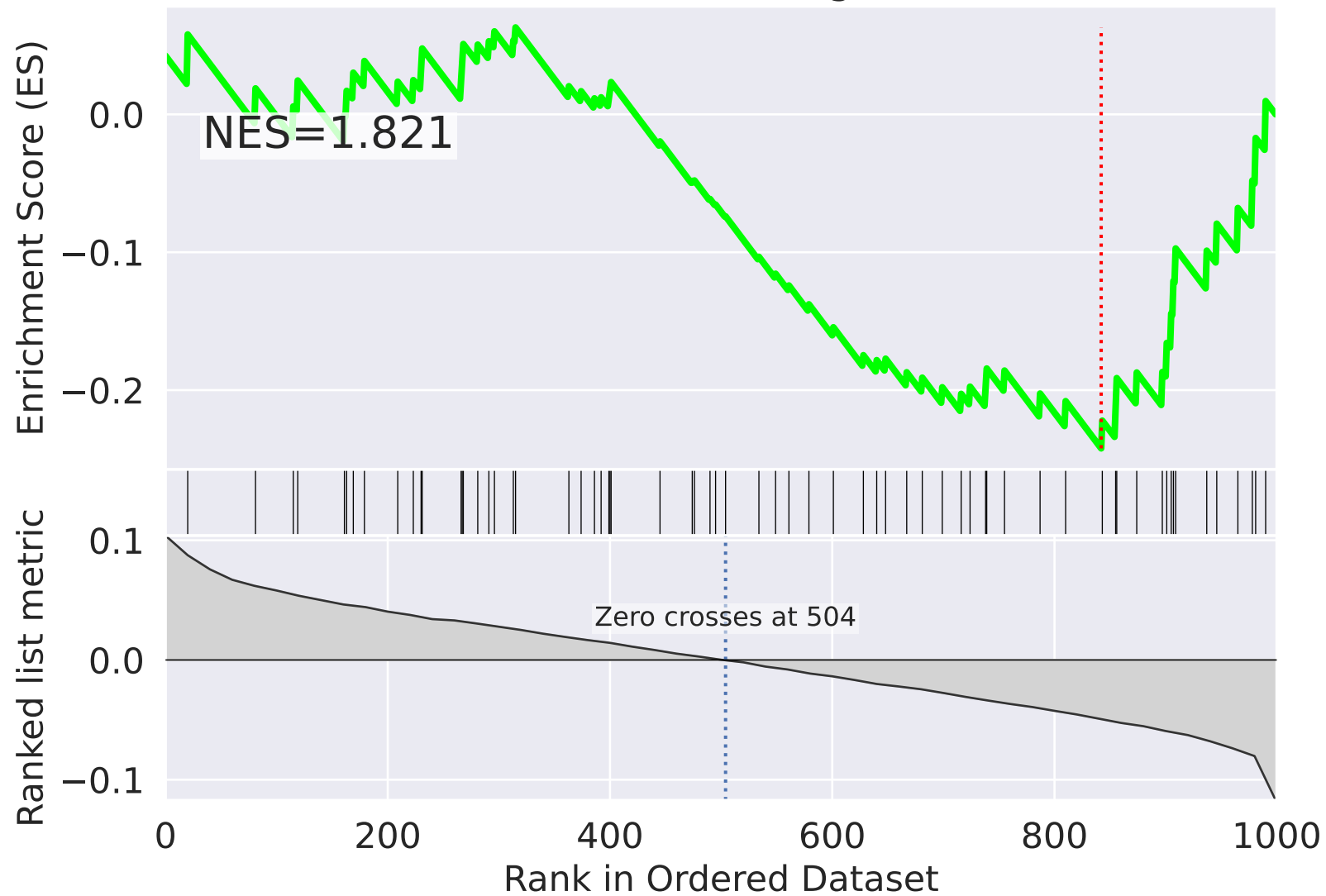
mitochondrial translational elongation (GO:0070125)



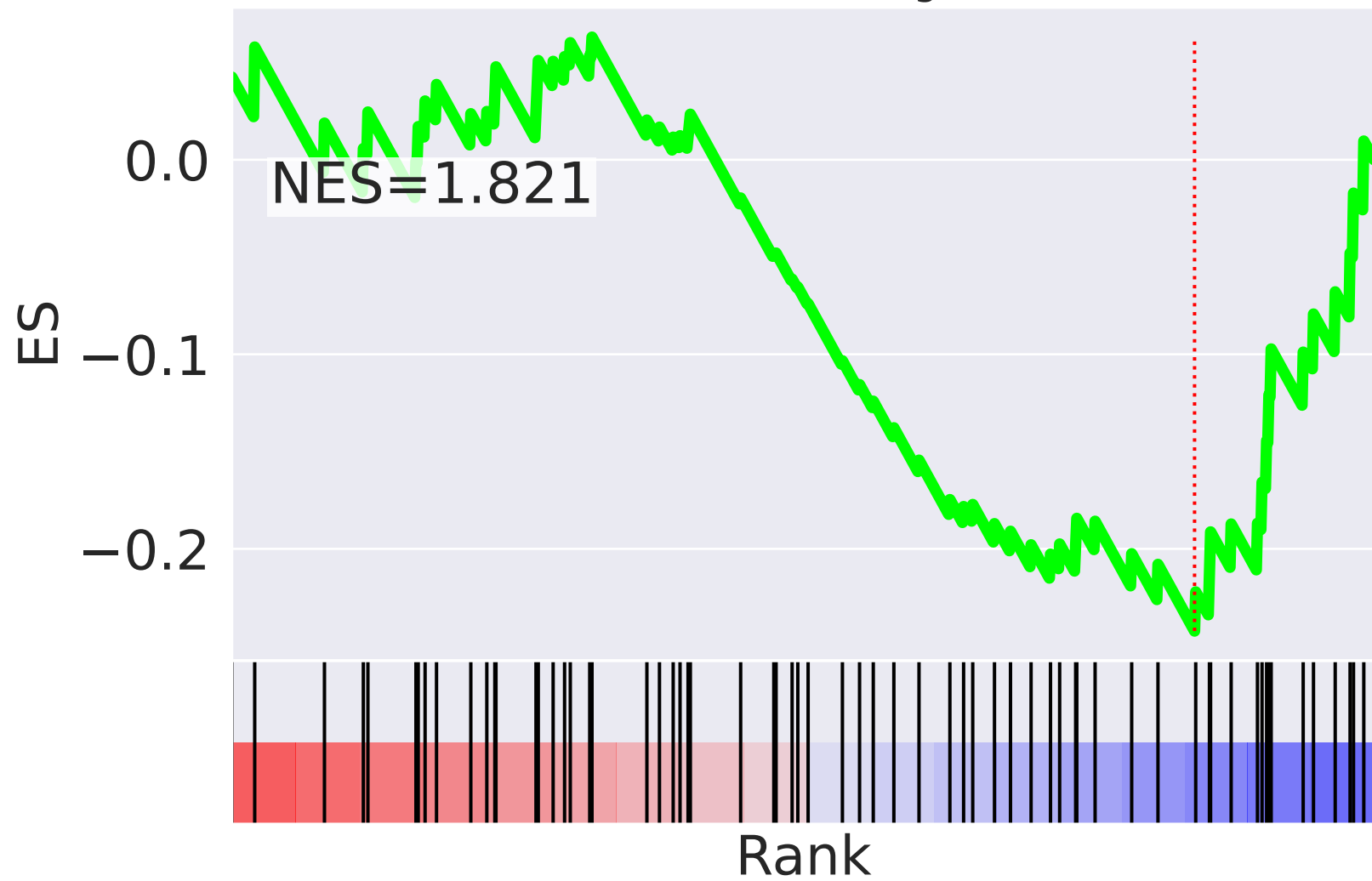
NES		SET
3.291		negative regulation of transcription, DNA-templated (GO:0045892)
-2.747		mitochondrial translation (GO:0032543)
-2.640		double-strand break repair via nonhomologous end joining (GO:0006303)
2.547		protein complex assembly (GO:0006461)
-2.414		phosphatidylinositol-mediated signaling (GO:0048015)
-2.391		transcription from RNA polymerase II promoter (GO:0006366)
2.375		protein sumoylation (GO:0016925)
-2.272		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-2.228		positive regulation of GTPase activity (GO:0043547)
2.125		gluconeogenesis (GO:0006094)
-2.108		Ras protein signal transduction (GO:0007265)
2.060		negative regulation of apoptotic process (GO:0043066)
-2.042		G1/S transition of mitotic cell cycle (GO:0000082)
2.039		cellular response to tumor necrosis factor (GO:0071356)
2.035		substrate adhesion-dependent cell spreading (GO:0034446)


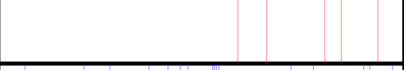
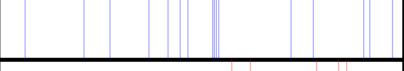

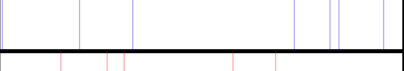
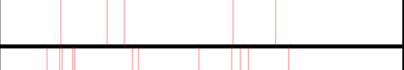
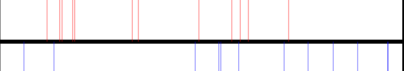

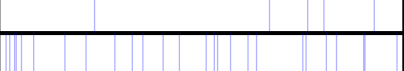

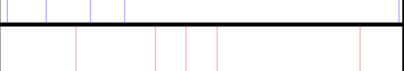
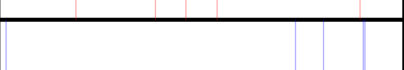



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=41$

mitochondrial translational elongation (GO:0070125)



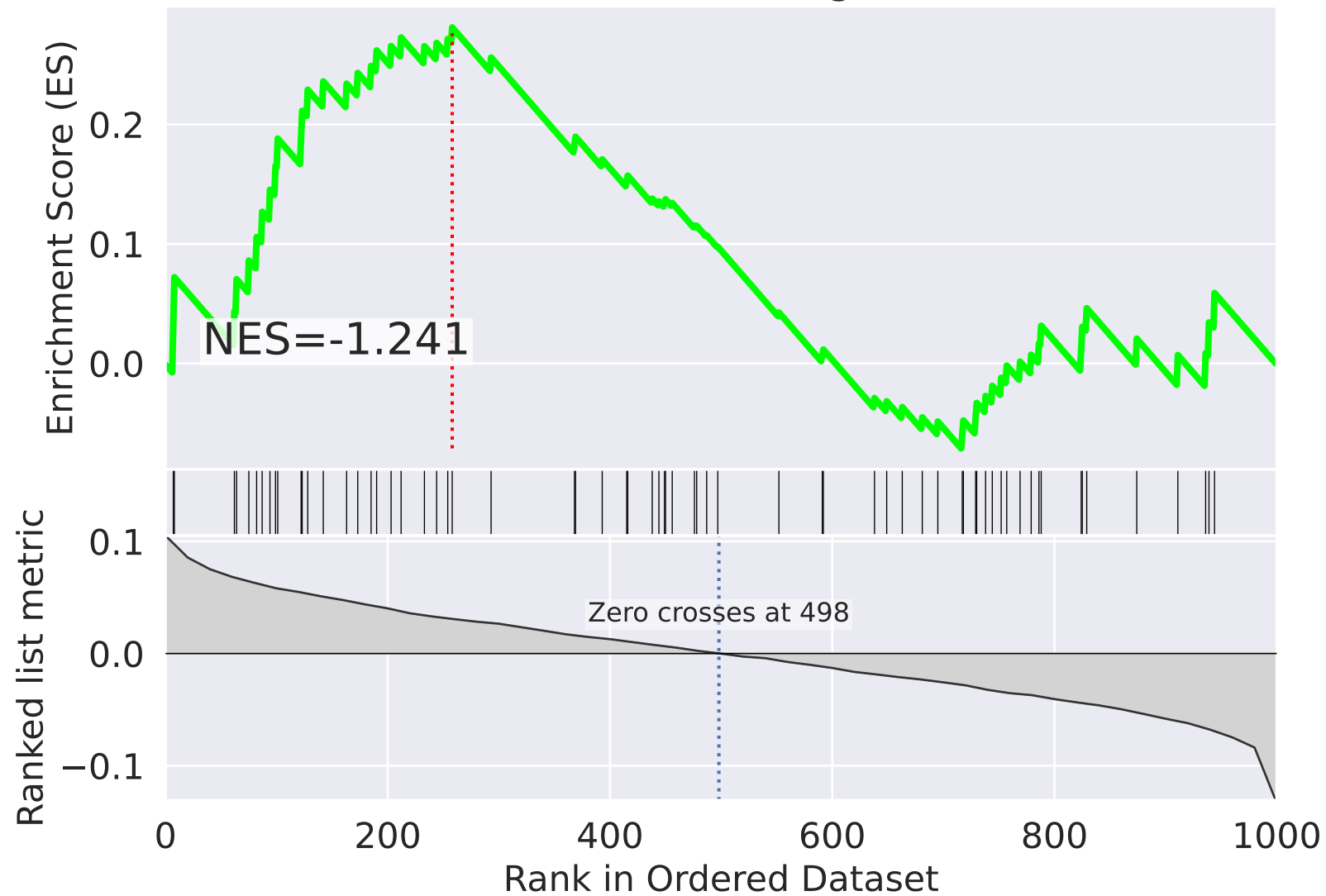
mitochondrial translational elongation (GO:0070125)



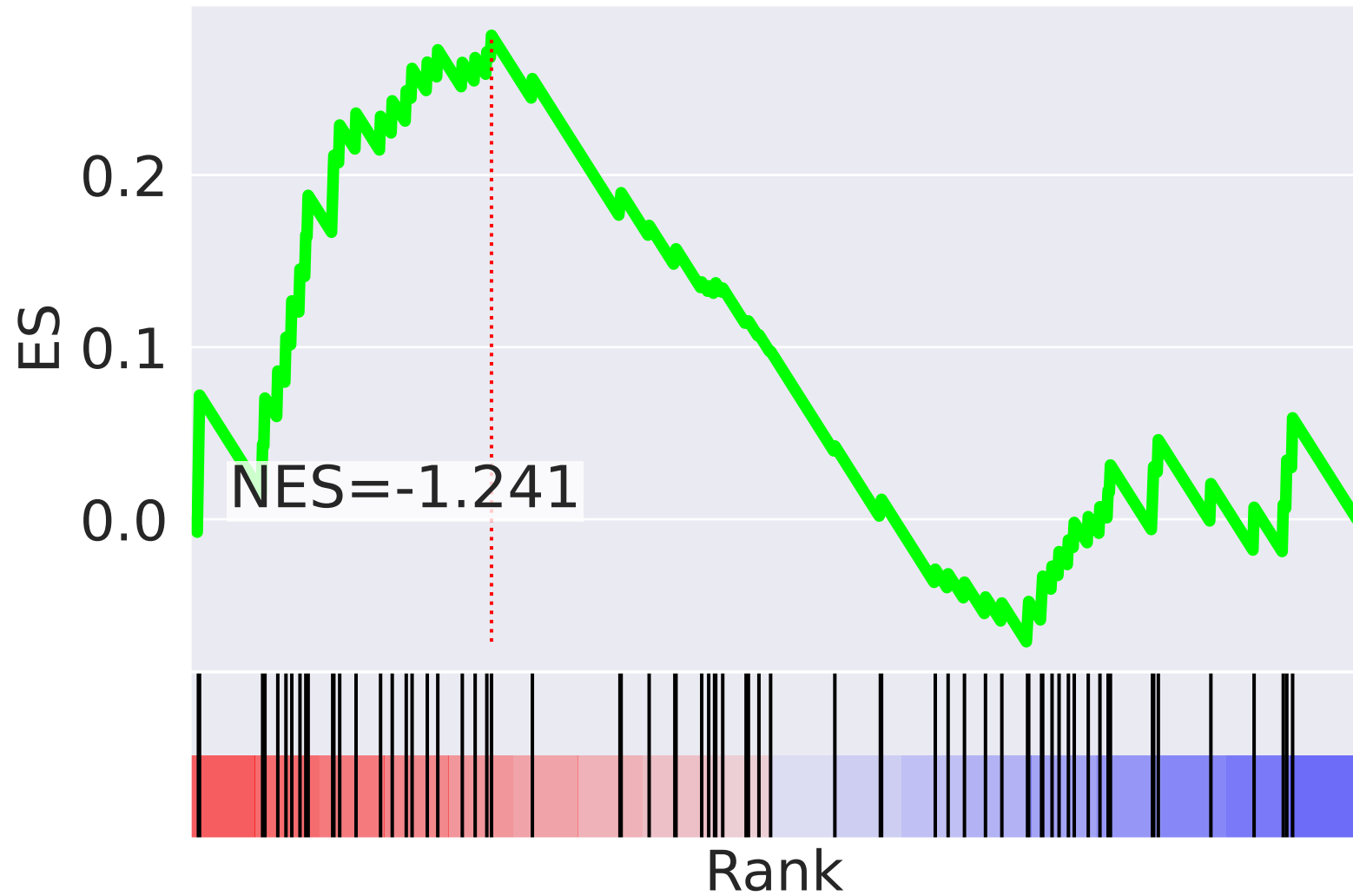
NES		SET
2.999		mitochondrion organization (GO:0007005)
2.435		cellular response to tumor necrosis factor (GO:0071356)
-2.342		protein complex assembly (GO:0006461)
2.270		cytokinesis (GO:0000910)
-2.239		negative regulation of translation (GO:0017148)
2.208		transcription from mitochondrial promoter (GO:0006390)
2.202		mitotic cell cycle (GO:0000278)
-2.151		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.140		mitotic spindle organization (GO:0007052)
-2.113		signal transduction (GO:0007165)
-2.111		canonical glycolysis (GO:0061621)
2.083		iron-sulfur cluster assembly (GO:0016226)
-2.022		positive regulation of GTPase activity (GO:0043547)
2.019		mitochondrial respiratory chain complex I assembly (GO:0032981)
1.997		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=42$

mitochondrial translational elongation (GO:0070125)



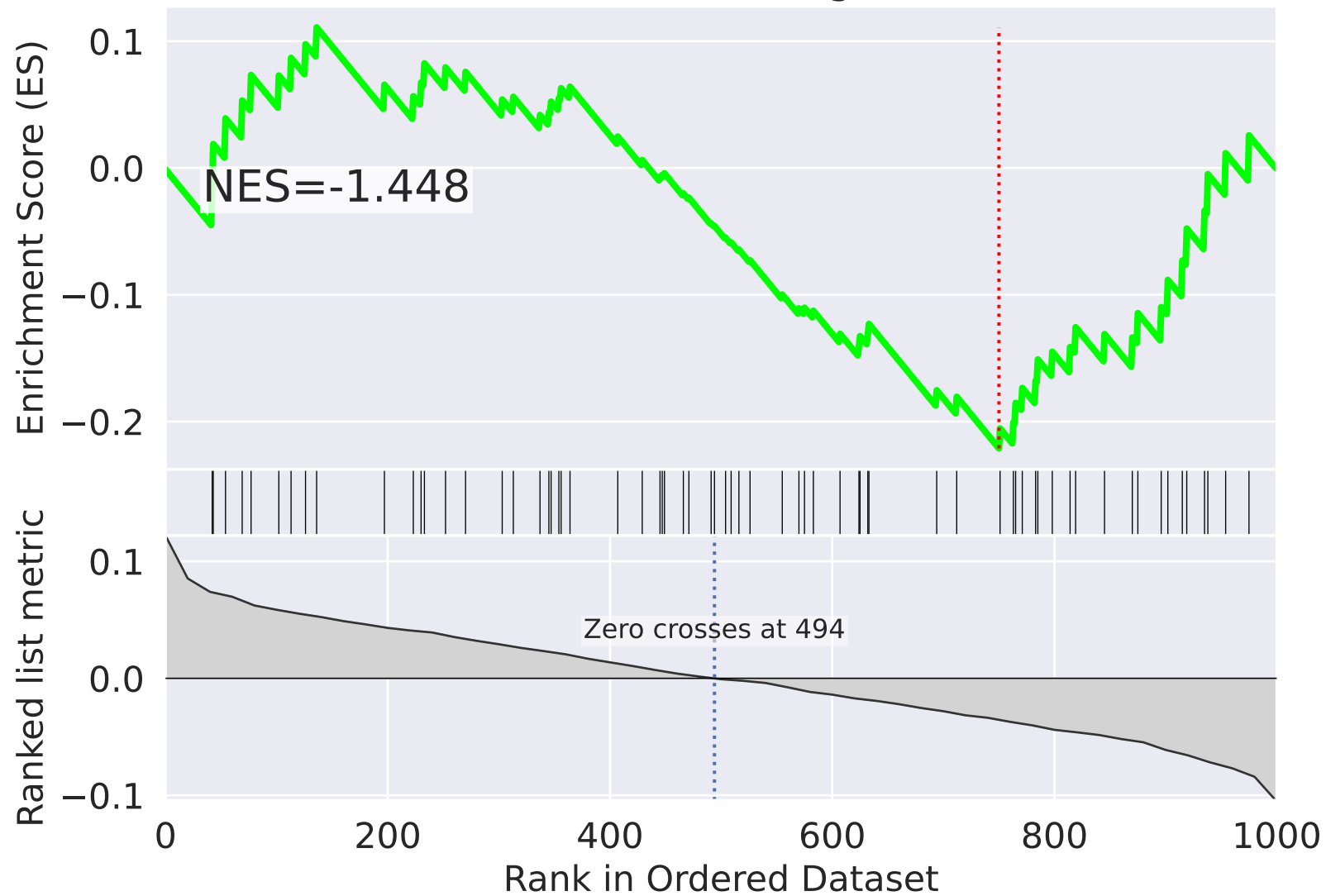
mitochondrial translational elongation (GO:0070125)



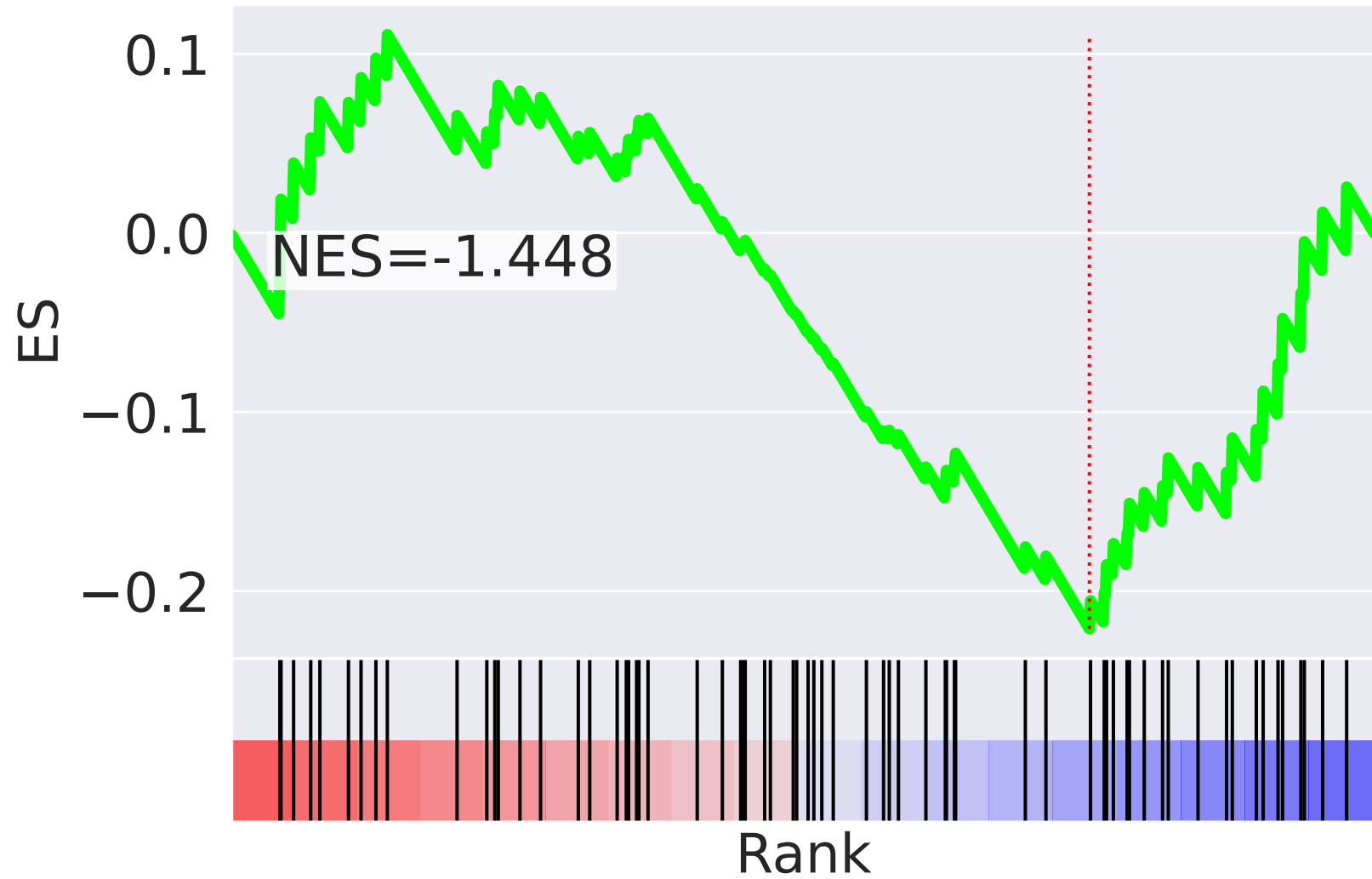
NES		SET
-3.719		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.282		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.871		IRE1-mediated unfolded protein response (GO:0036498)
2.658		regulation of cell motility (GO:2000145)
2.589		positive regulation of transcription, DNA-templated (GO:0045893)
2.418		ERBB2 signaling pathway (GO:0038128)
2.402		protein K63-linked ubiquitination (GO:0070534)
2.382		leukocyte migration (GO:0050900)
2.359		peptidyl-serine phosphorylation (GO:0018105)
-2.358		cellular respiration (GO:0045333)
2.269		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.202		histone H4 acetylation (GO:0043967)
2.152		epidermal growth factor receptor signaling pathway (GO:0007173)
2.151		cell differentiation (GO:0030154)
2.132		Fc-epsilon receptor signaling pathway (GO:0038095)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=43$

mitochondrial translational elongation (GO:0070125)



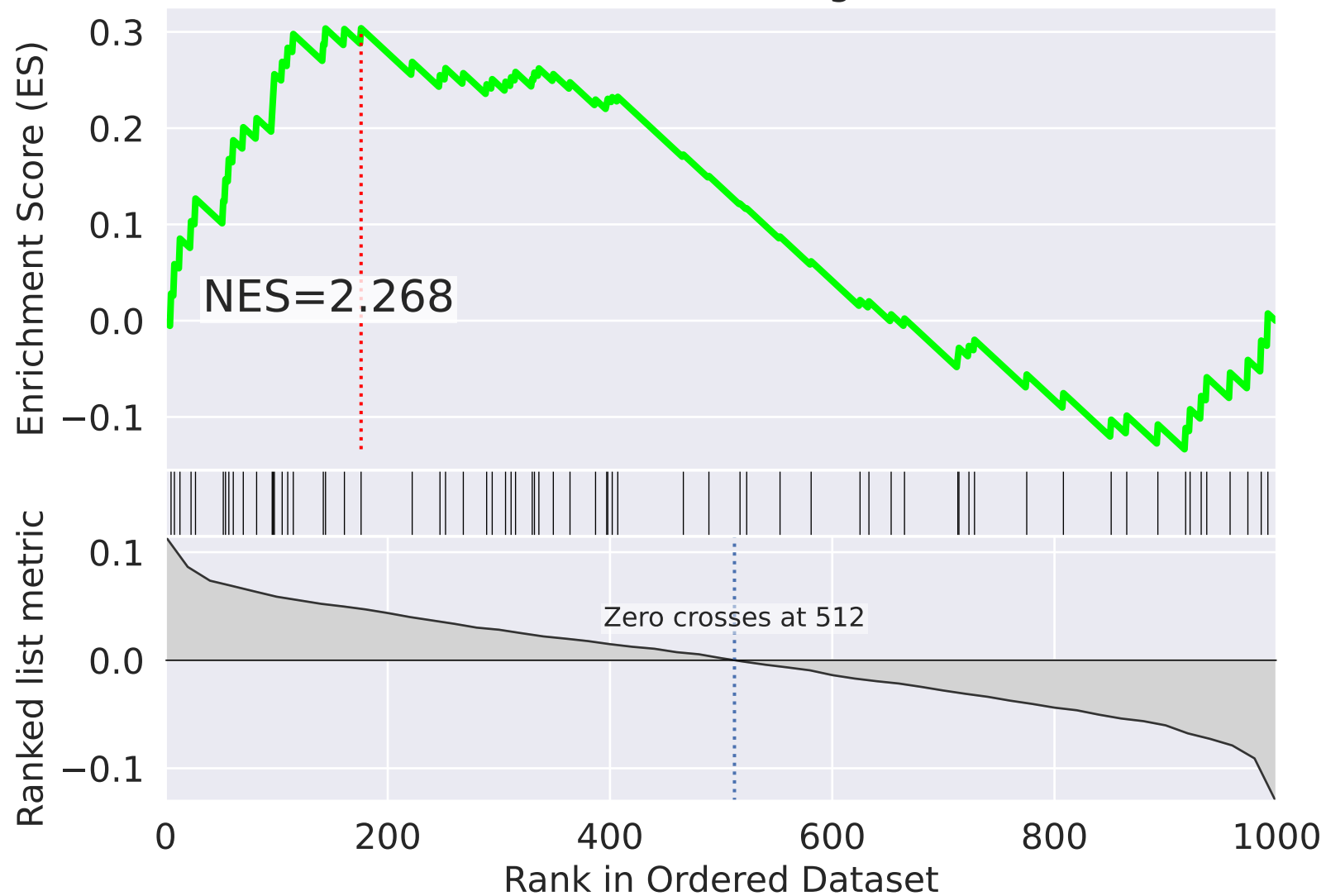
mitochondrial translational elongation (GO:0070125)



