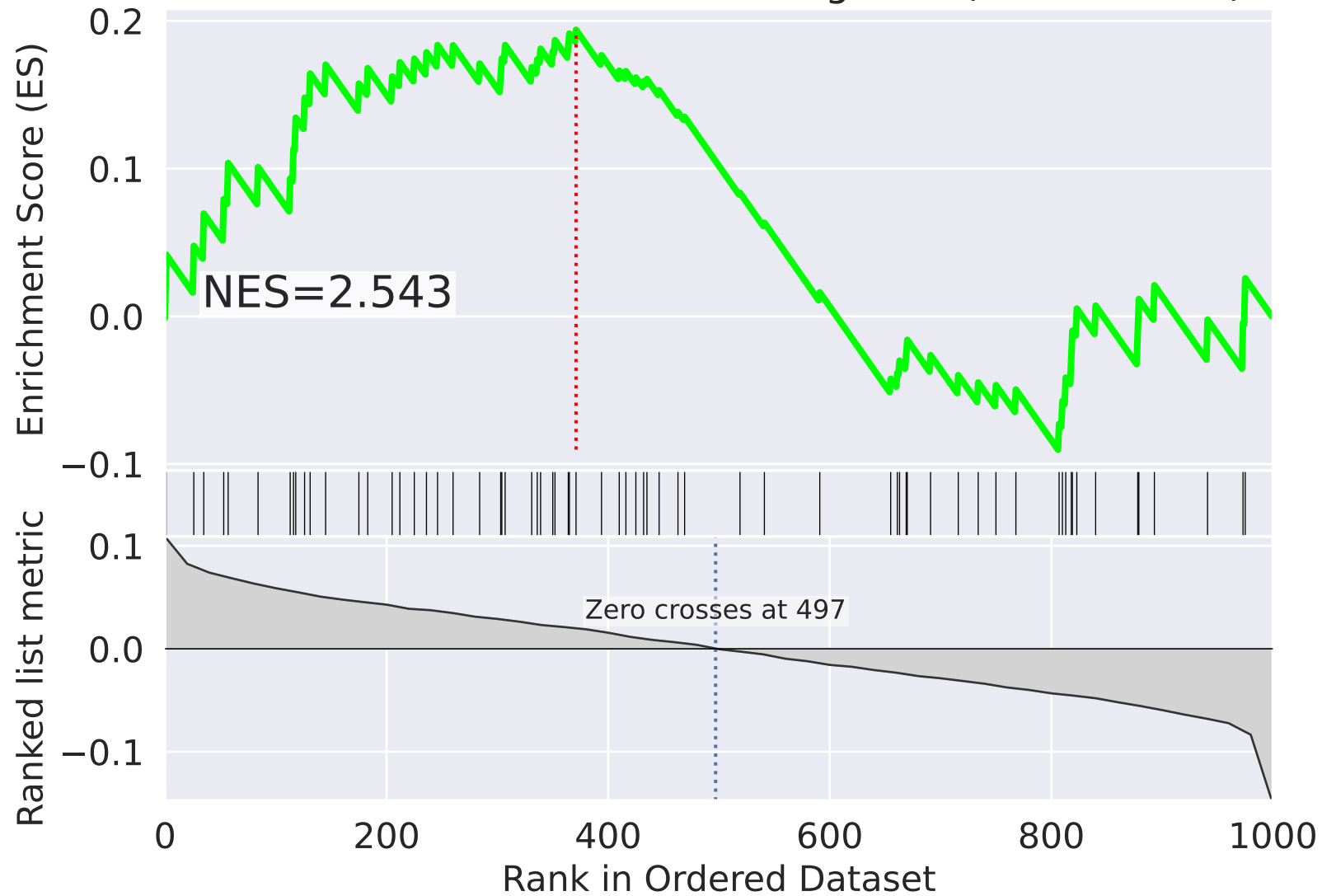
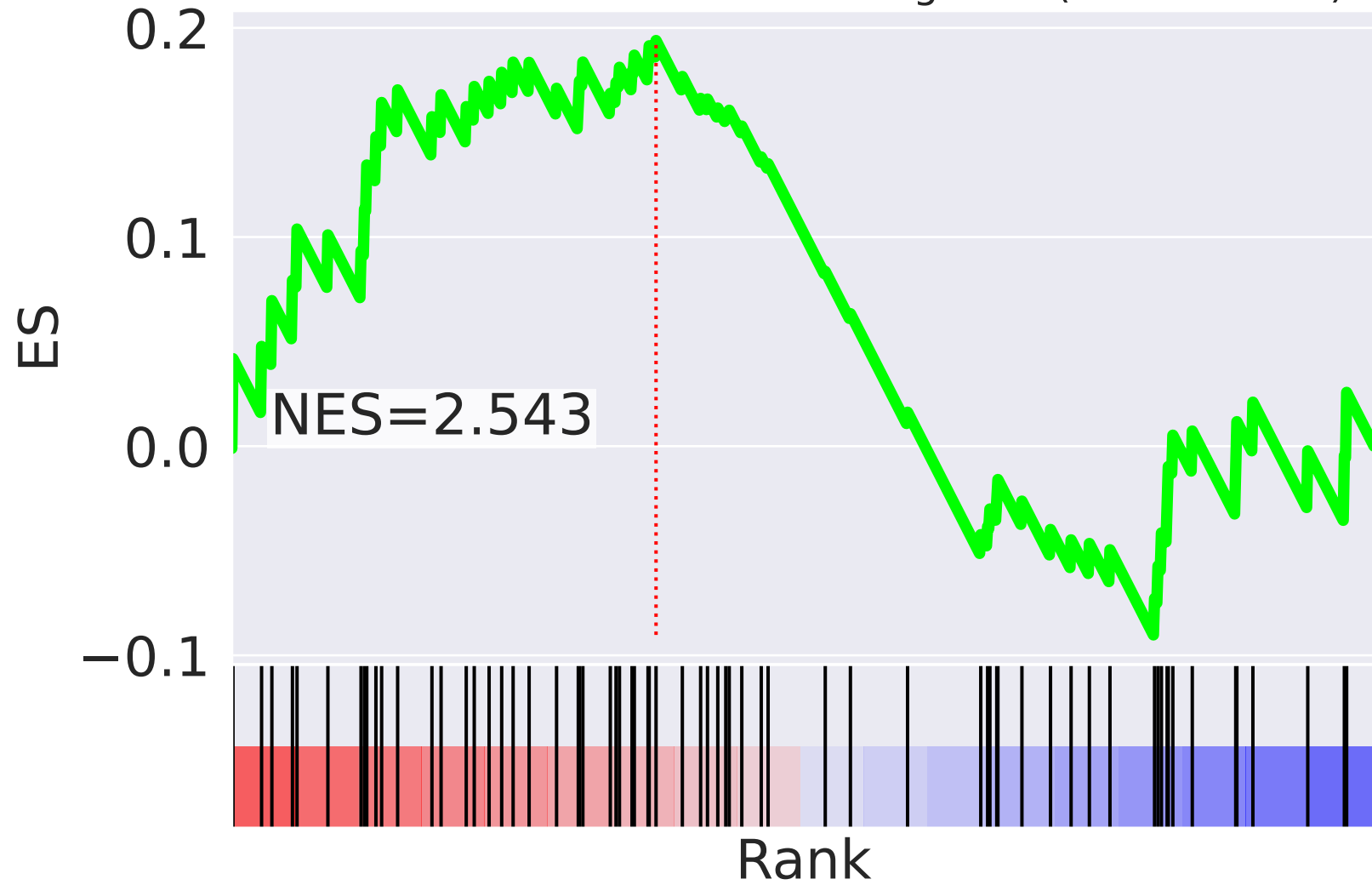


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=1$

mitochondrial translational elongation (GO:0070125)



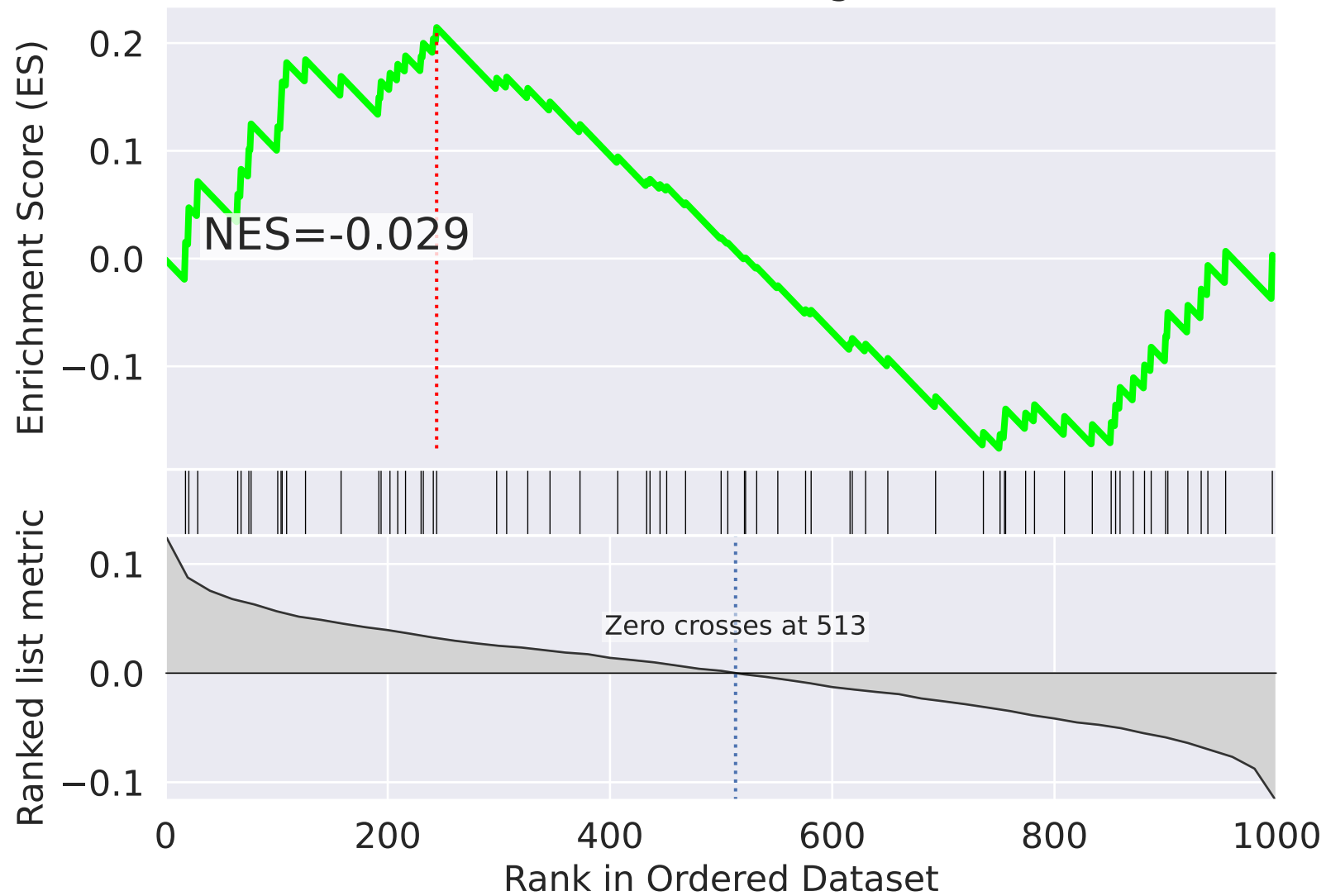
mitochondrial translational elongation (GO:0070125)



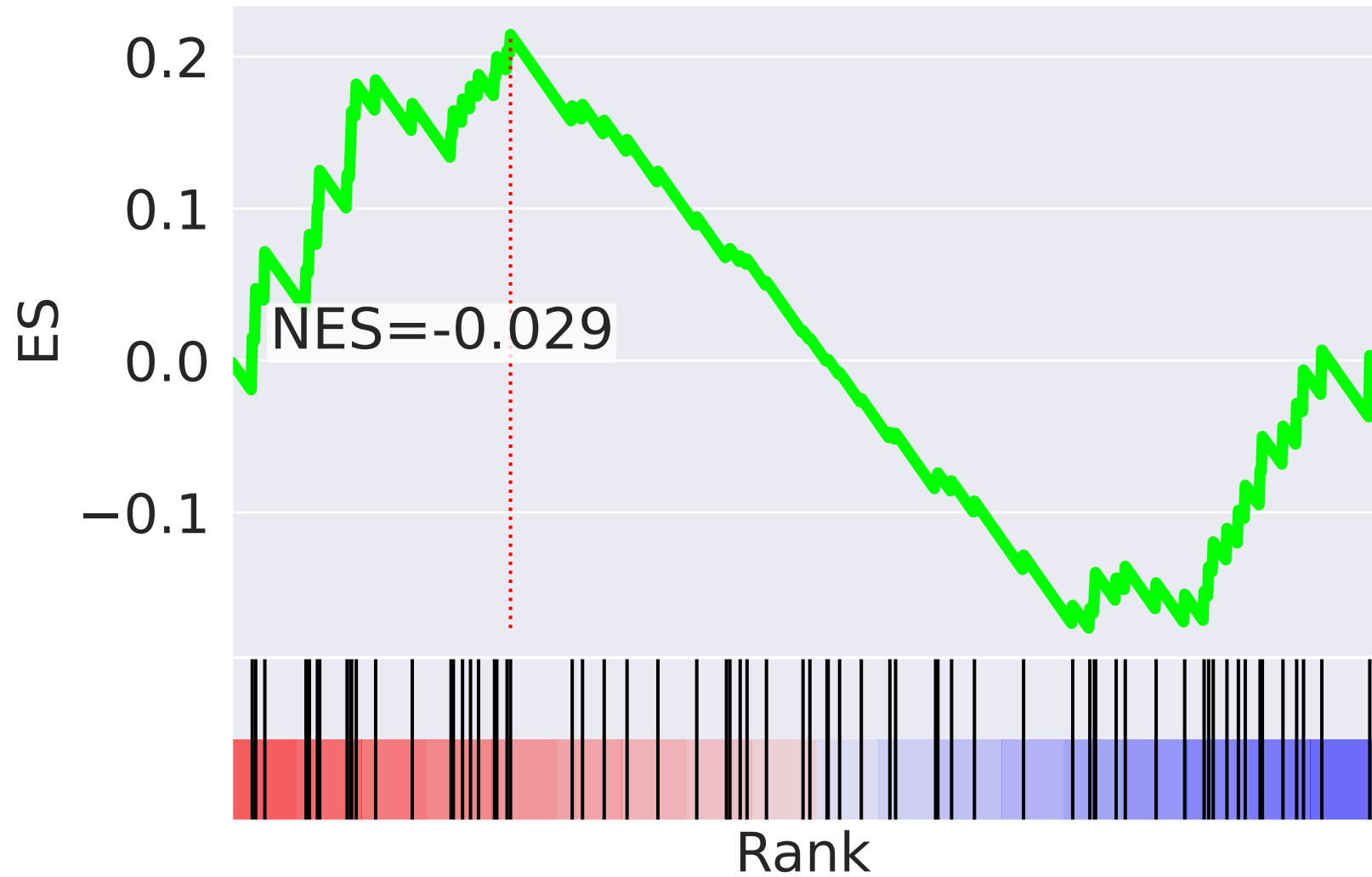
NES		SET
2.543		mitochondrial translational elongation (GO:0070125)
-2.396		mitochondrial translational termination (GO:0070126)
2.264		RNA splicing (GO:0008380)
2.257		protein autophosphorylation (GO:0046777)
-2.242		protein ubiquitination (GO:0016567)
2.176		response to virus (GO:0009615)
2.071		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.028		regulation of macroautophagy (GO:0016241)
2.009		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
1.990		DNA replication (GO:0006260)
-1.973		cellular response to amino acid stimulus (GO:0071230)
1.922		protein dephosphorylation (GO:0006470)
1.906		RNA secondary structure unwinding (GO:0010501)
-1.901		positive regulation of mitotic cell cycle (GO:0045931)
-1.900		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)




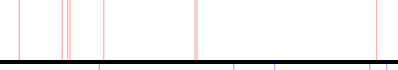







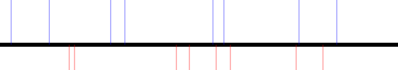
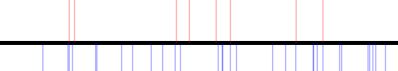
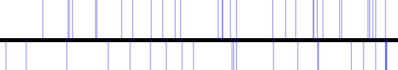

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=2$

mitochondrial translational elongation (GO:0070125)



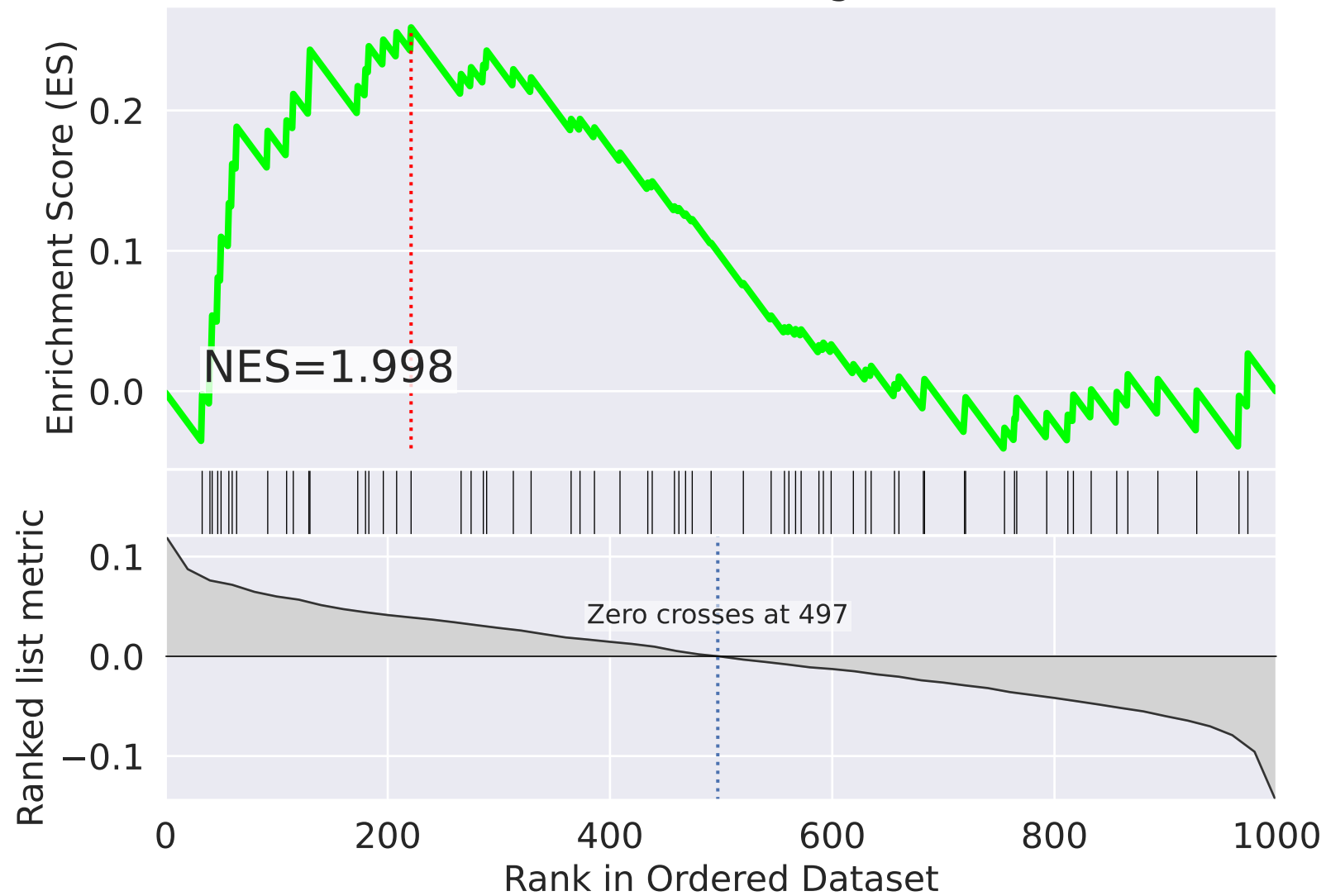
mitochondrial translational elongation (GO:0070125)



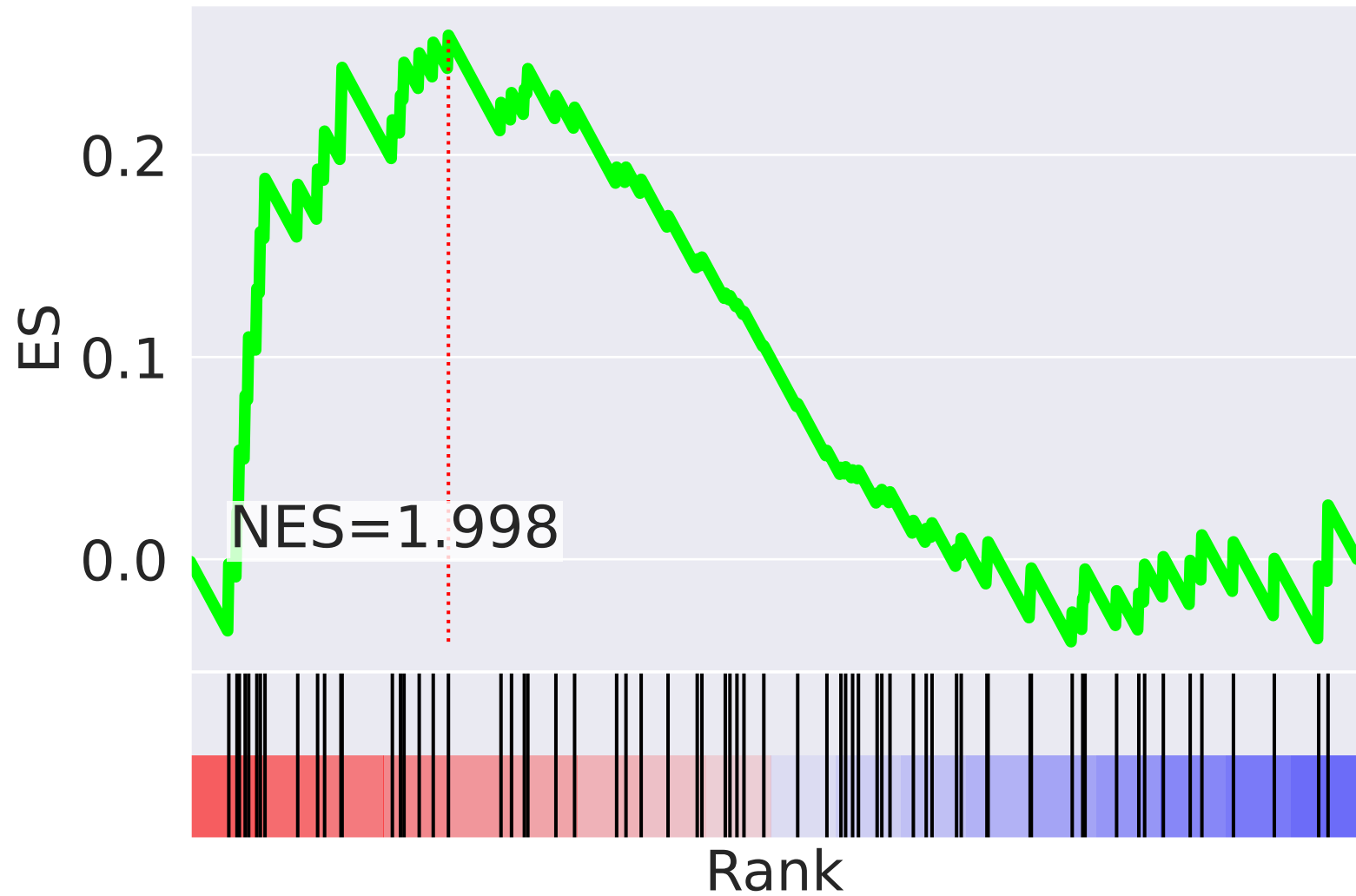
NES		SET
-2.698		innate immune response (GO:0045087)
-2.512		DNA replication (GO:0006260)
-2.463		histone H3 acetylation (GO:0043966)
2.423		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.318		inflammatory response (GO:0006954)
-2.317		telomere capping (GO:0016233)
-2.265		regulation of cell cycle (GO:0051726)
-2.209		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
-2.169		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.153		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-2.152		generation of precursor metabolites and energy (GO:0006091)
-2.135		tricarboxylic acid cycle (GO:0006099)
2.083		regulation of apoptotic process (GO:0042981)
-2.081		protein deubiquitination (GO:0016579)
-2.024		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 $z=3$

mitochondrial translational elongation (GO:0070125)


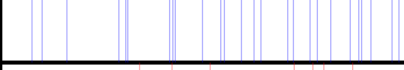

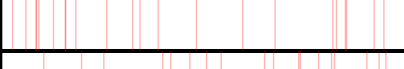


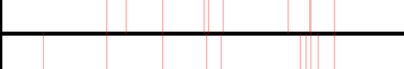
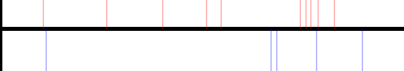

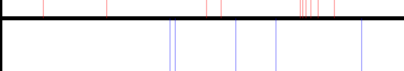
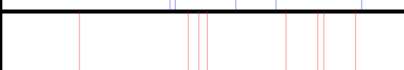


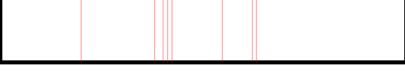



mitochondrial translational elongation (GO:0070125)



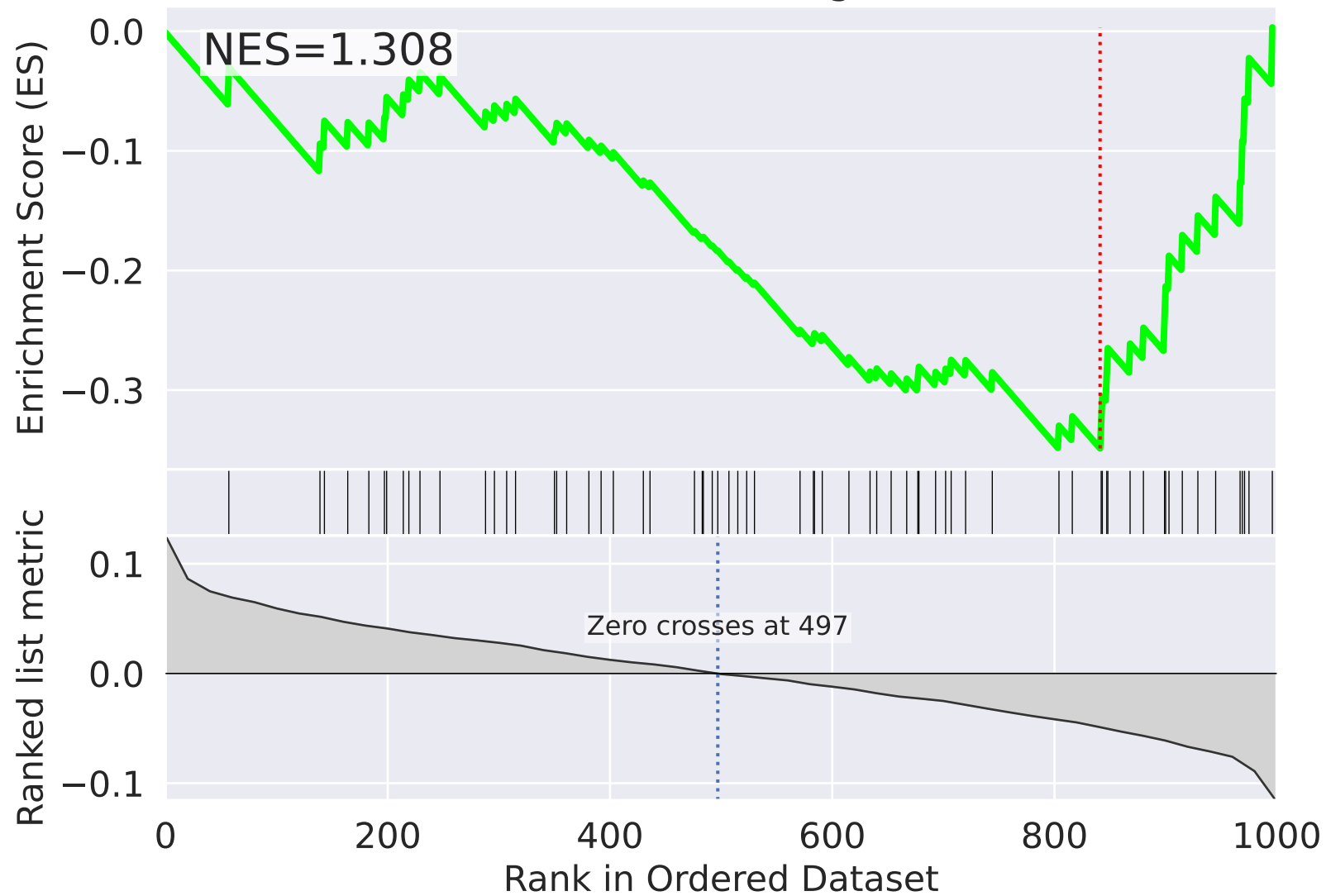
NES

SET

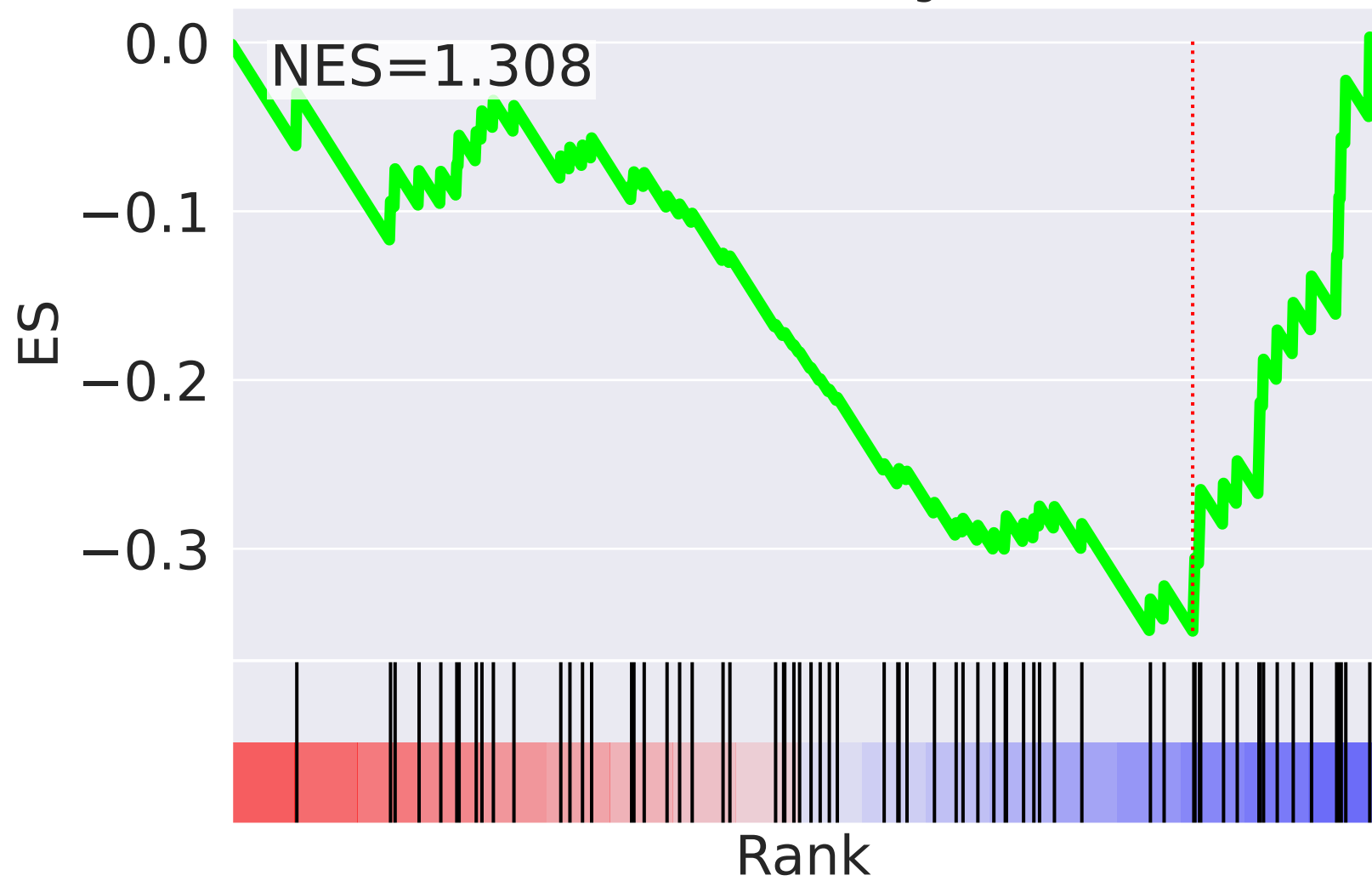
-4.000		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.254		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.658		platelet aggregation (GO:0070527)
2.517		positive regulation of apoptotic process (GO:0043065)
2.513		DNA repair (GO:0006281)
2.356		integrin-mediated signaling pathway (GO:0007229)
2.345		double-strand break repair via nonhomologous end joining (GO:0006303)
2.291		DNA synthesis involved in DNA repair (GO:0000731)
-2.271		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.251		strand displacement (GO:0000732)
-2.184		cellular respiration (GO:0045333)
2.164		multicellular organism development (GO:0007275)
2.113		protein sumoylation (GO:0016925)
-2.048		DNA-dependent DNA replication (GO:0006261)
2.045		IRE1-mediated unfolded protein response (GO:0036498)




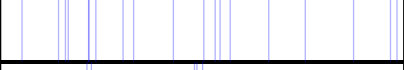

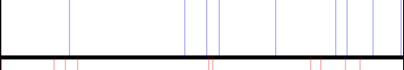


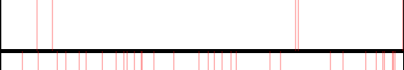
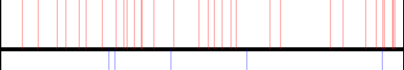

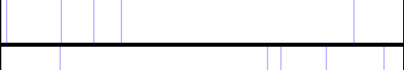
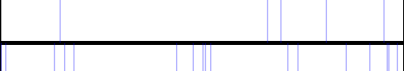
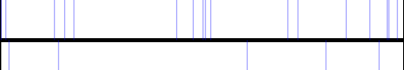
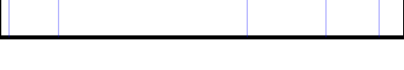
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=4$

mitochondrial translational elongation (GO:0070125)



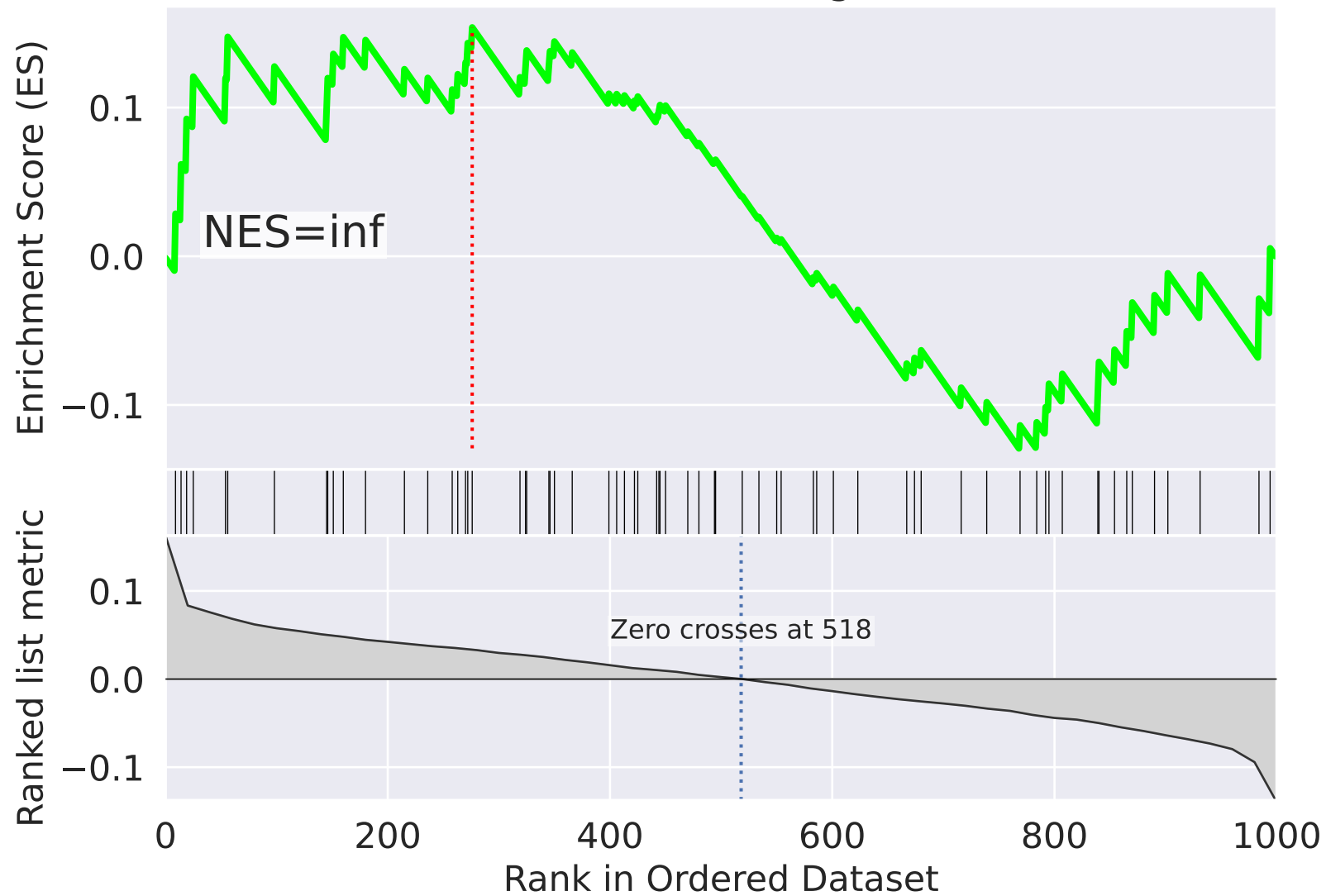
mitochondrial translational elongation (GO:0070125)



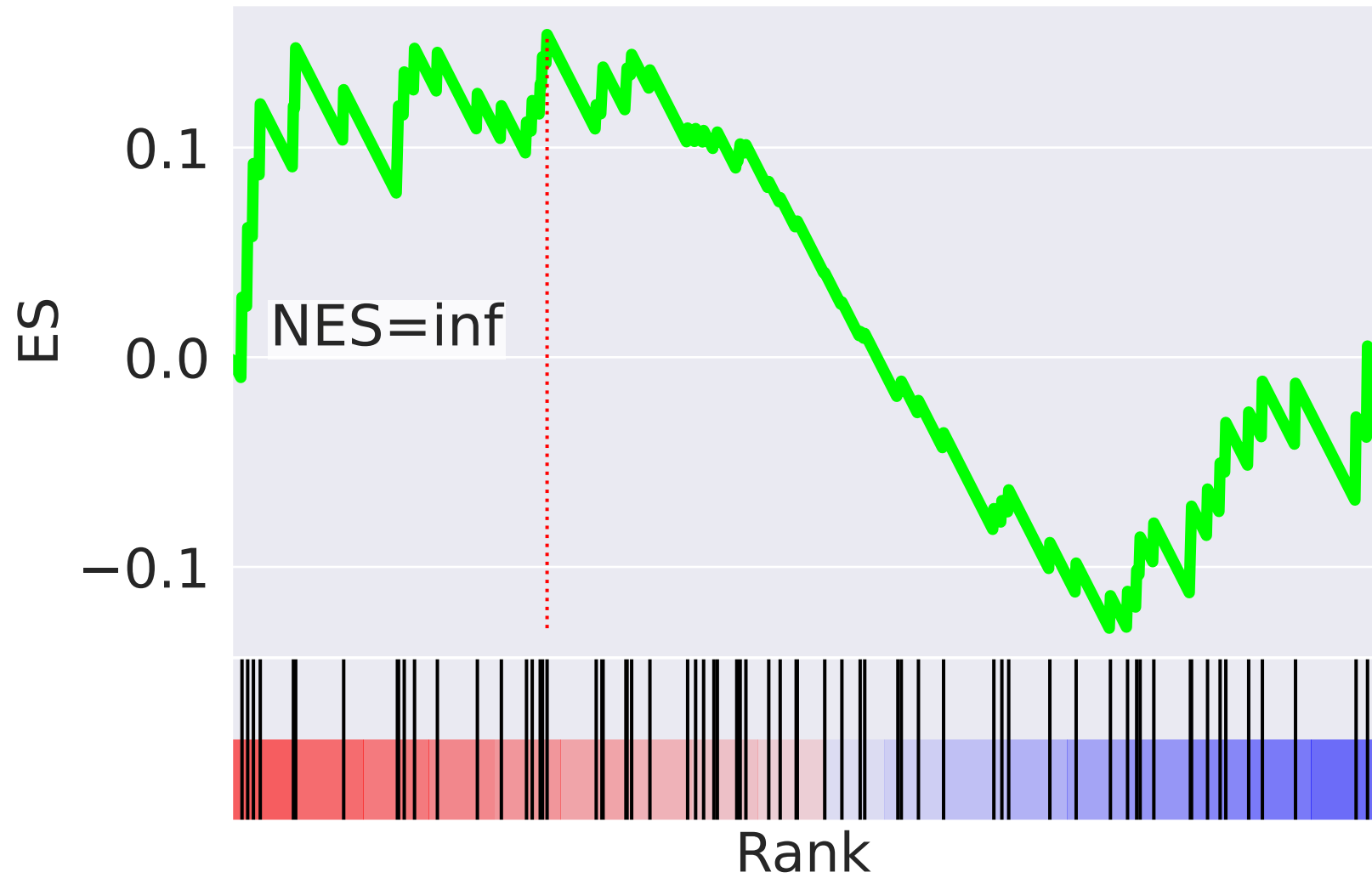
NES		SET
-2.538		RNA secondary structure unwinding (GO:0010501)
-2.454		blood coagulation (GO:0007596)
-2.338		mitochondrion organization (GO:0007005)
-2.297		DNA replication (GO:0006260)
-2.286		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.237		transcription, DNA-templated (GO:0006351)
2.114		Ras protein signal transduction (GO:0007265)
2.109		ERBB2 signaling pathway (GO:0038128)
2.069		post-Golgi vesicle-mediated transport (GO:0006892)
1.987		translation (GO:0006412)
-1.874		cytokinesis (GO:0000910)
-1.797		cellular response to hypoxia (GO:0071456)
-1.795		positive regulation of telomere maintenance via telomerase (GO:0032212)
-1.680		transcription initiation from RNA polymerase II promoter (GO:0006367)
-1.638		positive regulation of protein catabolic process (GO:0045732)

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)

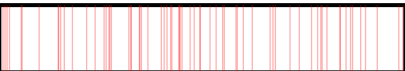



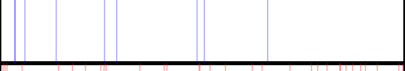
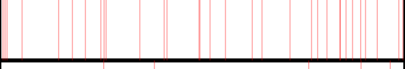






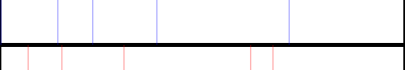
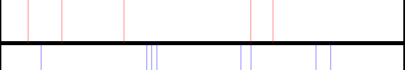
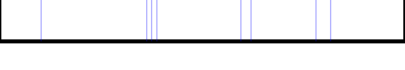


mitochondrial translational elongation (GO:0070125)



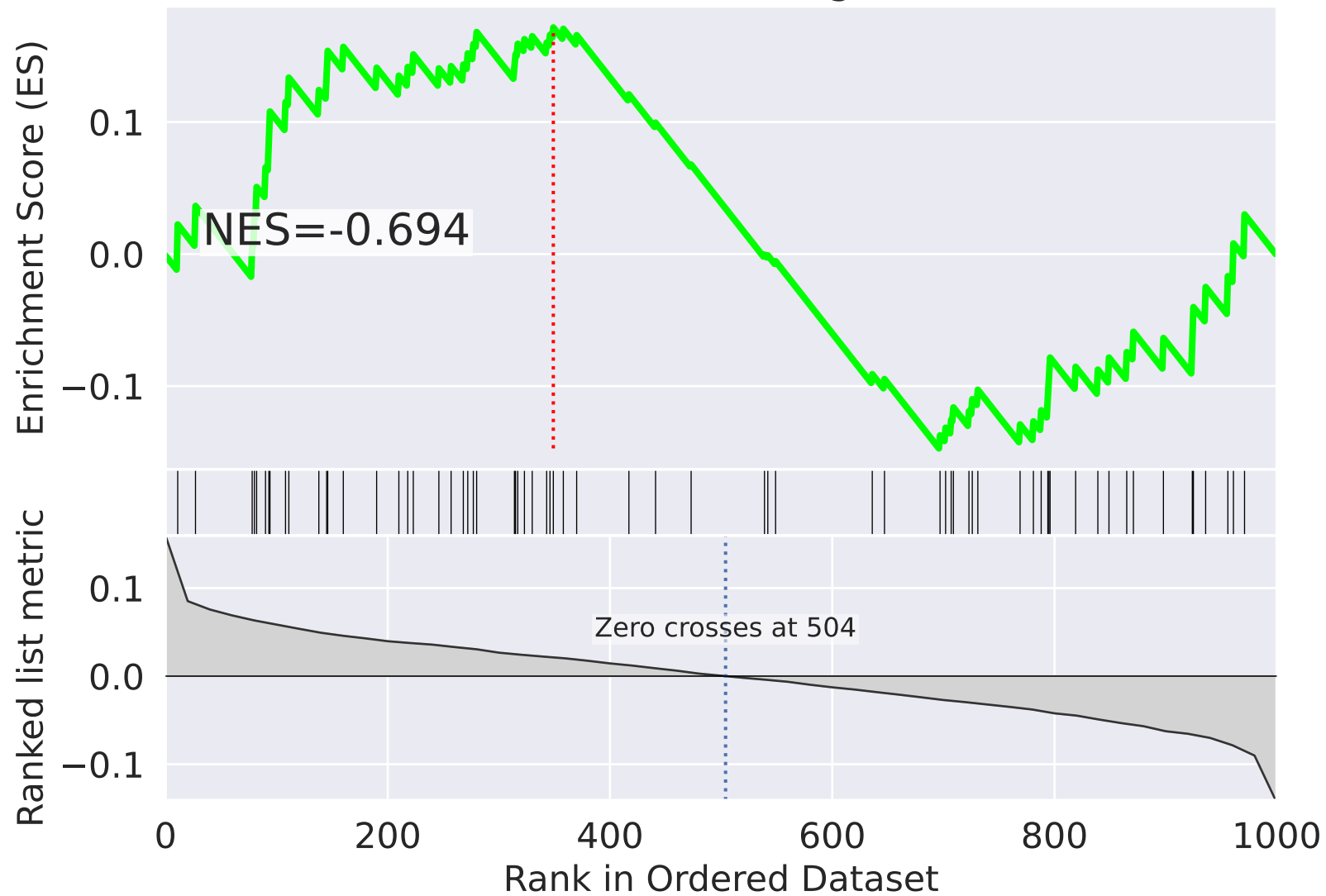
NES

SET

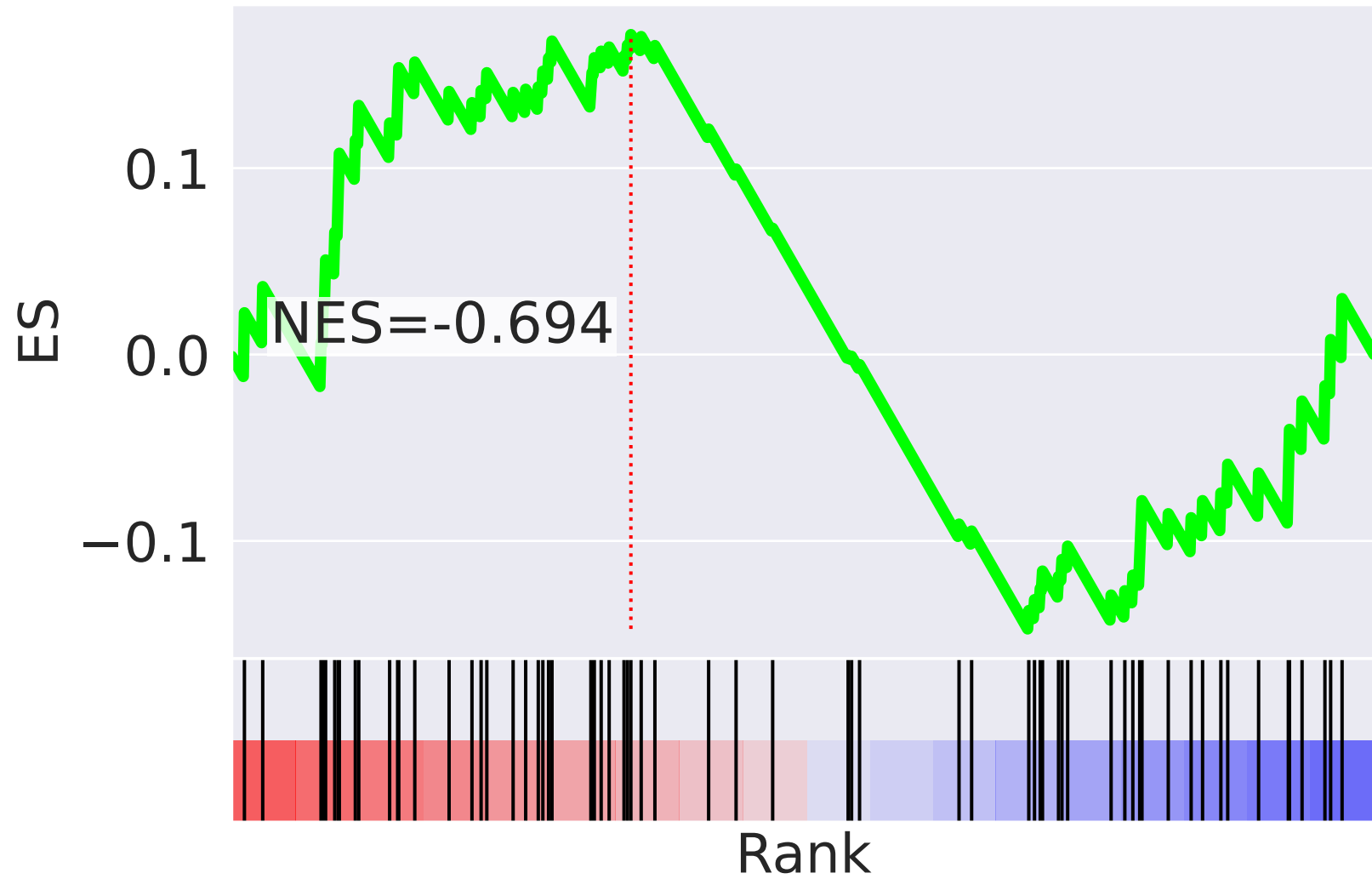
inf		mitochondrial translational elongation (GO:0070125)
inf		mitochondrial translational termination (GO:0070126)
-2.995		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.665		tricarboxylic acid cycle (GO:0006099)
-2.598		movement of cell or subcellular component (GO:0006928)
2.521		translation (GO:0006412)
2.325		positive regulation of GTPase activity (GO:0043547)
2.278		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.276		cellular iron ion homeostasis (GO:0006879)
-2.265		double-strand break repair via homologous recombination (GO:0000724)
-2.247		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.205		strand displacement (GO:0000732)
-2.112		cellular response to tumor necrosis factor (GO:0071356)
2.084		transcription from mitochondrial promoter (GO:0006390)
-2.082		response to ionizing radiation (GO:0010212)

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

mitochondrial translational elongation (GO:0070125)



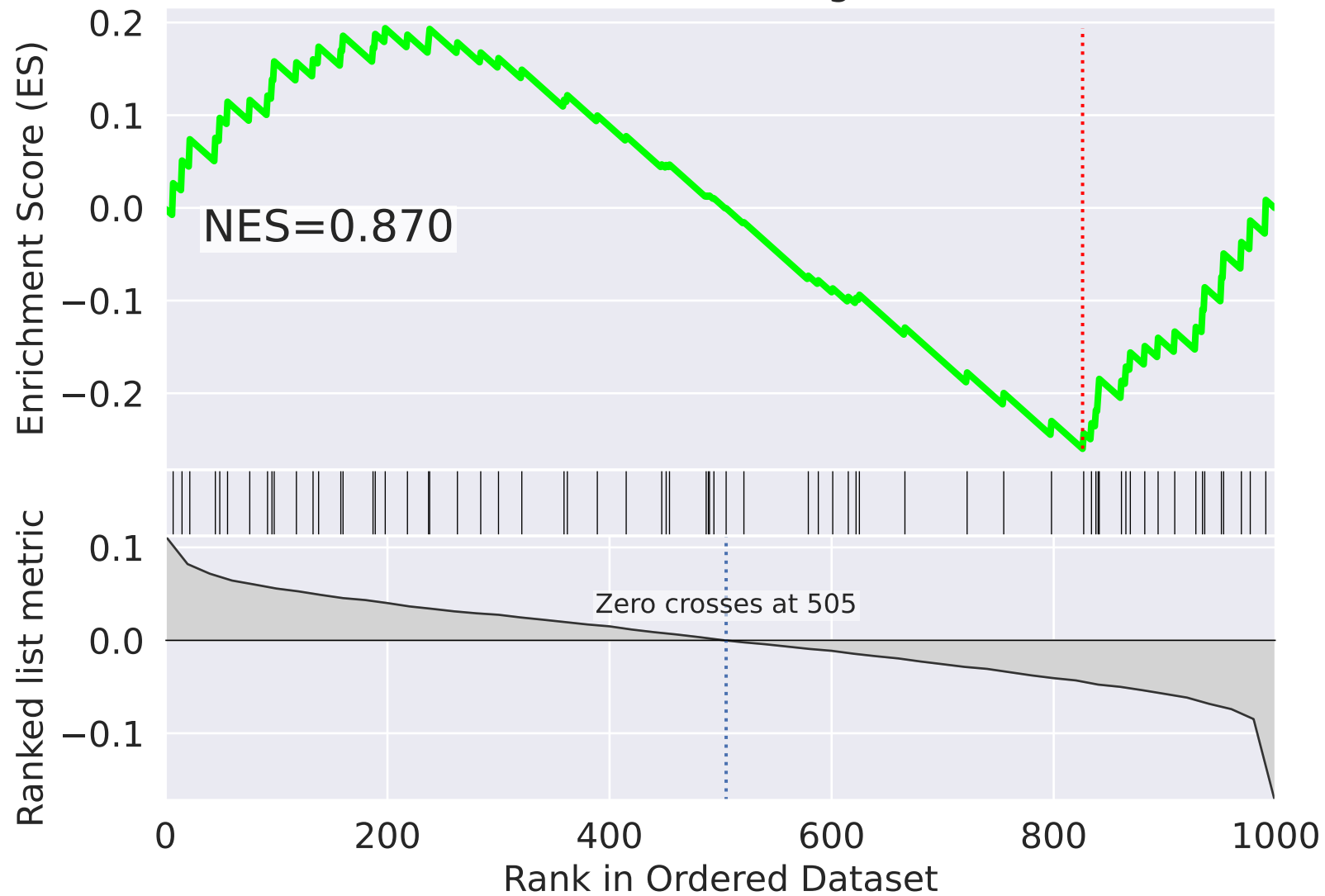
mitochondrial translational elongation (GO:0070125)



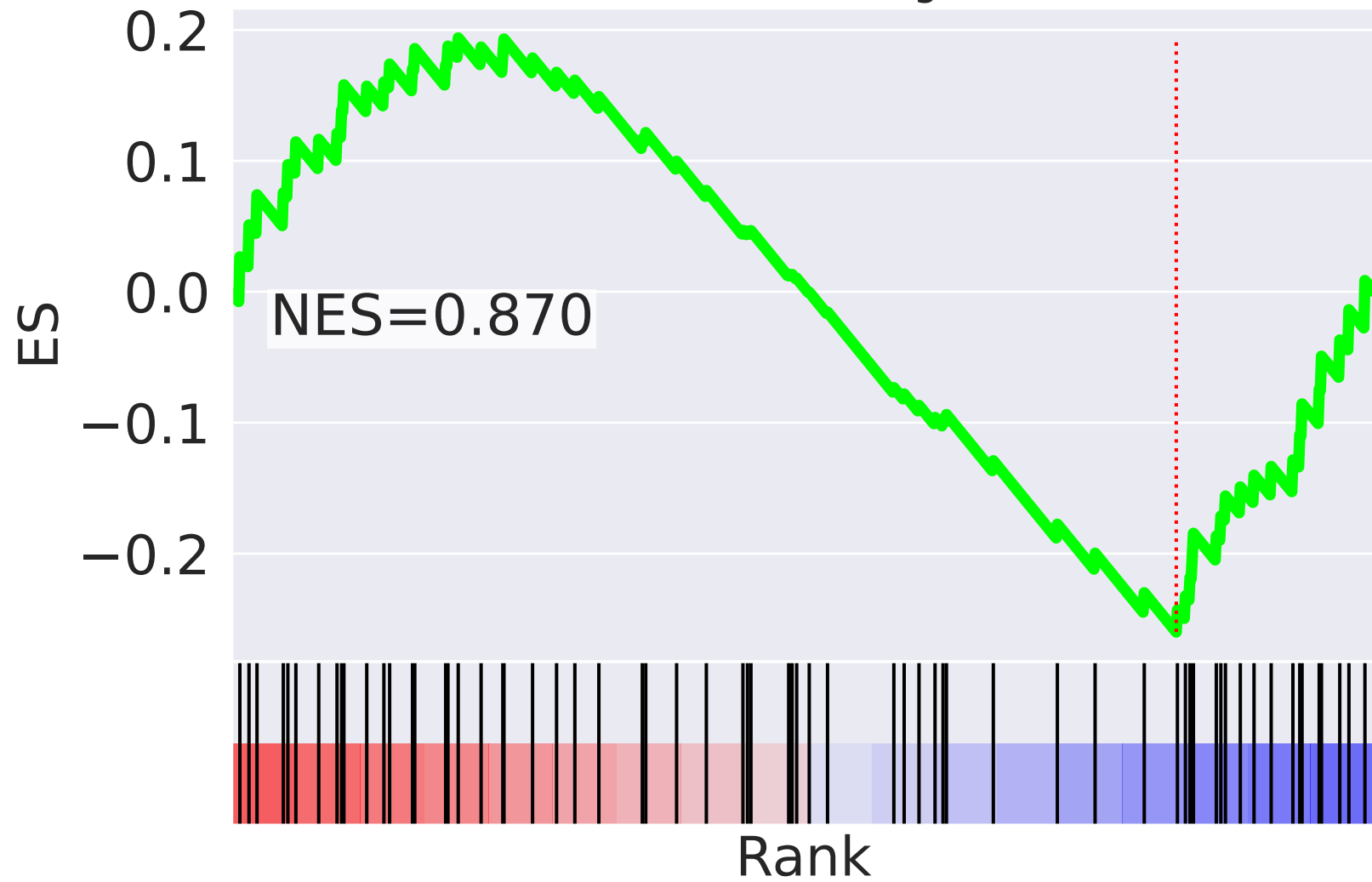
NES		SET
-3.469		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.870		intracellular signal transduction (GO:0035556)
-2.810		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.505		nucleotide-excision repair (GO:0006289)
2.494		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.384		positive regulation of transcription, DNA-templated (GO:0045893)
2.350		neutrophil degranulation (GO:0043312)
2.272		regulation of cell cycle (GO:0051726)
2.248		positive regulation of viral genome replication (GO:0045070)
2.158		tRNA modification (GO:0006400)
2.158		RNA metabolic process (GO:0016070)
2.114		transcription-coupled nucleotide-excision repair (GO:0006283)
2.106		oxidation-reduction process (GO:0055114)
2.049		chromosome segregation (GO:0007059)
1.953		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)

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)



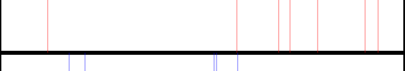
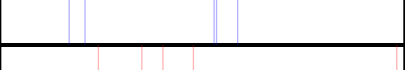


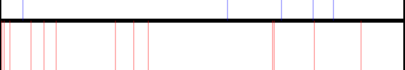



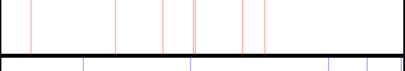

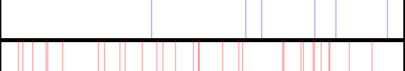




mitochondrial translational elongation (GO:0070125)



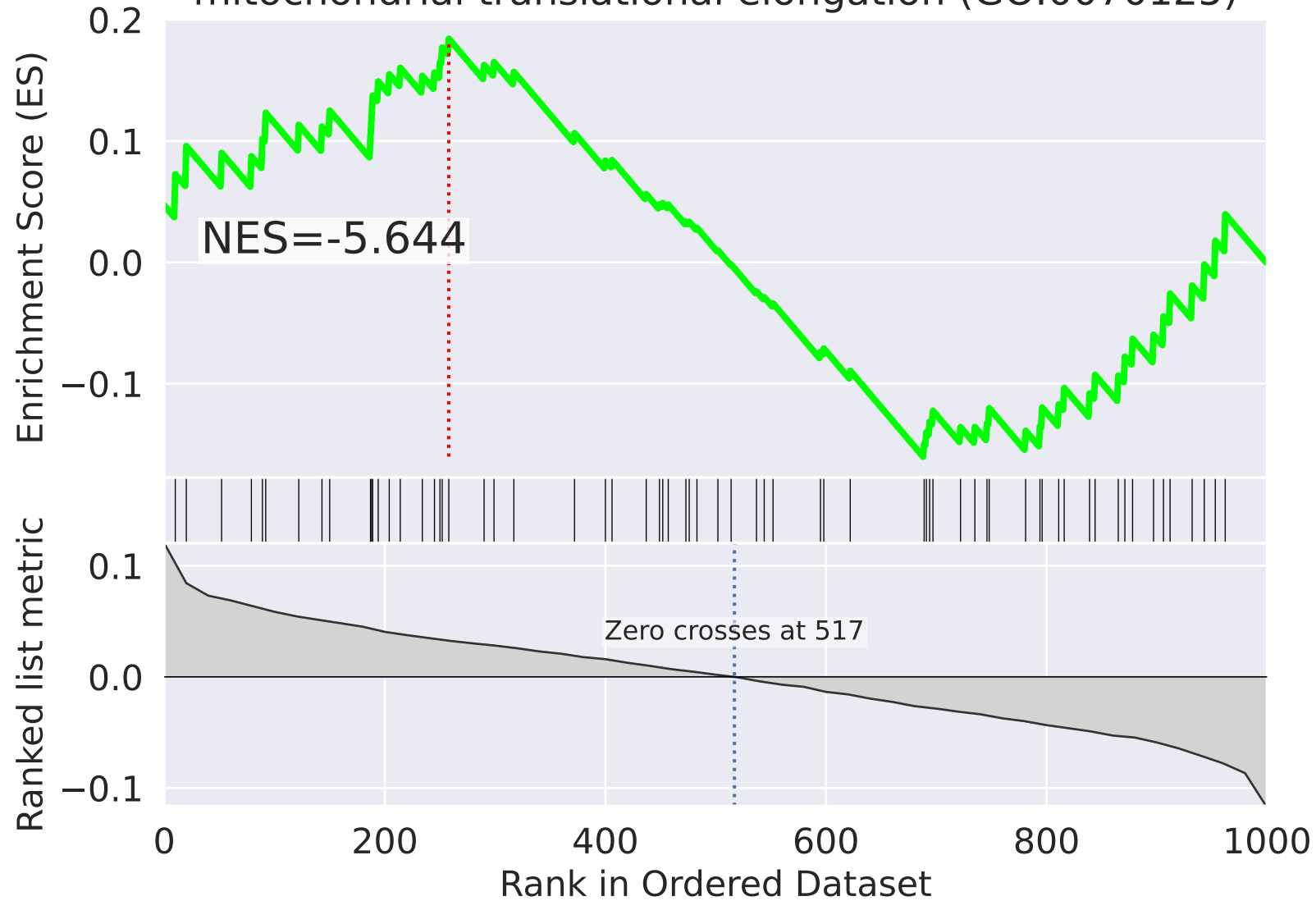
NES

SET

2.869		neutrophil degranulation (GO:0043312)
2.103		Ras protein signal transduction (GO:0007265)
2.102		response to virus (GO:0009615)
-2.097		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.086		positive regulation of DNA replication (GO:0045740)
2.061		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-1.980		positive regulation of cytokinesis (GO:0032467)
1.978		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
1.975		telomere maintenance via recombination (GO:0000722)
1.951		mitotic spindle organization (GO:0007052)
-1.935		transcription, DNA-templated (GO:0006351)
1.927		ERBB2 signaling pathway (GO:0038128)
-1.916		DNA-dependent DNA replication (GO:0006261)
-1.914		positive regulation by host of viral transcription (GO:0043923)
1.883		positive regulation of cell proliferation (GO:0008284)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1

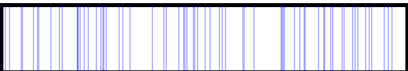


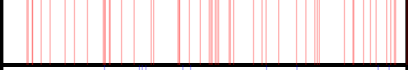
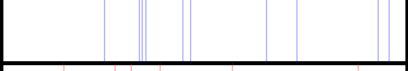
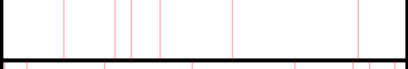







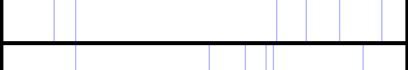

NES=-5.644

Rank



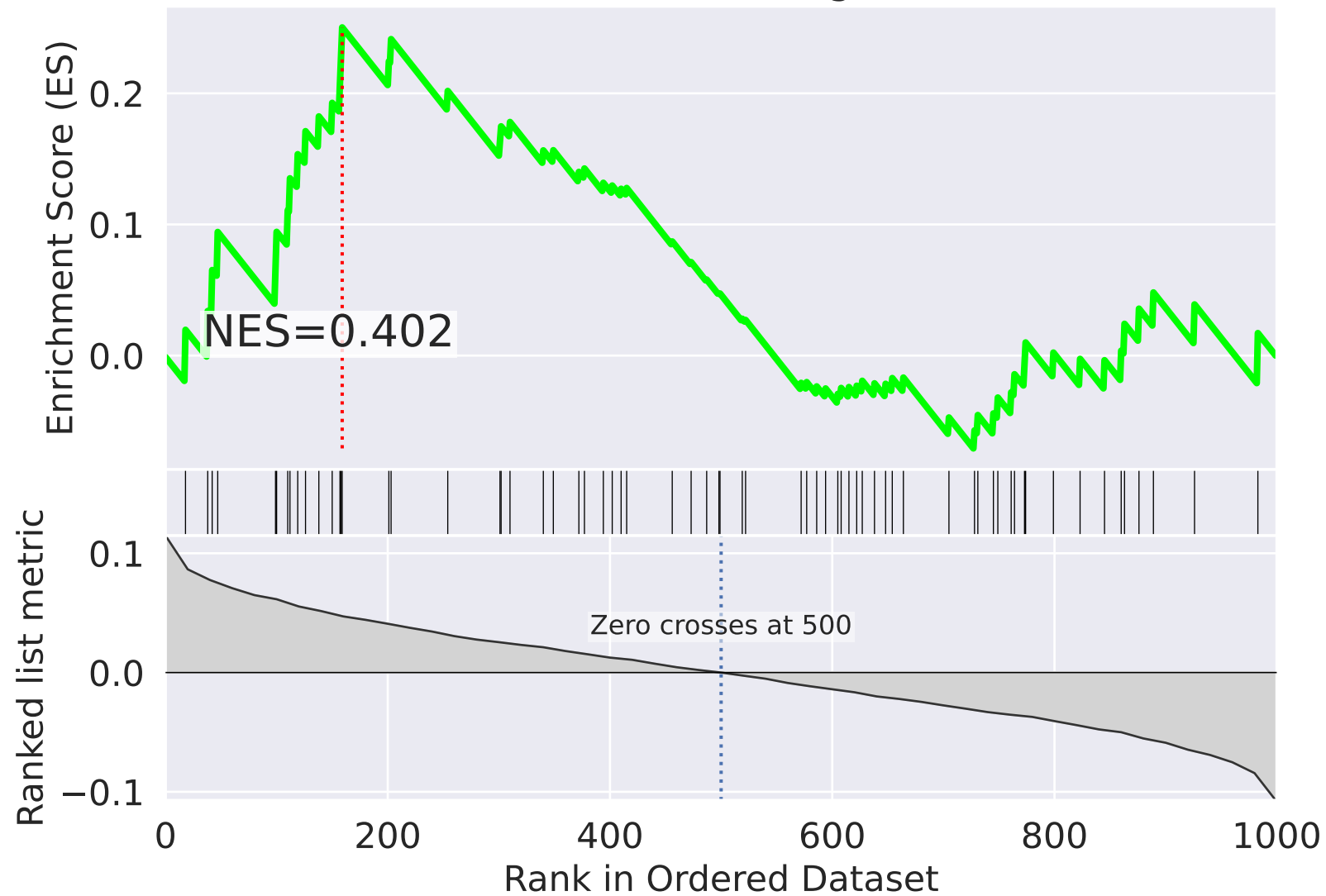
NES

SET

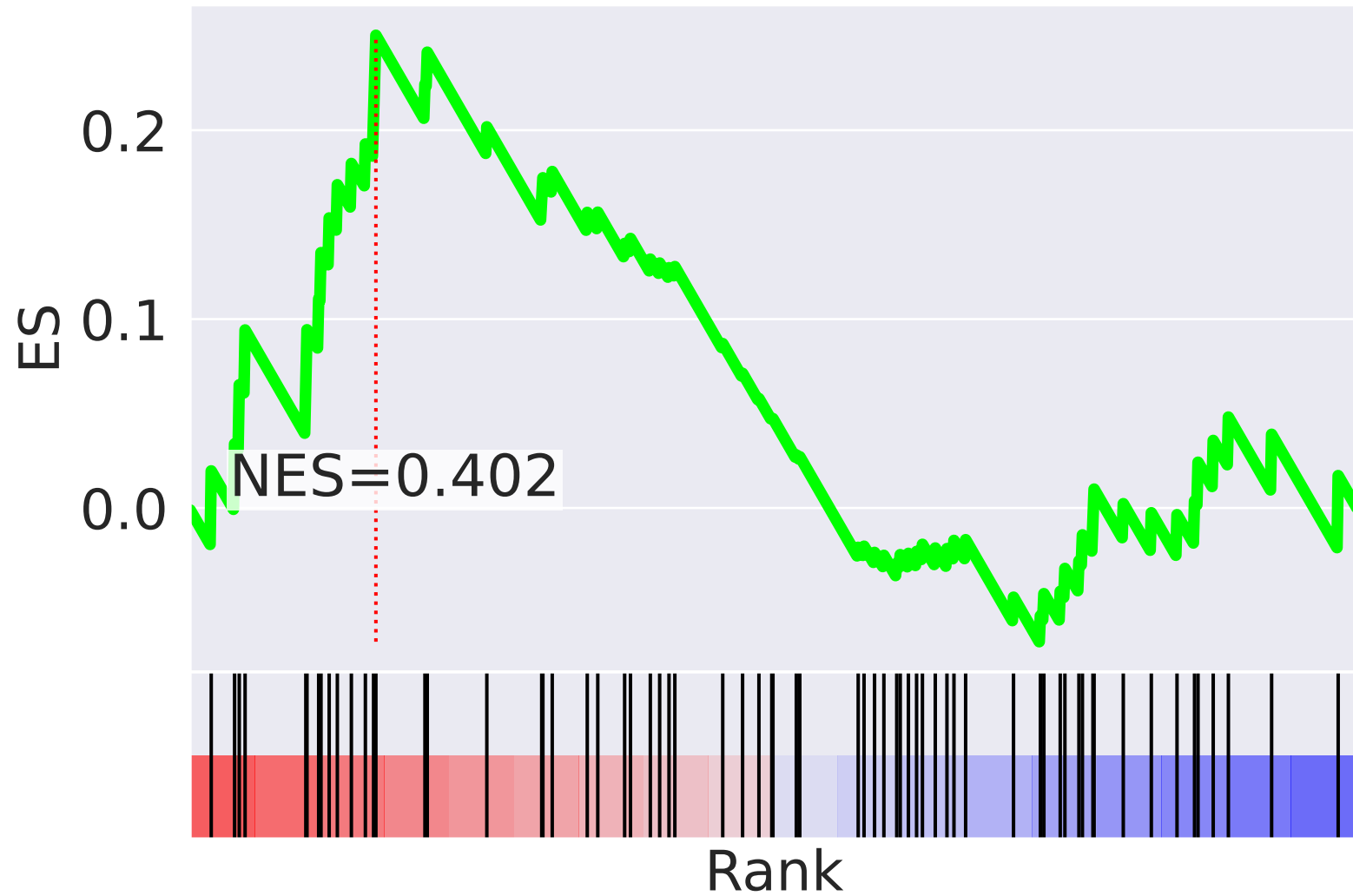
-5.668		mitochondrial translational termination (GO:0070126)
-5.644		mitochondrial translational elongation (GO:0070125)
2.938		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.821		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.428		double-strand break repair via nonhomologous end joining (GO:0006303)
2.411		cellular nitrogen compound metabolic process (GO:0034641)
2.358		regulation of apoptotic process (GO:0042981)
-2.211		DNA synthesis involved in DNA repair (GO:0000731)
-2.088		DNA replication (GO:0006260)
2.087		intracellular protein transport (GO:0006886)
2.077		negative regulation of transcription, DNA-templated (GO:0045892)
2.027		tricarboxylic acid cycle (GO:0006099)
-2.021		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.001		T cell costimulation (GO:0031295)
-1.919		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 $z=9$

mitochondrial translational elongation (GO:0070125)