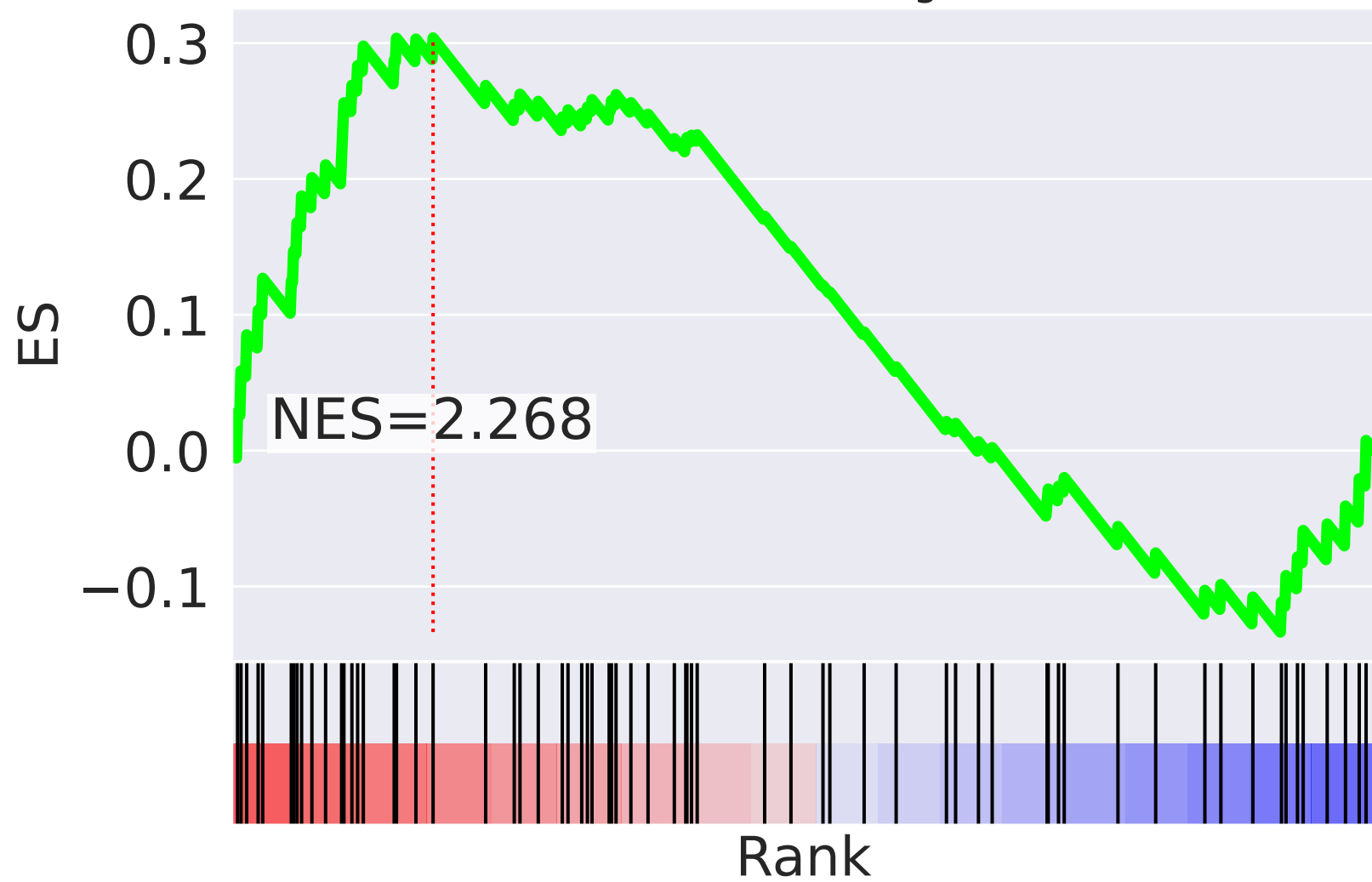
NES		SET
-3.052		DNA replication (GO:0006260)
-2.700		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.610		positive regulation of transcription, DNA-templated (GO:0045893)
2.531		signal transduction (GO:0007165)
-2.450		cell cycle arrest (GO:0007050)
-2.425		chromosome segregation (GO:0007059)
2.408		ATP-dependent chromatin remodeling (GO:0043044)
2.403		mRNA processing (GO:0006397)
2.379		positive regulation of DNA replication (GO:0045740)
2.257		Ras protein signal transduction (GO:0007265)
2.256		microtubule-based movement (GO:0007018)
2.230		ubiquitin-dependent protein catabolic process (GO:0006511)
-2.181		negative regulation of translation (GO:0017148)
-2.174		cellular response to tumor necrosis factor (GO:0071356)
-2.097		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=44$

mitochondrial translational elongation (GO:0070125)

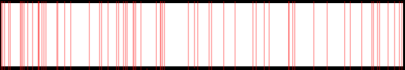
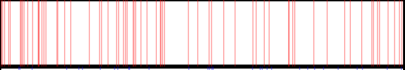
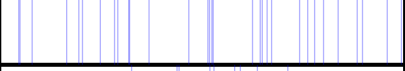
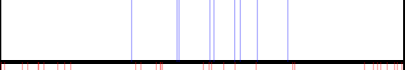
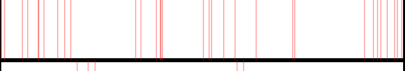
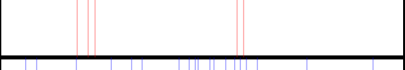
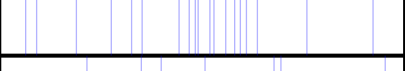
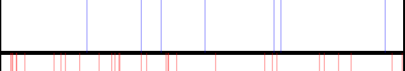




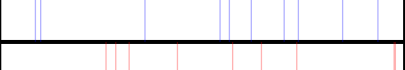
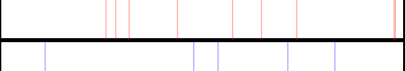



mitochondrial translational elongation (GO:0070125)



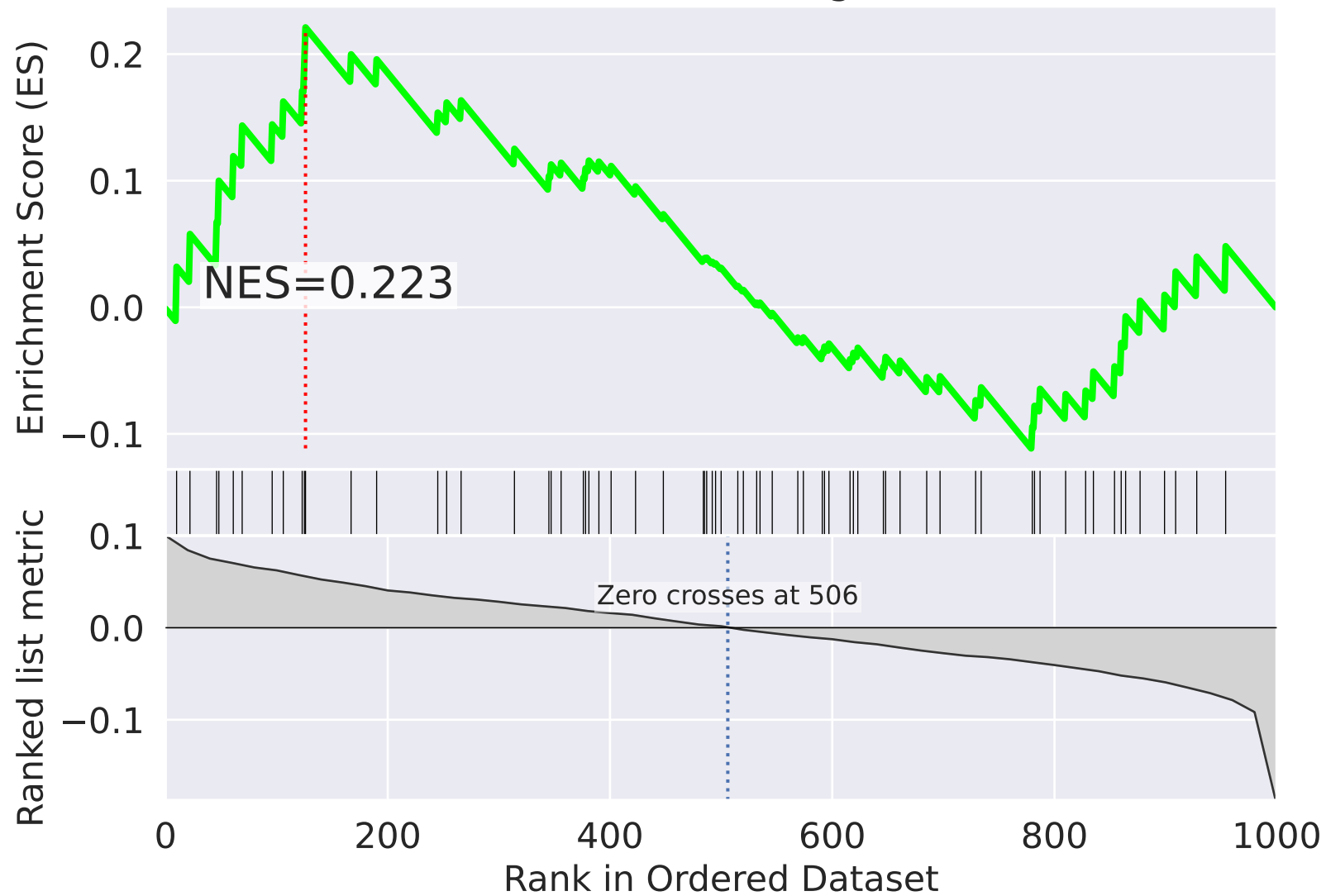
NES

SET

2.463		mitochondrial translational termination (GO:0070126)
2.268		mitochondrial translational elongation (GO:0070125)
-2.115		positive regulation of cell proliferation (GO:0008284)
-2.028		RNA export from nucleus (GO:0006405)
2.027		translation (GO:0006412)
1.995		lysosomal transport (GO:0007041)
-1.987		mRNA export from nucleus (GO:0006406)
-1.952		nervous system development (GO:0007399)
1.936		mitochondrial respiratory chain complex I assembly (GO:0032981)
1.934		endosomal transport (GO:0016197)
1.925		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.827		regulation of transcription, DNA-templated (GO:0006355)
-1.808		double-strand break repair via homologous recombination (GO:0000724)
1.798		movement of cell or subcellular component (GO:0006928)
-1.794		positive regulation of telomere maintenance via telomerase (GO:0032212)

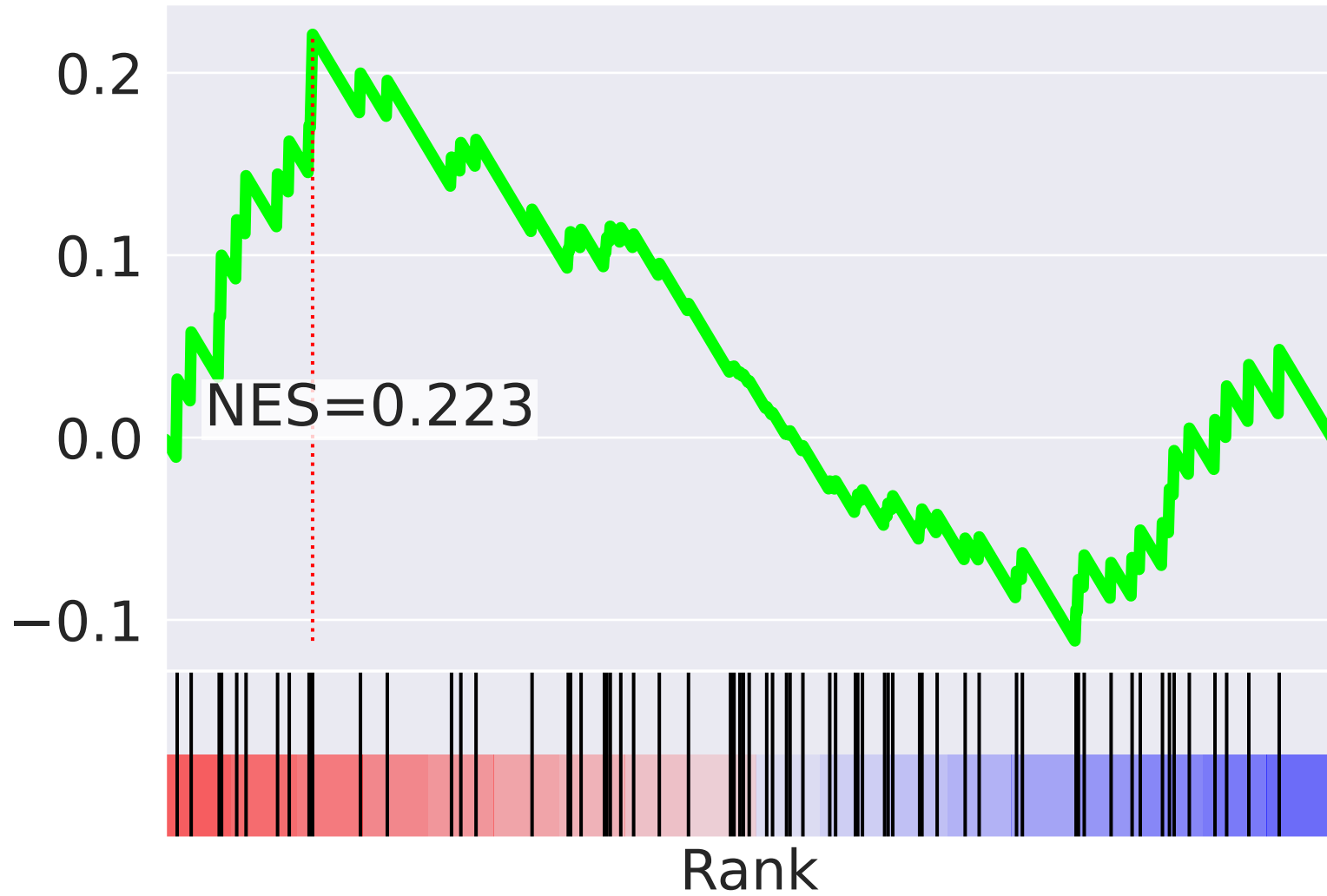
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=45$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

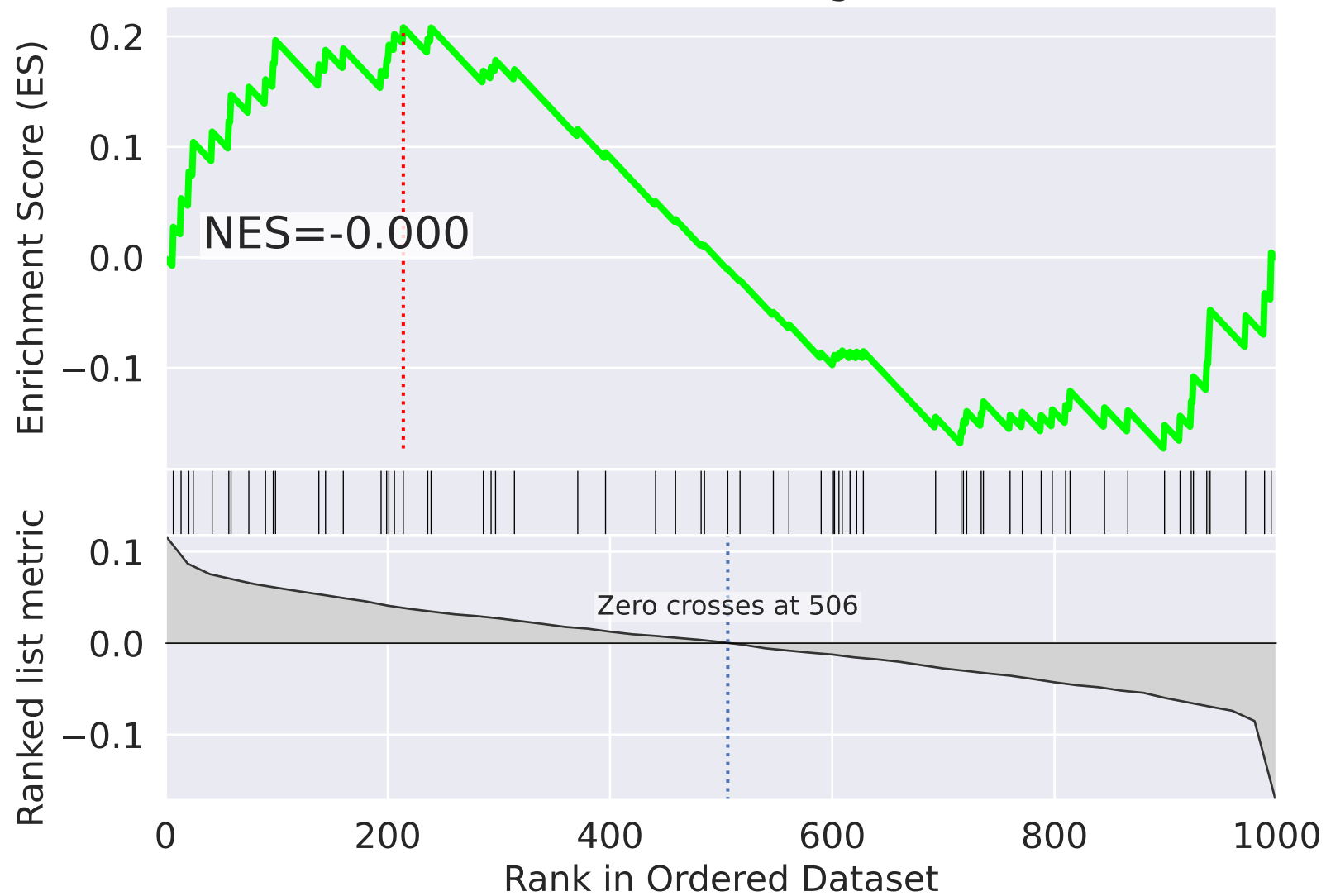
ES



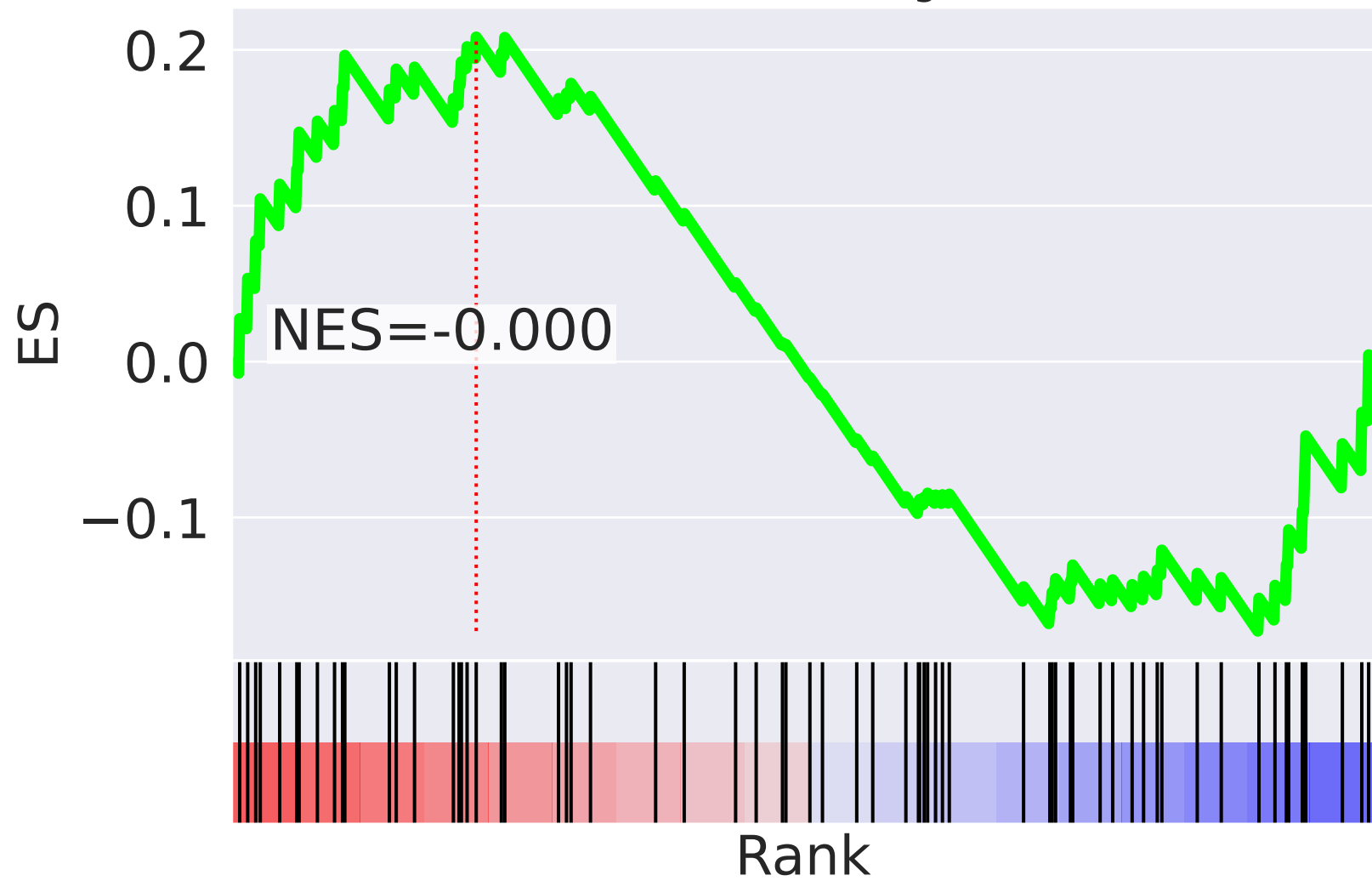
NES		SET
-3.145		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.004		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.795		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.469		multicellular organism development (GO:0007275)
2.323		regulation of cell adhesion (GO:0030155)
-2.284		regulation of lipid metabolic process (GO:0019216)
2.227		transcription initiation from RNA polymerase I promoter (GO:0006361)
2.227		transcription elongation from RNA polymerase I promoter (GO:0006362)
2.227		termination of RNA polymerase I transcription (GO:0006363)
-2.166		cellular respiration (GO:0045333)
-2.141		IRE1-mediated unfolded protein response (GO:0036498)
2.132		cellular response to hypoxia (GO:0071456)
-2.095		cell growth (GO:0016049)
-2.002		ciliary basal body docking (GO:0097711)
1.926		transcription, DNA-templated (GO:0006351)



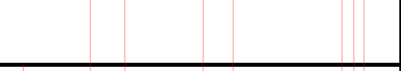
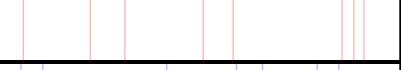
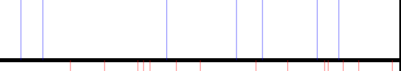
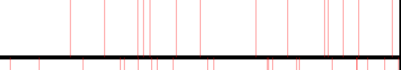
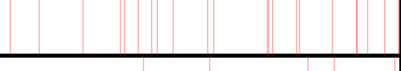


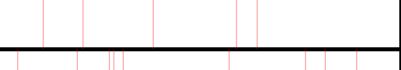
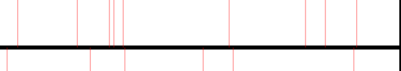


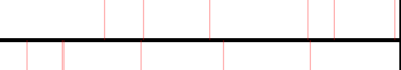
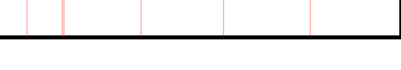
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=46$

mitochondrial translational elongation (GO:0070125)



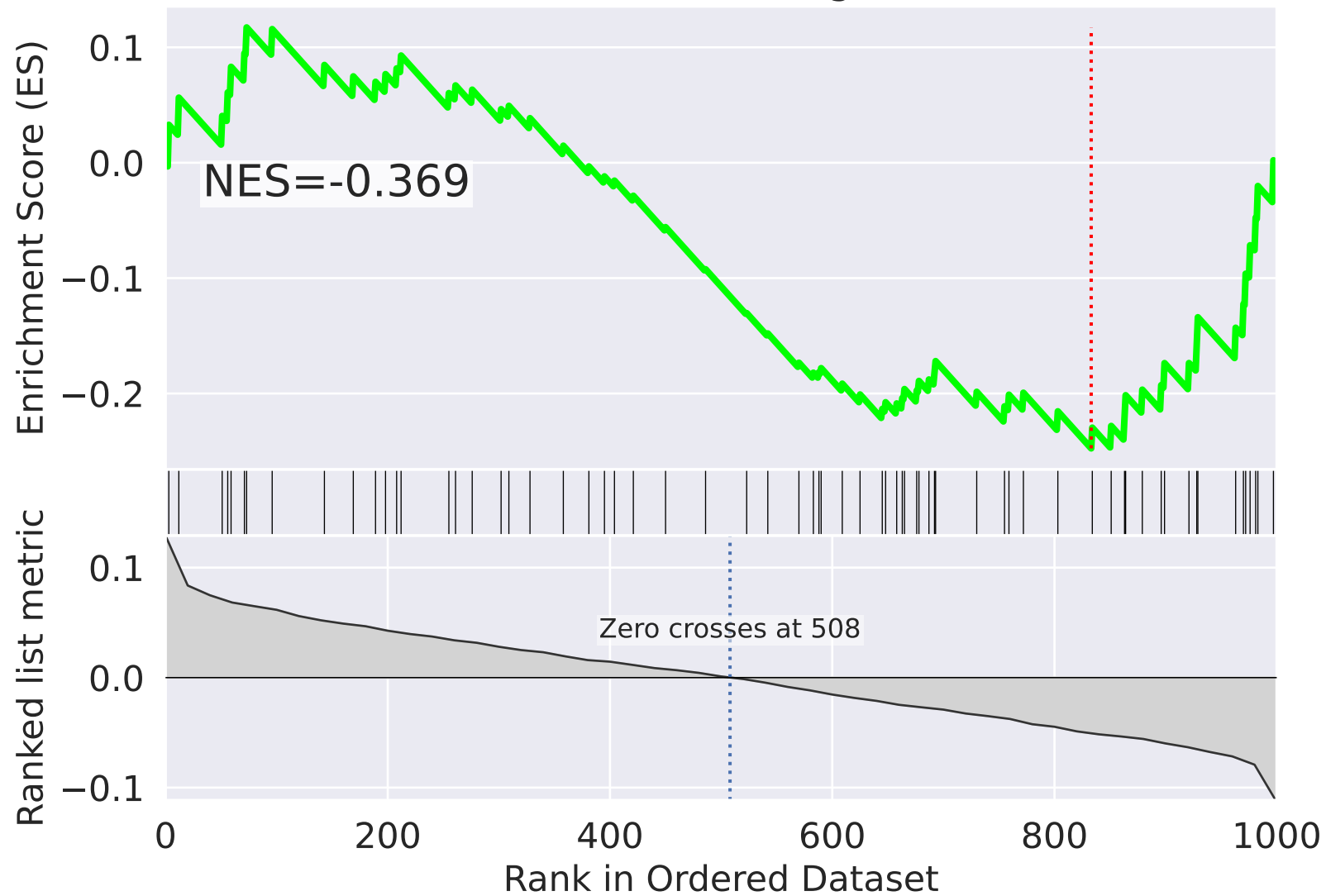
mitochondrial translational elongation (GO:0070125)



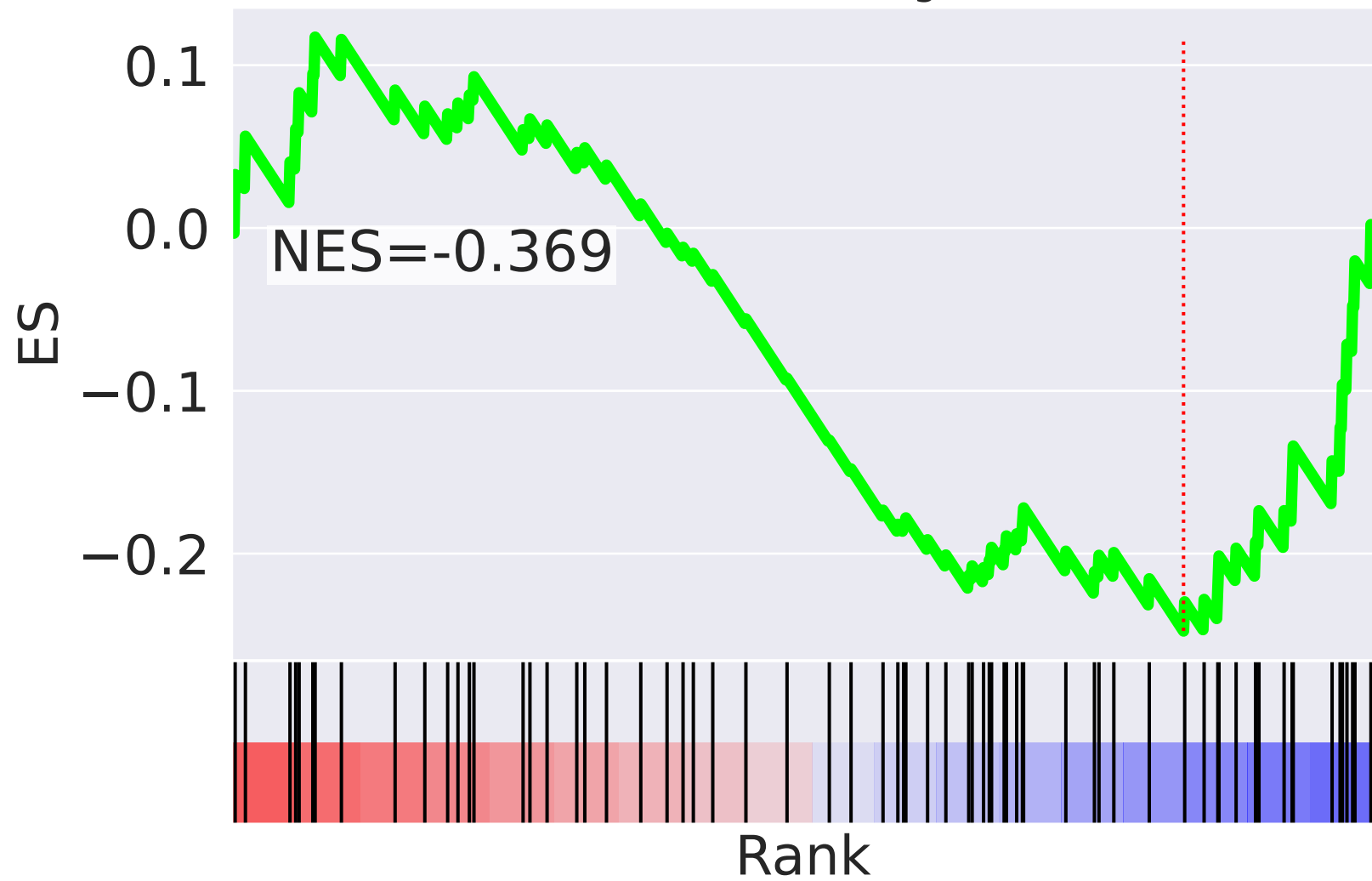
NES		SET
2.610		cellular response to DNA damage stimulus (GO:0006974)
2.539		mitotic metaphase plate congression (GO:0007080)
2.194		nucleus organization (GO:0006997)
2.177		cell separation after cytokinesis (GO:0000920)
-2.159		nervous system development (GO:0007399)
2.135		ubiquitin-dependent protein catabolic process (GO:0006511)
2.102		positive regulation of apoptotic process (GO:0043065)
2.075		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
-2.060		tricarboxylic acid cycle (GO:0006099)
1.987		positive regulation of type I interferon production (GO:0032481)
1.986		Golgi organization (GO:0007030)
1.966		viral budding via host ESCRT complex (GO:0039702)
-1.963		platelet degranulation (GO:0002576)
1.950		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
1.901		regulation of cell motility (GO:2000145)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=47$

mitochondrial translational elongation (GO:0070125)





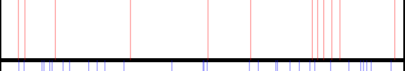

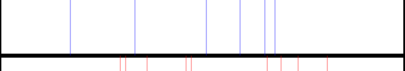

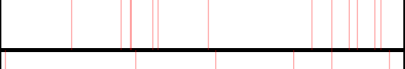



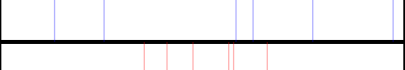




mitochondrial translational elongation (GO:0070125)