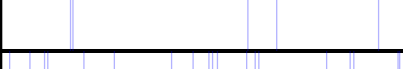
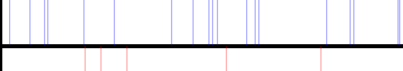
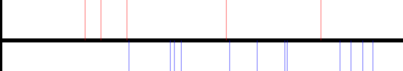
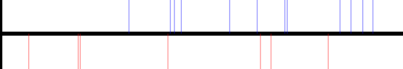


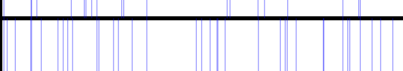



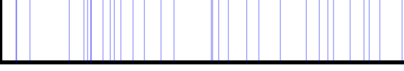



mitochondrial translational elongation (GO:0070125)



NES

SET

2.847		neutrophil degranulation (GO:0043312)
-2.485		DNA-dependent DNA replication (GO:0006261)
-2.369		RNA export from nucleus (GO:0006405)
-2.360		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.200		mRNA export from nucleus (GO:0006406)
2.187		regulation of lipid metabolic process (GO:0019216)
-2.046		protein phosphorylation (GO:0006468)
2.039		cellular protein modification process (GO:0006464)
-2.038		mRNA 3'-end processing (GO:0031124)
-2.012		transcription from RNA polymerase II promoter (GO:0006366)
-1.993		regulation of transcription from RNA polymerase II promoter (GO:0006357)
1.932		substrate adhesion-dependent cell spreading (GO:0034446)
1.927		cellular response to amino acid stimulus (GO:0071230)
1.854		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-1.842		mRNA splicing, via spliceosome (GO:0000398)

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)

ES

0.2

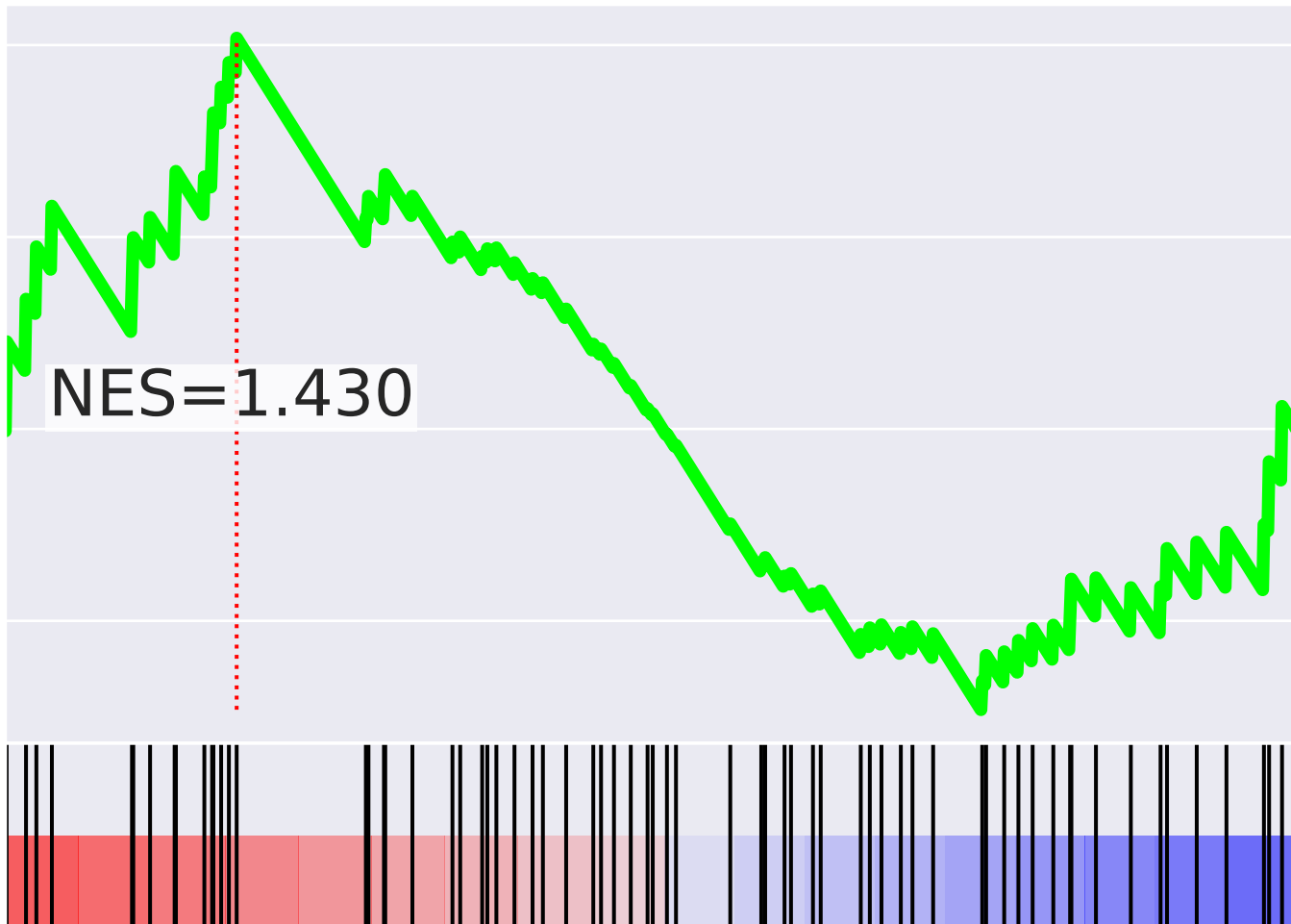
0.1

0.0

-0.1

NES=1.430

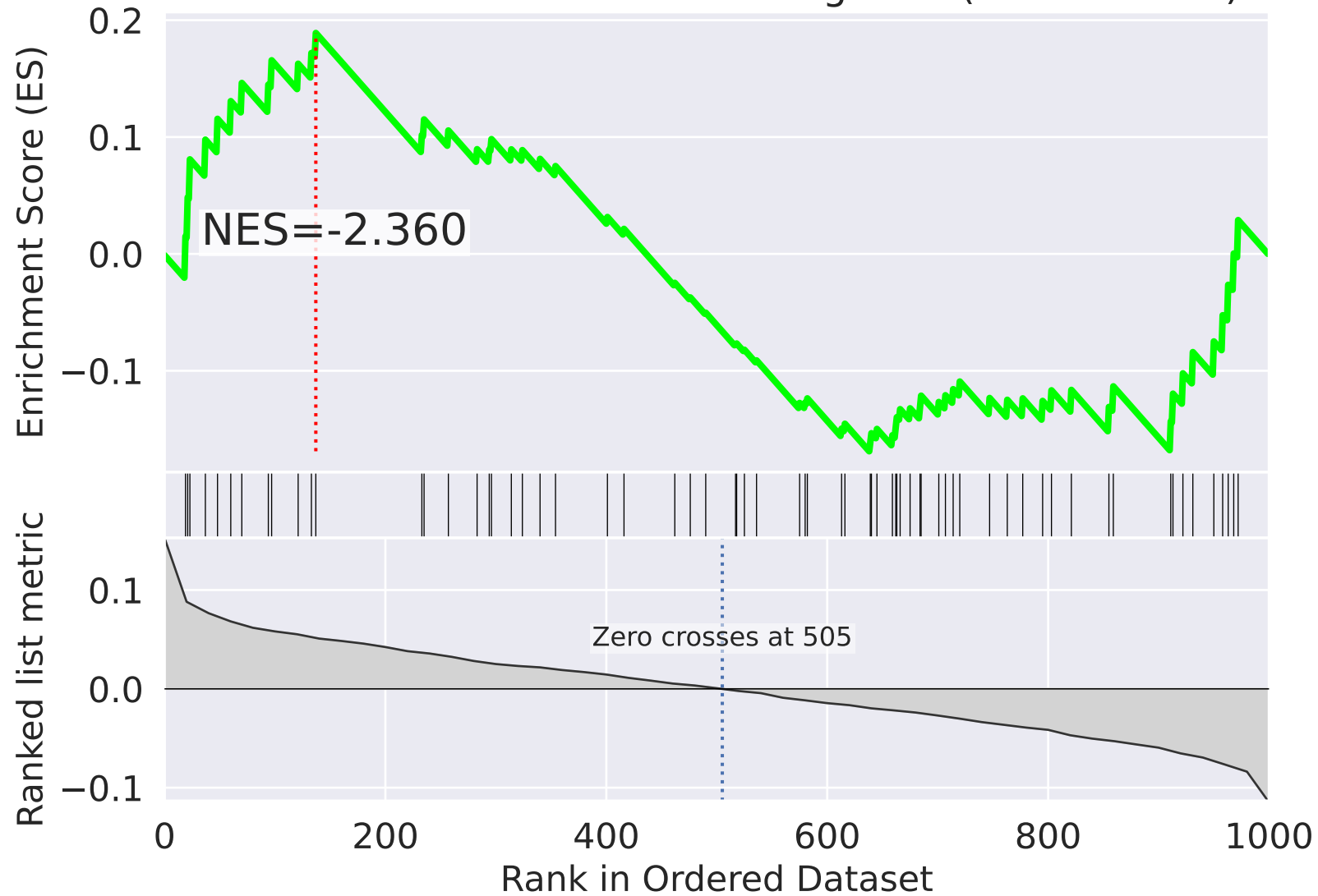
Rank



NES	SET
-2.860	RNA metabolic process (GO:0016070)
-2.814	positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.499	positive regulation by host of viral transcription (GO:0043923)
2.490	Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.470	endosomal transport (GO:0016197)
-2.288	cellular iron ion homeostasis (GO:0006879)
-2.239	generation of precursor metabolites and energy (GO:0006091)
2.211	chromosome segregation (GO:0007059)
-2.115	protein stabilization (GO:0050821)
2.109	ERK1 and ERK2 cascade (GO:0070371)
2.102	epidermal growth factor receptor signaling pathway (GO:0007173)
2.101	T cell costimulation (GO:0031295)
2.073	mitochondrial respiratory chain complex I assembly (GO:0032981)
2.067	axon guidance (GO:0007411)
2.049	transcription initiation from RNA polymerase I promoter (GO:0006361)

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)

ES

0.2

0.1



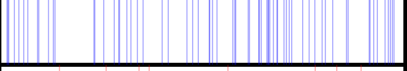





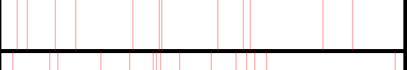
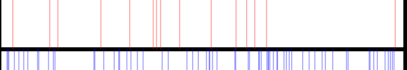
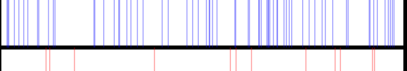

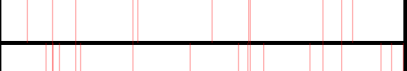
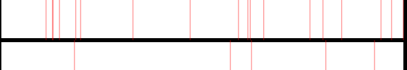
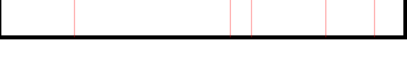
0.0

-0.1

NES=-2.360

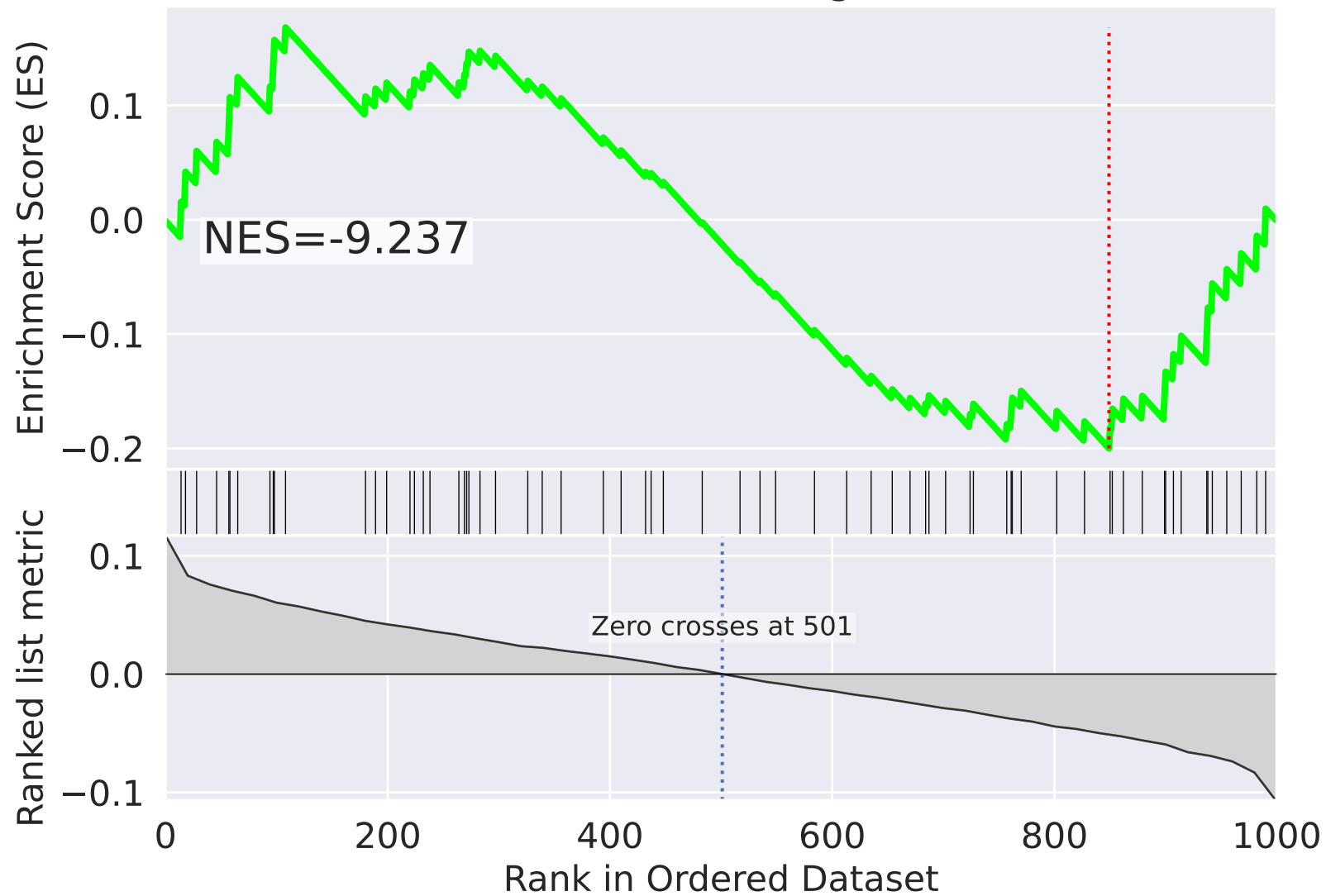
Rank



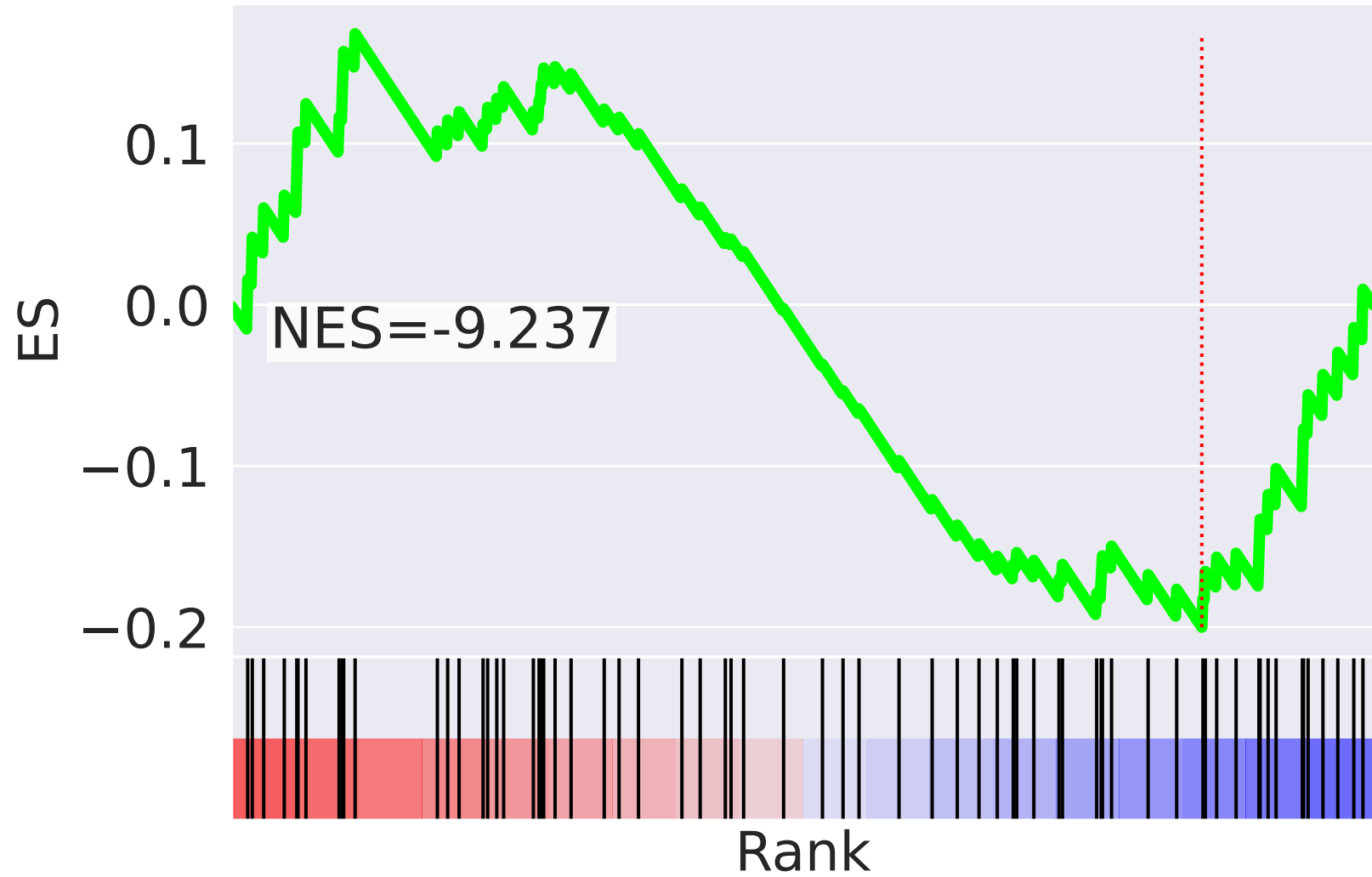
NES		SET
2.684		protein homooligomerization (GO:0051260)
2.646		mitotic cytokinesis (GO:0000281)
-2.360		mitochondrial translational elongation (GO:0070125)
2.308		substantia nigra development (GO:0021762)
2.255		cell separation after cytokinesis (GO:0000920)
-2.196		protein K63-linked ubiquitination (GO:0070534)
2.129		positive regulation of protein catabolic process (GO:0045732)
2.121		regulation of lipid metabolic process (GO:0019216)
2.101		leukocyte migration (GO:0050900)
2.087		sister chromatid cohesion (GO:0007062)
-2.078		mitochondrial translational termination (GO:0070126)
2.064		mitotic metaphase plate congression (GO:0007080)
2.044		epidermal growth factor receptor signaling pathway (GO:0007173)
2.041		MAPK cascade (GO:0000165)
1.928		regulation of centrosome duplication (GO:0010824)

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)

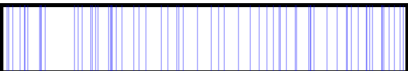


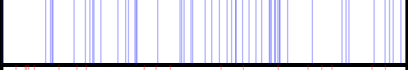



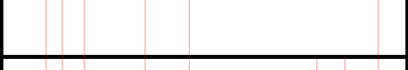
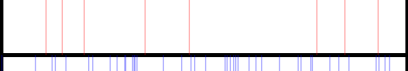
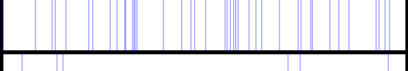
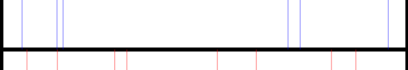
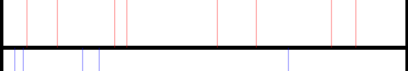
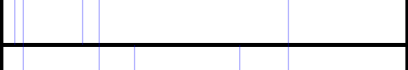
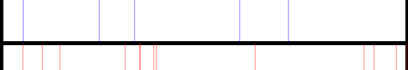
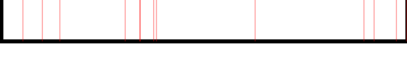


mitochondrial translational elongation (GO:0070125)



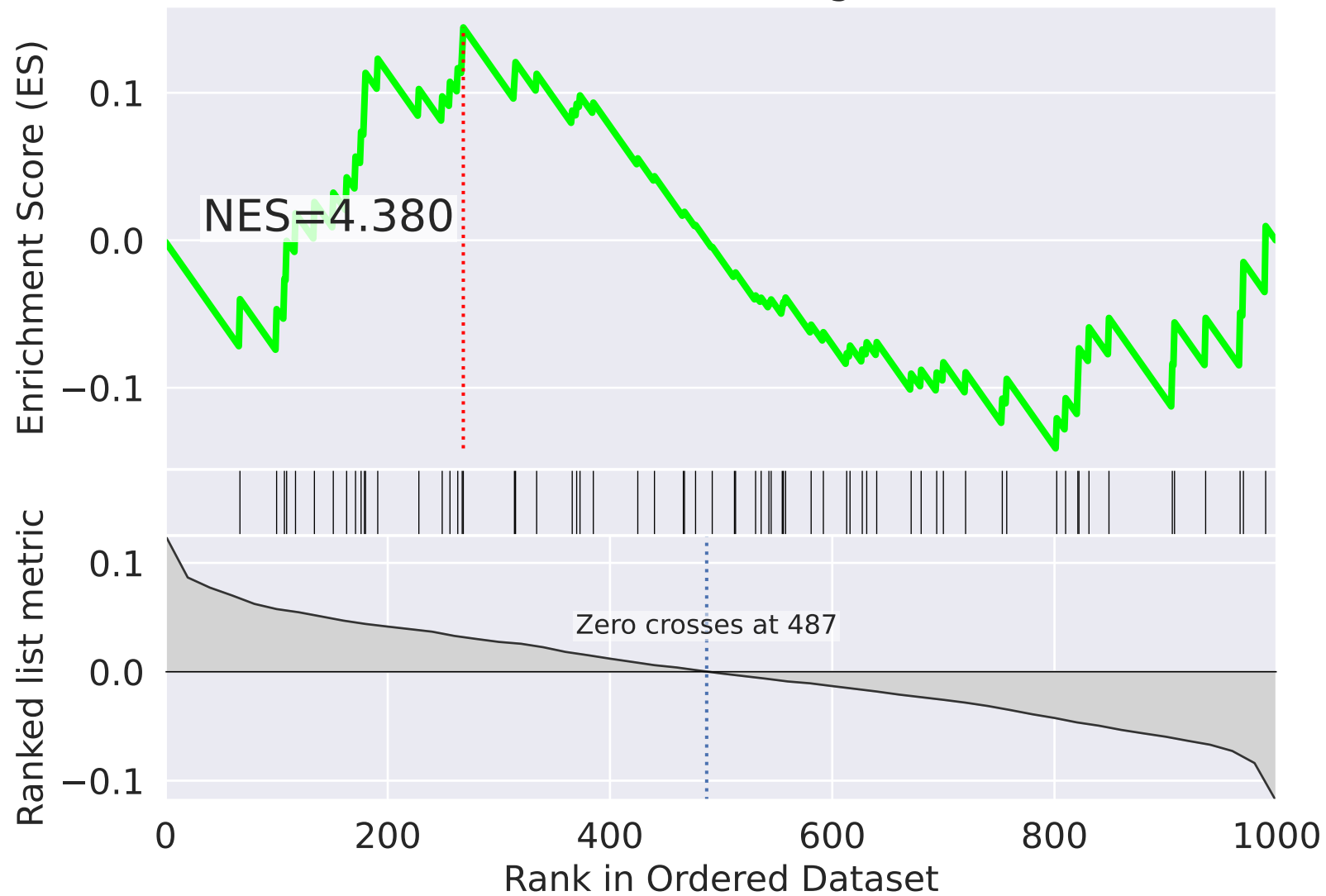
NES

SET

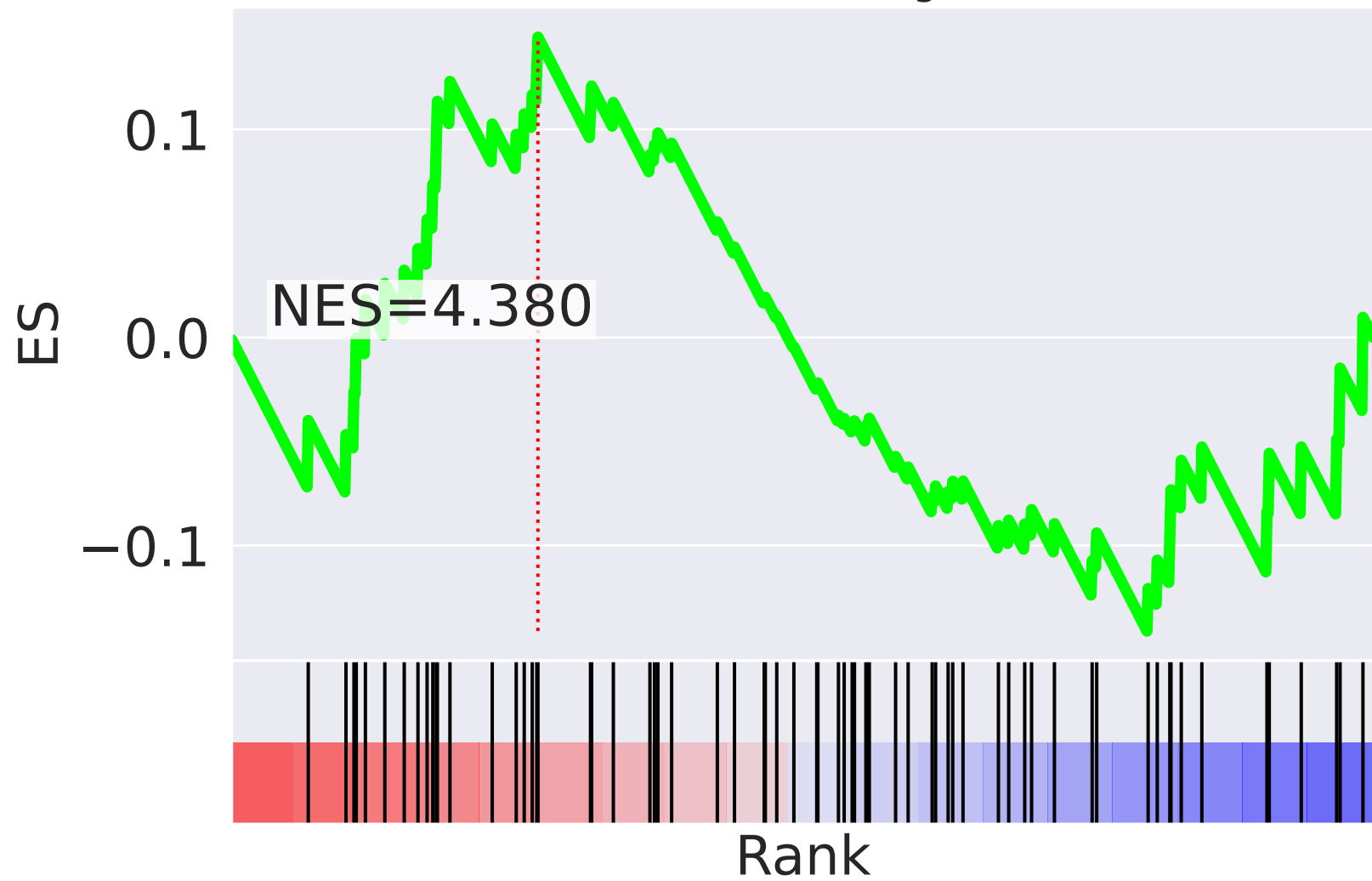
-9.237		mitochondrial translational elongation (GO:0070125)
-8.702		mitochondrial translational termination (GO:0070126)
-2.814		regulation of transcription, DNA-templated (GO:0006355)
-2.675		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.275		mRNA export from nucleus (GO:0006406)
2.242		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.212		nucleus organization (GO:0006997)
2.184		viral budding via host ESCRT complex (GO:0039702)
2.183		viral life cycle (GO:0019058)
-2.171		positive regulation of transcription, DNA-templated (GO:0045893)
-2.074		phosphatidylinositol biosynthetic process (GO:0006661)
2.031		tricarboxylic acid cycle (GO:0006099)
-2.019		telomere maintenance (GO:0000723)
-2.008		telomere capping (GO:0016233)
1.981		ER to Golgi vesicle-mediated transport (GO:0006888)

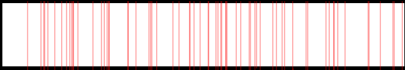
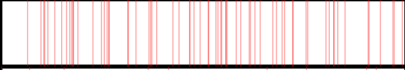


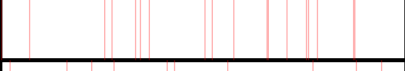
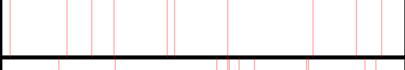
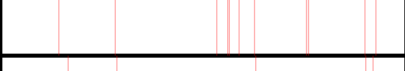
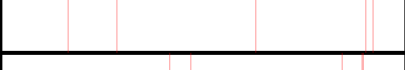
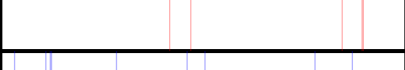

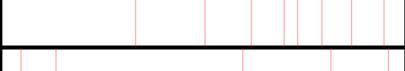
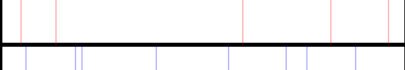



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=13$

mitochondrial translational elongation (GO:0070125)



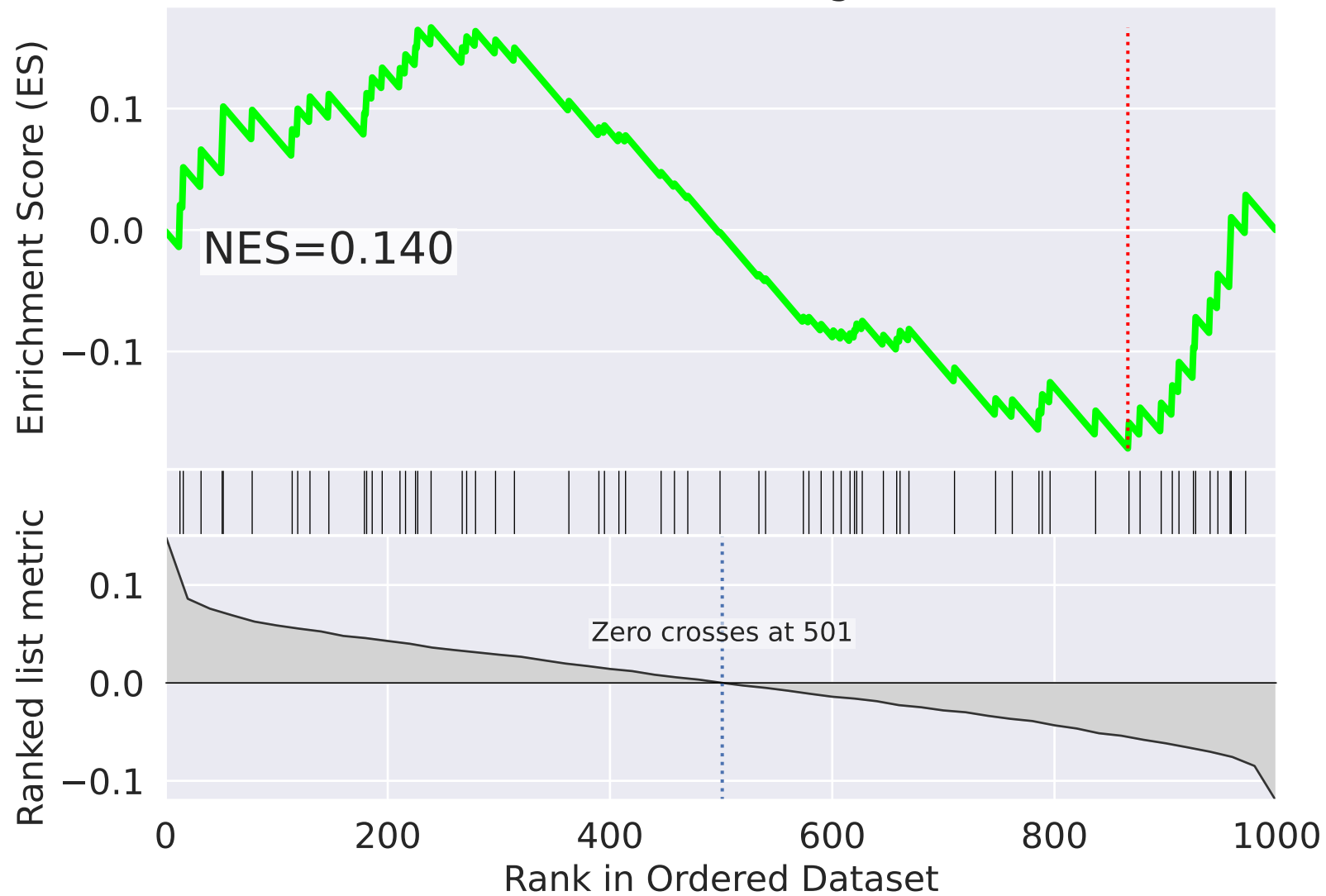
mitochondrial translational elongation (GO:0070125)



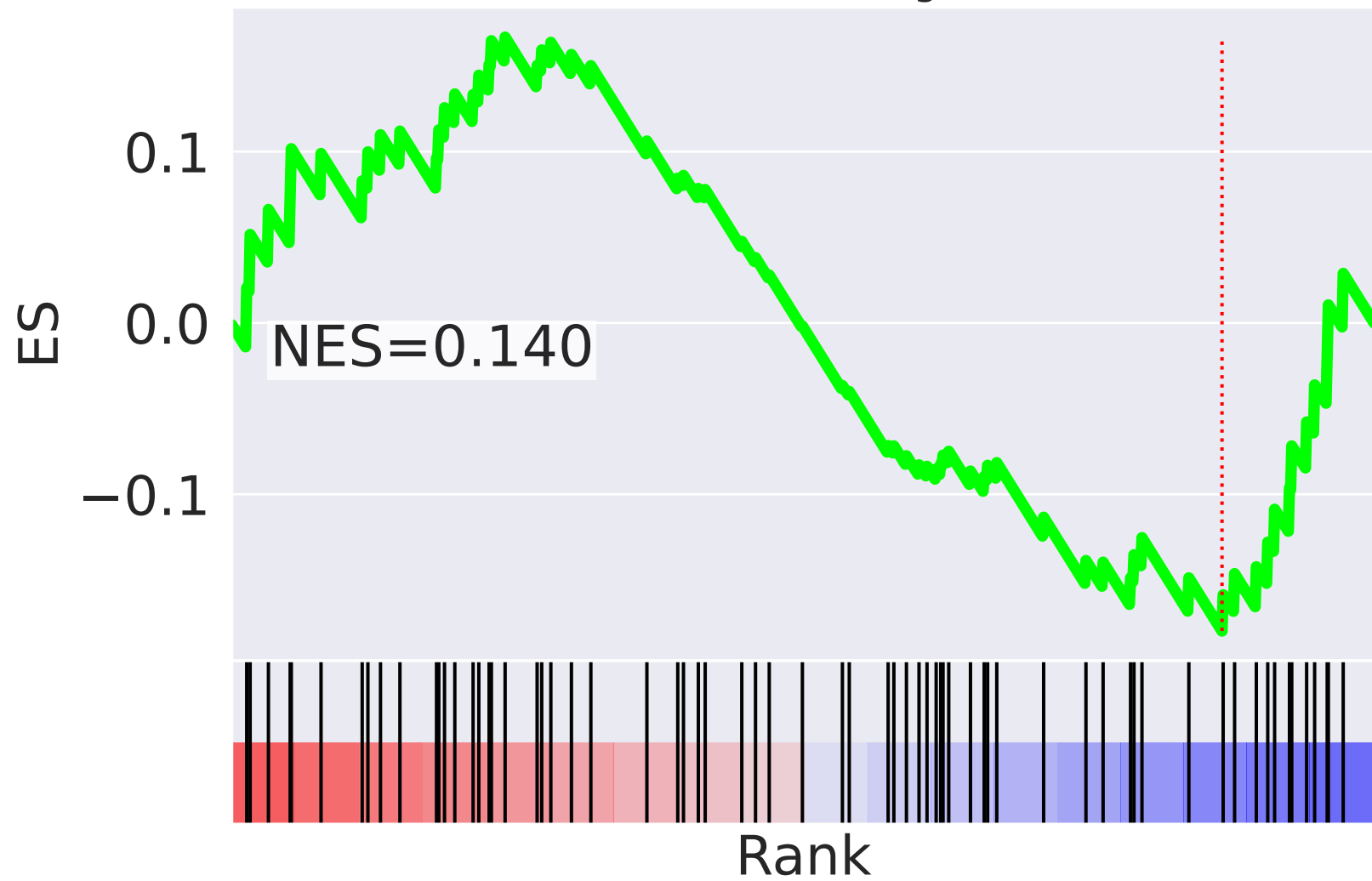
NES		SET
4.380		mitochondrial translational elongation (GO:0070125)
4.283		mitochondrial translational termination (GO:0070126)
2.871		double-strand break repair (GO:0006302)
2.616		positive regulation of GTPase activity (GO:0043547)
2.452		cellular response to DNA damage stimulus (GO:0006974)
2.429		retrograde transport, endosome to Golgi (GO:0042147)
2.303		positive regulation of gene expression (GO:0010628)
2.301		mitotic spindle organization (GO:0007052)
2.294		proteolysis (GO:0006508)
-2.212		mitotic cytokinesis (GO:0000281)
2.197		cell migration (GO:0016477)
2.086		CENP-A containing nucleosome assembly (GO:0034080)
-2.032		oxidation-reduction process (GO:0055114)
1.996		sister chromatid cohesion (GO:0007062)
-1.980		inflammatory response (GO:0006954)

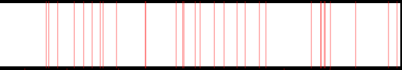

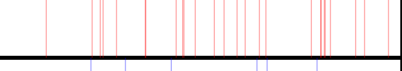

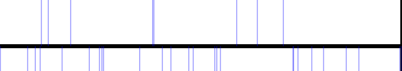
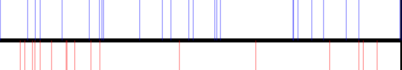


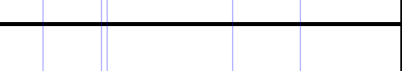
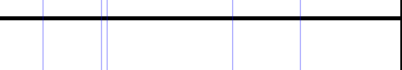
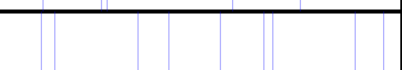




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=14$

mitochondrial translational elongation (GO:0070125)



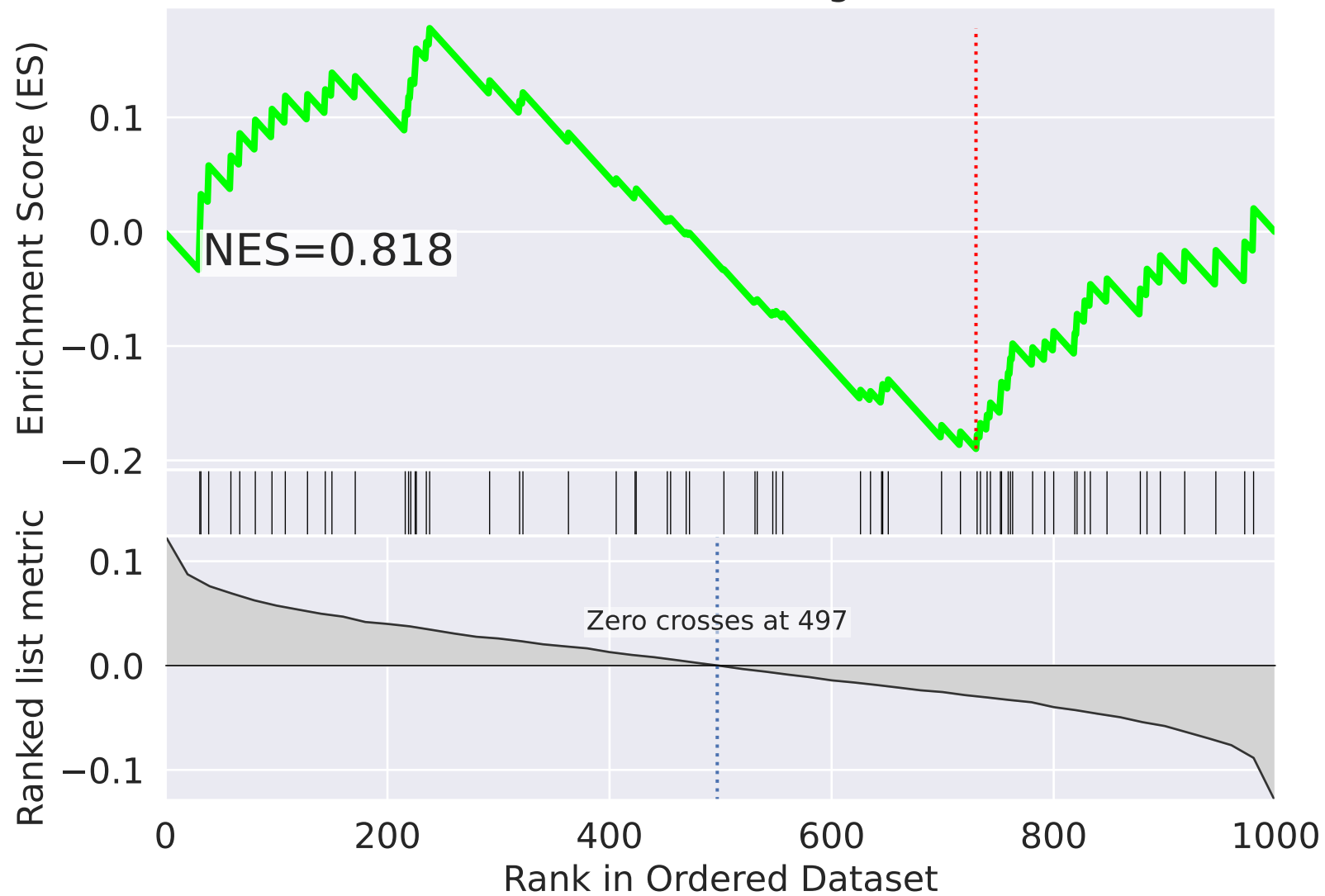
mitochondrial translational elongation (GO:0070125)



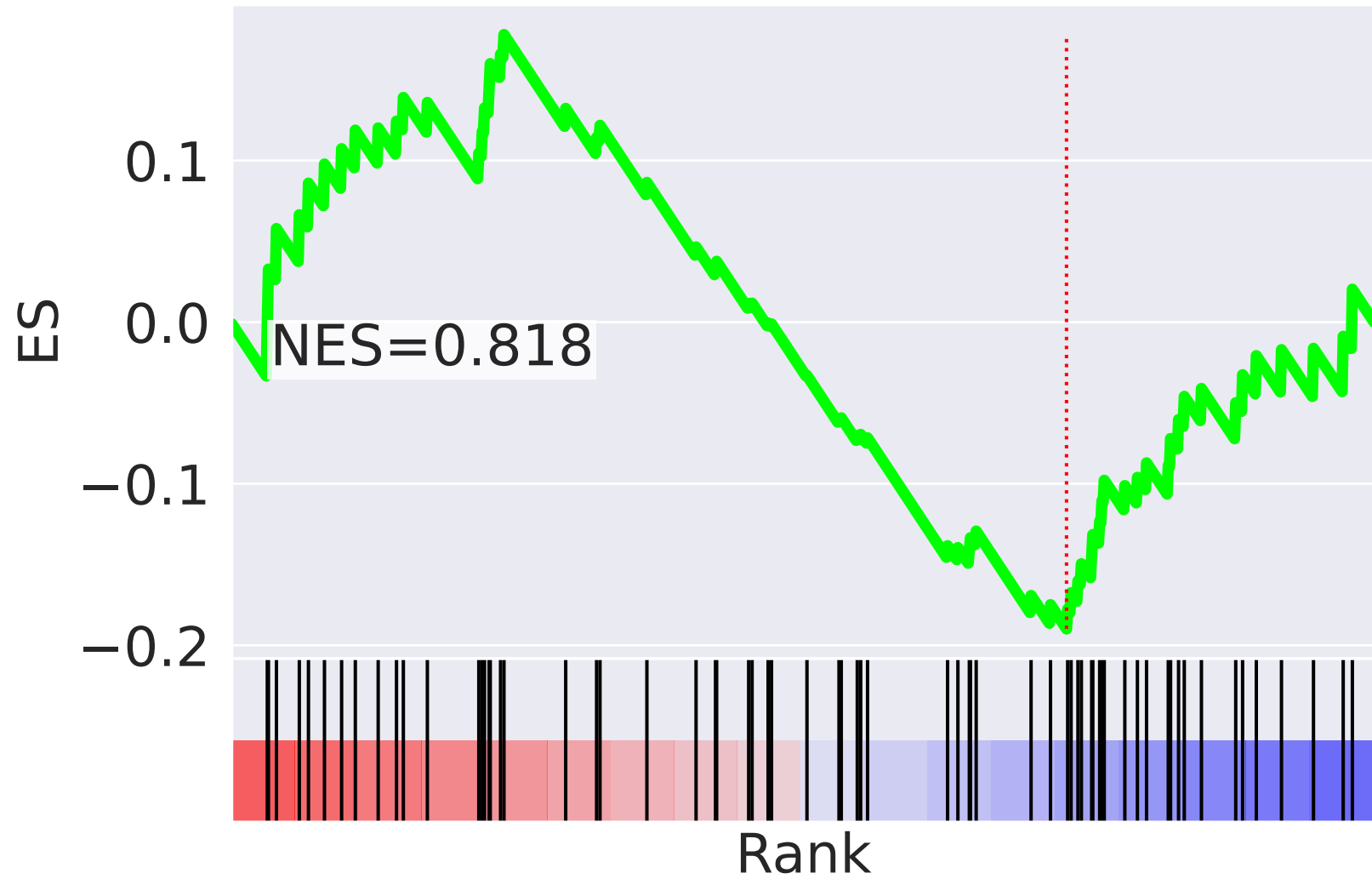
NES		SET
3.230		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.657		cellular iron ion homeostasis (GO:0006879)
2.531		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.341		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-2.337		protein homooligomerization (GO:0051260)
-2.322		signal transduction (GO:0007165)
2.282		post-translational protein modification (GO:0043687)
-2.280		regulation of cellular response to heat (GO:1900034)
-2.254		transcription initiation from RNA polymerase I promoter (GO:0006361)
-2.254		transcription elongation from RNA polymerase I promoter (GO:0006362)
-2.254		termination of RNA polymerase I transcription (GO:0006363)
-2.252		Golgi organization (GO:0007030)
-2.122		regulation of defense response to virus by virus (GO:0050690)
-2.077		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-2.017		ATP-dependent chromatin remodeling (GO:0043044)

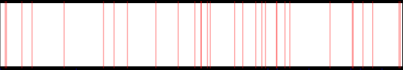

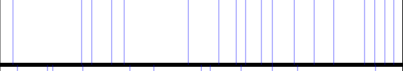
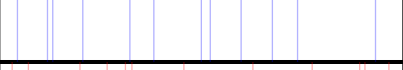
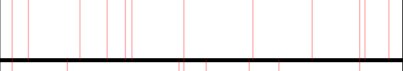
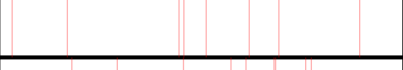
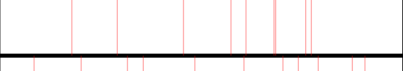





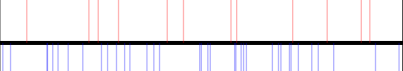
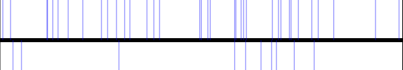
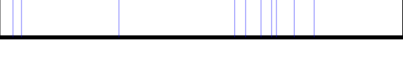
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=15$

mitochondrial translational elongation (GO:0070125)



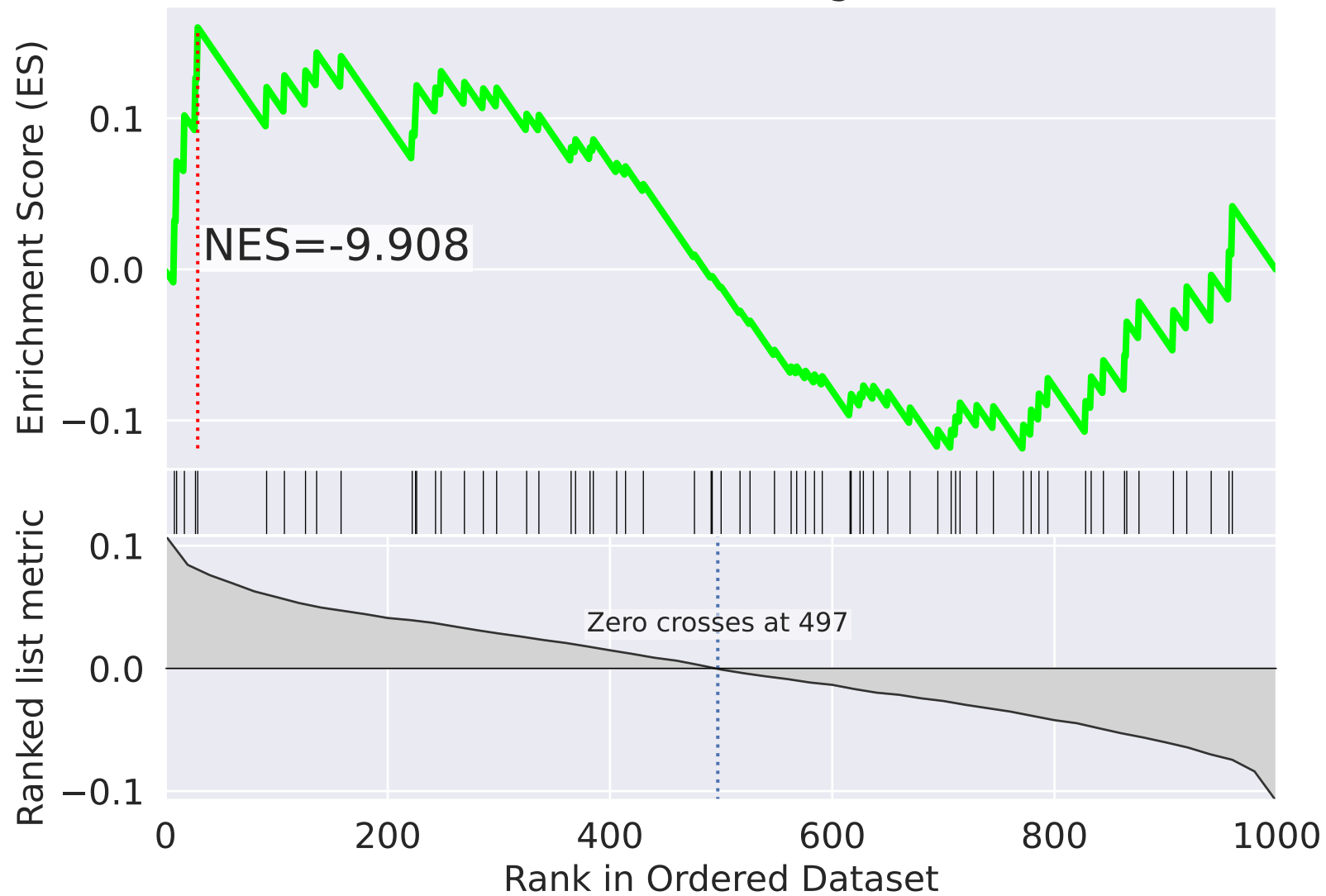
mitochondrial translational elongation (GO:0070125)



NES		SET
2.473		protein deubiquitination (GO:0016579)
-2.316		protein import into nucleus (GO:0006606)
-2.285		DNA repair (GO:0006281)
-2.262		chromatin remodeling (GO:0006338)
2.260		mitotic metaphase plate congression (GO:0007080)
2.226		microtubule-based movement (GO:0007018)
2.212		protein dephosphorylation (GO:0006470)
2.212		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-2.121		Golgi organization (GO:0007030)
2.086		spermatogenesis (GO:0007283)
-2.075		DNA-dependent DNA replication (GO:0006261)
-2.050		RNA secondary structure unwinding (GO:0010501)
1.987		RNA splicing (GO:0008380)
-1.951		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-1.939		strand displacement (GO:0000732)

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)

ES

0.1

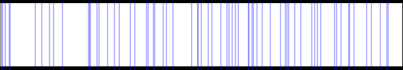
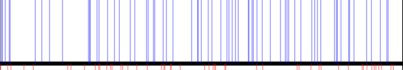
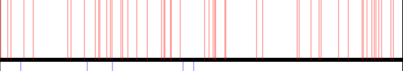
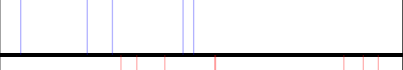



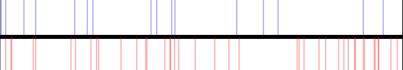
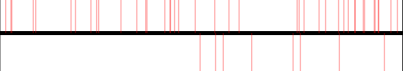
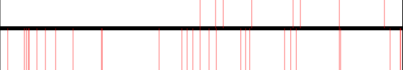
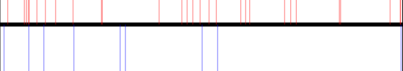



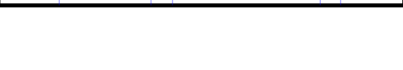
0.0

-0.1

NES=-9.908

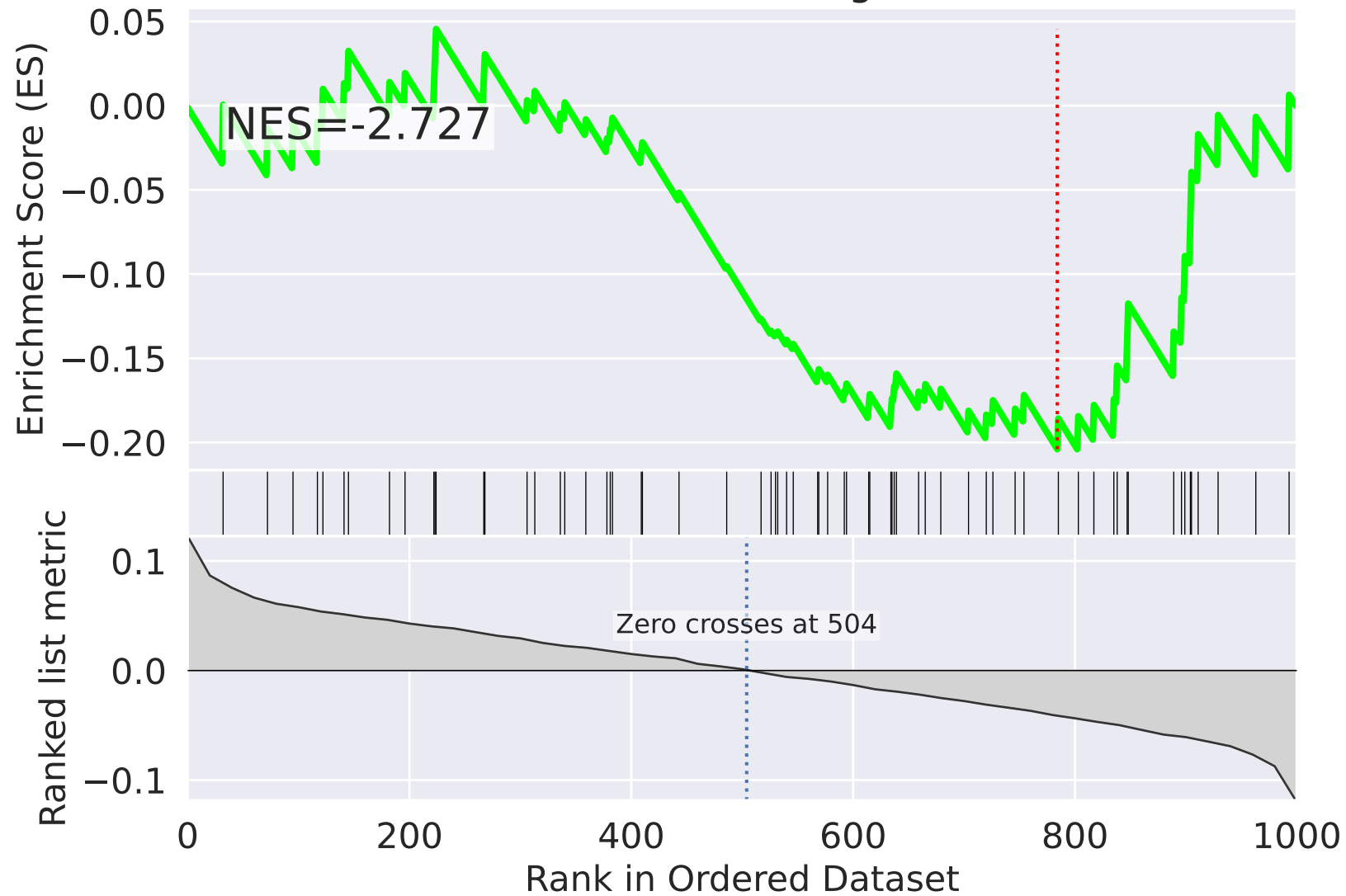
Rank



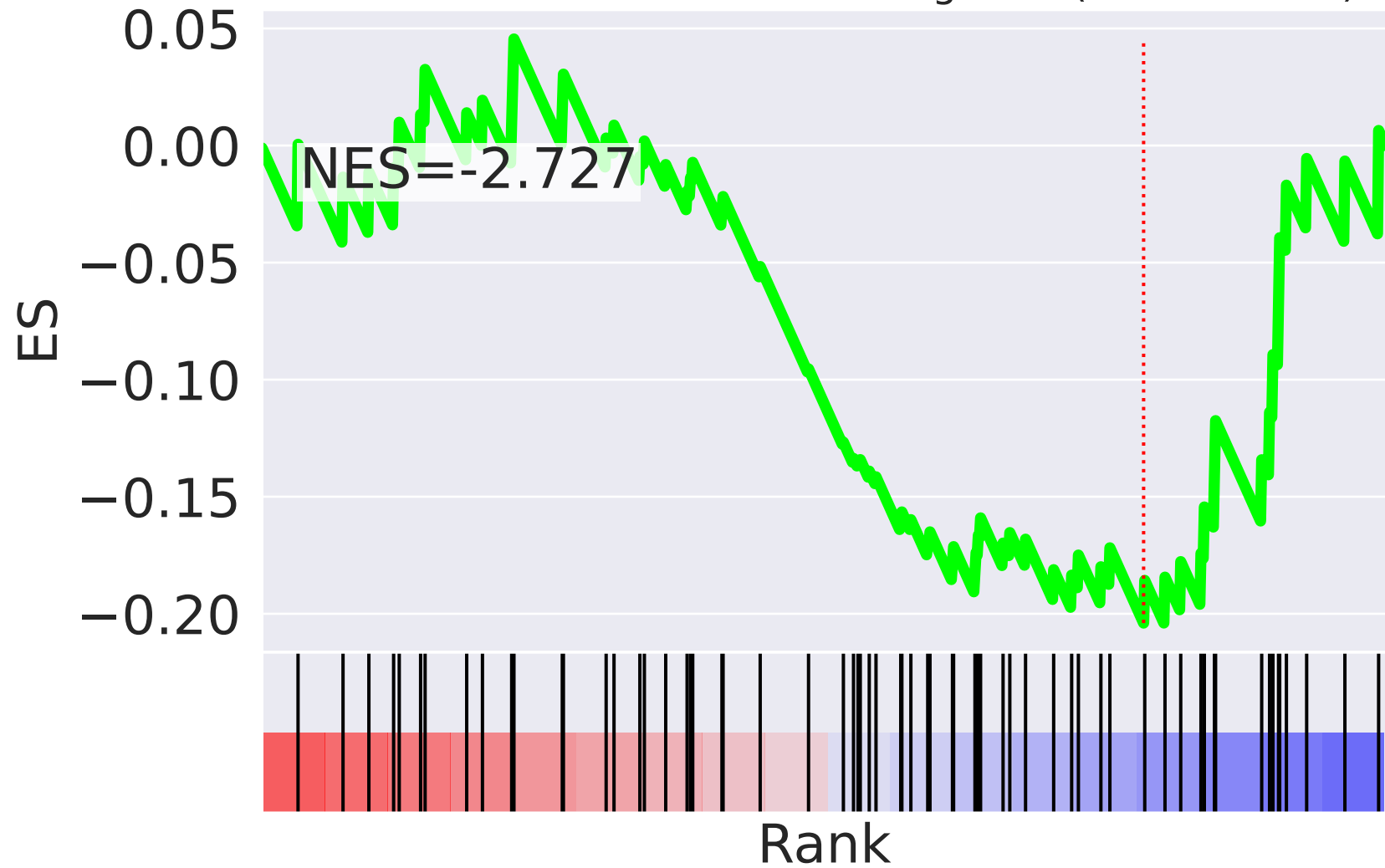
NES		SET
-9.908		mitochondrial translational elongation (GO:0070125)
-9.786		mitochondrial translational termination (GO:0070126)
2.884		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.752		cellular response to hypoxia (GO:0071456)
2.541		androgen receptor signaling pathway (GO:0030521)
-2.301		IRE1-mediated unfolded protein response (GO:0036498)
-2.065		positive regulation of telomere maintenance via telomerase (GO:0032212)
-2.043		negative regulation of cell proliferation (GO:0008285)
2.004		positive regulation of transcription, DNA-templated (GO:0045893)
1.962		cell growth (GO:0016049)
1.946		neutrophil degranulation (GO:0043312)
-1.936		tRNA modification (GO:0006400)
-1.920		protein dephosphorylation (GO:0006470)
-1.915		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-1.887		cellular iron ion homeostasis (GO:0006879)

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)


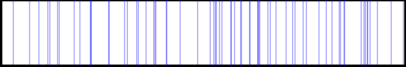

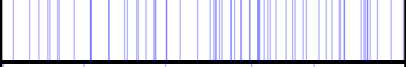


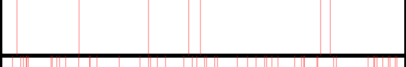
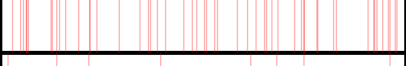
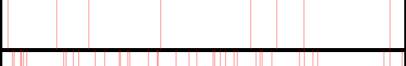
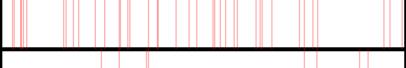
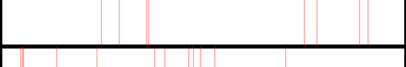
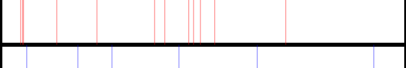
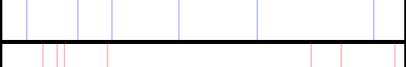




mitochondrial translational elongation (GO:0070125)



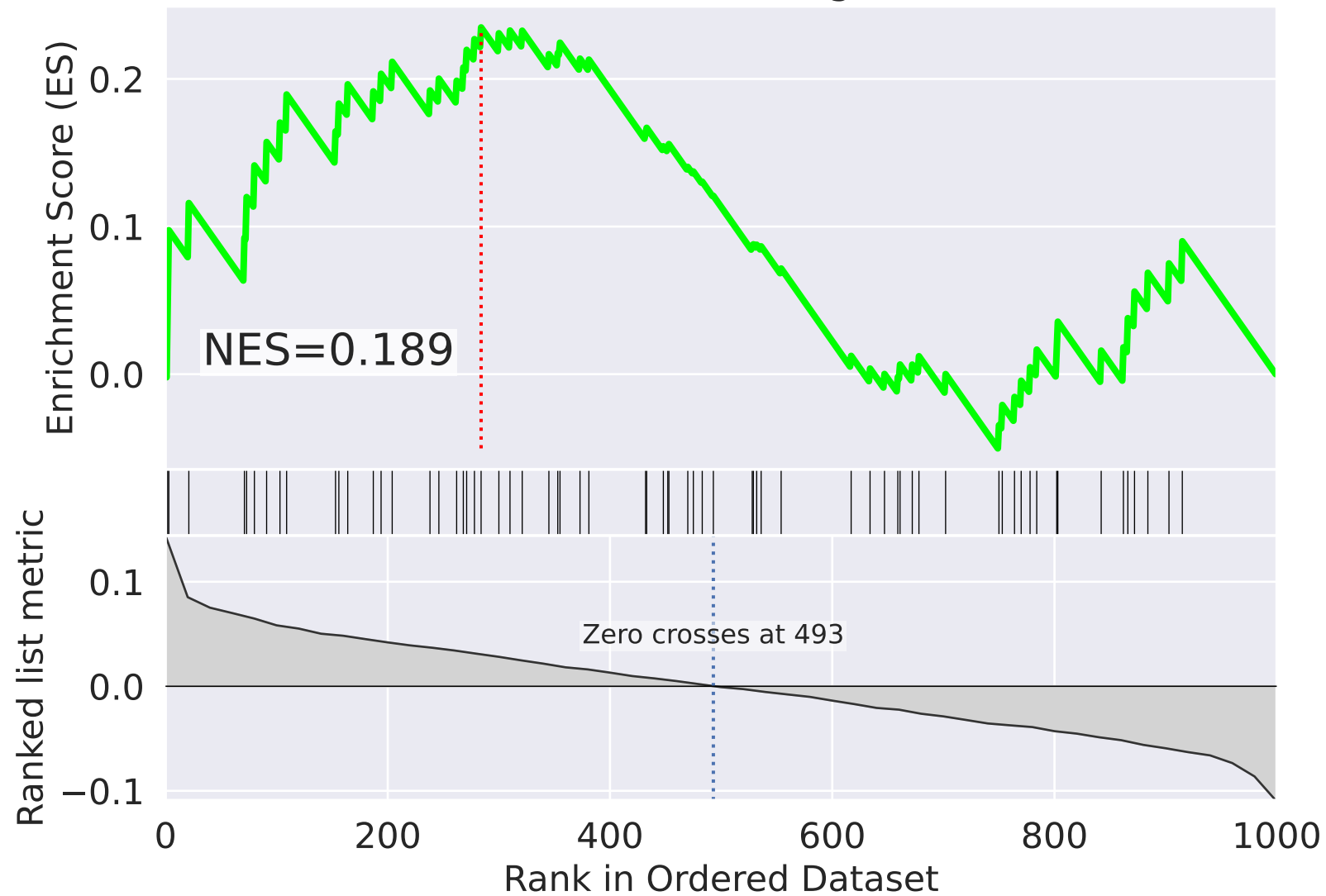
NES

SET

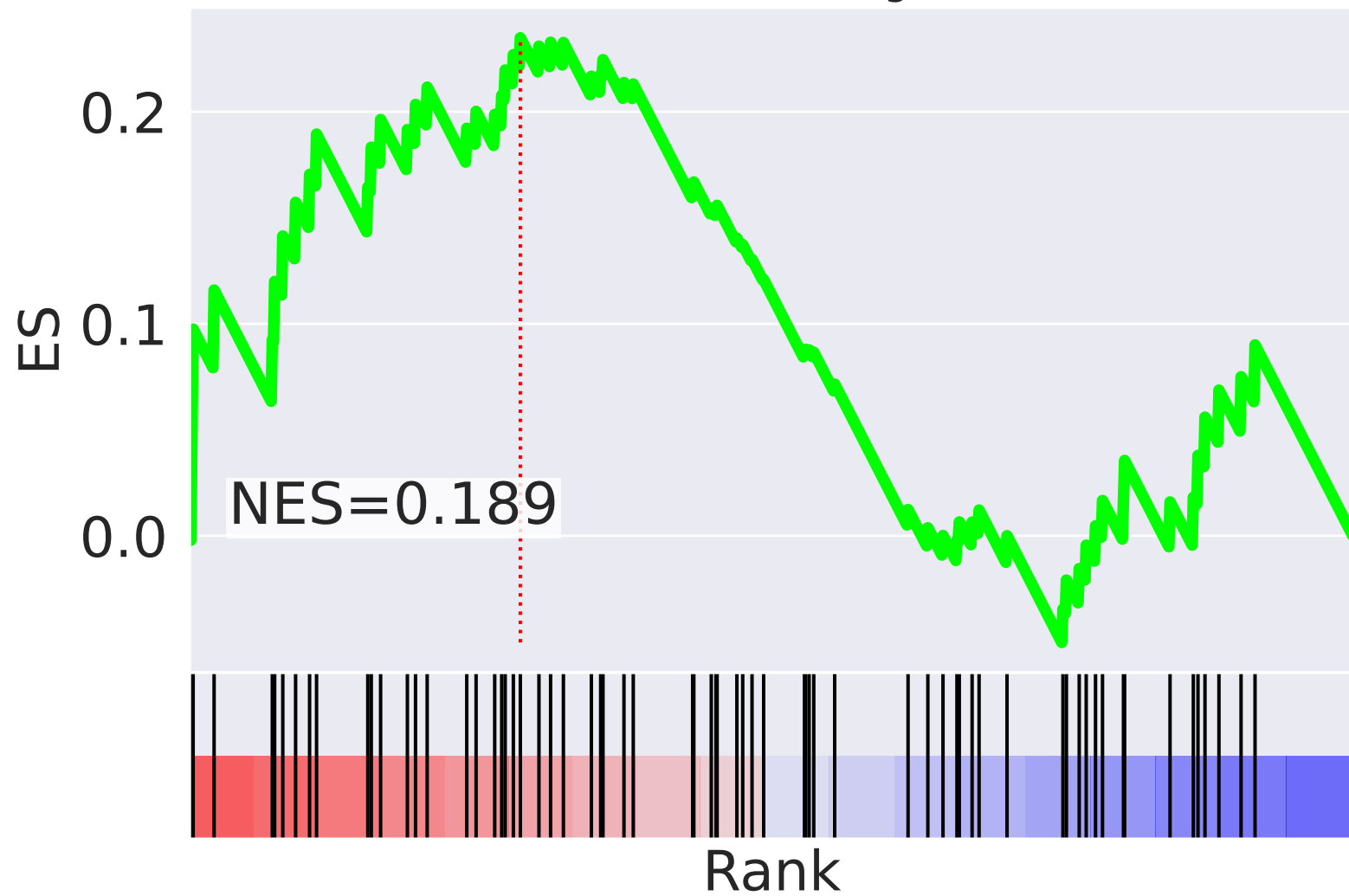
-2.758		tricarboxylic acid cycle (GO:0006099)
-2.727		mitochondrial translational elongation (GO:0070125)
-2.506		cellular respiration (GO:0045333)
-2.427		mitochondrial translational termination (GO:0070126)
-2.395		intrinsic apoptotic signaling pathway (GO:0097193)
-2.373		positive regulation of gene expression (GO:0010628)
2.367		positive regulation of gene expression, epigenetic (GO:0045815)
2.292		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.230		regulation of apoptotic process (GO:0042981)
2.225		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.223		regulation of cell cycle (GO:0051726)
2.189		chromatin remodeling (GO:0006338)
-2.149		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
2.032		negative regulation of telomere maintenance via telomerase (GO:0032211)
-2.029		generation of precursor metabolites and energy (GO:0006091)