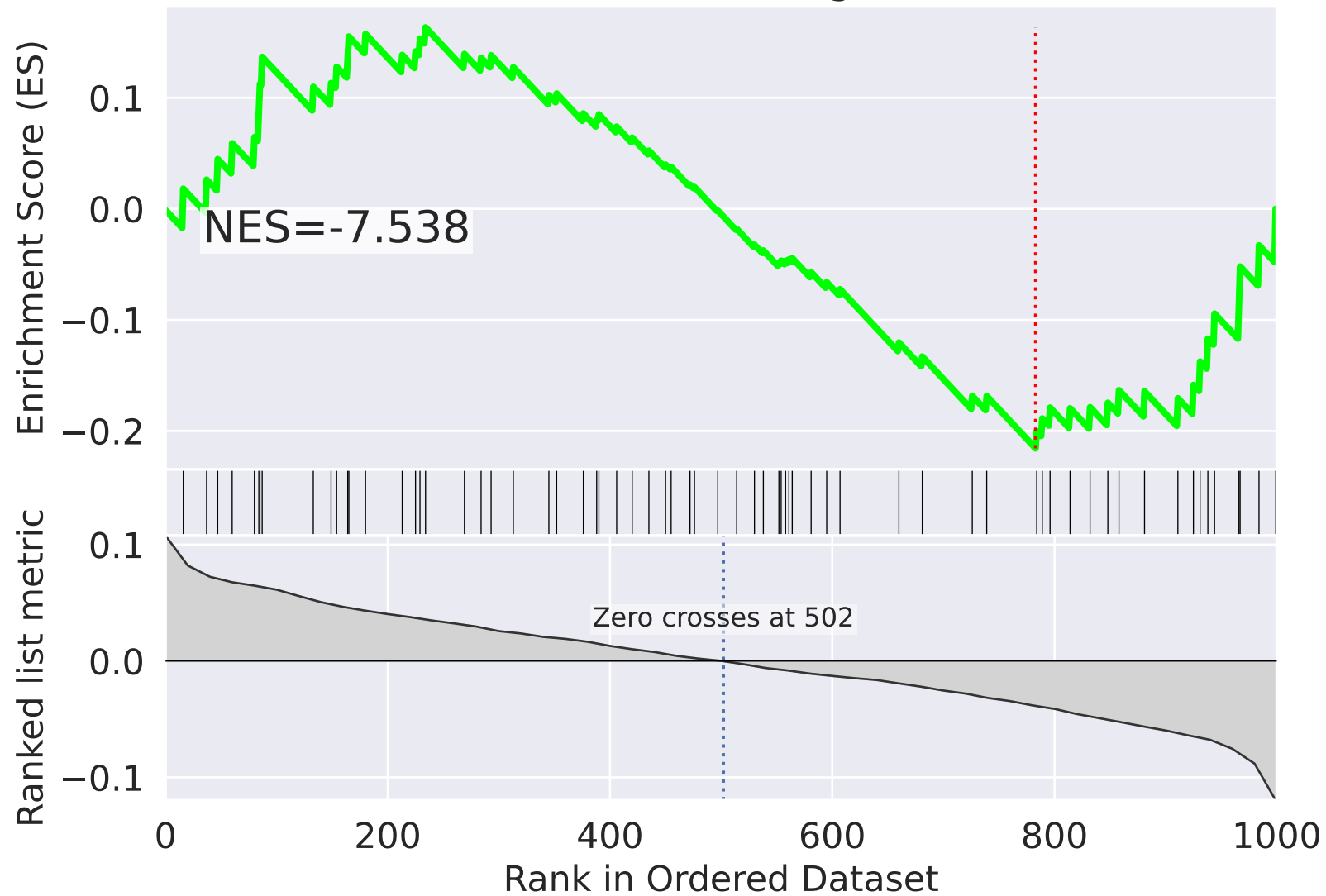
NES

SET

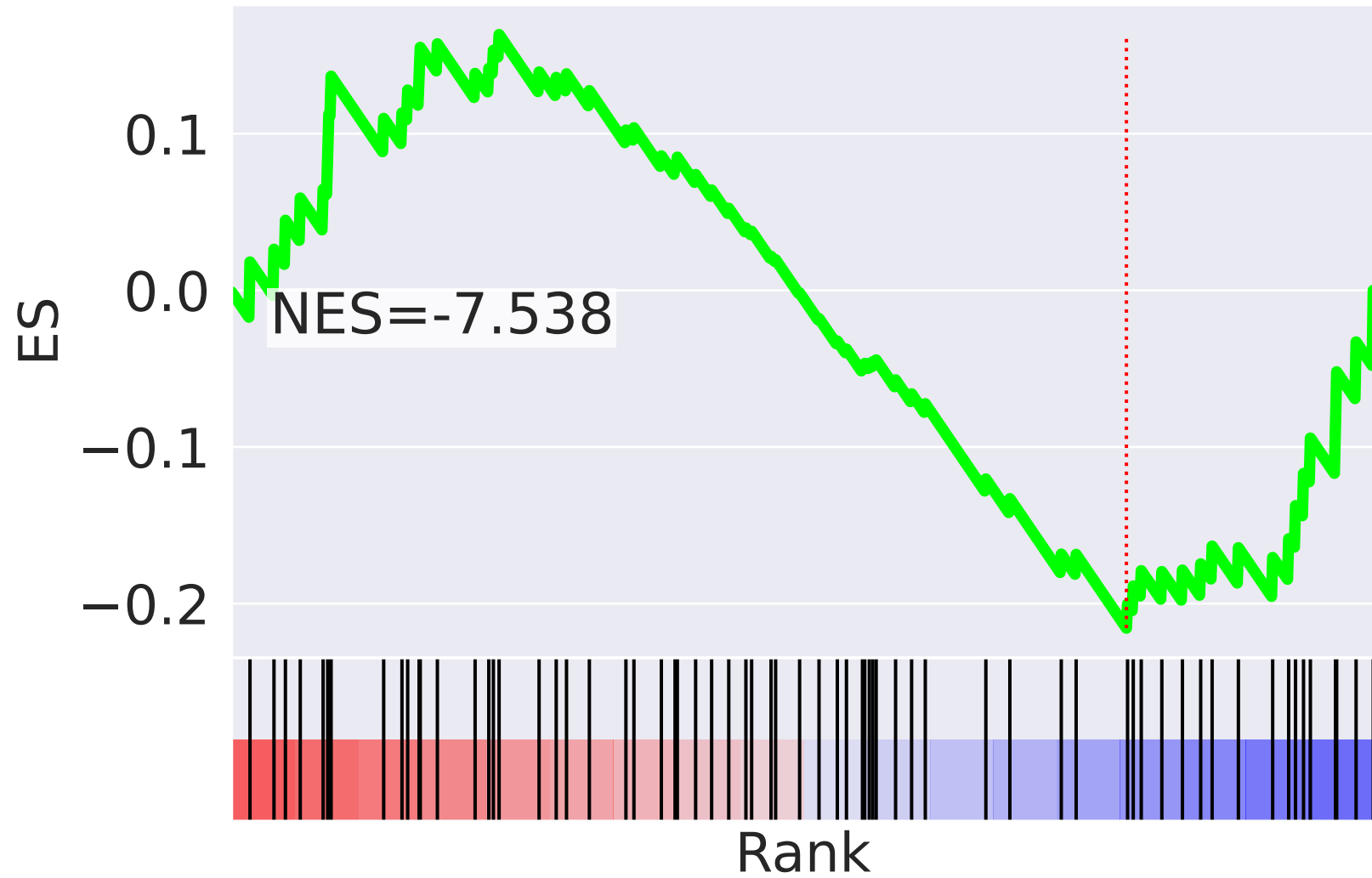
2.893		axon guidance (GO:0007411)
2.887		Fc-epsilon receptor signaling pathway (GO:0038095)
2.737		epidermal growth factor receptor signaling pathway (GO:0007173)
2.602		platelet activation (GO:0030168)
2.578		leukocyte migration (GO:0050900)
-2.576		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.417		negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.396		double-strand break repair (GO:0006302)
2.377		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.365		cell differentiation (GO:0030154)
-2.285		transcription from mitochondrial promoter (GO:0006390)
-2.279		positive regulation of protein catabolic process (GO:0045732)
-2.193		DNA damage response, detection of DNA damage (GO:0042769)
2.152		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
2.151		ERBB2 signaling pathway (GO:0038128)

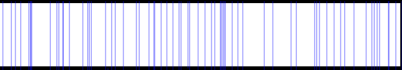
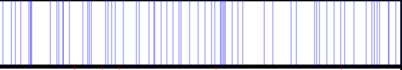
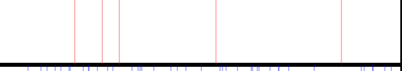
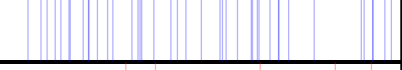



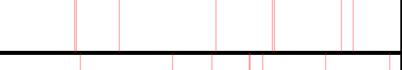
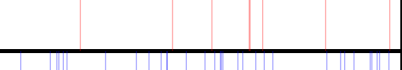
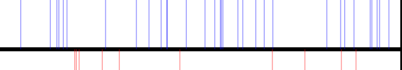




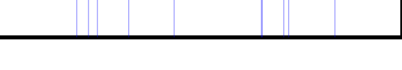
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=48$

mitochondrial translational elongation (GO:0070125)



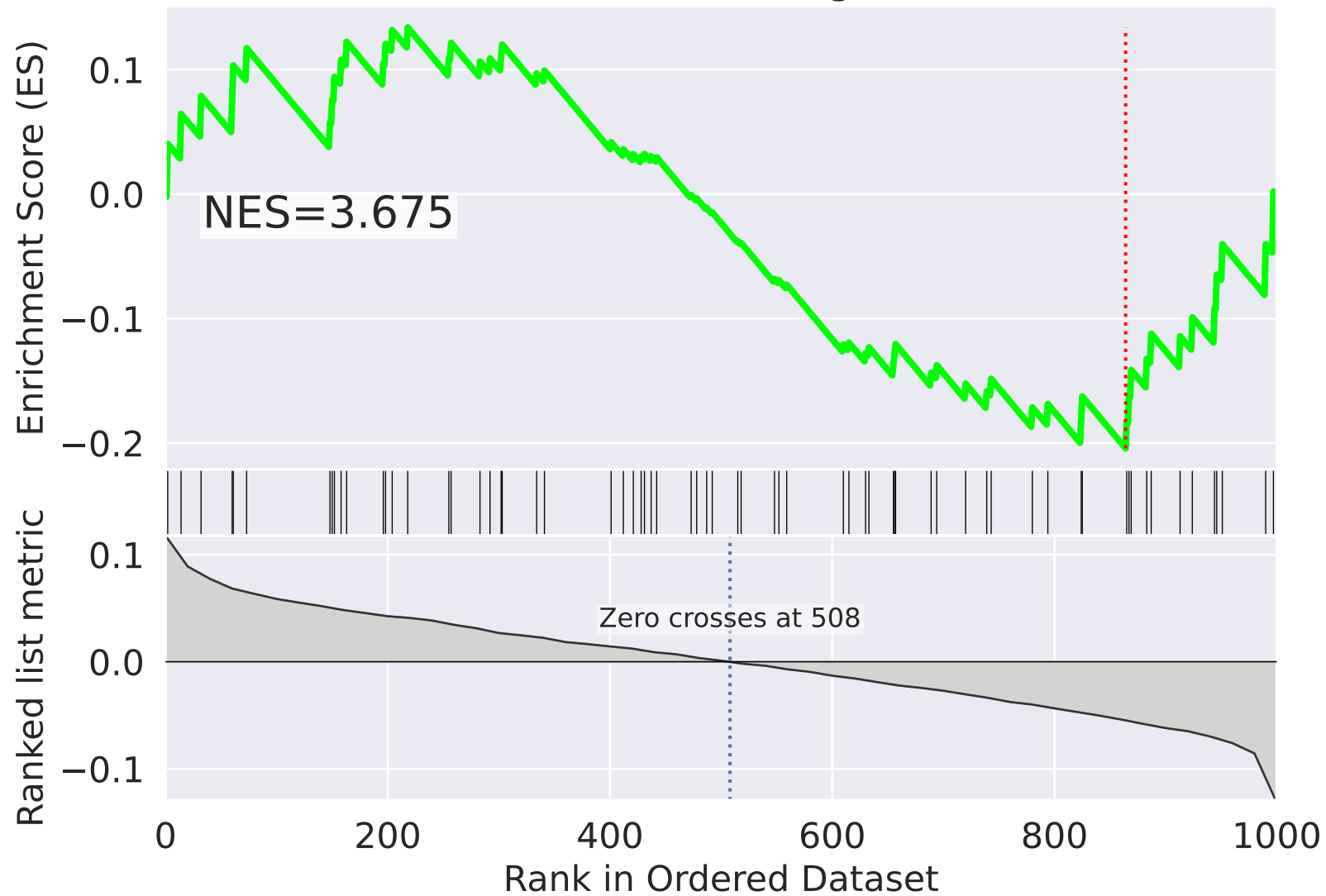
mitochondrial translational elongation (GO:0070125)



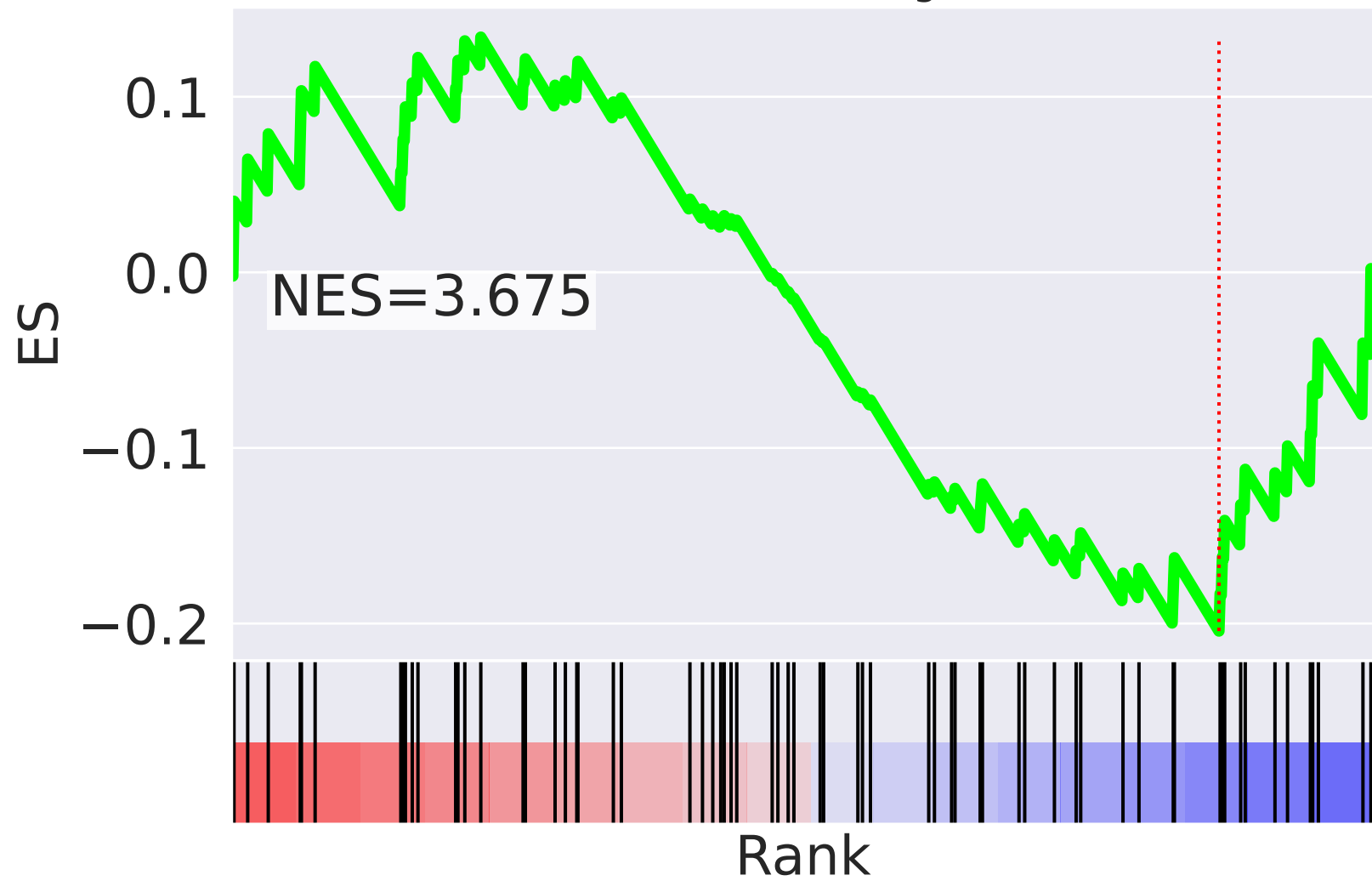
NES		SET
-7.538		mitochondrial translational elongation (GO:0070125)
-7.481		mitochondrial translational termination (GO:0070126)
2.576		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-2.487		positive regulation of transcription, DNA-templated (GO:0045893)
2.485		DNA replication initiation (GO:0006270)
-2.412		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.270		leukocyte migration (GO:0050900)
2.171		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.155		interstrand cross-link repair (GO:0036297)
-2.052		translation (GO:0006412)
2.036		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-1.976		Golgi organization (GO:0007030)
1.963		telomere maintenance via recombination (GO:0000722)
-1.933		protein autoubiquitination (GO:0051865)
-1.917		Ras protein signal transduction (GO:0007265)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=49$

mitochondrial translational elongation (GO:0070125)

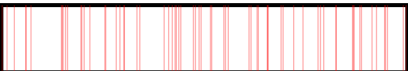


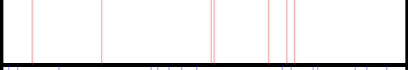

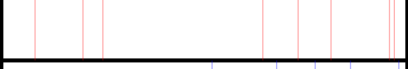



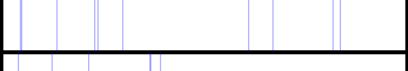
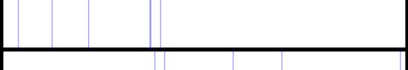
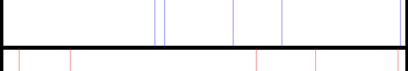
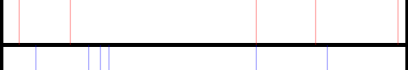
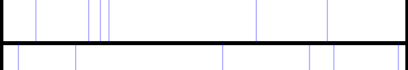
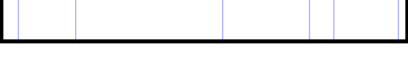


mitochondrial translational elongation (GO:0070125)



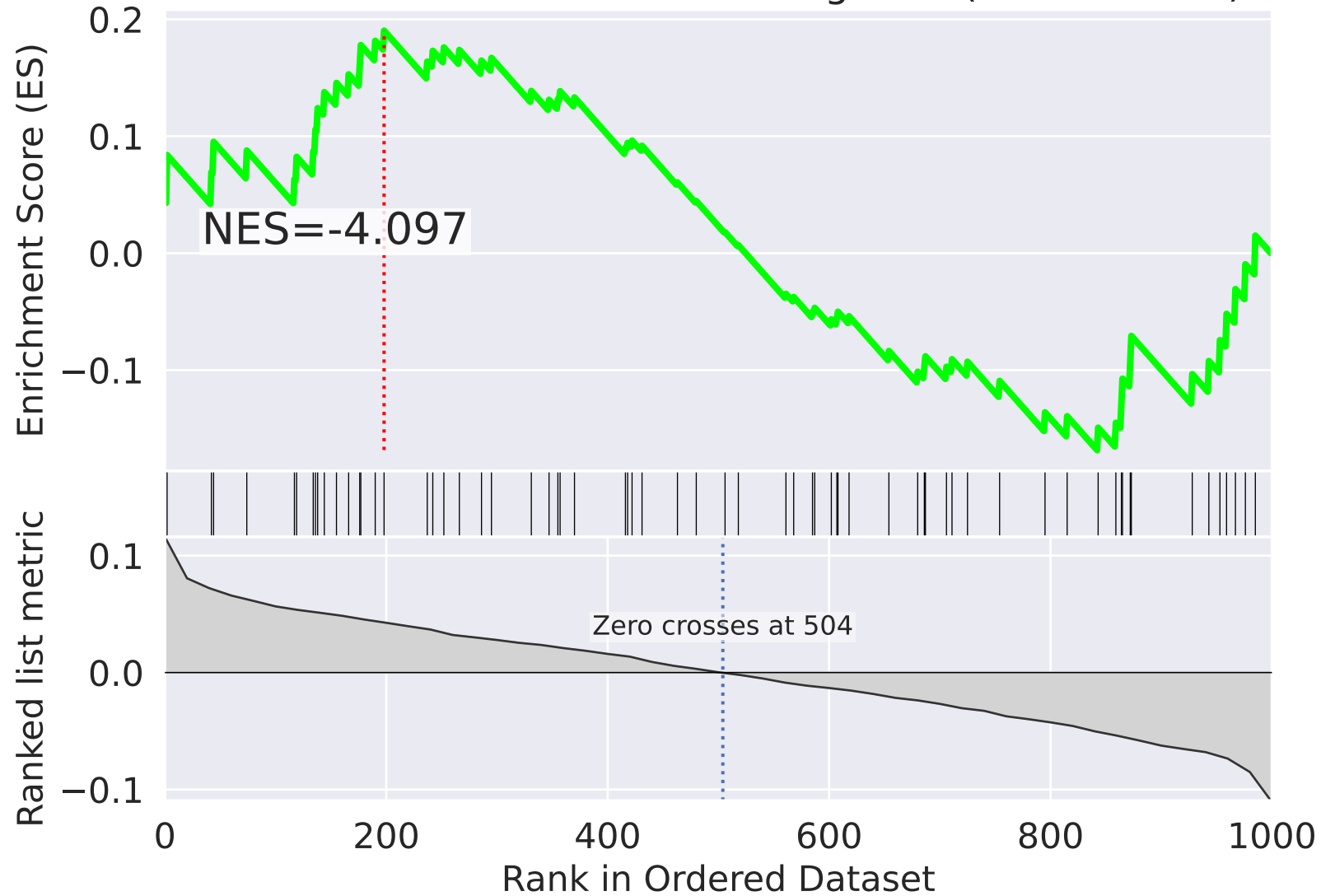
NES

SET

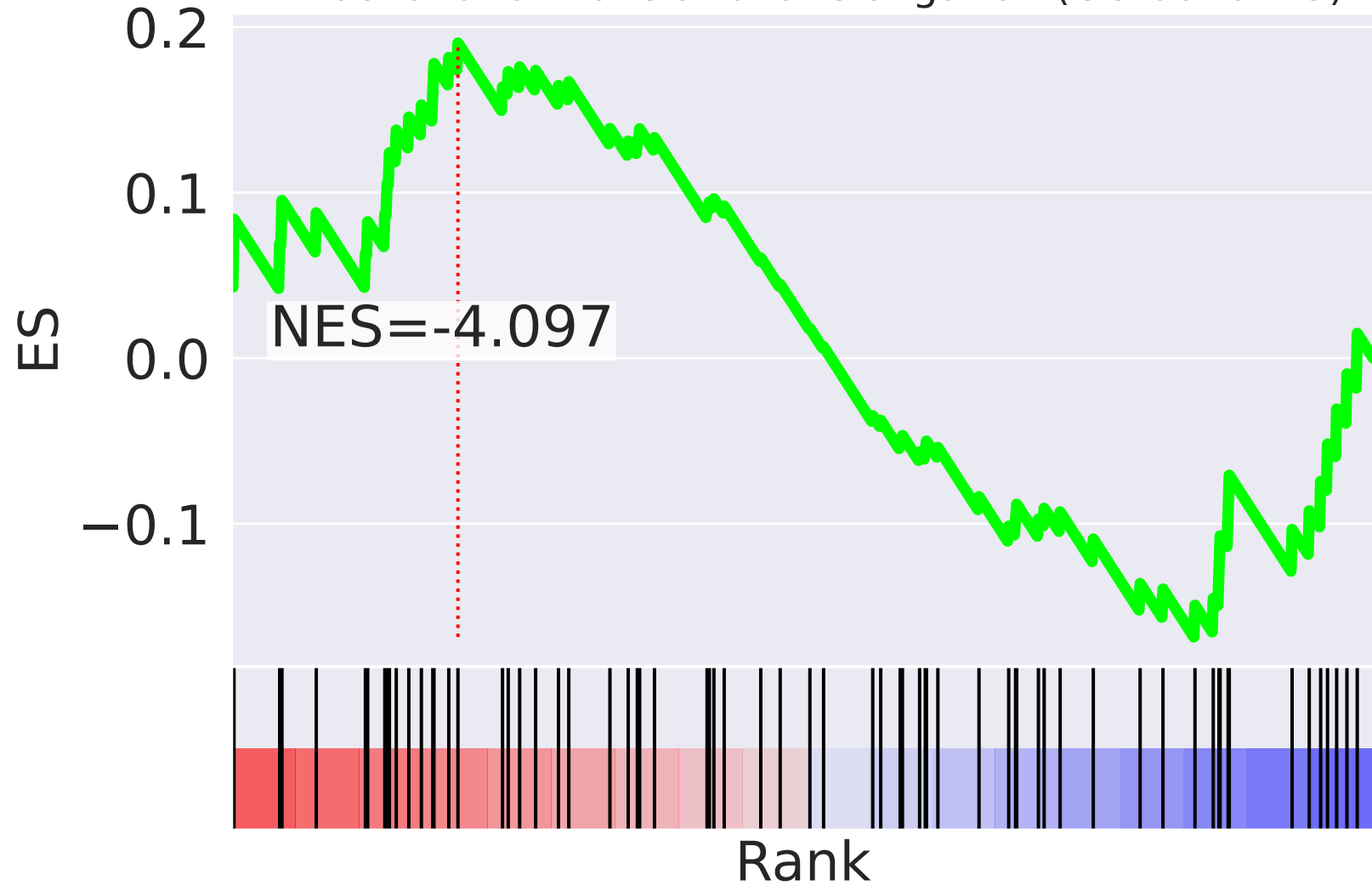
3.926		mitochondrial translational termination (GO:0070126)
3.675		mitochondrial translational elongation (GO:0070125)
-2.980		regulation of transcription, DNA-templated (GO:0006355)
2.743		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.679		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
2.557		cell growth (GO:0016049)
-2.416		cholesterol biosynthetic process (GO:0006695)
-2.394		regulation of cholesterol biosynthetic process (GO:0045540)
2.368		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.322		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.321		positive regulation of viral genome replication (GO:0045070)
-2.219		platelet degranulation (GO:0002576)
2.096		positive regulation of GTPase activity (GO:0043547)
-2.091		regulation of cell motility (GO:2000145)
-2.072		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=50$

mitochondrial translational elongation (GO:0070125)



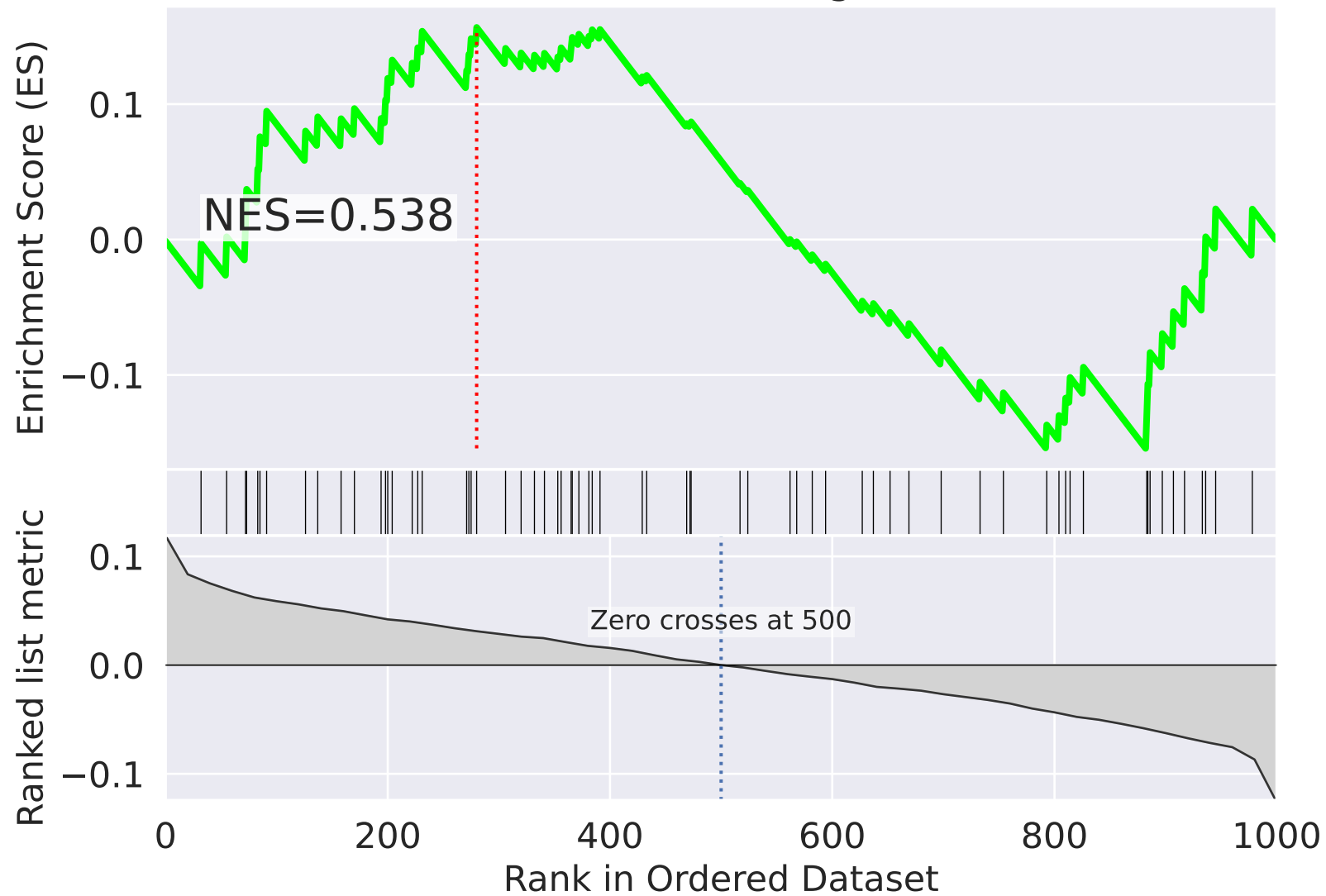
mitochondrial translational elongation (GO:0070125)



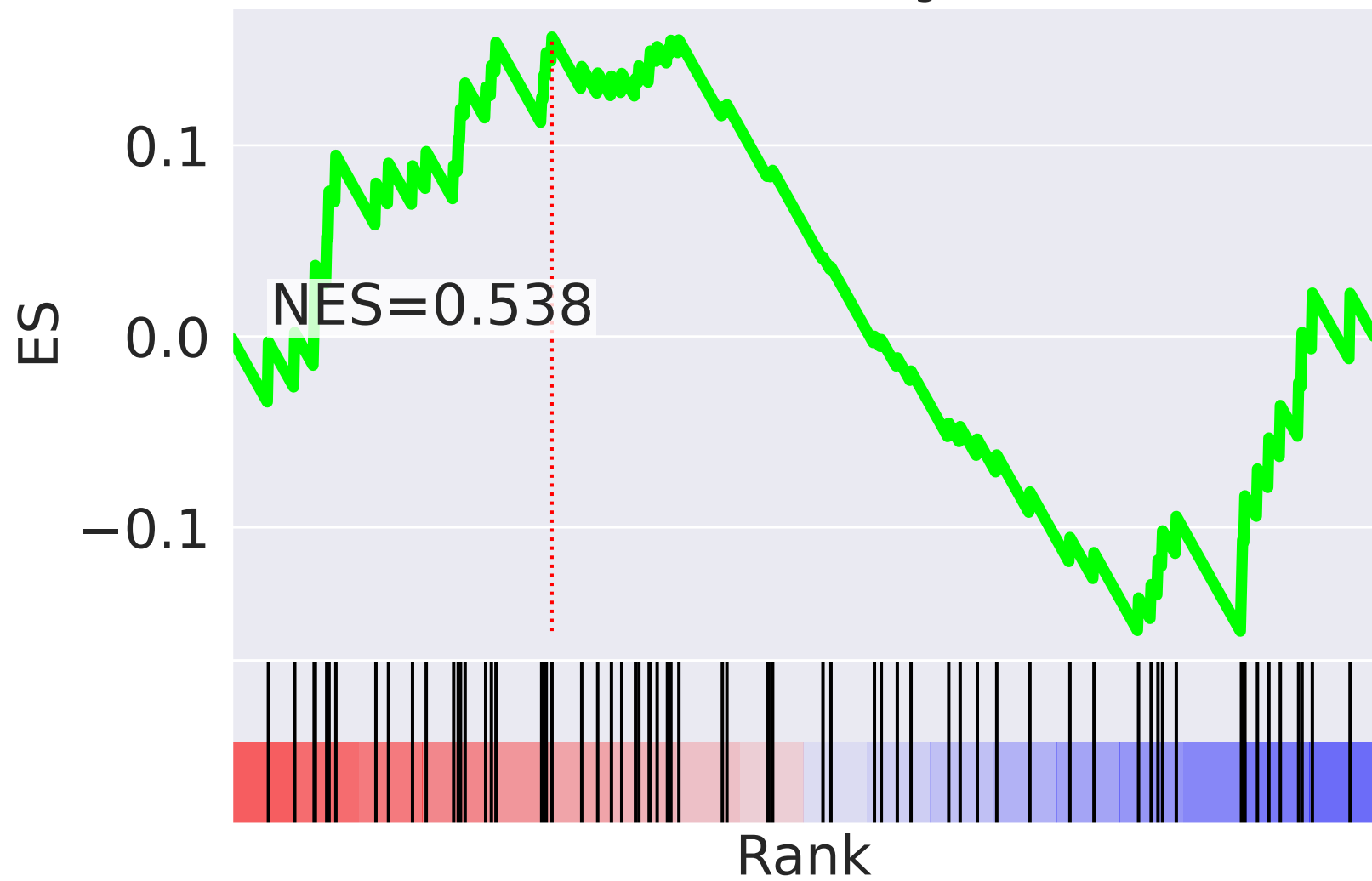
NES		SET
-4.097		mitochondrial translational elongation (GO:0070125)
-3.530		mitochondrial translational termination (GO:0070126)
2.757		mRNA splicing, via spliceosome (GO:0000398)
-2.658		protein phosphorylation (GO:0006468)
-2.568		peptidyl-serine phosphorylation (GO:0018105)
-2.526		tricarboxylic acid cycle (GO:0006099)
-2.477		substantia nigra development (GO:0021762)
-2.439		telomere maintenance via recombination (GO:0000722)
-2.318		mitotic cell cycle (GO:0000278)
2.228		protein ubiquitination (GO:0016567)
-2.128		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.116		response to ionizing radiation (GO:0010212)
-2.095		cellular response to amino acid starvation (GO:0034198)
2.042		mRNA processing (GO:0006397)
-1.988		DNA replication initiation (GO:0006270)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=51$

mitochondrial translational elongation (GO:0070125)