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)



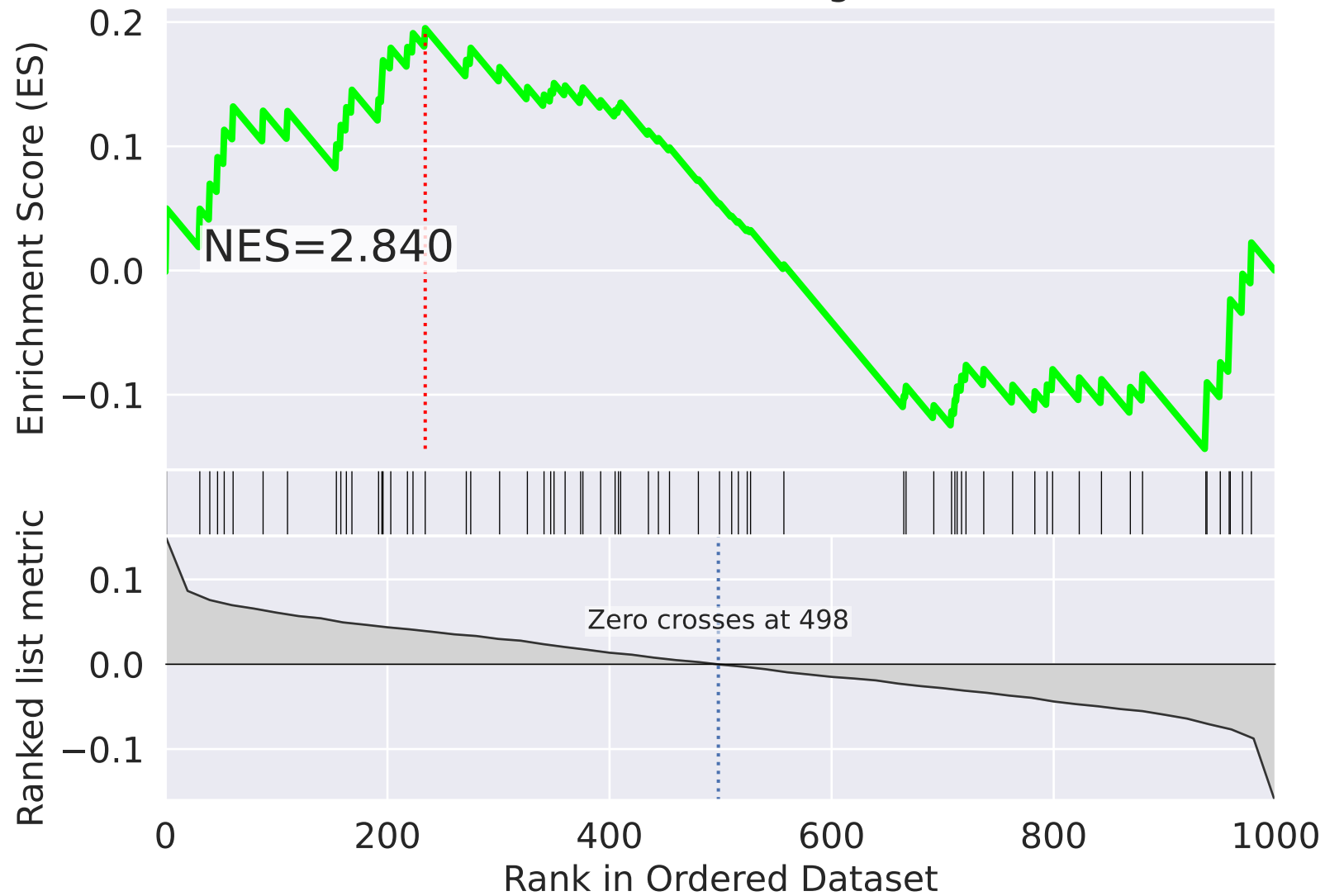
mitochondrial translational elongation (GO:0070125)



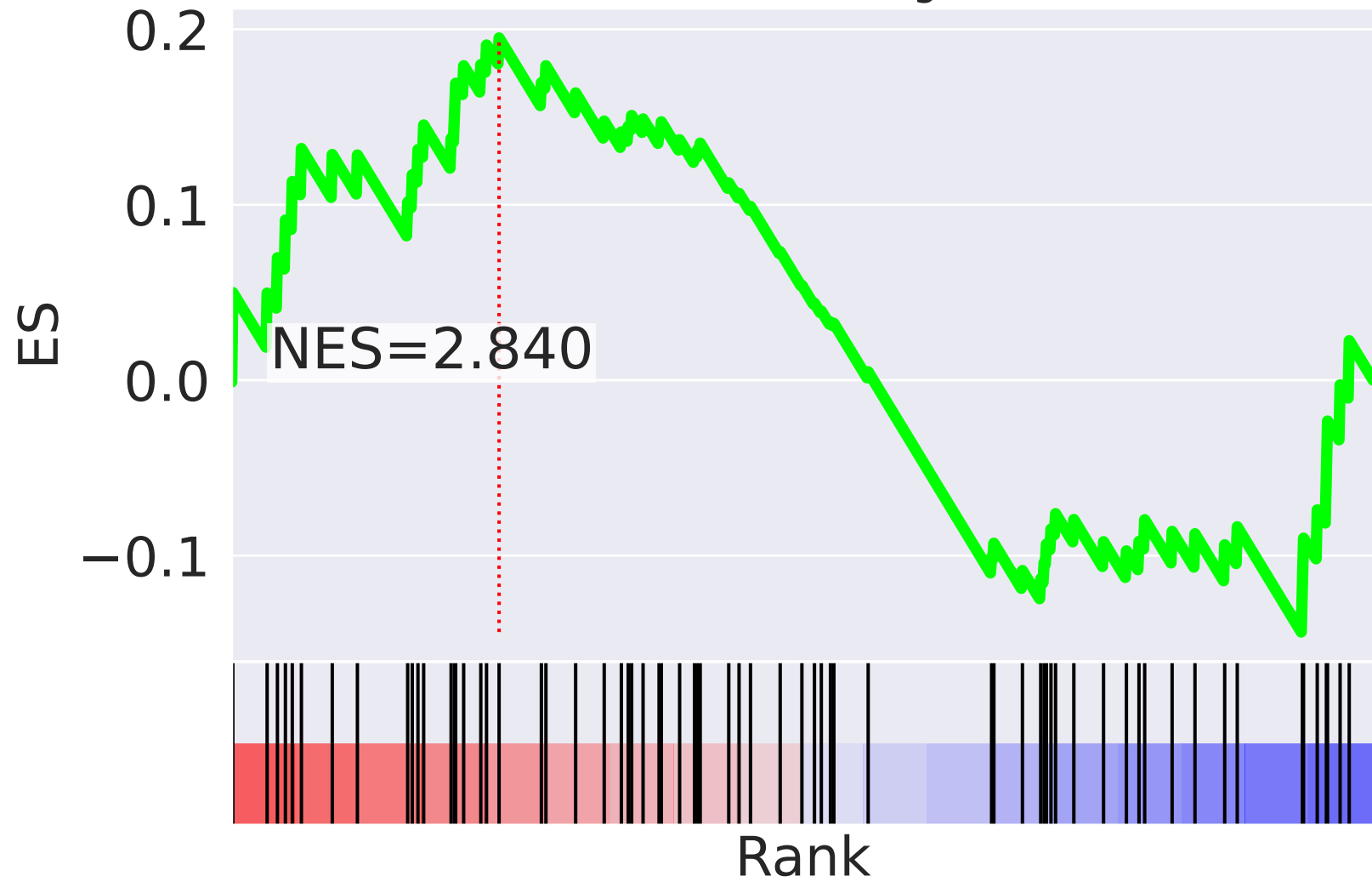
NES		SET
2.582		cytokinesis (GO:0000910)
2.559		positive regulation of DNA repair (GO:0045739)
2.411		ciliary basal body docking (GO:0097711)
2.366		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.249		protein K11-linked ubiquitination (GO:0070979)
-2.234		tRNA aminoacylation for protein translation (GO:0006418)
2.206		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.204		ephrin receptor signaling pathway (GO:0048013)
-2.152		T cell receptor signaling pathway (GO:0050852)
2.141		double-strand break repair (GO:0006302)
2.108		COPII vesicle coating (GO:0048208)
2.050		apoptotic process (GO:0006915)
-2.003		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-1.967		positive regulation of protein targeting to mitochondrion (GO:1903955)
-1.945		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)

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)



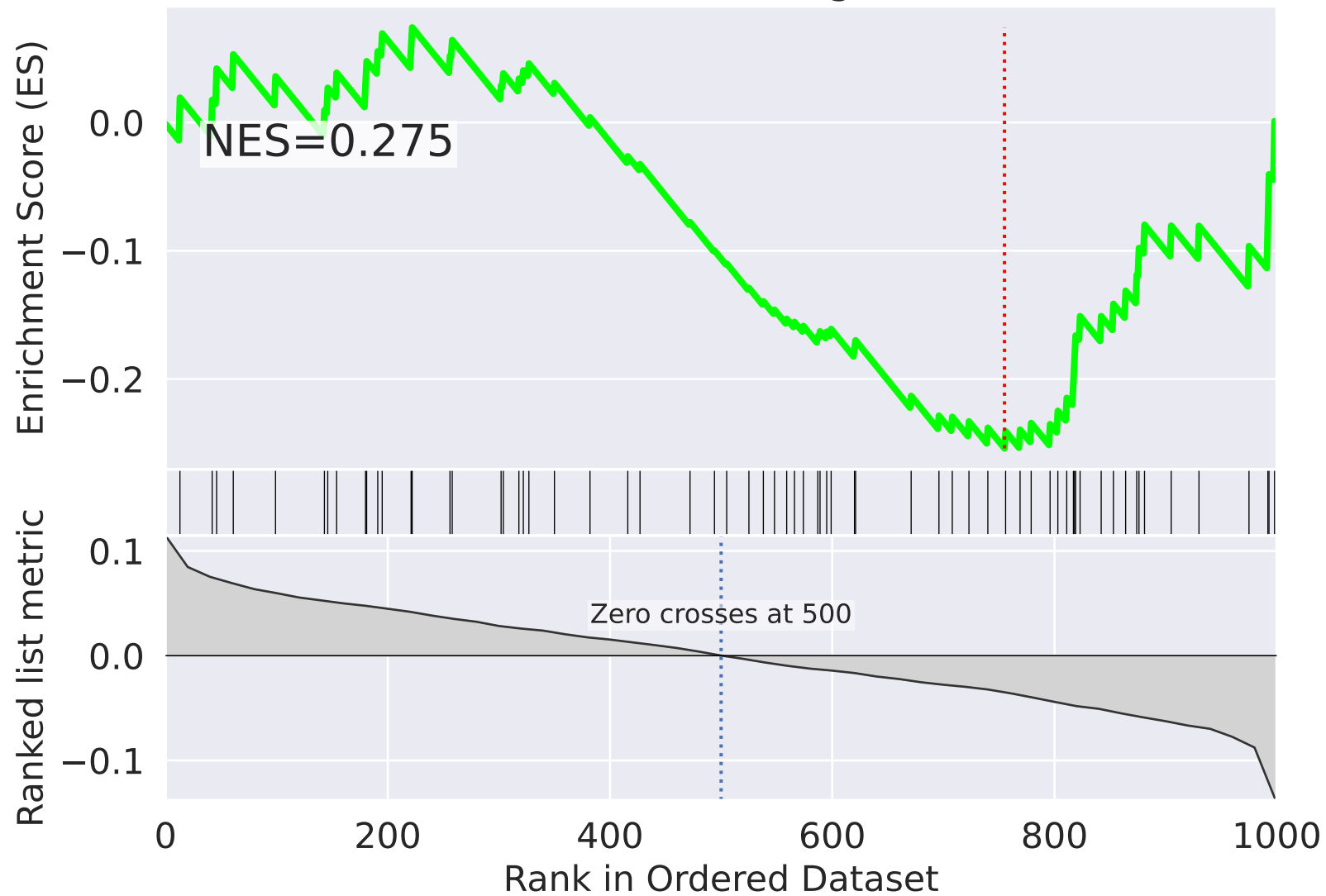
mitochondrial translational elongation (GO:0070125)



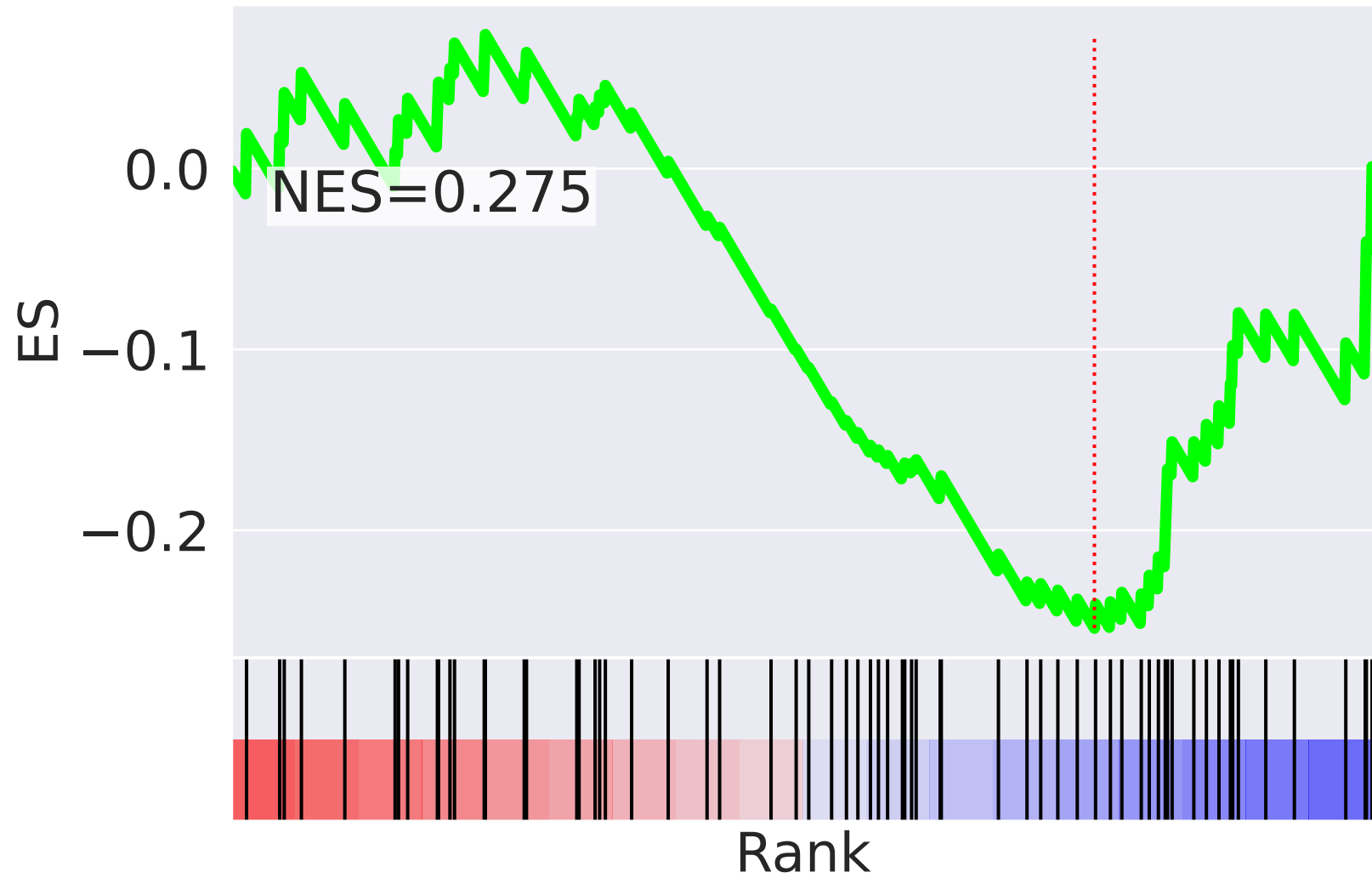
NES		SET
2.840		mitochondrial translational elongation (GO:0070125)
-2.644		cellular respiration (GO:0045333)
2.550		mitochondrial translational termination (GO:0070126)
2.522		CENP-A containing nucleosome assembly (GO:0034080)
-2.488		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.488		retrograde protein transport, ER to cytosol (GO:0030970)
-2.405		mitotic cytokinesis (GO:0000281)
2.246		proteolysis (GO:0006508)
2.081		telomere maintenance (GO:0000723)
2.059		protein targeting to mitochondrion (GO:0006626)
-2.055		rRNA processing (GO:0006364)
-2.038		nervous system development (GO:0007399)
2.004		telomere capping (GO:0016233)
-1.967		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-1.942		T cell receptor signaling pathway (GO:0050852)



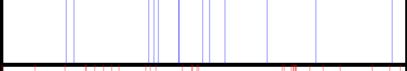
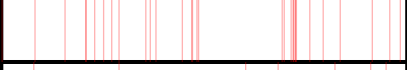
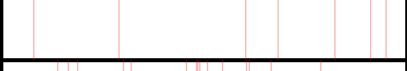
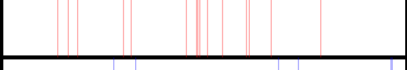
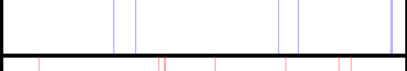
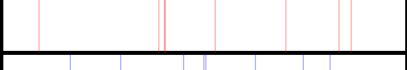
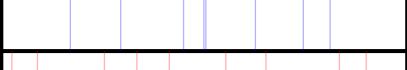




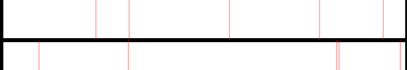
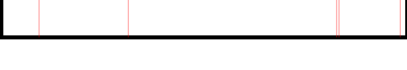
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=20$

mitochondrial translational elongation (GO:0070125)



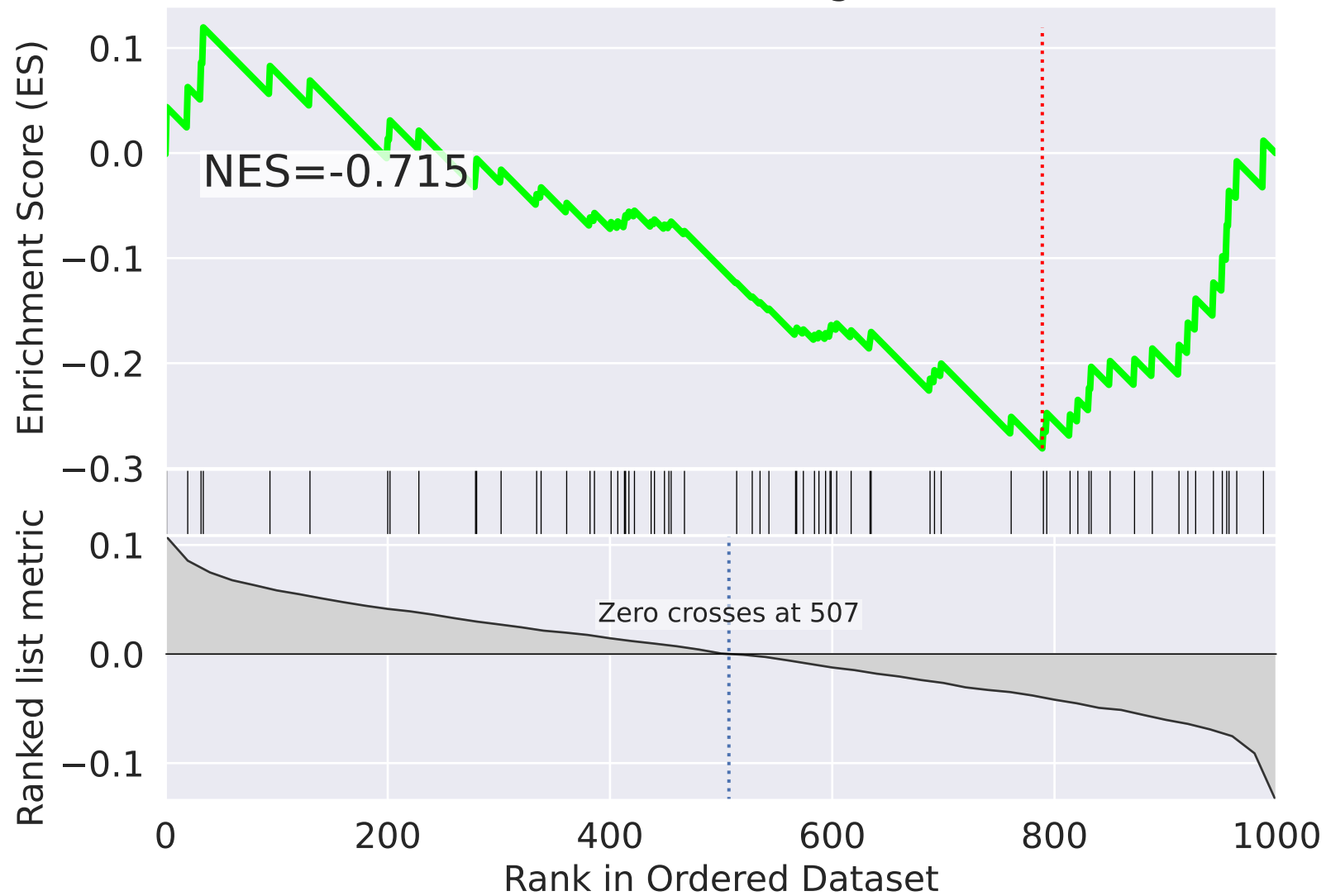
mitochondrial translational elongation (GO:0070125)



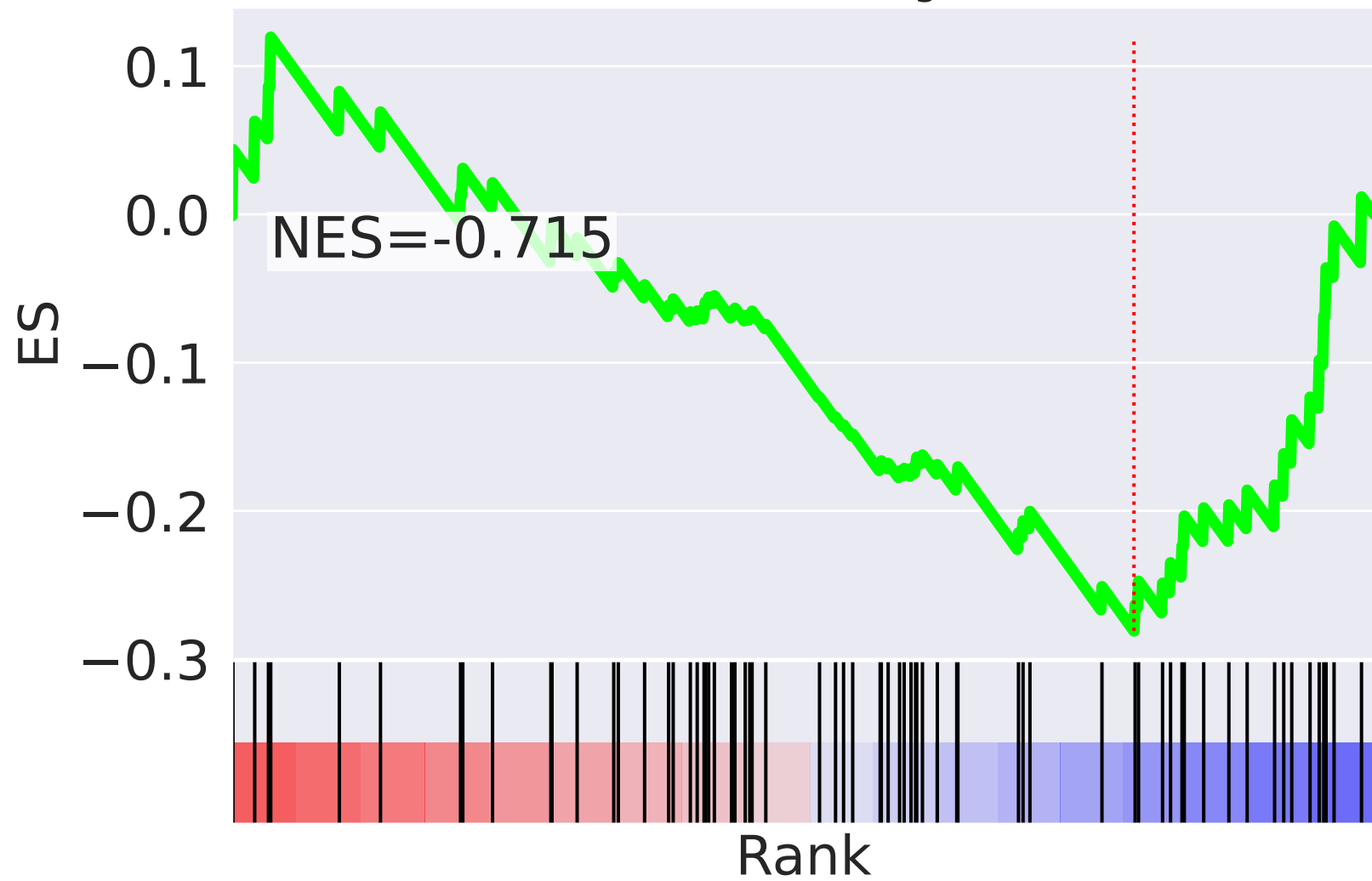
NES		SET
2.993		positive regulation of GTPase activity (GO:0043547)
2.756		androgen receptor signaling pathway (GO:0030521)
-2.631		protein stabilization (GO:0050821)
2.581		positive regulation of cell proliferation (GO:0008284)
2.542		cell-matrix adhesion (GO:0007160)
2.382		sister chromatid cohesion (GO:0007062)
-2.375		positive regulation by host of viral transcription (GO:0043923)
2.373		interstrand cross-link repair (GO:0036297)
-2.282		positive regulation of TOR signaling (GO:0032008)
2.034		tRNA aminoacylation for protein translation (GO:0006418)
-2.010		DNA replication initiation (GO:0006270)
1.928		positive regulation of protein phosphorylation (GO:0001934)
-1.889		cellular protein localization (GO:0034613)
1.888		regulation of DNA replication (GO:0006275)
1.848		positive regulation of DNA repair (GO:0045739)




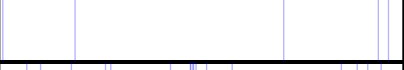
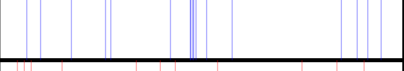




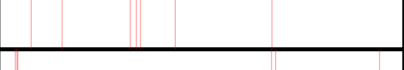
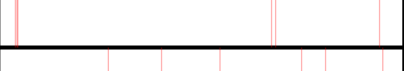
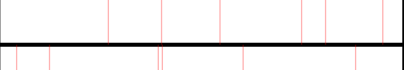


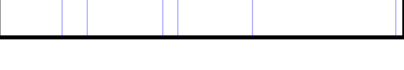
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=21$

mitochondrial translational elongation (GO:0070125)



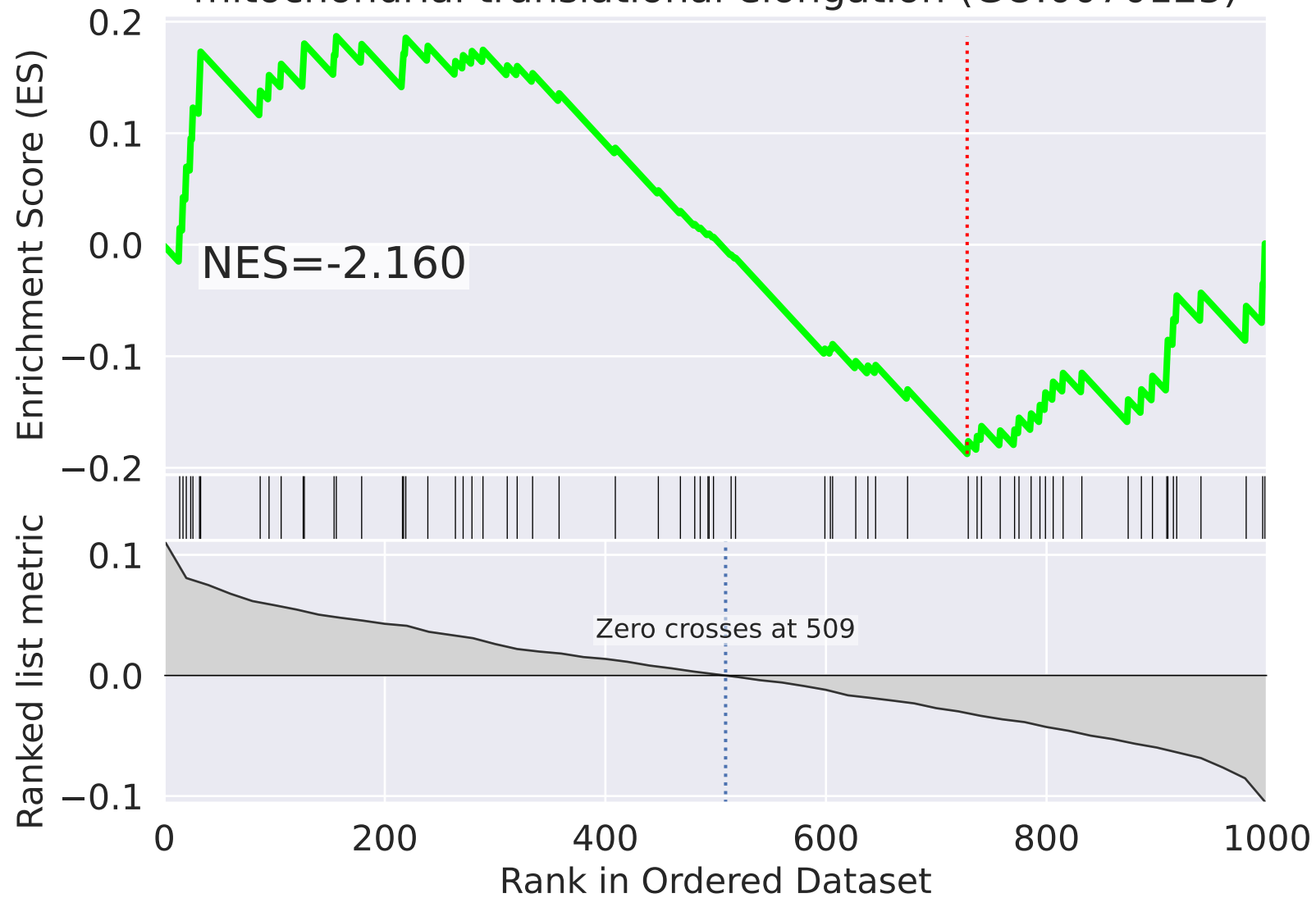
mitochondrial translational elongation (GO:0070125)



NES		SET
2.817		retrograde transport, endosome to Golgi (GO:0042147)
2.684		intracellular signal transduction (GO:0035556)
2.454		cell-matrix adhesion (GO:0007160)
-2.281		cellular respiration (GO:0045333)
-2.182		apoptotic process (GO:0006915)
2.086		epidermal growth factor receptor signaling pathway (GO:0007173)
2.072		substrate adhesion-dependent cell spreading (GO:0034446)
-2.070		regulation of apoptotic process (GO:0042981)
-1.966		transcription elongation from RNA polymerase II promoter (GO:0006368)
1.852		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
1.827		aerobic respiration (GO:0009060)
1.762		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
1.748		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
1.727		regulation of cell cycle (GO:0051726)
-1.727		phosphatidylinositol biosynthetic process (GO:0006661)

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)



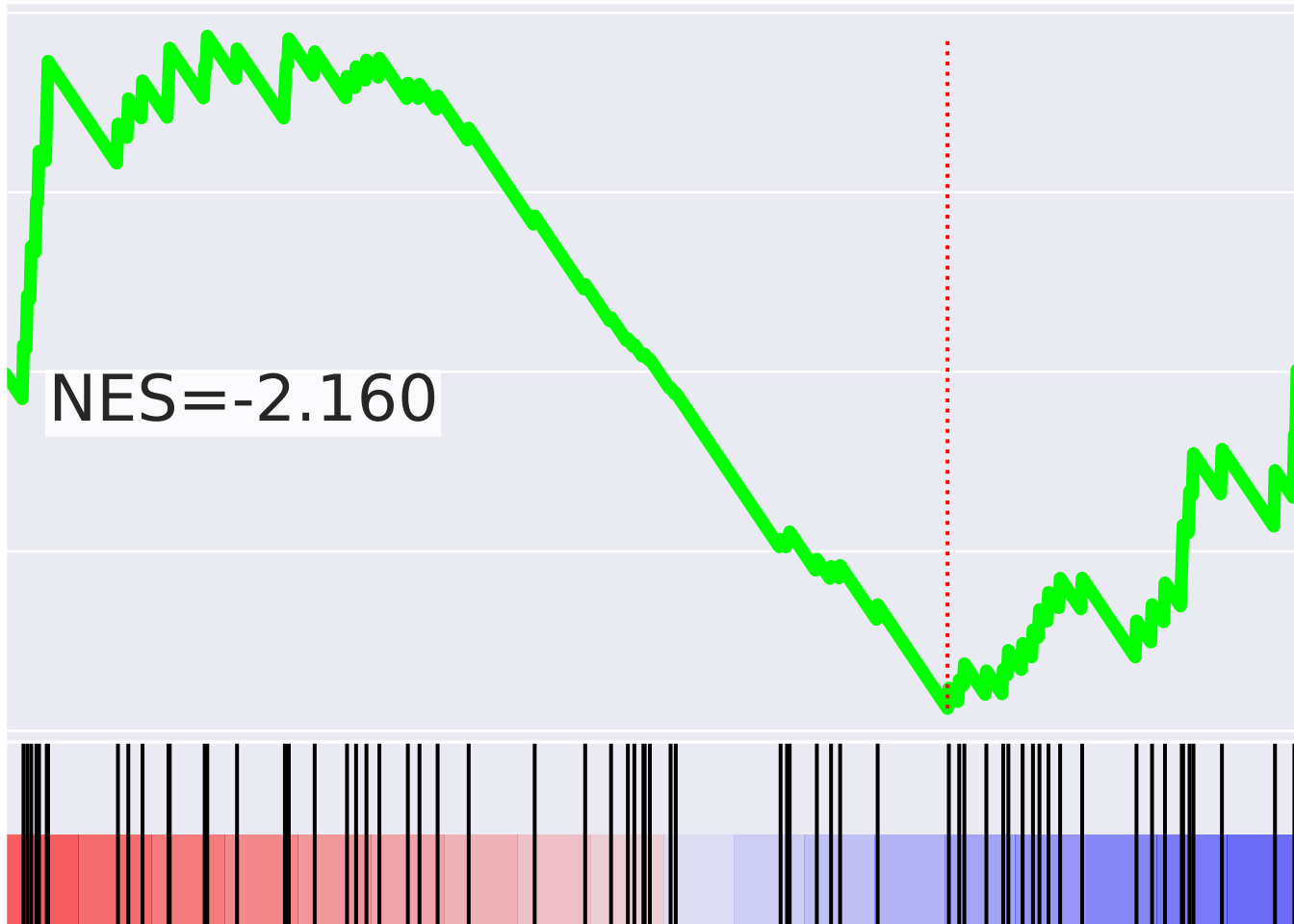
mitochondrial translational elongation (GO:0070125)

ES

NES=-2.160

0.2
0.1
0.0
-0.1
-0.2

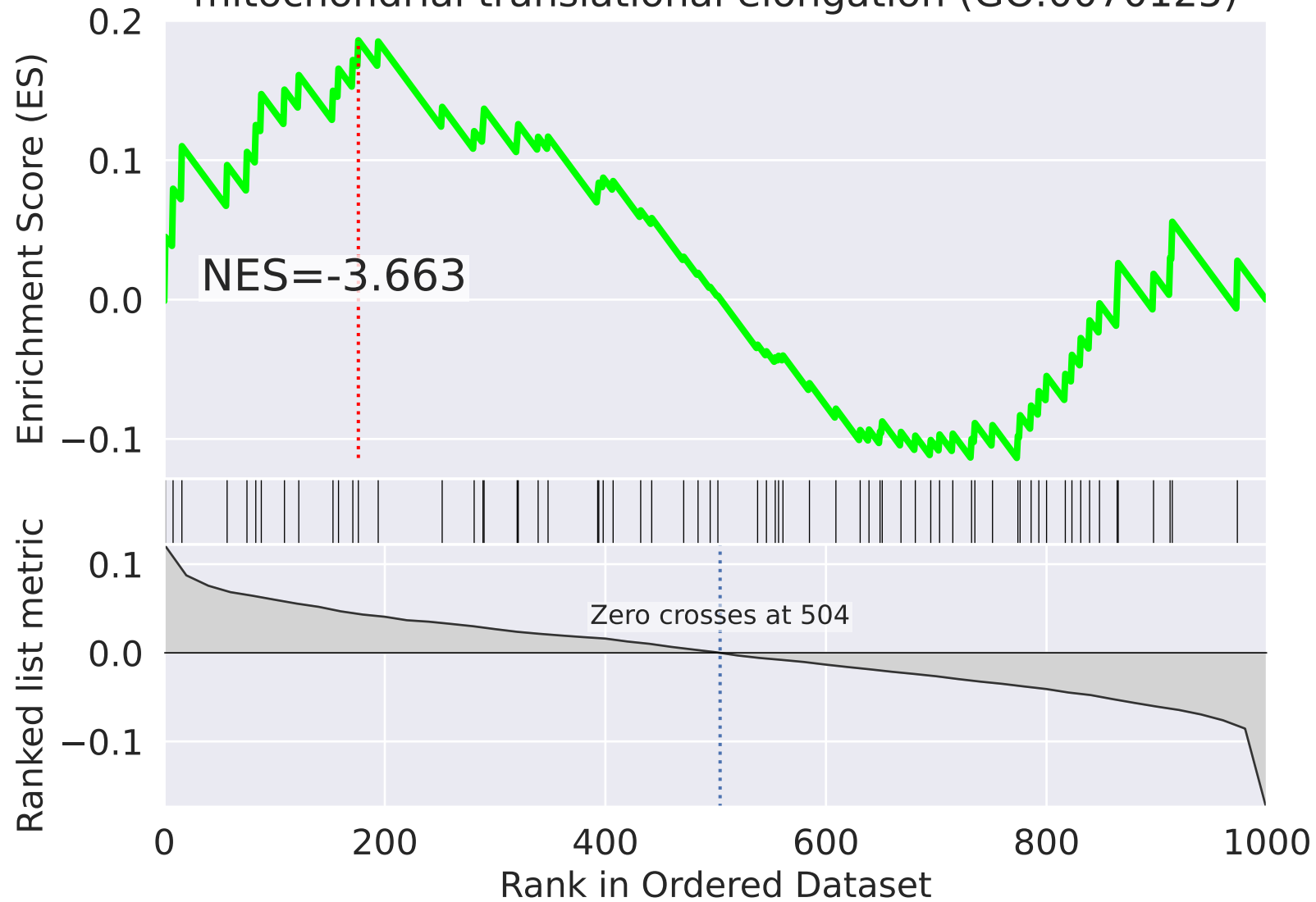
Rank



NES		SET
2.763		double-strand break repair via homologous recombination (GO:0000724)
2.572		proteolysis (GO:0006508)
2.450		RNA secondary structure unwinding (GO:0010501)
-2.415		intracellular protein transport (GO:0006886)
2.364		reciprocal meiotic recombination (GO:0007131)
2.359		CENP-A containing nucleosome assembly (GO:0034080)
-2.343		mitochondrial translational termination (GO:0070126)
2.334		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.222		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.167		mitotic cell cycle (GO:0000278)
-2.160		mitochondrial translational elongation (GO:0070125)
2.114		positive regulation of gene expression (GO:0010628)
-2.104		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.102		response to virus (GO:0009615)
2.009		strand displacement (GO:0000732)

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)



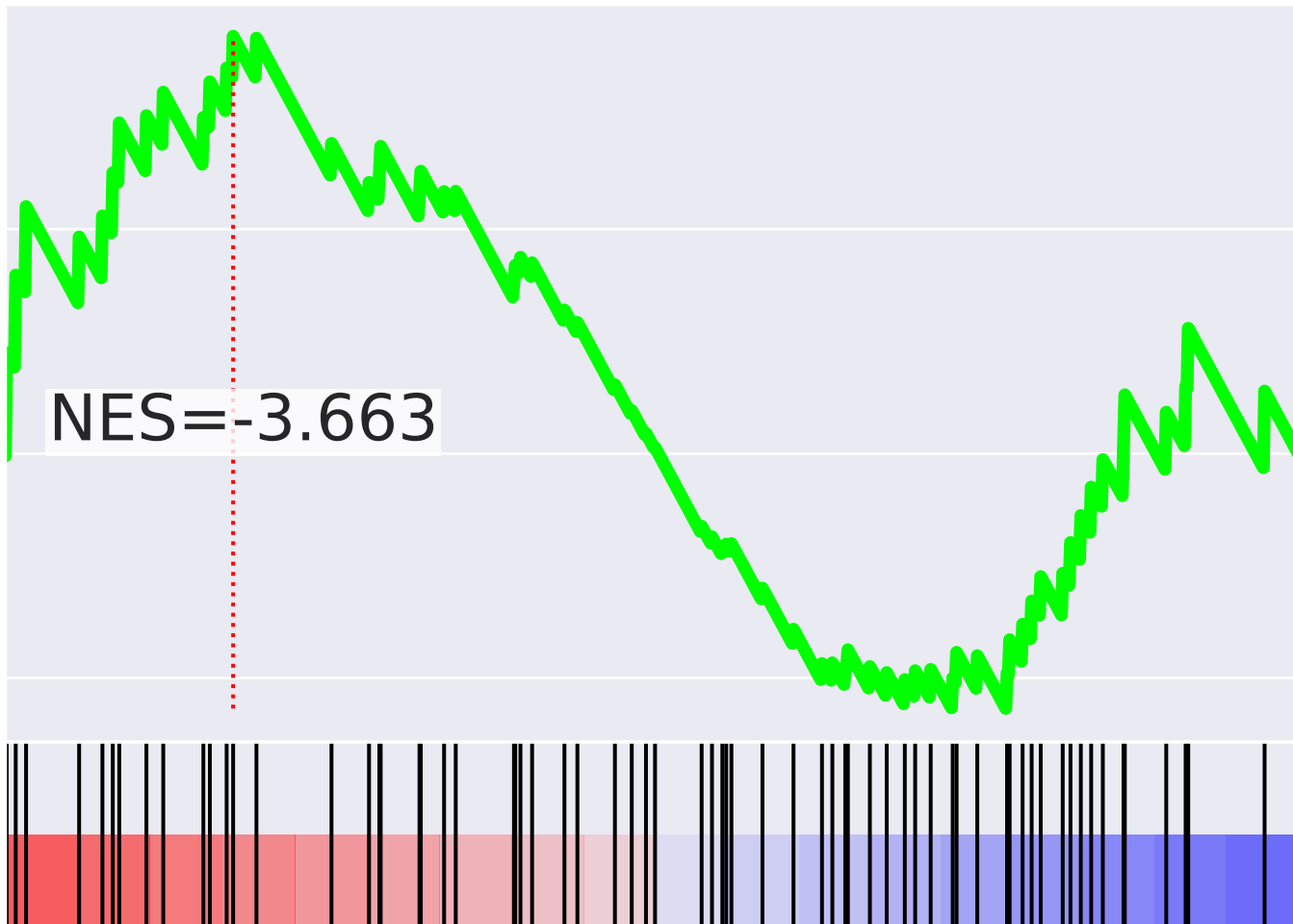
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1

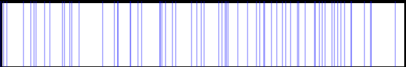
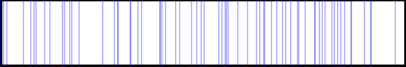



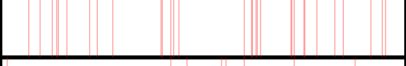
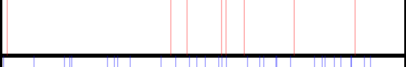
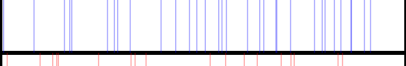
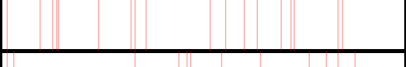

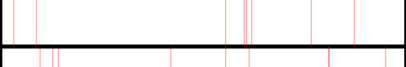
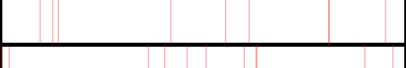
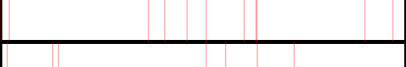
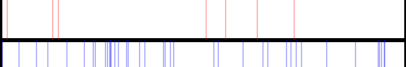

NES=-3.663

Rank



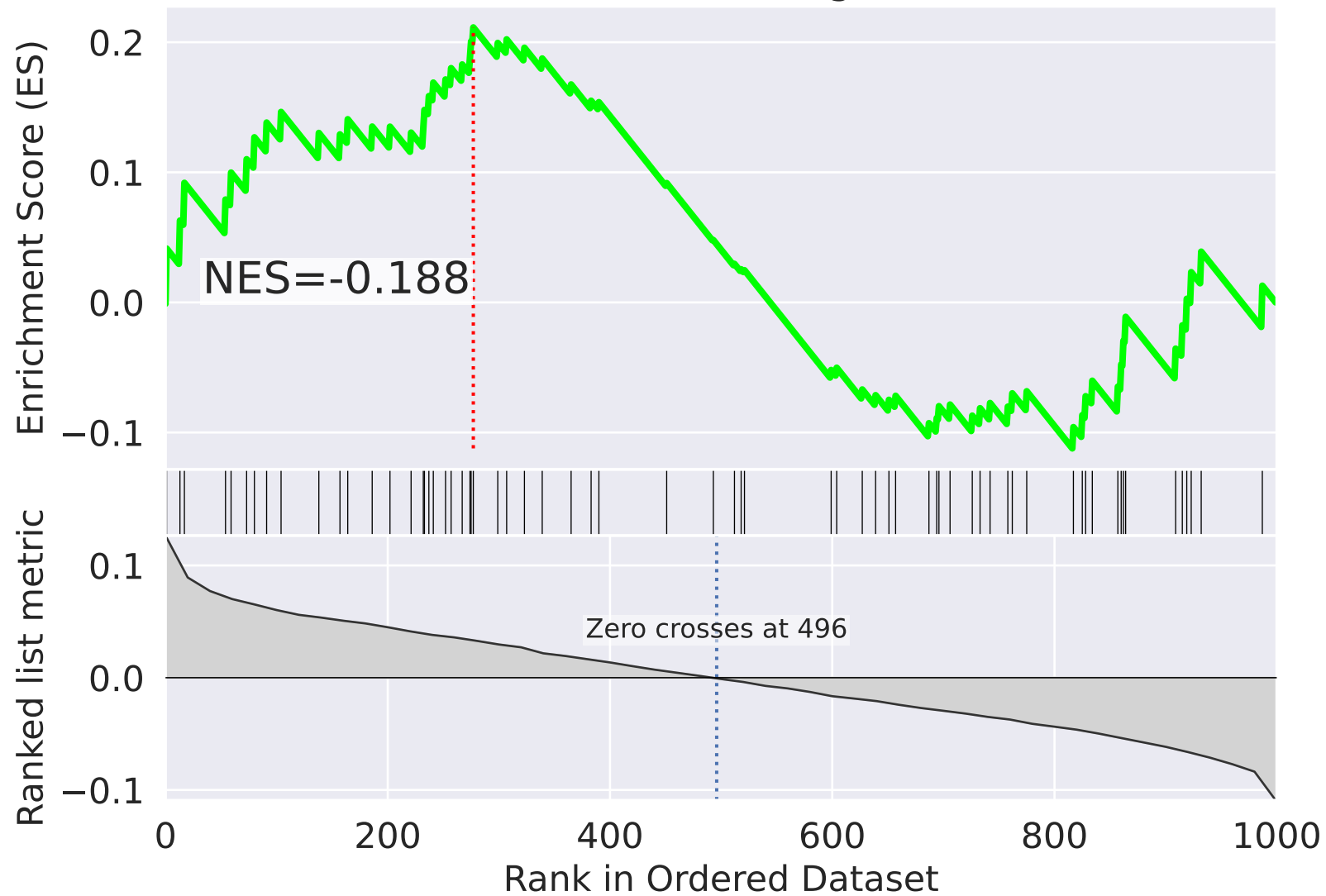
NES

SET

-3.929		mitochondrial translational termination (GO:0070126)
-3.663		mitochondrial translational elongation (GO:0070125)
3.135		Fc-epsilon receptor signaling pathway (GO:0038095)
3.008		signal transduction (GO:0007165)
2.983		positive regulation of protein phosphorylation (GO:0001934)
2.964		positive regulation of cell proliferation (GO:0008284)
2.784		protein autophosphorylation (GO:0046777)
-2.659		translation (GO:0006412)
2.578		MAPK cascade (GO:0000165)
2.550		protein phosphorylation (GO:0006468)
2.522		regulation of cell proliferation (GO:0042127)
2.448		insulin receptor signaling pathway (GO:0008286)
2.341		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.317		ERBB2 signaling pathway (GO:0038128)
-2.294		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 $z=24$

mitochondrial translational elongation (GO:0070125)



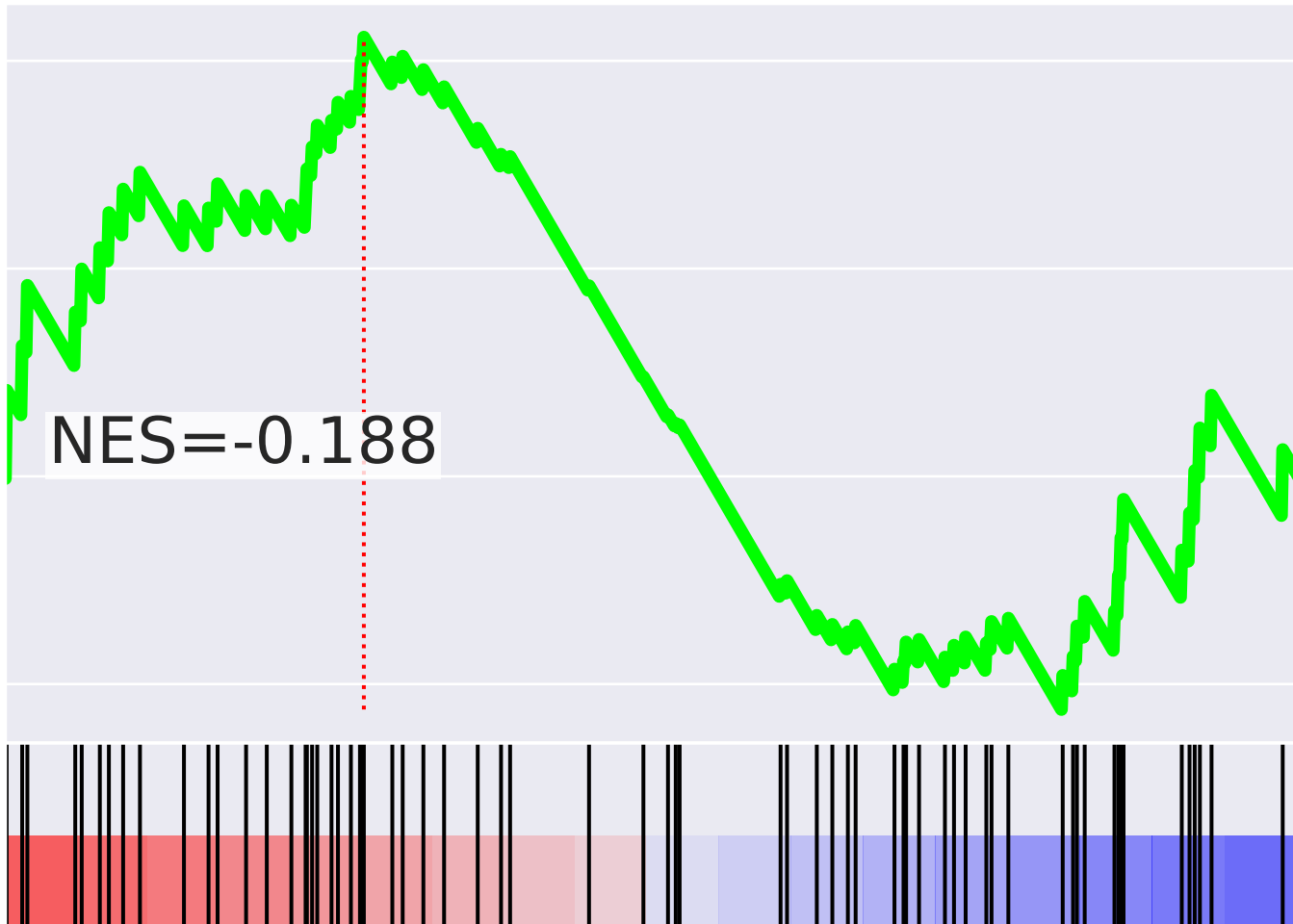
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1







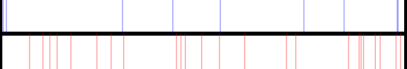
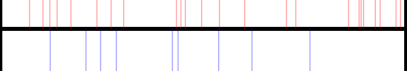

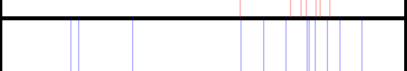

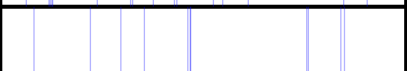

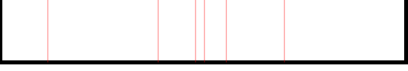

NES=-0.188

Rank



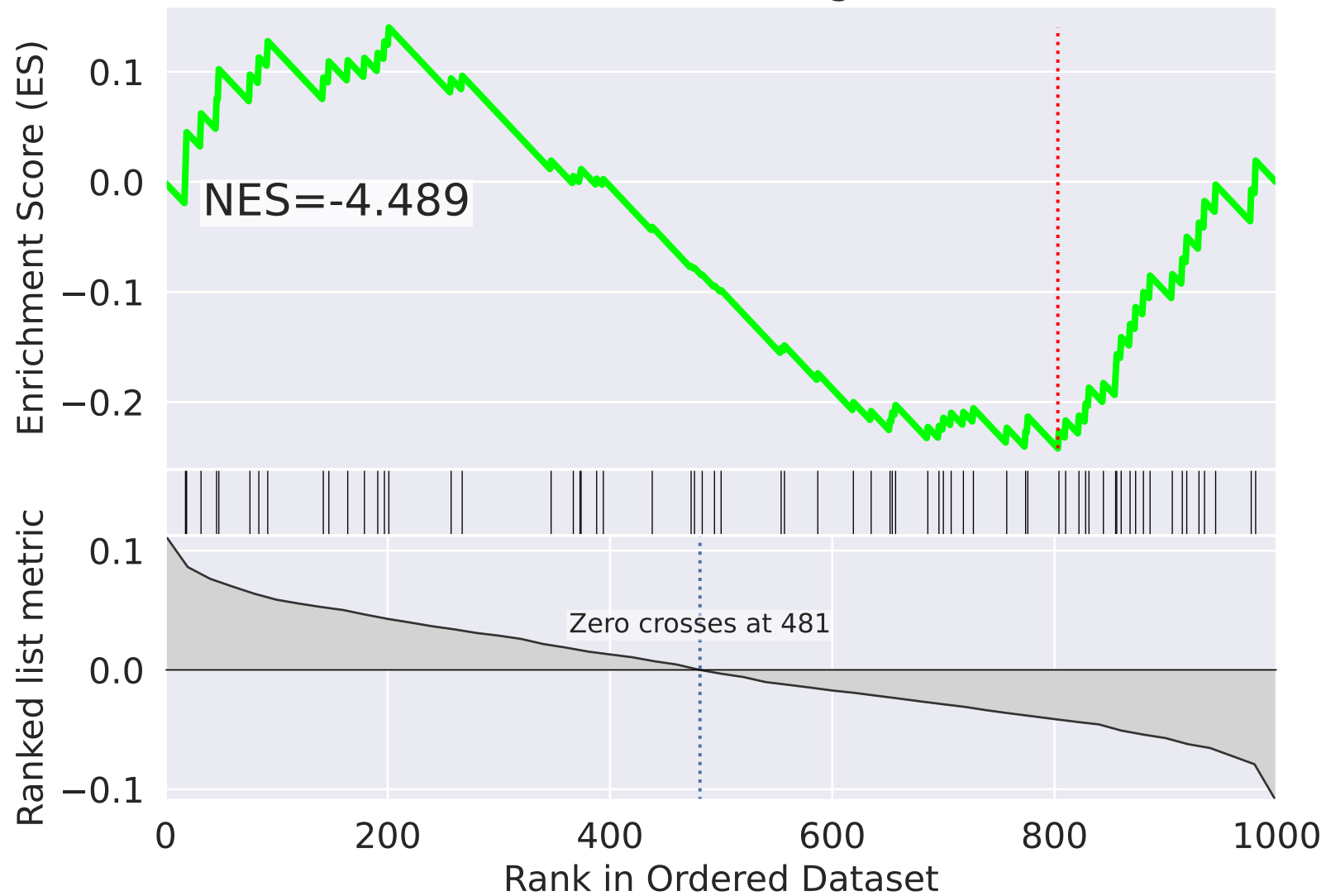
NES

SET

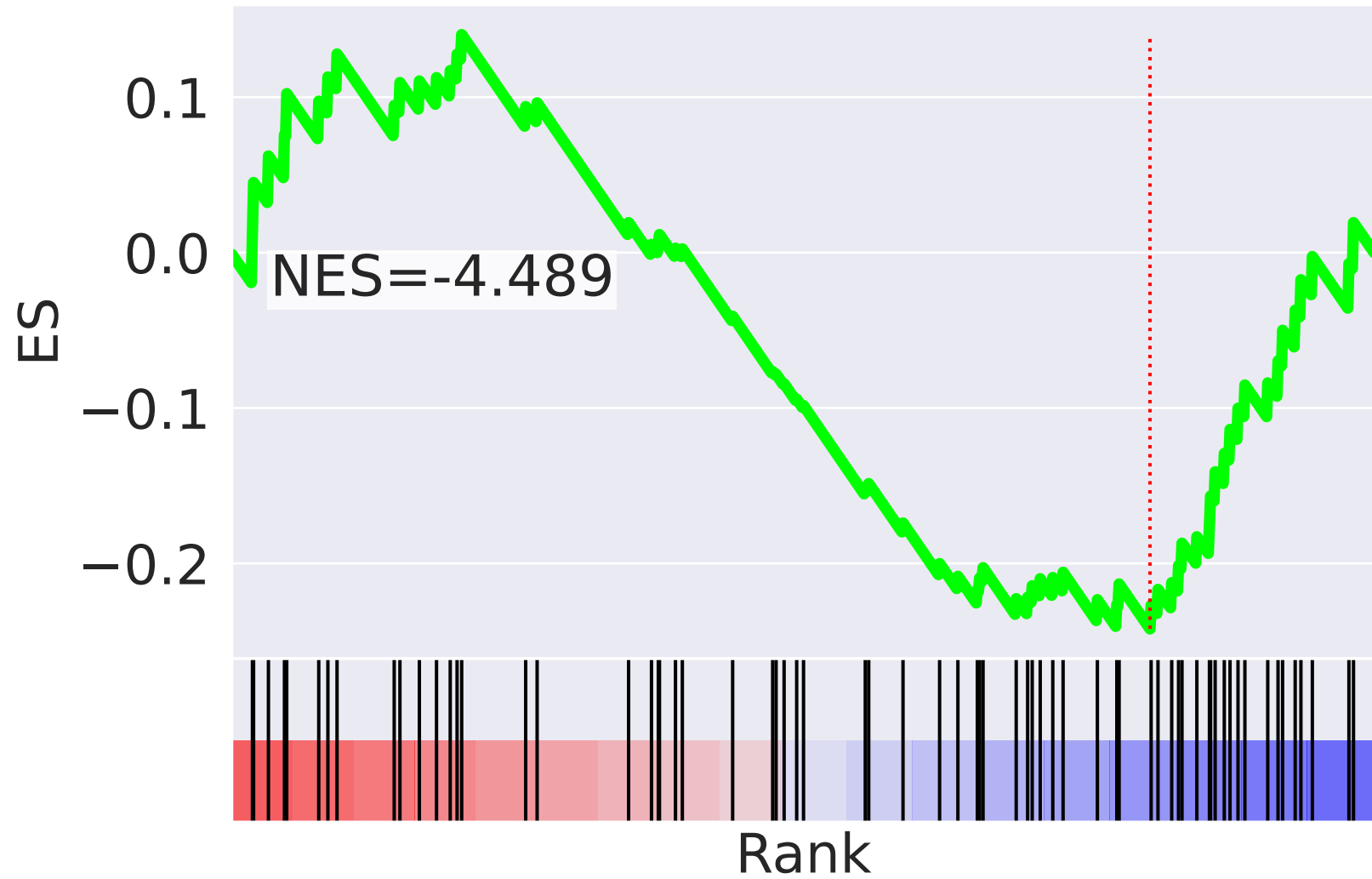
-2.990		generation of precursor metabolites and energy (GO:0006091)
2.613		positive regulation of GTPase activity (GO:0043547)
2.487		telomere maintenance (GO:0000723)
-2.474		protein ubiquitination (GO:0016567)
-2.462		nucleotide-excision repair (GO:0006289)
-2.454		cellular response to DNA damage stimulus (GO:0006974)
-2.322		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.302		regulation of transcription, DNA-templated (GO:0006355)
-2.250		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.240		intracellular protein transport (GO:0006886)
-2.200		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.194		G1/S transition of mitotic cell cycle (GO:0000082)
-2.184		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.164		RNA secondary structure unwinding (GO:0010501)
2.134		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)

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)

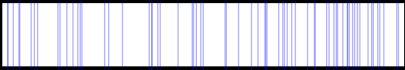
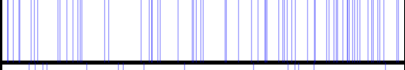




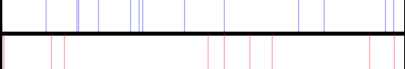
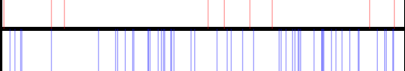
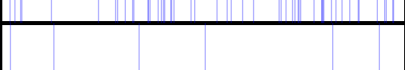
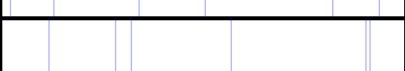



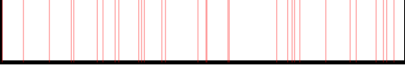



mitochondrial translational elongation (GO:0070125)



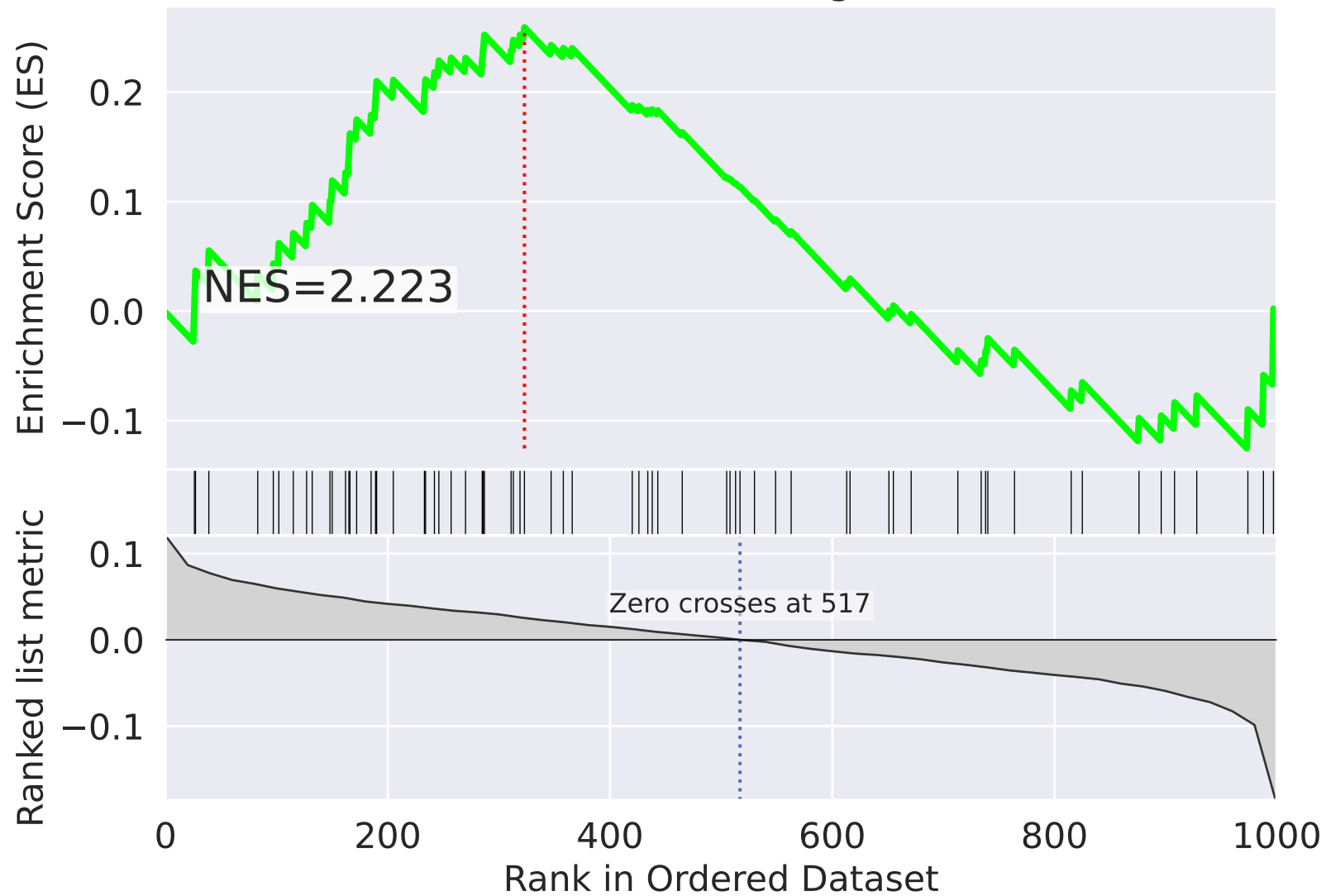
NES

SET

-4.521		mitochondrial translational termination (GO:0070126)
-4.489		mitochondrial translational elongation (GO:0070125)
-2.918		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-2.791		axon guidance (GO:0007411)
-2.685		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.581		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.560		Fc-epsilon receptor signaling pathway (GO:0038095)
2.471		intracellular signal transduction (GO:0035556)
-2.355		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.311		phosphatidylinositol biosynthetic process (GO:0006661)
-2.255		transcription-coupled nucleotide-excision repair (GO:0006283)
-2.255		transcription from RNA polymerase II promoter (GO:0006366)
2.222		viral budding via host ESCRT complex (GO:0039702)
-2.197		ERBB2 signaling pathway (GO:0038128)
2.187		mitochondrial respiratory chain complex I assembly (GO:0032981)

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)