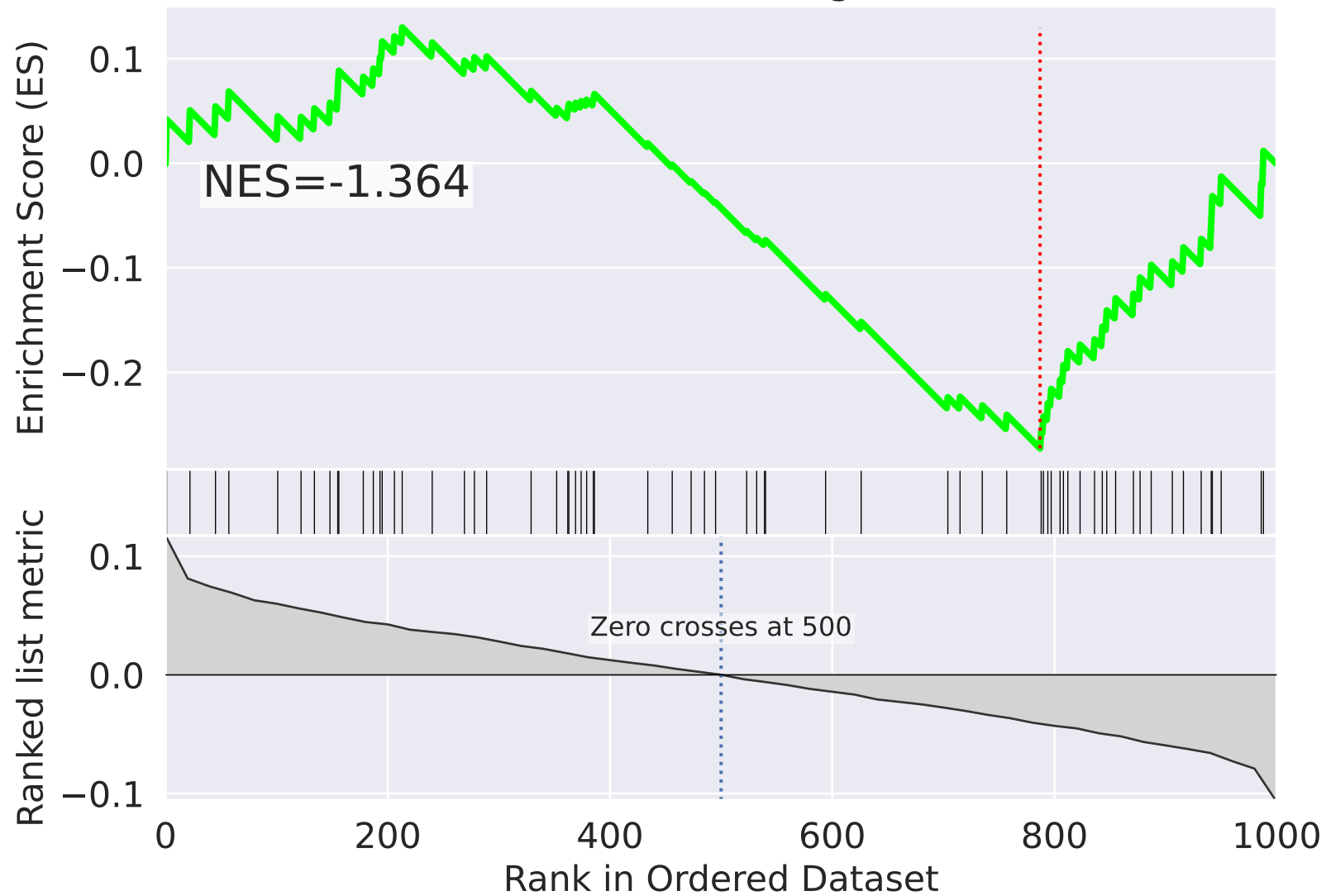
mitochondrial translational elongation (GO:0070125)



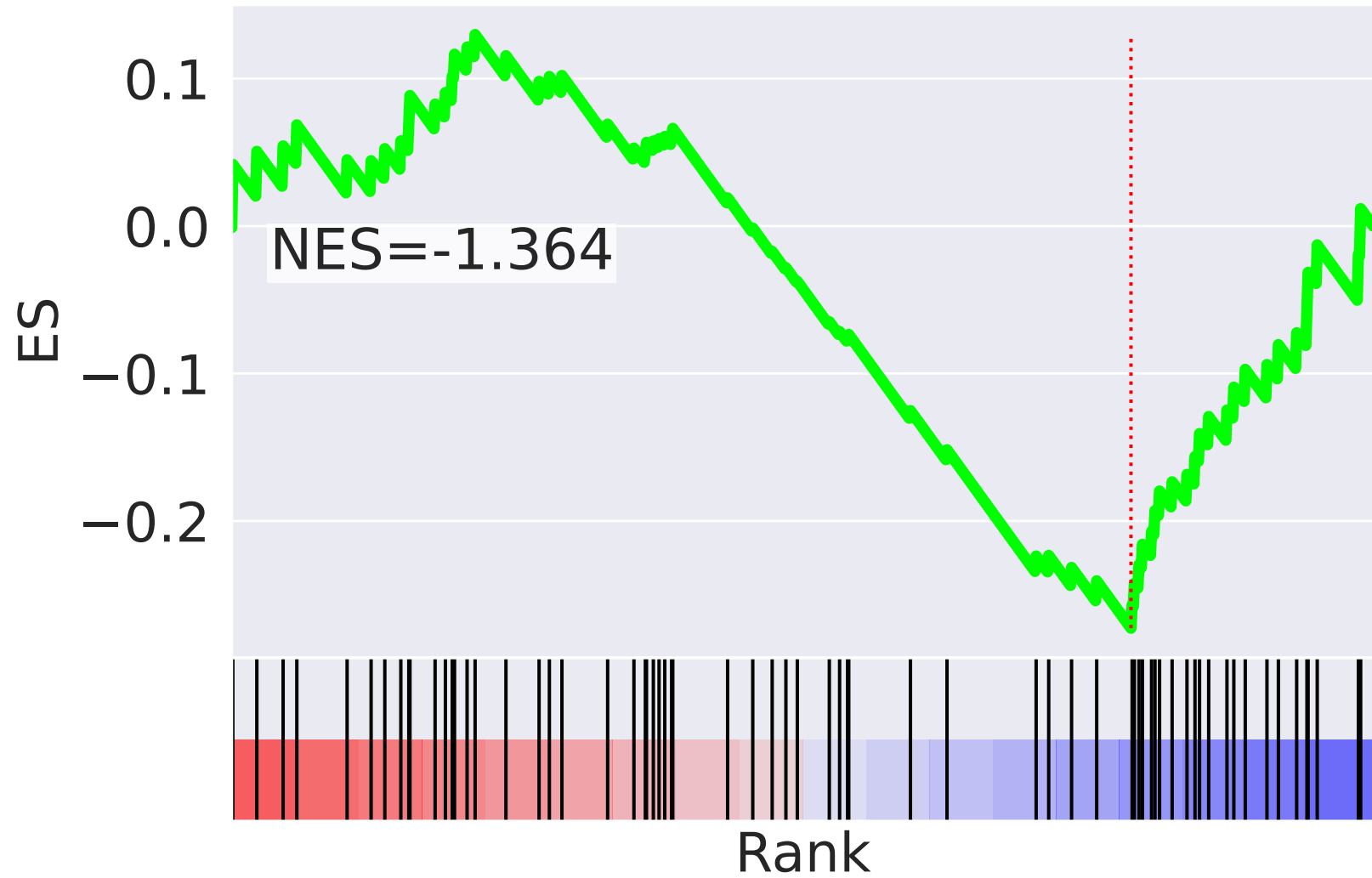
NES		SET
-2.963		tRNA modification (GO:0006400)
2.654		transcription from RNA polymerase II promoter (GO:0006366)
2.451		DNA synthesis involved in DNA repair (GO:0000731)
2.434		strand displacement (GO:0000732)
2.387		mitotic spindle organization (GO:0007052)
2.317		cellular response to tumor necrosis factor (GO:0071356)
-2.226		rRNA processing (GO:0006364)
-2.186		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.115		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.102		DNA replication (GO:0006260)
2.093		telomere maintenance (GO:0000723)
-1.979		endosomal transport (GO:0016197)
1.935		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-1.929		insulin receptor signaling pathway (GO:0008286)
1.904		mitotic metaphase plate congression (GO:0007080)





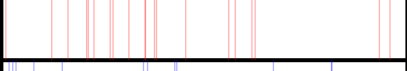
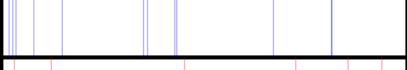
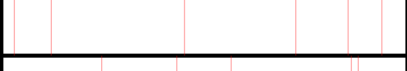

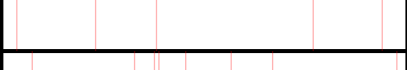
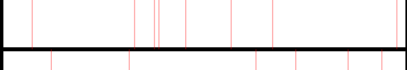
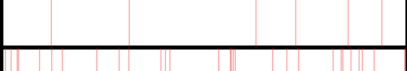
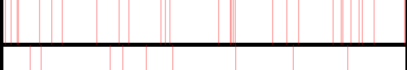

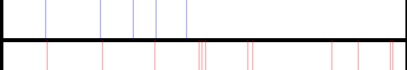

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=52$

mitochondrial translational elongation (GO:0070125)



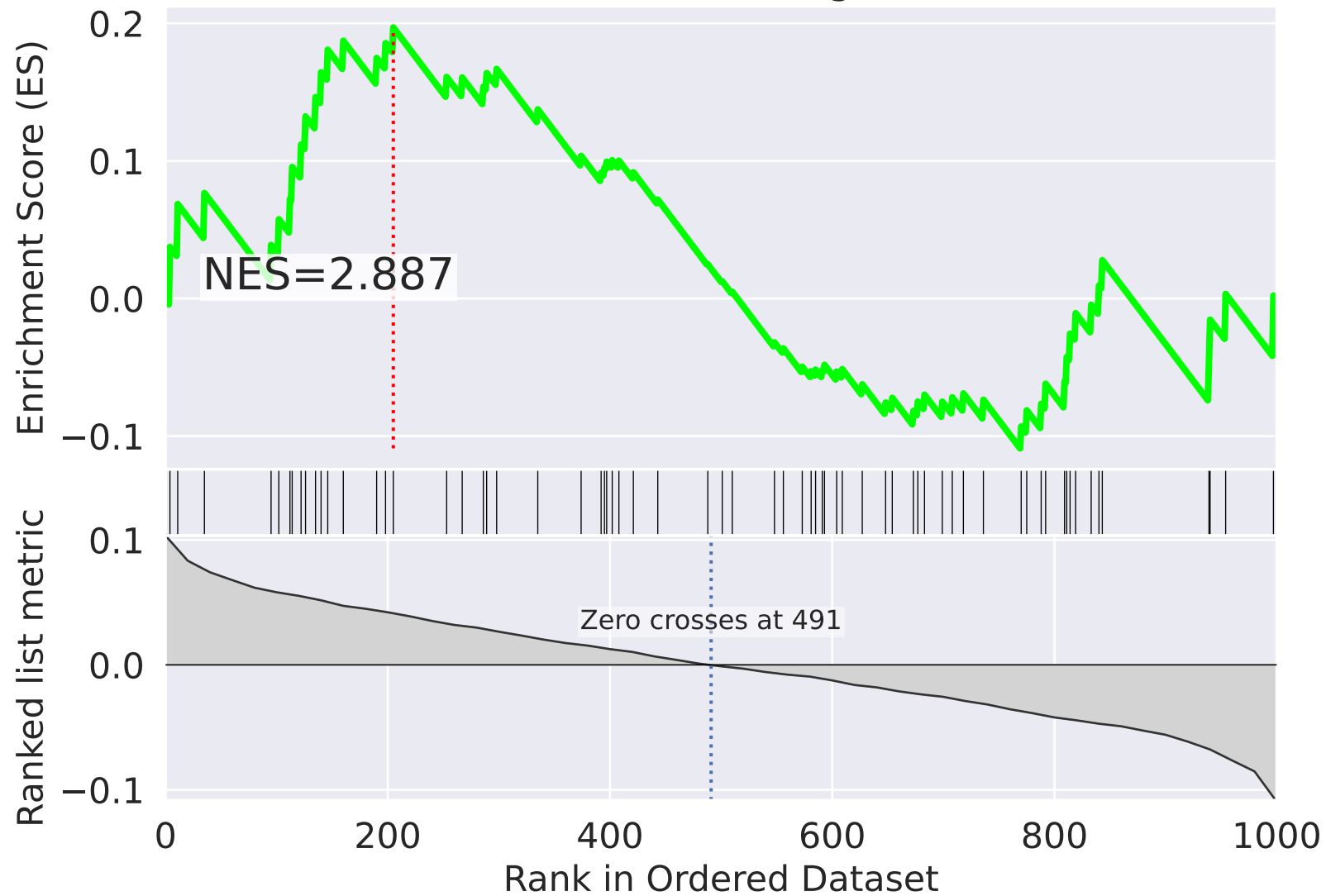
mitochondrial translational elongation (GO:0070125)



NES		SET
3.052		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.614		positive regulation of cell migration (GO:0030335)
2.525		COPII vesicle coating (GO:0048208)
-2.512		protein autophosphorylation (GO:0046777)
2.309		membrane organization (GO:0061024)
-2.288		protein phosphorylation (GO:0006468)
2.208		RNA metabolic process (GO:0016070)
2.185		positive regulation of cytokinesis (GO:0032467)
2.164		heart development (GO:0007507)
2.160		substantia nigra development (GO:0021762)
2.109		mRNA processing (GO:0006397)
2.098		neutrophil degranulation (GO:0043312)
2.046		Golgi organization (GO:0007030)
-2.028		transcription from mitochondrial promoter (GO:0006390)
2.022		mitotic cell cycle (GO:0000278)


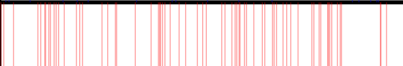


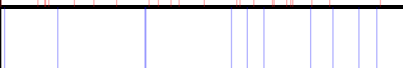

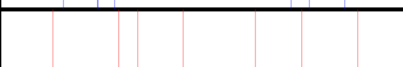
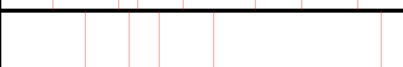




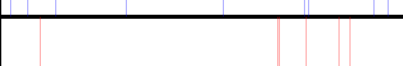
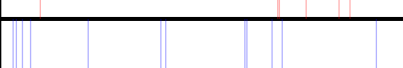
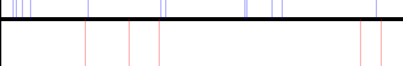
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=53$

mitochondrial translational elongation (GO:0070125)



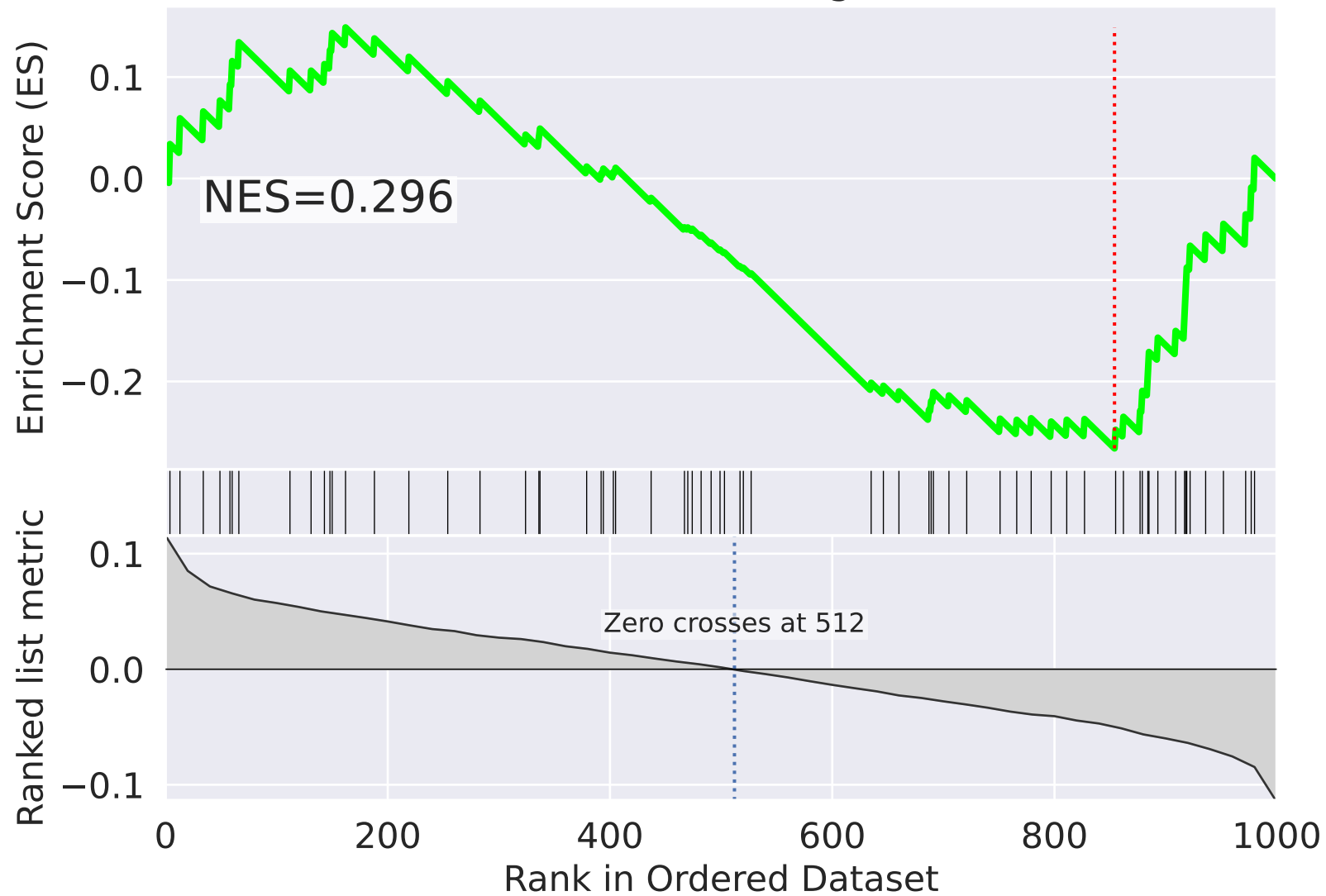
mitochondrial translational elongation (GO:0070125)



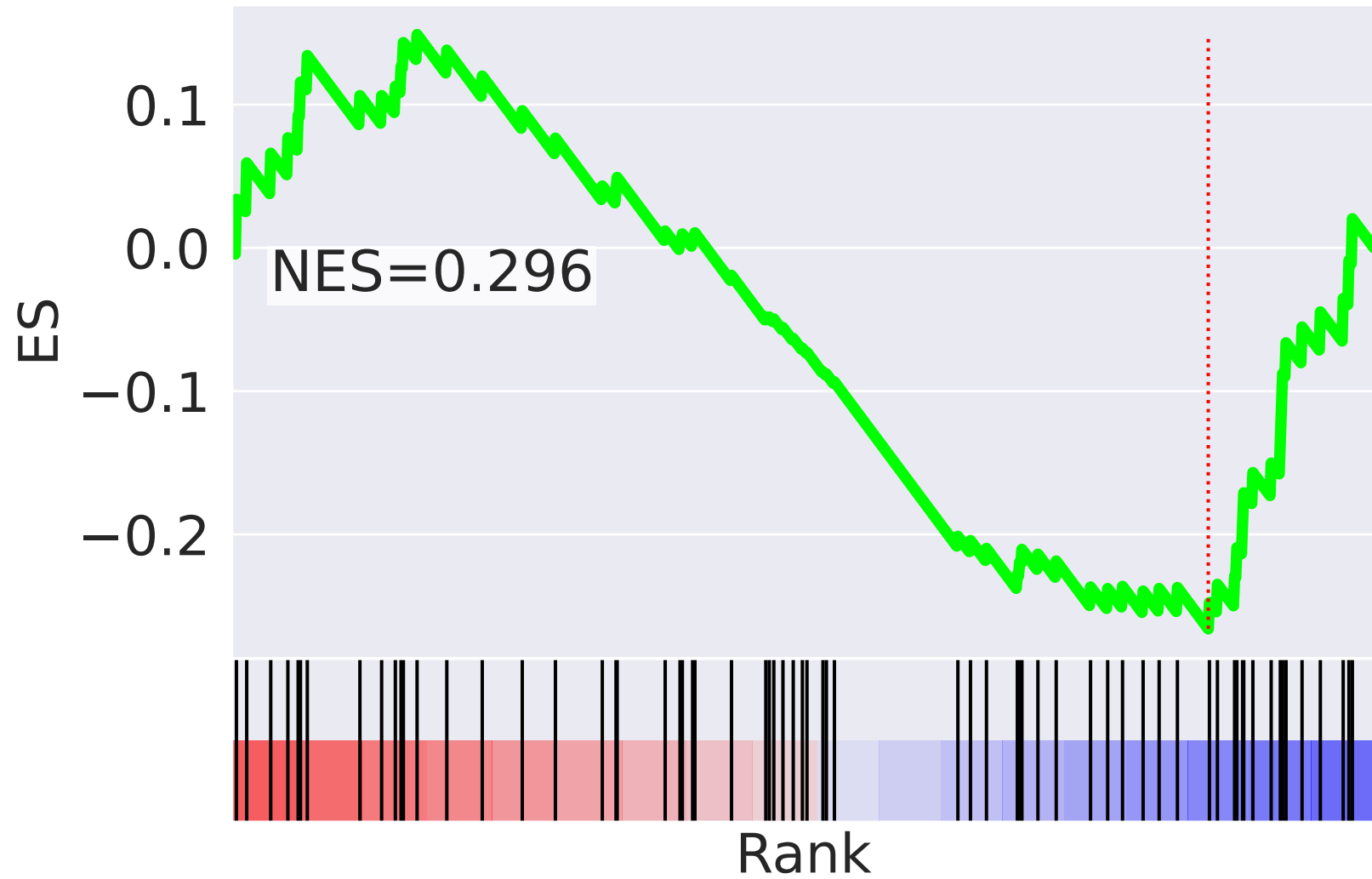
NES		SET
-3.191		G2/M transition of mitotic cell cycle (GO:0000086)
2.976		mitochondrial translational termination (GO:0070126)
2.887		mitochondrial translational elongation (GO:0070125)
2.666		mitochondrial translation (GO:0032543)
-2.575		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-2.529		negative regulation of translation (GO:0017148)
2.436		intracellular protein transport (GO:0006886)
2.426		canonical glycolysis (GO:0061621)
-2.352		cell cycle arrest (GO:0007050)
-2.351		negative regulation of cell proliferation (GO:0008285)
2.324		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-2.291		transforming growth factor beta receptor signaling pathway (GO:0007179)
2.272		aerobic respiration (GO:0009060)
-2.174		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.143		gluconeogenesis (GO:0006094)




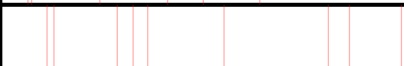


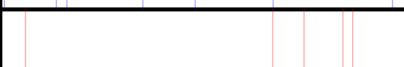
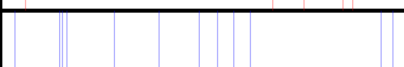


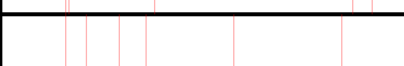
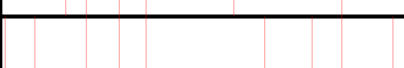



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=54$

mitochondrial translational elongation (GO:0070125)



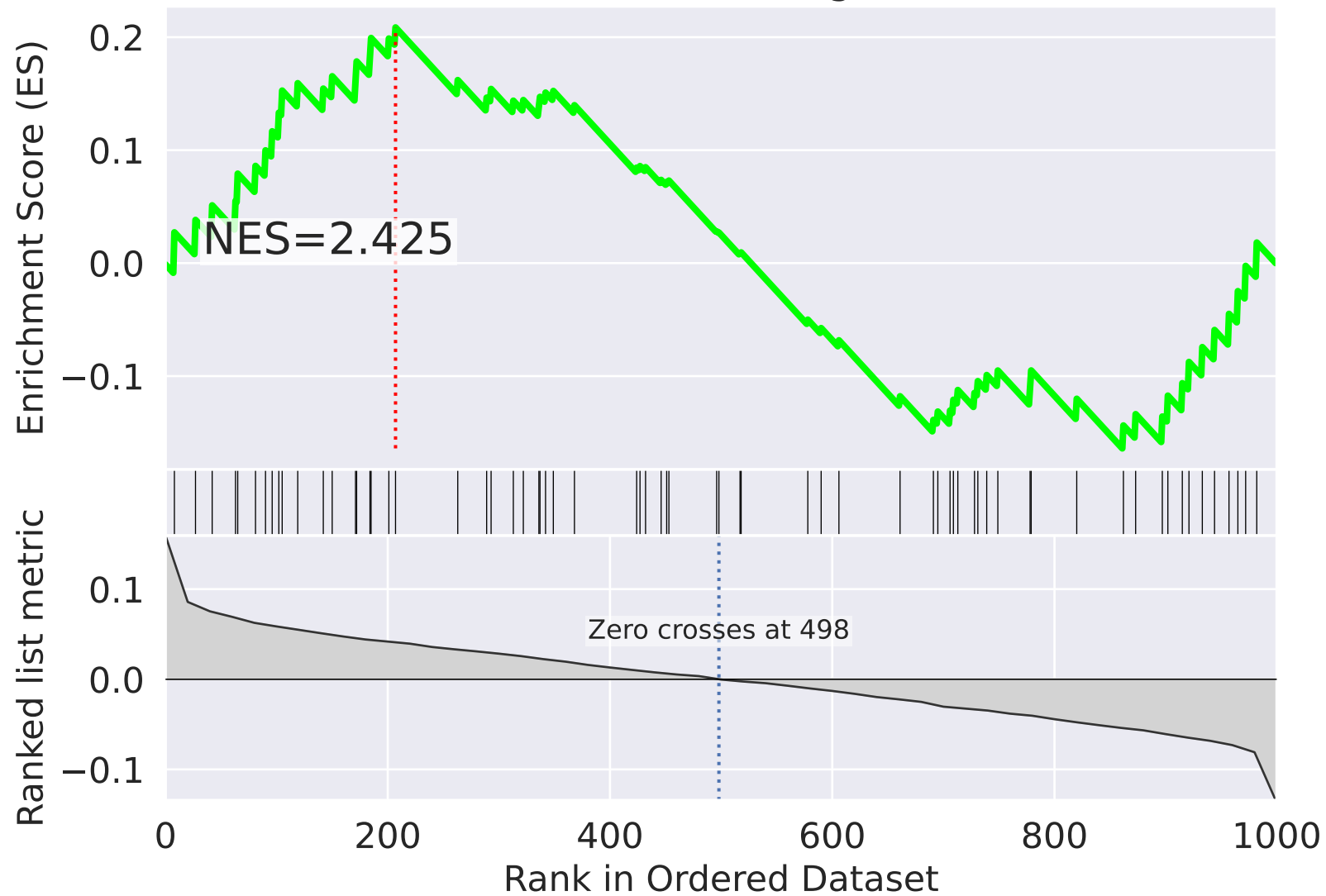
mitochondrial translational elongation (GO:0070125)



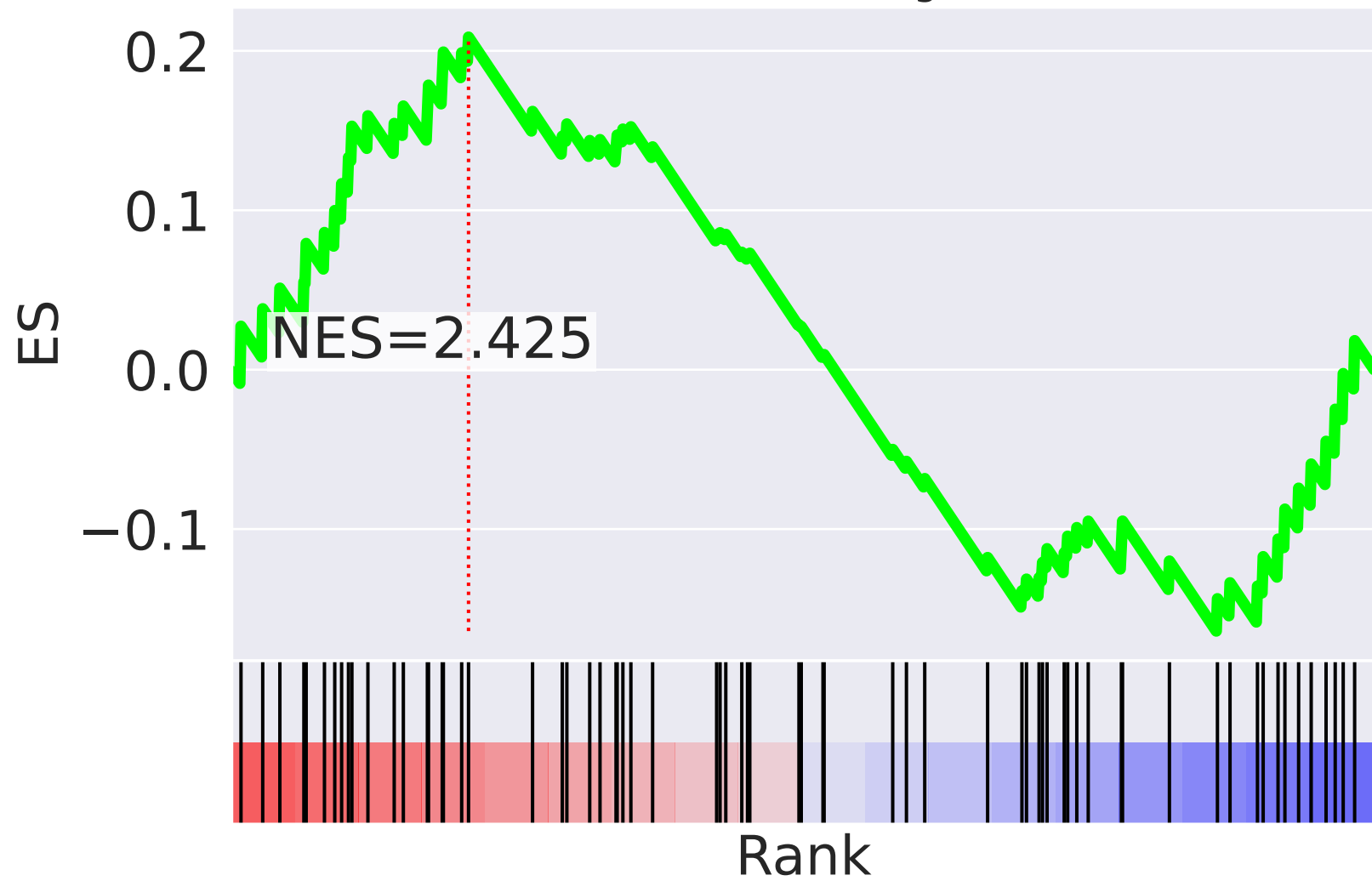
NES		SET
2.579		protein homooligomerization (GO:0051260)
-2.278		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.200		RNA metabolic process (GO:0016070)
2.171		tRNA aminoacylation for protein translation (GO:0006418)
2.073		negative regulation of cell growth (GO:0030308)
-2.037		cellular response to amino acid starvation (GO:0034198)
2.033		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-2.000		protein phosphorylation (GO:0006468)
-1.968		transcription, DNA-templated (GO:0006351)
1.947		inflammatory response (GO:0006954)
1.945		T cell costimulation (GO:0031295)
1.918		phosphatidylinositol-mediated signaling (GO:0048015)
1.917		chromosome segregation (GO:0007059)
-1.871		regulation of mRNA stability (GO:0043488)
1.805		positive regulation of DNA repair (GO:0045739)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=55$

mitochondrial translational elongation (GO:0070125)

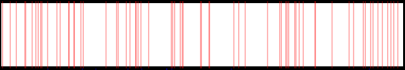

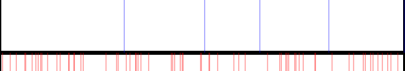
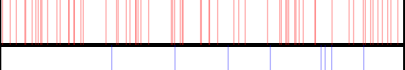

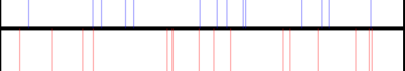
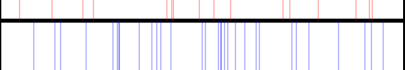
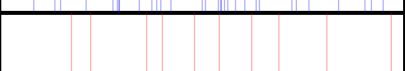




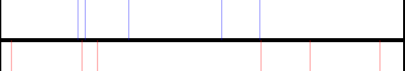
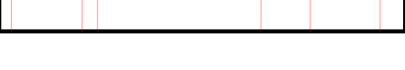



mitochondrial translational elongation (GO:0070125)



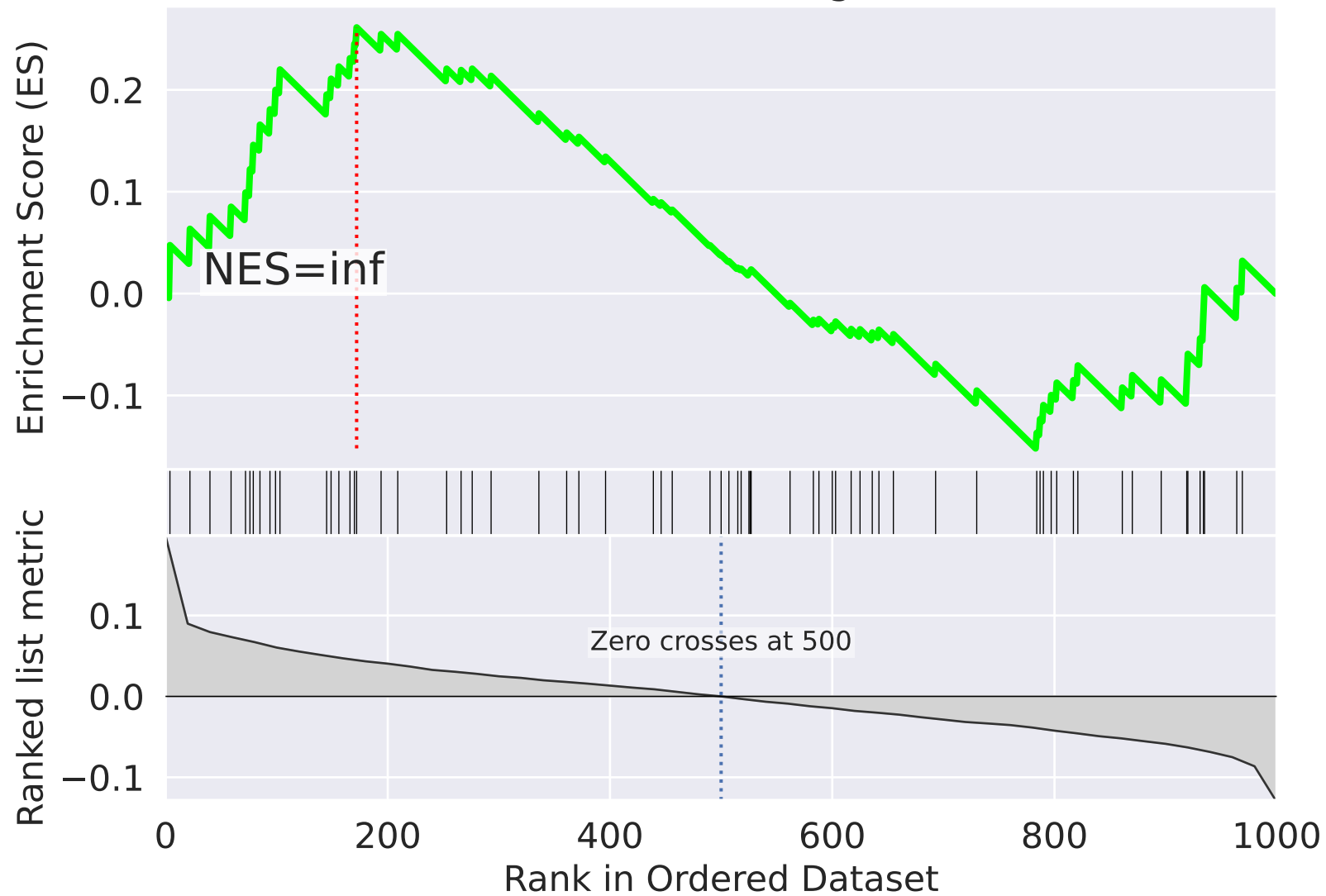
NES

SET

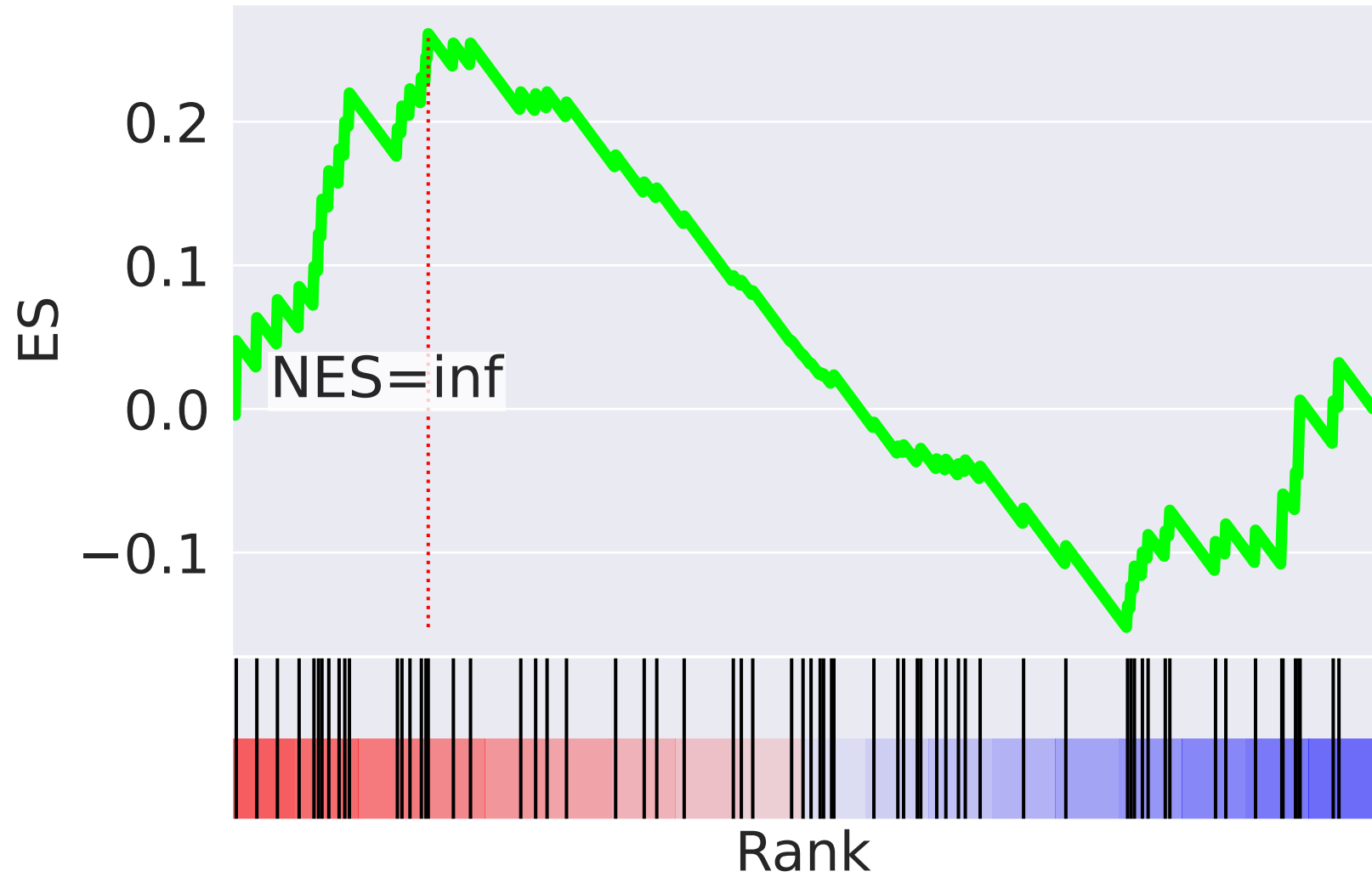
2.425		mitochondrial translational elongation (GO:0070125)
-2.306		double-strand break repair via homologous recombination (GO:0000724)
-2.215		positive regulation of telomere maintenance via telomerase (GO:0032212)
2.158		mitochondrial translational termination (GO:0070126)
-2.073		rRNA processing (GO:0006364)
-2.054		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.005		regulation of signal transduction by p53 class mediator (GO:1901796)
-1.956		mitochondrial respiratory chain complex I assembly (GO:0032981)
1.933		retrograde transport, endosome to Golgi (GO:0042147)
1.926		MAPK cascade (GO:0000165)
1.922		regulation of cell motility (GO:2000145)
1.911		RNA secondary structure unwinding (GO:0010501)
-1.896		substrate adhesion-dependent cell spreading (GO:0034446)
-1.888		DNA-dependent DNA replication (GO:0006261)
1.878		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)

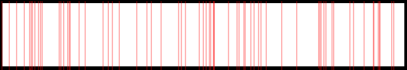
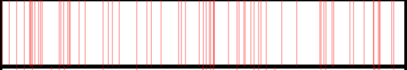
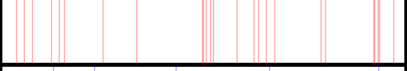

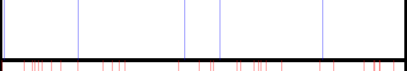
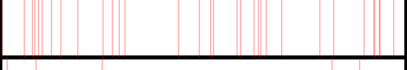
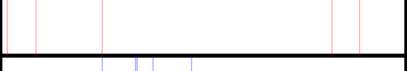
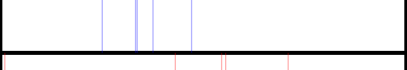
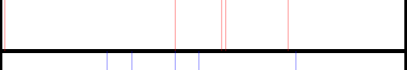



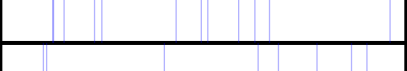


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=56$

mitochondrial translational elongation (GO:0070125)



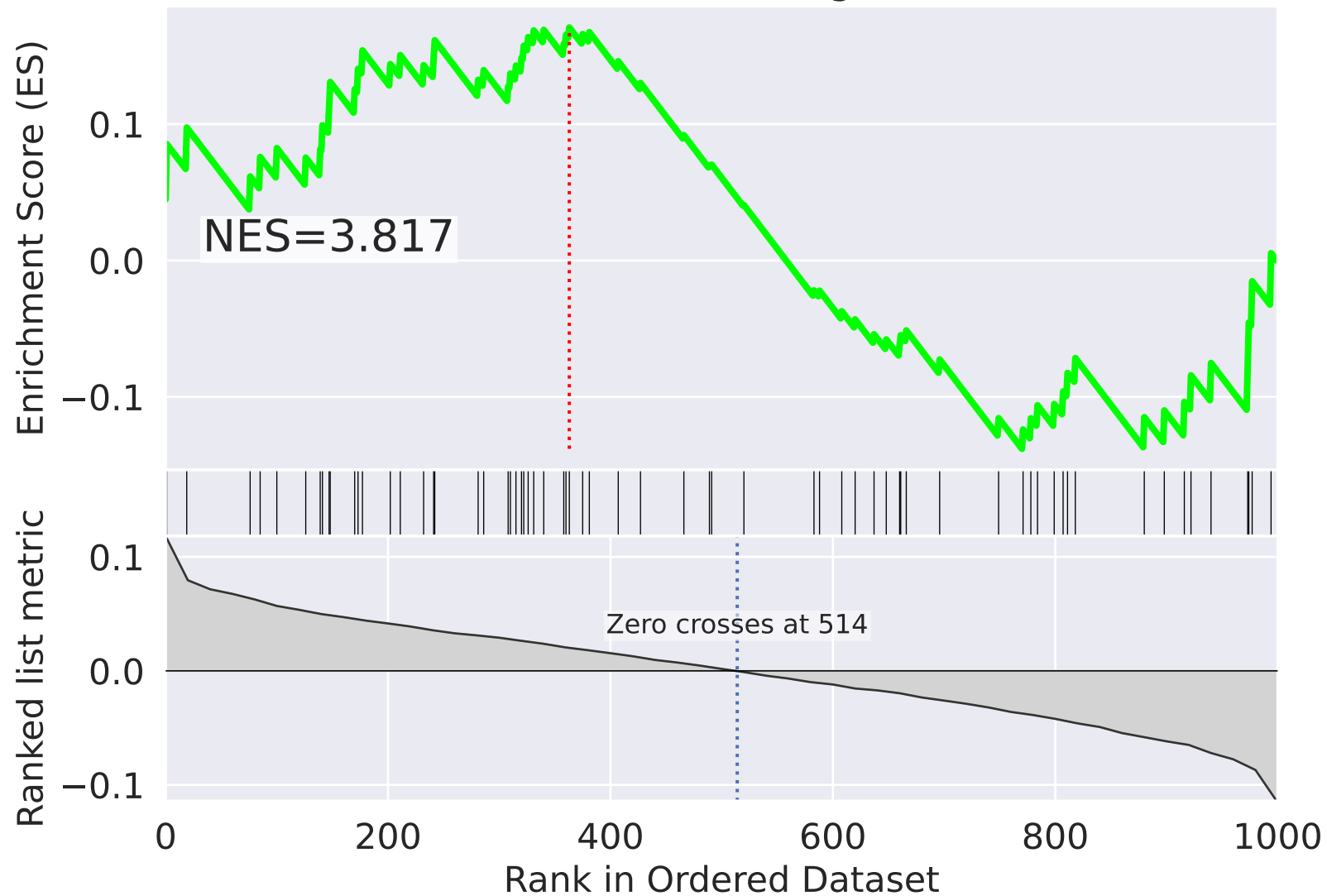
mitochondrial translational elongation (GO:0070125)



NES		SET
inf		mitochondrial translational elongation (GO:0070125)
inf		mitochondrial translational termination (GO:0070126)
2.515		mitochondrial translation (GO:0032543)
-2.476		cholesterol biosynthetic process (GO:0006695)
-2.340		nucleotide-excision repair (GO:0006289)
2.204		translation (GO:0006412)
2.174		transcription from mitochondrial promoter (GO:0006390)
-2.072		DNA-dependent DNA replication (GO:0006261)
2.062		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-2.013		nucleosome disassembly (GO:0006337)
1.983		regulation of macroautophagy (GO:0016241)
-1.978		histone H4 acetylation (GO:0043967)
-1.959		regulation of cholesterol biosynthetic process (GO:0045540)
-1.926		protein import into nucleus (GO:0006606)
-1.870		regulation of transcription, DNA-templated (GO:0006355)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=57$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

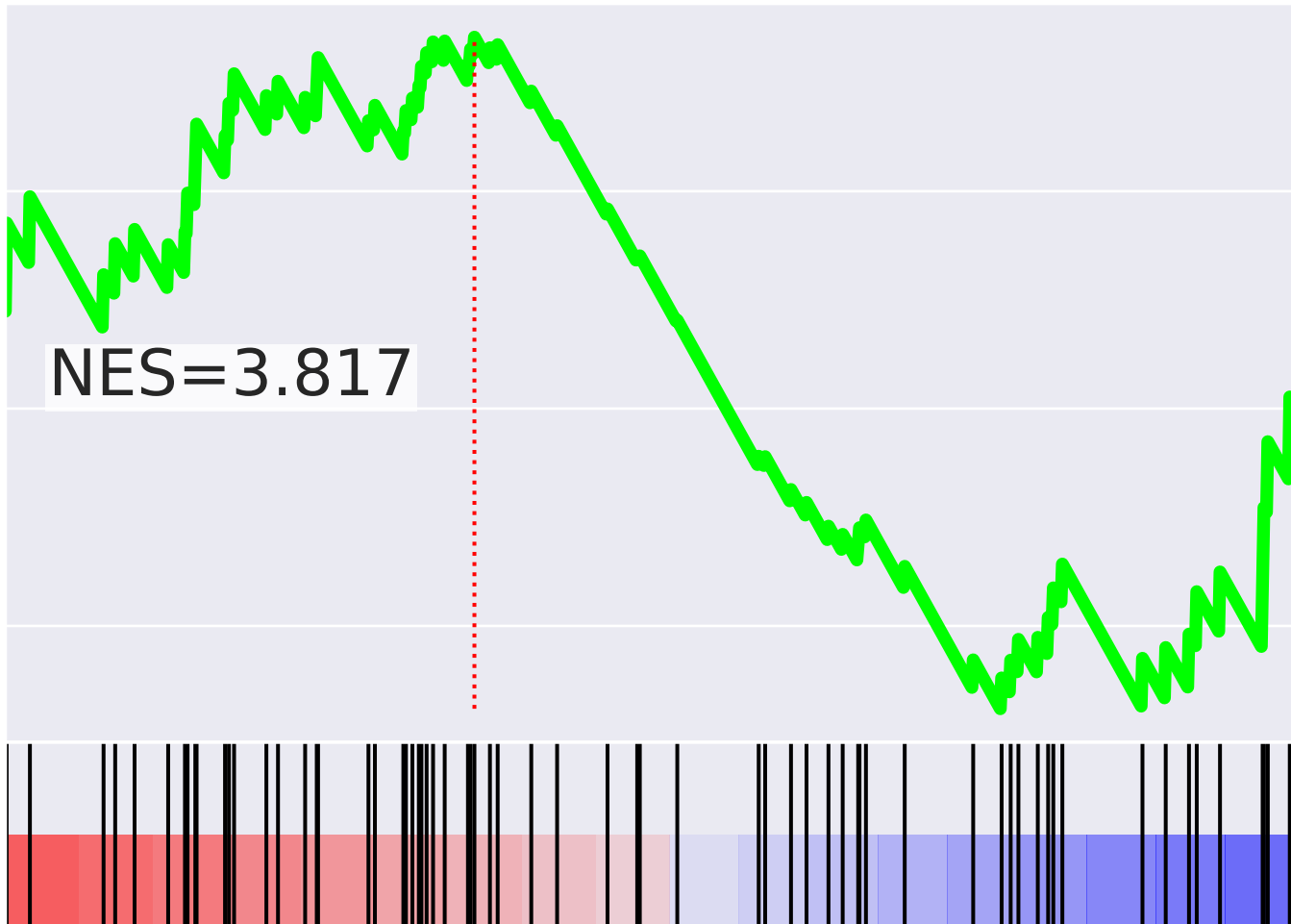
NES=3.817

0.1

0.0

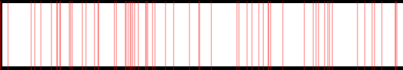
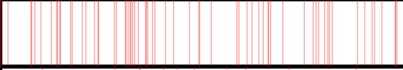
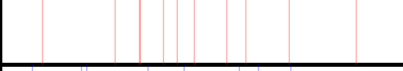
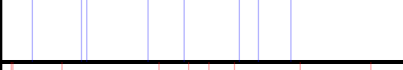

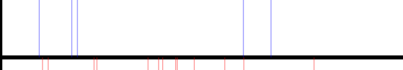
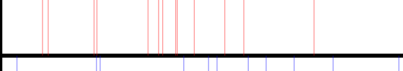
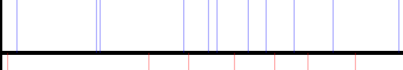



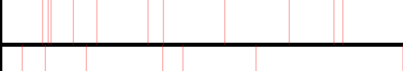


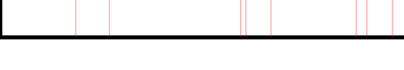
-0.1

Rank



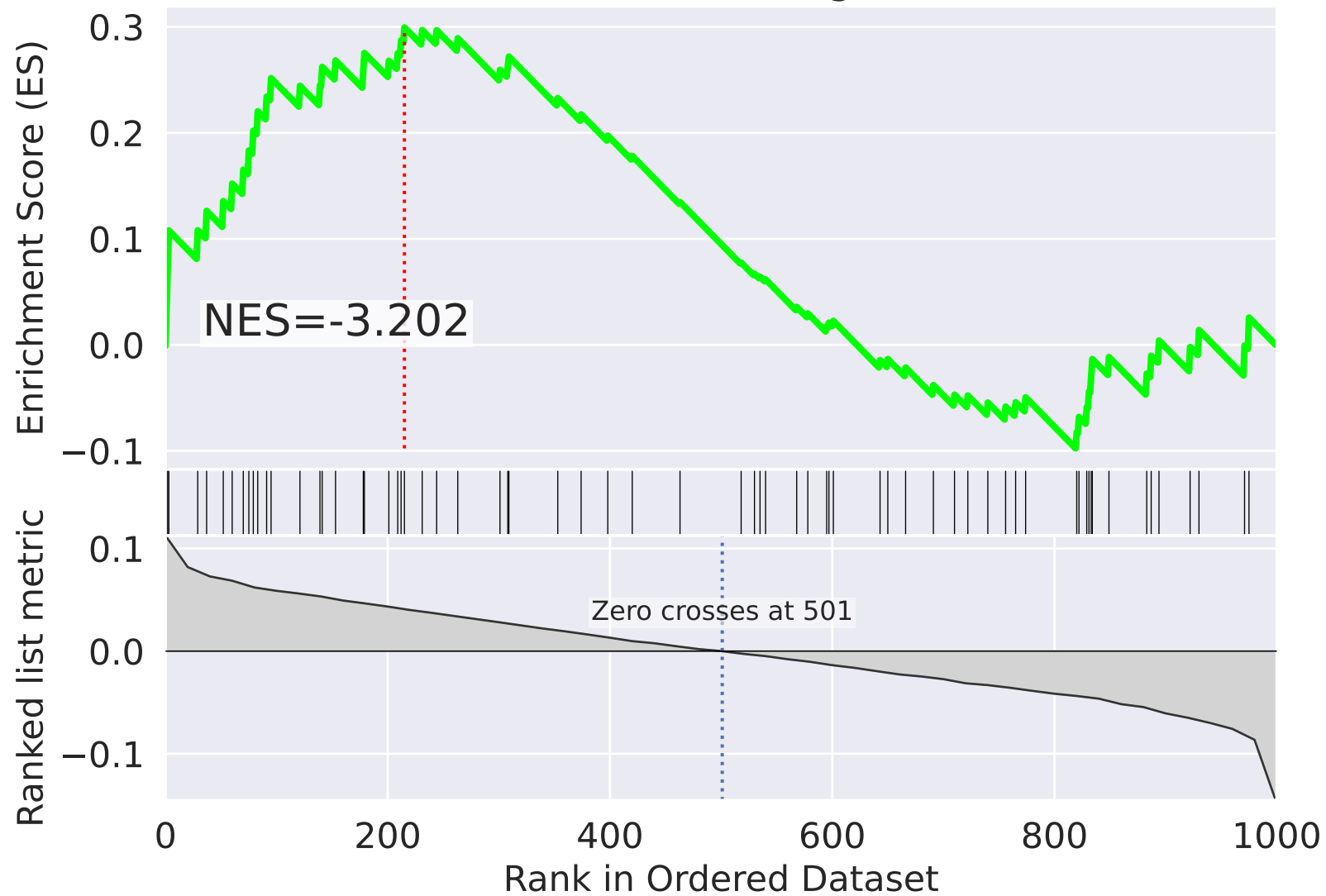
NES

SET

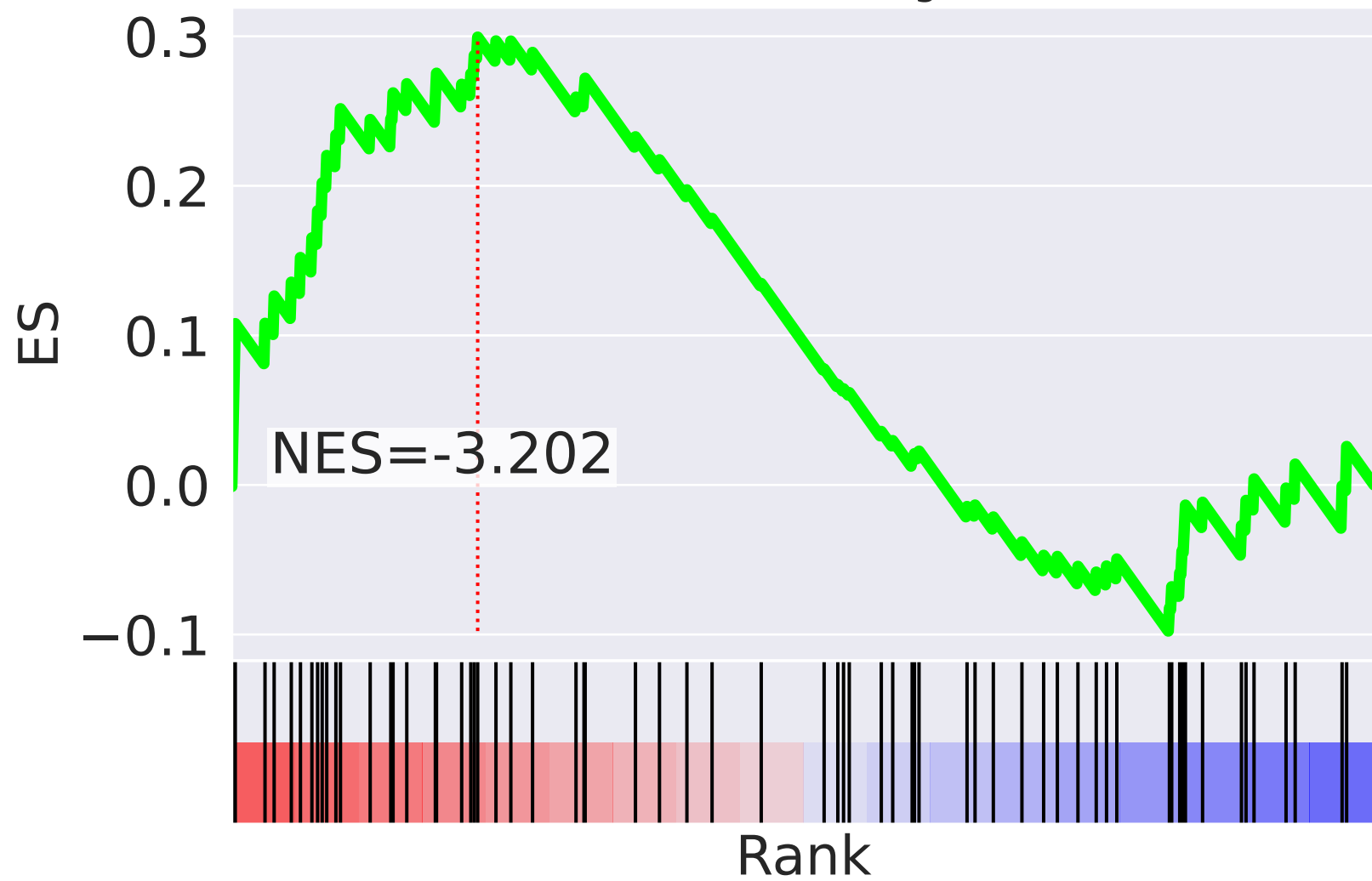
3.817		mitochondrial translational elongation (GO:0070125)
3.675		mitochondrial translational termination (GO:0070126)
2.866		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.722		IRE1-mediated unfolded protein response (GO:0036498)
2.680		Golgi organization (GO:0007030)
-2.613		DNA damage checkpoint (GO:0000077)
2.520		Fc-epsilon receptor signaling pathway (GO:0038095)
-2.215		endosomal transport (GO:0016197)
2.190		intracellular protein transport (GO:0006886)
-2.178		protein sumoylation (GO:0016925)
2.161		retrograde transport, endosome to Golgi (GO:0042147)
2.157		epidermal growth factor receptor signaling pathway (GO:0007173)
2.151		Wnt signaling pathway (GO:0016055)
2.140		ER to Golgi vesicle-mediated transport (GO:0006888)
2.130		substantia nigra development (GO:0021762)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=58$

mitochondrial translational elongation (GO:0070125)

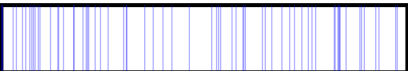
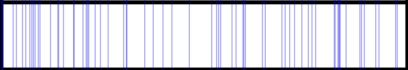

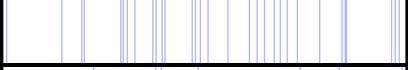



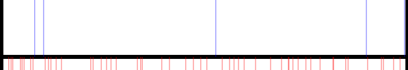
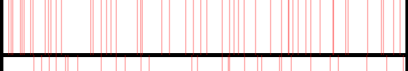
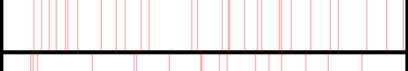
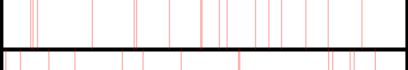

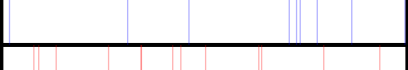

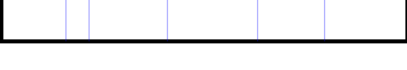


mitochondrial translational elongation (GO:0070125)



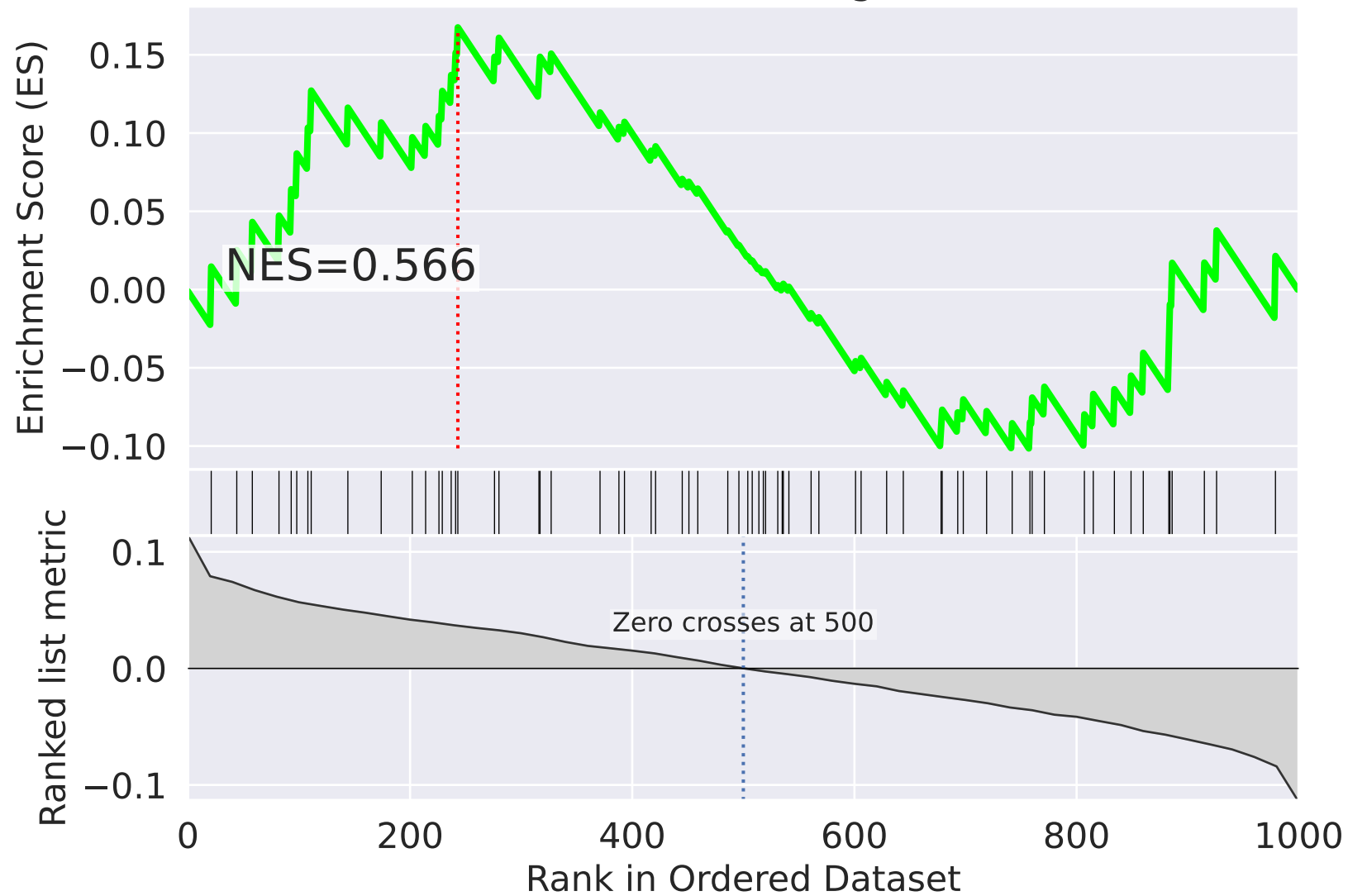
NES

SET

-3.202		mitochondrial translational elongation (GO:0070125)
-3.069		mitochondrial translational termination (GO:0070126)
-2.976		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.909		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.758		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.486		cellular respiration (GO:0045333)
-2.392		tRNA aminoacylation for protein translation (GO:0006418)
-2.335		iron-sulfur cluster assembly (GO:0016226)
2.270		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.259		negative regulation of apoptotic process (GO:0043066)
2.251		transcription initiation from RNA polymerase II promoter (GO:0006367)
2.230		regulation of cellular response to heat (GO:1900034)
-2.143		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.093		positive regulation of cell migration (GO:0030335)
-2.087		regulation of defense response to virus by virus (GO:0050690)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=59$

mitochondrial translational elongation (GO:0070125)