ES

0.2

0.1

0.0

-0.1

NES=2.223

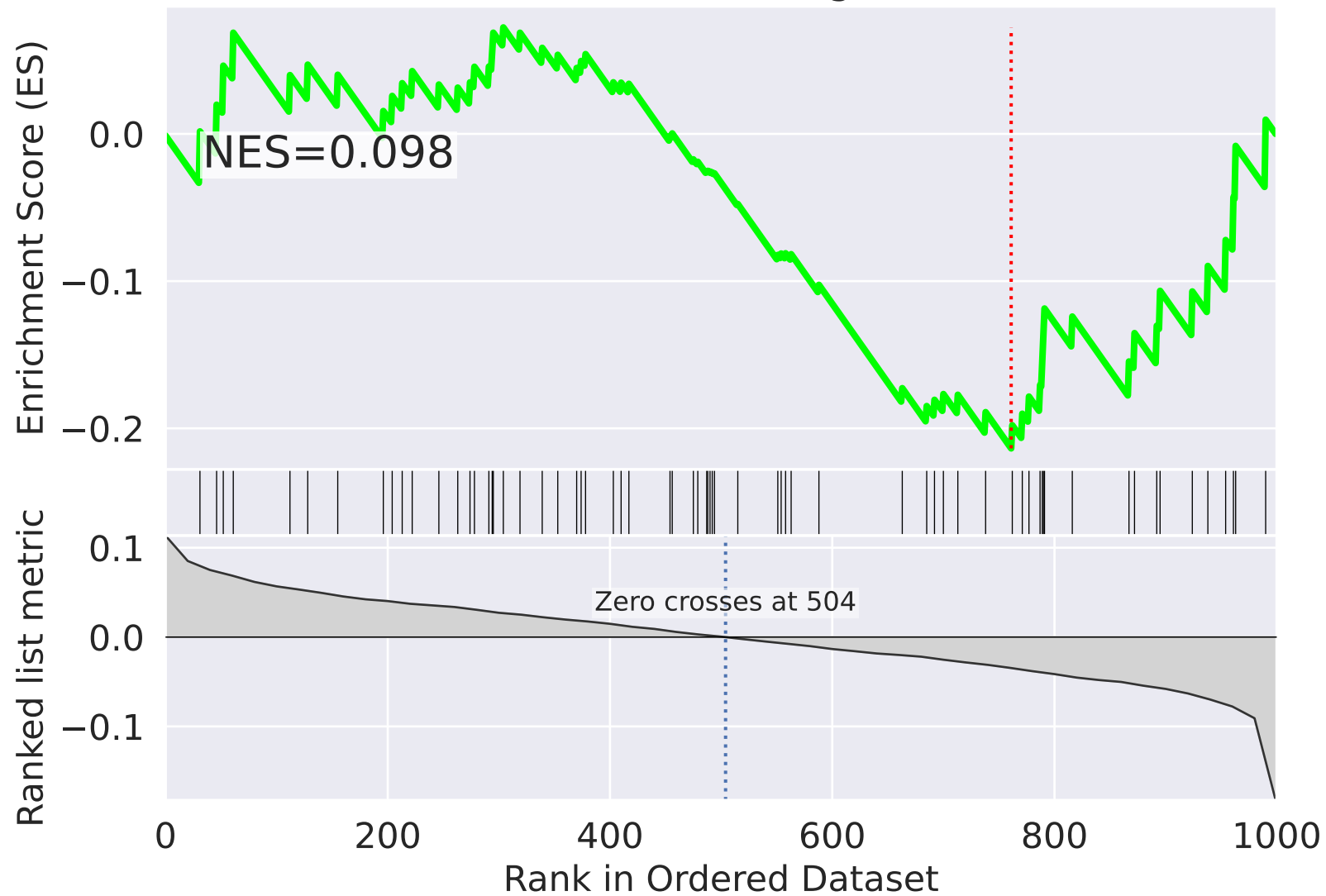
Rank



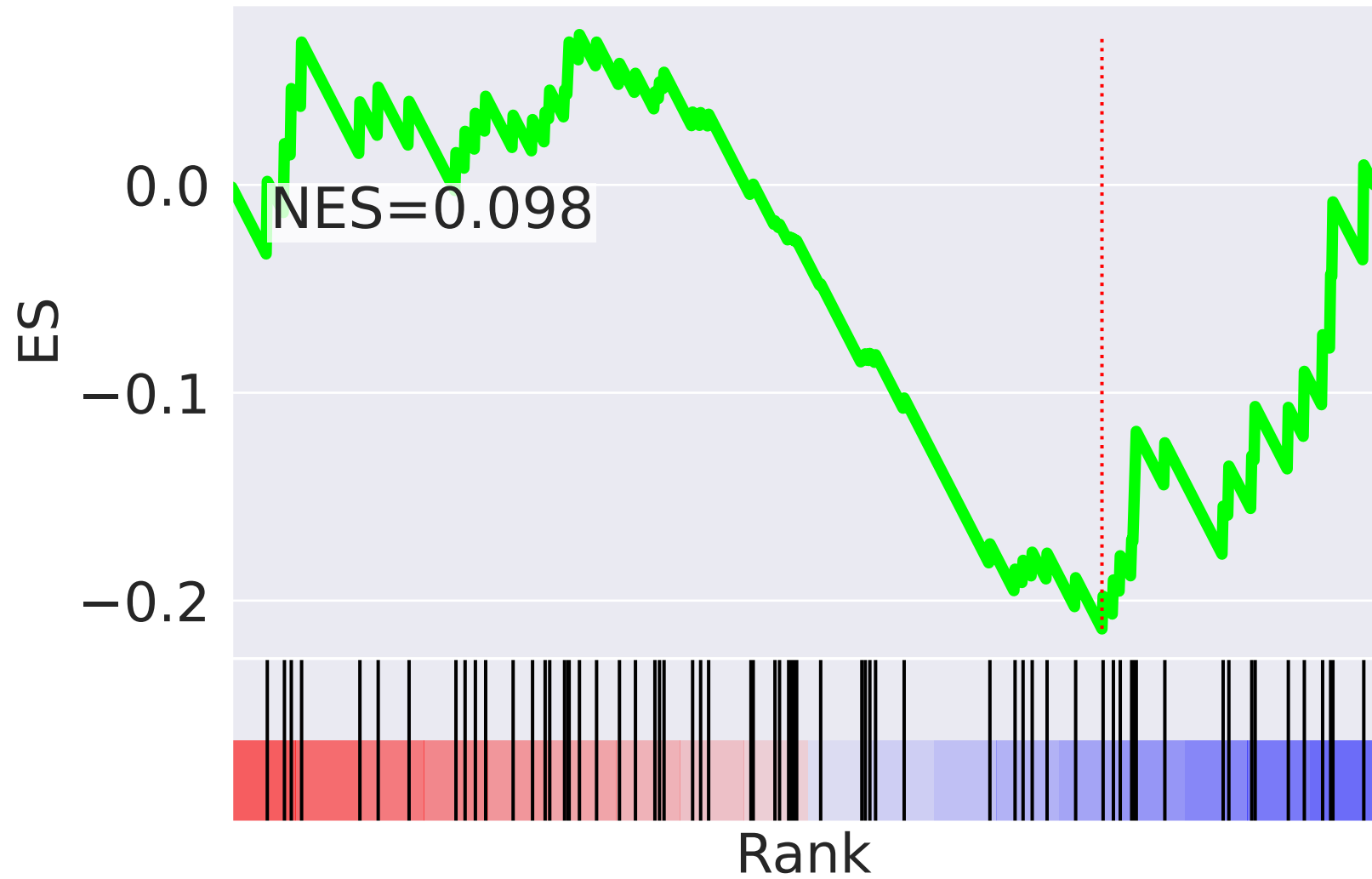
NES		SET
3.182		positive regulation of apoptotic process (GO:0043065)
-2.739		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.594		rRNA processing (GO:0006364)
-2.434		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.338		transcription from RNA polymerase II promoter (GO:0006366)
-2.295		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.223		mitochondrial translational elongation (GO:0070125)
2.217		translation (GO:0006412)
2.102		double-strand break repair via homologous recombination (GO:0000724)
-1.994		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-1.991		cellular respiration (GO:0045333)
-1.990		transcription initiation from RNA polymerase I promoter (GO:0006361)
-1.990		transcription elongation from RNA polymerase I promoter (GO:0006362)
-1.990		termination of RNA polymerase I transcription (GO:0006363)
1.924		reciprocal meiotic recombination (GO:0007131)

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)



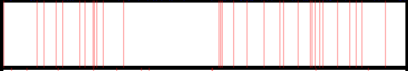
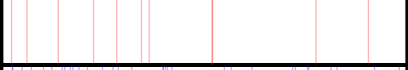




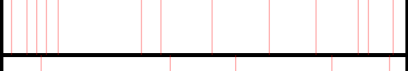
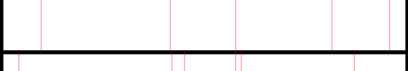
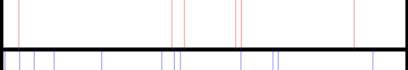
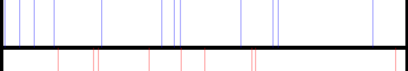
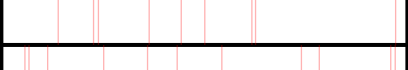
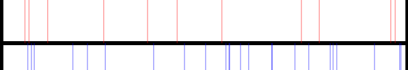



mitochondrial translational elongation (GO:0070125)



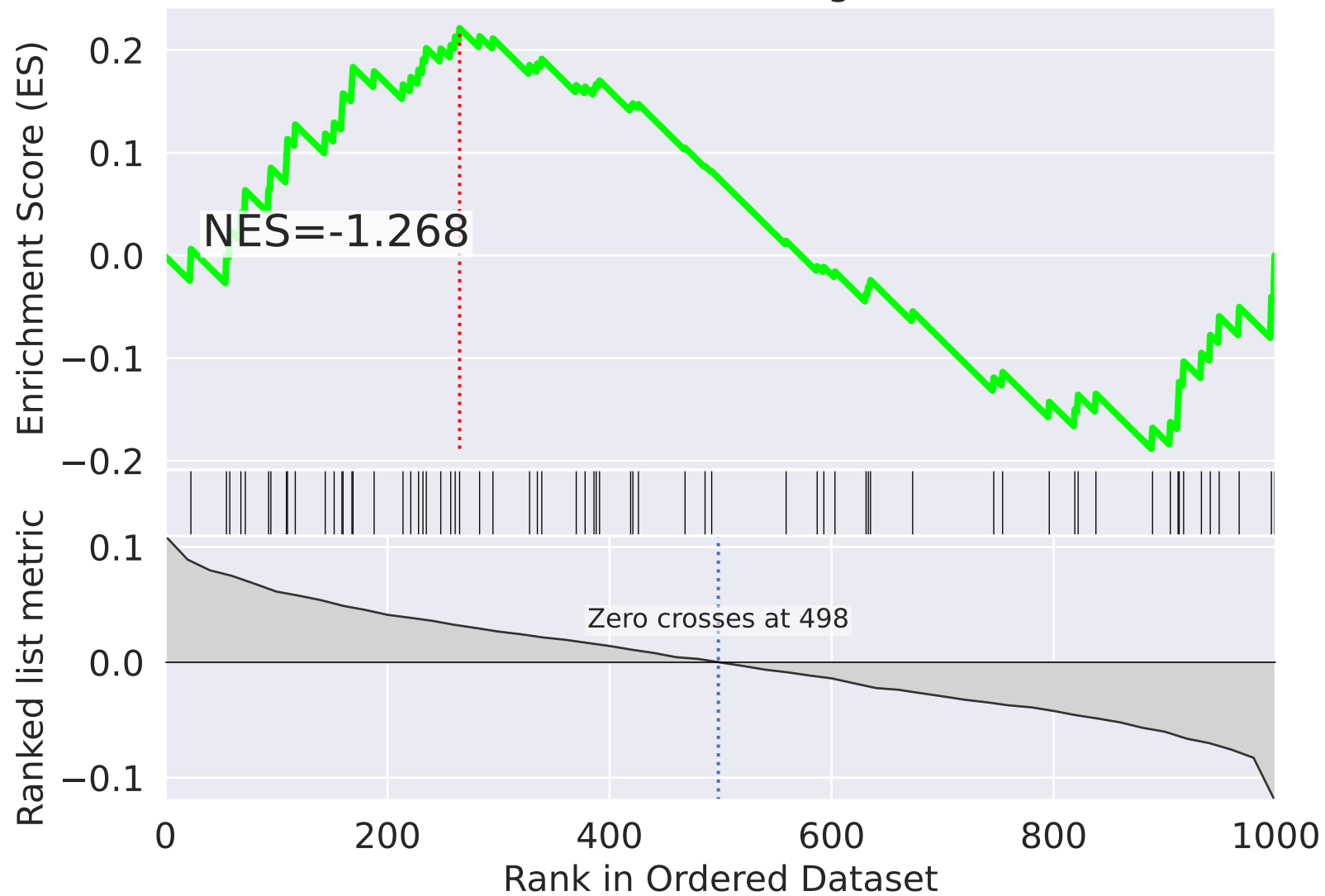
NES

SET

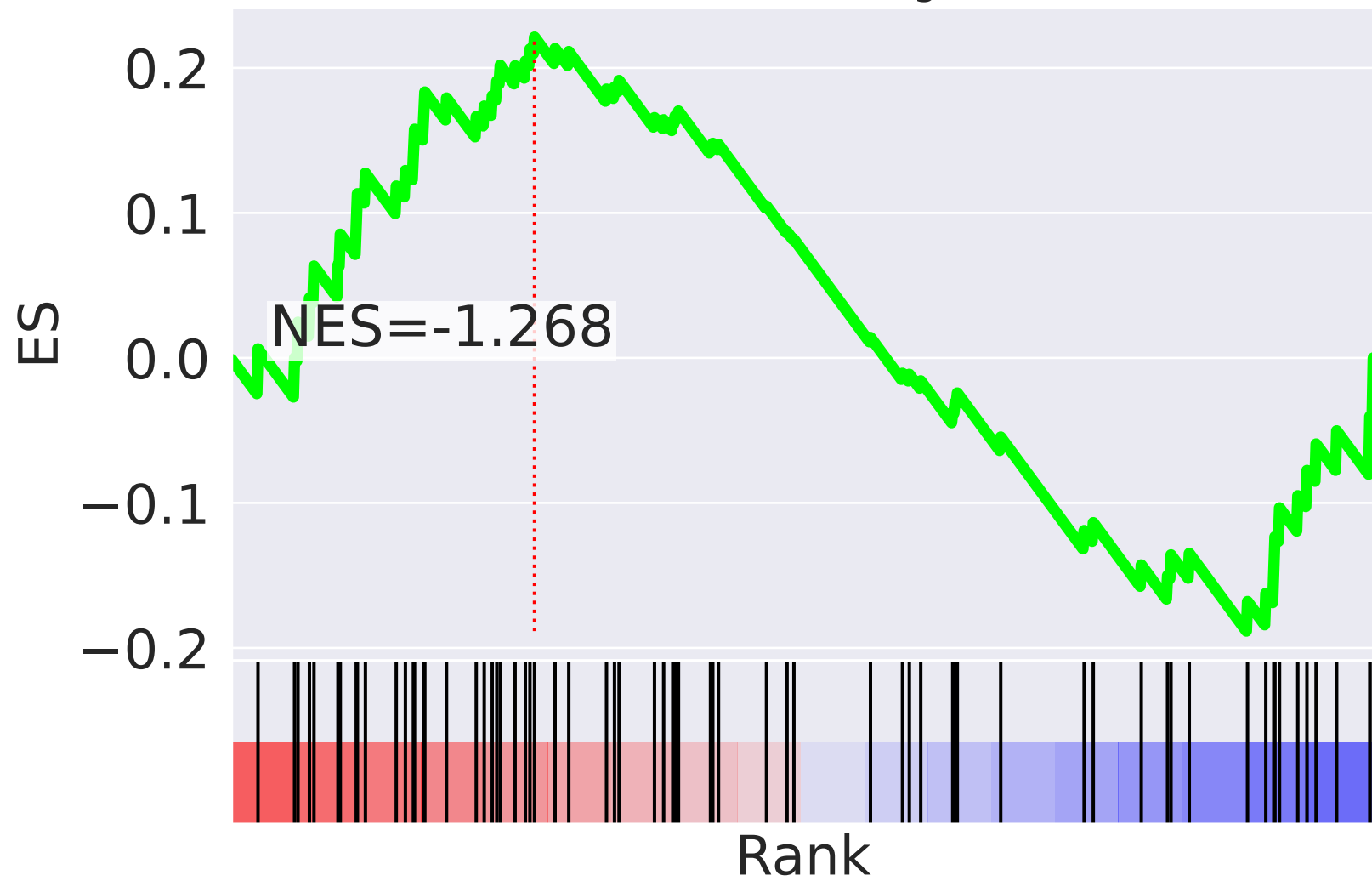
-3.296		transcription from RNA polymerase II promoter (GO:0006366)
-3.223		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
3.112		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.058		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.790		negative regulation of transcription, DNA-templated (GO:0045892)
-2.760		transcription-coupled nucleotide-excision repair (GO:0006283)
-2.637		chromatin remodeling (GO:0006338)
2.558		mitotic metaphase plate congression (GO:0007080)
2.512		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.492		iron-sulfur cluster assembly (GO:0016226)
2.411		chromosome segregation (GO:0007059)
-2.390		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.262		transforming growth factor beta receptor signaling pathway (GO:0007179)
2.199		generation of precursor metabolites and energy (GO:0006091)
-2.115		regulation of transcription, DNA-templated (GO:0006355)



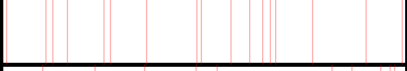
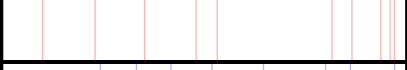
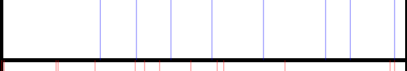


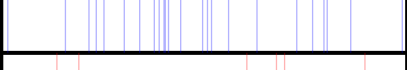

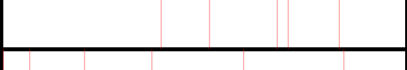


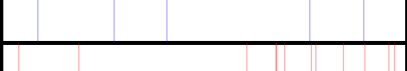
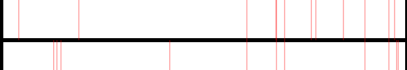

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=28$

mitochondrial translational elongation (GO:0070125)



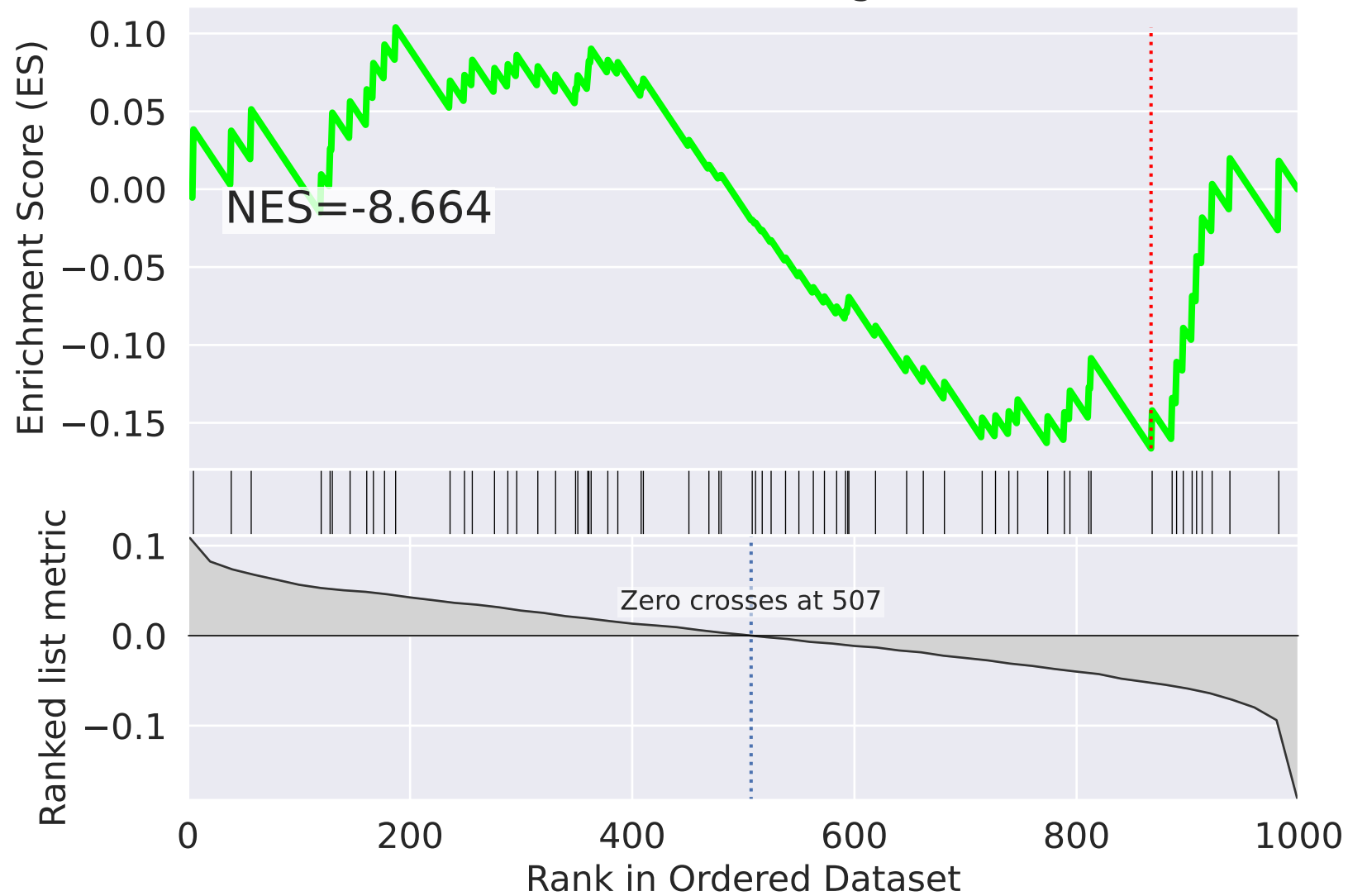
mitochondrial translational elongation (GO:0070125)



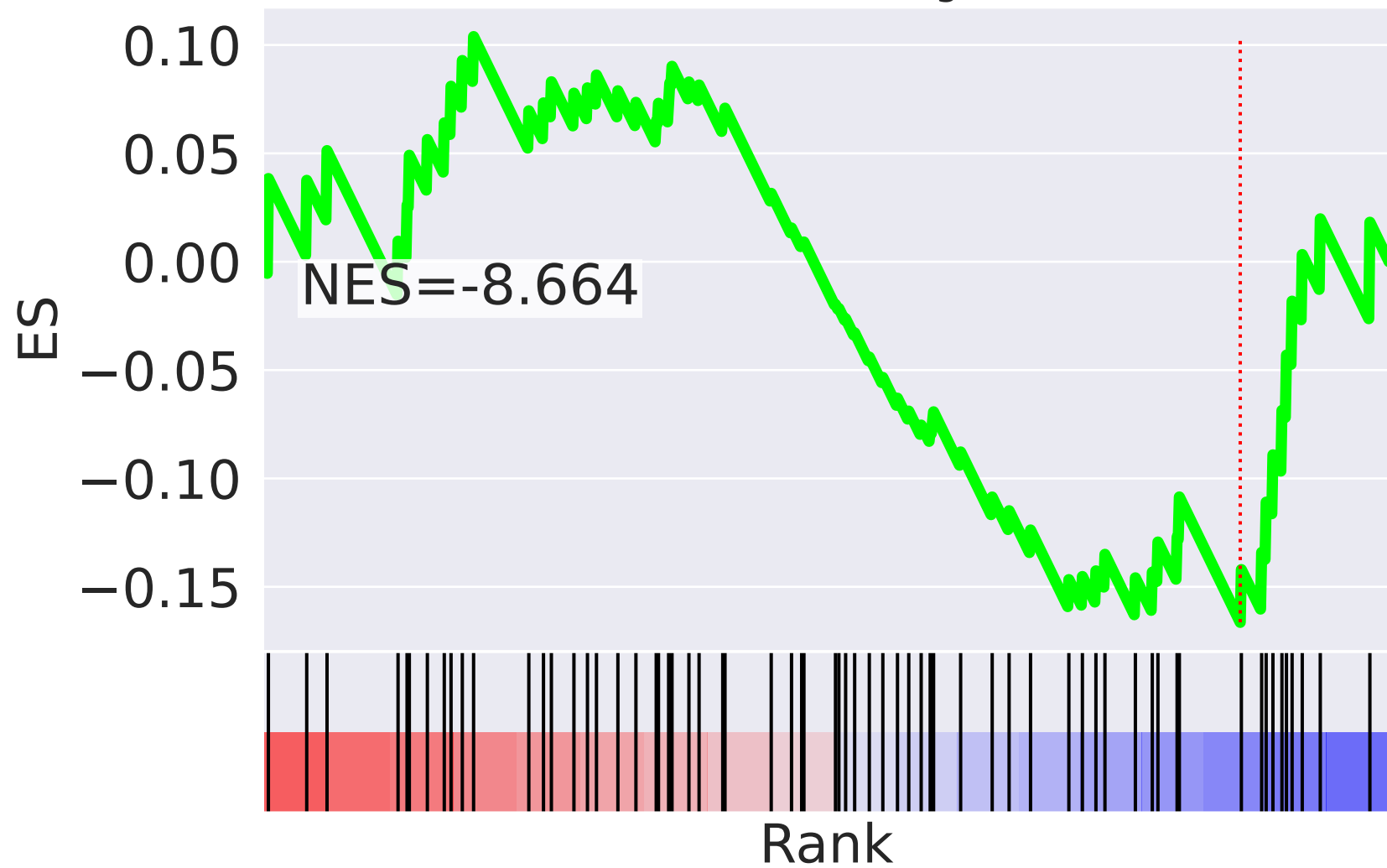
NES		SET
2.478		viral life cycle (GO:0019058)
2.454		macroautophagy (GO:0016236)
2.437		apoptotic process (GO:0006915)
2.236		protein polyubiquitination (GO:0000209)
-2.220		integrin-mediated signaling pathway (GO:0007229)
2.177		ubiquitin-dependent protein catabolic process (GO:0006511)
2.166		multivesicular body assembly (GO:0036258)
-2.157		regulation of transcription, DNA-templated (GO:0006355)
2.075		viral budding via host ESCRT complex (GO:0039702)
1.994		nucleosome disassembly (GO:0006337)
1.959		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-1.947		tricarboxylic acid cycle (GO:0006099)
-1.933		lysosomal transport (GO:0007041)
1.916		mitotic metaphase plate congression (GO:0007080)
1.877		endosomal transport (GO:0016197)

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

mitochondrial translational elongation (GO:0070125)



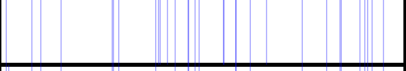
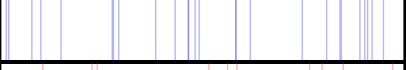
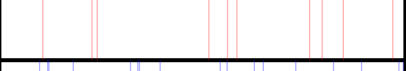
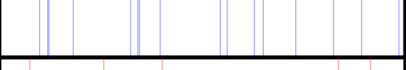
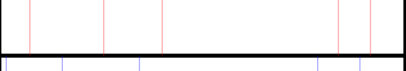
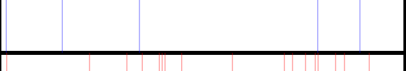


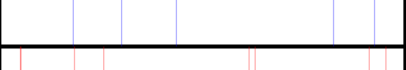
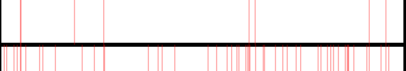
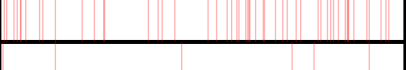
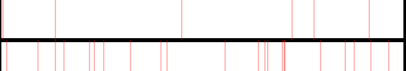
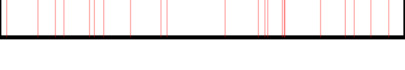


mitochondrial translational elongation (GO:0070125)



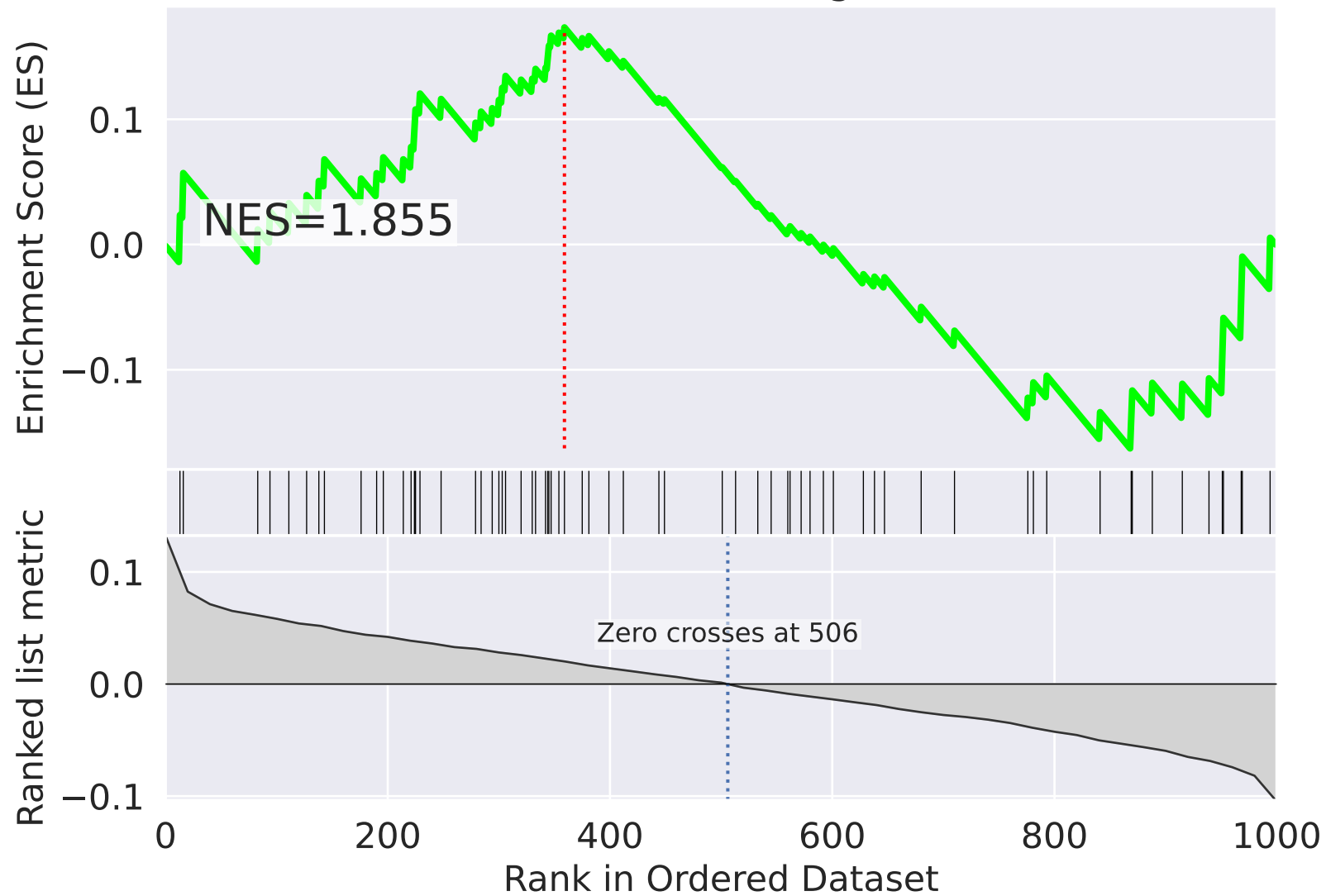
NES

SET

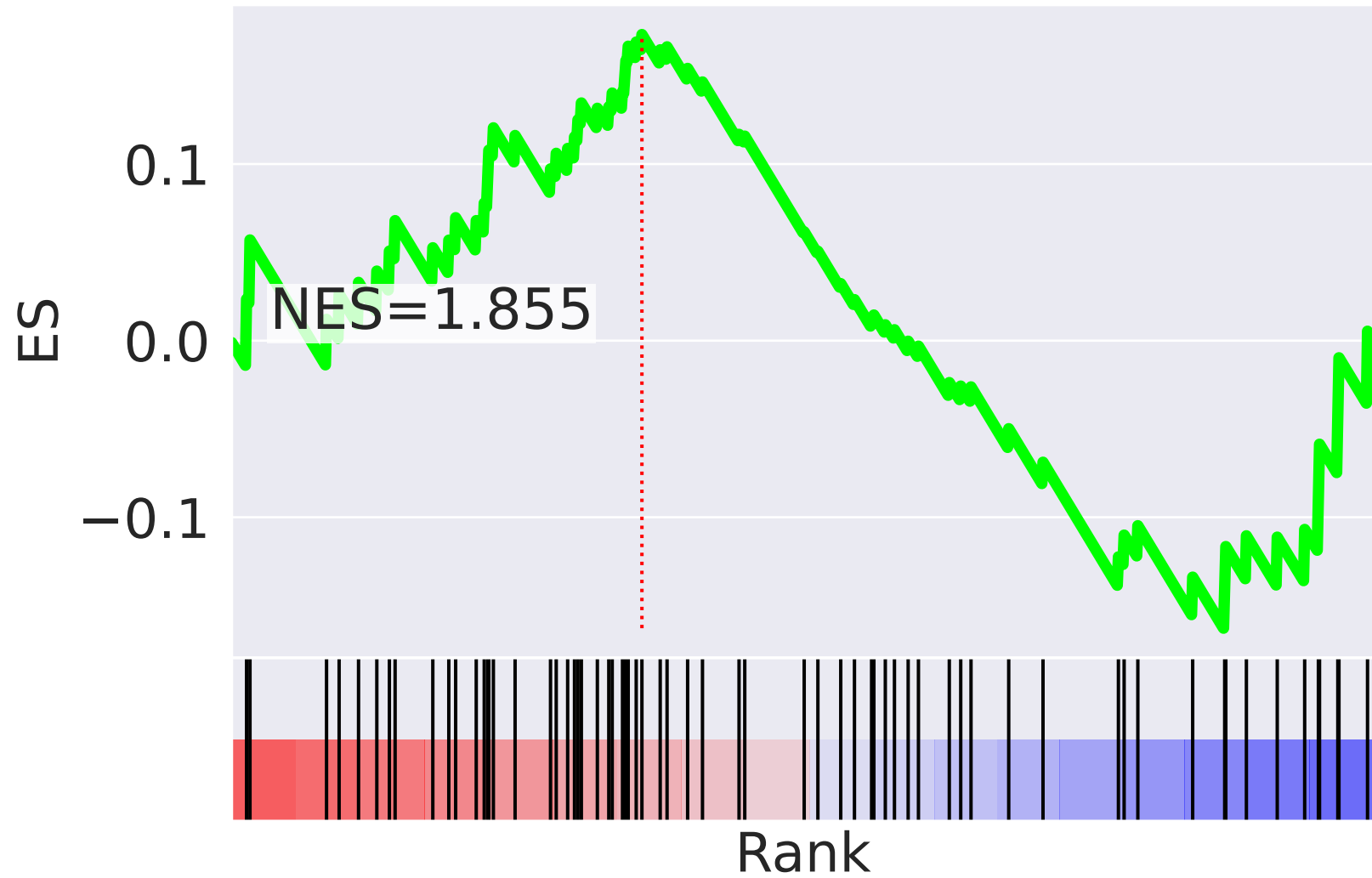
-8.974		mitochondrial translational termination (GO:0070126)
-8.664		mitochondrial translational elongation (GO:0070125)
-3.395		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.930		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.745		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.549		mitochondrion organization (GO:0007005)
2.525		positive regulation of type I interferon production (GO:0032481)
-2.495		cellular respiration (GO:0045333)
2.424		apoptotic process (GO:0006915)
2.400		platelet aggregation (GO:0070527)
-2.353		DNA-dependent DNA replication (GO:0006261)
2.305		androgen receptor signaling pathway (GO:0030521)
2.304		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.286		chromosome segregation (GO:0007059)
2.283		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 $z=30$

mitochondrial translational elongation (GO:0070125)



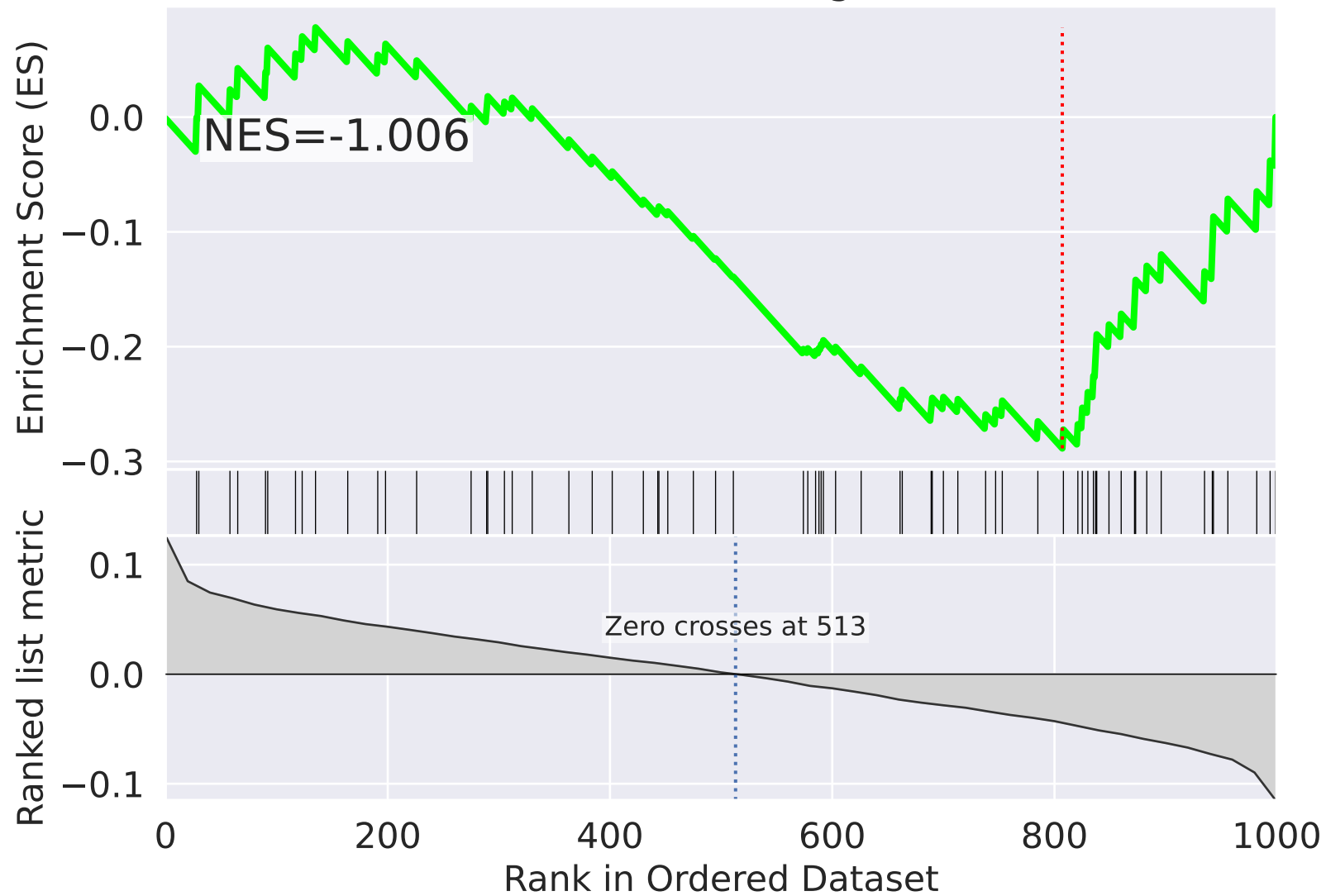
mitochondrial translational elongation (GO:0070125)



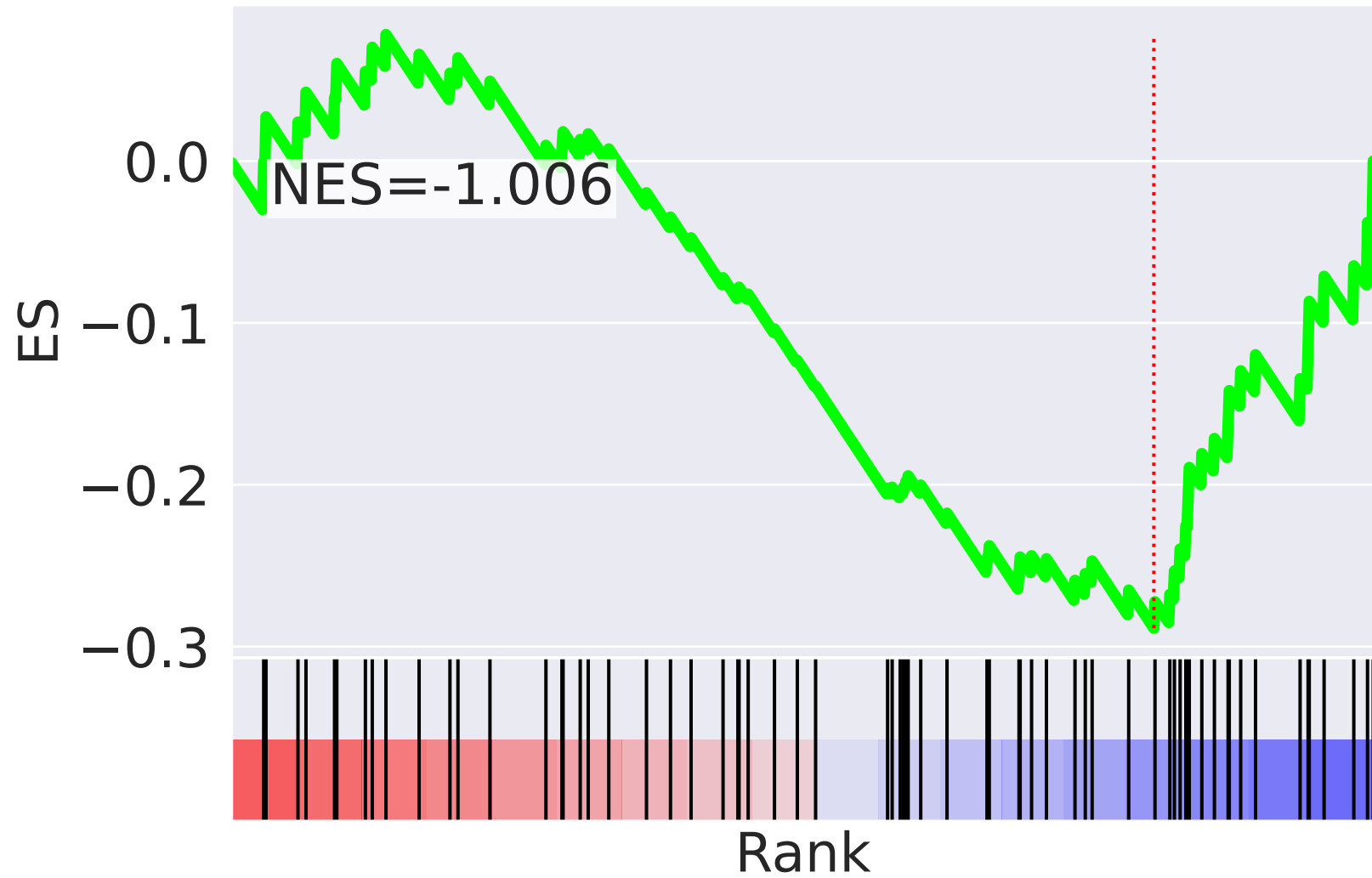
NES		SET
2.601		ERBB2 signaling pathway (GO:0038128)
-2.558		DNA replication (GO:0006260)
-2.519		transforming growth factor beta receptor signaling pathway (GO:0007179)
-2.484		cell cycle arrest (GO:0007050)
-2.445		cellular response to hypoxia (GO:0071456)
2.373		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.372		cell migration (GO:0016477)
2.370		positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900740)
2.358		execution phase of apoptosis (GO:0097194)
-2.268		cellular protein localization (GO:0034613)
-2.202		membrane organization (GO:0061024)
2.150		phosphatidylinositol biosynthetic process (GO:0006661)
-2.127		cellular response to amino acid starvation (GO:0034198)
2.112		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.098		protein K63-linked ubiquitination (GO:0070534)

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)



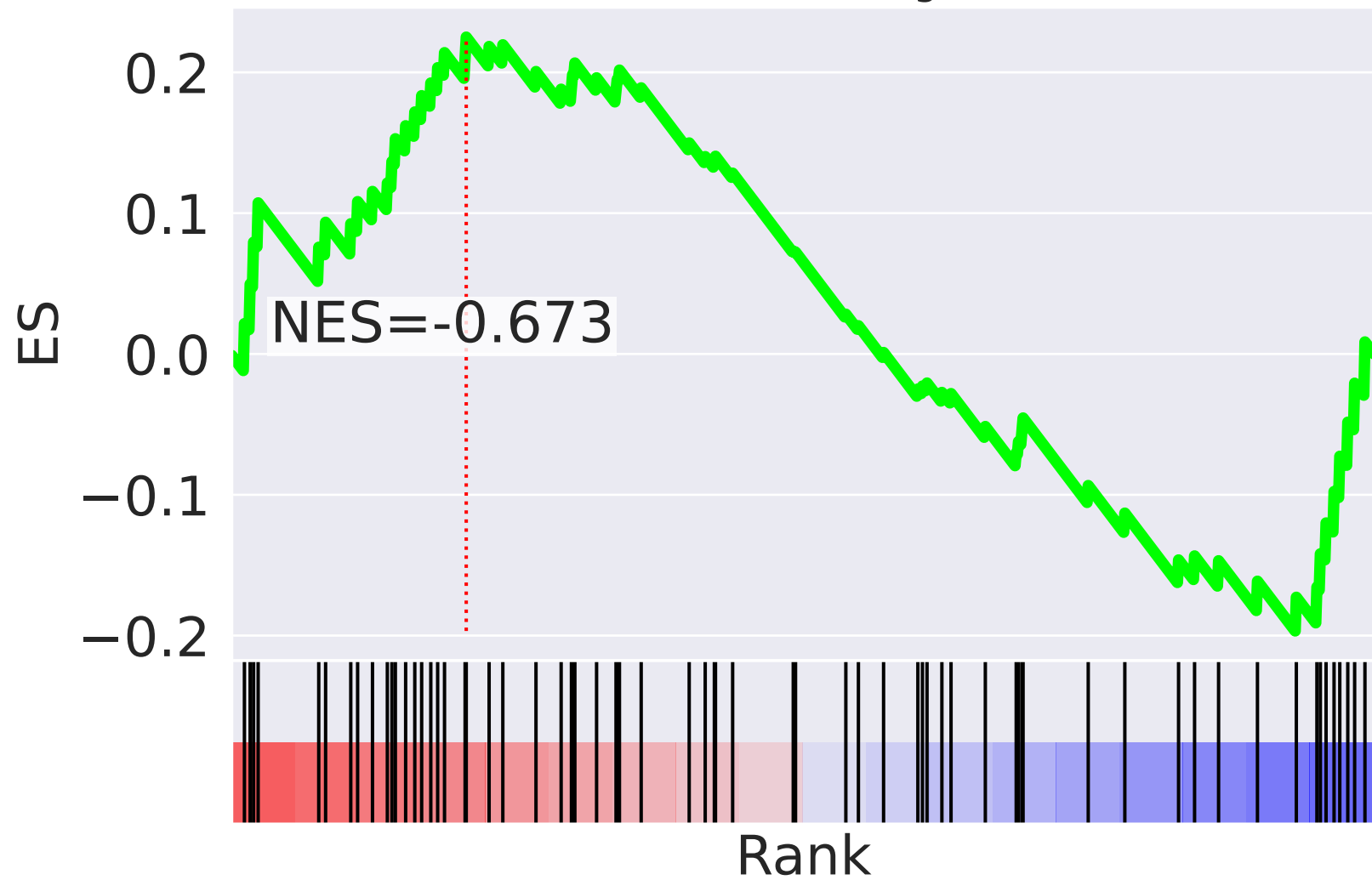
NES		SET
2.926		transcription, DNA-templated (GO:0006351)
2.740		tRNA modification (GO:0006400)
-2.589		ERK1 and ERK2 cascade (GO:0070371)
2.326		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
-2.289		protein import into nucleus (GO:0006606)
-2.193		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.179		response to endoplasmic reticulum stress (GO:0034976)
2.168		phosphatidylinositol biosynthetic process (GO:0006661)
2.086		histone H3 acetylation (GO:0043966)
2.052		double-strand break repair (GO:0006302)
2.008		proteolysis (GO:0006508)
1.954		T cell receptor signaling pathway (GO:0050852)
-1.938		cellular response to epidermal growth factor stimulus (GO:0071364)
-1.822		protein K11-linked ubiquitination (GO:0070979)
-1.768		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)






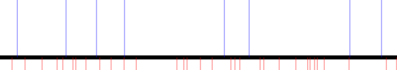
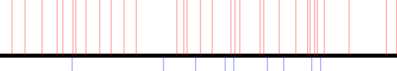
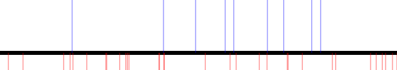
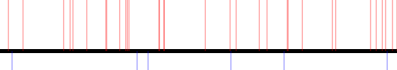



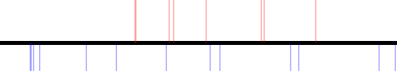
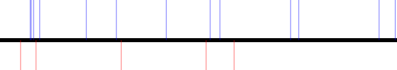
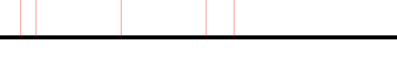
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=32$

mitochondrial translational elongation (GO:0070125)



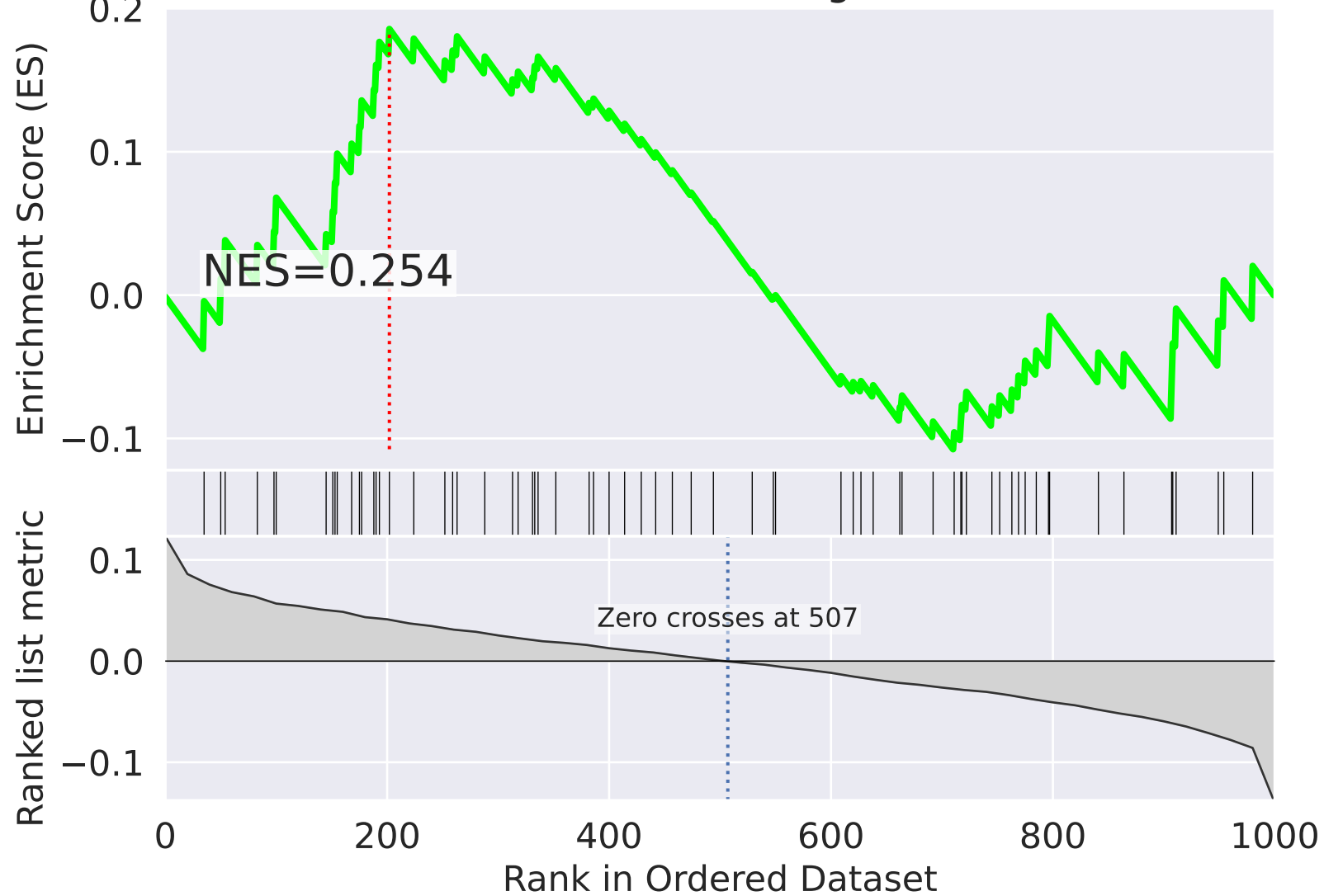
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.480		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.461		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.424		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.414		cytokinesis (GO:0000910)
-2.397		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.315		rRNA processing (GO:0006364)
2.280		mRNA splicing, via spliceosome (GO:0000398)
-2.223		protein dephosphorylation (GO:0006470)
2.219		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-2.186		fibroblast growth factor receptor signaling pathway (GO:0008543)
2.129		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.120		nucleosome disassembly (GO:0006337)
2.047		multicellular organism development (GO:0007275)
-1.981		protein stabilization (GO:0050821)
1.958		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)

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)

ES

NES=0.254

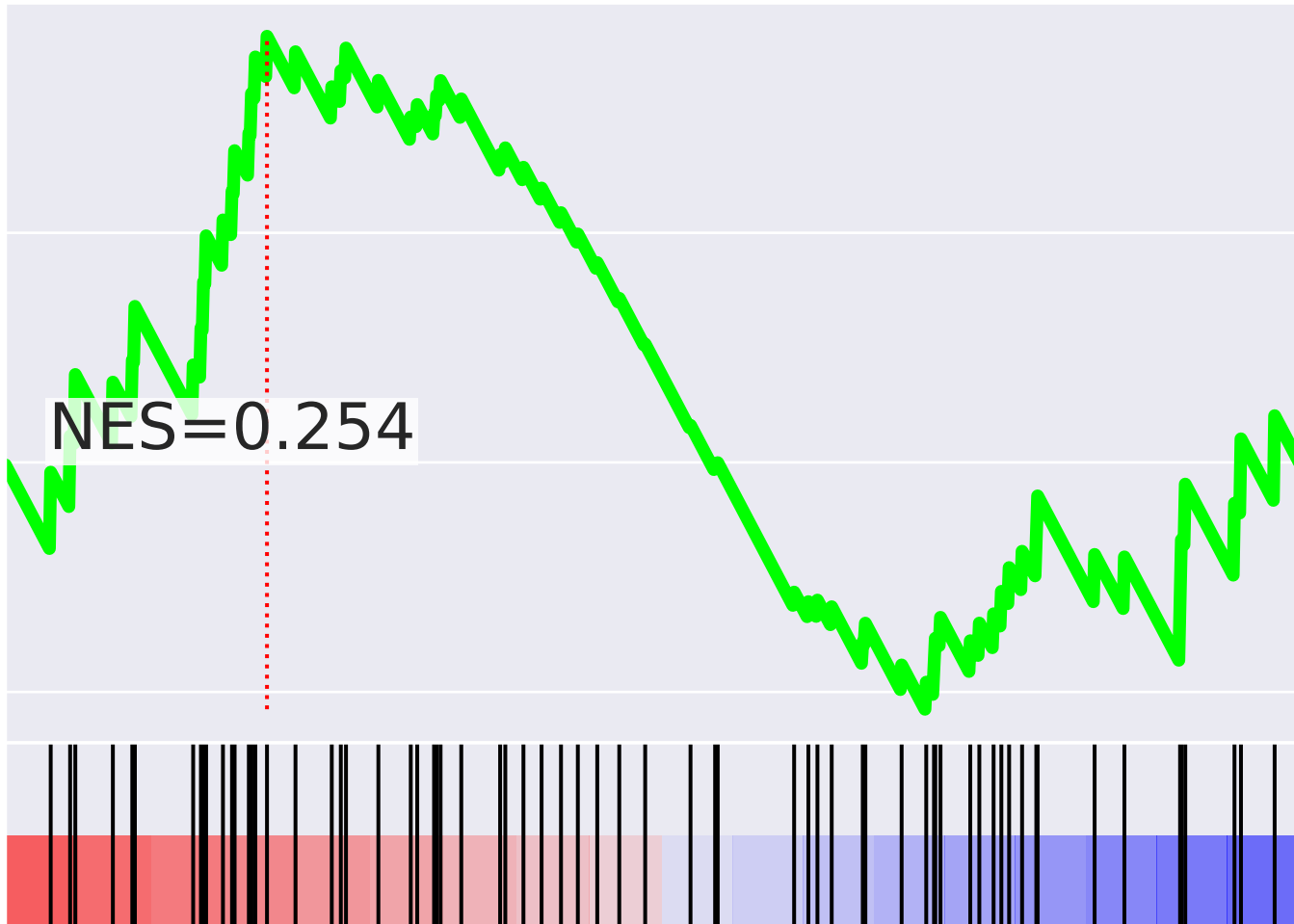
-0.1

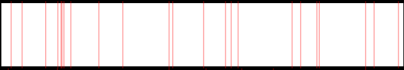



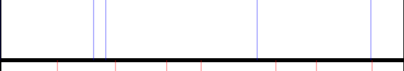

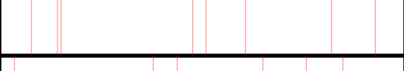
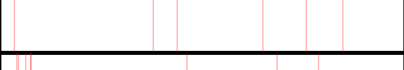


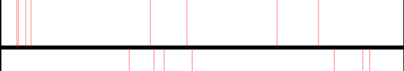

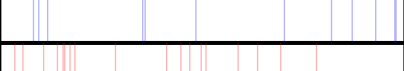
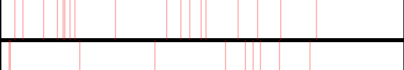
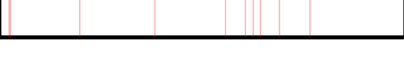
0.0

0.1

0.2

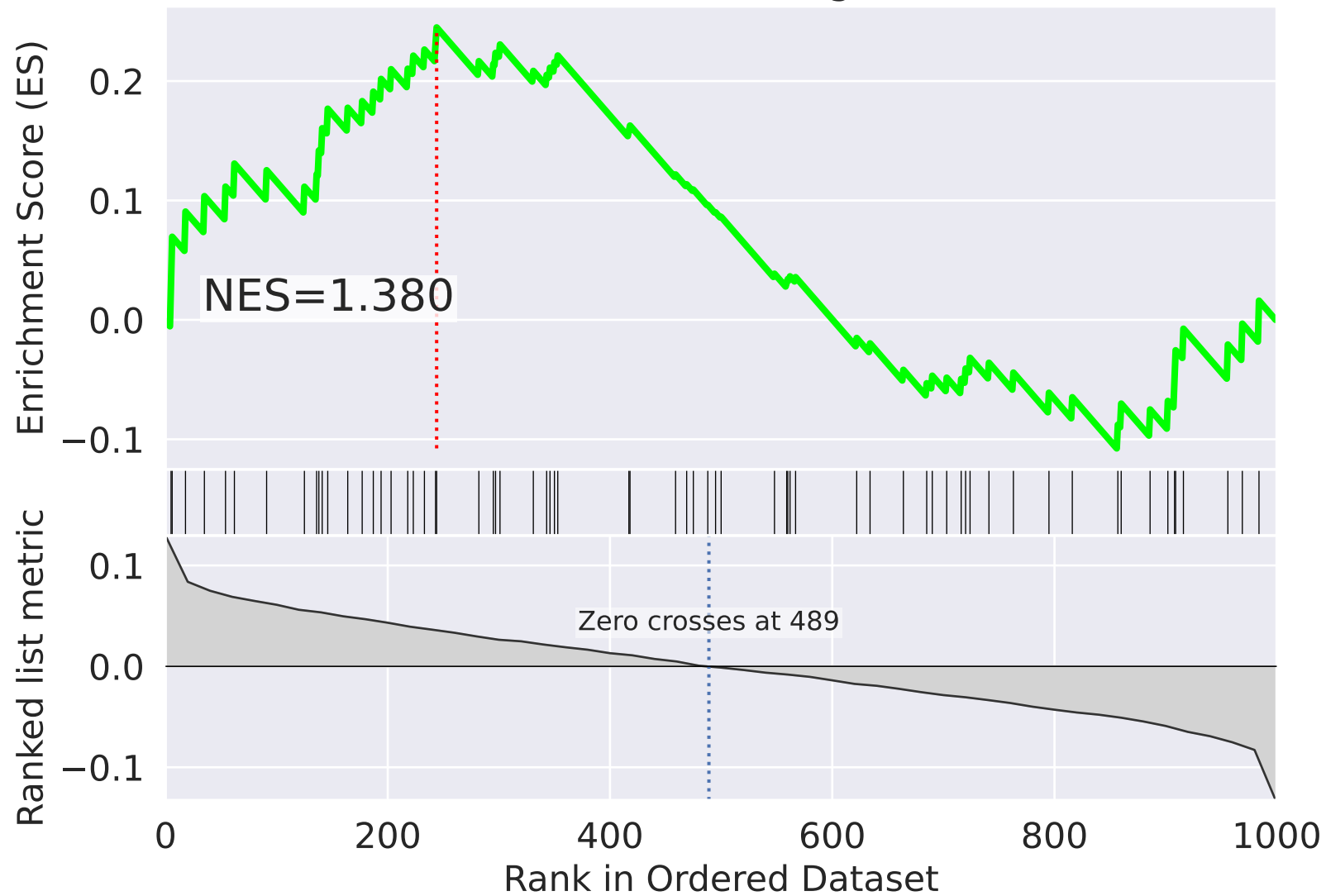
Rank



NES		SET
3.173		positive regulation of apoptotic process (GO:0043065)
2.671		innate immune response (GO:0045087)
-2.604		nucleosome disassembly (GO:0006337)
-2.503		retrograde protein transport, ER to cytosol (GO:0030970)
-2.503		ubiquitin-dependent ERAD pathway (GO:0030433)
2.489		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.392		regulation of cell proliferation (GO:0042127)
2.391		aerobic respiration (GO:0009060)
2.317		multivesicular body assembly (GO:0036258)
2.297		positive regulation of GTPase activity (GO:0043547)
2.282		viral life cycle (GO:0019058)
2.264		intracellular protein transport (GO:0006886)
-2.257		chromatin remodeling (GO:0006338)
2.199		MAPK cascade (GO:0000165)
2.195		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 $z=34$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1



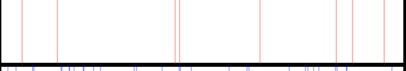
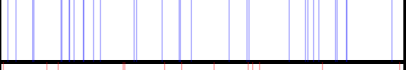
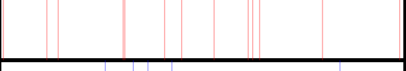

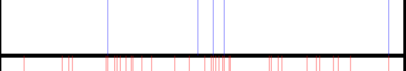
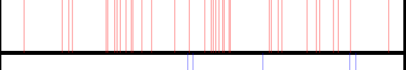
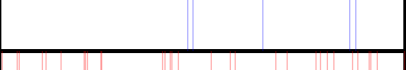
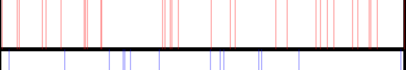
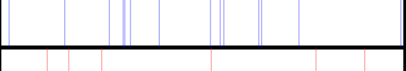


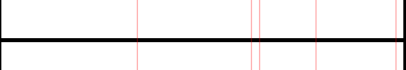
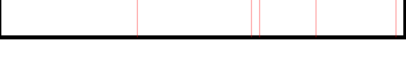
0.0

-0.1

NES=1.380

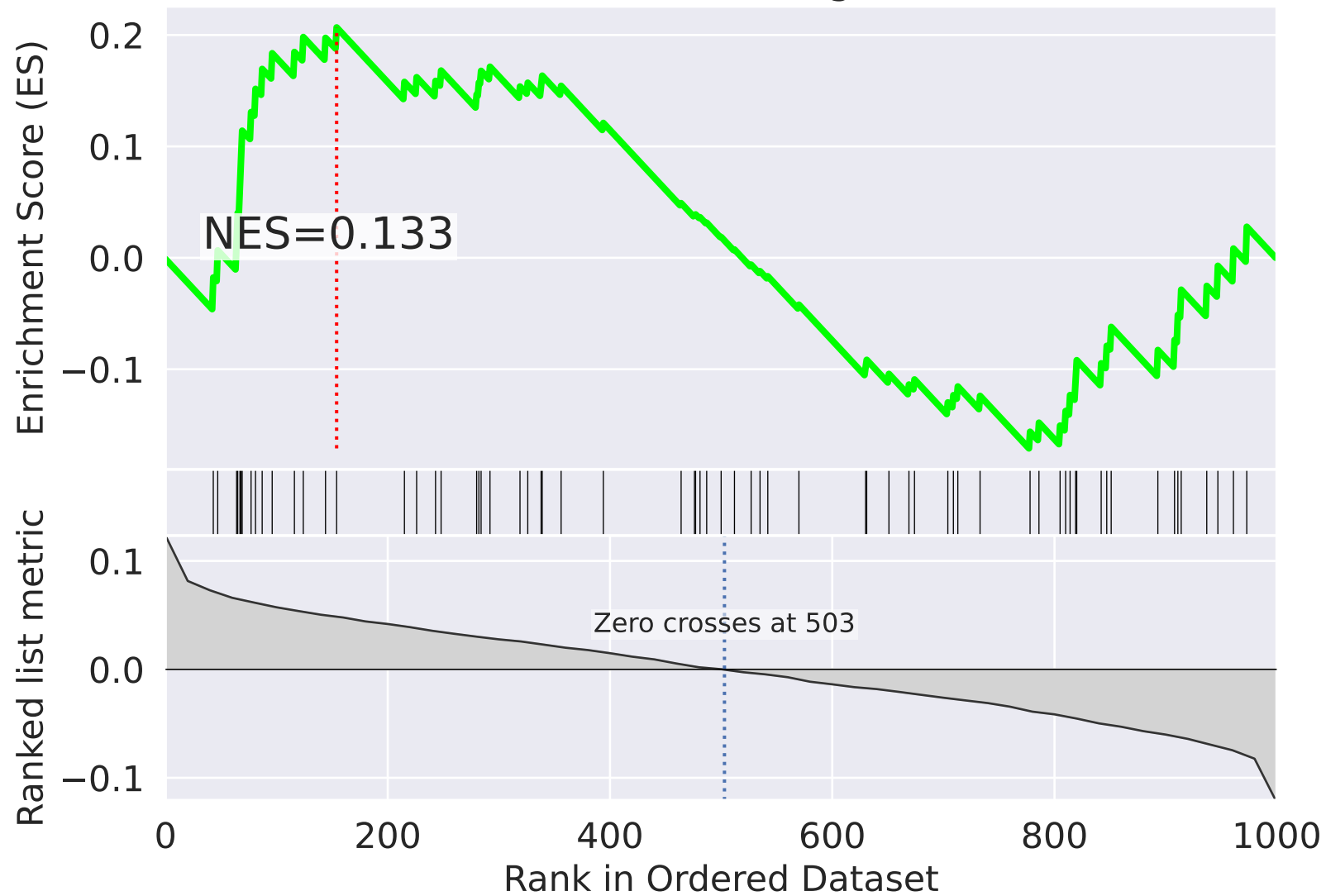
Rank



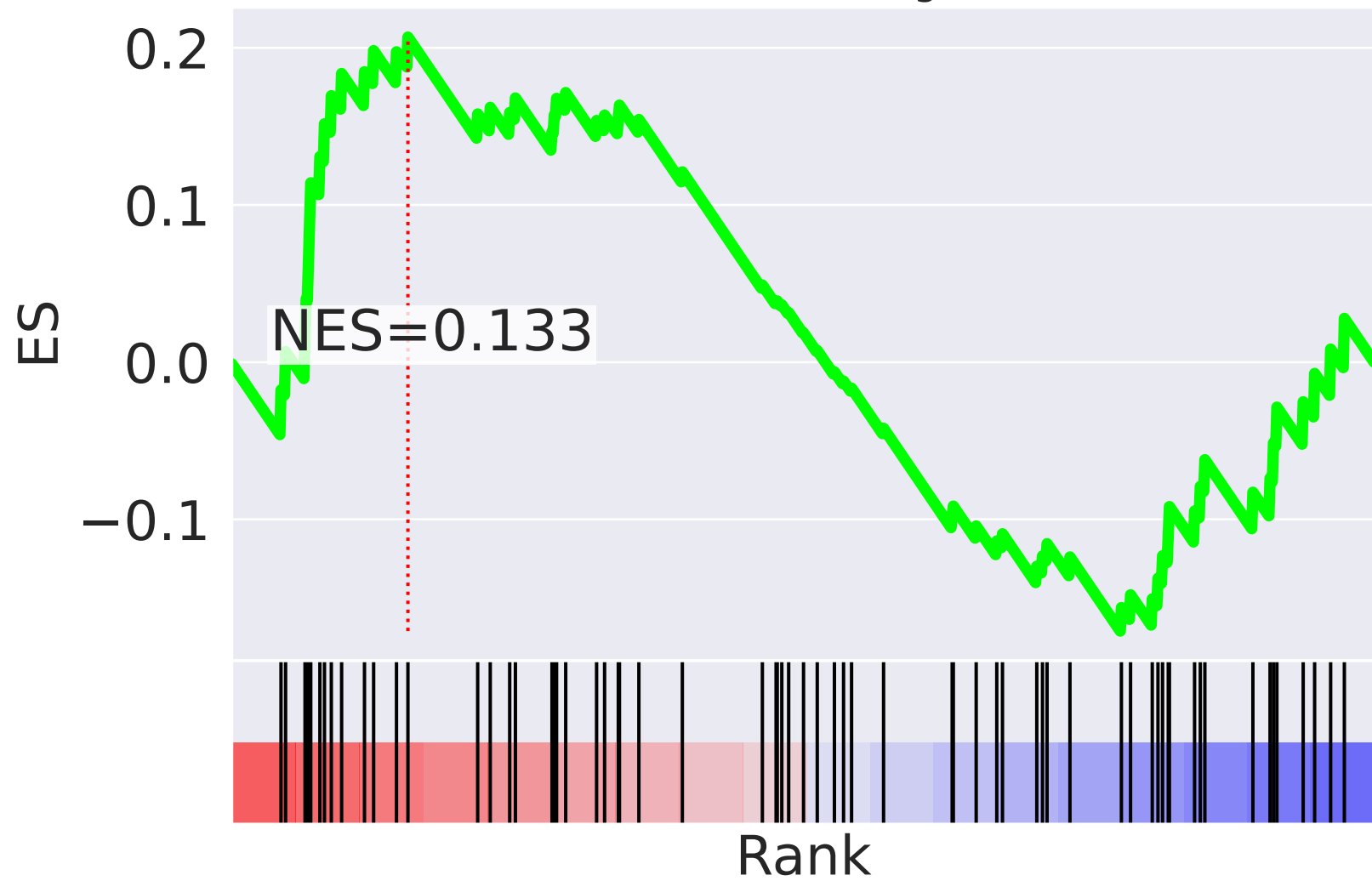
NES		SET
2.851		Ras protein signal transduction (GO:0007265)
-2.372		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.342		protein homooligomerization (GO:0051260)
-2.149		mRNA splicing, via spliceosome (GO:0000398)
2.148		protein stabilization (GO:0050821)
-2.137		regulation of lipid metabolic process (GO:0019216)
-2.074		nucleosome disassembly (GO:0006337)
2.045		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-1.969		mitochondrial respiratory chain complex IV assembly (GO:0033617)
1.940		positive regulation of cell proliferation (GO:0008284)
-1.928		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
1.914		positive regulation of cell growth (GO:0030307)
1.886		negative regulation of canonical Wnt signaling pathway (GO:0090090)
1.877		ubiquitin-dependent ERAD pathway (GO:0030433)
1.877		retrograde protein transport, ER to cytosol (GO:0030970)

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)



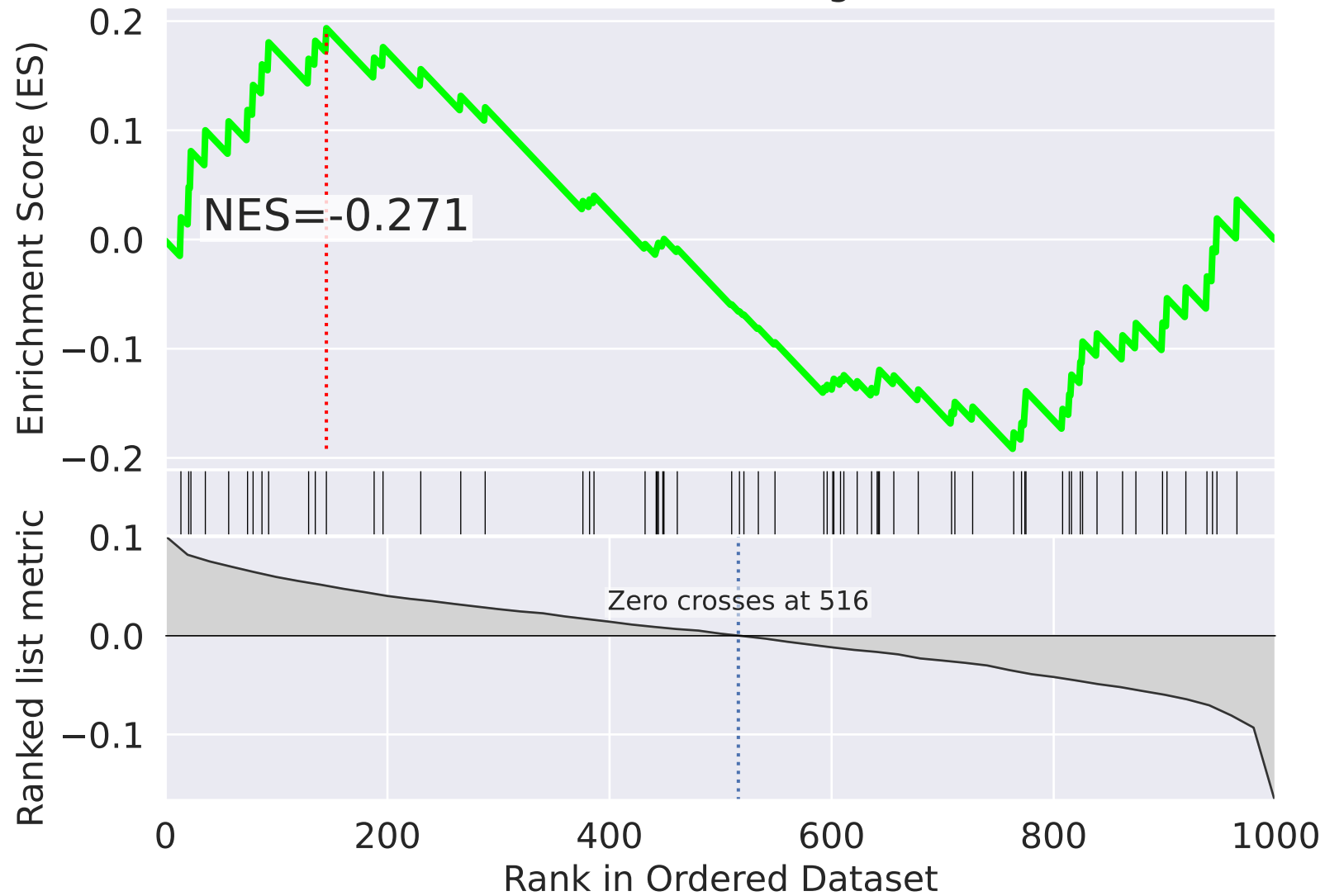
mitochondrial translational elongation (GO:0070125)



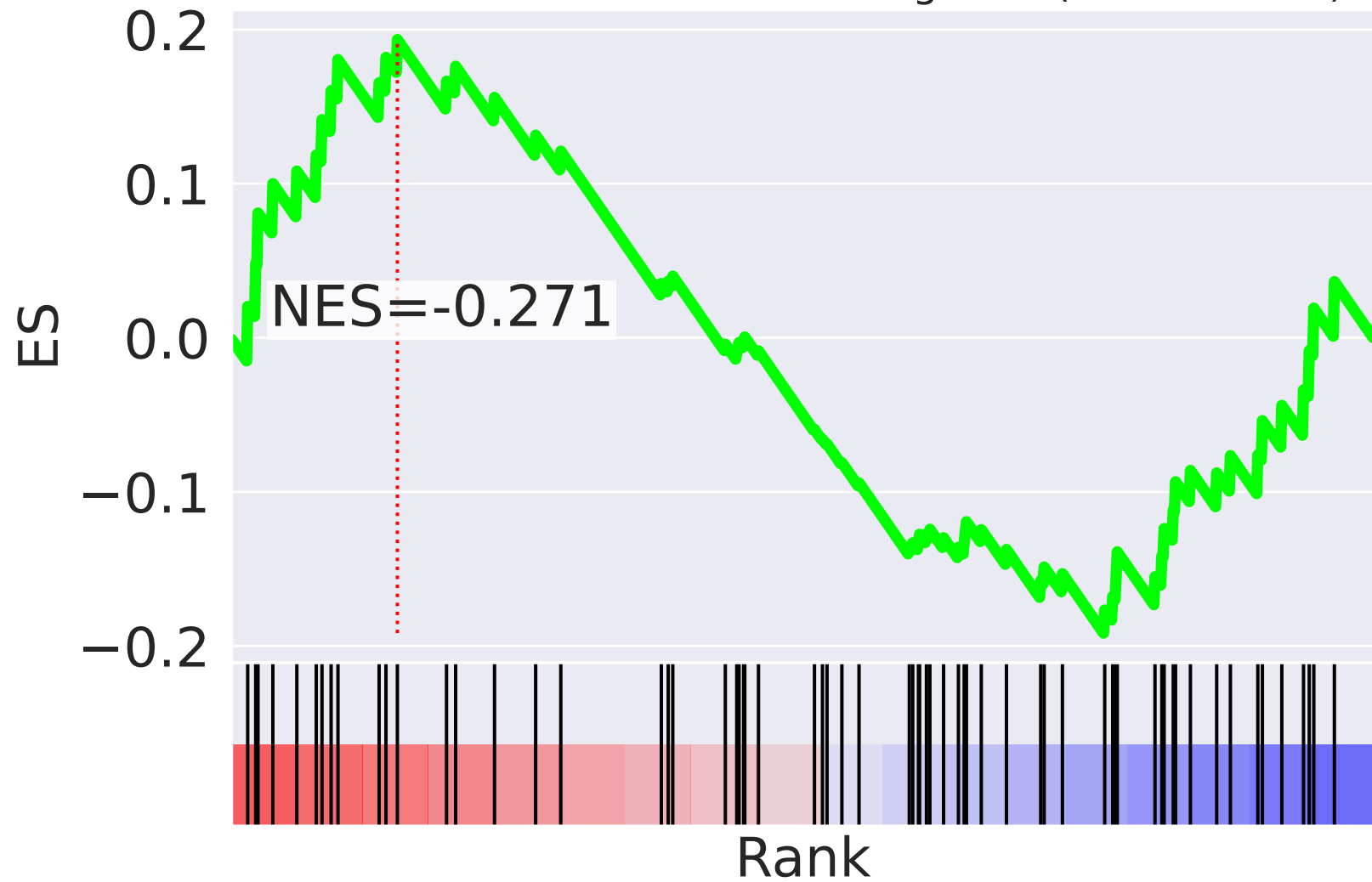
NES		SET
2.393		protein deubiquitination (GO:0016579)
-2.337		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.306		protein sumoylation (GO:0016925)
2.272		protein autoubiquitination (GO:0051865)
-2.243		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.111		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-2.077		generation of precursor metabolites and energy (GO:0006091)
1.988		protein K11-linked ubiquitination (GO:0070979)
-1.982		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
1.970		protein K48-linked ubiquitination (GO:0070936)
1.899		chromosome segregation (GO:0007059)
-1.895		positive regulation of cytokinesis (GO:0032467)
-1.865		COPII vesicle coating (GO:0048208)
-1.845		intracellular transport of virus (GO:0075733)
1.804		phosphatidylinositol biosynthetic process (GO:0006661)

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)

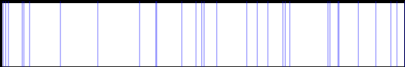
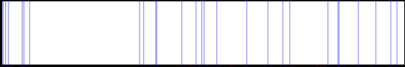







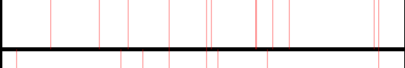




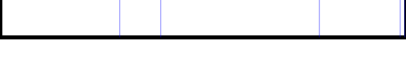


mitochondrial translational elongation (GO:0070125)



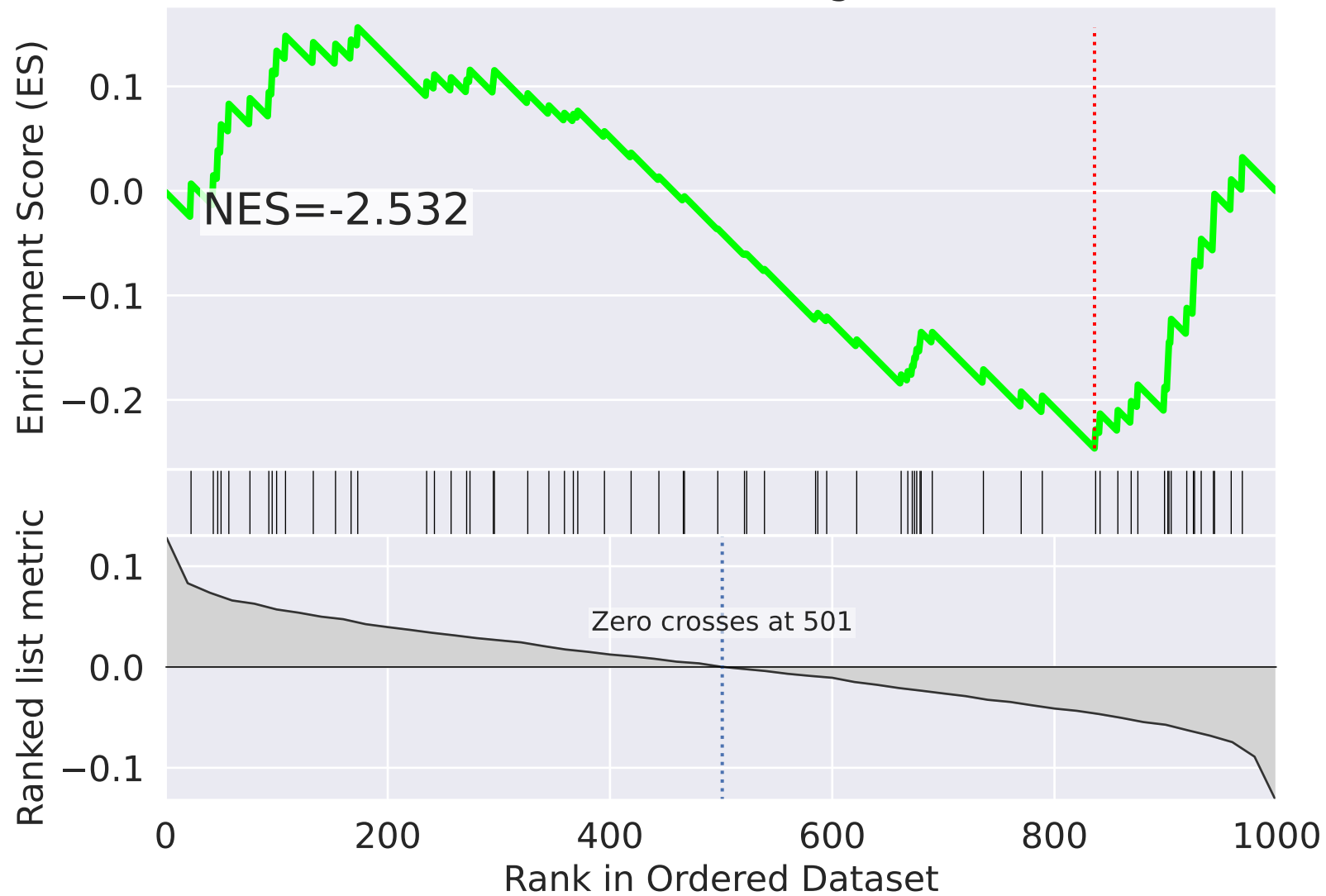
NES

SET

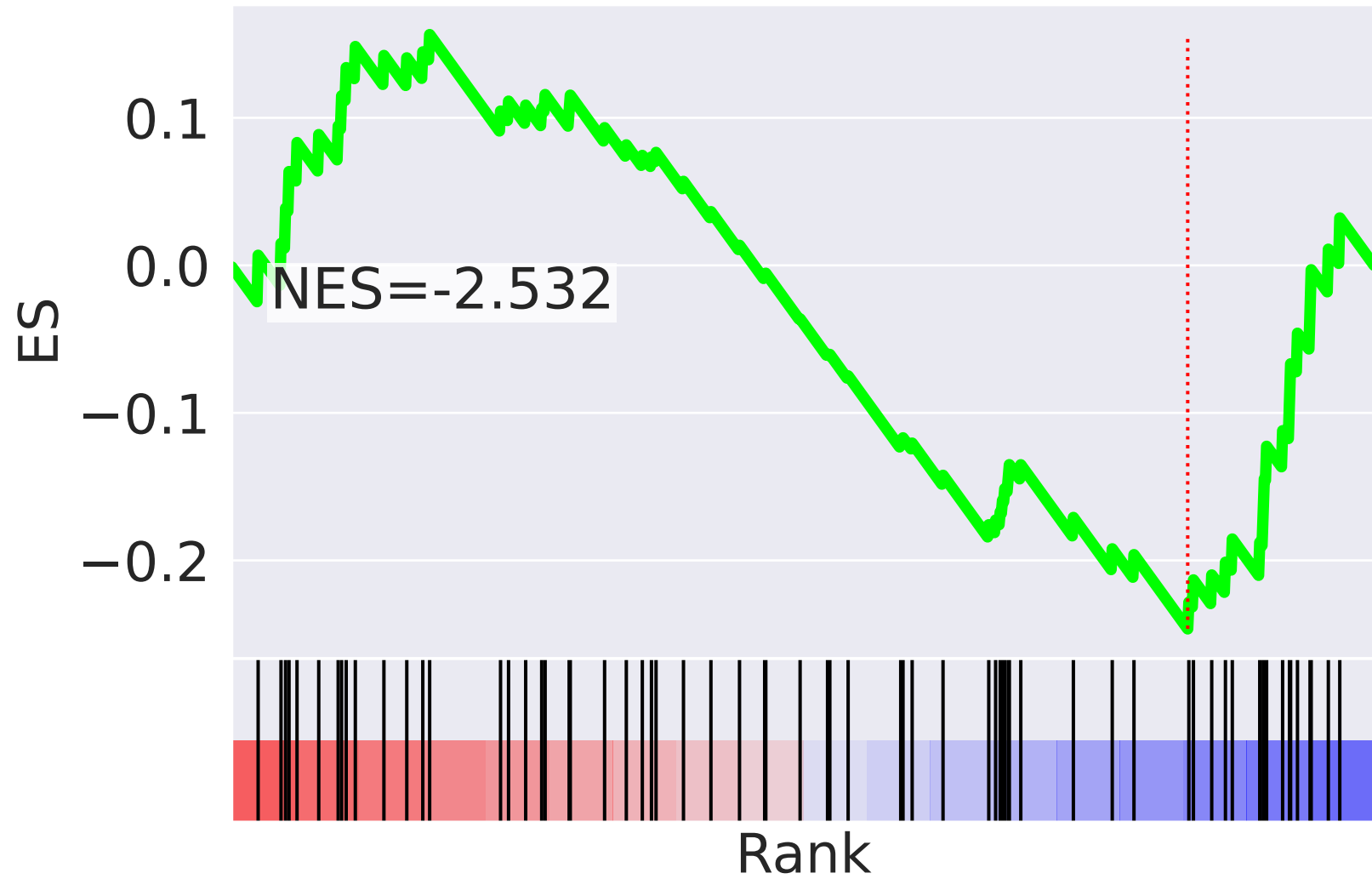
-3.120		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.996		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.650		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.547		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.519		positive regulation of DNA replication (GO:0045740)
2.349		telomere capping (GO:0016233)
2.245		cellular response to DNA damage stimulus (GO:0006974)
2.242		canonical glycolysis (GO:0061621)
2.240		cell growth (GO:0016049)
2.237		leukocyte migration (GO:0050900)
2.180		cell migration (GO:0016477)
2.168		regulation of cell proliferation (GO:0042127)
2.134		phosphatidylinositol-mediated signaling (GO:0048015)
2.133		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
-2.100		mitochondrial respiratory chain complex IV assembly (GO:0033617)

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)



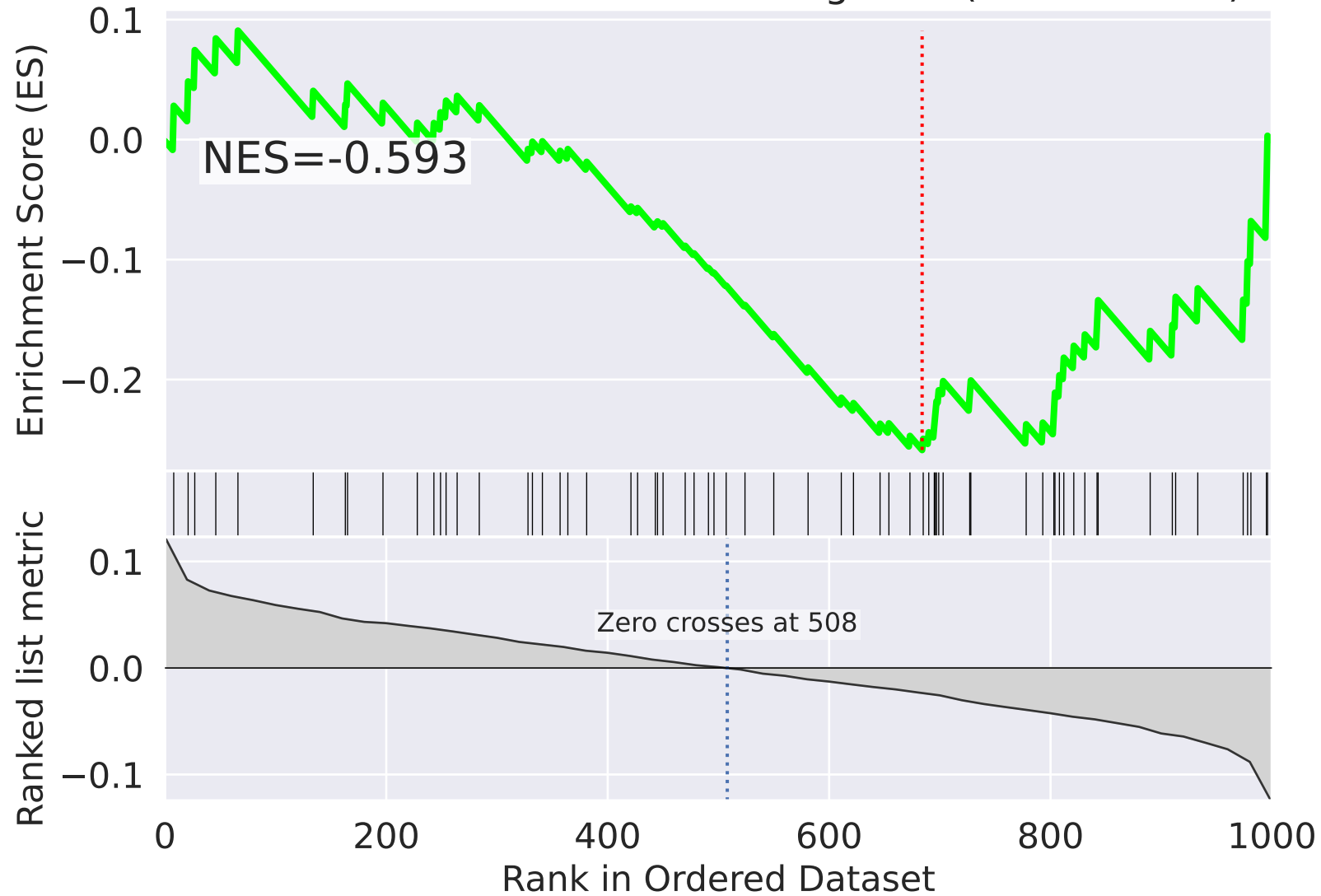
mitochondrial translational elongation (GO:0070125)



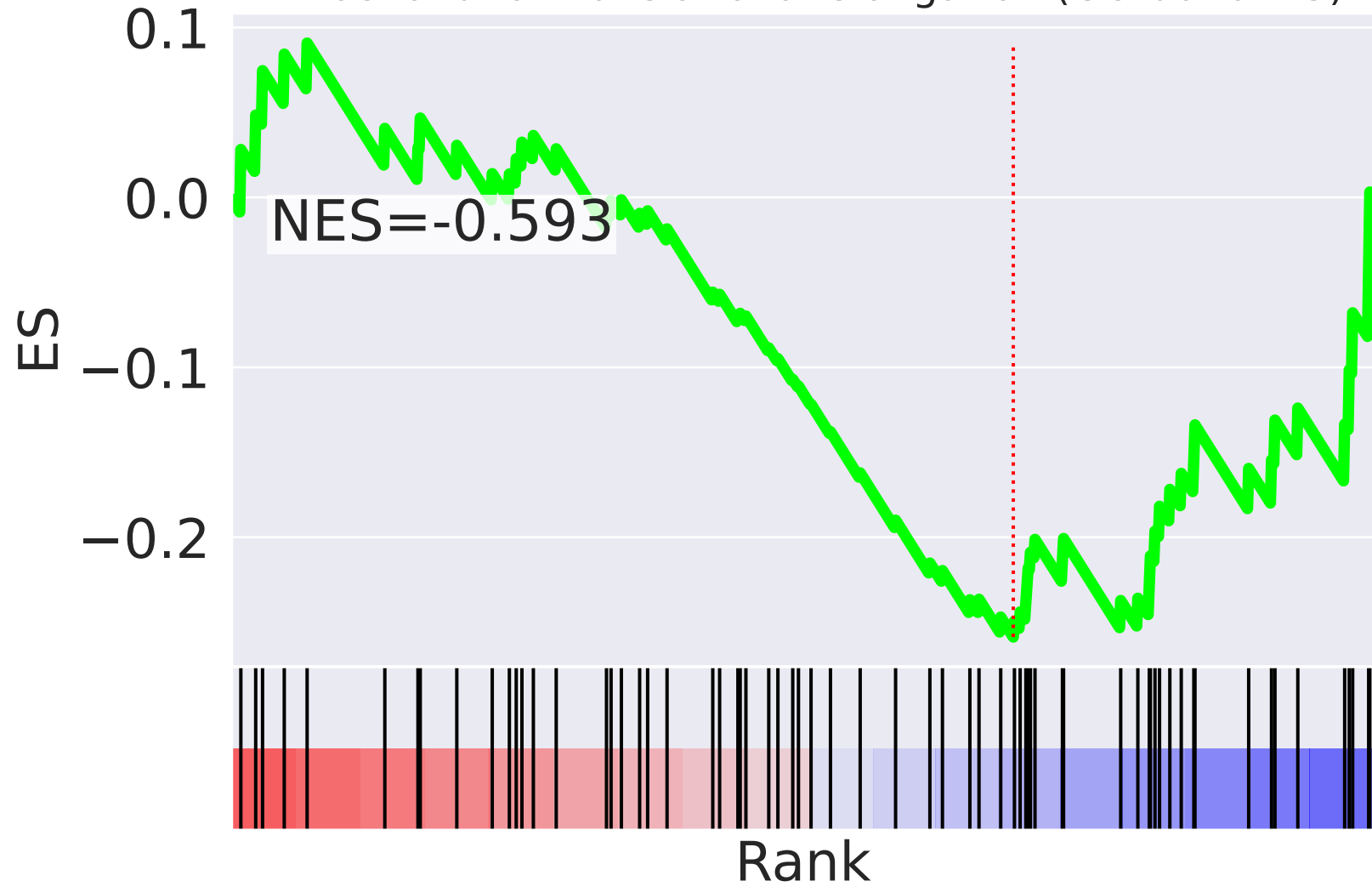
NES		SET
2.864		macroautophagy (GO:0016236)
2.730		apoptotic process (GO:0006915)
-2.649		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.534		mitochondrial translational termination (GO:0070126)
2.533		positive regulation of gene expression, epigenetic (GO:0045815)
-2.532		mitochondrial translational elongation (GO:0070125)
2.460		protein deubiquitination (GO:0016579)
2.402		RNA export from nucleus (GO:0006405)
2.382		termination of RNA polymerase II transcription (GO:0006369)
-2.368		DNA damage response, detection of DNA damage (GO:0042769)
-2.353		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.305		transcription initiation from RNA polymerase I promoter (GO:0006361)
2.305		transcription elongation from RNA polymerase I promoter (GO:0006362)
2.305		termination of RNA polymerase I transcription (GO:0006363)
2.192		viral process (GO:0016032)



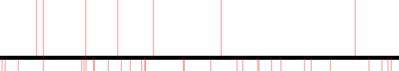
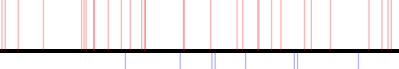
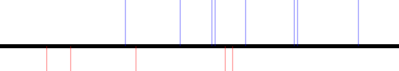
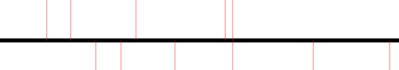



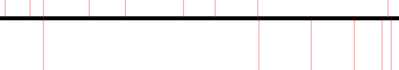
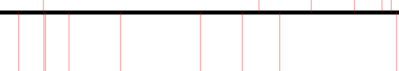




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=38$

mitochondrial translational elongation (GO:0070125)



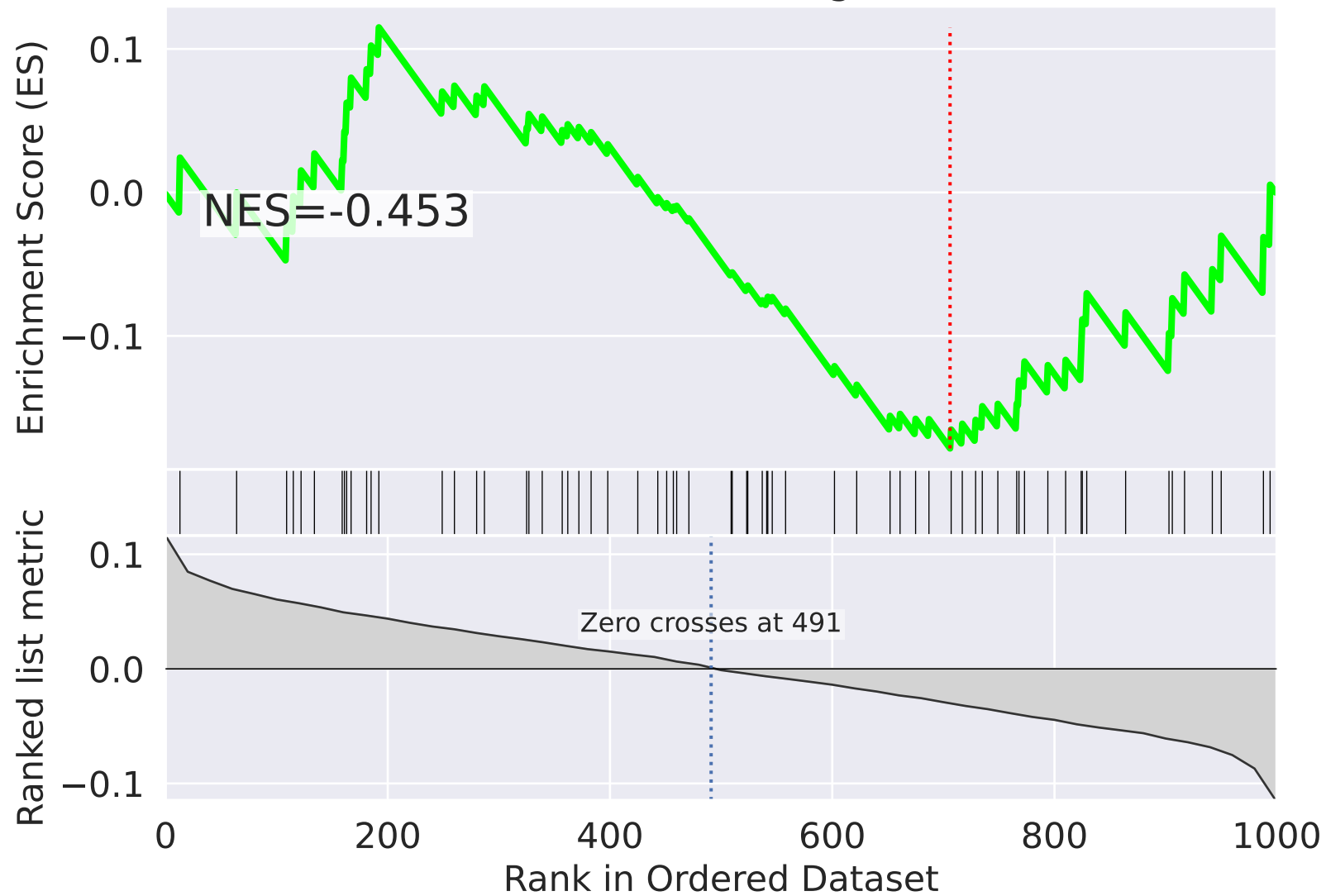
mitochondrial translational elongation (GO:0070125)



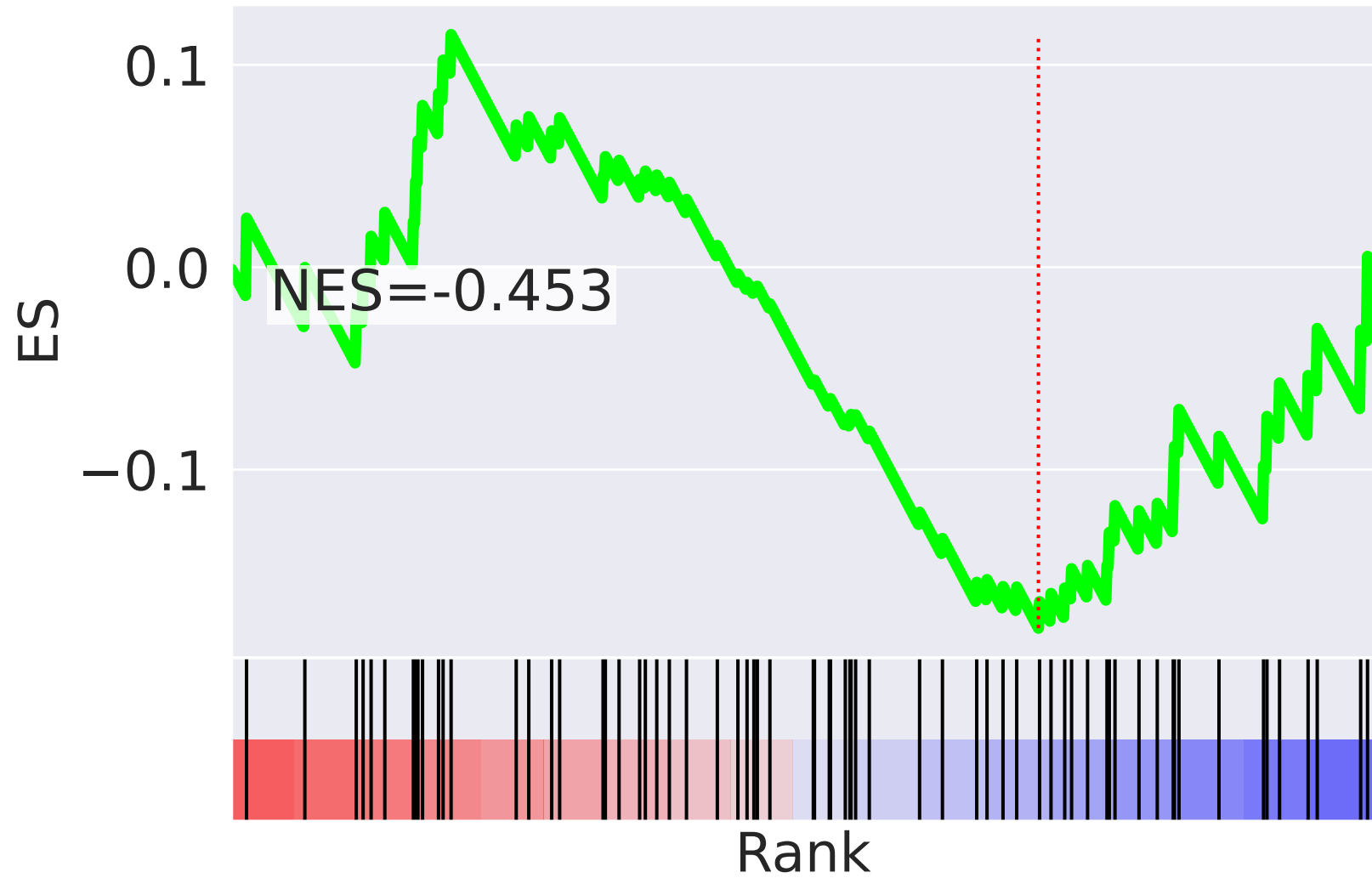
NES		SET
2.595		response to virus (GO:0009615)
-2.430		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.387		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.298		mRNA splicing, via spliceosome (GO:0000398)
-2.234		protein import into nucleus (GO:0006606)
2.210		proteolysis (GO:0006508)
2.139		positive regulation of protein targeting to mitochondrion (GO:1903955)
-2.029		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.011		nucleotide-excision repair (GO:0006289)
2.010		RNA export from nucleus (GO:0006405)
1.985		RNA metabolic process (GO:0016070)
1.976		tRNA modification (GO:0006400)
1.949		snRNA transcription from RNA polymerase II promoter (GO:0042795)
1.911		platelet activation (GO:0030168)
-1.892		telomere maintenance via recombination (GO:0000722)

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)




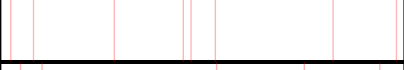
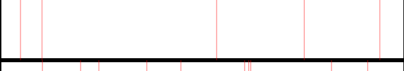
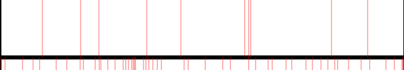
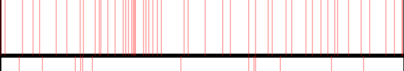


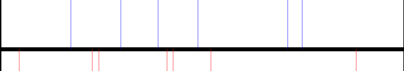
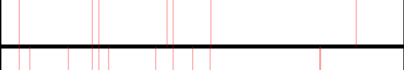
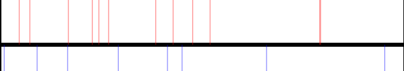
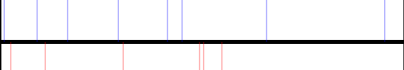

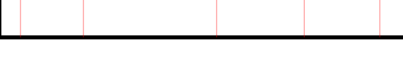


mitochondrial translational elongation (GO:0070125)



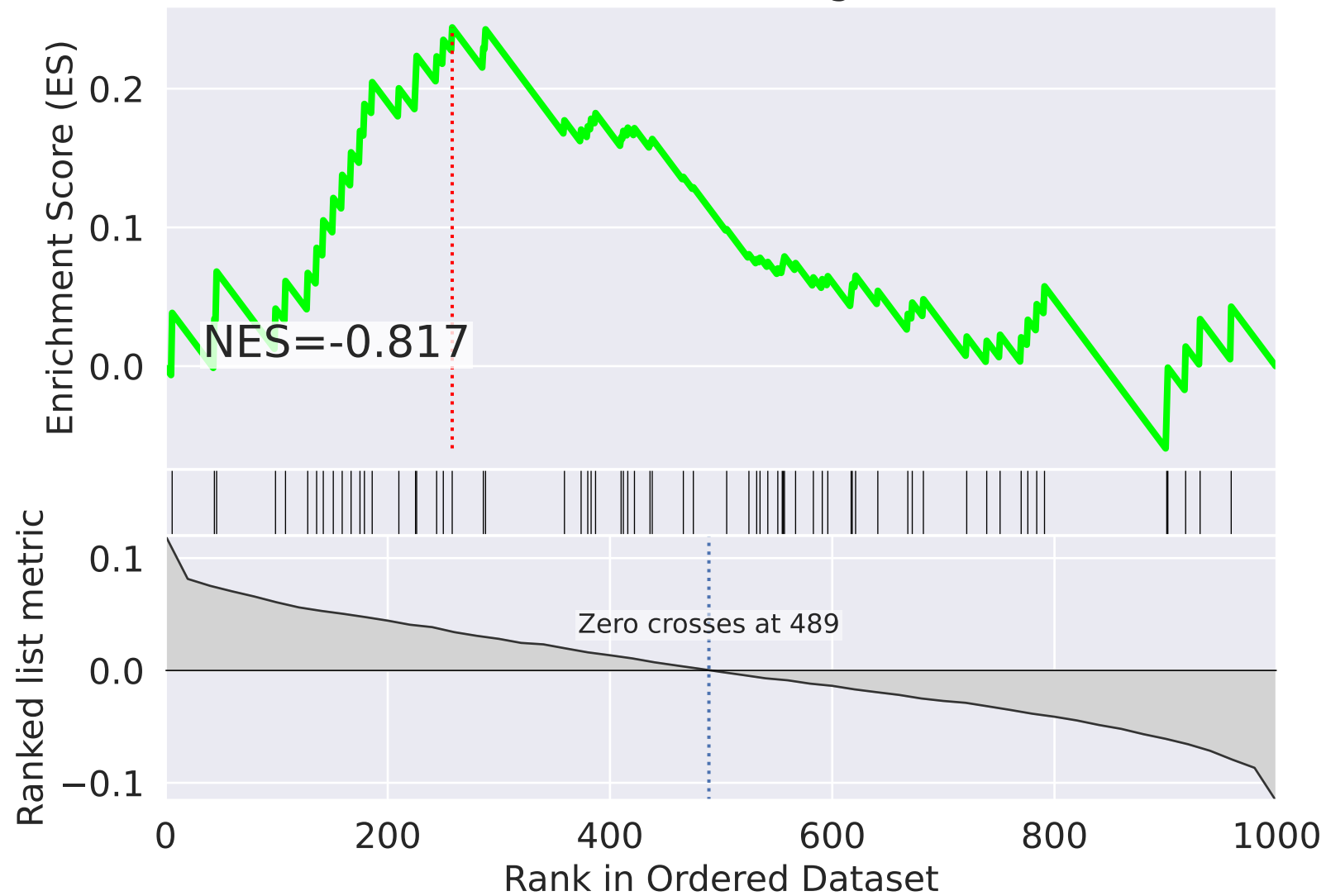
NES

SET

2.547		positive regulation of gene expression (GO:0010628)
2.452		generation of precursor metabolites and energy (GO:0006091)
-2.377		cellular iron ion homeostasis (GO:0006879)
2.318		interstrand cross-link repair (GO:0036297)
2.228		canonical glycolysis (GO:0061621)
2.224		Ras protein signal transduction (GO:0007265)
2.180		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.139		Fc-epsilon receptor signaling pathway (GO:0038095)
-2.093		membrane organization (GO:0061024)
-2.069		aerobic respiration (GO:0009060)
2.068		peptidyl-serine phosphorylation (GO:0018105)
2.040		protein phosphorylation (GO:0006468)
-2.033		rRNA processing (GO:0006364)
2.008		protein K48-linked ubiquitination (GO:0070936)
1.996		gluconeogenesis (GO:0006094)

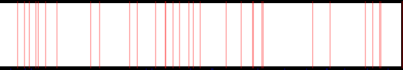




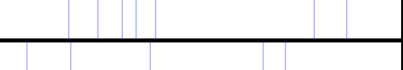



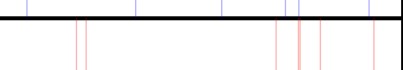
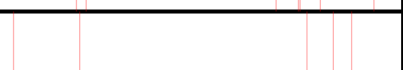




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=40$

mitochondrial translational elongation (GO:0070125)



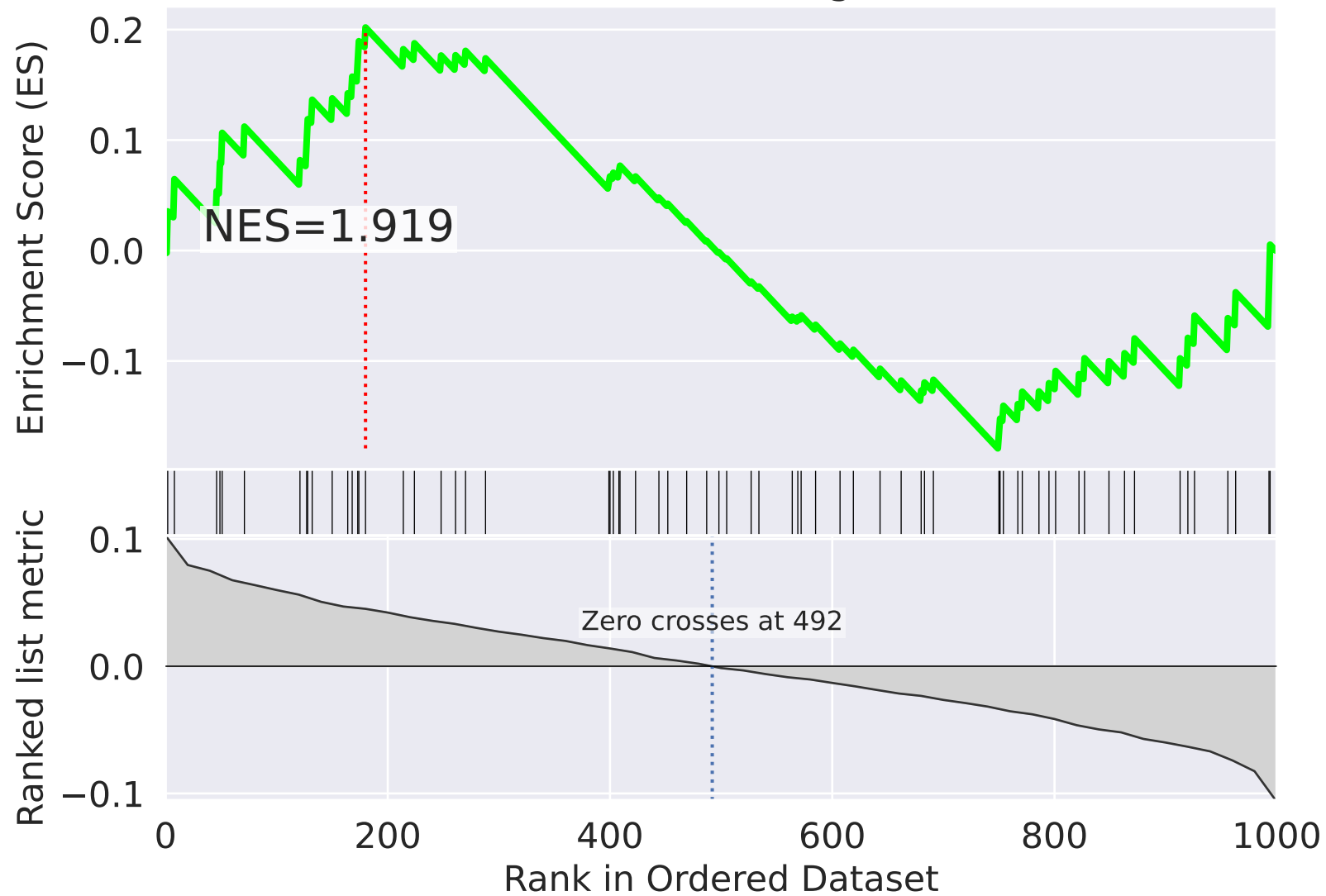
mitochondrial translational elongation (GO:0070125)



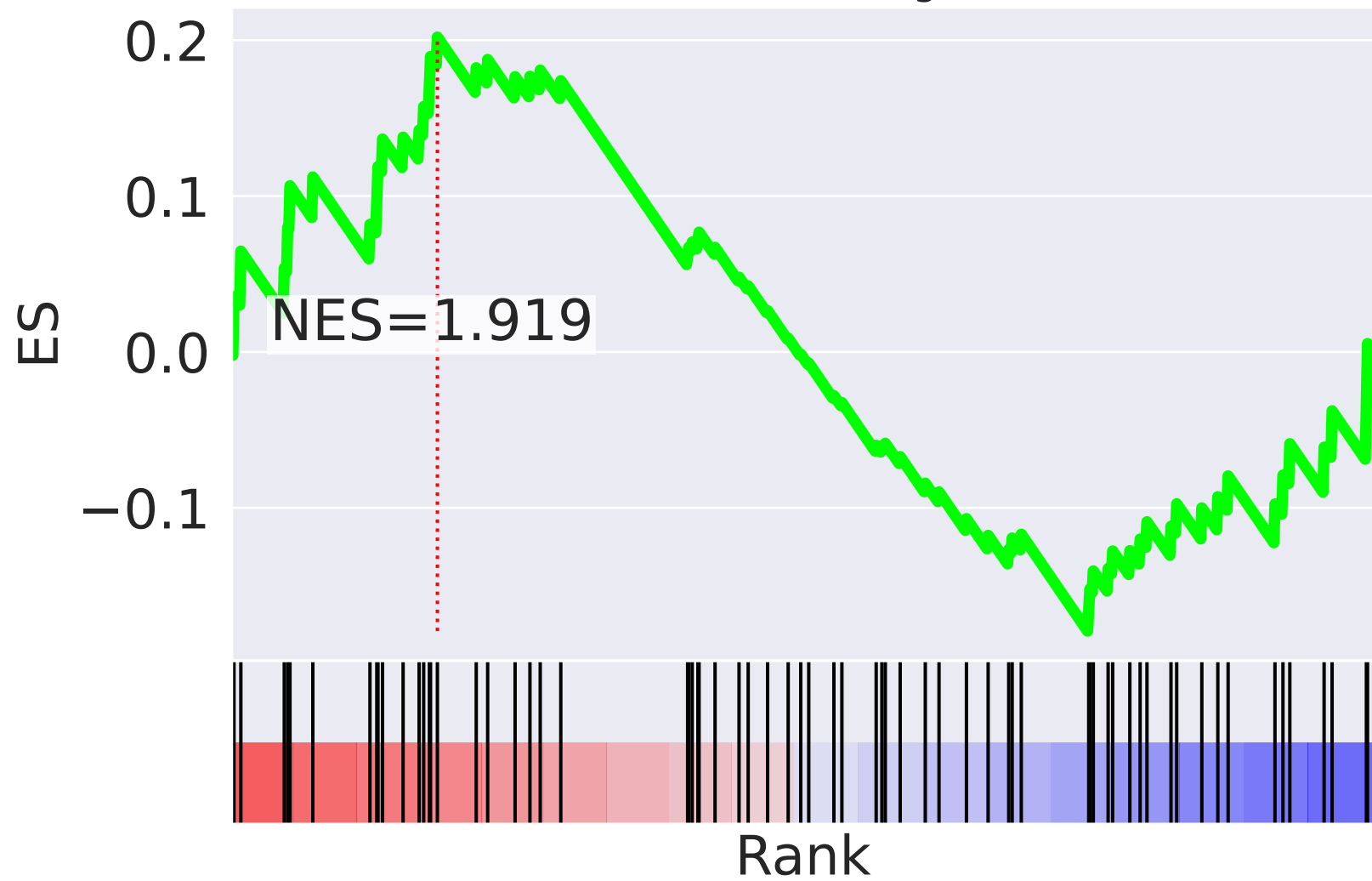
NES		SET
3.031		negative regulation of transcription, DNA-templated (GO:0045892)
-2.663		G1/S transition of mitotic cell cycle (GO:0000082)
2.529		oxidation-reduction process (GO:0055114)
-2.451		substantia nigra development (GO:0021762)
-2.409		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.372		IRE1-mediated unfolded protein response (GO:0036498)
-2.230		positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900740)
-2.220		MAPK cascade (GO:0000165)
2.164		protein sumoylation (GO:0016925)
-2.141		ciliary basal body docking (GO:0097711)
2.102		negative regulation of translation (GO:0017148)
2.079		substrate adhesion-dependent cell spreading (GO:0034446)
-2.066		translation (GO:0006412)
-2.065		ubiquitin-dependent protein catabolic process (GO:0006511)
2.002		regulation of cell adhesion (GO:0030155)

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)



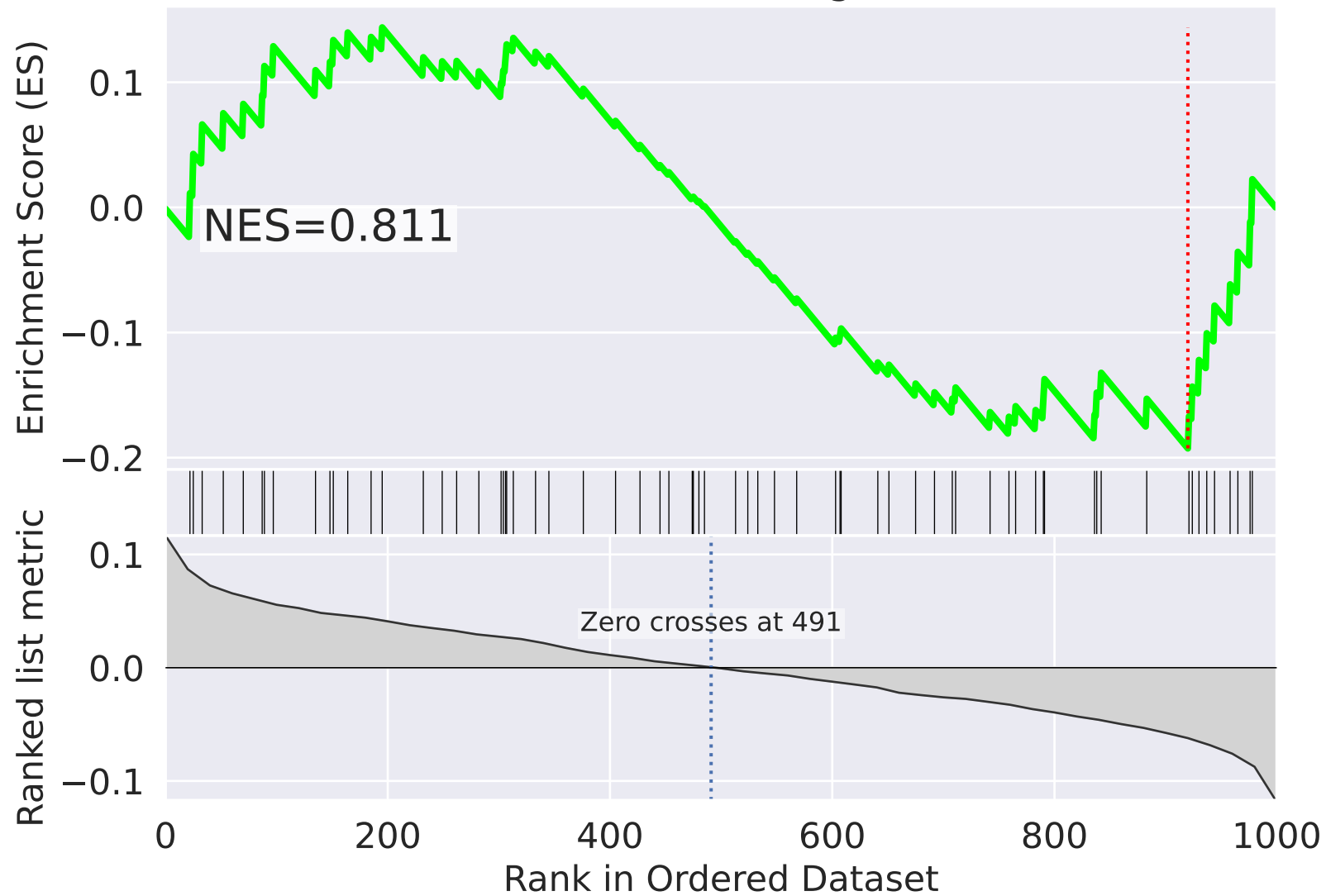
mitochondrial translational elongation (GO:0070125)



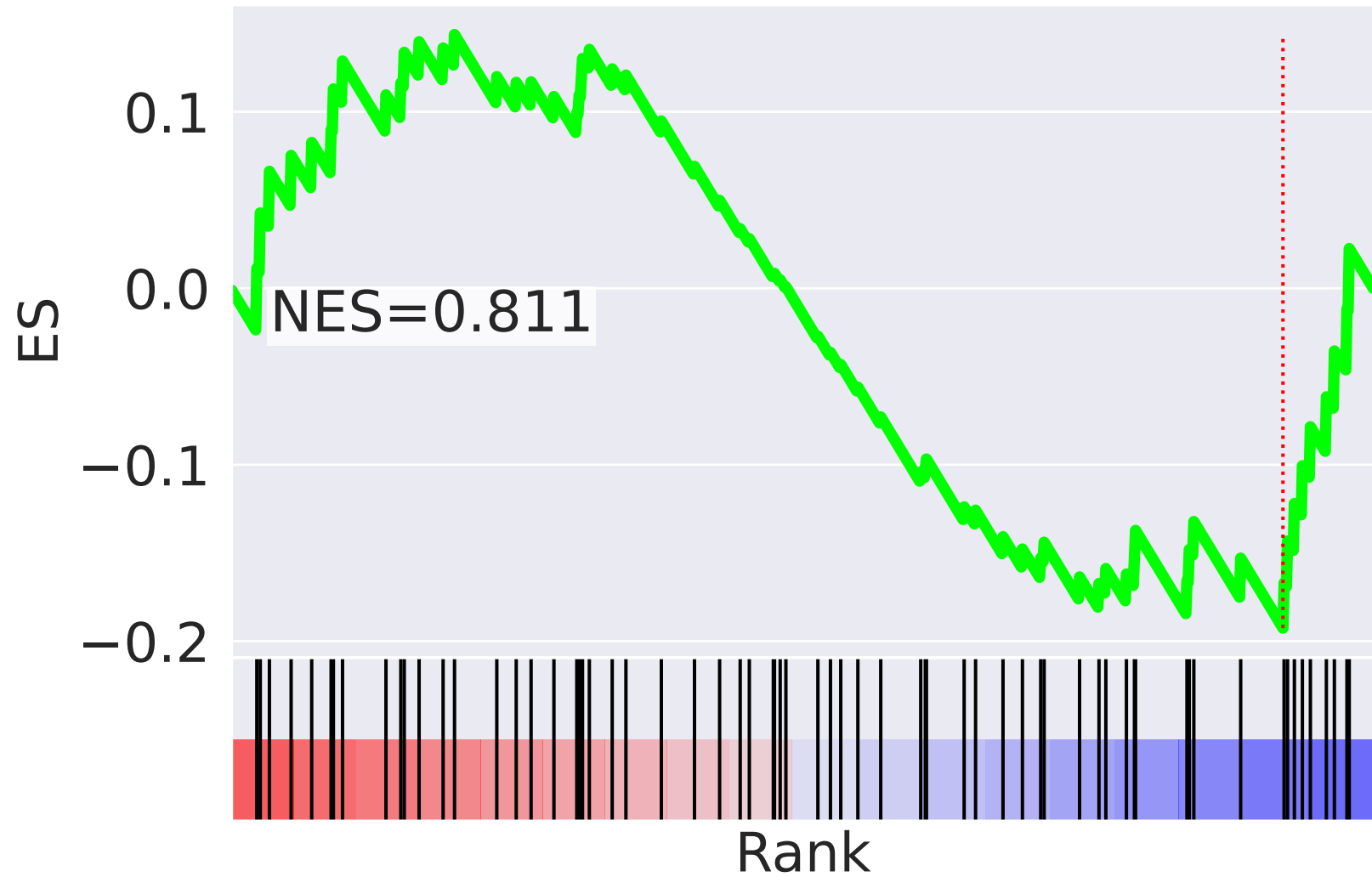
NES		SET
-2.861		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.619		cellular protein modification process (GO:0006464)
2.464		mitochondrion organization (GO:0007005)
2.247		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
-2.239		integrin-mediated signaling pathway (GO:0007229)
2.199		mitotic cell cycle (GO:0000278)
2.189		telomere maintenance (GO:0000723)
2.120		inflammatory response (GO:0006954)
2.096		cellular response to tumor necrosis factor (GO:0071356)
-2.095		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.088		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
2.021		protein stabilization (GO:0050821)
2.002		negative regulation of telomere maintenance via telomerase (GO:0032211)
1.994		mitochondrial translational termination (GO:0070126)
1.919		mitochondrial translational elongation (GO:0070125)

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)



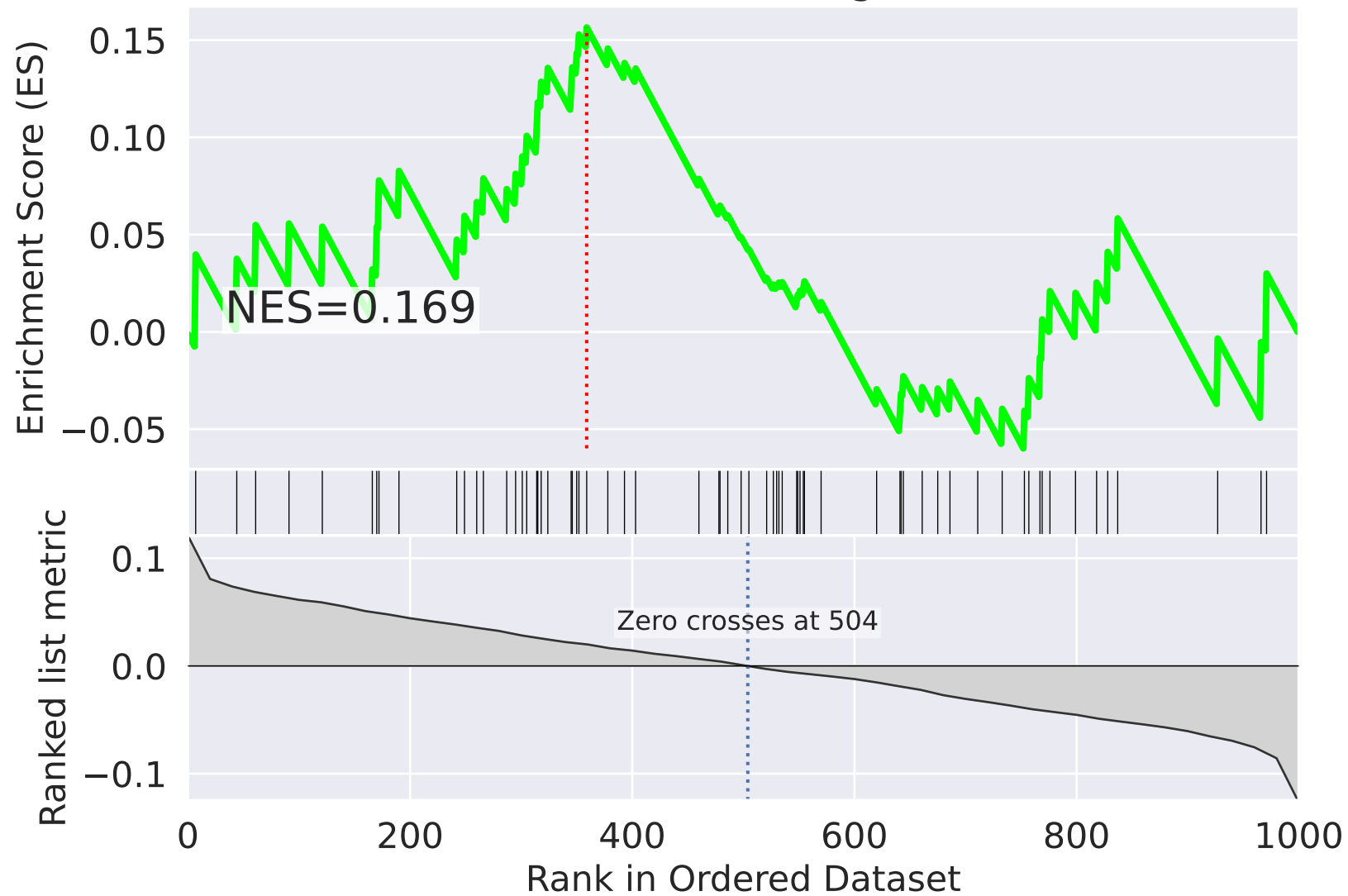
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.512		protein polyubiquitination (GO:0000209)
2.510		ERBB2 signaling pathway (GO:0038128)
2.367		response to ionizing radiation (GO:0010212)
2.283		IRE1-mediated unfolded protein response (GO:0036498)
2.255		leukocyte migration (GO:0050900)
-2.210		positive regulation of cell proliferation (GO:0008284)
-2.146		negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.118		histone H4 acetylation (GO:0043967)
2.091		iron-sulfur cluster assembly (GO:0016226)
-2.070		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
2.012		endosomal transport (GO:0016197)
-2.012		tRNA modification (GO:0006400)
1.996		double-strand break repair via homologous recombination (GO:0000724)
-1.899		retrograde transport, endosome to Golgi (GO:0042147)
1.899		macroautophagy (GO:0016236)

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)



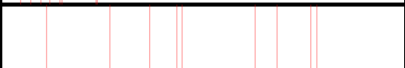
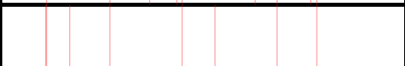
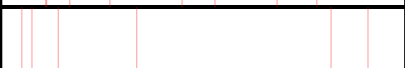


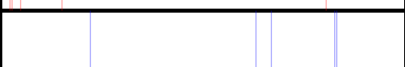





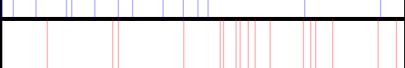

ES

0.15
0.10
0.05
0.00
-0.05

NES=0.169

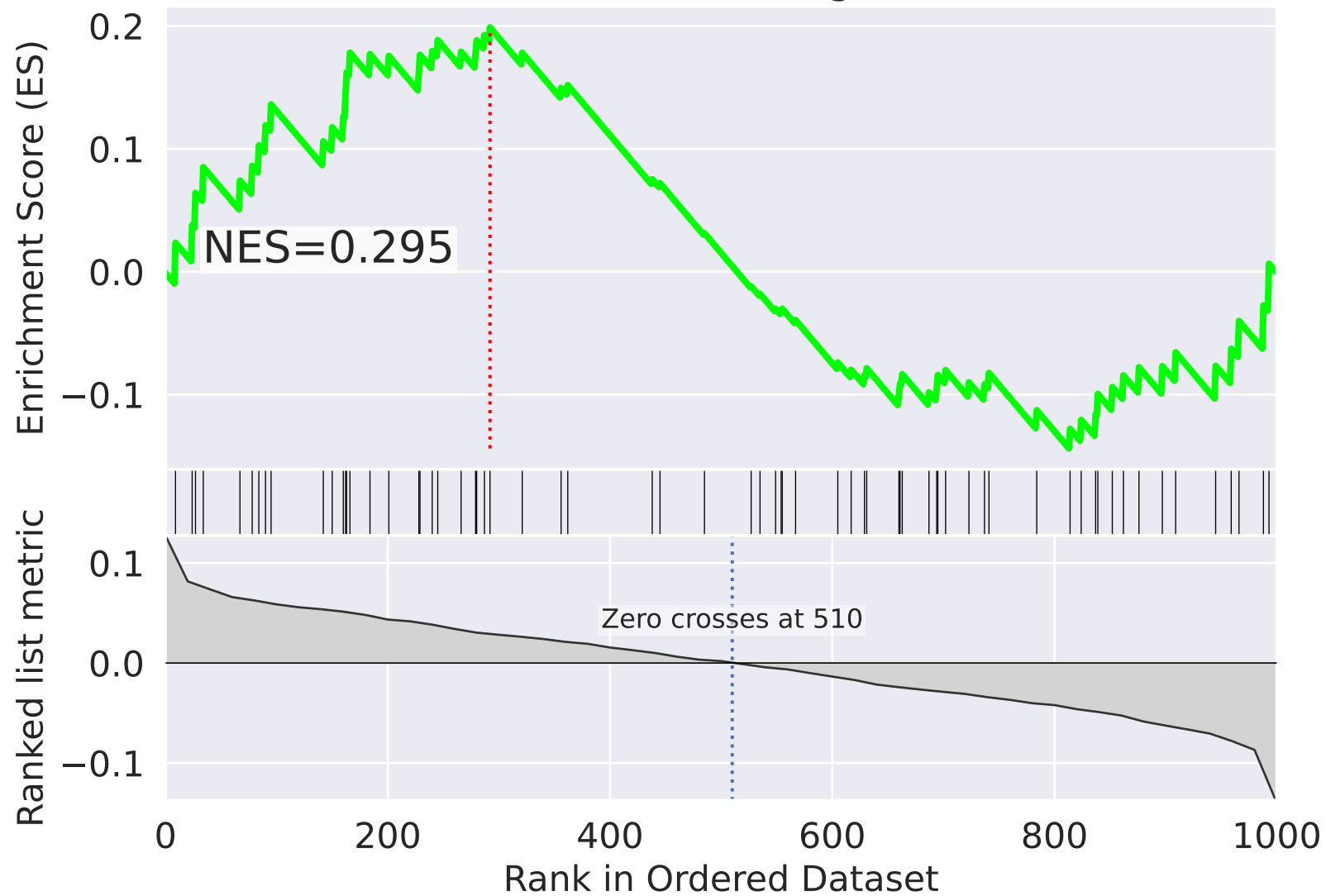
Rank



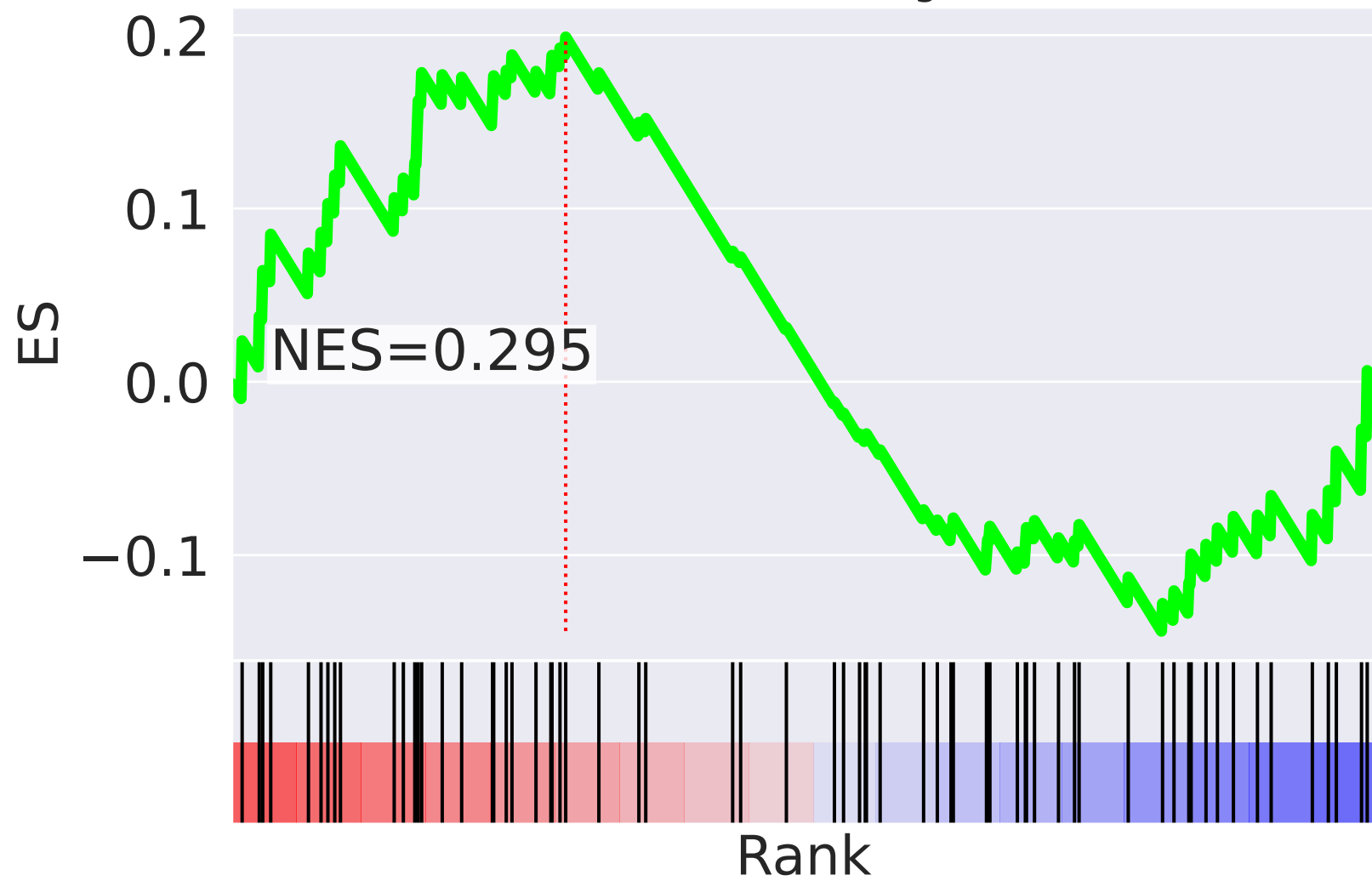
NES		SET
2.690		rRNA processing (GO:0006364)
2.451		interstrand cross-link repair (GO:0036297)
2.429		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.399		microtubule-based movement (GO:0007018)
2.362		ATP-dependent chromatin remodeling (GO:0043044)
-2.362		regulation of transcription, DNA-templated (GO:0006355)
2.351		protein K63-linked ubiquitination (GO:0070534)
-2.289		positive regulation of type I interferon production (GO:0032481)
2.255		mRNA processing (GO:0006397)
-2.182		negative regulation of translation (GO:0017148)
2.115		mitotic cell cycle (GO:0000278)
-2.065		transcription, DNA-templated (GO:0006351)
-1.957		cell cycle arrest (GO:0007050)
1.933		G2/M transition of mitotic cell cycle (GO:0000086)
1.918		mRNA splicing, via spliceosome (GO:0000398)






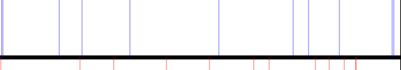

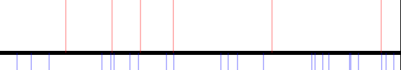





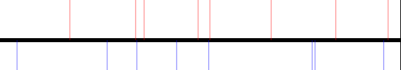

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=44$

mitochondrial translational elongation (GO:0070125)



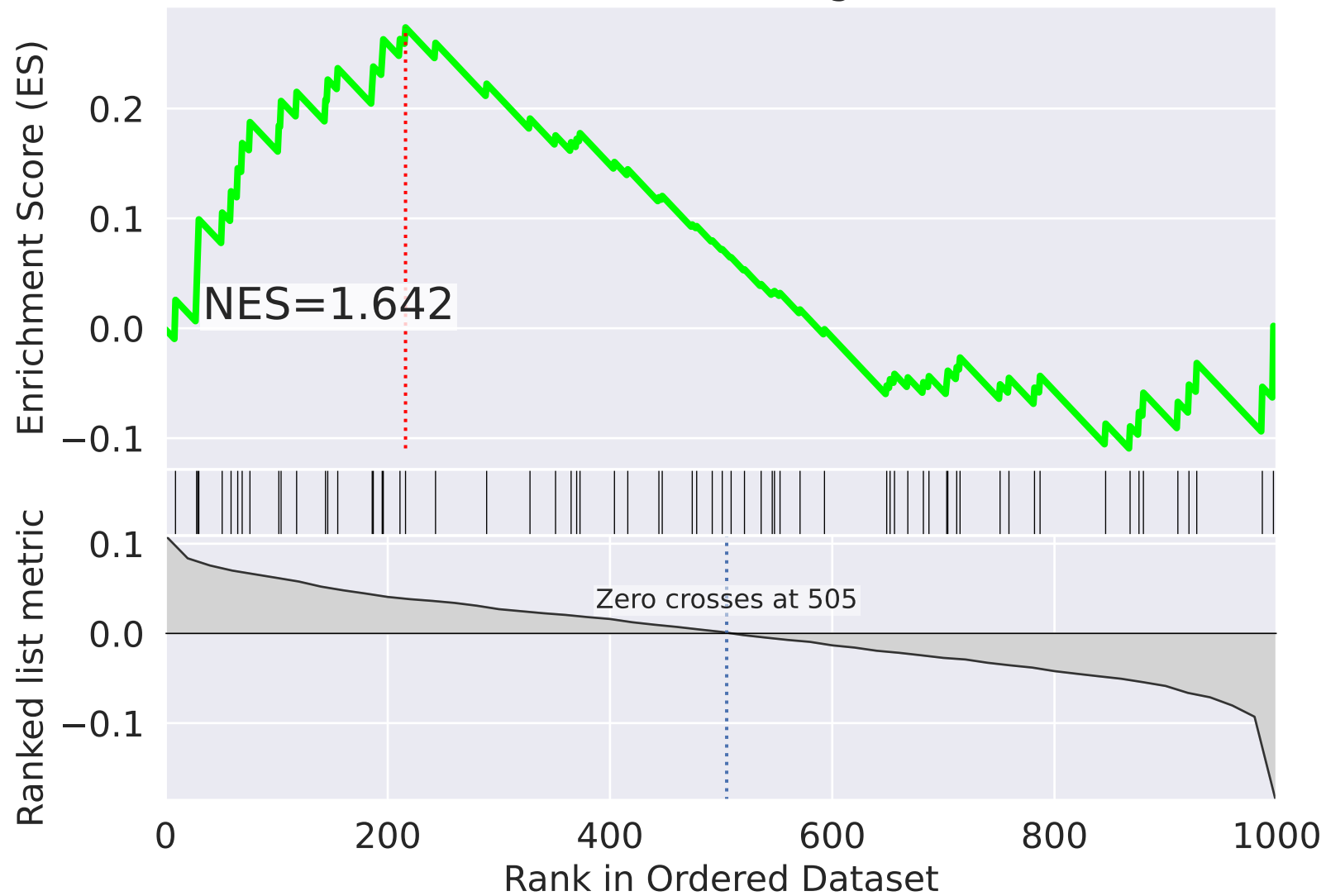
mitochondrial translational elongation (GO:0070125)