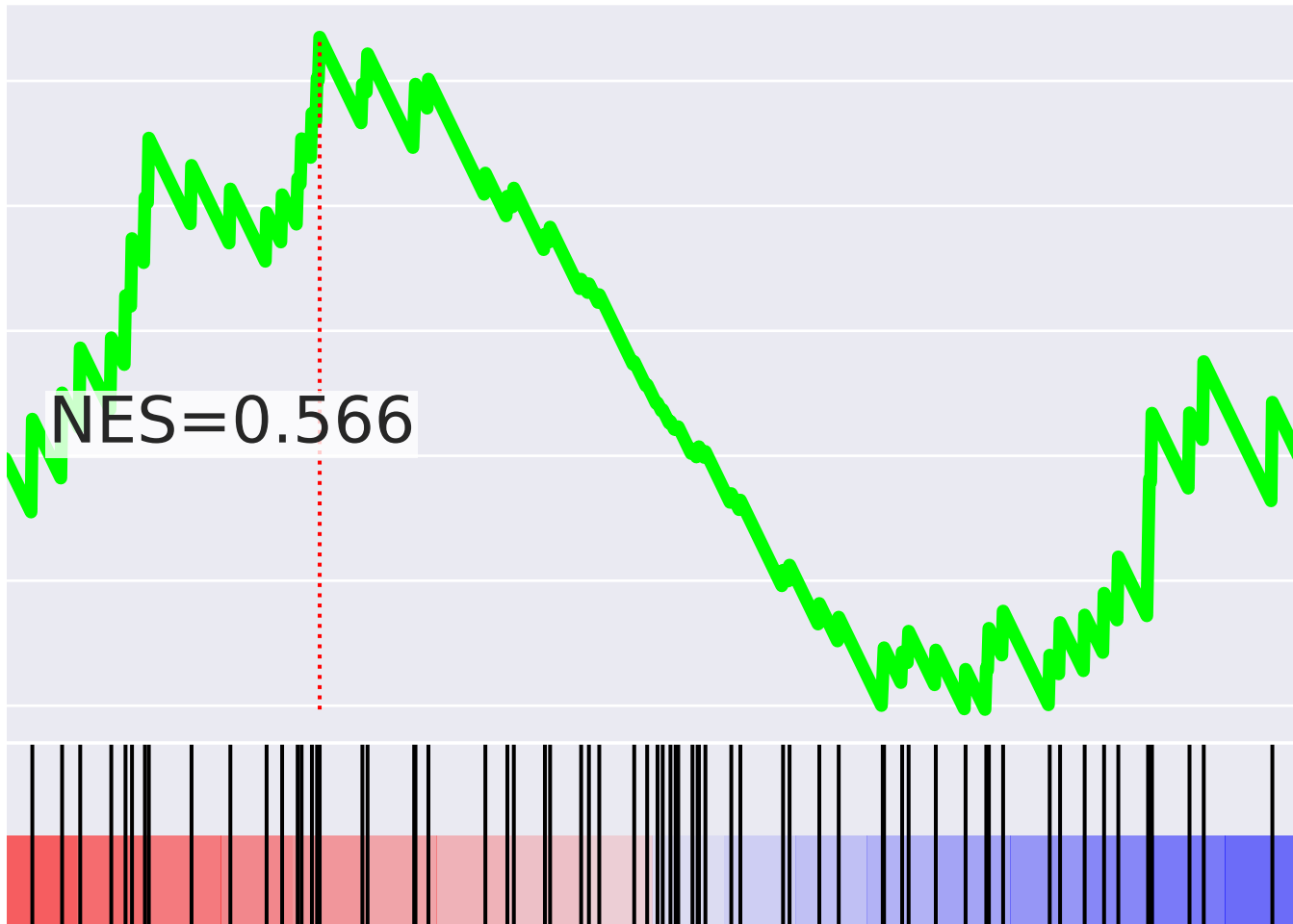
mitochondrial translational elongation (GO:0070125)

ES

0.15
0.10
0.05
0.00
-0.05
-0.10

NES=0.566

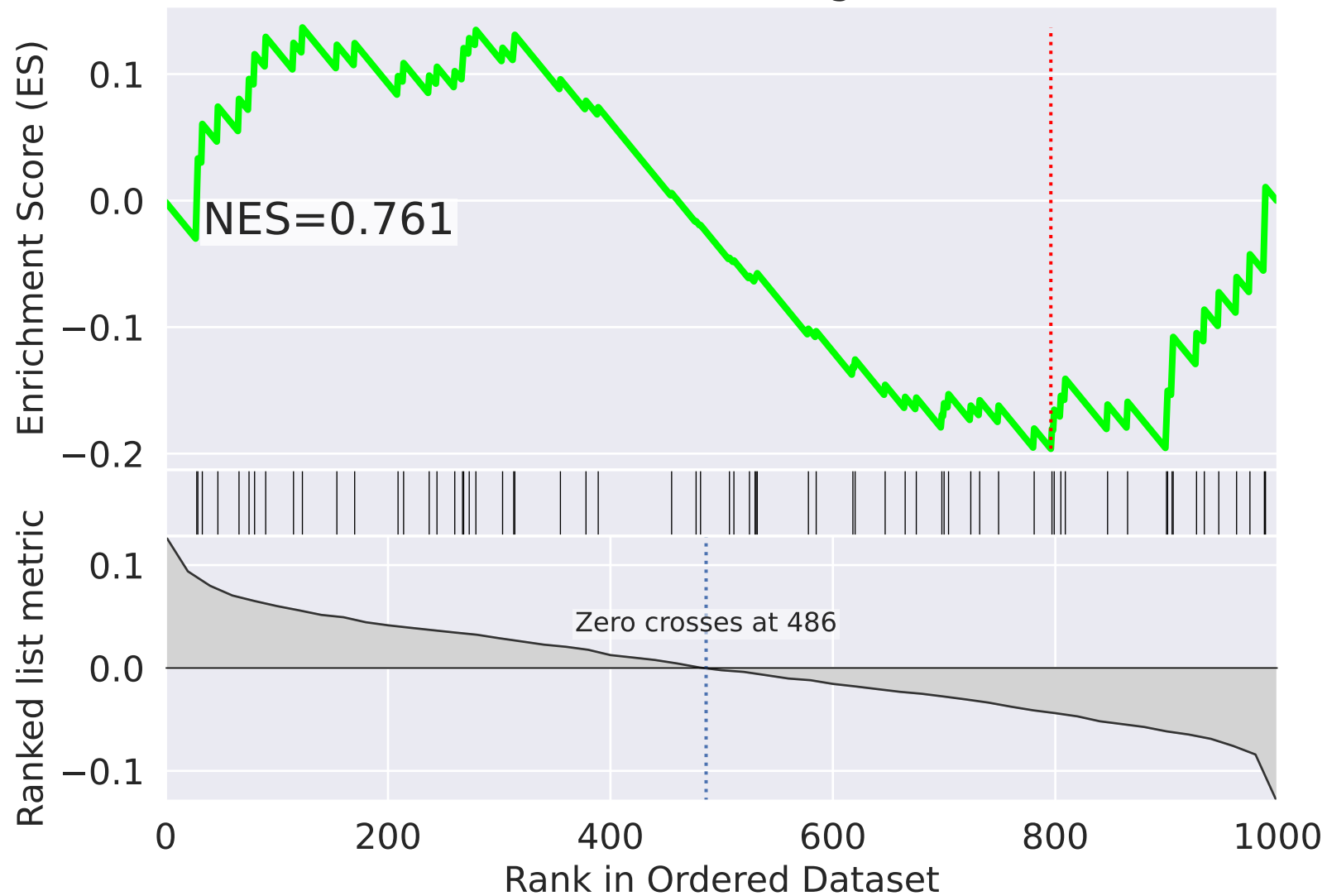
Rank



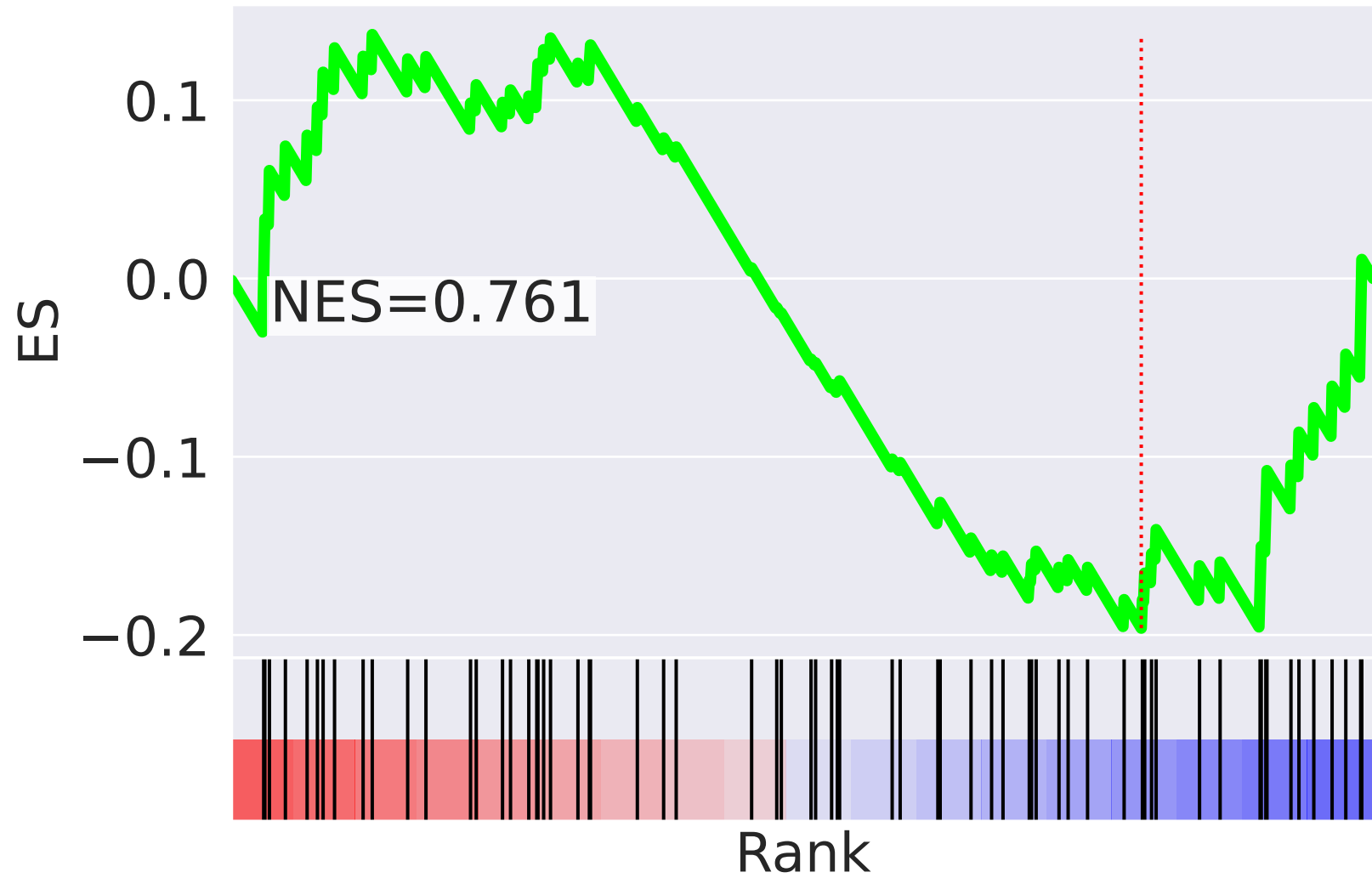
NES		SET
2.514		response to endoplasmic reticulum stress (GO:0034976)
2.418		cell-matrix adhesion (GO:0007160)
2.327		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-2.314		IRE1-mediated unfolded protein response (GO:0036498)
-2.272		proteolysis (GO:0006508)
-2.224		vesicle-mediated transport (GO:0016192)
-2.205		negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.150		RNA export from nucleus (GO:0006405)
2.142		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
-2.120		innate immune response (GO:0045087)
-2.108		positive regulation of viral genome replication (GO:0045070)
-2.055		axon guidance (GO:0007411)
-2.027		Fc-epsilon receptor signaling pathway (GO:0038095)
2.008		platelet aggregation (GO:0070527)
1.998		DNA replication (GO:0006260)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=60$

mitochondrial translational elongation (GO:0070125)



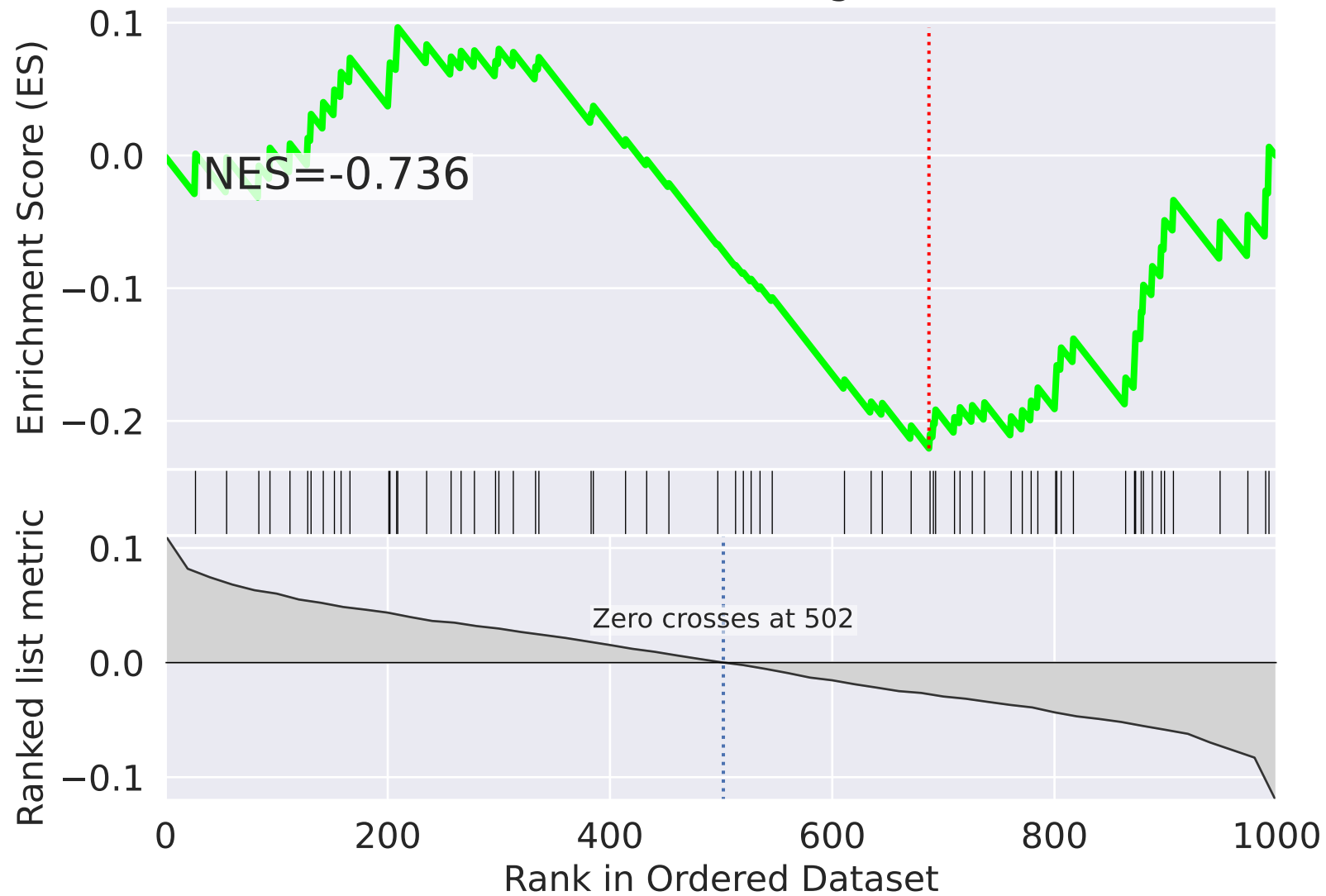
mitochondrial translational elongation (GO:0070125)



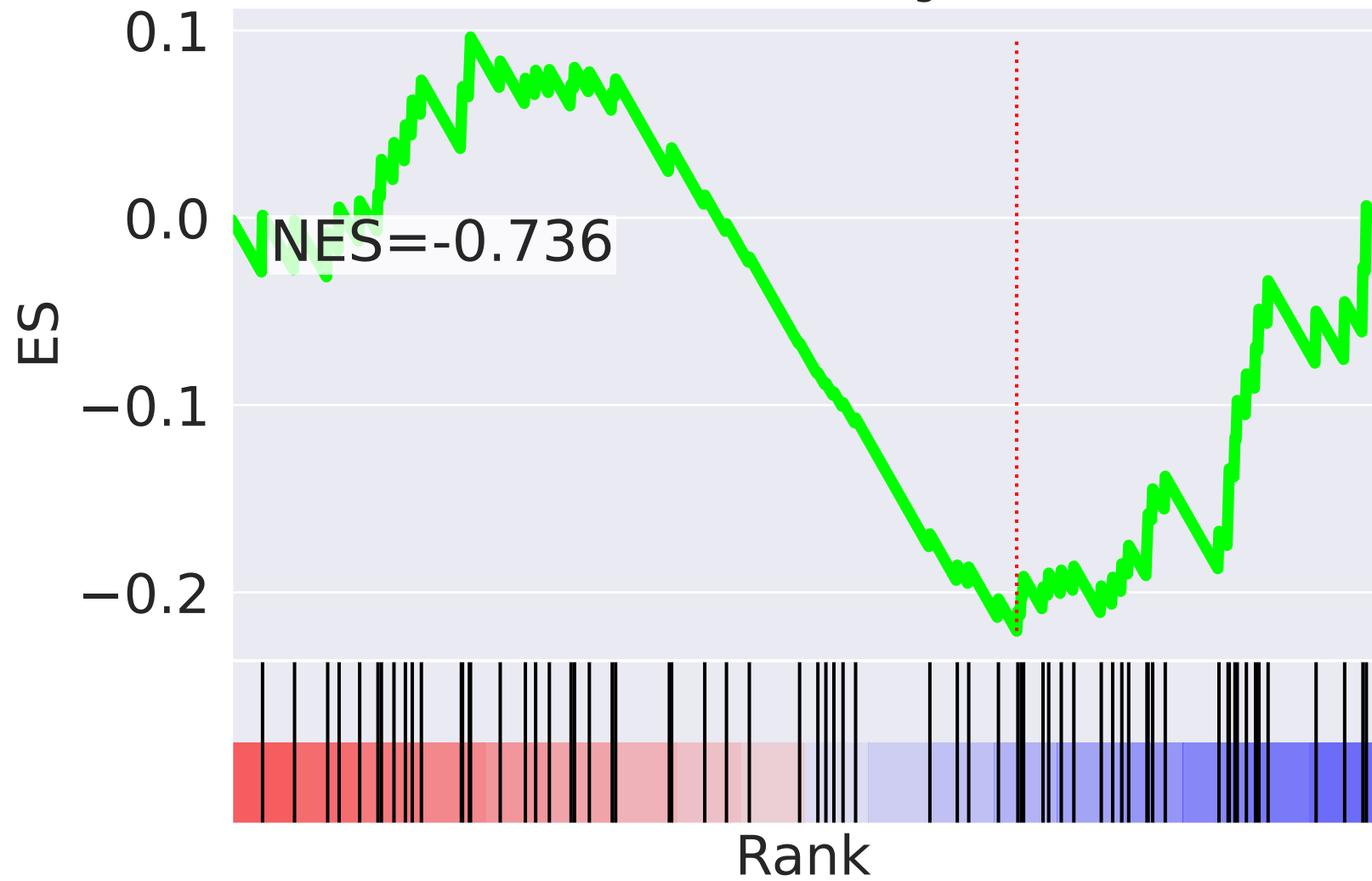
NES		SET
-2.759		positive regulation of protein phosphorylation (GO:0001934)
-2.520		negative regulation of apoptotic process (GO:0043066)
2.449		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.443		cellular response to hypoxia (GO:0071456)
2.386		RNA metabolic process (GO:0016070)
2.322		heart development (GO:0007507)
-2.322		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.280		regulation of defense response to virus by virus (GO:0050690)
-2.274		movement of cell or subcellular component (GO:0006928)
-2.232		ephrin receptor signaling pathway (GO:0048013)
-2.228		rRNA processing (GO:0006364)
-1.995		execution phase of apoptosis (GO:0097194)
-1.932		response to ionizing radiation (GO:0010212)
1.882		nucleus organization (GO:0006997)
-1.865		DNA synthesis involved in DNA repair (GO:0000731)


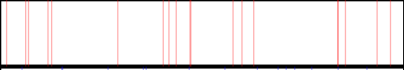


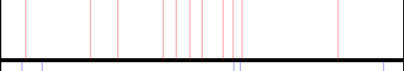
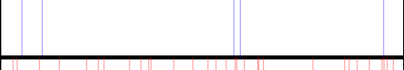
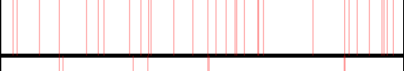
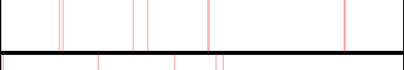



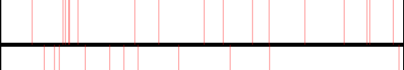



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=61$

mitochondrial translational elongation (GO:0070125)



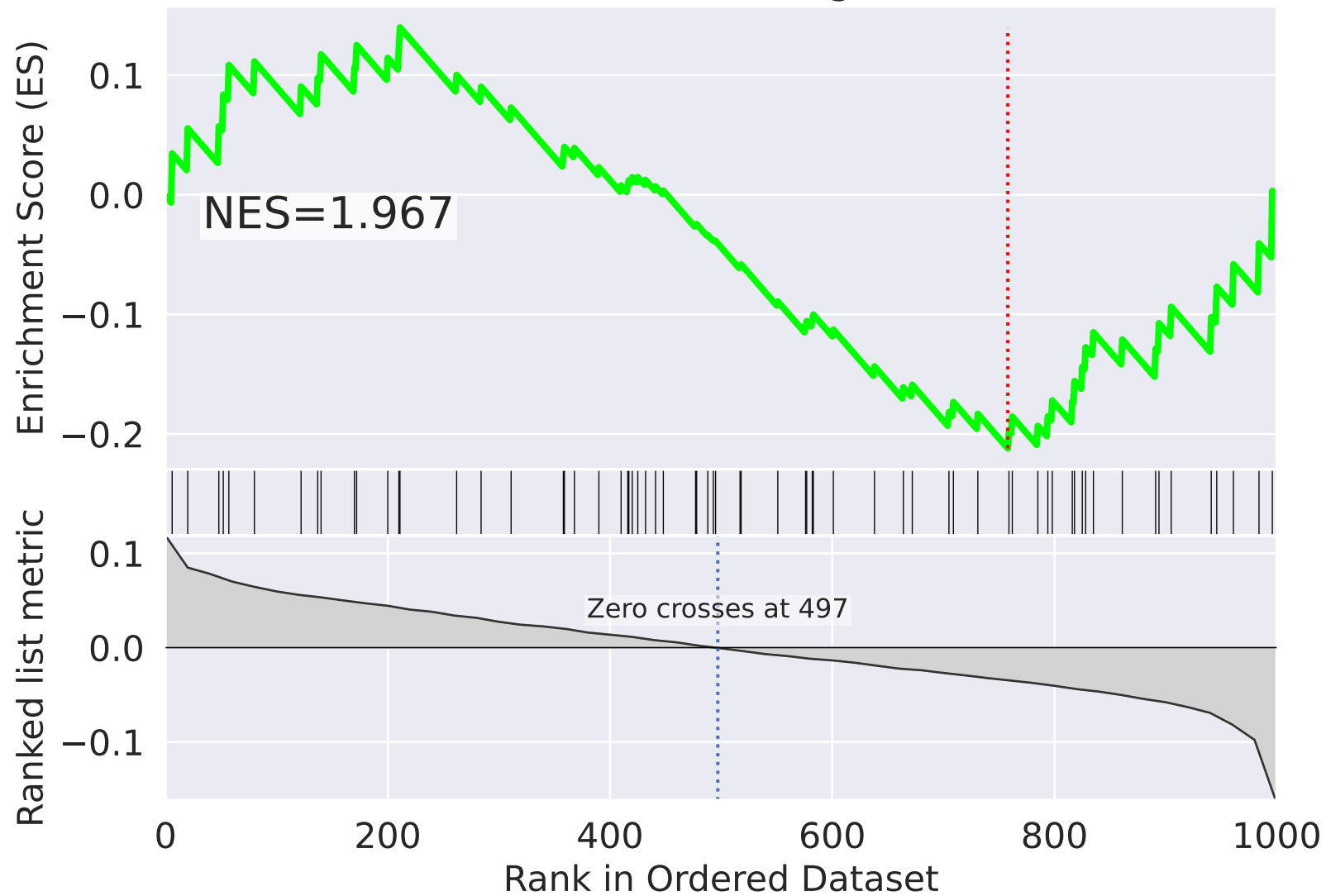
mitochondrial translational elongation (GO:0070125)



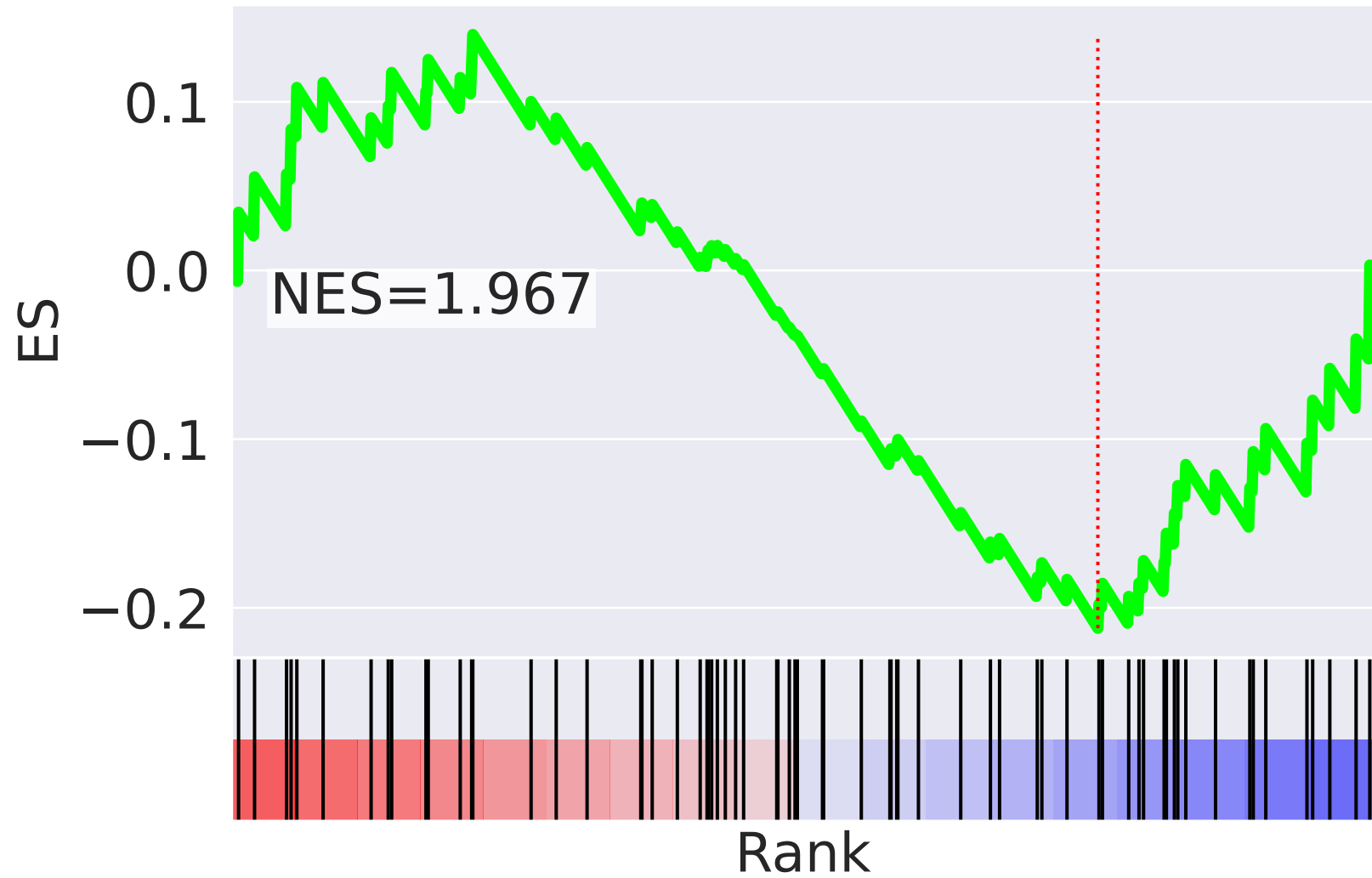
NES		SET
2.784		histone H3 acetylation (GO:0043966)
2.752		mRNA export from nucleus (GO:0006406)
-2.746		sister chromatid cohesion (GO:0007062)
2.411		protein import into nucleus (GO:0006606)
2.353		mitotic nuclear envelope disassembly (GO:0007077)
-2.307		DNA-dependent DNA replication (GO:0006261)
2.304		positive regulation of cell proliferation (GO:0008284)
2.304		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.253		positive regulation of mitotic cell cycle (GO:0045931)
2.206		inflammatory response (GO:0006954)
-2.165		positive regulation of telomere maintenance via telomerase (GO:0032212)
2.164		G2/M transition of mitotic cell cycle (GO:0000086)
2.161		positive regulation of gene expression (GO:0010628)
2.110		histone H4 acetylation (GO:0043967)
2.106		protein targeting to mitochondrion (GO:0006626)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=62$

mitochondrial translational elongation (GO:0070125)



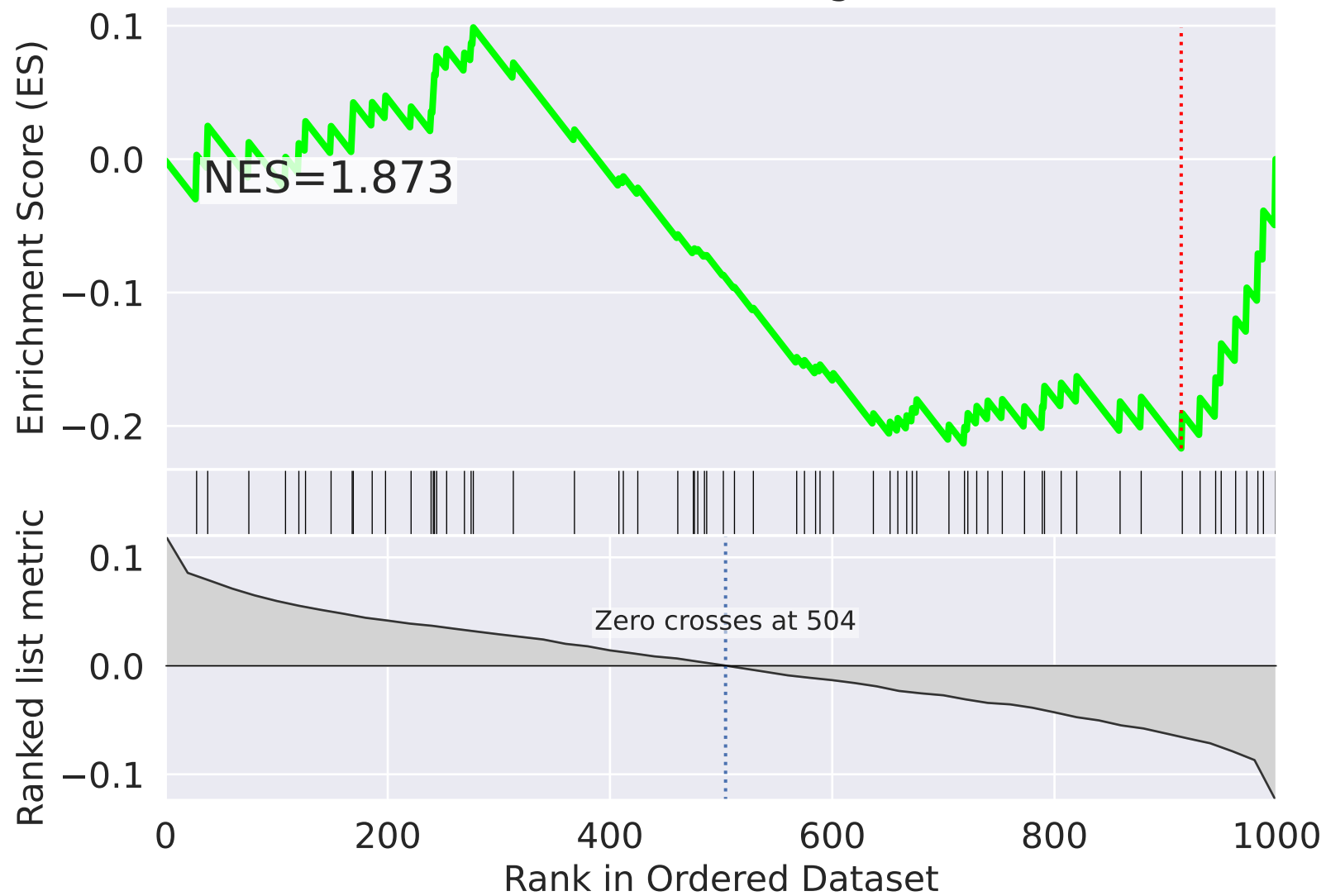
mitochondrial translational elongation (GO:0070125)



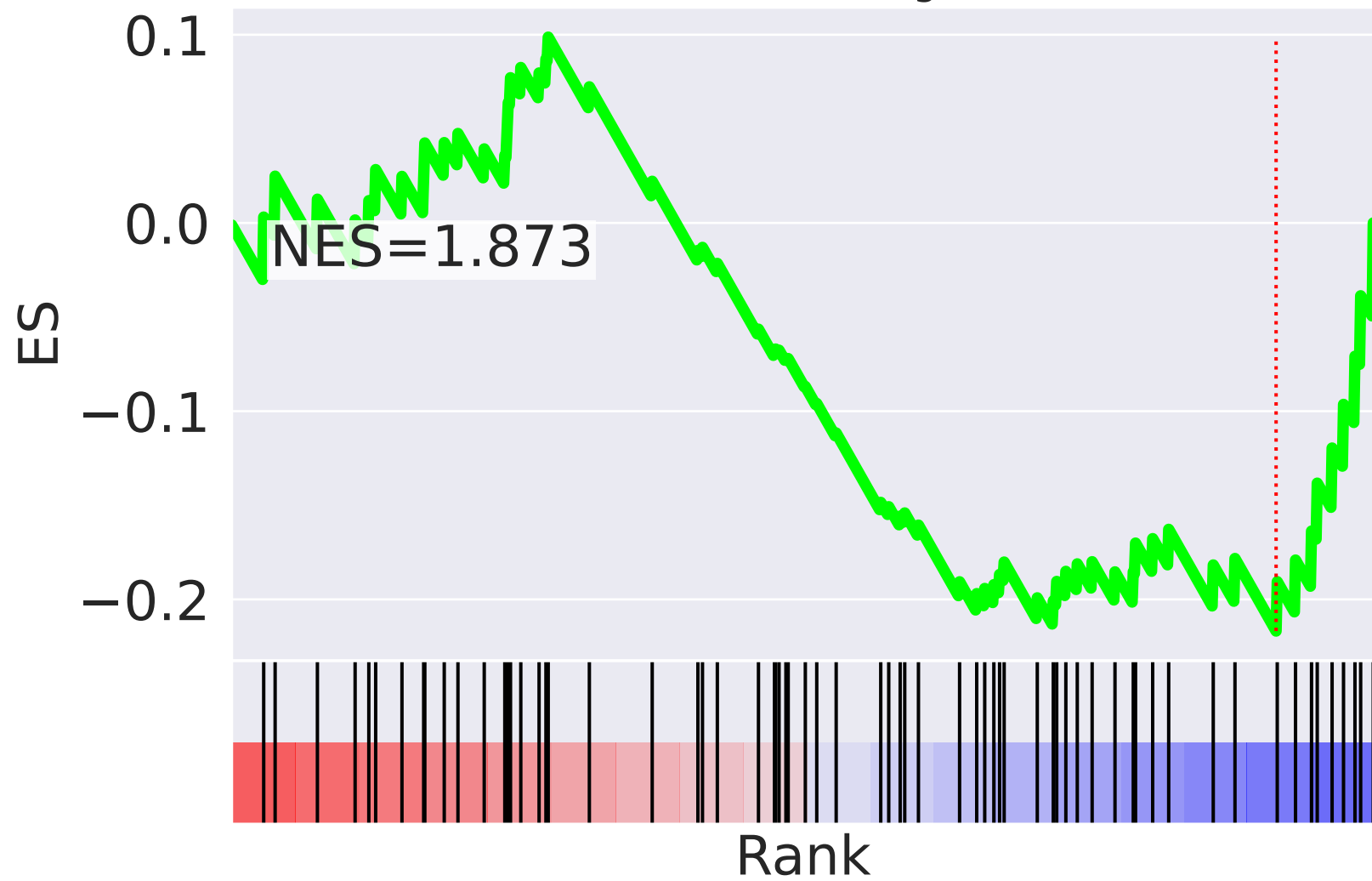
NES		SET
-3.121		positive regulation of TOR signaling (GO:0032008)
-2.795		cell cycle arrest (GO:0007050)
2.771		double-strand break repair via homologous recombination (GO:0000724)
2.636		reciprocal meiotic recombination (GO:0007131)
2.466		regulation of defense response to virus by virus (GO:0050690)
-2.367		protein polyubiquitination (GO:0000209)
-2.346		cellular response to amino acid stimulus (GO:0071230)
2.334		strand displacement (GO:0000732)
2.273		DNA repair (GO:0006281)
2.264		cellular response to hypoxia (GO:0071456)
-2.264		protein homooligomerization (GO:0051260)
2.219		positive regulation of gene expression (GO:0010628)
-2.204		regulation of macroautophagy (GO:0016241)
2.126		cellular response to epidermal growth factor stimulus (GO:0071364)
-2.102		substantia nigra development (GO:0021762)



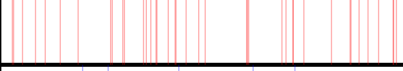


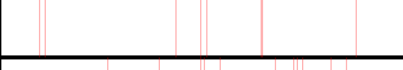
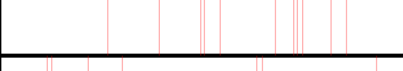

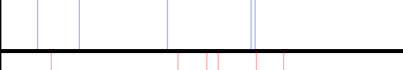
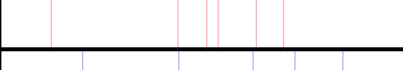
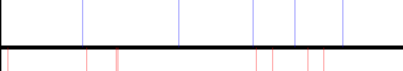
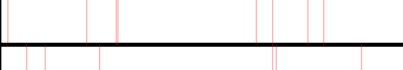
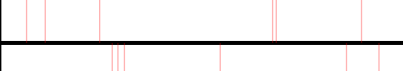


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=63$

mitochondrial translational elongation (GO:0070125)



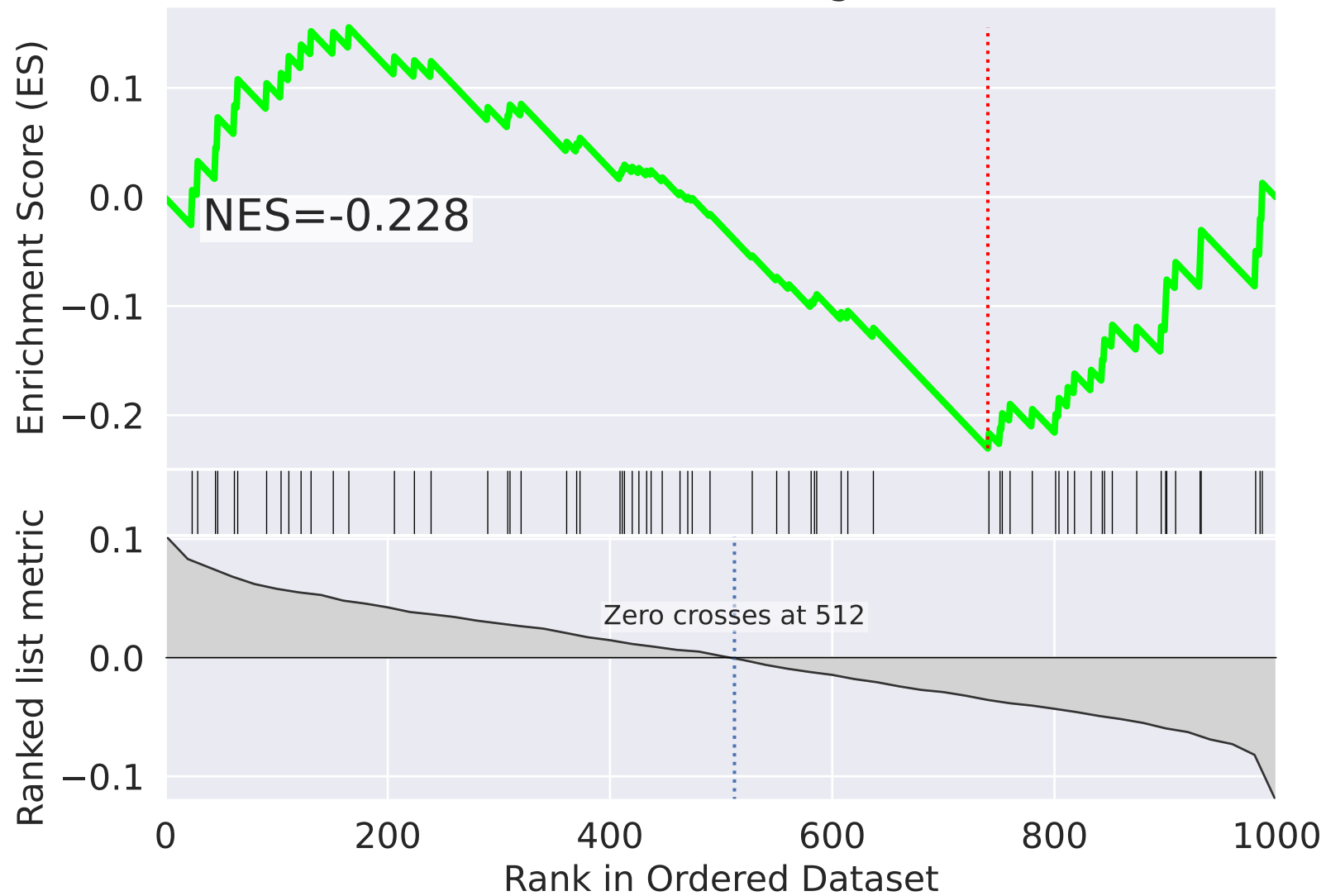
mitochondrial translational elongation (GO:0070125)



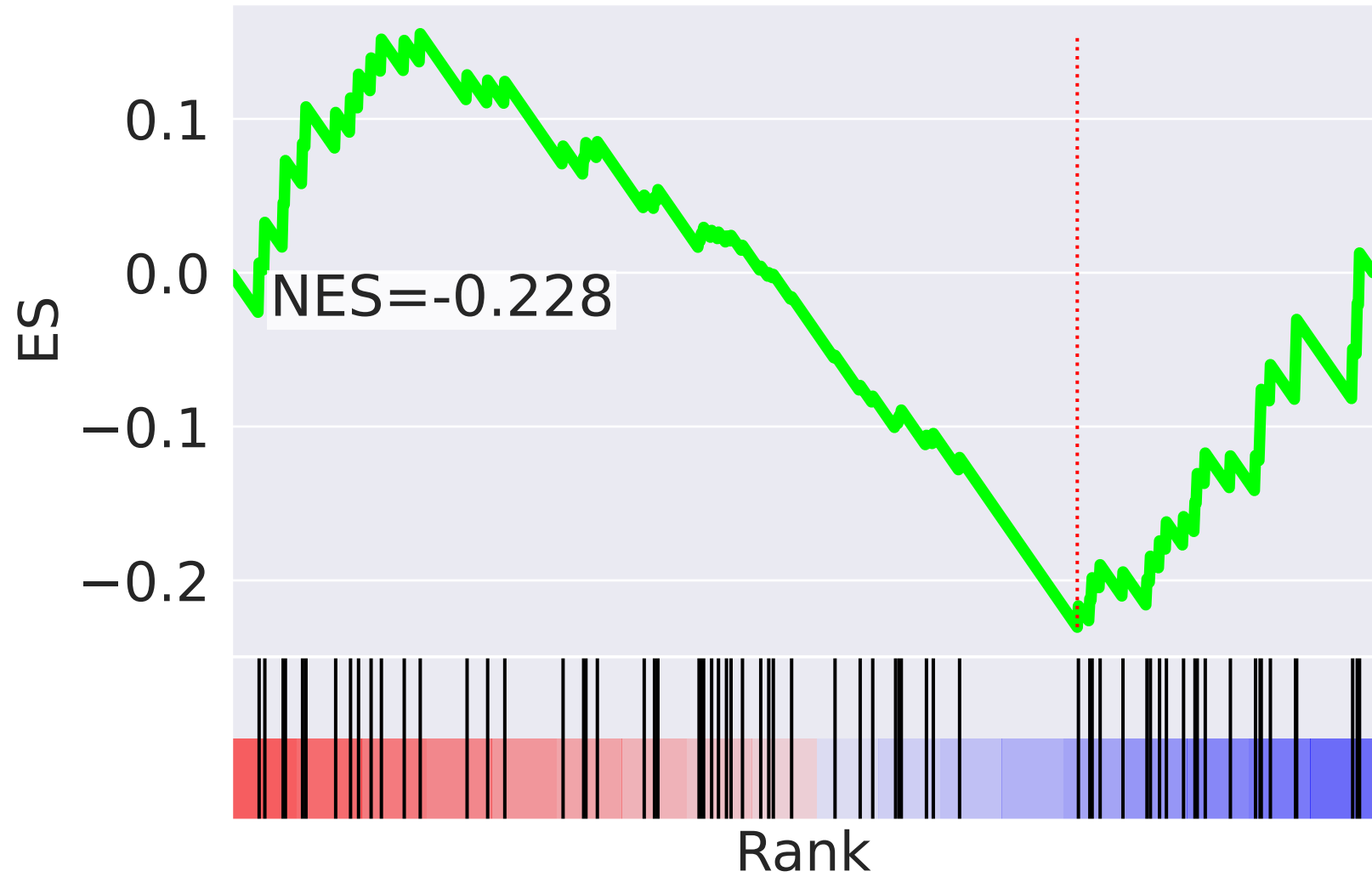
NES		SET
2.947		chromatin remodeling (GO:0006338)
2.528		peptidyl-serine phosphorylation (GO:0018105)
2.449		positive regulation of transcription, DNA-templated (GO:0045893)
-2.315		cellular protein localization (GO:0034613)
2.309		regulation of cellular response to heat (GO:1900034)
2.302		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.301		regulation of mRNA stability (GO:0043488)
2.295		positive regulation of gene expression, epigenetic (GO:0045815)
-2.294		regulation of cell adhesion (GO:0030155)
2.158		T cell costimulation (GO:0031295)
-2.140		cellular response to amino acid stimulus (GO:0071230)
2.109		cell migration (GO:0016477)
2.032		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
2.032		ERK1 and ERK2 cascade (GO:0070371)
2.009		T cell receptor signaling pathway (GO:0050852)




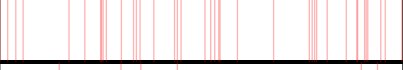
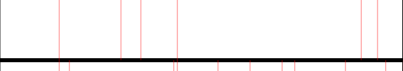
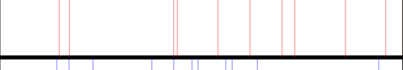


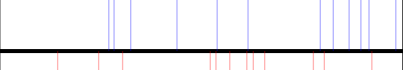
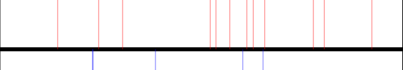
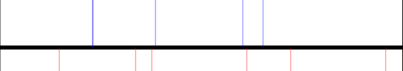
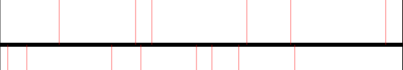
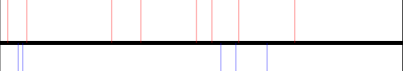

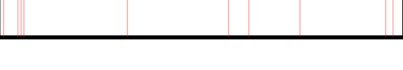
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=64$

mitochondrial translational elongation (GO:0070125)



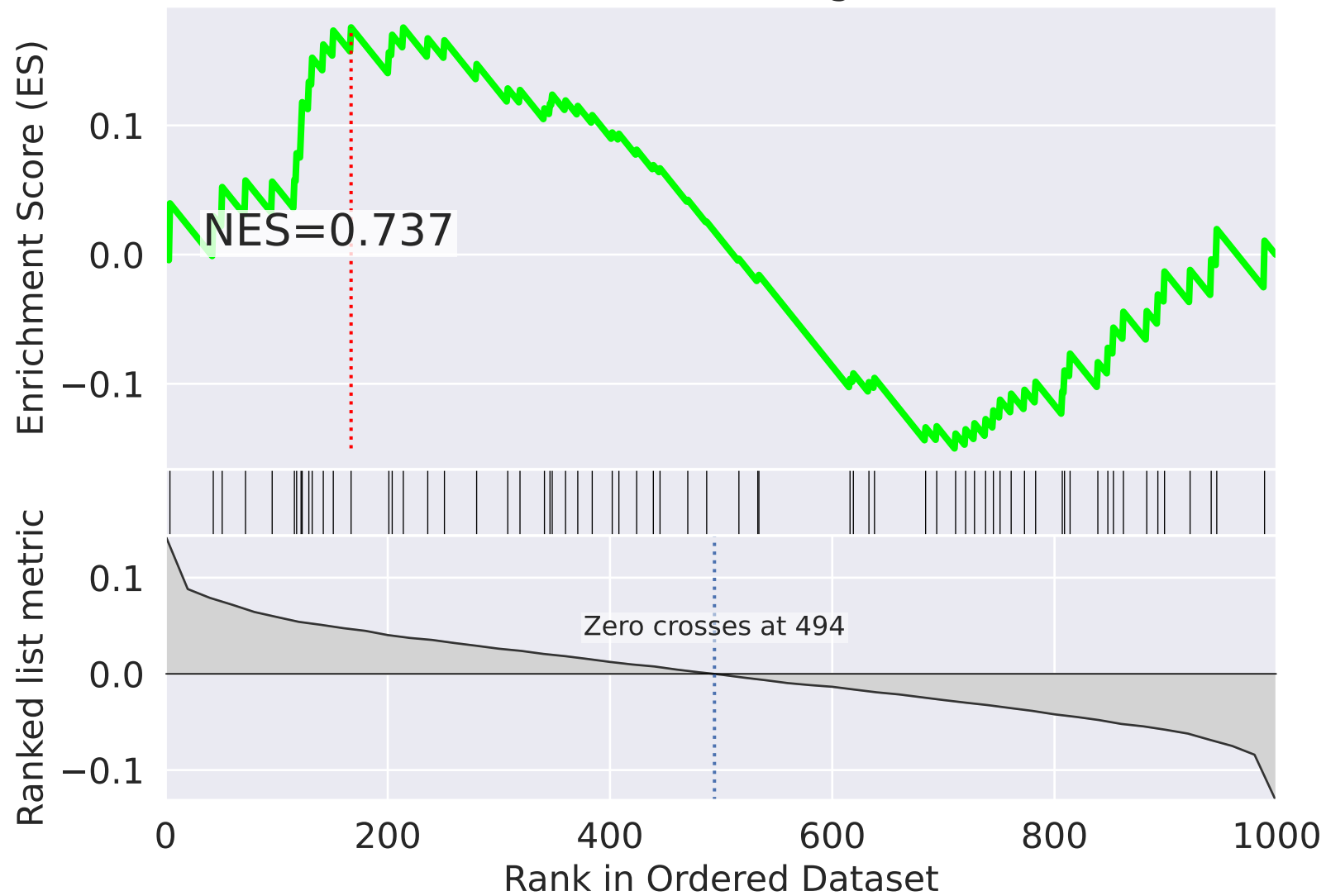
mitochondrial translational elongation (GO:0070125)



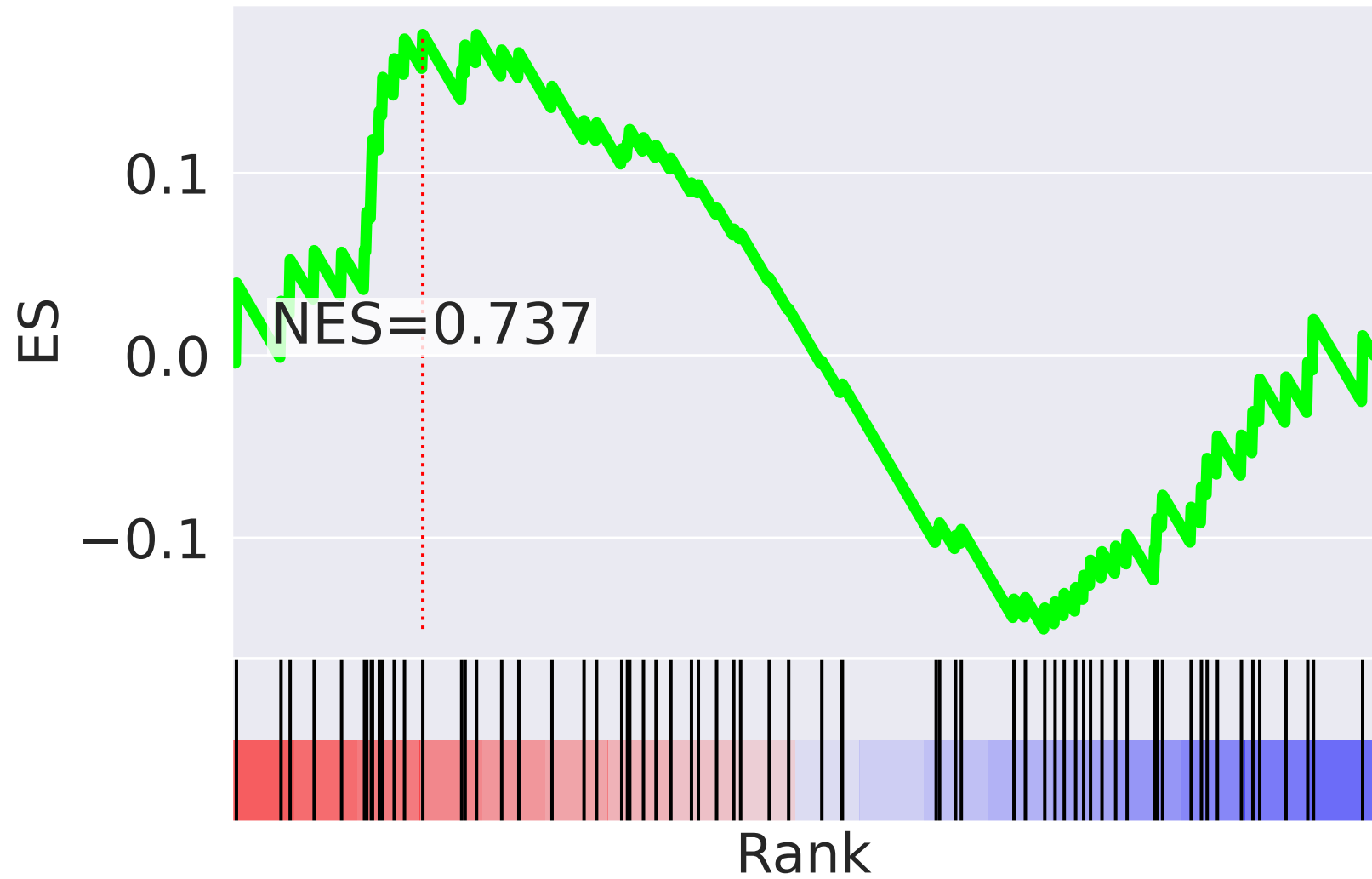
NES		SET
3.139		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-2.955		transcription, DNA-templated (GO:0006351)
-2.773		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
2.754		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.682		ERK1 and ERK2 cascade (GO:0070371)
2.360		positive regulation of gene expression (GO:0010628)
-2.320		histone H3 acetylation (GO:0043966)
2.295		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.169		RNA splicing (GO:0008380)
2.159		regulation of cholesterol biosynthetic process (GO:0045540)
-2.093		cytokinesis (GO:0000910)
2.057		regulation of protein stability (GO:0031647)
2.038		regulation of apoptotic process (GO:0042981)
-2.014		execution phase of apoptosis (GO:0097194)
2.005		Ras protein signal transduction (GO:0007265)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=65$

mitochondrial translational elongation (GO:0070125)



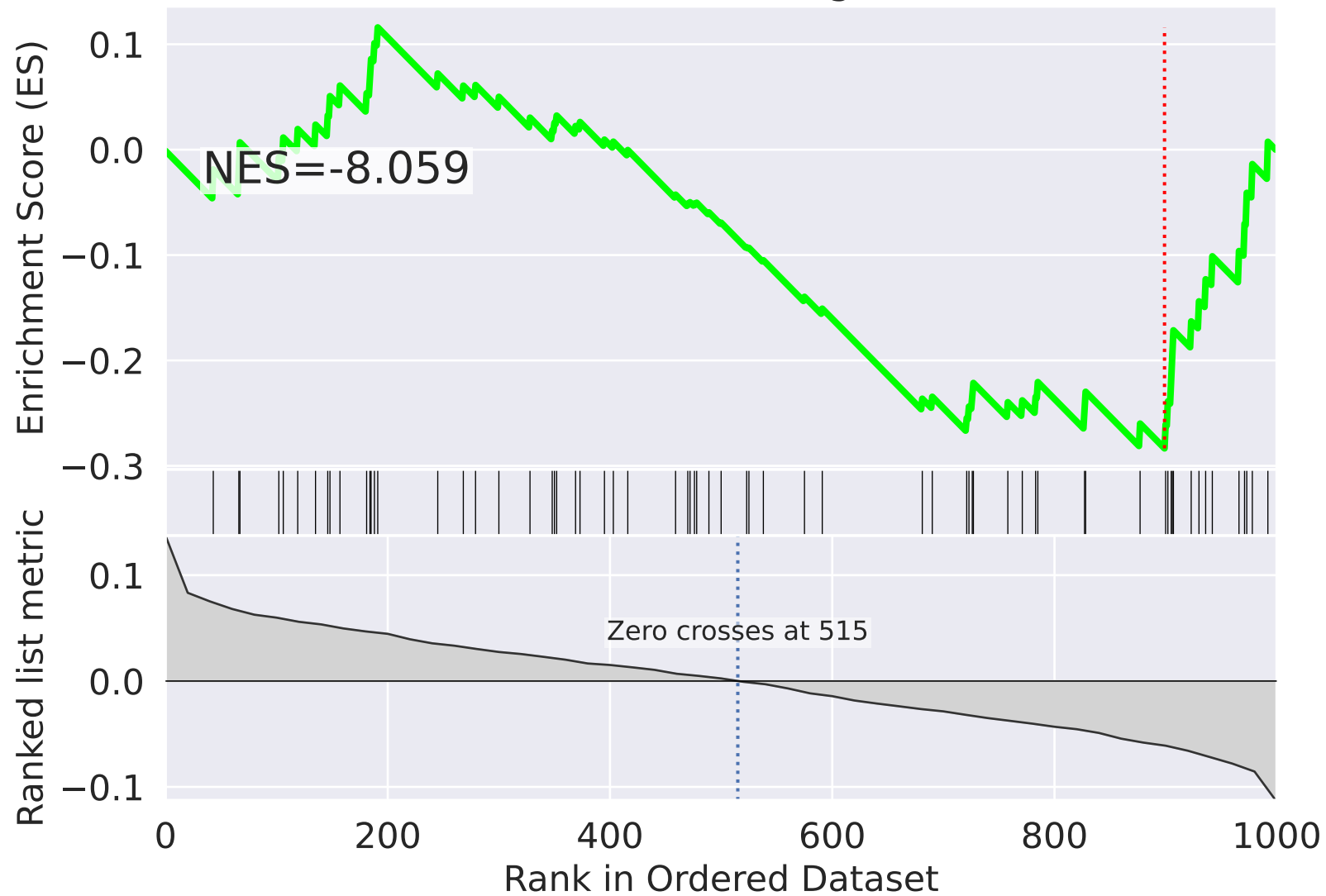
mitochondrial translational elongation (GO:0070125)