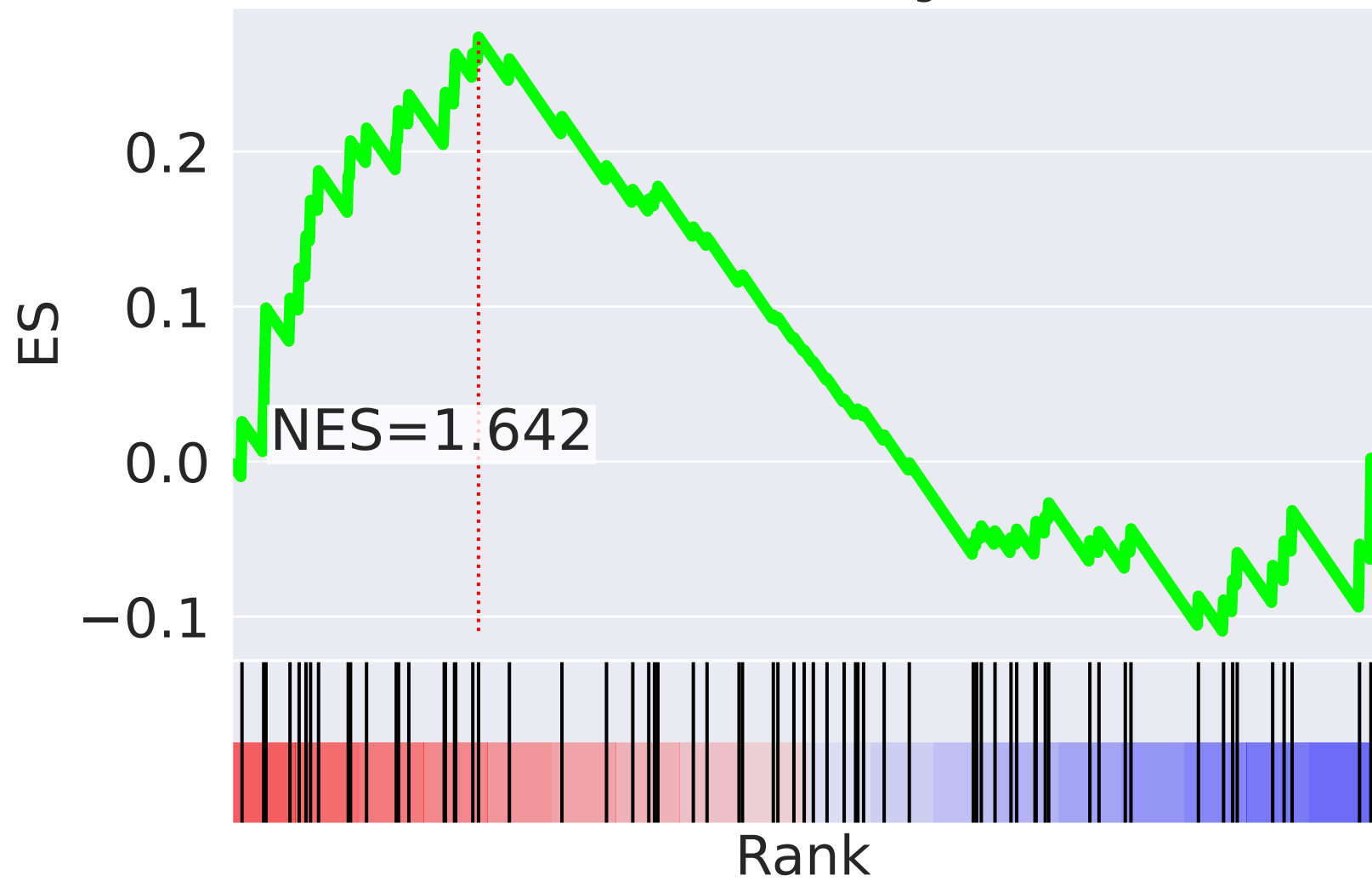
NES		SET
2.283		mRNA processing (GO:0006397)
-2.152		protein stabilization (GO:0050821)
2.075		movement of cell or subcellular component (GO:0006928)
2.038		response to virus (GO:0009615)
1.976		substantia nigra development (GO:0021762)
-1.943		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
1.897		transcription elongation from RNA polymerase II promoter (GO:0006368)
1.893		DNA duplex unwinding (GO:0032508)
-1.855		regulation of transcription, DNA-templated (GO:0006355)
-1.846		RNA export from nucleus (GO:0006405)
-1.826		mitotic cytokinesis (GO:0000281)
1.797		heart development (GO:0007507)
1.784		mitochondrial respiratory chain complex IV assembly (GO:0033617)
1.773		regulation of apoptotic process (GO:0042981)
-1.763		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)


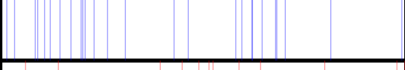
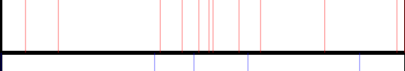
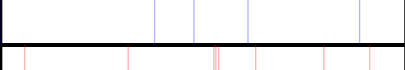


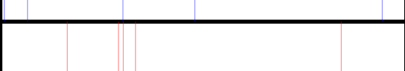
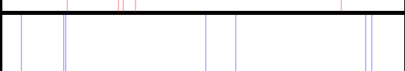

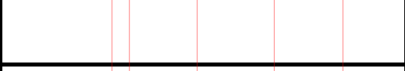
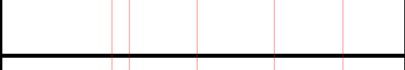

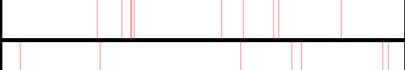
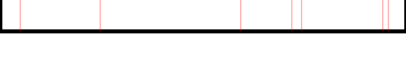

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=45$

mitochondrial translational elongation (GO:0070125)



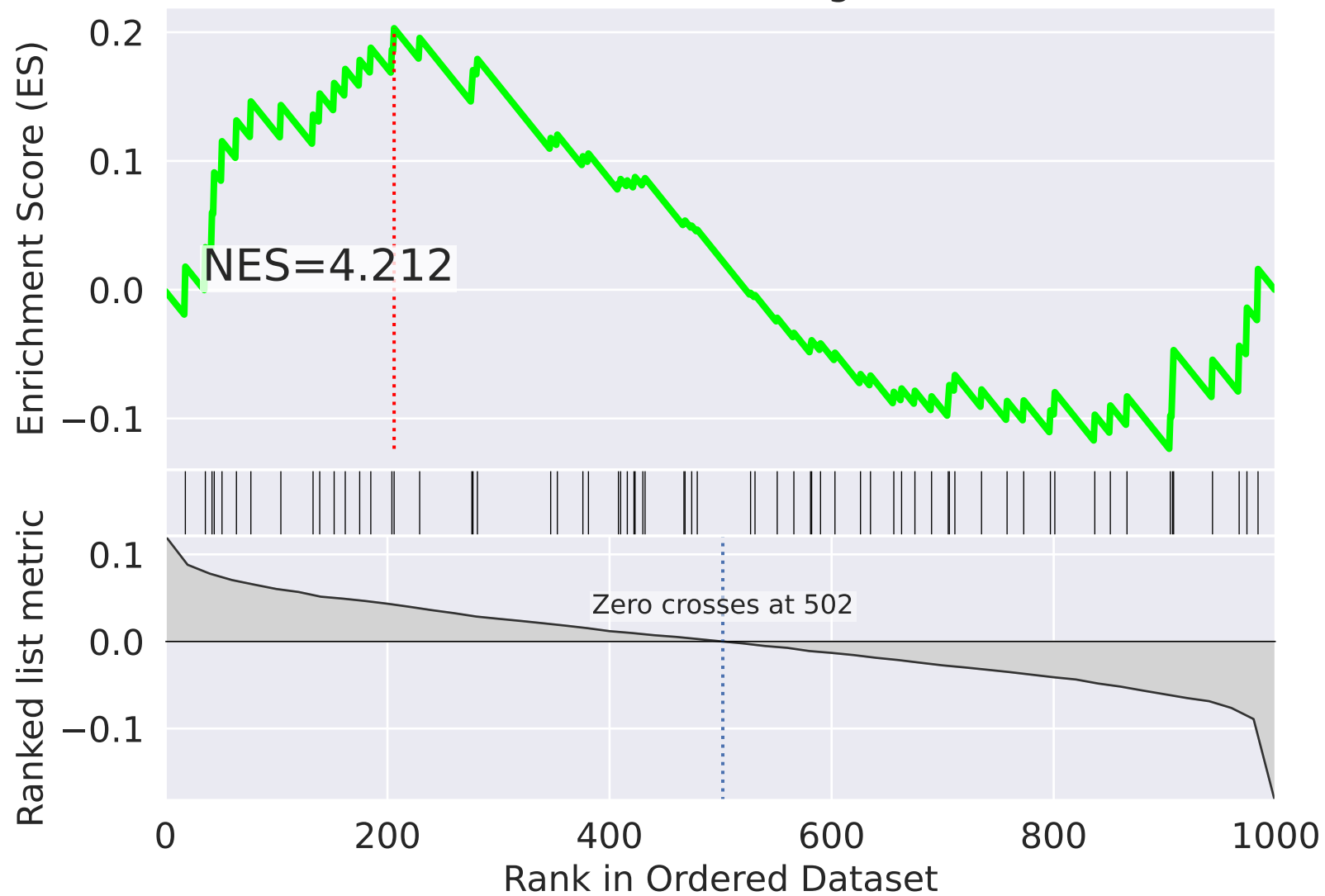
mitochondrial translational elongation (GO:0070125)



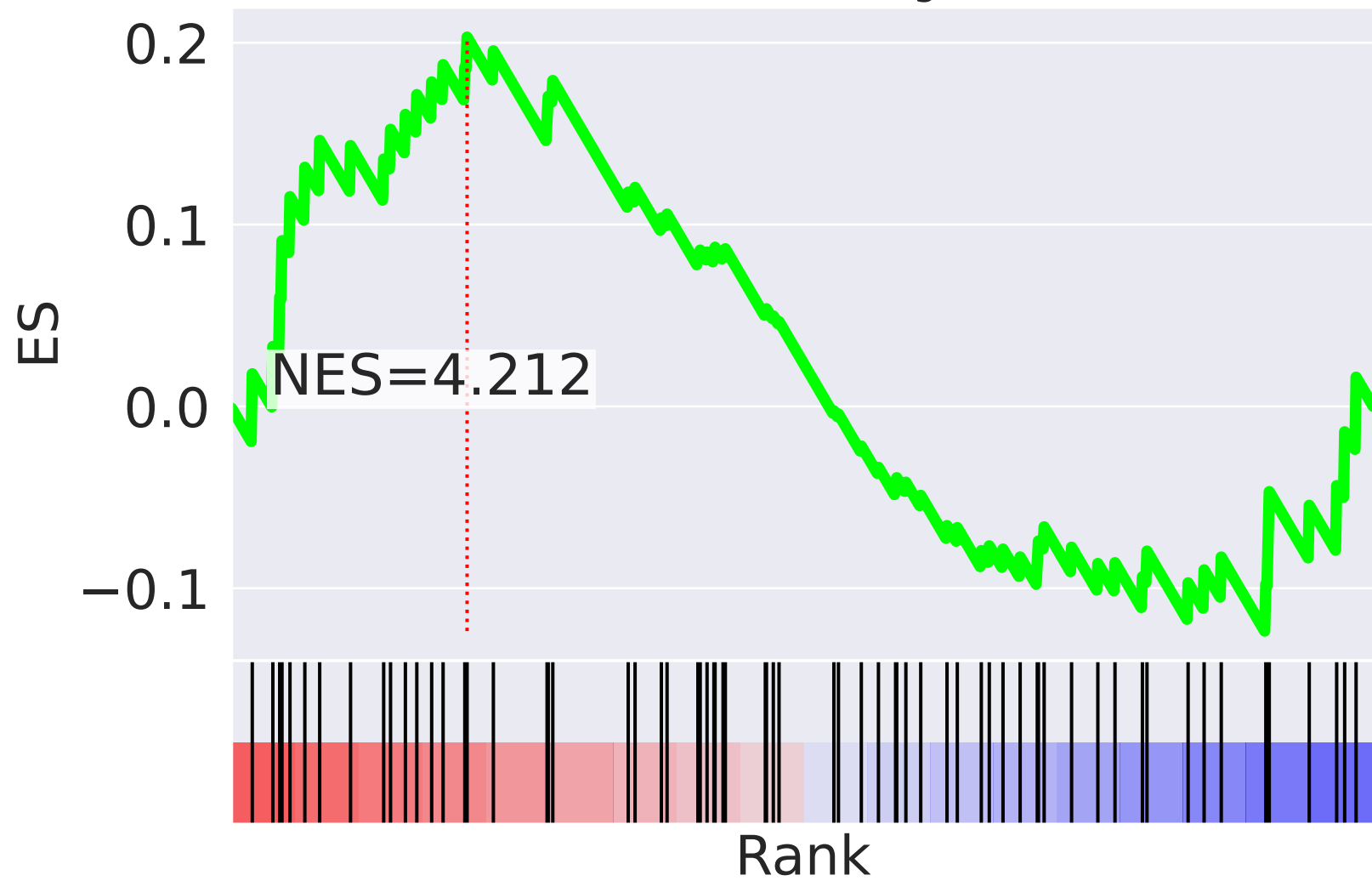
NES		SET
-3.439		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.149		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.822		ephrin receptor signaling pathway (GO:0048013)
-2.771		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.613		multicellular organism development (GO:0007275)
-2.251		cellular respiration (GO:0045333)
-2.248		DNA-dependent DNA replication (GO:0006261)
2.192		cellular response to hypoxia (GO:0071456)
-2.089		nervous system development (GO:0007399)
-1.936		iron-sulfur cluster assembly (GO:0016226)
1.914		termination of RNA polymerase I transcription (GO:0006363)
1.914		transcription initiation from RNA polymerase I promoter (GO:0006361)
1.914		transcription elongation from RNA polymerase I promoter (GO:0006362)
1.900		protein polyubiquitination (GO:0000209)
1.892		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 $z=46$

mitochondrial translational elongation (GO:0070125)

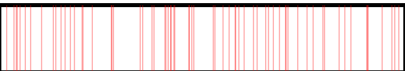





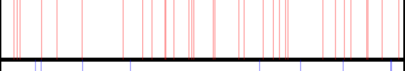
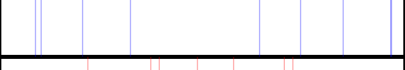
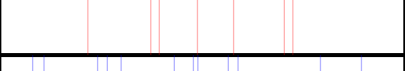
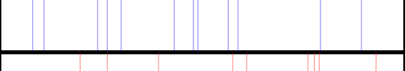
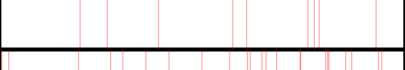

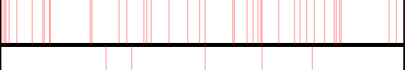

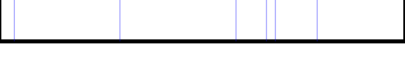


mitochondrial translational elongation (GO:0070125)



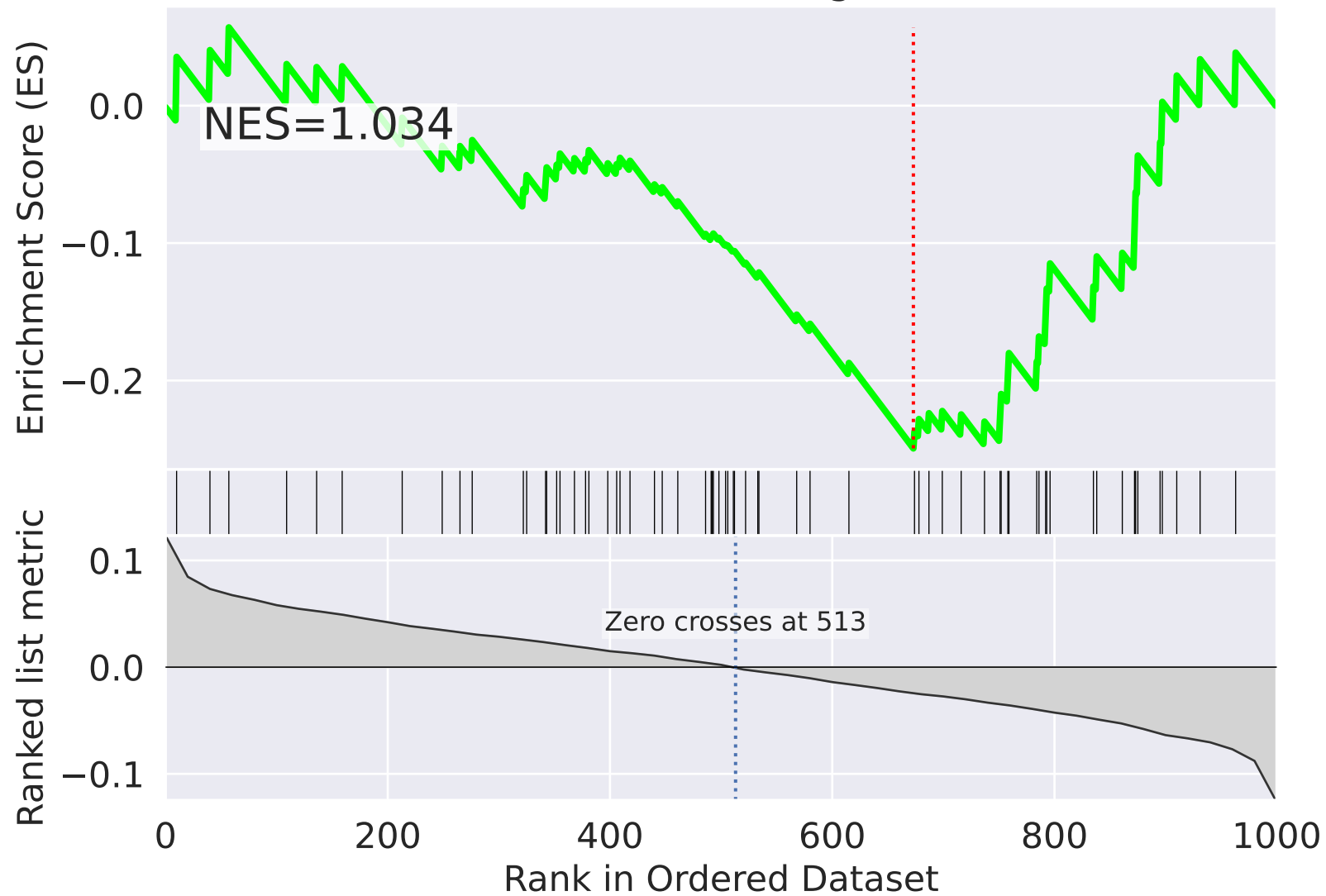
NES

SET

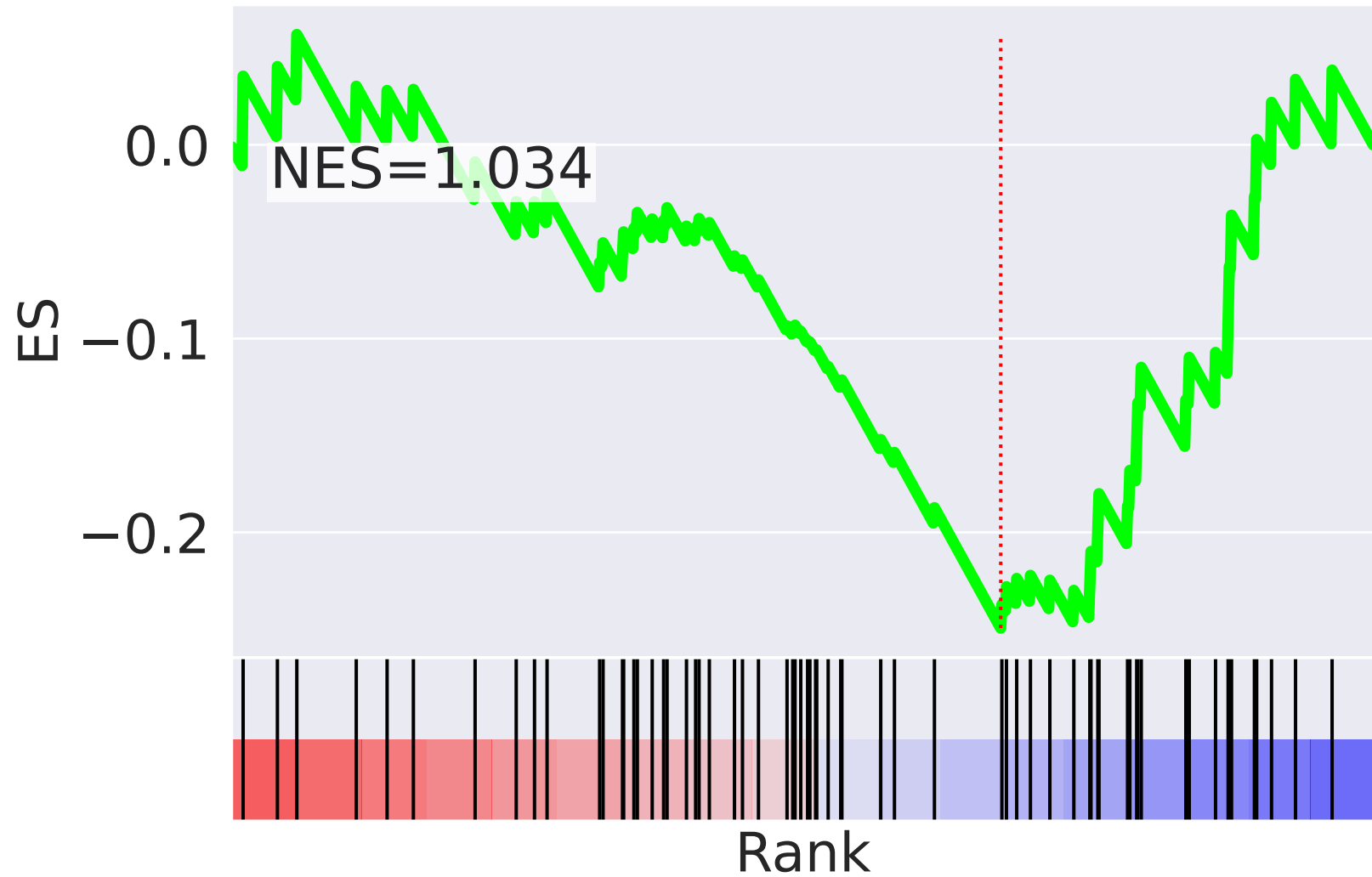
4.212		mitochondrial translational elongation (GO:0070125)
4.115		mitochondrial translational termination (GO:0070126)
2.938		insulin receptor signaling pathway (GO:0008286)
2.896		mitotic metaphase plate congression (GO:0007080)
-2.745		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.449		cell separation after cytokinesis (GO:0000920)
2.430		translation (GO:0006412)
-2.310		movement of cell or subcellular component (GO:0006928)
2.302		nucleus organization (GO:0006997)
-2.258		RNA splicing (GO:0008380)
2.254		transcription, DNA-templated (GO:0006351)
2.243		positive regulation of apoptotic process (GO:0043065)
2.152		positive regulation of transcription, DNA-templated (GO:0045893)
2.145		positive regulation of type I interferon production (GO:0032481)
-2.143		cellular nitrogen compound metabolic process (GO:0034641)

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)





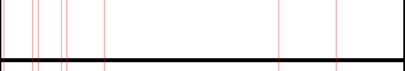


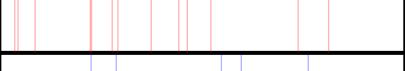






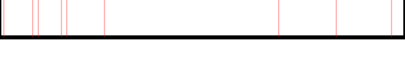


mitochondrial translational elongation (GO:0070125)



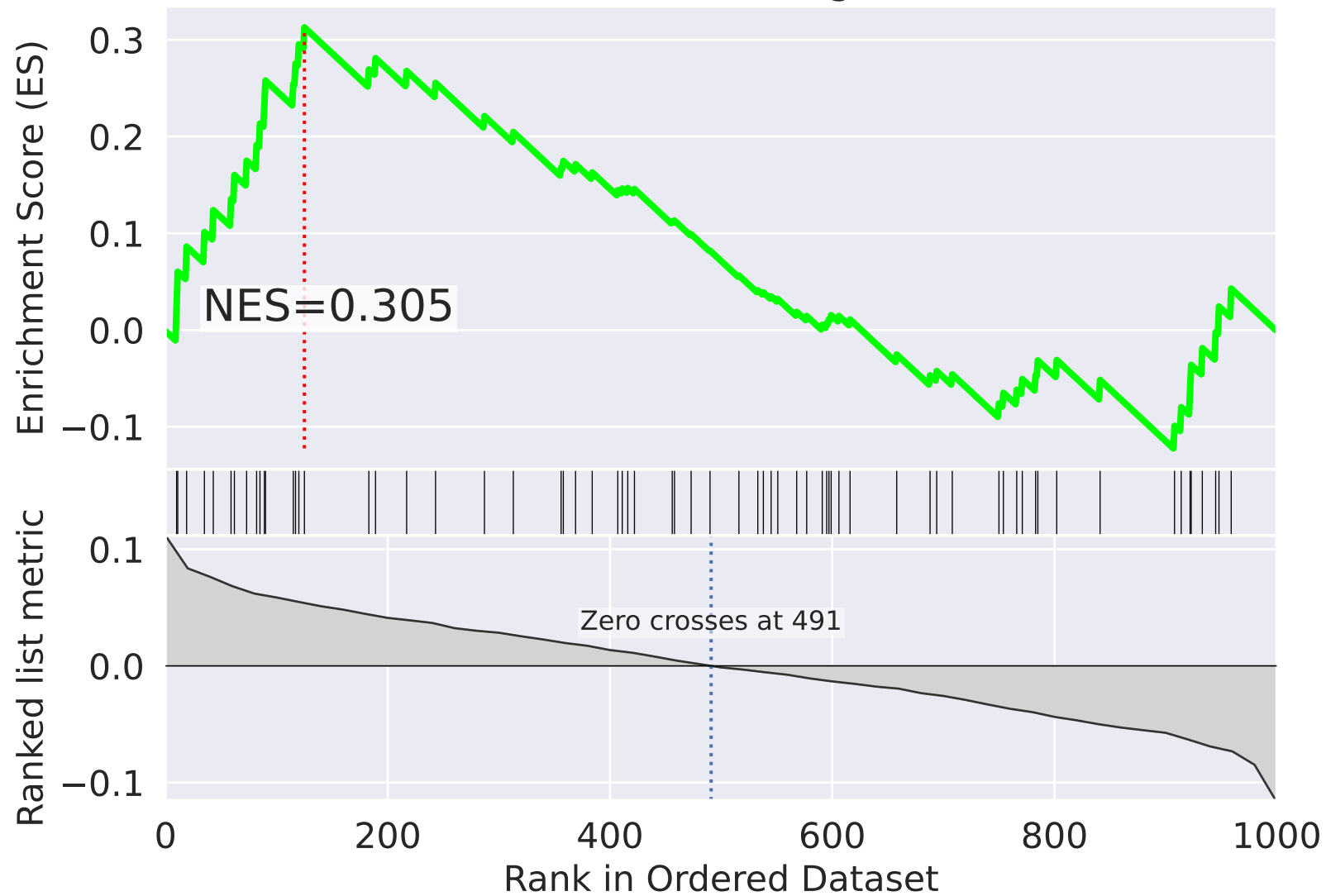
NES

SET

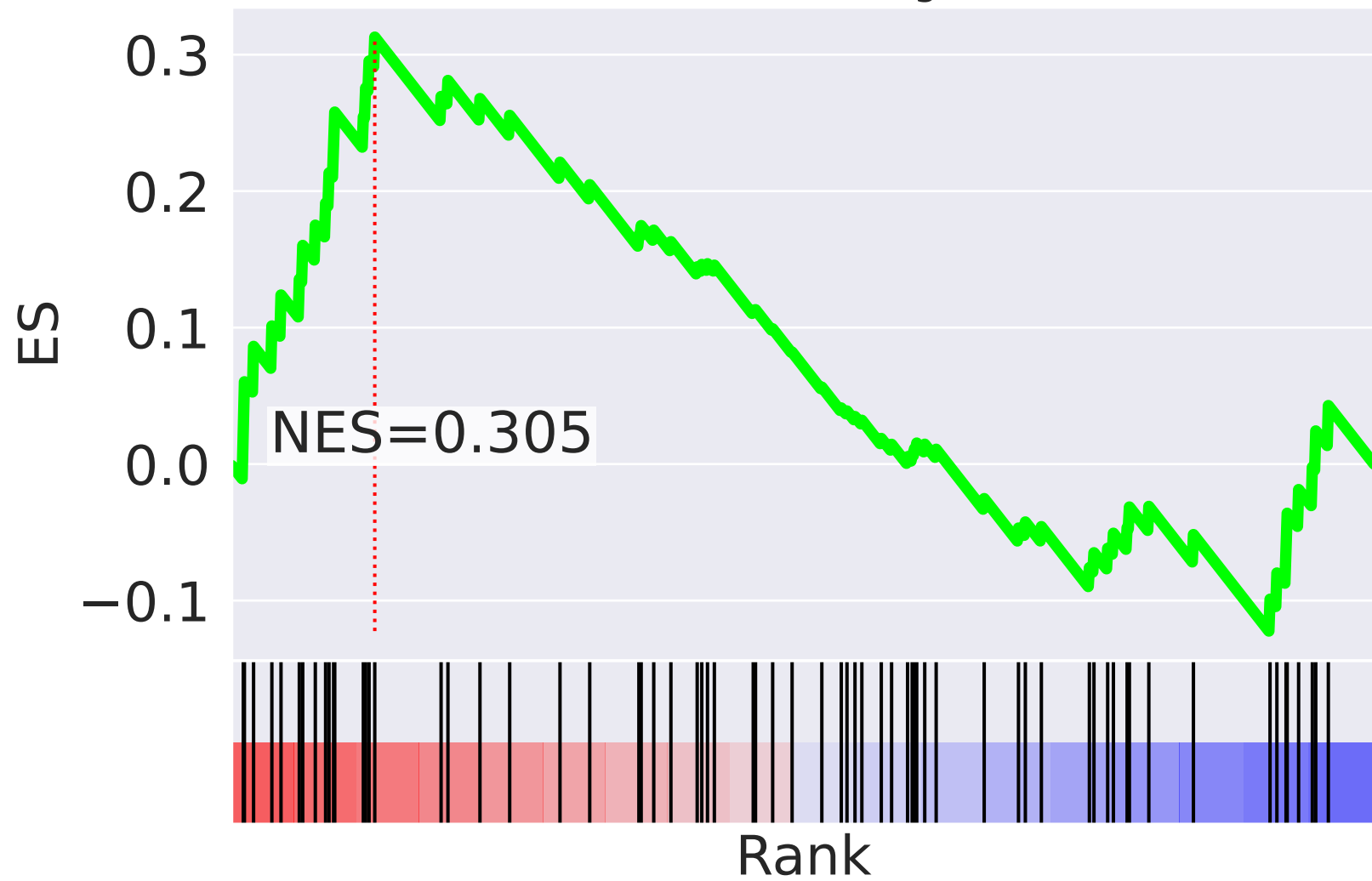
3.039		intracellular transport of virus (GO:0075733)
3.025		cell differentiation (GO:0030154)
2.895		DNA replication initiation (GO:0006270)
2.833		regulation of glucose transport (GO:0010827)
2.833		tRNA export from nucleus (GO:0006409)
2.833		regulation of gene silencing by miRNA (GO:0060964)
2.789		viral process (GO:0016032)
2.778		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.774		telomere capping (GO:0016233)
2.742		protein sumoylation (GO:0016925)
2.691		phosphatidylinositol-mediated signaling (GO:0048015)
2.630		double-strand break repair (GO:0006302)
2.612		T cell costimulation (GO:0031295)
2.607		mitotic nuclear envelope disassembly (GO:0007077)
2.603		viral transcription (GO:0019083)




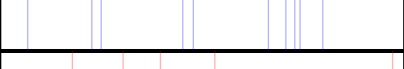
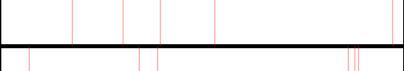
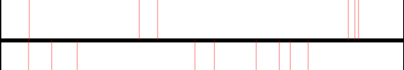
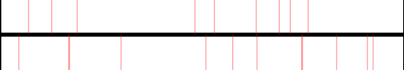
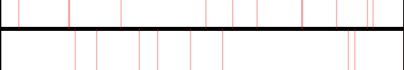
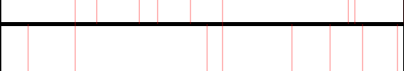
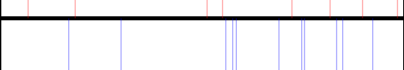
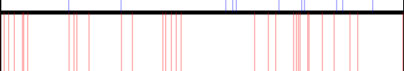




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=48$

mitochondrial translational elongation (GO:0070125)



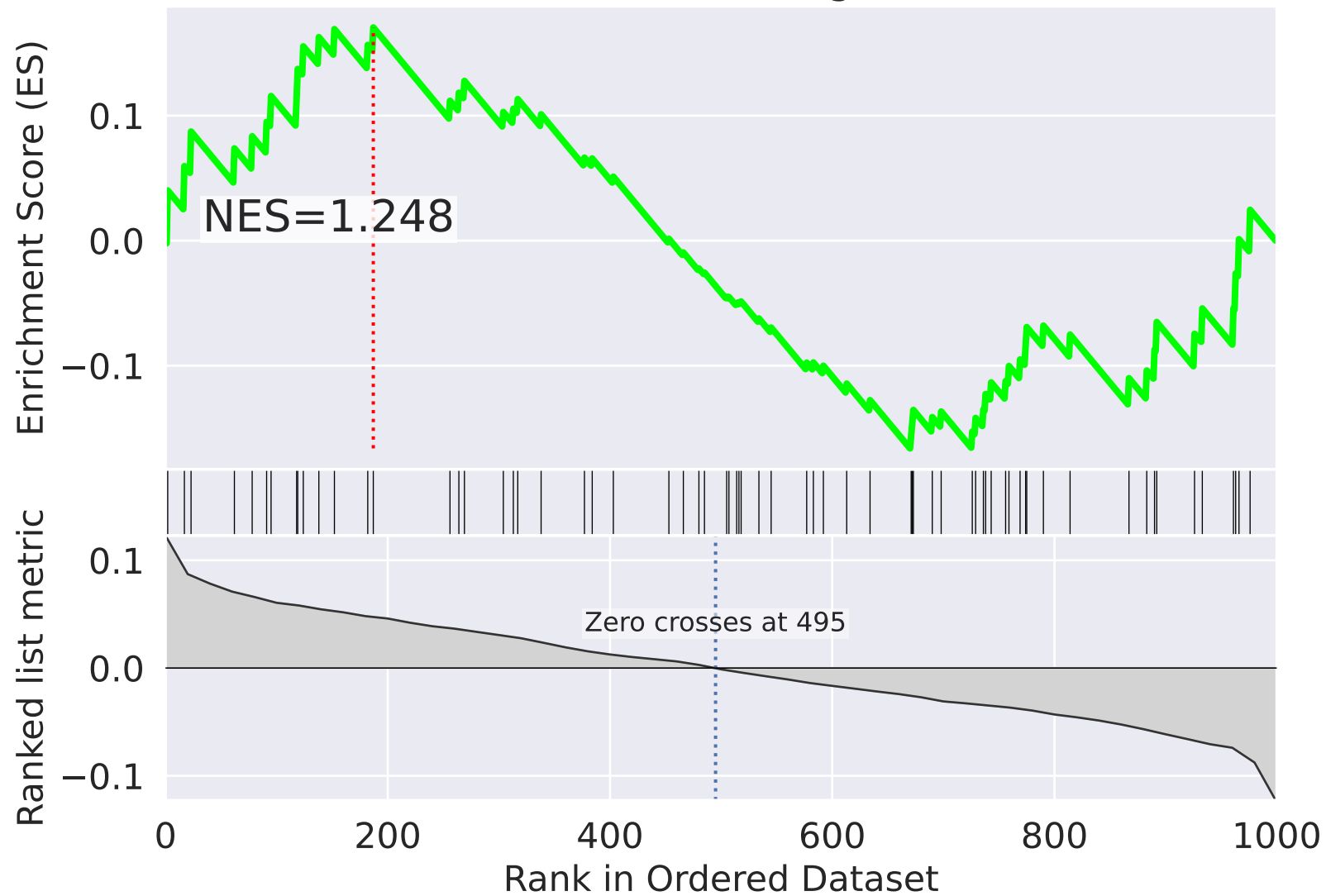
mitochondrial translational elongation (GO:0070125)



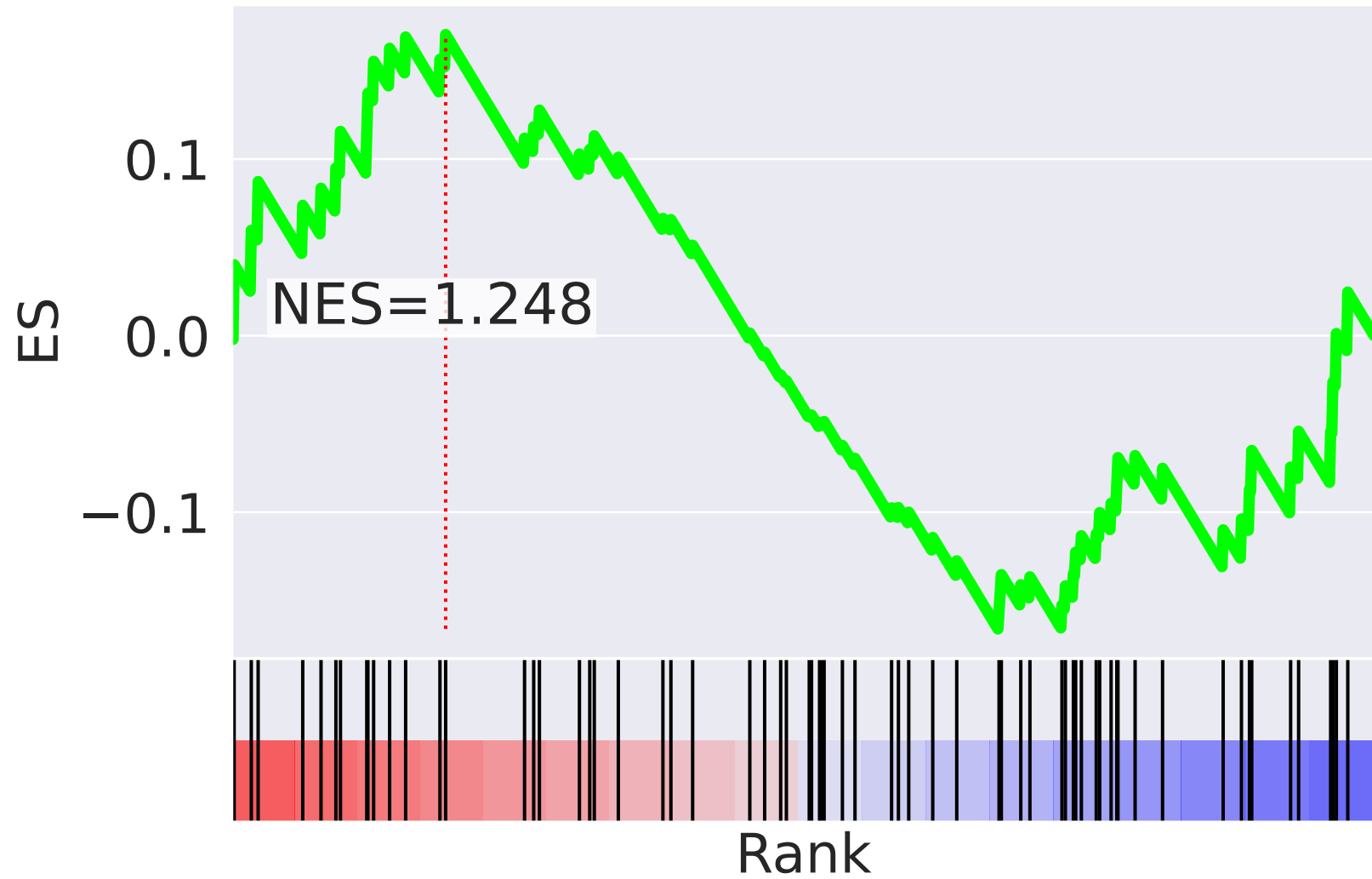
NES		SET
-2.853		transforming growth factor beta receptor signaling pathway (GO:0007179)
2.417		intrinsic apoptotic signaling pathway (GO:0097193)
2.402		protein dephosphorylation (GO:0006470)
-2.388		Ras protein signal transduction (GO:0007265)
2.253		DNA replication initiation (GO:0006270)
2.232		termination of RNA polymerase II transcription (GO:0006369)
2.215		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.159		mitotic metaphase plate congression (GO:0007080)
2.149		RNA export from nucleus (GO:0006405)
2.139		protein import into nucleus (GO:0006606)
-2.122		endosomal transport (GO:0016197)
2.103		negative regulation of transcription, DNA-templated (GO:0045892)
-2.071		regulation of cell adhesion (GO:0030155)
-2.025		integrin-mediated signaling pathway (GO:0007229)
-2.008		regulation of cholesterol biosynthetic process (GO:0045540)

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)



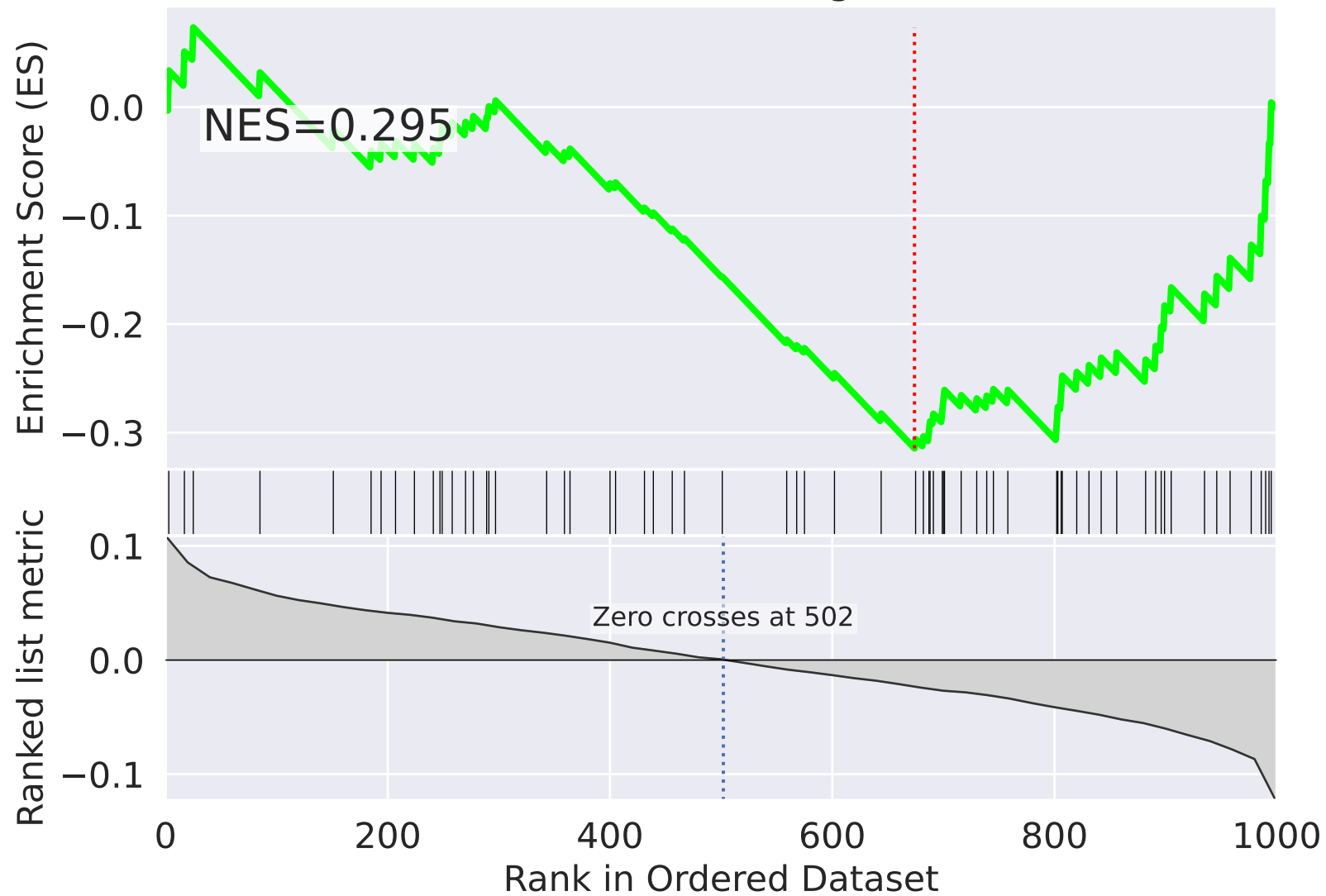
mitochondrial translational elongation (GO:0070125)



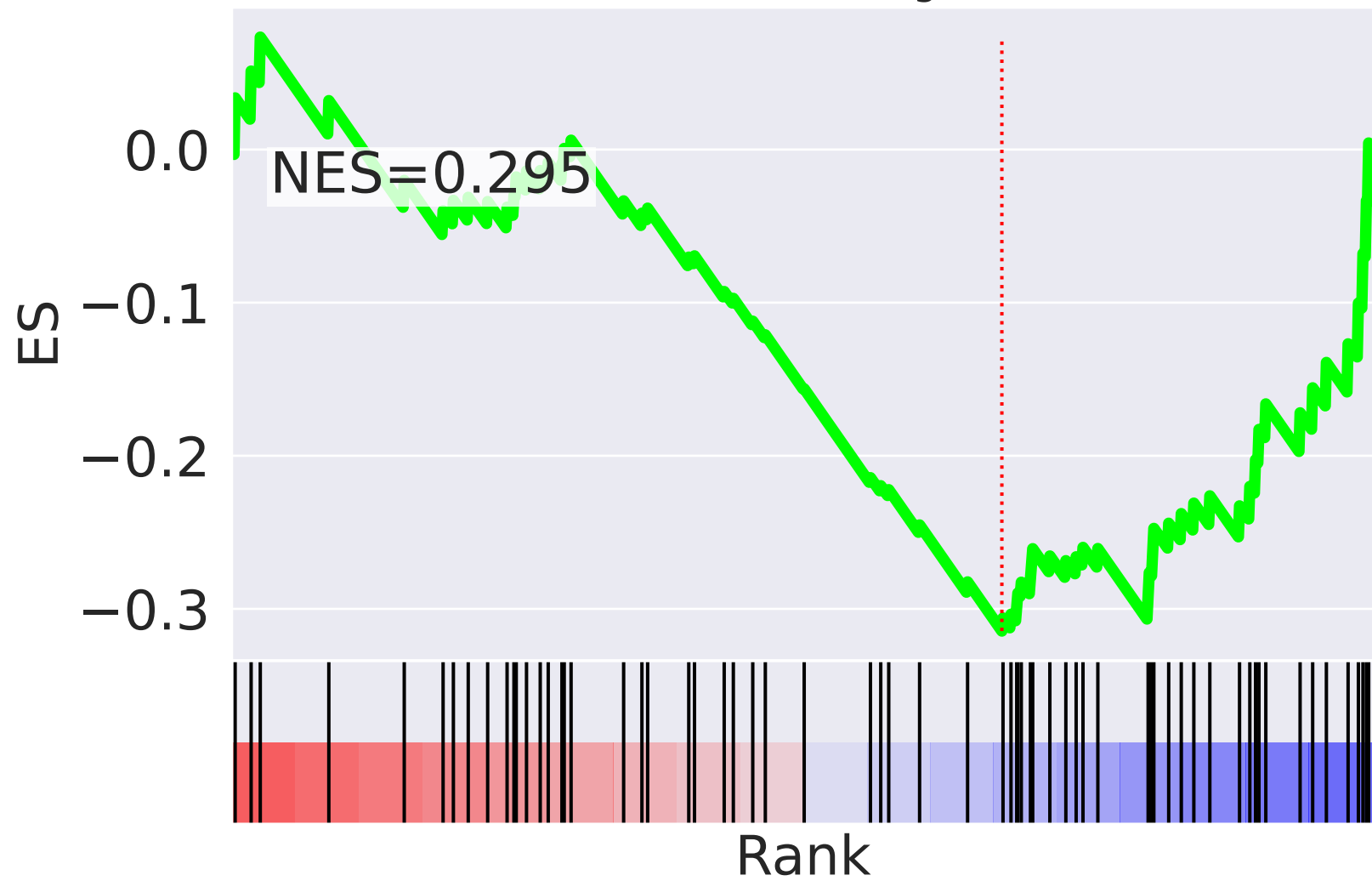
NES		SET
-3.055		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.506		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.460		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.306		cholesterol biosynthetic process (GO:0006695)
2.242		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.226		regulation of mRNA stability (GO:0043488)
-2.219		regulation of transcription, DNA-templated (GO:0006355)
-2.167		regulation of cholesterol biosynthetic process (GO:0045540)
-2.138		cellular response to epidermal growth factor stimulus (GO:0071364)
-2.069		protein dephosphorylation (GO:0006470)
1.998		macroautophagy (GO:0016236)
-1.986		snRNA transcription from RNA polymerase II promoter (GO:0042795)
1.983		cell growth (GO:0016049)
1.904		cellular protein modification process (GO:0006464)
1.891		positive regulation of apoptotic process (GO:0043065)






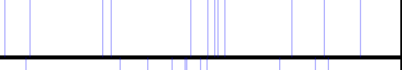

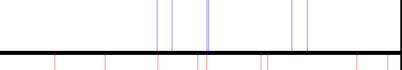
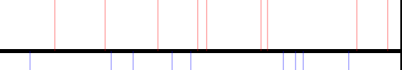




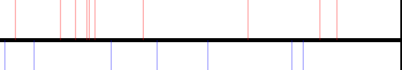
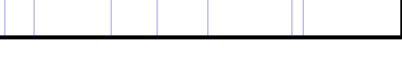
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=50$

mitochondrial translational elongation (GO:0070125)



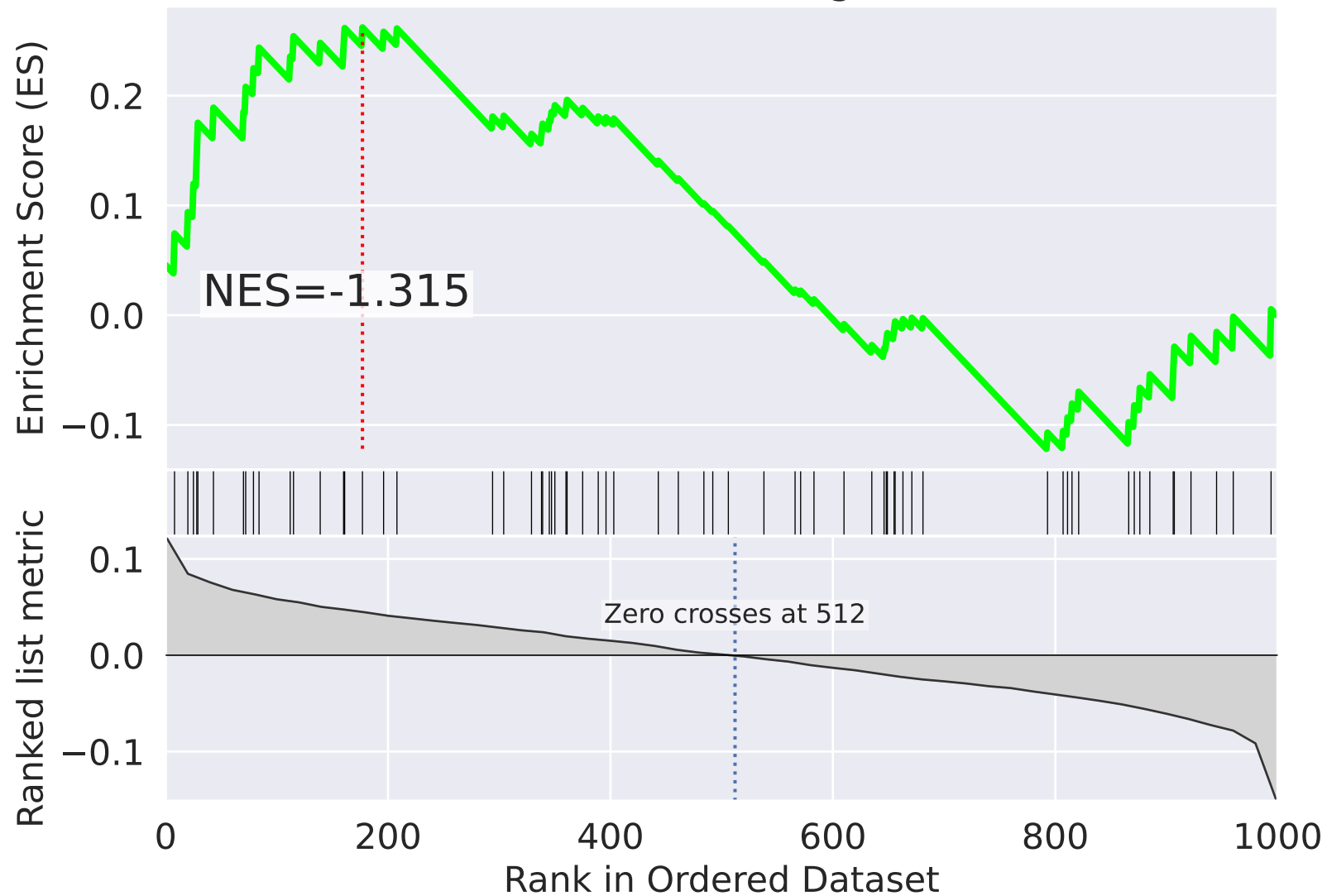
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.613		telomere maintenance via recombination (GO:0000722)
-2.576		positive regulation of TOR signaling (GO:0032008)
-2.478		mitotic cell cycle (GO:0000278)
2.452		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.383		ERK1 and ERK2 cascade (GO:0070371)
-2.282		protein phosphorylation (GO:0006468)
-2.250		ephrin receptor signaling pathway (GO:0048013)
-2.207		T cell costimulation (GO:0031295)
2.163		RNA export from nucleus (GO:0006405)
-2.130		intracellular signal transduction (GO:0035556)
-2.069		platelet activation (GO:0030168)
1.981		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-1.965		phosphatidylinositol-mediated signaling (GO:0048015)
1.960		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-1.953		peptidyl-serine phosphorylation (GO:0018105)

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)



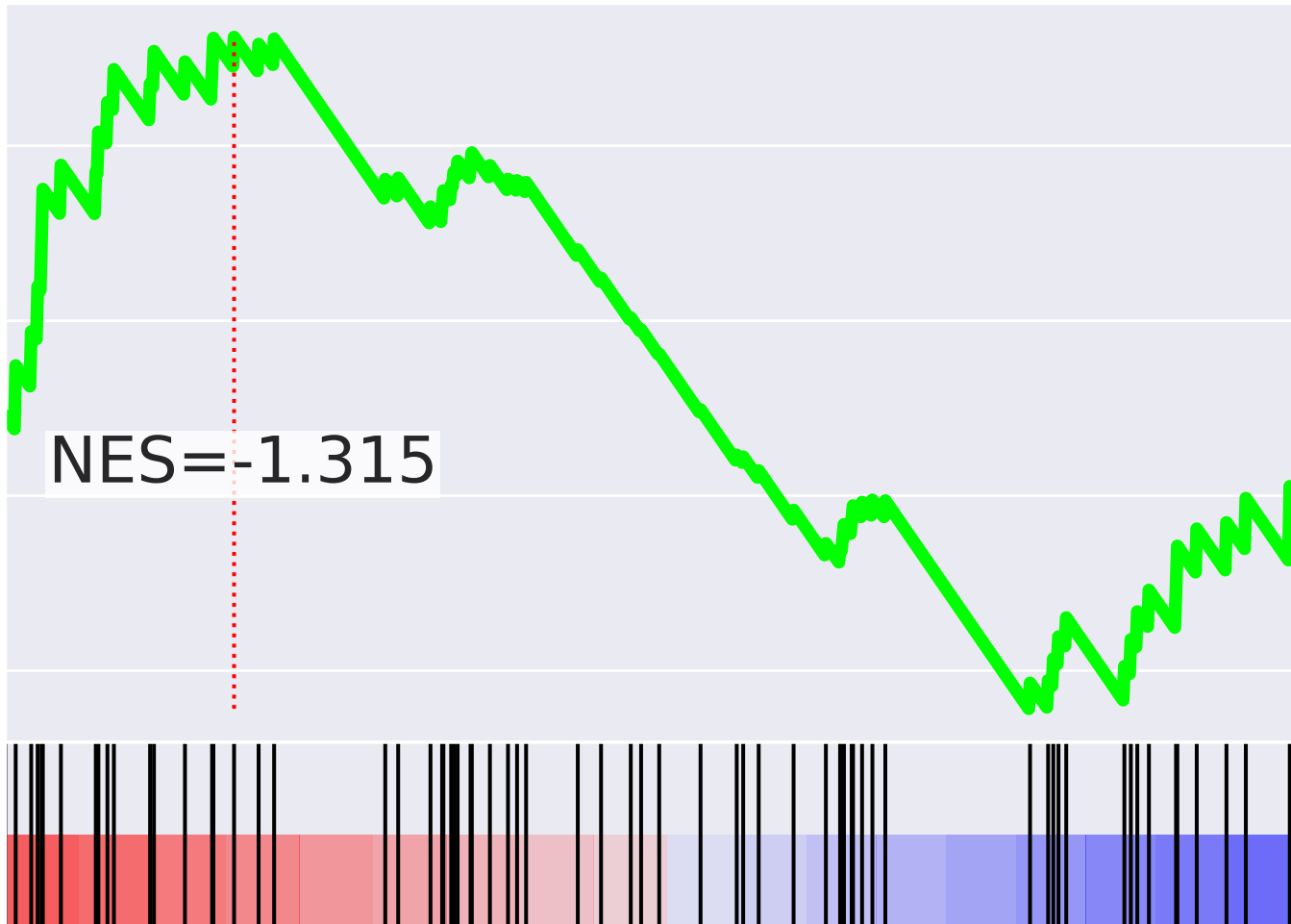
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1

NES=-1.315

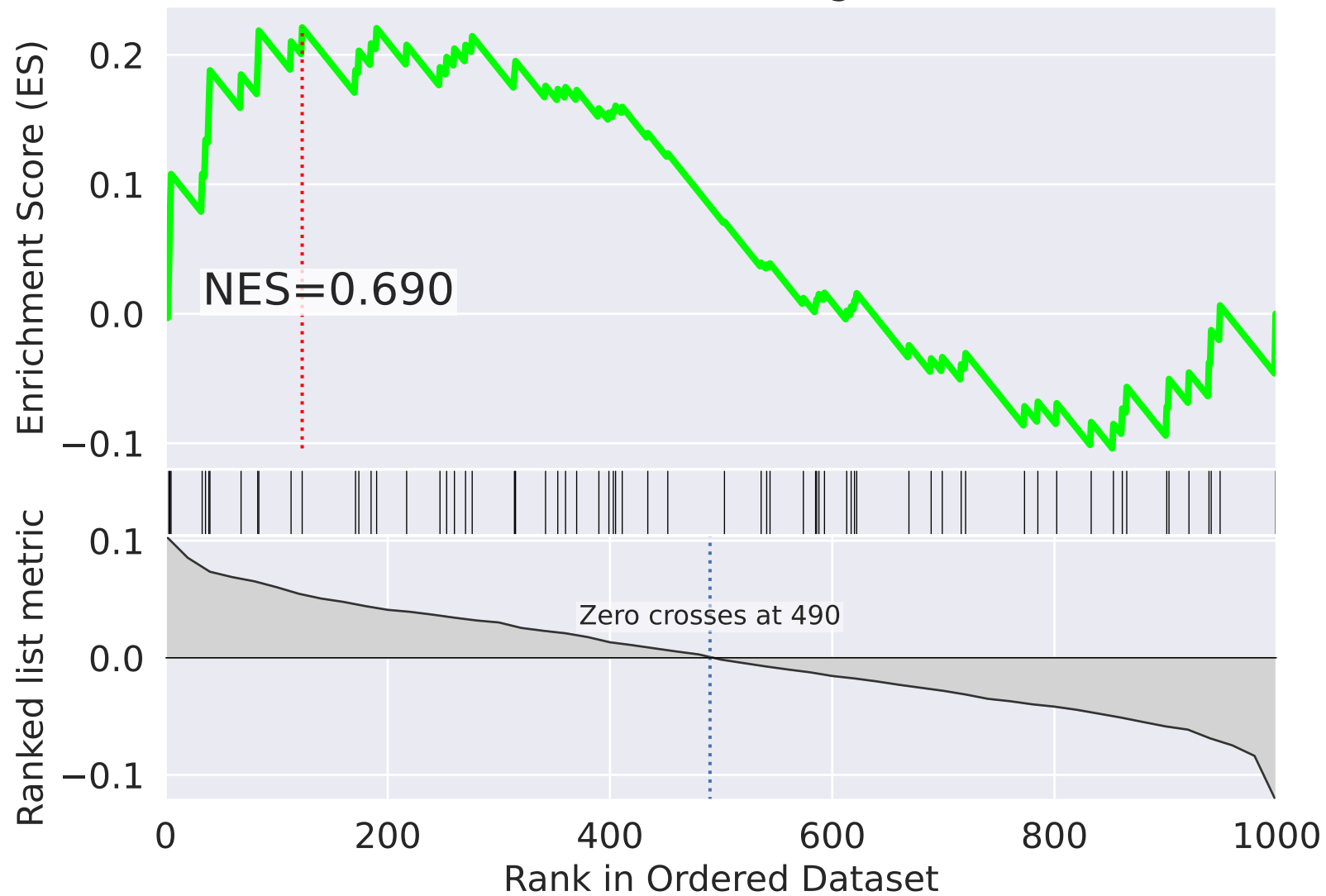
Rank



NES		SET
-2.464		retrograde transport, endosome to Golgi (GO:0042147)
2.339		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.291		cellular response to tumor necrosis factor (GO:0071356)
-2.280		lysosomal transport (GO:0007041)
-2.257		rRNA processing (GO:0006364)
2.248		mitotic spindle organization (GO:0007052)
-2.216		tRNA modification (GO:0006400)
-2.206		protein sumoylation (GO:0016925)
2.196		strand displacement (GO:0000732)
2.152		DNA synthesis involved in DNA repair (GO:0000731)
-2.137		negative regulation of translation (GO:0017148)
2.094		negative regulation of cell proliferation (GO:0008285)
-2.037		tRNA aminoacylation for protein translation (GO:0006418)
-2.028		innate immune response (GO:0045087)
-2.021		regulation of cellular response to heat (GO:1900034)

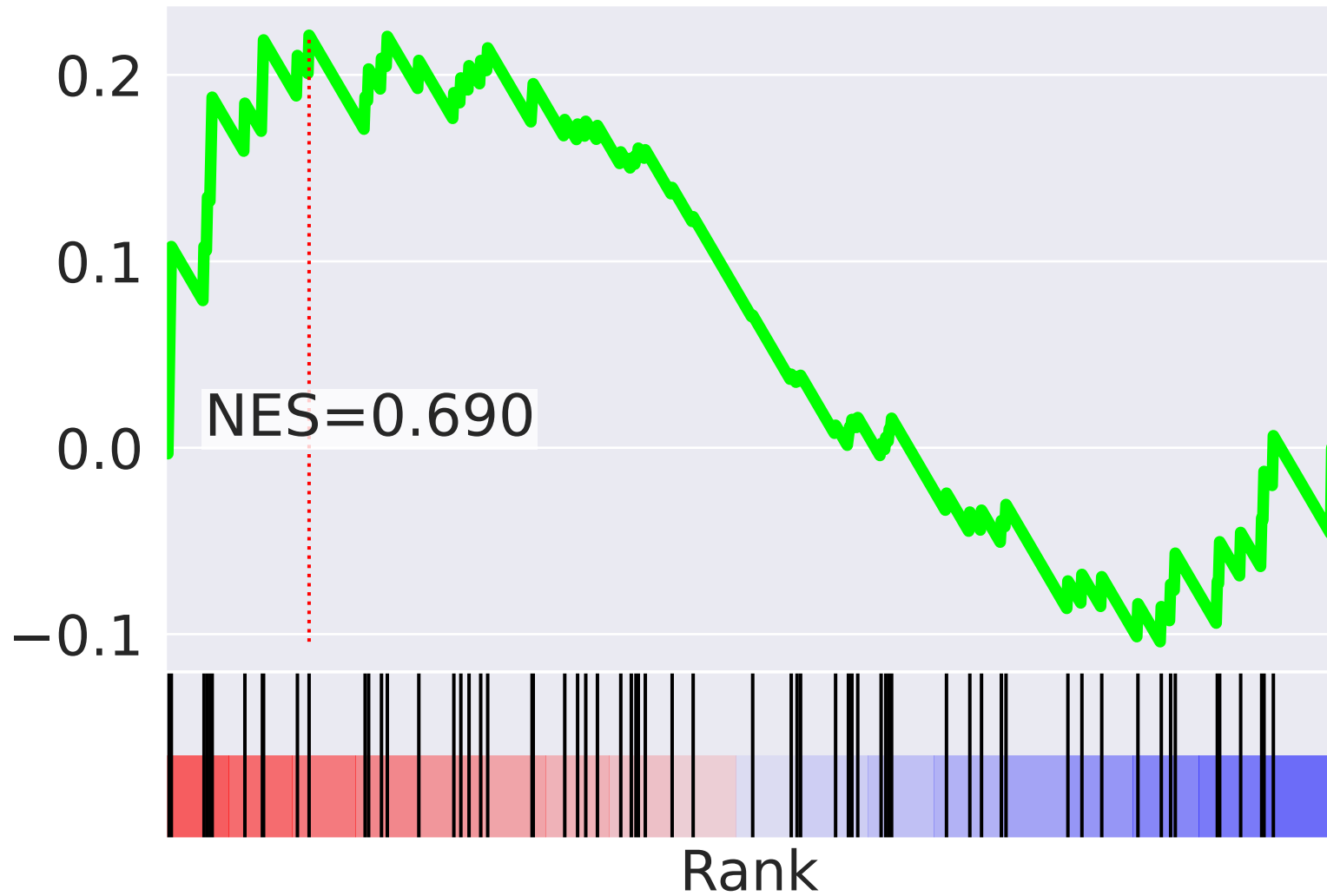
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=52$

mitochondrial translational elongation (GO:0070125)







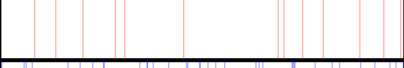
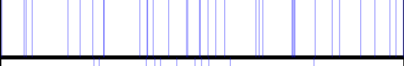



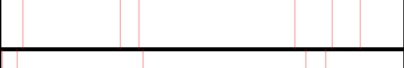
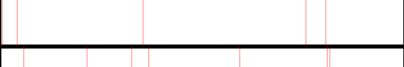

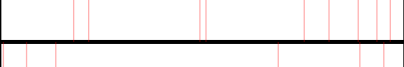
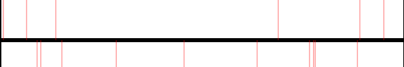
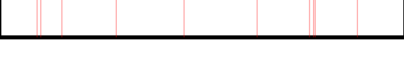
mitochondrial translational elongation (GO:0070125)

ES



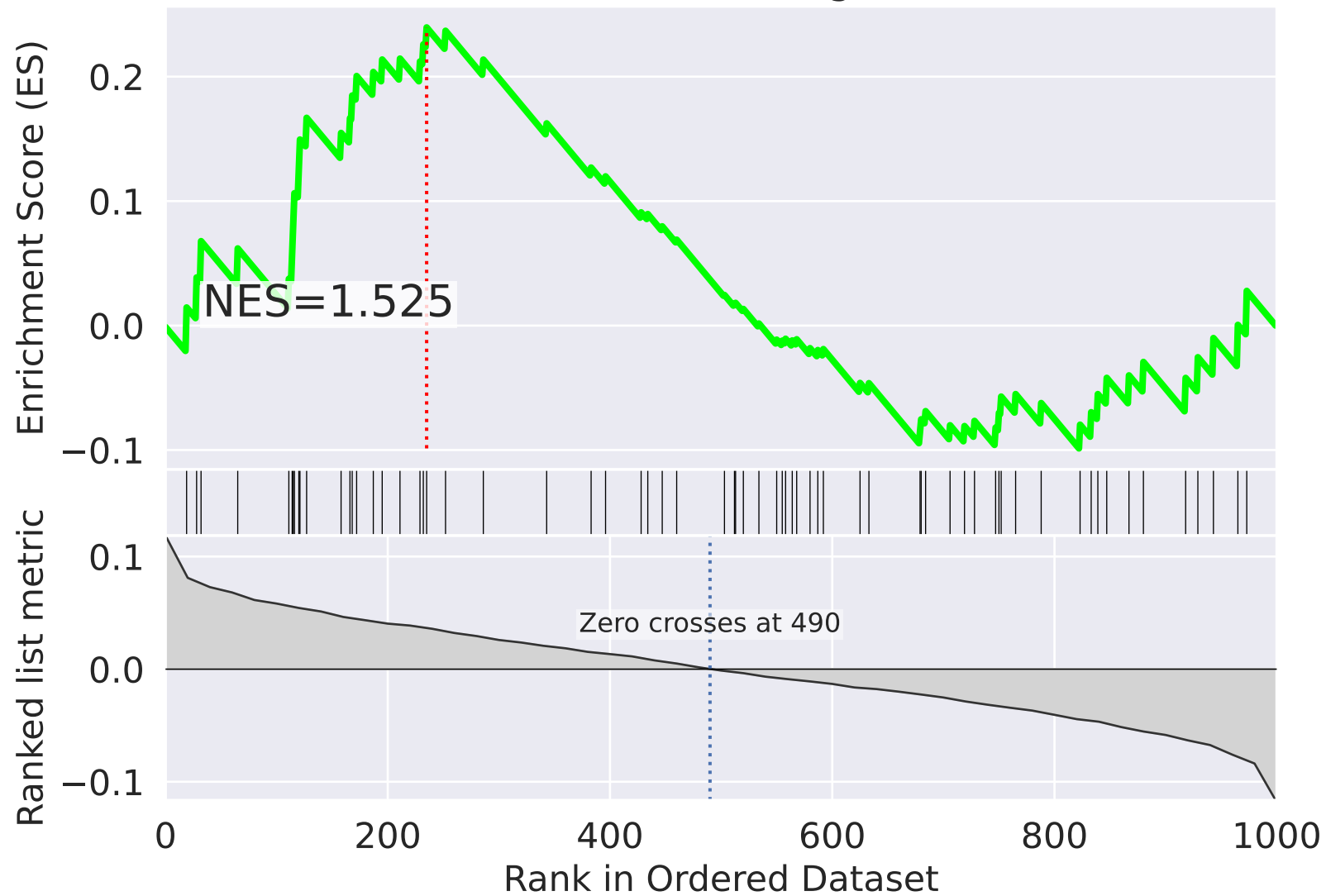
NES

SET

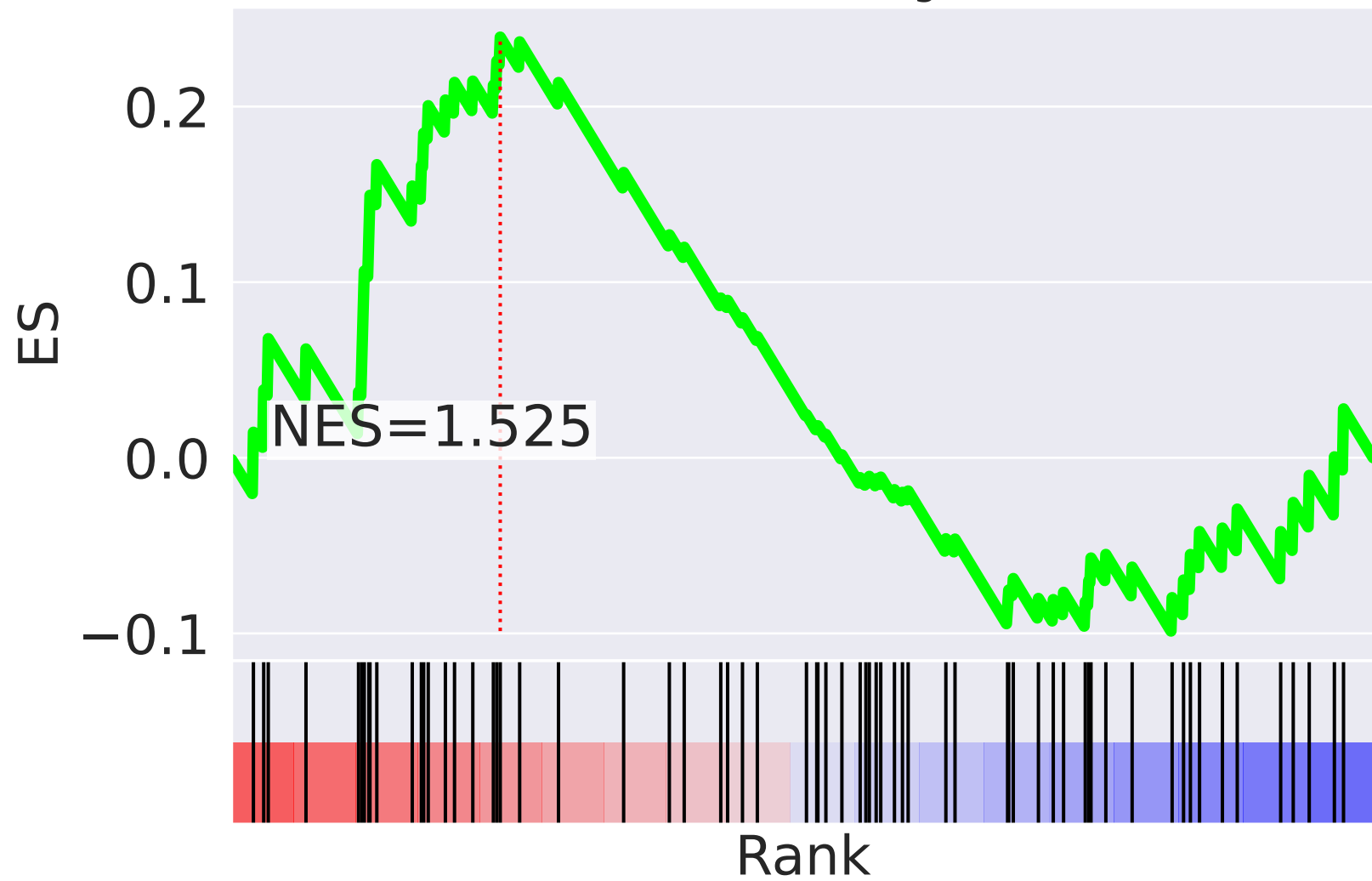
2.815		mitotic metaphase plate congression (GO:0007080)
-2.520		protein autophosphorylation (GO:0046777)
2.431		membrane organization (GO:0061024)
2.393		regulation of cell proliferation (GO:0042127)
2.387		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.332		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-2.324		mitotic nuclear envelope disassembly (GO:0007077)
-2.277		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.172		transcription from RNA polymerase II promoter (GO:0006366)
2.126		cell differentiation (GO:0030154)
2.111		cellular respiration (GO:0045333)
2.101		nucleus organization (GO:0006997)
2.078		movement of cell or subcellular component (GO:0006928)
2.048		COPII vesicle coating (GO:0048208)
2.028		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 $z=53$

mitochondrial translational elongation (GO:0070125)