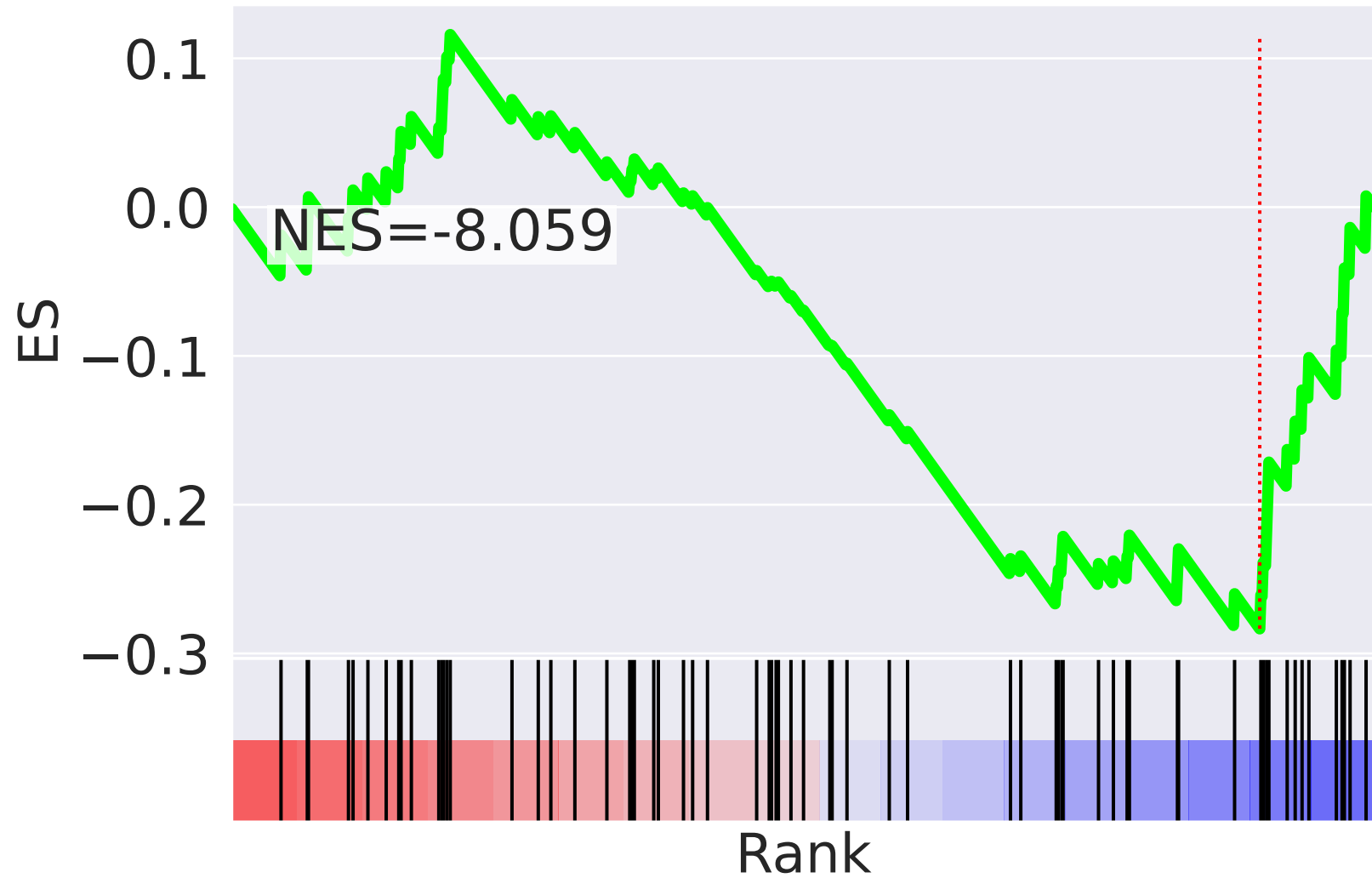
NES		SET
-2.599		retrograde transport, endosome to Golgi (GO:0042147)
2.523		gluconeogenesis (GO:0006094)
-2.427		cellular nitrogen compound metabolic process (GO:0034641)
2.298		positive regulation of viral genome replication (GO:0045070)
2.127		canonical glycolysis (GO:0061621)
-2.080		oxidation-reduction process (GO:0055114)
1.968		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
1.923		vesicle-mediated transport (GO:0016192)
1.908		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
1.838		cellular response to epidermal growth factor stimulus (GO:0071364)
1.804		mitotic metaphase plate congression (GO:0007080)
-1.770		generation of precursor metabolites and energy (GO:0006091)
1.732		T cell costimulation (GO:0031295)
1.723		protein autophosphorylation (GO:0046777)
1.720		intrinsic apoptotic signaling pathway (GO:0097193)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=66$

mitochondrial translational elongation (GO:0070125)

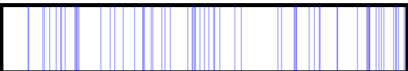
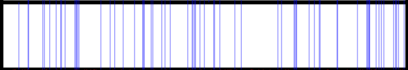
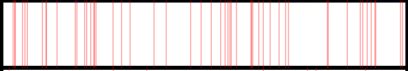

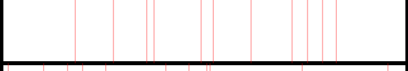
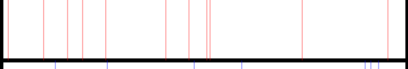
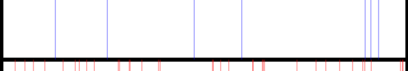
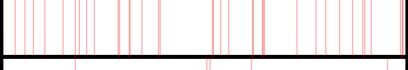

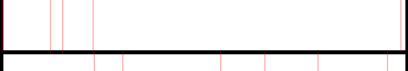

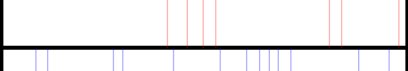





mitochondrial translational elongation (GO:0070125)



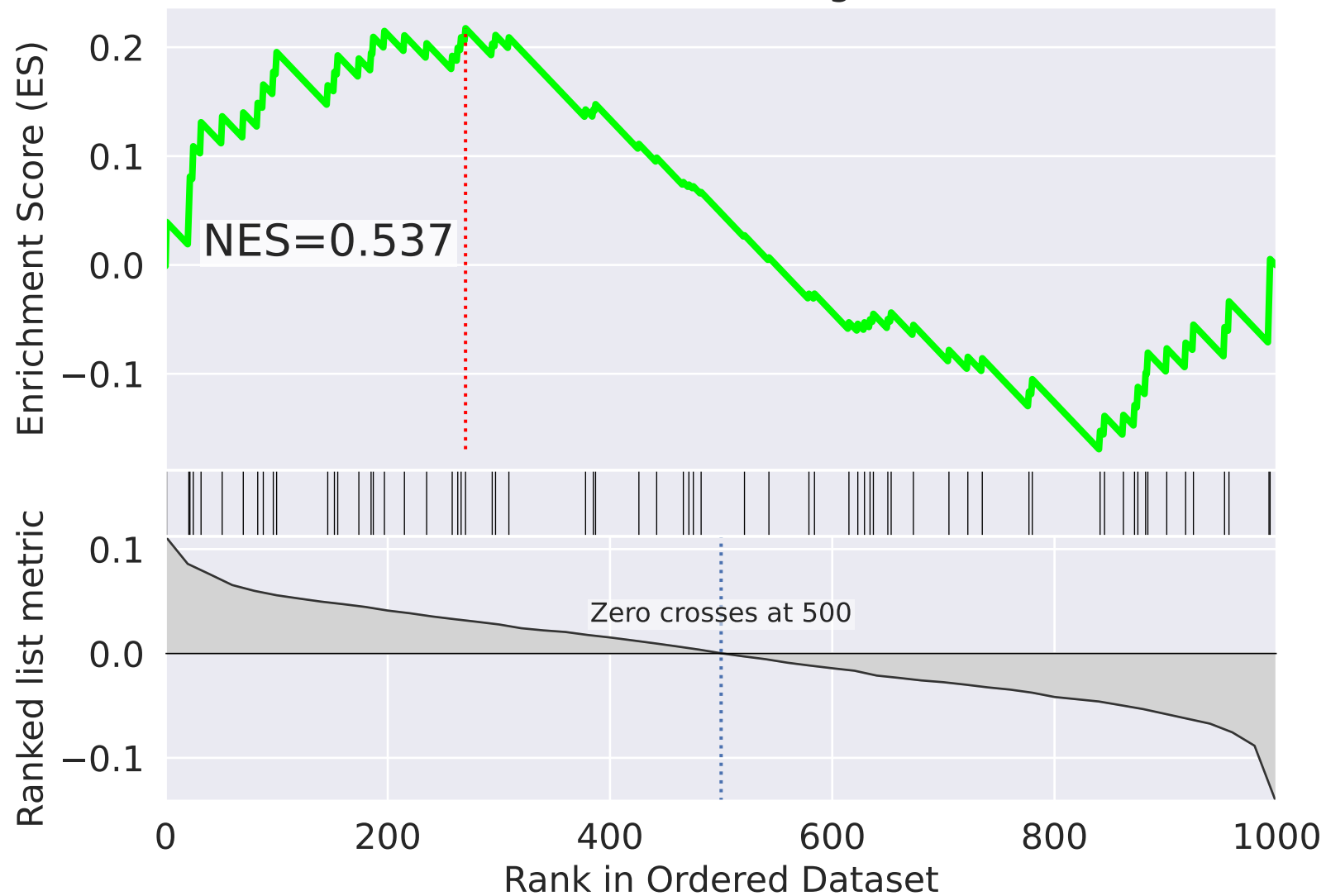
NES

SET

-8.222		mitochondrial translational termination (GO:0070126)
-8.059		mitochondrial translational elongation (GO:0070125)
3.348		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.440		regulation of protein stability (GO:0031647)
2.341		positive regulation of gene expression (GO:0010628)
2.247		regulation of mRNA stability (GO:0043488)
-2.106		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.082		regulation of transcription from RNA polymerase II promoter (GO:0006357)
1.996		cellular response to tumor necrosis factor (GO:0071356)
1.978		cytokinesis (GO:0000910)
1.977		cell differentiation (GO:0030154)
1.967		termination of RNA polymerase II transcription (GO:0006369)
-1.945		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-1.939		aerobic respiration (GO:0009060)
-1.889		membrane organization (GO:0061024)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=67$

mitochondrial translational elongation (GO:0070125)



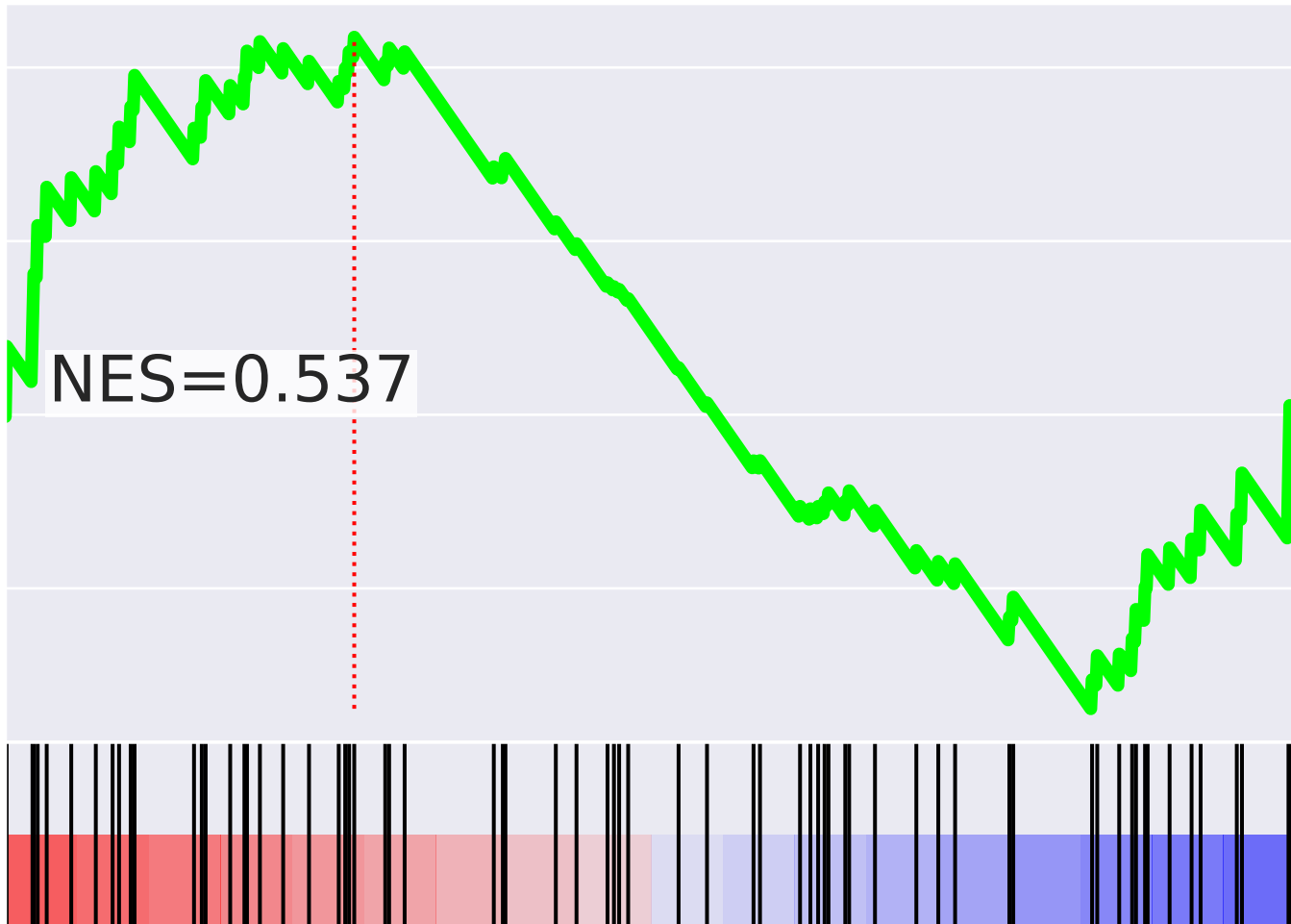
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1



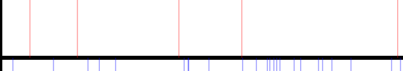
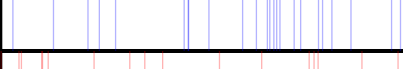

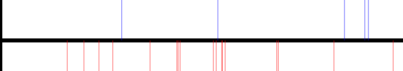
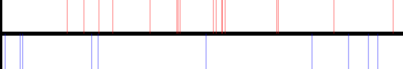



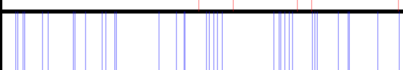
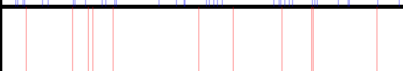



NES=0.537

Rank



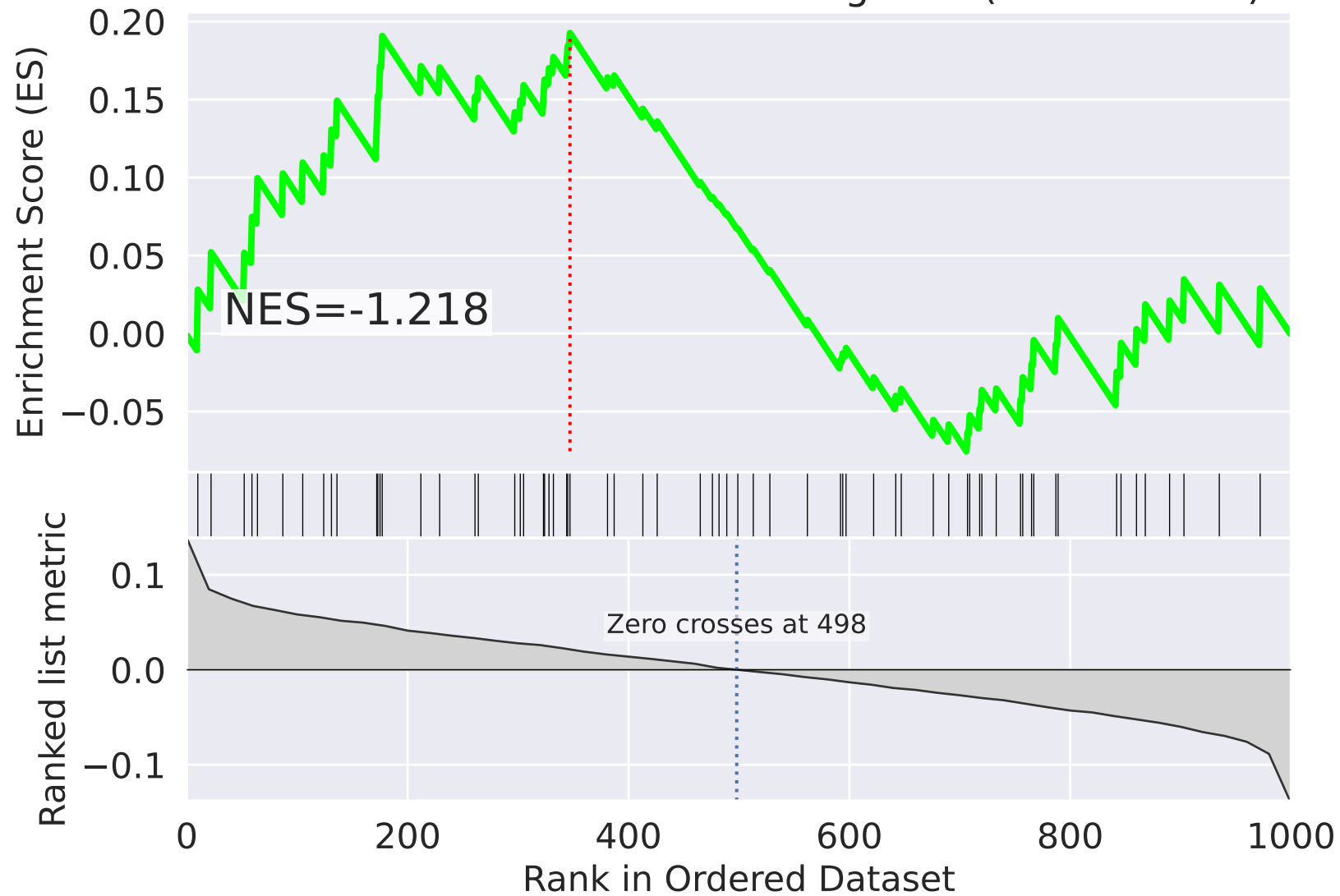
NES

SET

-3.139		chromatin remodeling (GO:0006338)
2.632		intracellular signal transduction (GO:0035556)
2.547		cholesterol biosynthetic process (GO:0006695)
-2.499		regulation of transcription, DNA-templated (GO:0006355)
2.465		mitochondrion organization (GO:0007005)
-2.404		cytokinesis (GO:0000910)
2.319		G2/M transition of mitotic cell cycle (GO:0000086)
-2.288		double-strand break repair via homologous recombination (GO:0000724)
-2.116		nervous system development (GO:0007399)
2.086		peptidyl-serine phosphorylation (GO:0018105)
2.082		platelet activation (GO:0030168)
-2.079		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.063		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.037		protein deubiquitination (GO:0016579)
2.035		substrate adhesion-dependent cell spreading (GO:0034446)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=68$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.20
0.15
0.10
0.05
0.00
-0.05

NES=-1.218

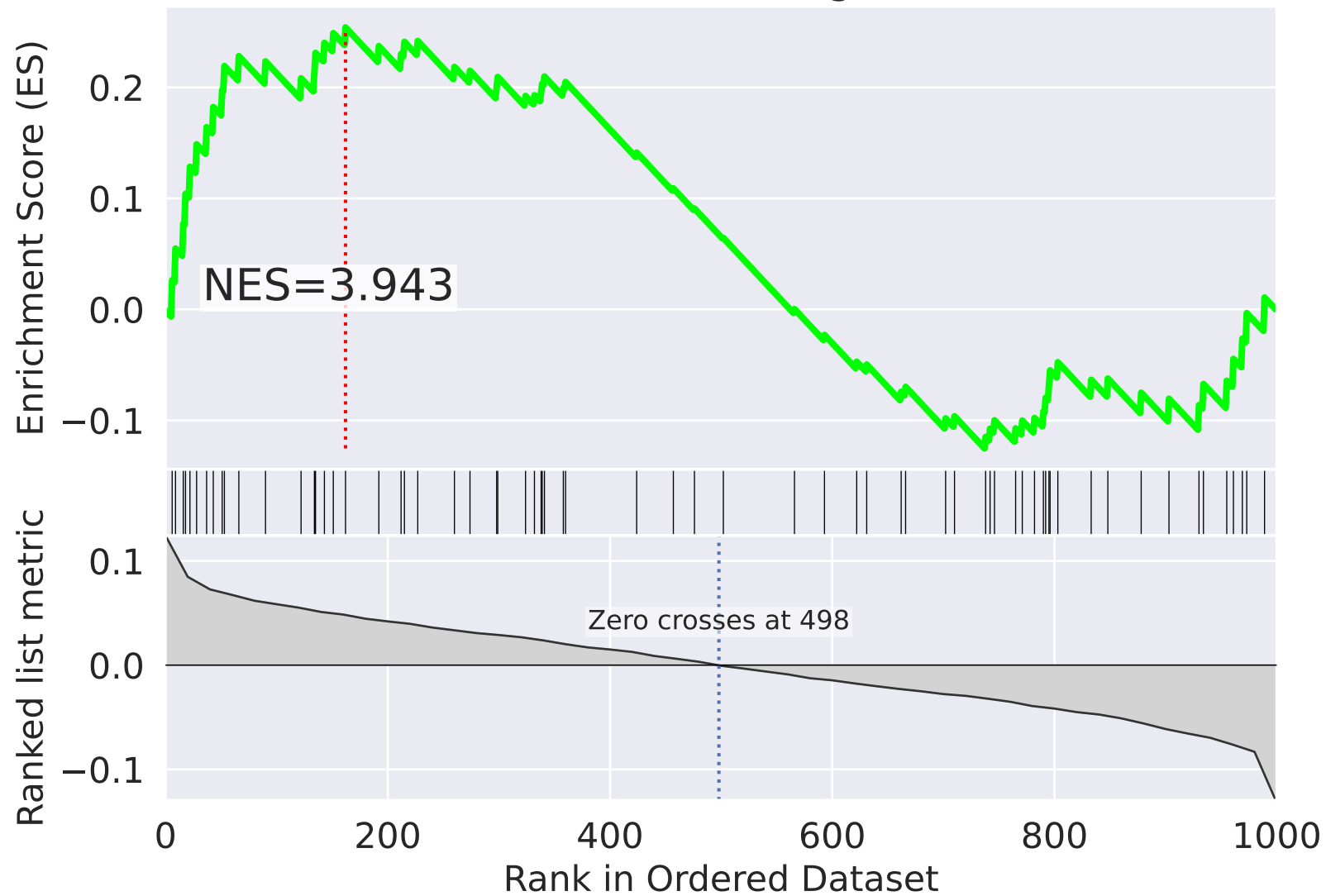
Rank



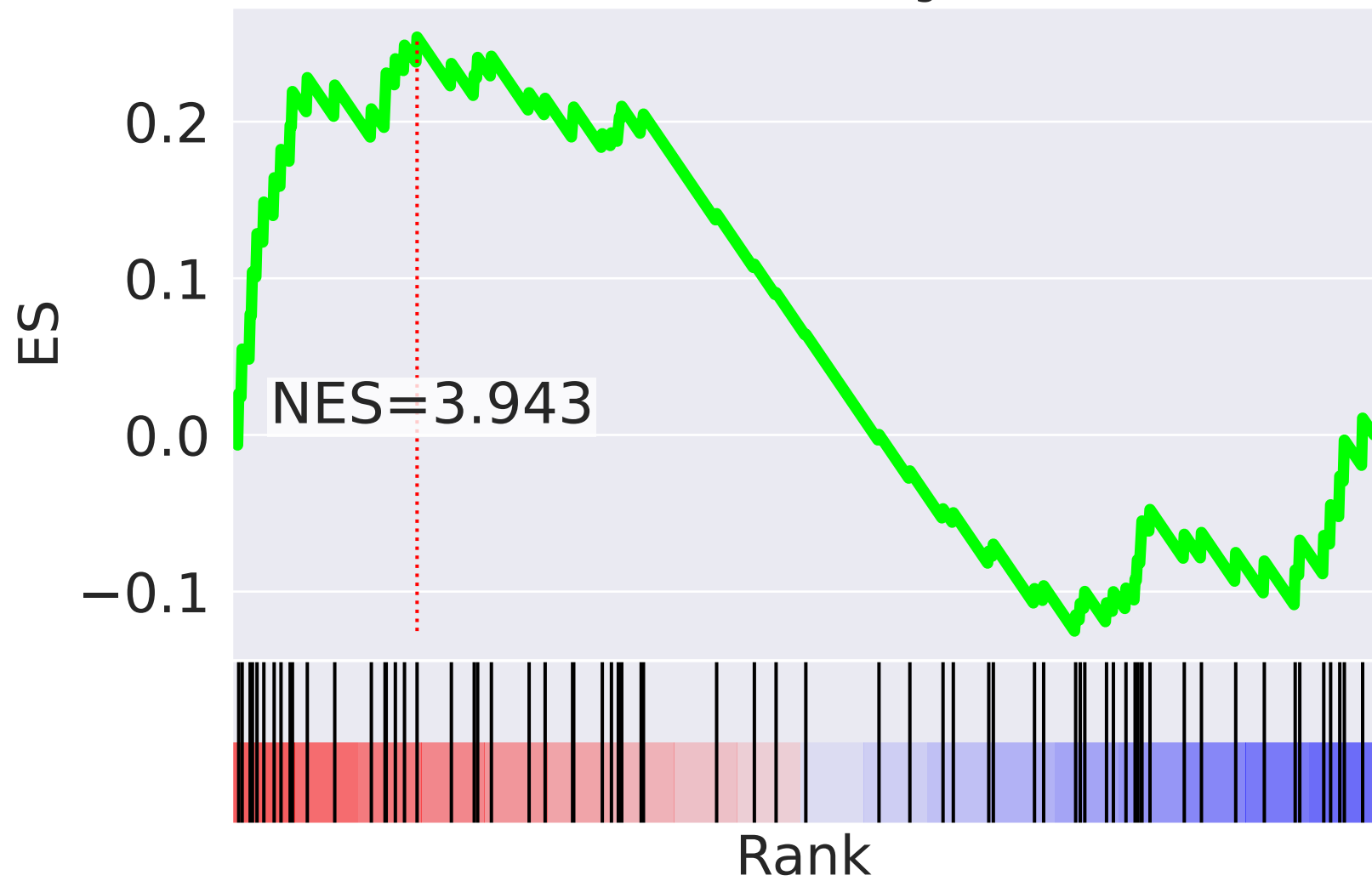
NES		SET
2.503		phosphatidylinositol-mediated signaling (GO:0048015)
-2.365		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
2.222		canonical glycolysis (GO:0061621)
2.213		ephrin receptor signaling pathway (GO:0048013)
-2.145		ciliary basal body docking (GO:0097711)
2.118		protein K11-linked ubiquitination (GO:0070979)
-2.058		regulation of transcription, DNA-templated (GO:0006355)
-2.021		regulation of DNA replication (GO:0006275)
-1.967		regulation of protein stability (GO:0031647)
1.946		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-1.897		tRNA aminoacylation for protein translation (GO:0006418)
1.876		blood coagulation (GO:0007596)
1.866		positive regulation of apoptotic process (GO:0043065)
-1.820		double-strand break repair via nonhomologous end joining (GO:0006303)
1.809		cell differentiation (GO:0030154)






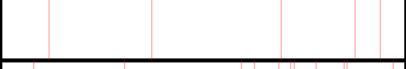

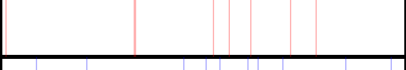


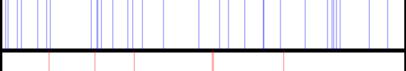

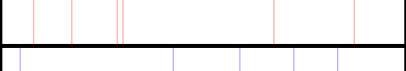

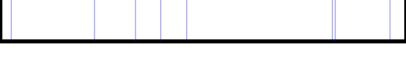
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=69$

mitochondrial translational elongation (GO:0070125)



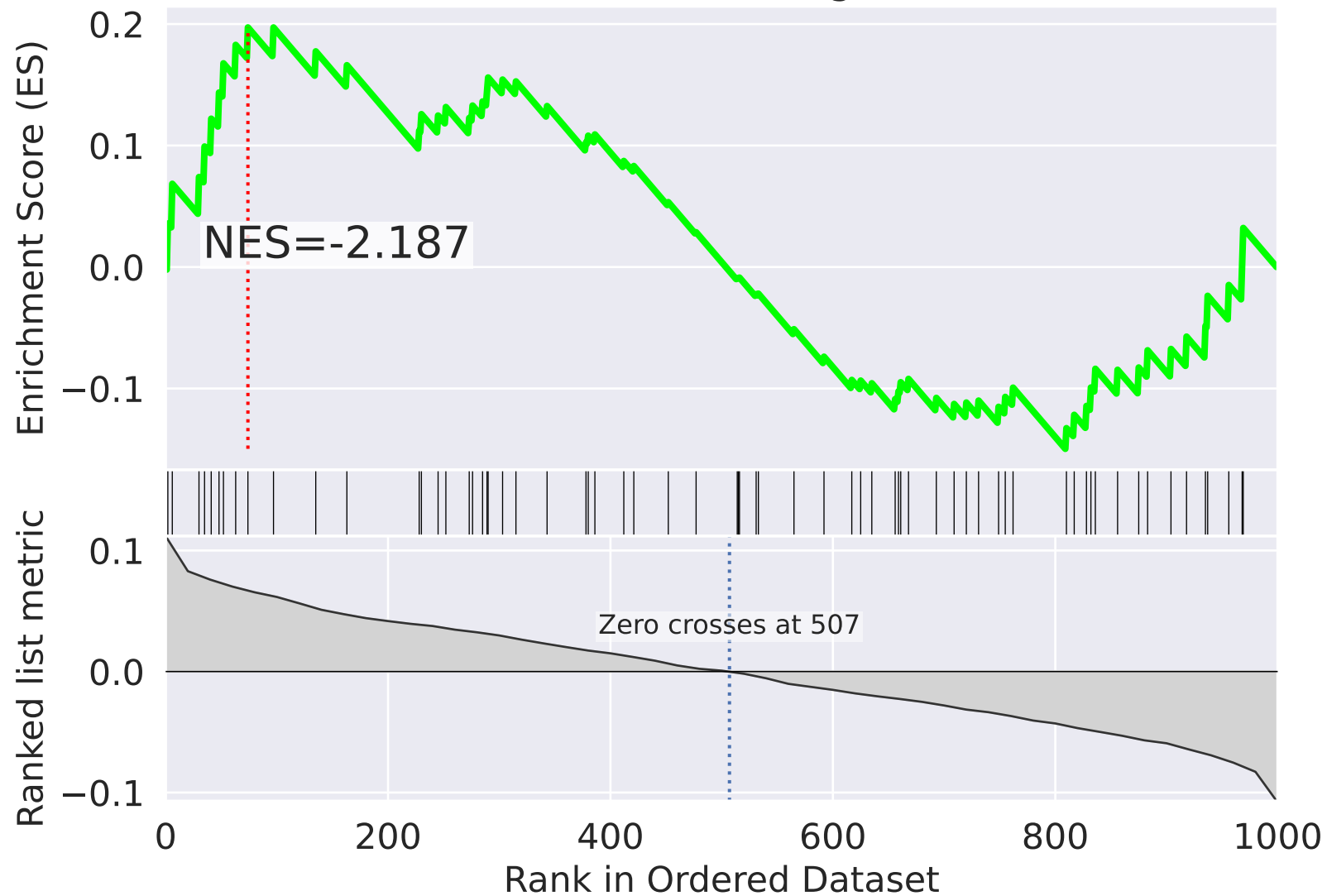
mitochondrial translational elongation (GO:0070125)



NES		SET
4.155		mitochondrial translational termination (GO:0070126)
3.943		mitochondrial translational elongation (GO:0070125)
2.887		positive regulation of cell migration (GO:0030335)
2.670		positive regulation of DNA replication (GO:0045740)
-2.592		strand displacement (GO:0000732)
2.512		RNA secondary structure unwinding (GO:0010501)
2.441		regulation of mRNA stability (GO:0043488)
2.396		cellular response to epidermal growth factor stimulus (GO:0071364)
-2.174		retrograde transport, endosome to Golgi (GO:0042147)
-2.102		cellular response to DNA damage stimulus (GO:0006974)
-2.056		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.021		positive regulation of cell growth (GO:0030307)
1.929		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-1.929		cytokinesis (GO:0000910)
-1.918		regulation of apoptotic process (GO:0042981)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=70$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1

0.0

-0.1

NES=-2.187

Rank



NES		SET
2.893		protein autophosphorylation (GO:0046777)
2.733		positive regulation of DNA replication (GO:0045740)
-2.461		negative regulation of cell proliferation (GO:0008285)
2.434		cellular response to epidermal growth factor stimulus (GO:0071364)
2.340		positive regulation of cell migration (GO:0030335)
-2.307		tRNA aminoacylation for protein translation (GO:0006418)
2.281		cellular response to tumor necrosis factor (GO:0071356)
2.272		positive regulation of protein phosphorylation (GO:0001934)
2.206		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-2.200		protein deubiquitination (GO:0016579)
2.195		negative regulation of apoptotic process (GO:0043066)
-2.187		mitochondrial translational elongation (GO:0070125)
-2.155		RNA splicing (GO:0008380)
2.130		nucleotide-excision repair (GO:0006289)
2.082		epidermal growth factor receptor signaling pathway (GO:0007173)