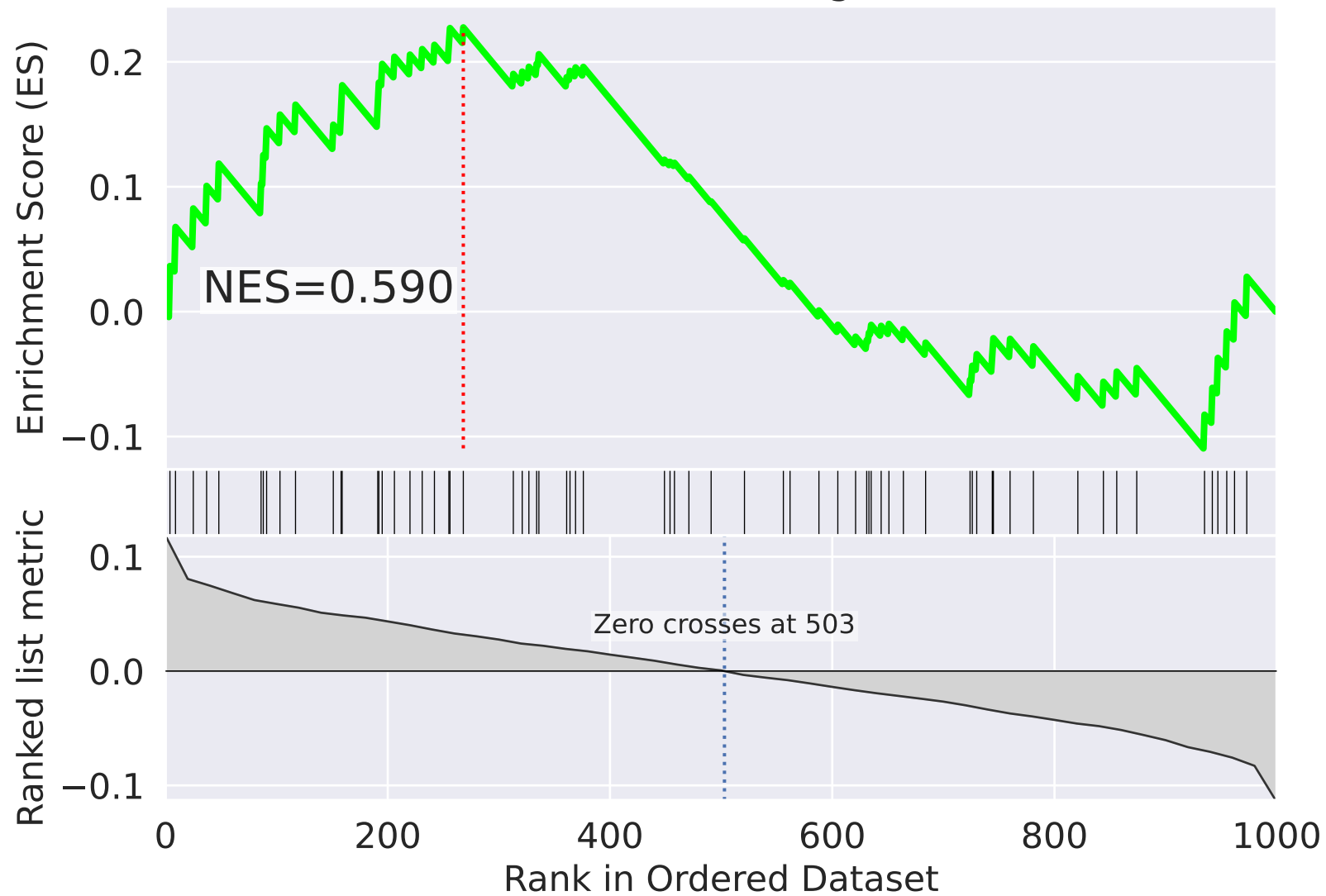
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.816		G2/M transition of mitotic cell cycle (GO:0000086)
-2.652		transforming growth factor beta receptor signaling pathway (GO:0007179)
2.476		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.434		positive regulation of cytokinesis (GO:0032467)
-2.304		G1/S transition of mitotic cell cycle (GO:0000082)
2.304		proteolysis (GO:0006508)
2.303		translation (GO:0006412)
2.261		regulation of protein stability (GO:0031647)
2.114		ERBB2 signaling pathway (GO:0038128)
-2.094		substrate adhesion-dependent cell spreading (GO:0034446)
-2.084		integrin-mediated signaling pathway (GO:0007229)
-2.082		protein complex assembly (GO:0006461)
2.045		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.042		aerobic respiration (GO:0009060)
-2.000		negative regulation of translation (GO:0017148)

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)




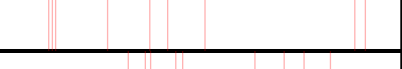
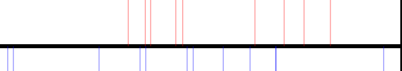
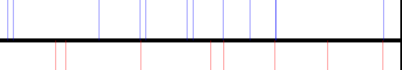
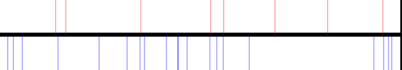
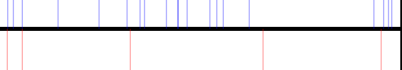
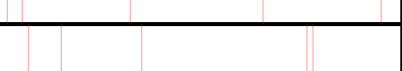
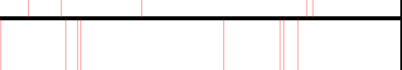
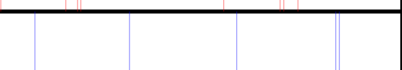




ES

0.2
0.1
0.0
-0.1

NES=0.590

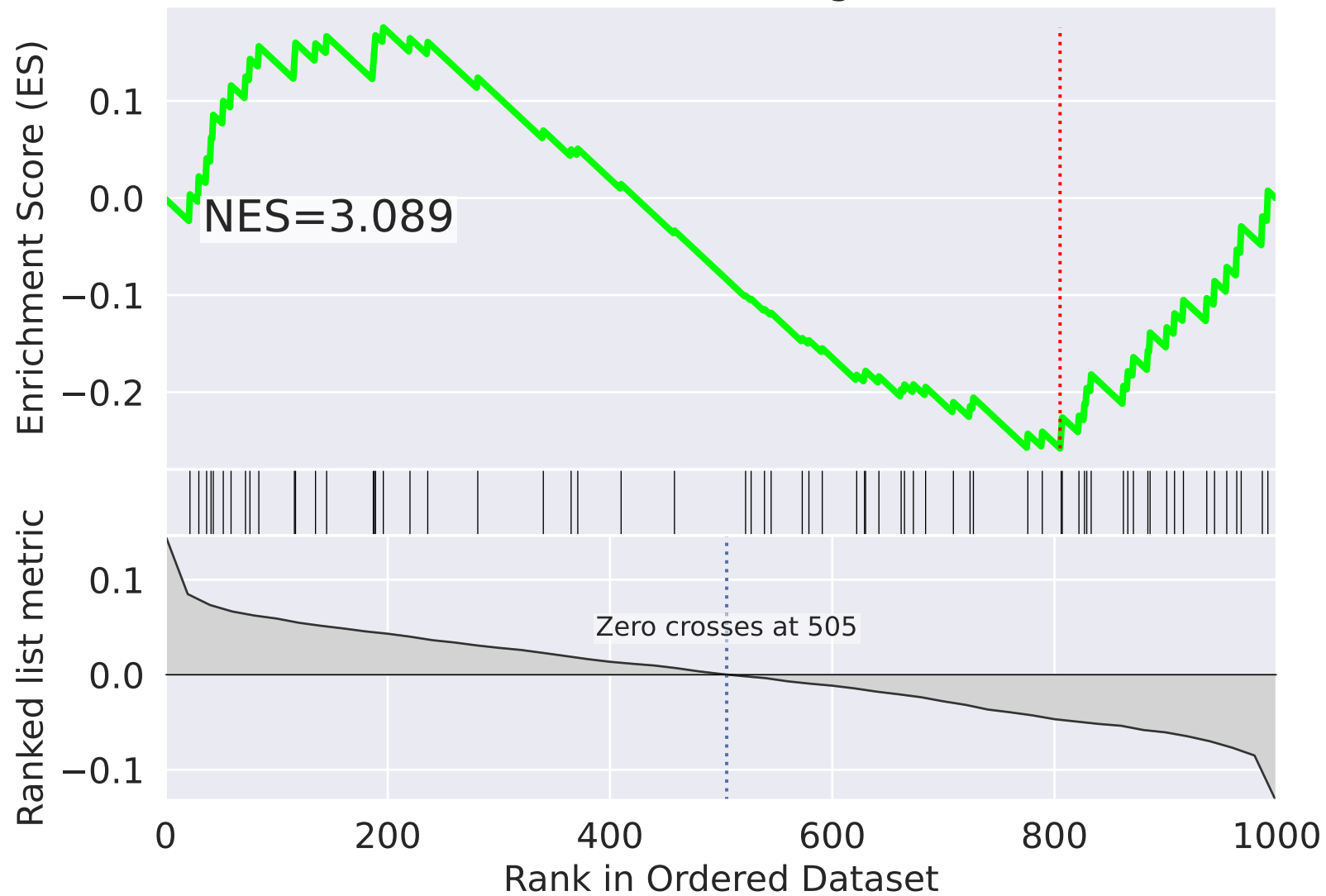
Rank



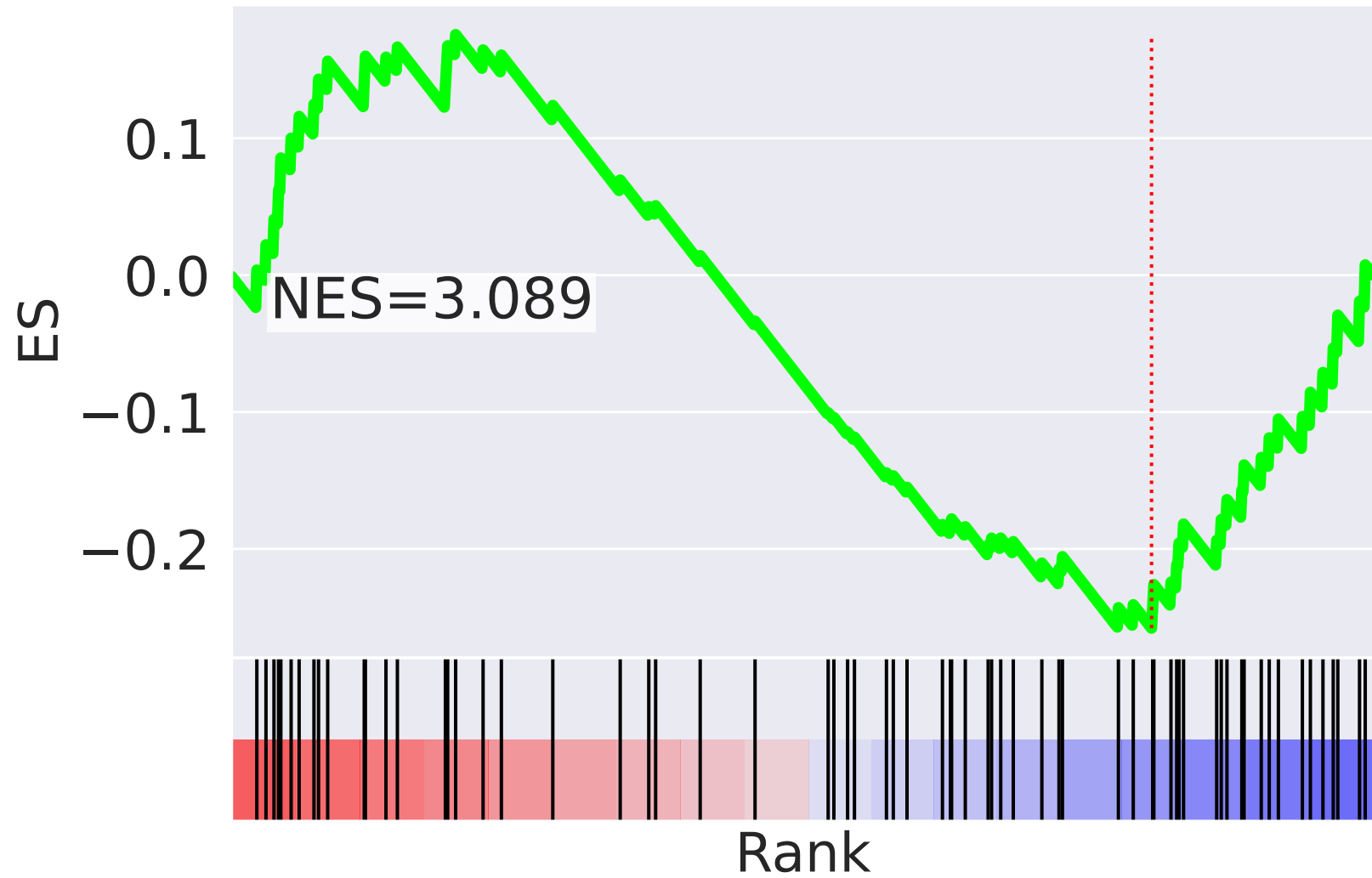
NES		SET
-2.665		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.302		T cell costimulation (GO:0031295)
2.296		phosphatidylinositol-mediated signaling (GO:0048015)
2.289		insulin receptor signaling pathway (GO:0008286)
2.241		tRNA aminoacylation for protein translation (GO:0006418)
-2.221		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.171		protein homooligomerization (GO:0051260)
-2.115		transcription from RNA polymerase II promoter (GO:0006366)
2.090		positive regulation of pri-miRNA transcription from RNA polymerase II promoter (GO:1902895)
2.047		regulation of defense response to virus by virus (GO:0050690)
2.001		cell separation after cytokinesis (GO:0000920)
-1.959		protein K48-linked ubiquitination (GO:0070936)
-1.953		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-1.941		transcription, DNA-templated (GO:0006351)
1.912		regulation of lipid metabolic process (GO:0019216)


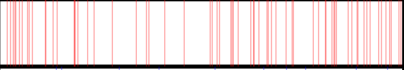
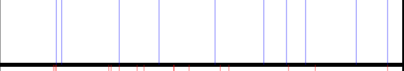
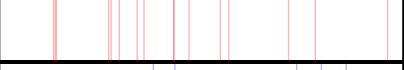
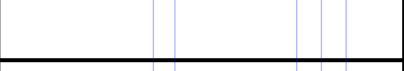

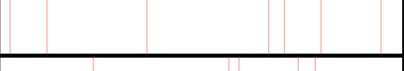


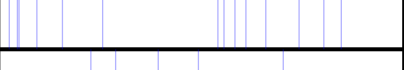

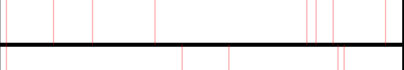


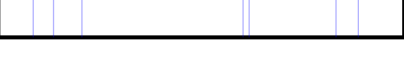
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=55$

mitochondrial translational elongation (GO:0070125)



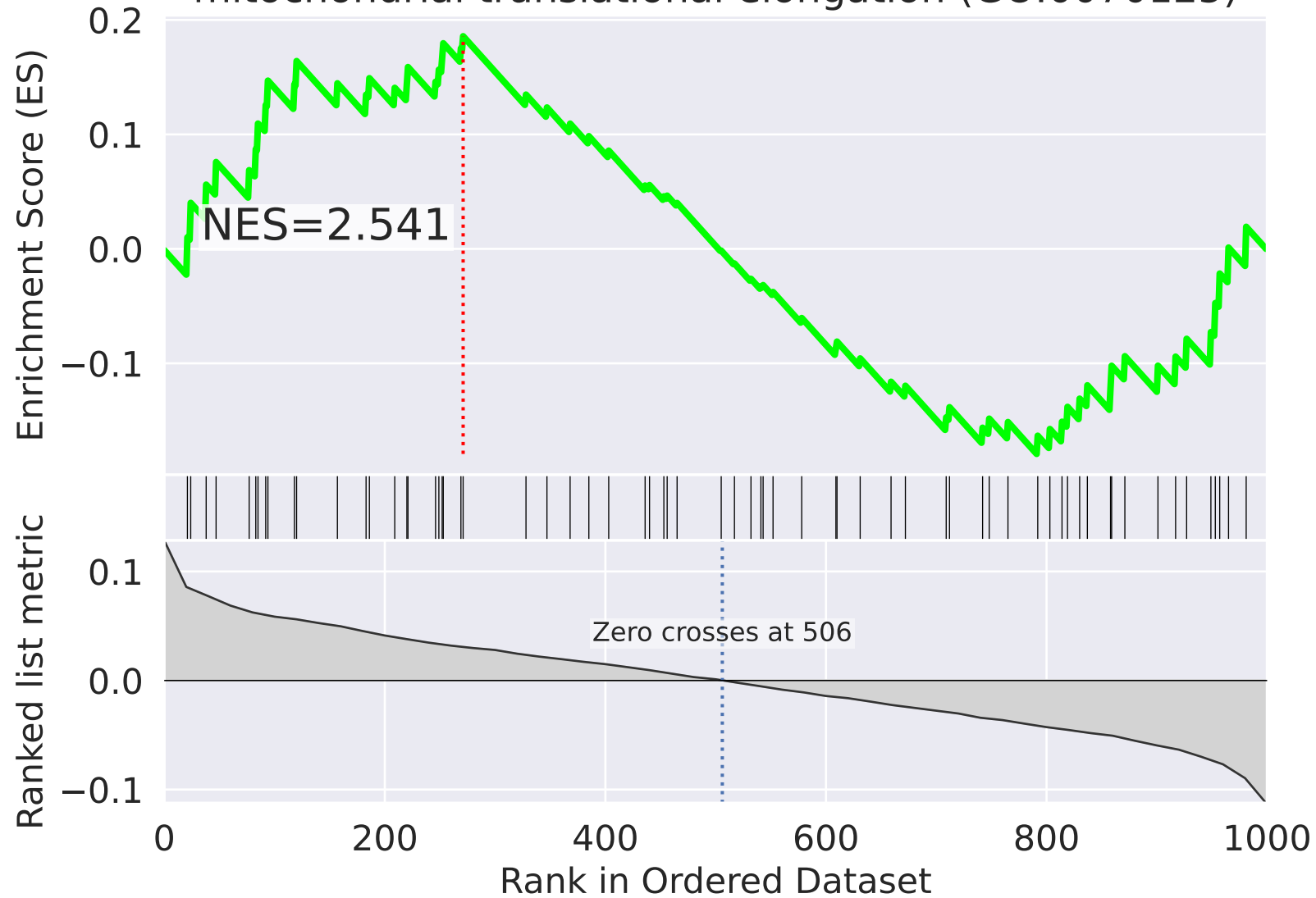
mitochondrial translational elongation (GO:0070125)



NES		SET
3.089		mitochondrial translational elongation (GO:0070125)
2.943		mitochondrial translational termination (GO:0070126)
-2.624		double-strand break repair via homologous recombination (GO:0000724)
2.357		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.342		retrograde protein transport, ER to cytosol (GO:0030970)
-2.342		ubiquitin-dependent ERAD pathway (GO:0030433)
2.262		innate immune response (GO:0045087)
2.236		cellular response to hypoxia (GO:0071456)
-2.220		chromatin remodeling (GO:0006338)
-2.208		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-2.188		DNA-dependent DNA replication (GO:0006261)
2.130		regulation of cell cycle (GO:0051726)
2.097		positive regulation of mitotic cell cycle (GO:0045931)
2.058		proteolysis (GO:0006508)
-2.039		positive regulation of gene expression, epigenetic (GO:0045815)

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)



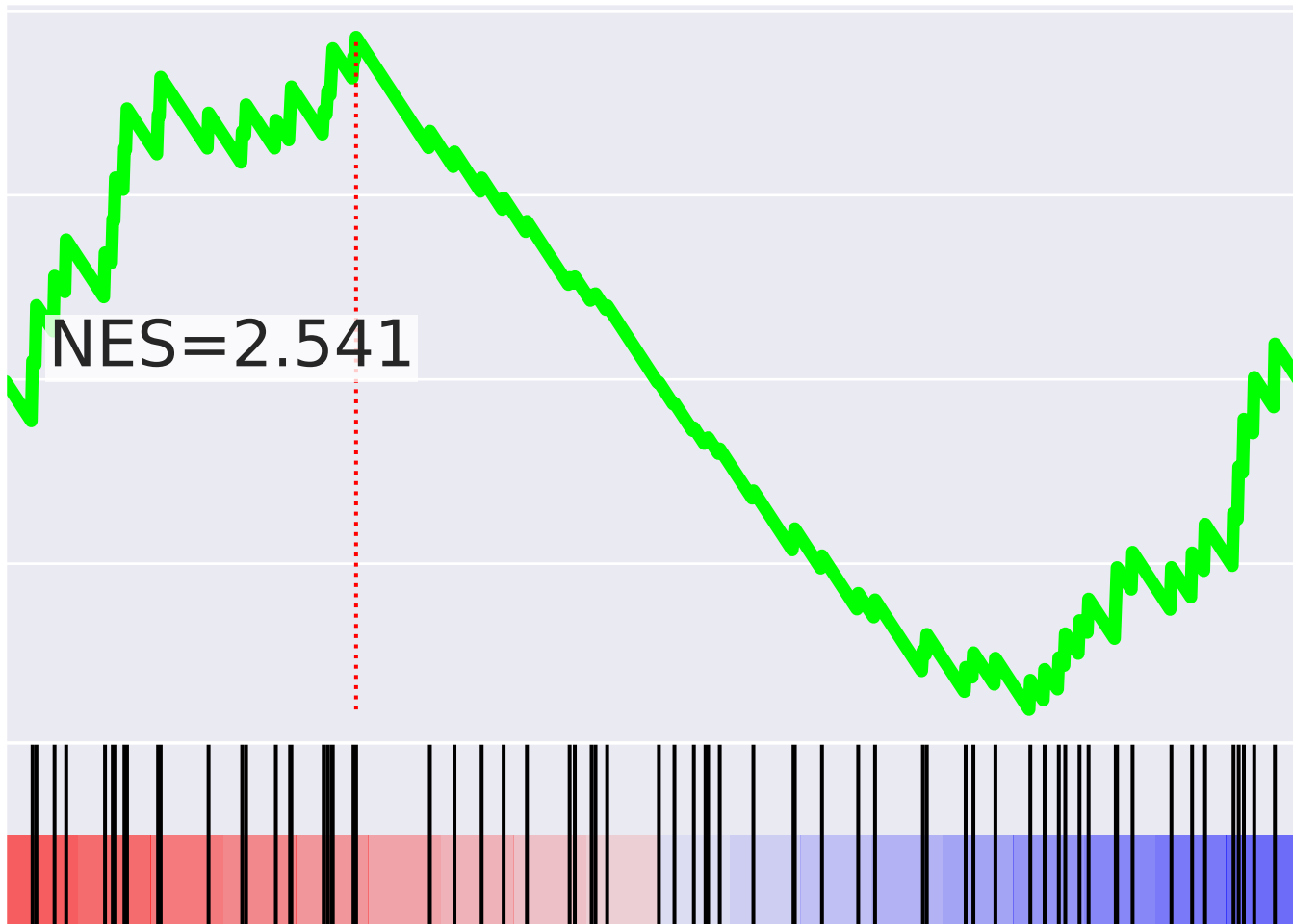
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1

NES=2.541

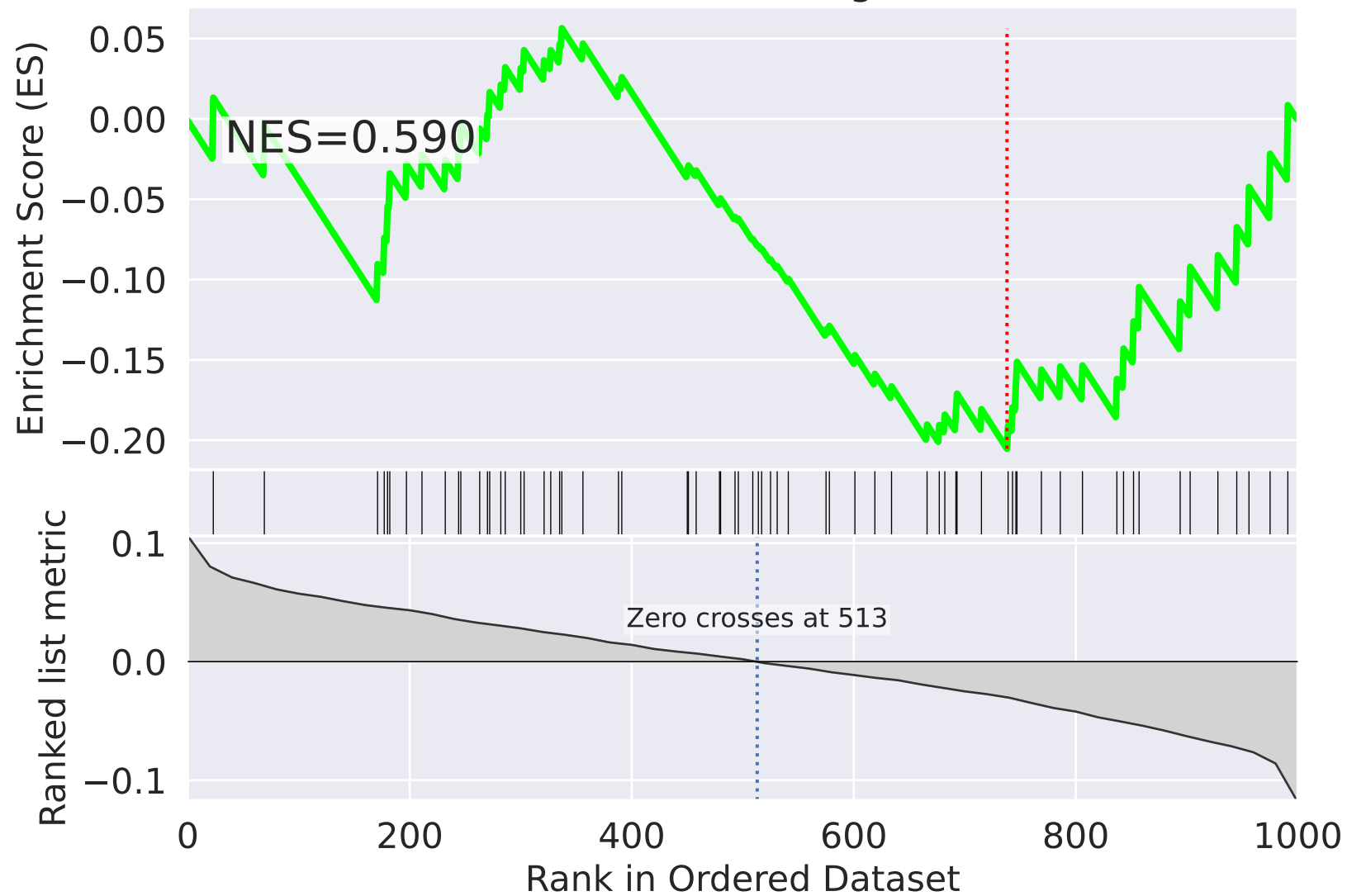
Rank



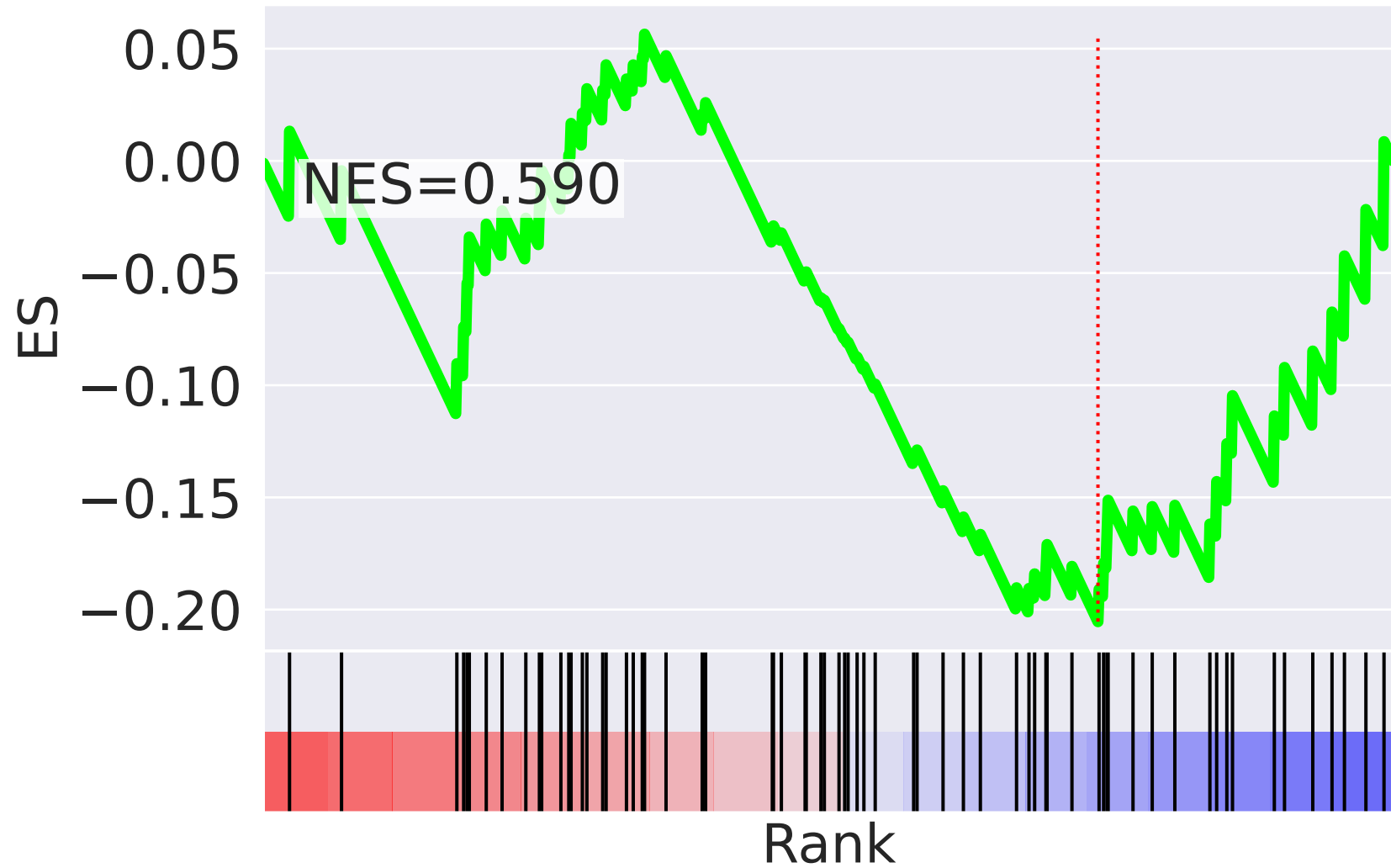
NES		SET
-3.076		snRNA transcription from RNA polymerase II promoter (GO:0042795)
3.008		mitochondrial translation (GO:0032543)
2.541		mitochondrial translational elongation (GO:0070125)
2.519		regulation of macroautophagy (GO:0016241)
2.461		mitochondrial translational termination (GO:0070126)
-2.449		protein targeting to mitochondrion (GO:0006626)
-2.405		RNA splicing (GO:0008380)
2.194		CENP-A containing nucleosome assembly (GO:0034080)
-2.148		mRNA splicing, via spliceosome (GO:0000398)
-2.043		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.039		spermatogenesis (GO:0007283)
-2.008		positive regulation of protein phosphorylation (GO:0001934)
1.994		proteolysis (GO:0006508)
-1.944		regulation of cell adhesion (GO:0030155)
-1.935		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 $z=57$

mitochondrial translational elongation (GO:0070125)



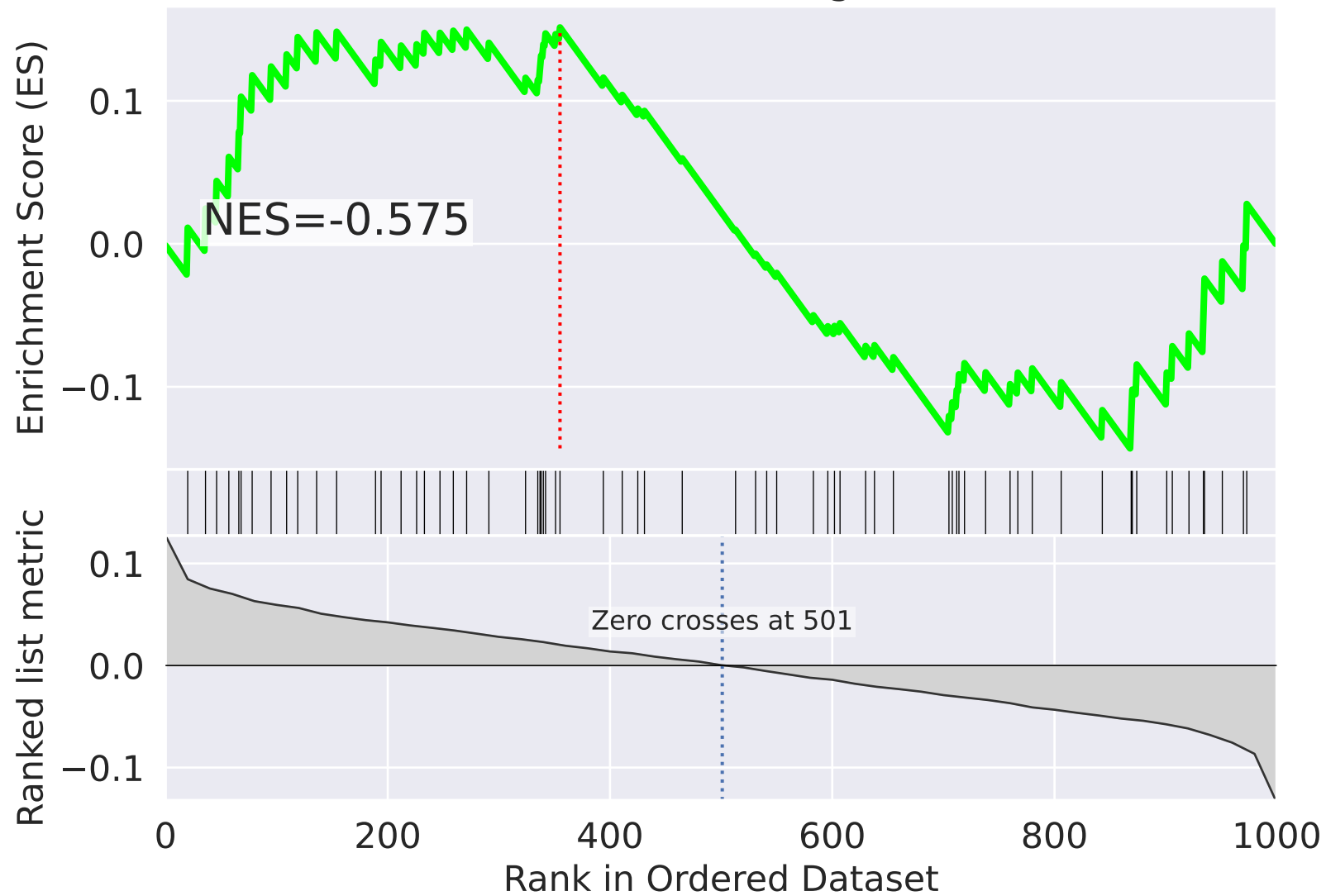
mitochondrial translational elongation (GO:0070125)



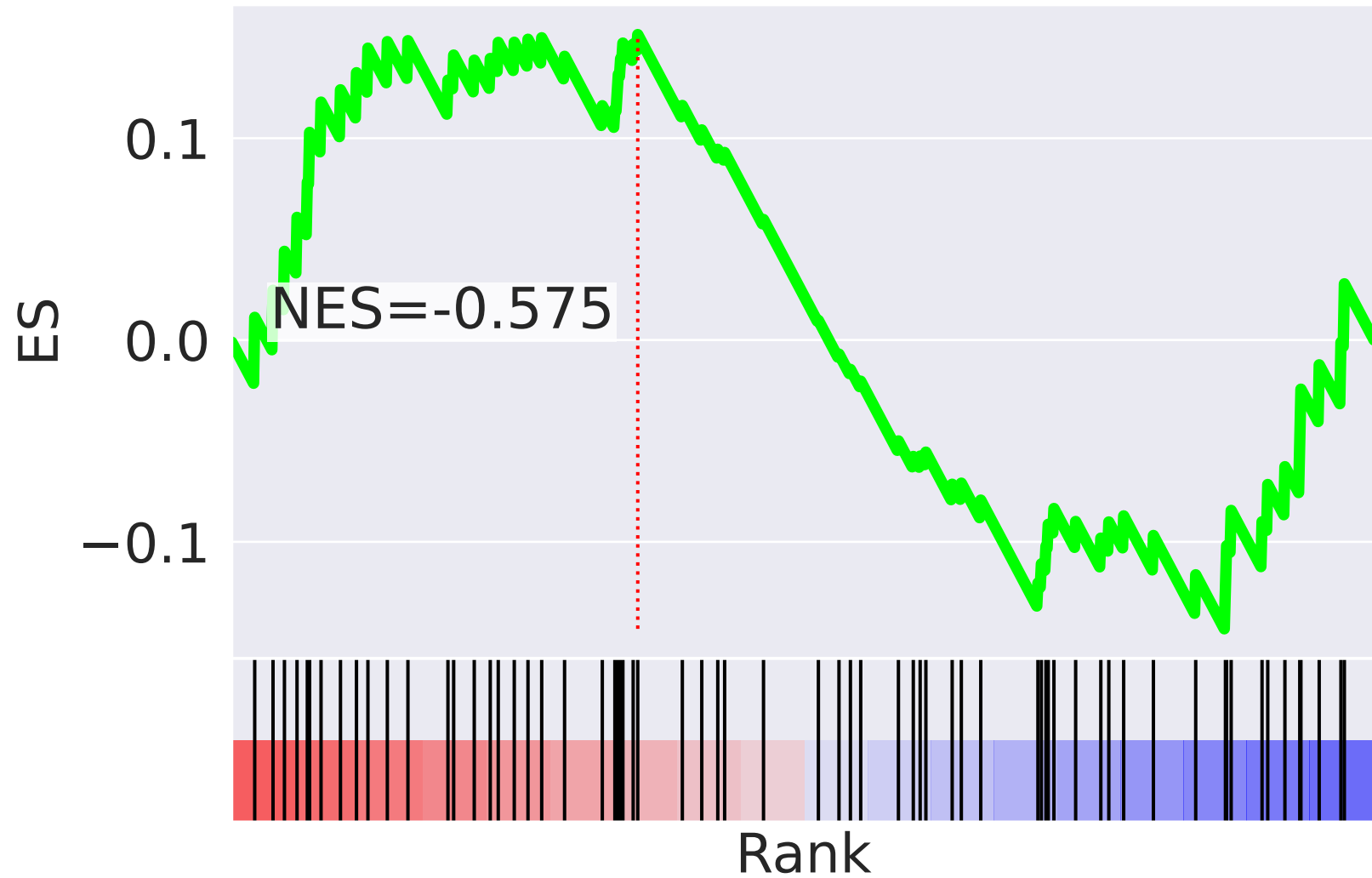
NES		SET
2.873		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.350		protein sumoylation (GO:0016925)
-2.254		mitochondrion organization (GO:0007005)
2.226		Golgi organization (GO:0007030)
-2.221		positive regulation of TOR signaling (GO:0032008)
-2.186		mitotic nuclear envelope disassembly (GO:0007077)
2.045		Fc-epsilon receptor signaling pathway (GO:0038095)
2.044		cellular response to tumor necrosis factor (GO:0071356)
-2.036		viral transcription (GO:0019083)
-2.017		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-2.007		viral process (GO:0016032)
-1.984		intracellular transport of virus (GO:0075733)
-1.982		cell differentiation (GO:0030154)
-1.981		tRNA export from nucleus (GO:0006409)
-1.981		regulation of glucose transport (GO:0010827)





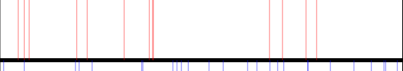
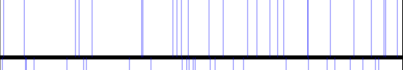
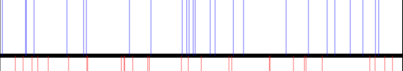
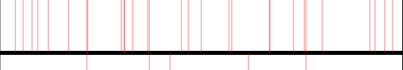

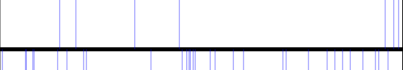
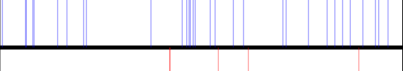


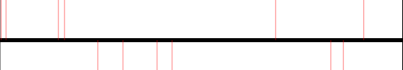

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=58$

mitochondrial translational elongation (GO:0070125)



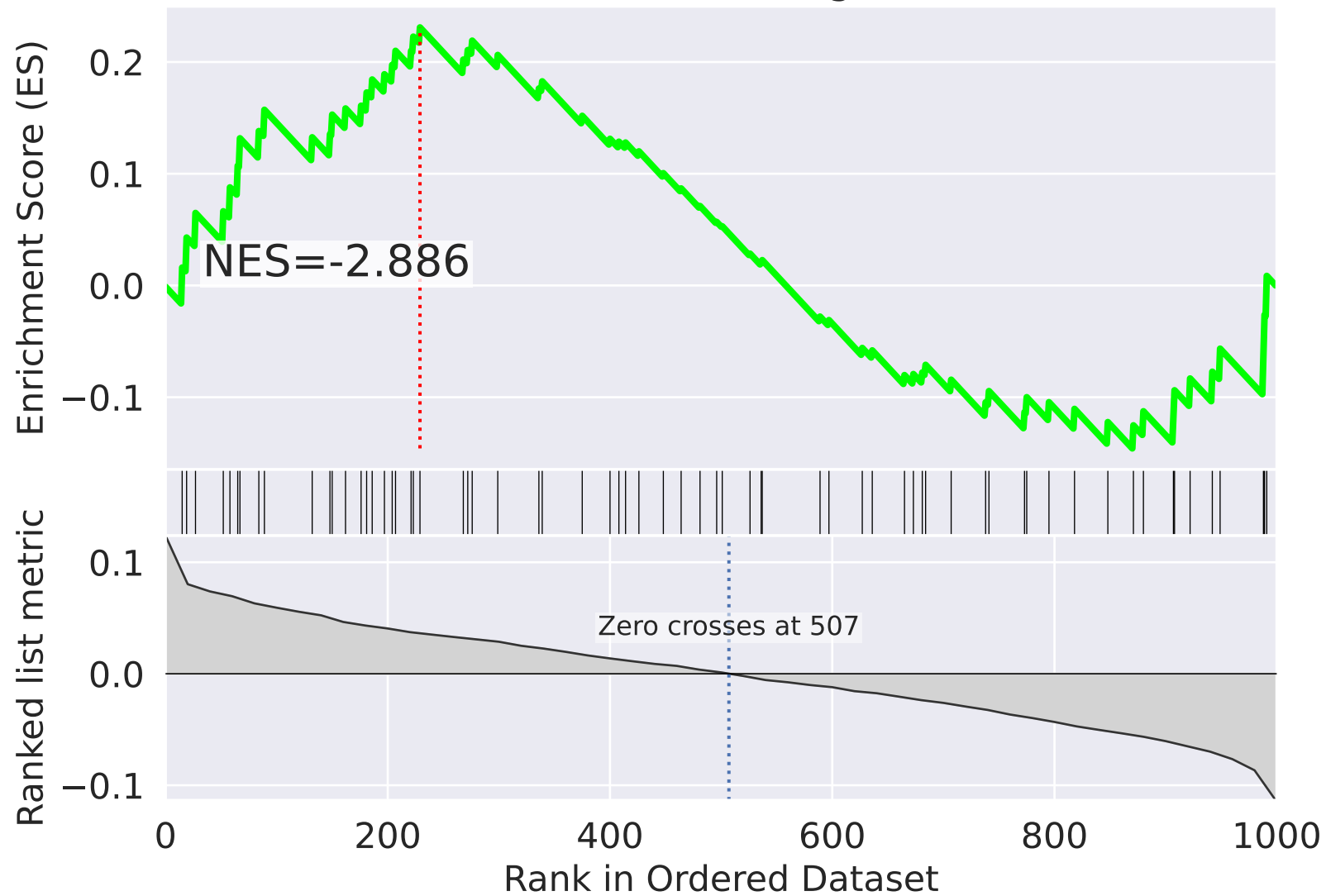
mitochondrial translational elongation (GO:0070125)



NES		SET
2.685		ATP-dependent chromatin remodeling (GO:0043044)
2.341		DNA duplex unwinding (GO:0032508)
2.334		regulation of DNA replication (GO:0006275)
2.307		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.291		positive regulation of cell migration (GO:0030335)
-2.207		protein ubiquitination (GO:0016567)
-2.162		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.101		negative regulation of apoptotic process (GO:0043066)
2.041		positive regulation of DNA replication (GO:0045740)
-2.023		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-1.981		mitochondrial respiratory chain complex I assembly (GO:0032981)
1.927		telomere maintenance (GO:0000723)
-1.916		tRNA aminoacylation for protein translation (GO:0006418)
1.909		RNA metabolic process (GO:0016070)
1.901		positive regulation by host of viral transcription (GO:0043923)

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

0.2

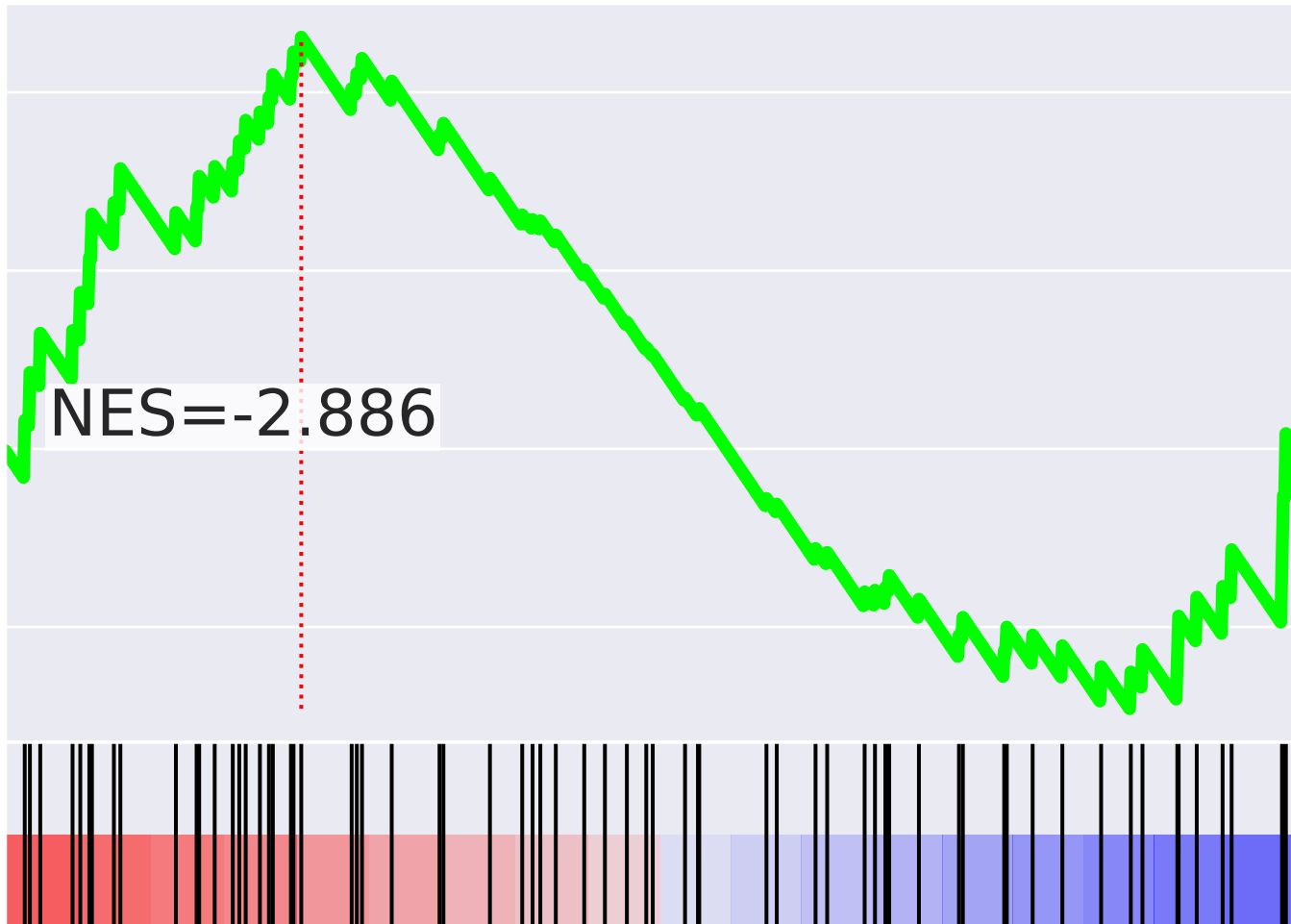
0.1

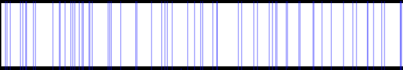
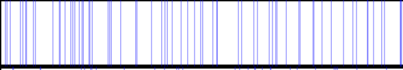
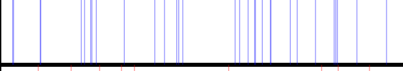
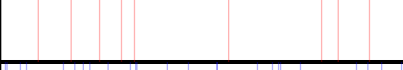
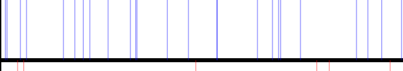
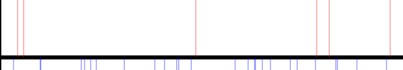


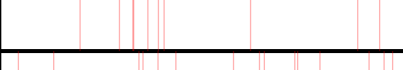
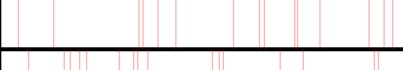
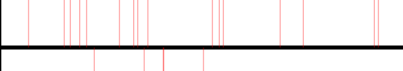
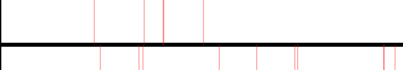
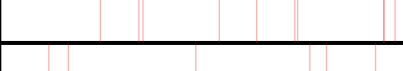
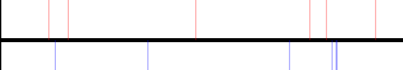
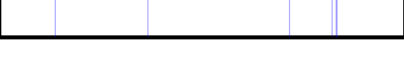
0.0

-0.1

NES=-2.886

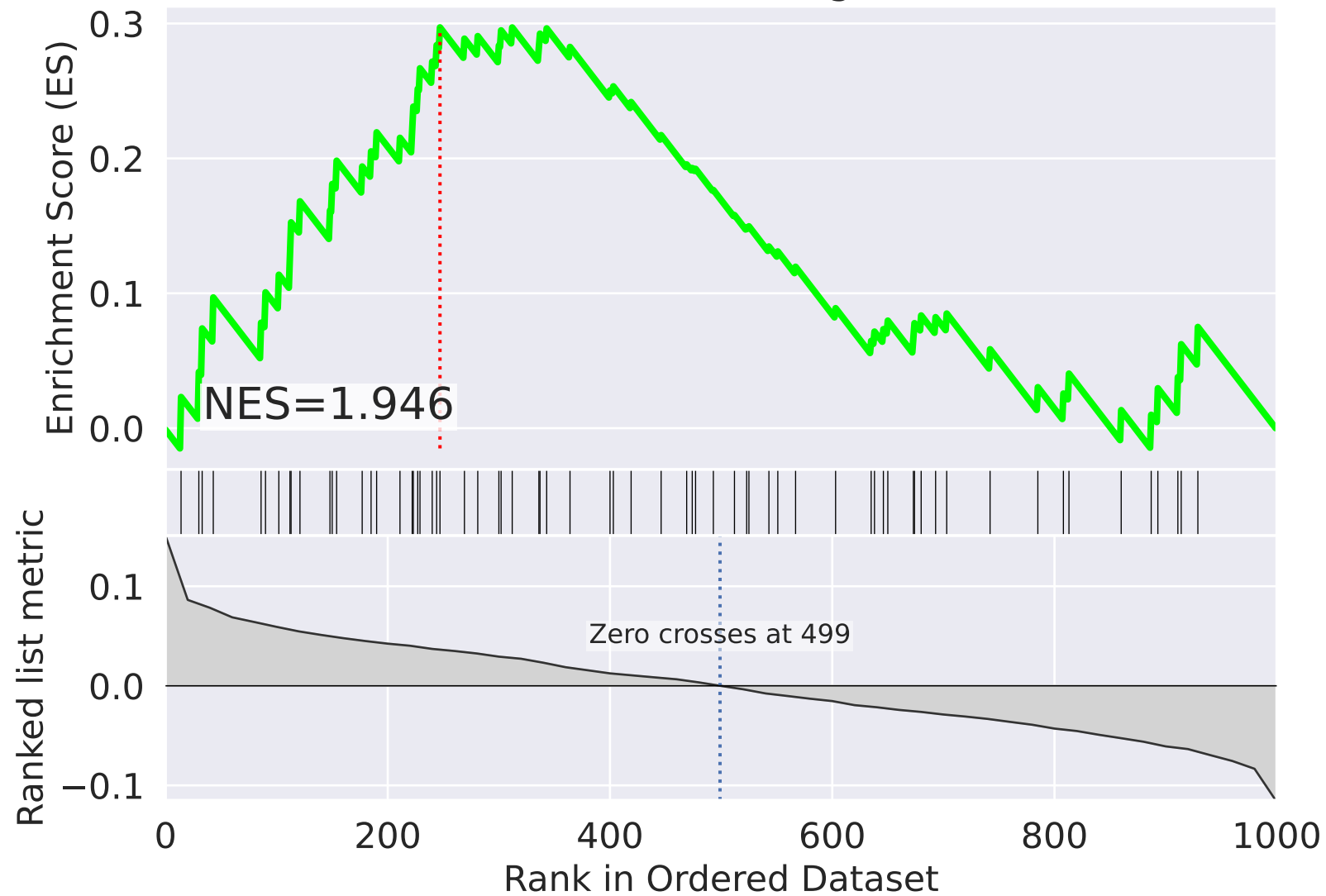
Rank



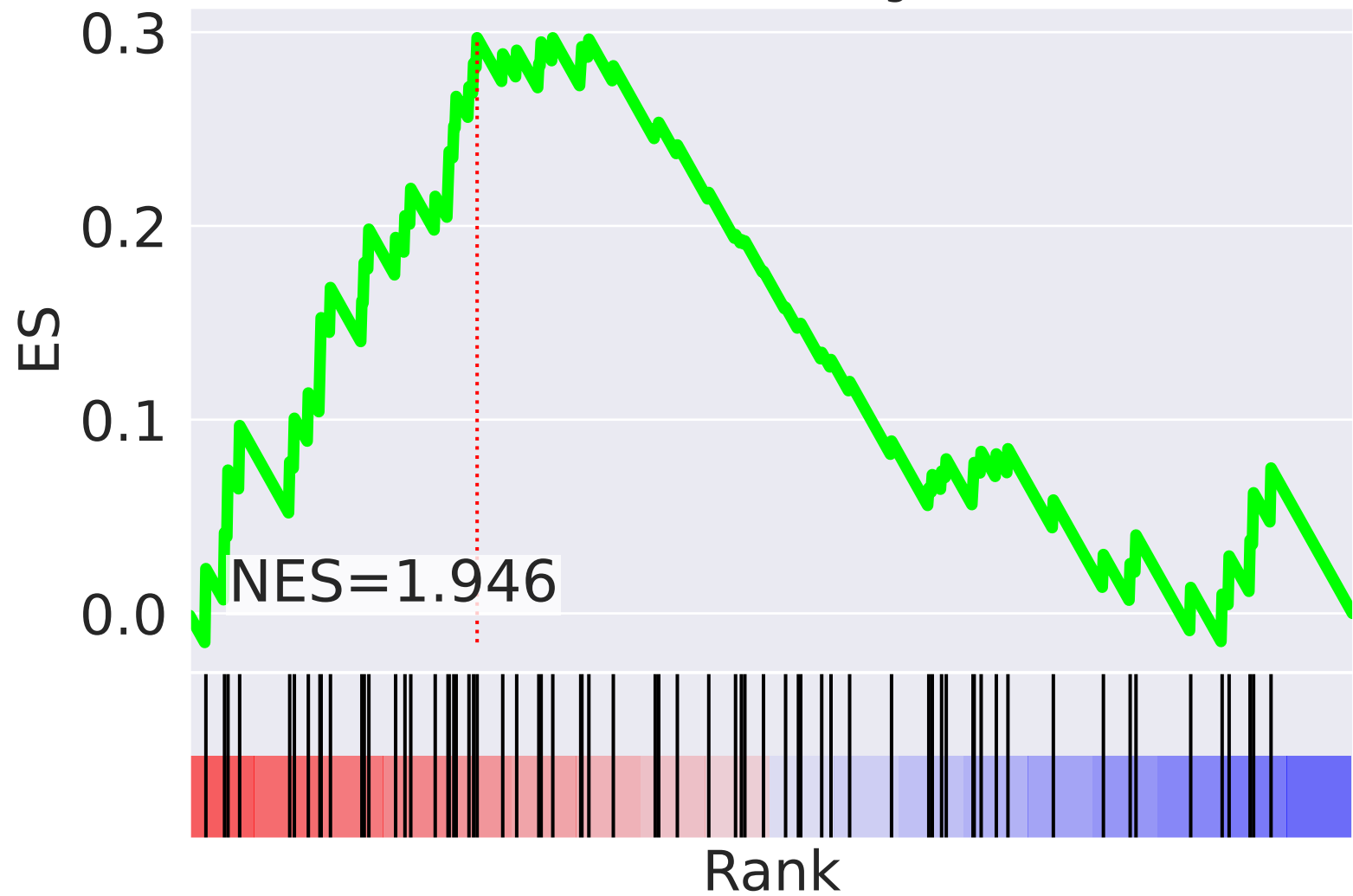
NES		SET
-2.991		mitochondrial translational termination (GO:0070126)
-2.886		mitochondrial translational elongation (GO:0070125)
-2.599		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.559		response to endoplasmic reticulum stress (GO:0034976)
-2.471		mitochondrial translation (GO:0032543)
2.445		cell-matrix adhesion (GO:0007160)
-2.428		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.308		tRNA aminoacylation for protein translation (GO:0006418)
2.278		double-strand break repair via homologous recombination (GO:0000724)
2.195		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
2.065		regulation of signal transduction by p53 class mediator (GO:1901796)
2.061		DNA-dependent DNA replication (GO:0006261)
2.016		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.010		platelet aggregation (GO:0070527)
-2.004		DNA duplex unwinding (GO:0032508)









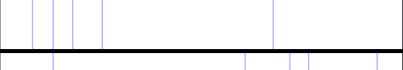
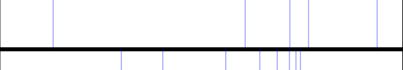

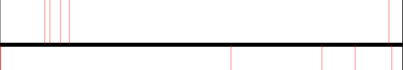


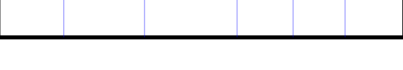
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=60$

mitochondrial translational elongation (GO:0070125)



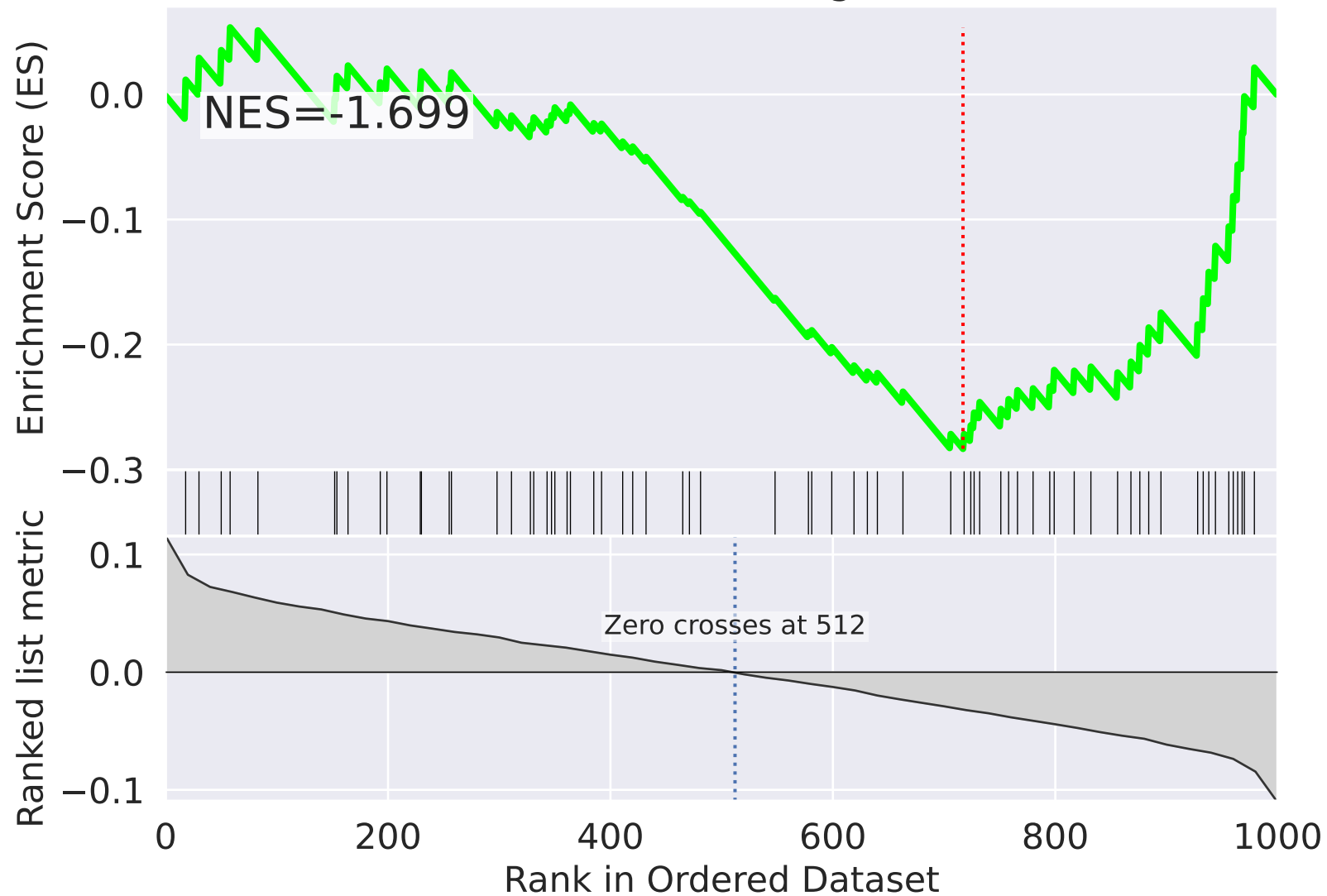
mitochondrial translational elongation (GO:0070125)



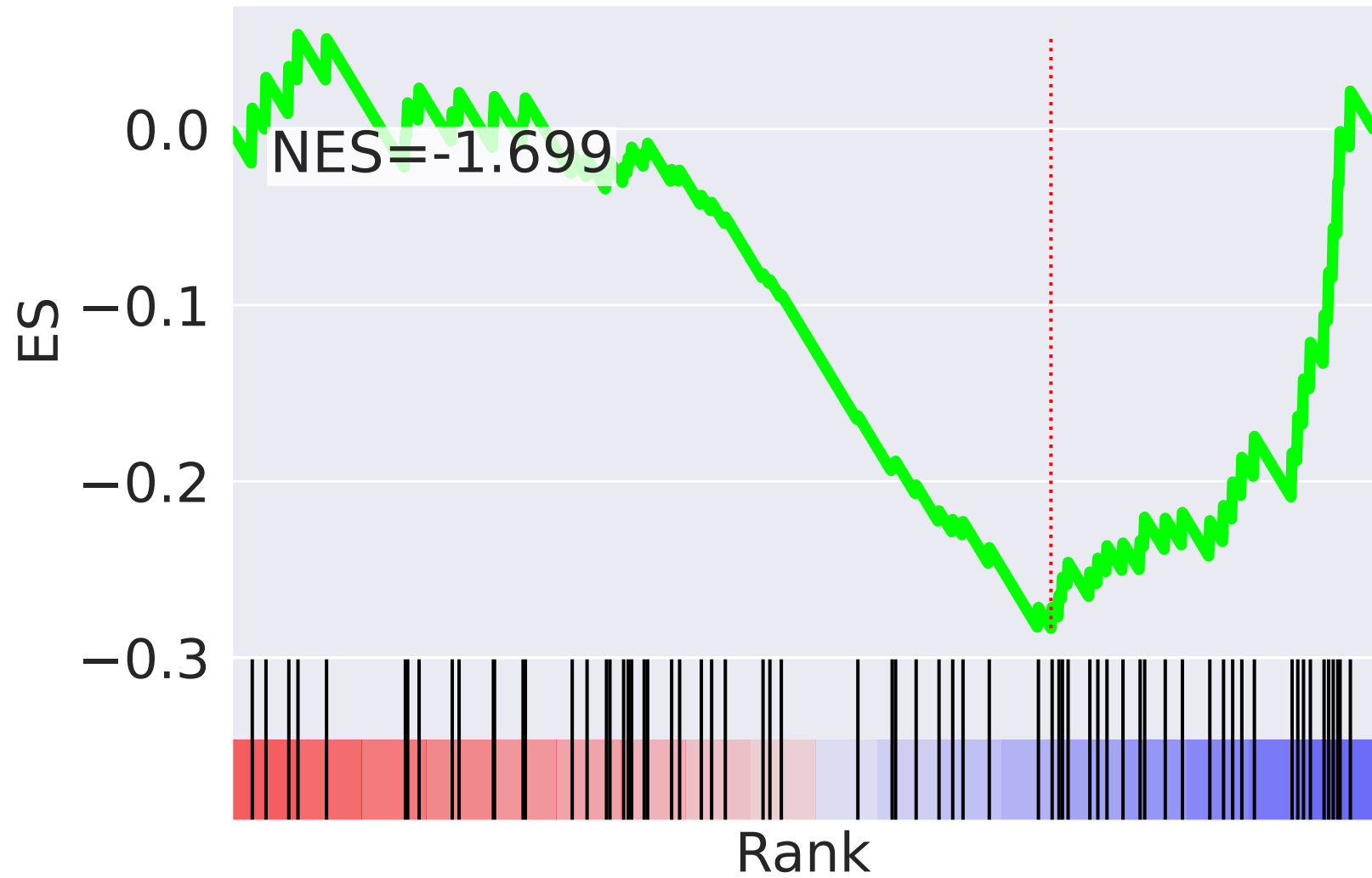
NES		SET
-2.800		Ras protein signal transduction (GO:0007265)
-2.698		positive regulation of viral genome replication (GO:0045070)
-2.587		positive regulation of protein phosphorylation (GO:0001934)
-2.294		regulation of defense response to virus by virus (GO:0050690)
-2.210		cellular nitrogen compound metabolic process (GO:0034641)
-2.182		protein K48-linked ubiquitination (GO:0070936)
-2.171		movement of cell or subcellular component (GO:0006928)
-2.157		positive regulation by host of viral transcription (GO:0043923)
-2.155		negative regulation of canonical Wnt signaling pathway (GO:0090090)
-2.118		execution phase of apoptosis (GO:0097194)
-2.099		response to ionizing radiation (GO:0010212)
2.074		cellular response to hypoxia (GO:0071456)
1.993		cellular protein localization (GO:0034613)
-1.982		ephrin receptor signaling pathway (GO:0048013)
-1.974		RNA secondary structure unwinding (GO:0010501)





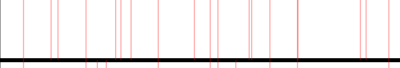

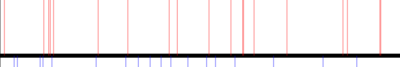

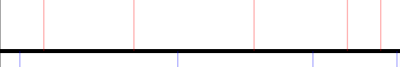
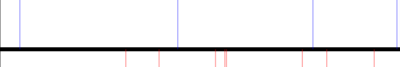
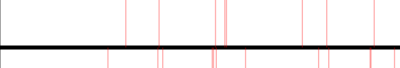

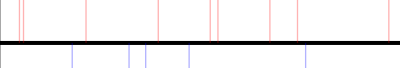


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=61$

mitochondrial translational elongation (GO:0070125)



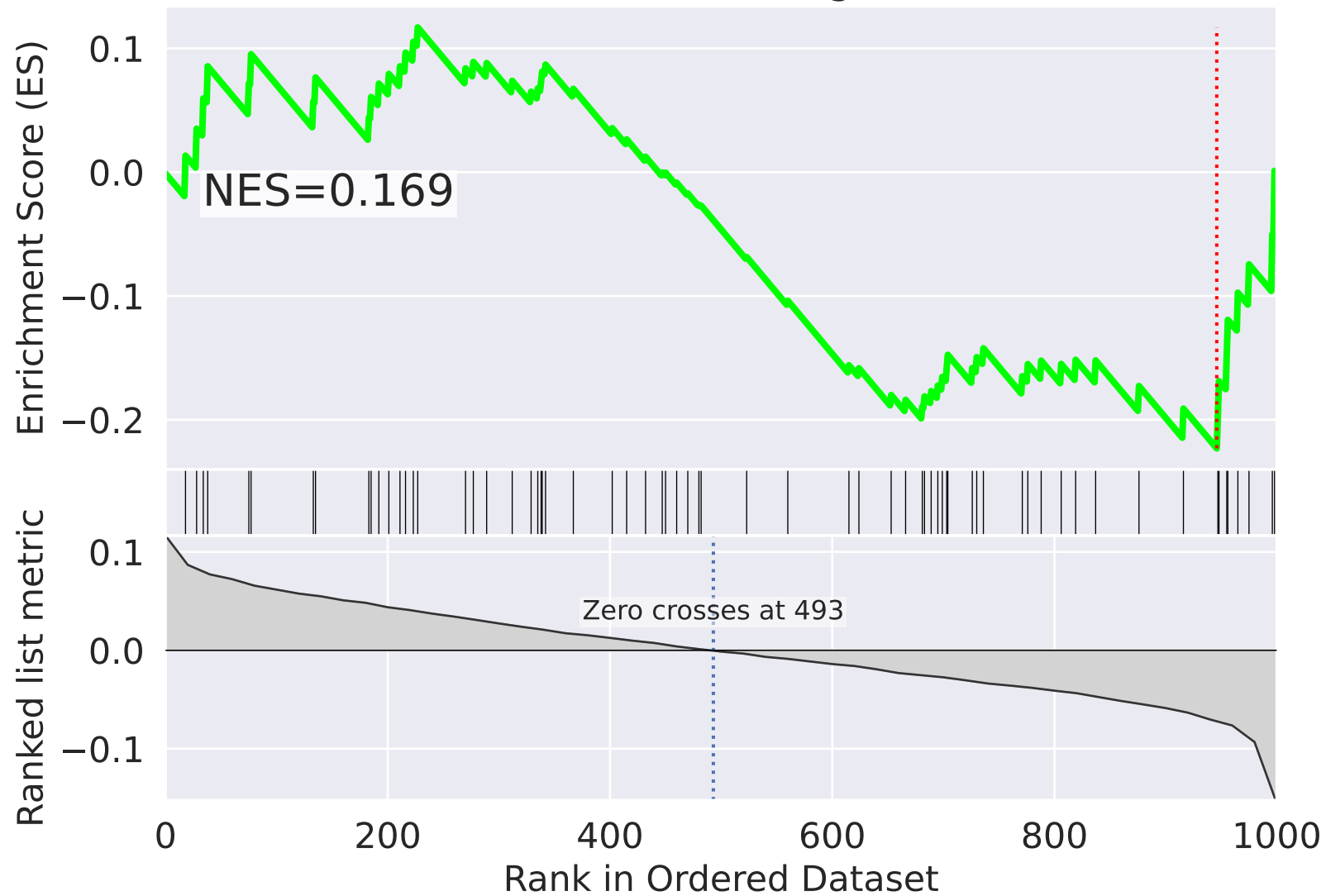
mitochondrial translational elongation (GO:0070125)



NES		SET
-3.174		sister chromatid cohesion (GO:0007062)
2.812		protein import into nucleus (GO:0006606)
2.525		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.488		insulin receptor signaling pathway (GO:0008286)
2.362		mRNA export from nucleus (GO:0006406)
2.360		mitotic nuclear envelope disassembly (GO:0007077)
2.357		DNA replication (GO:0006260)
-2.241		MAPK cascade (GO:0000165)
2.235		DNA damage checkpoint (GO:0000077)
-2.221		CENP-A containing nucleosome assembly (GO:0034080)
2.197		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.189		regulation of cholesterol biosynthetic process (GO:0045540)
2.187		intracellular transport of virus (GO:0075733)
-2.187		cellular respiration (GO:0045333)
-2.176		regulation of macroautophagy (GO:0016241)

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)

ES

NES=0.169

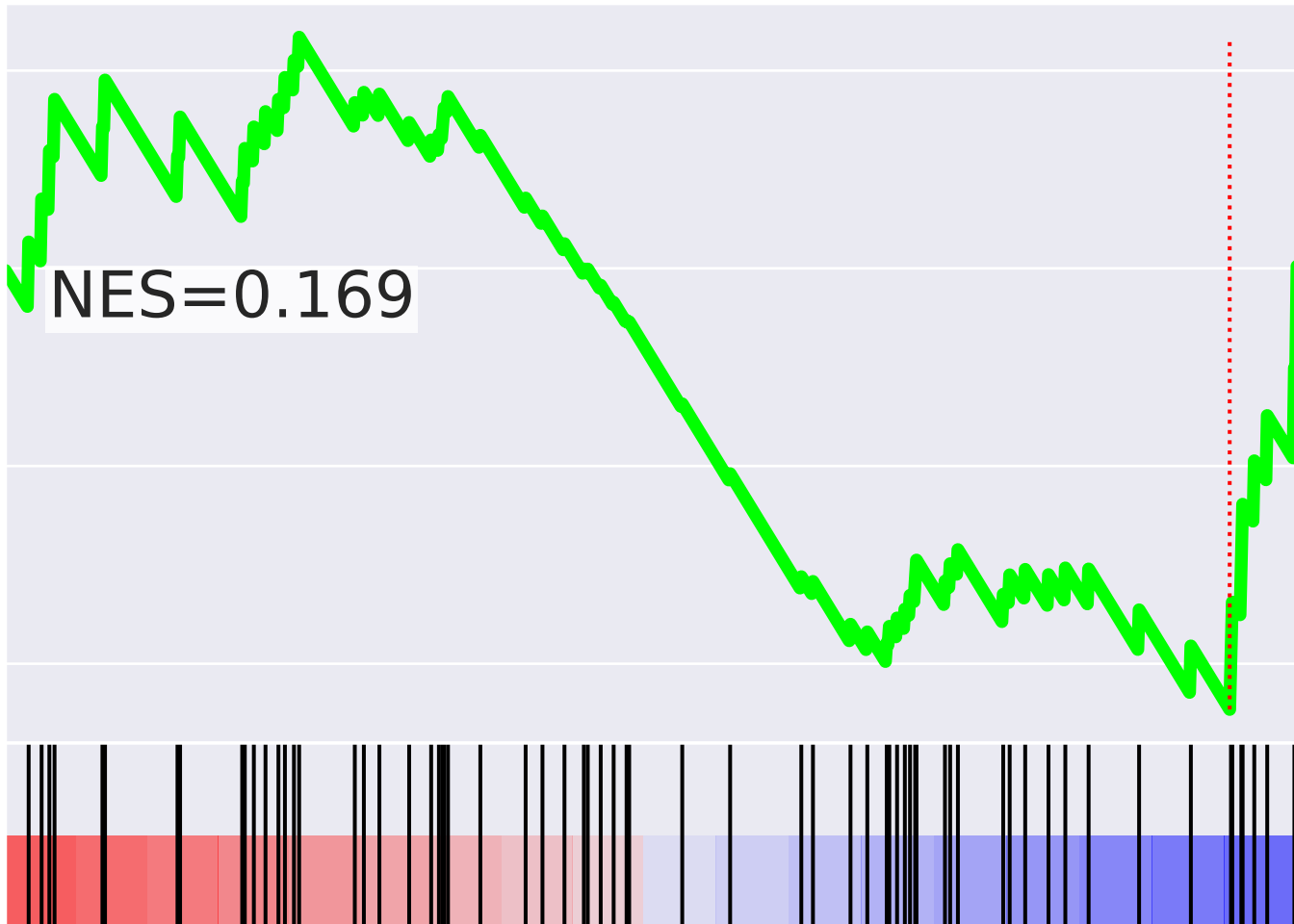
0.1

0.0

-0.1

-0.2

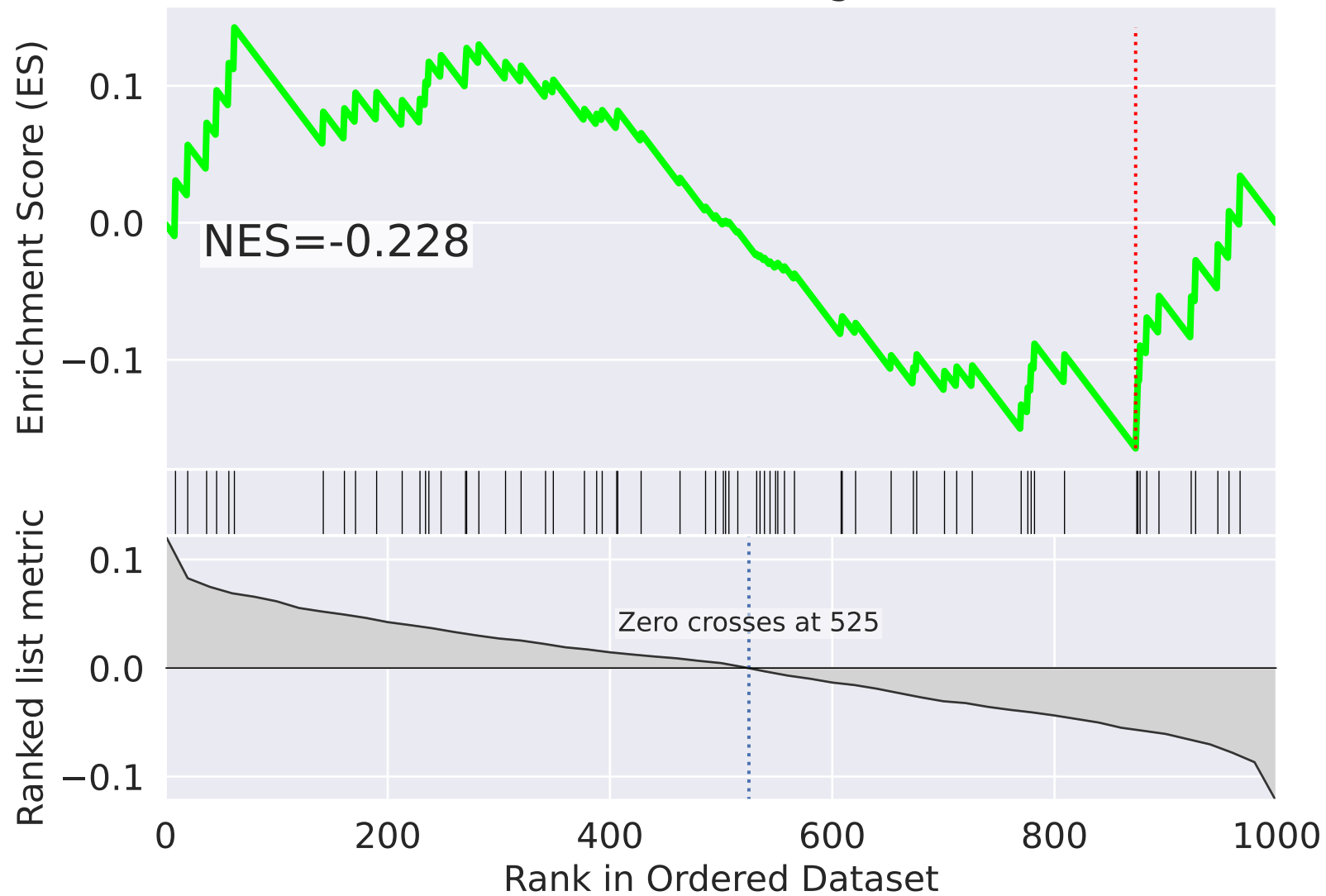
Rank



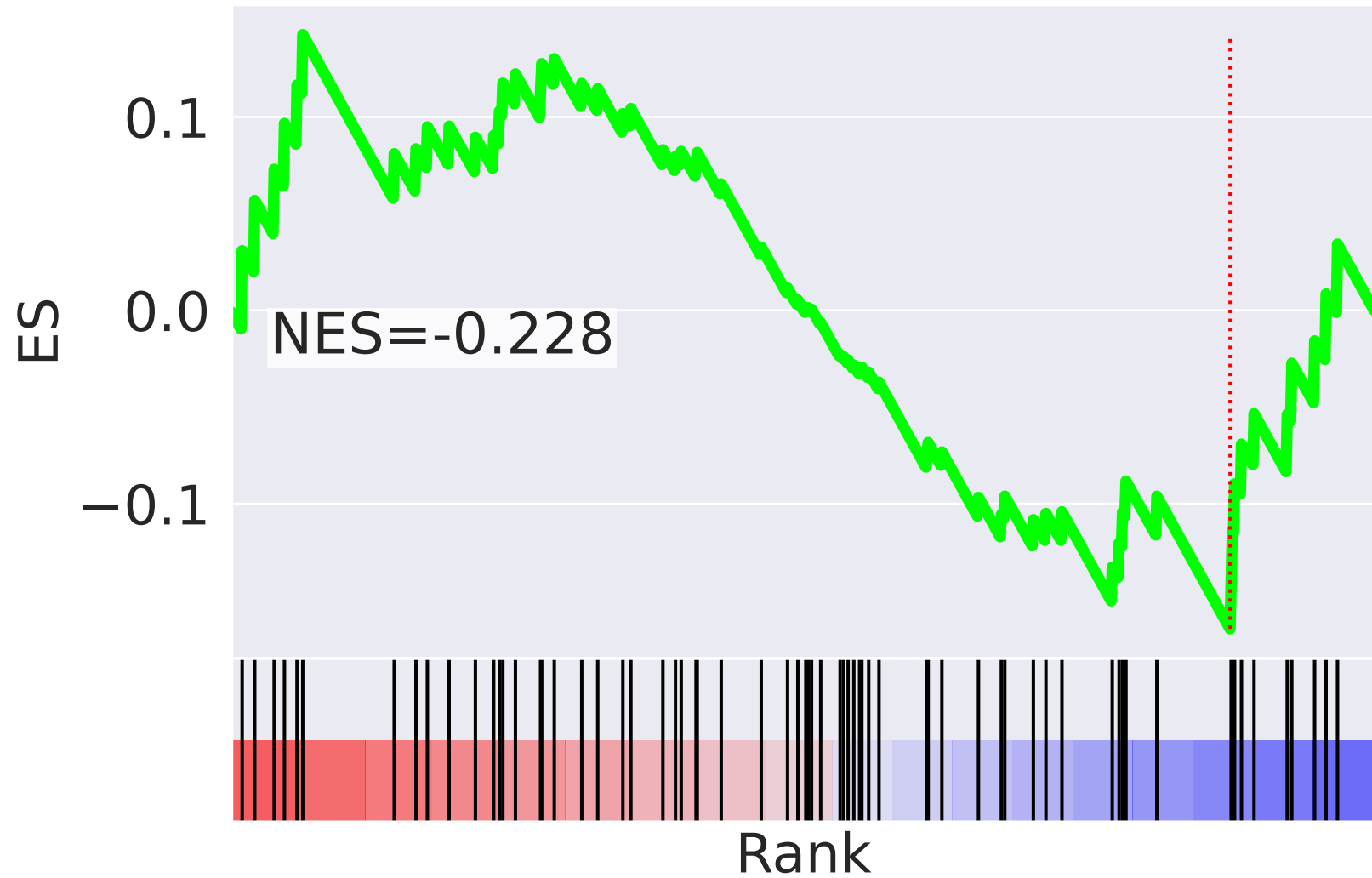
NES		SET
2.490		RNA secondary structure unwinding (GO:0010501)
2.381		regulation of defense response to virus by virus (GO:0050690)
2.241		protein phosphorylation (GO:0006468)
2.196		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.178		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
2.176		signal transduction (GO:0007165)
-2.158		positive regulation of protein targeting to mitochondrion (GO:1903955)
2.142		double-strand break repair via homologous recombination (GO:0000724)
2.132		negative regulation of apoptotic process (GO:0043066)
2.099		reciprocal meiotic recombination (GO:0007131)
-2.080		retrograde protein transport, ER to cytosol (GO:0030970)
-2.080		ubiquitin-dependent ERAD pathway (GO:0030433)
1.994		mRNA splicing, via spliceosome (GO:0000398)
1.970		positive regulation of telomere maintenance via telomerase (GO:0032212)
-1.966		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)



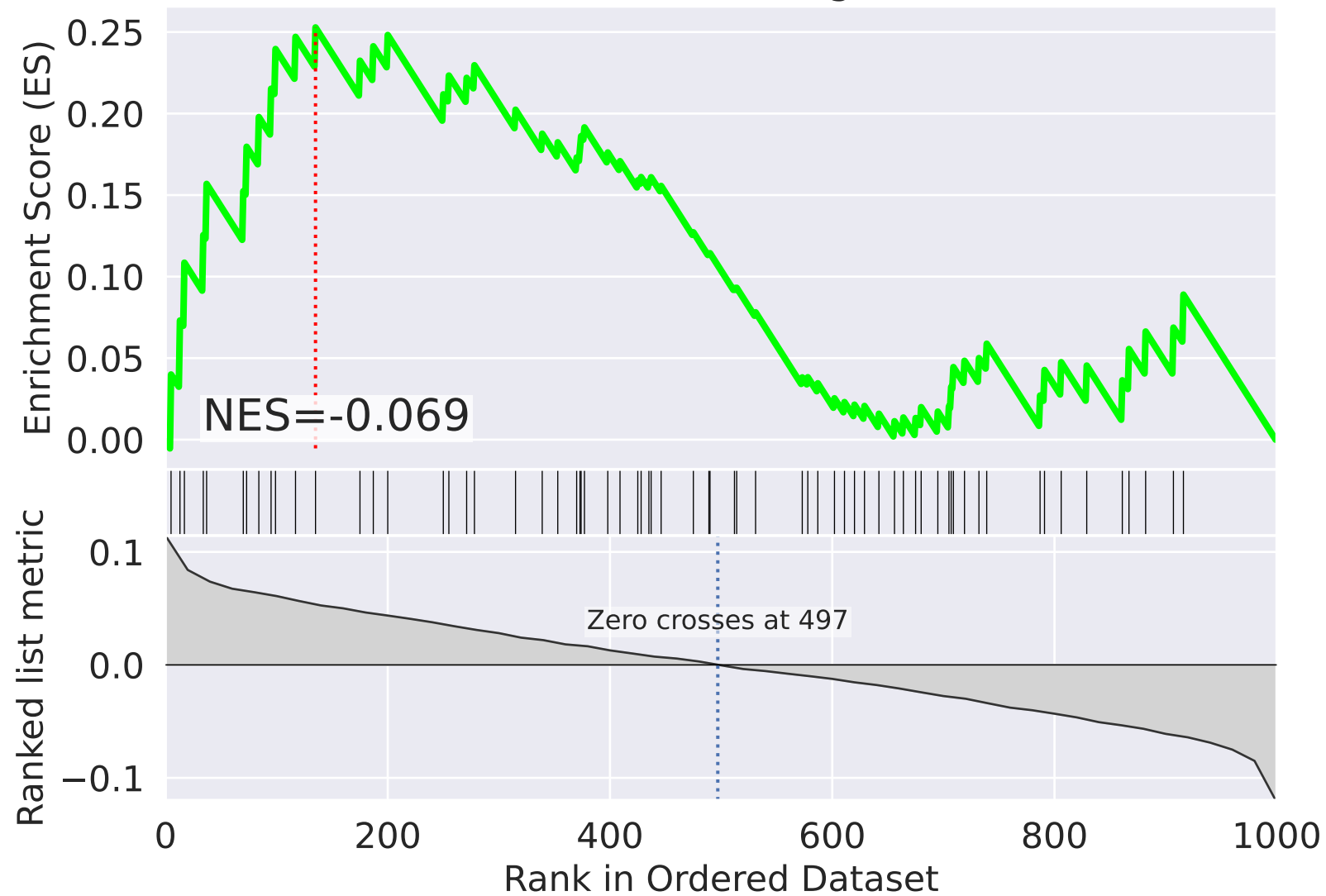
mitochondrial translational elongation (GO:0070125)



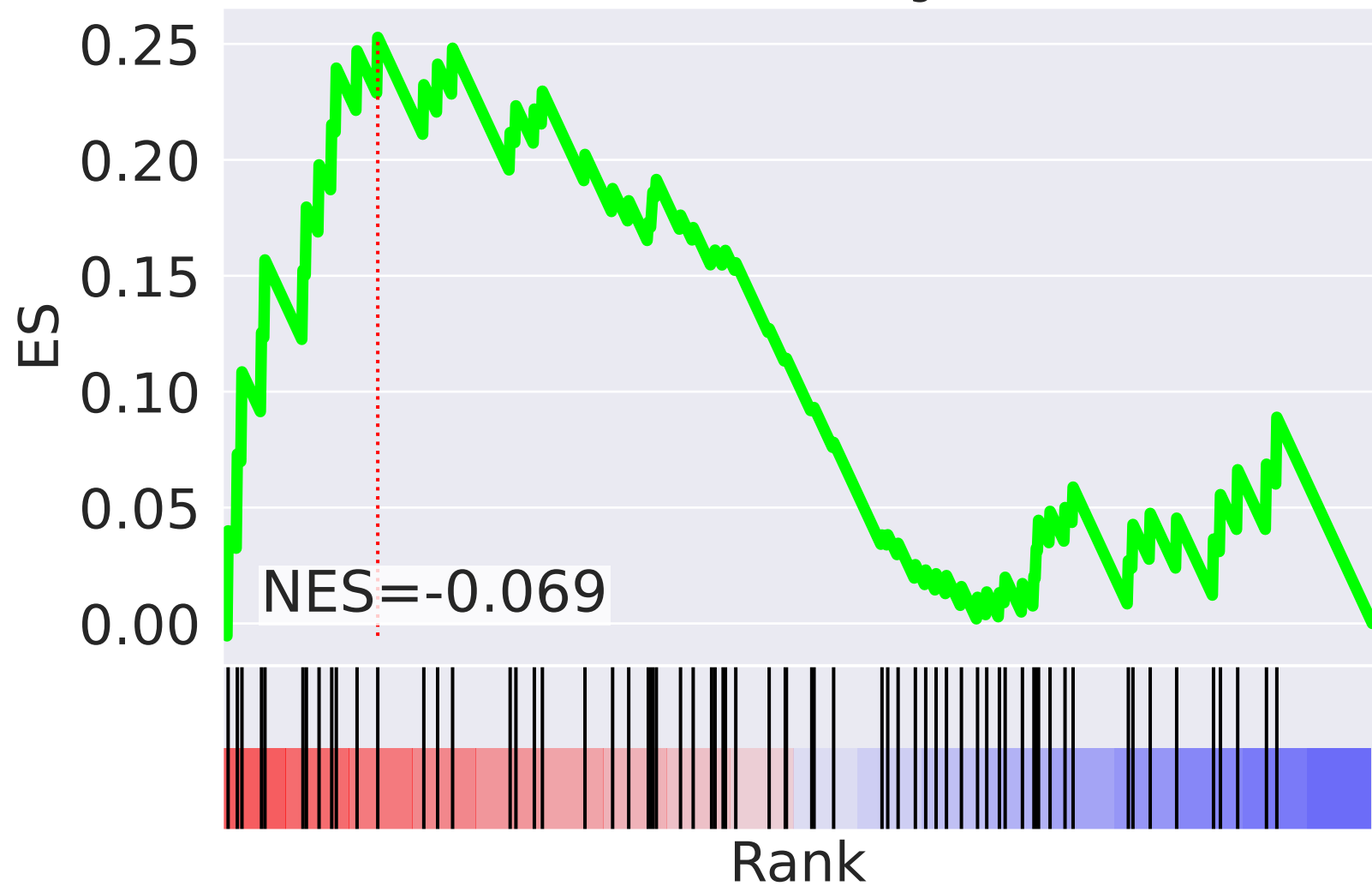
NES		SET
2.844		positive regulation of transcription, DNA-templated (GO:0045893)
2.599		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.580		regulation of cellular response to heat (GO:1900034)
2.385		cell migration (GO:0016477)
-2.367		regulation of macroautophagy (GO:0016241)
2.309		peptidyl-serine phosphorylation (GO:0018105)
-2.278		regulation of cell adhesion (GO:0030155)
2.259		T cell receptor signaling pathway (GO:0050852)
2.211		positive regulation of protein phosphorylation (GO:0001934)
-2.204		tRNA aminoacylation for protein translation (GO:0006418)
2.153		Fc-epsilon receptor signaling pathway (GO:0038095)
2.145		positive regulation of gene expression, epigenetic (GO:0045815)
2.056		cellular response to epidermal growth factor stimulus (GO:0071364)
2.034		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
2.027		anaphase-promoting complex-dependent catabolic process (GO:0031145)

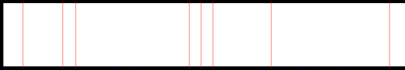



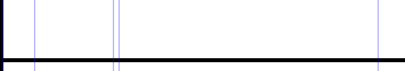

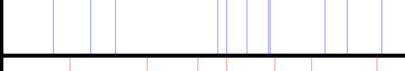
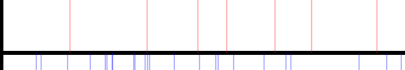


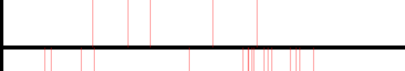


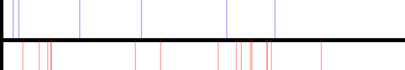

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=64$

mitochondrial translational elongation (GO:0070125)



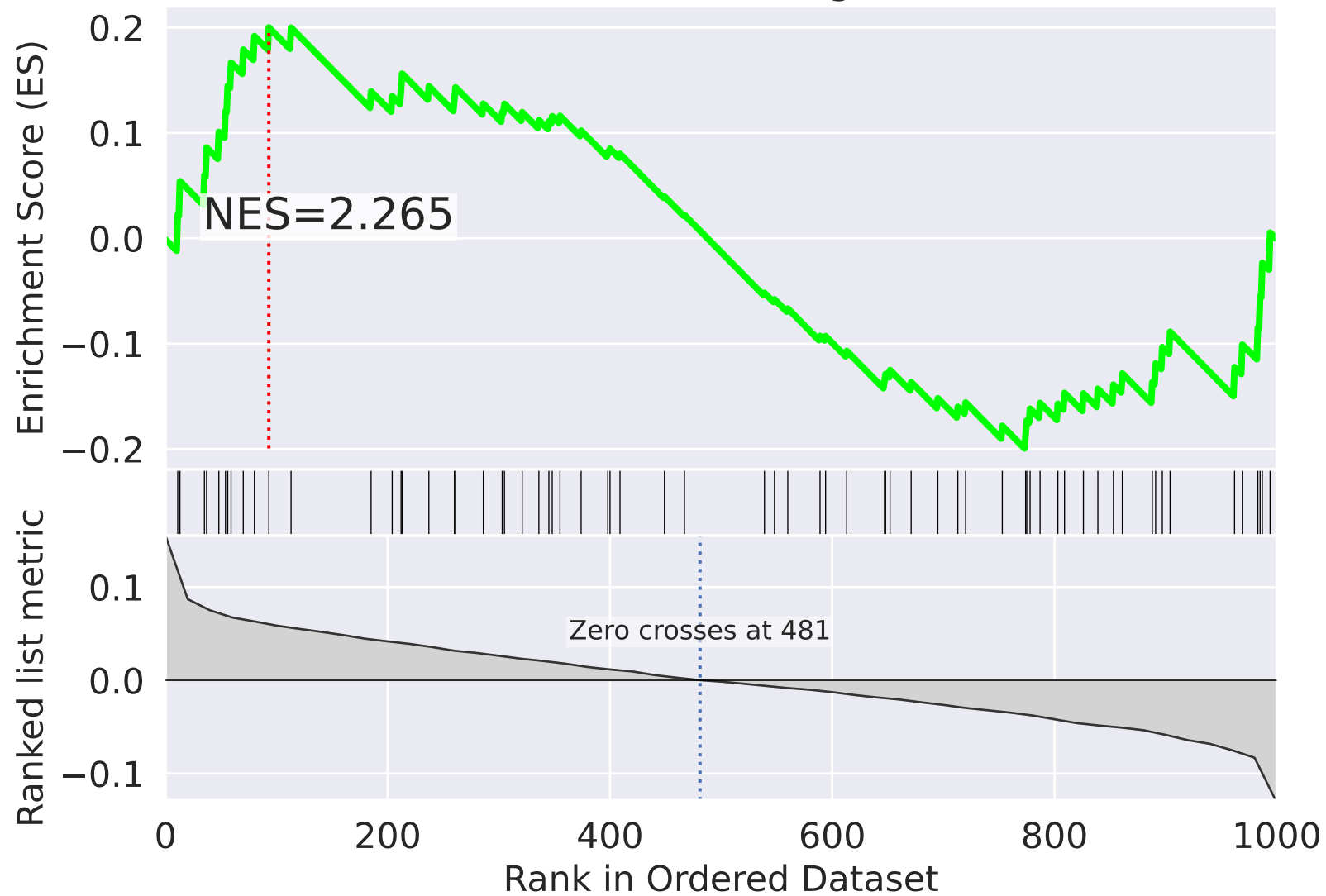
mitochondrial translational elongation (GO:0070125)



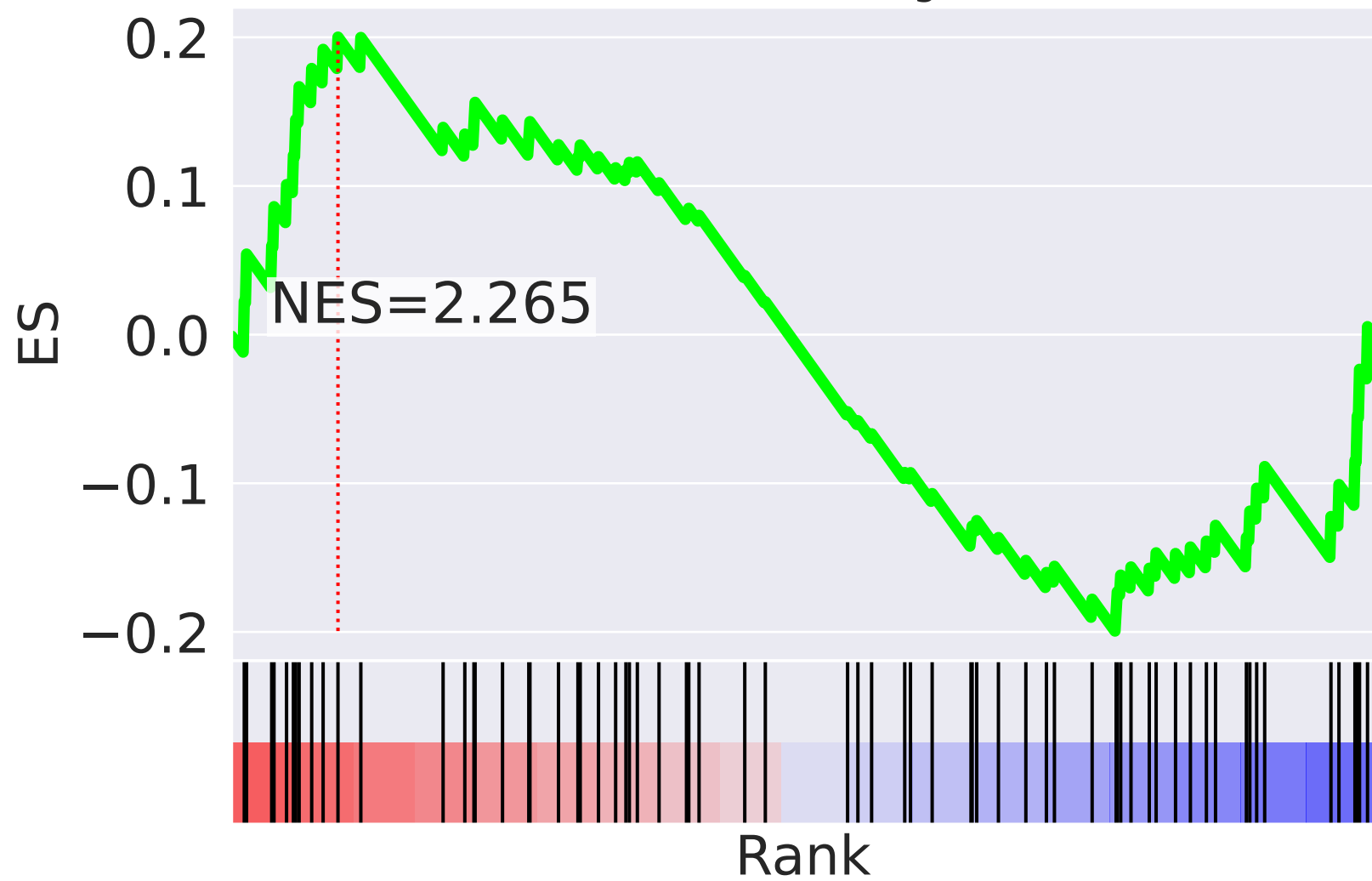
NES		SET
2.972		regulation of apoptotic process (GO:0042981)
-2.566		transcription, DNA-templated (GO:0006351)
2.550		ERK1 and ERK2 cascade (GO:0070371)
2.458		regulation of cholesterol biosynthetic process (GO:0045540)
-2.430		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.430		retrograde protein transport, ER to cytosol (GO:0030970)
-2.418		histone H3 acetylation (GO:0043966)
2.316		regulation of protein stability (GO:0031647)
-2.284		regulation of transcription, DNA-templated (GO:0006355)
-2.192		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
2.128		spermatogenesis (GO:0007283)
2.077		G2/M transition of mitotic cell cycle (GO:0000086)
-2.060		oxidation-reduction process (GO:0055114)
-2.044		positive regulation of protein targeting to mitochondrion (GO:1903955)
2.021		regulation of signal transduction by p53 class mediator (GO:1901796)

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)



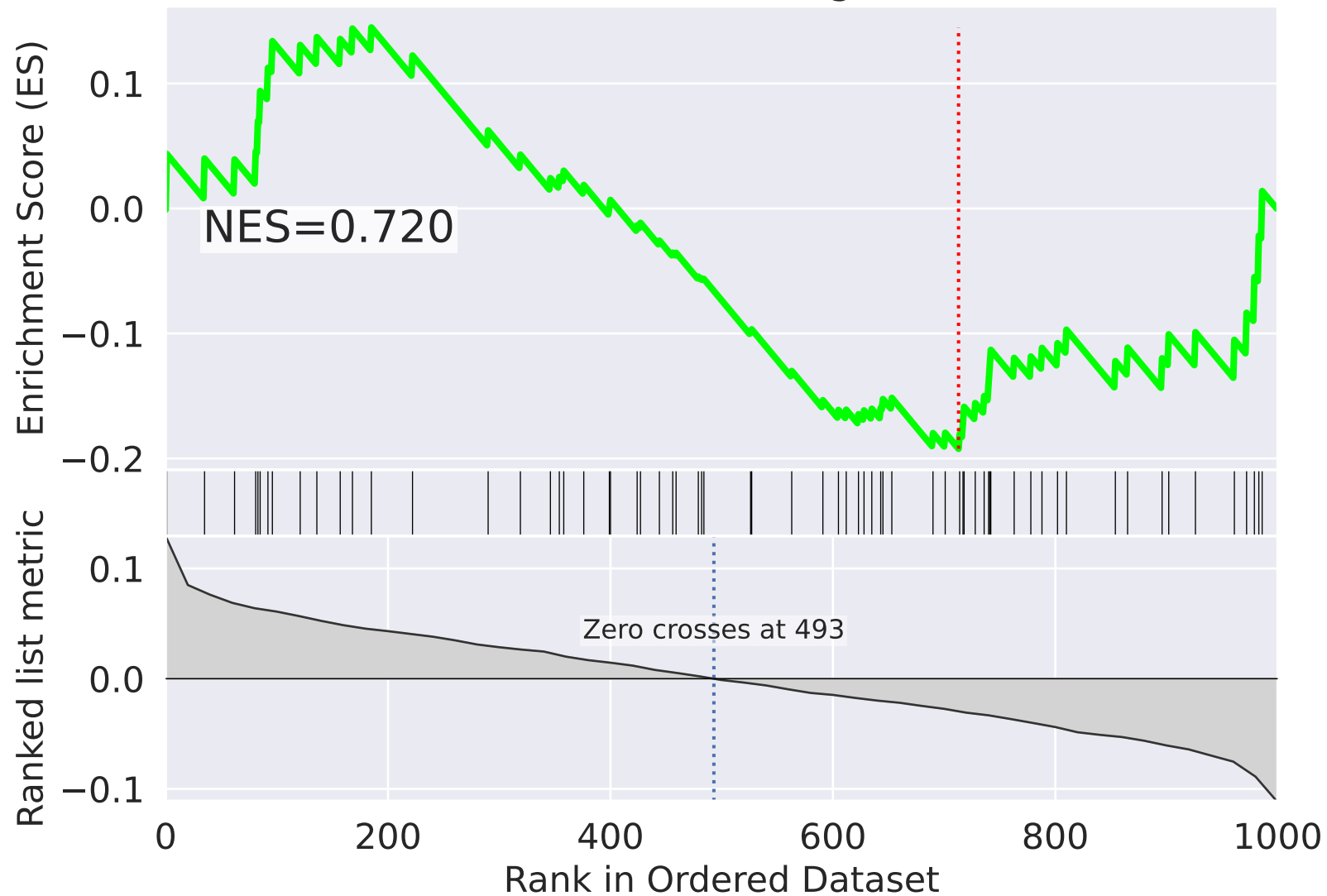
mitochondrial translational elongation (GO:0070125)



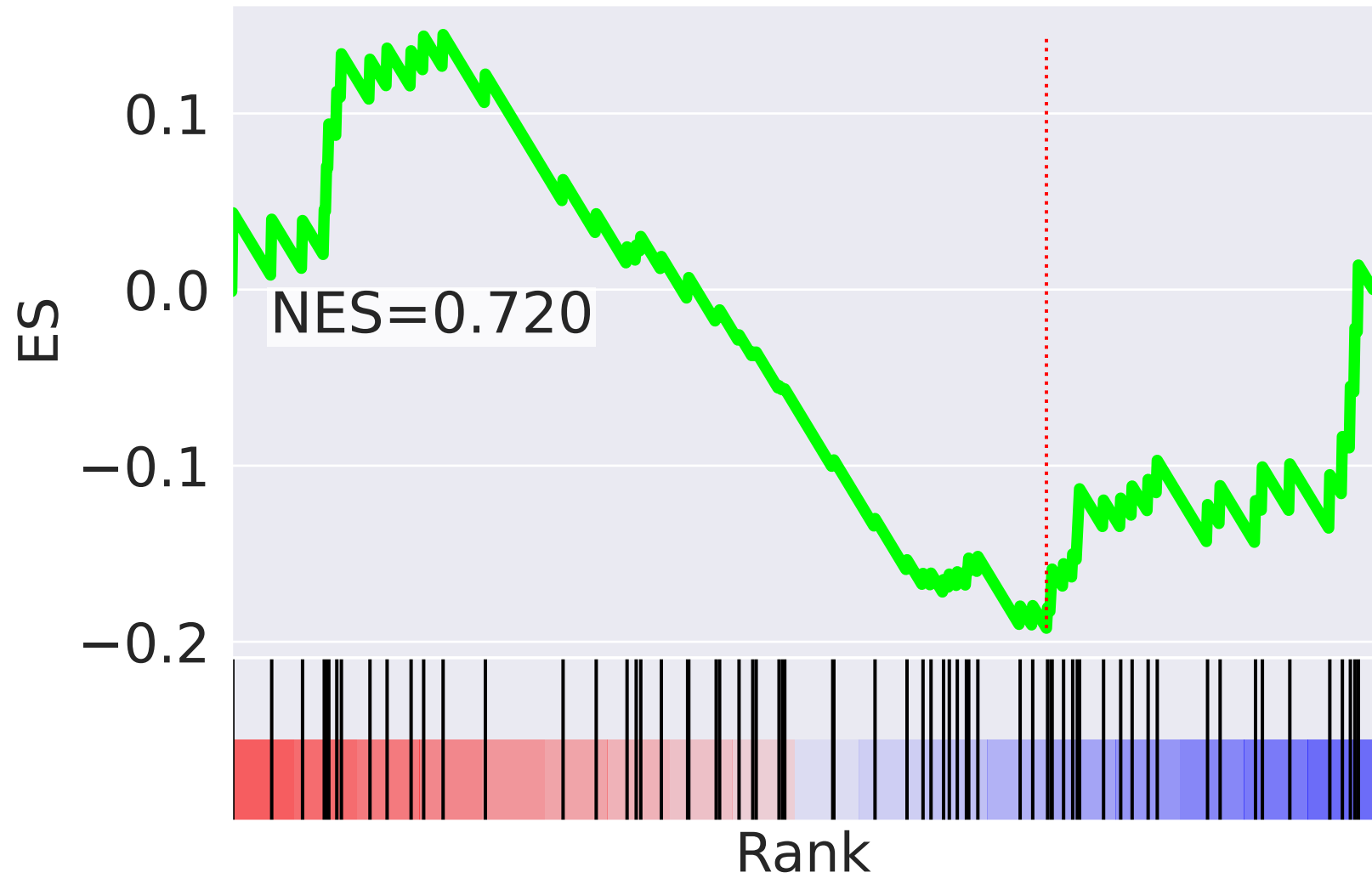
NES		SET
2.612		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.306		Ras protein signal transduction (GO:0007265)
2.265		mitochondrial translational elongation (GO:0070125)
-2.252		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
2.120		ERK1 and ERK2 cascade (GO:0070371)
-2.053		retrograde transport, endosome to Golgi (GO:0042147)
1.999		cellular response to amino acid starvation (GO:0034198)
-1.997		insulin receptor signaling pathway (GO:0008286)
1.978		vesicle-mediated transport (GO:0016192)
-1.939		transcription, DNA-templated (GO:0006351)
1.924		mitochondrial translational termination (GO:0070126)
-1.924		response to ionizing radiation (GO:0010212)
-1.841		platelet aggregation (GO:0070527)
-1.802		positive regulation of protein catabolic process (GO:0045732)
-1.801		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 $z=66$

mitochondrial translational elongation (GO:0070125)






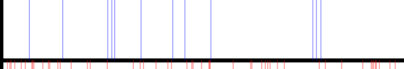
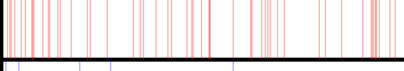
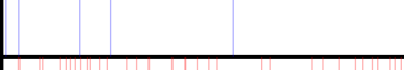
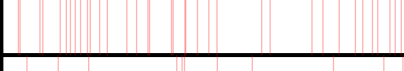
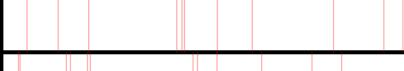
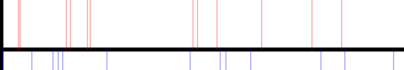
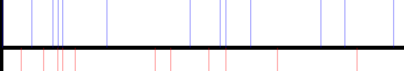


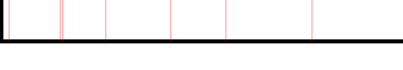


mitochondrial translational elongation (GO:0070125)



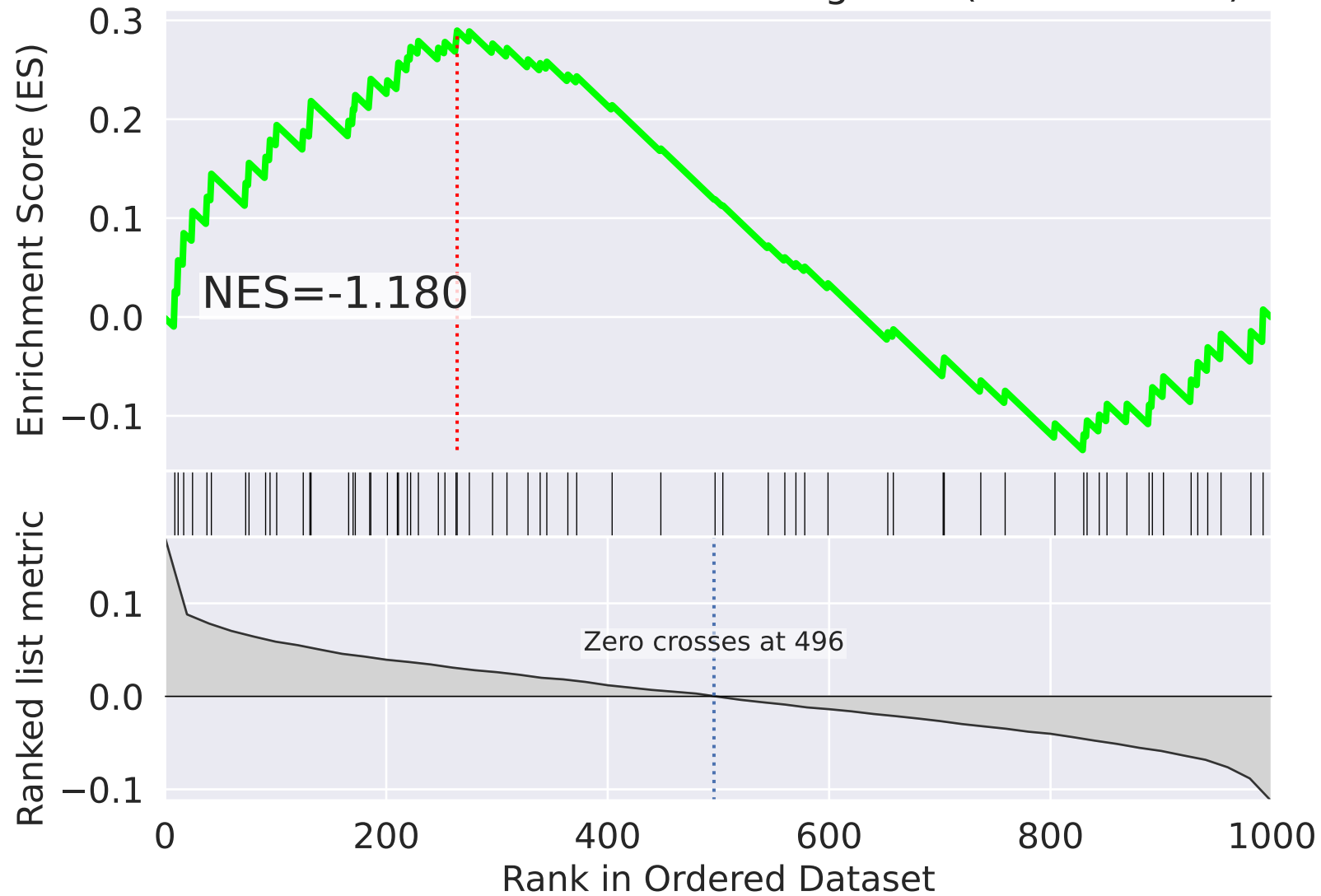
NES

SET

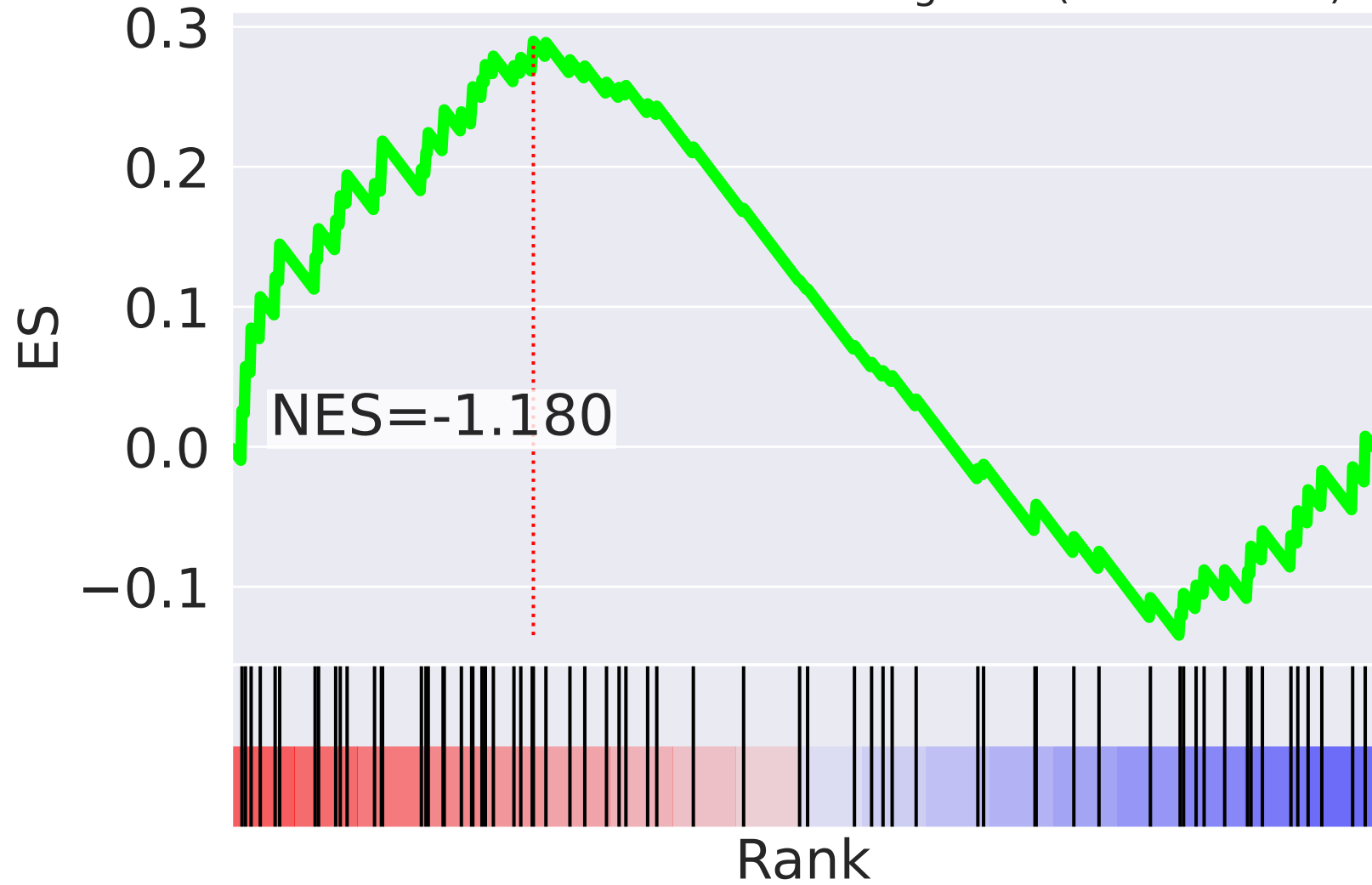
2.436		nucleosome disassembly (GO:0006337)
-2.261		positive regulation of telomere maintenance via telomerase (GO:0032212)
-2.238		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.168		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.146		protein complex assembly (GO:0006461)
-2.142		protein phosphorylation (GO:0006468)
2.126		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.105		regulation of cell adhesion (GO:0030155)
2.094		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.076		regulation of mRNA stability (GO:0043488)
2.059		chromatin remodeling (GO:0006338)
-2.044		Fc-epsilon receptor signaling pathway (GO:0038095)
1.979		positive regulation of gene expression (GO:0010628)
-1.967		T cell receptor signaling pathway (GO:0050852)
1.917		regulation of protein stability (GO:0031647)




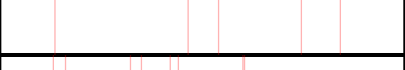
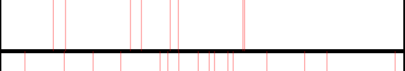
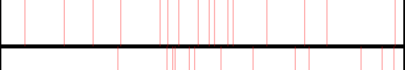
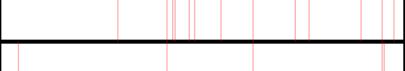
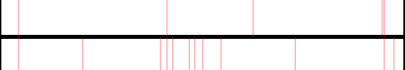
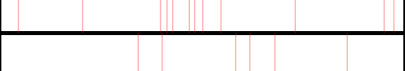
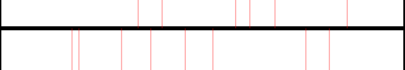
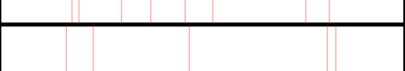


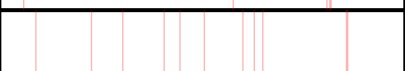
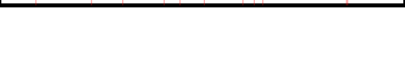
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=67$

mitochondrial translational elongation (GO:0070125)



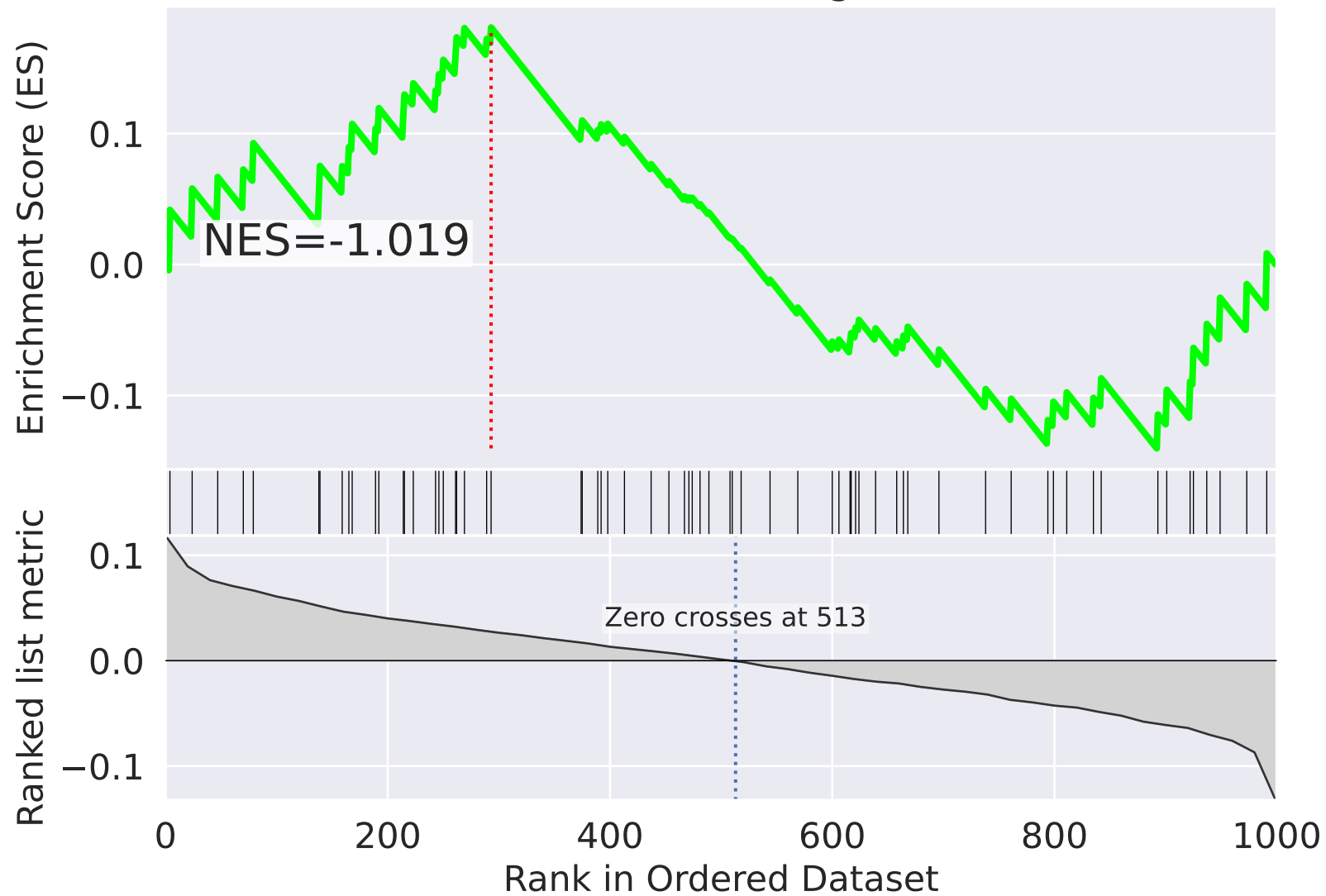
mitochondrial translational elongation (GO:0070125)



NES		SET
2.692		blood coagulation (GO:0007596)
-2.589		mRNA 3'-end processing (GO:0031124)
2.560		RNA metabolic process (GO:0016070)
2.374		cholesterol biosynthetic process (GO:0006695)
2.266		rRNA processing (GO:0006364)
2.200		mitochondrion organization (GO:0007005)
2.194		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.088		platelet activation (GO:0030168)
1.997		ephrin receptor signaling pathway (GO:0048013)
1.956		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
1.930		protein import into nucleus (GO:0006606)
1.917		execution phase of apoptosis (GO:0097194)
-1.887		termination of RNA polymerase II transcription (GO:0006369)
1.863		DNA-dependent DNA replication (GO:0006261)
1.820		regulation of mRNA stability (GO:0043488)

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)





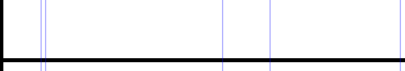

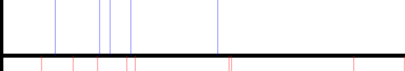

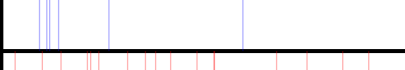


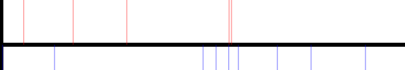

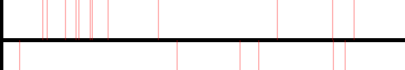
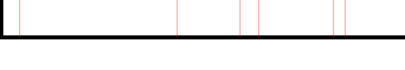
ES

0.1
0.0
-0.1

NES=-1.019

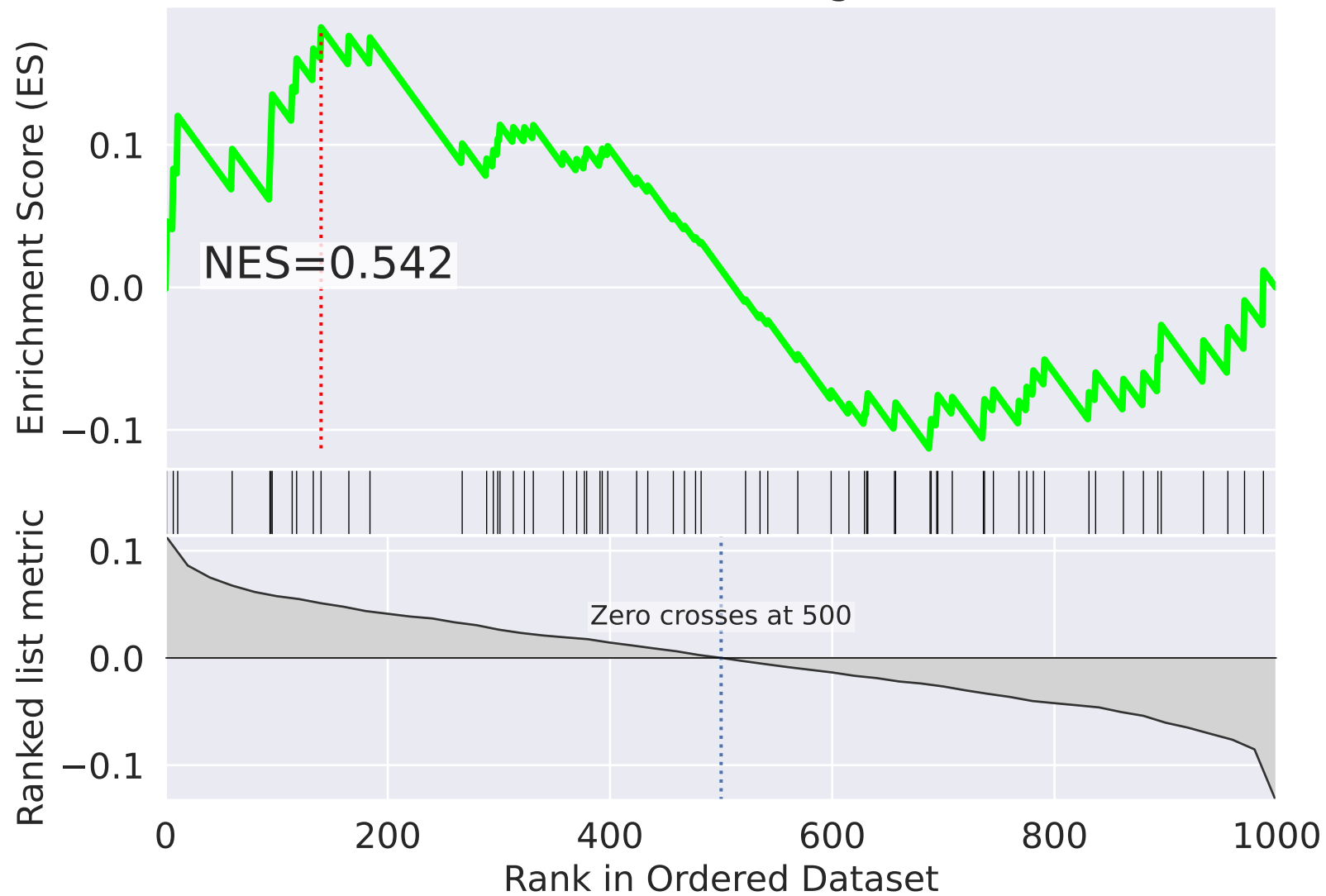
Rank



NES		SET
-2.927		protein dephosphorylation (GO:0006470)
-2.474		RNA export from nucleus (GO:0006405)
-2.259		regulation of transcription, DNA-templated (GO:0006355)
2.219		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.189		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.189		retrograde protein transport, ER to cytosol (GO:0030970)
-2.139		regulation of DNA replication (GO:0006275)
2.079		regulation of macroautophagy (GO:0016241)
-2.027		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
2.022		mitochondrion organization (GO:0007005)
1.971		transcription-coupled nucleotide-excision repair (GO:0006283)
1.923		cellular protein localization (GO:0034613)
-1.913		intracellular signal transduction (GO:0035556)
1.850		ephrin receptor signaling pathway (GO:0048013)
1.811		COPII vesicle coating (GO:0048208)

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)



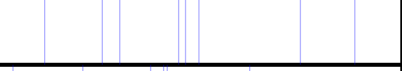



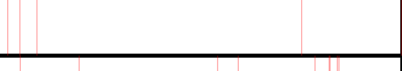



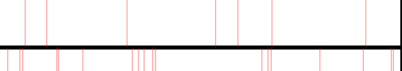
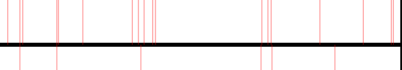


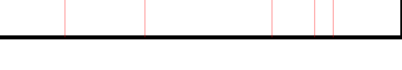
ES

0.1
0.0
-0.1

NES=0.542

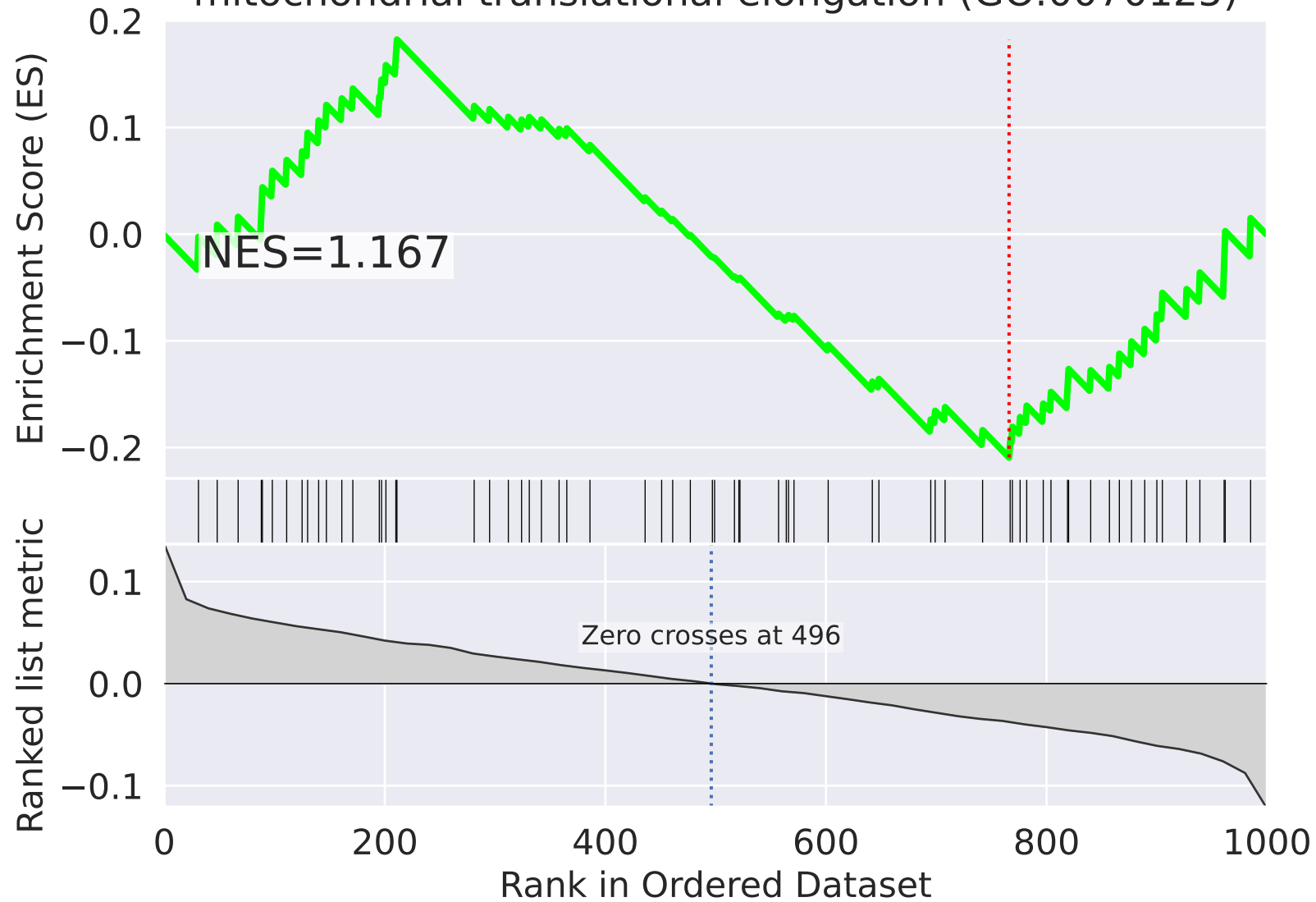
Rank



NES		SET
-3.287		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.436		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.410		regulation of apoptotic process (GO:0042981)
-2.354		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-2.316		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
2.290		innate immune response (GO:0045087)
2.276		positive regulation of DNA replication (GO:0045740)
2.263		tRNA modification (GO:0006400)
-2.253		cytokinesis (GO:0000910)
-2.194		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
2.170		negative regulation of translation (GO:0017148)
2.169		MAPK cascade (GO:0000165)
2.124		positive regulation of cell growth (GO:0030307)
2.081		cellular response to epidermal growth factor stimulus (GO:0071364)
2.020		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 $z=70$

mitochondrial translational elongation (GO:0070125)



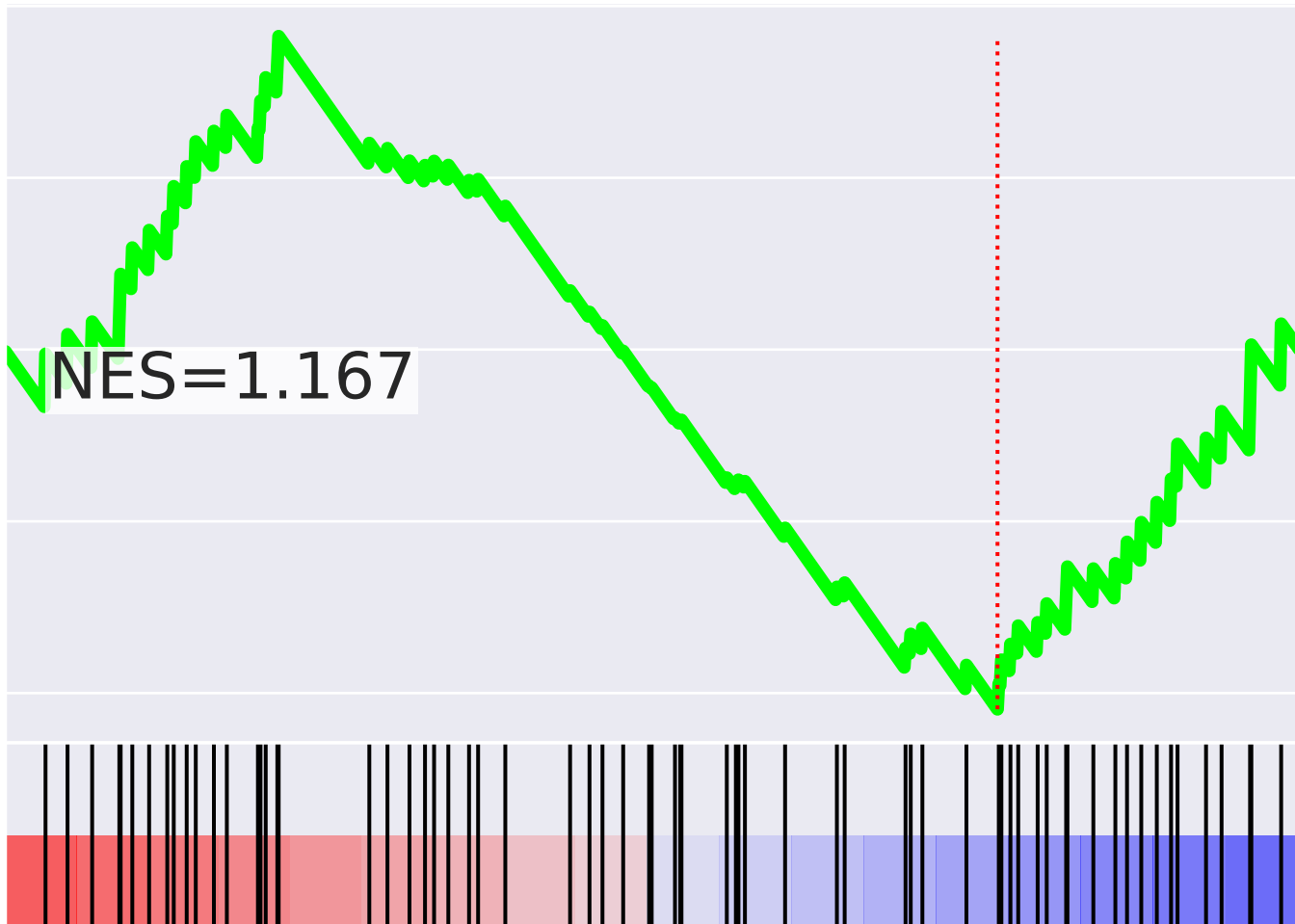
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1
-0.2

NES=1.167

Rank



NES		SET
-2.477		negative regulation of cell proliferation (GO:0008285)
2.134		interstrand cross-link repair (GO:0036297)
-2.131		positive regulation of TOR signaling (GO:0032008)
2.064		positive regulation of DNA replication (GO:0045740)
2.035		double-strand break repair via nonhomologous end joining (GO:0006303)
1.959		protein autophosphorylation (GO:0046777)
1.946		cellular response to tumor necrosis factor (GO:0071356)
1.907		RNA export from nucleus (GO:0006405)
-1.901		regulation of cell adhesion (GO:0030155)
-1.873		protein deubiquitination (GO:0016579)
-1.865		RNA splicing (GO:0008380)
1.864		response to ionizing radiation (GO:0010212)
-1.854		peptidyl-serine phosphorylation (GO:0018105)
1.801		transcription from mitochondrial promoter (GO:0006390)
1.795		CENP-A containing nucleosome assembly (GO:0034080)