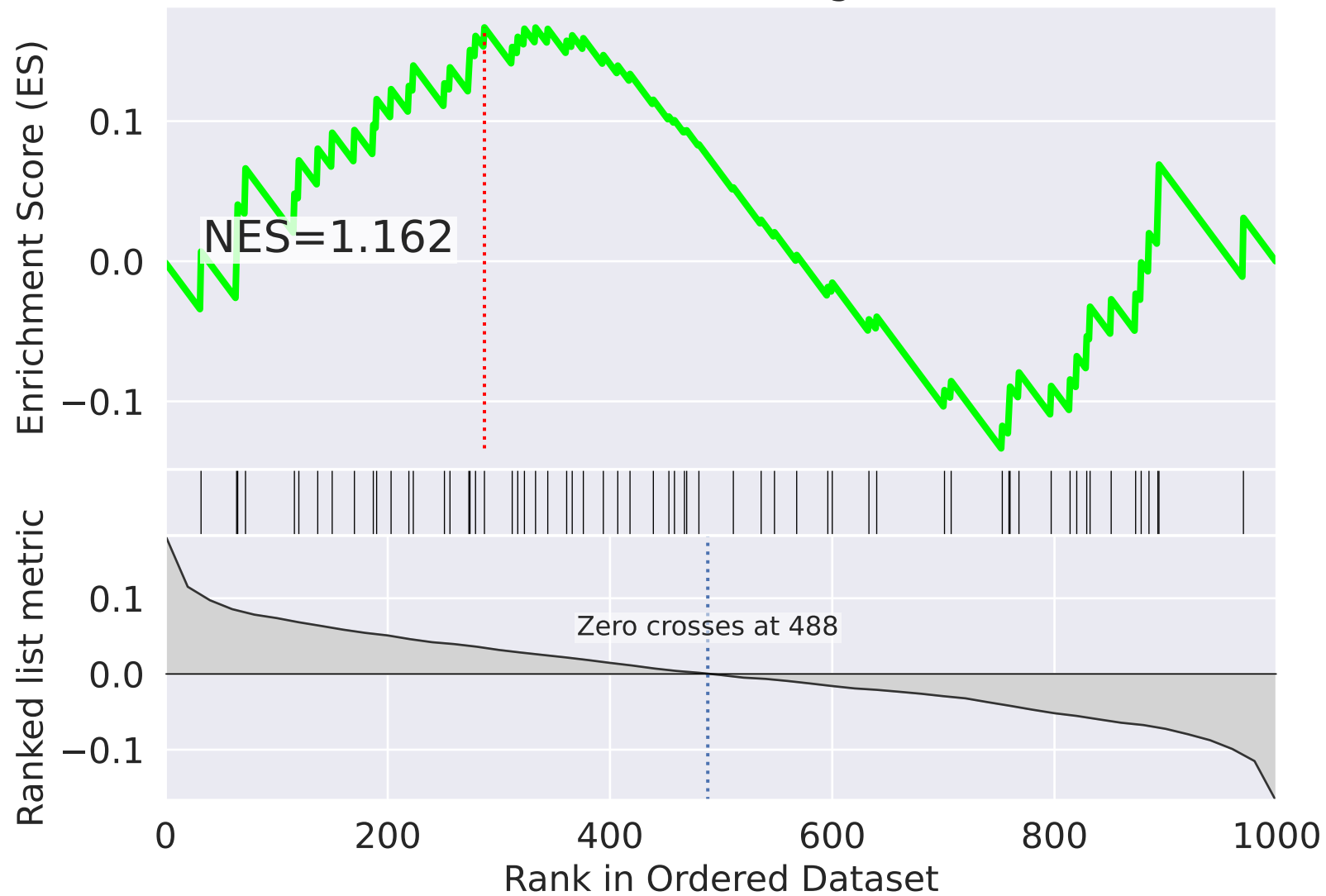
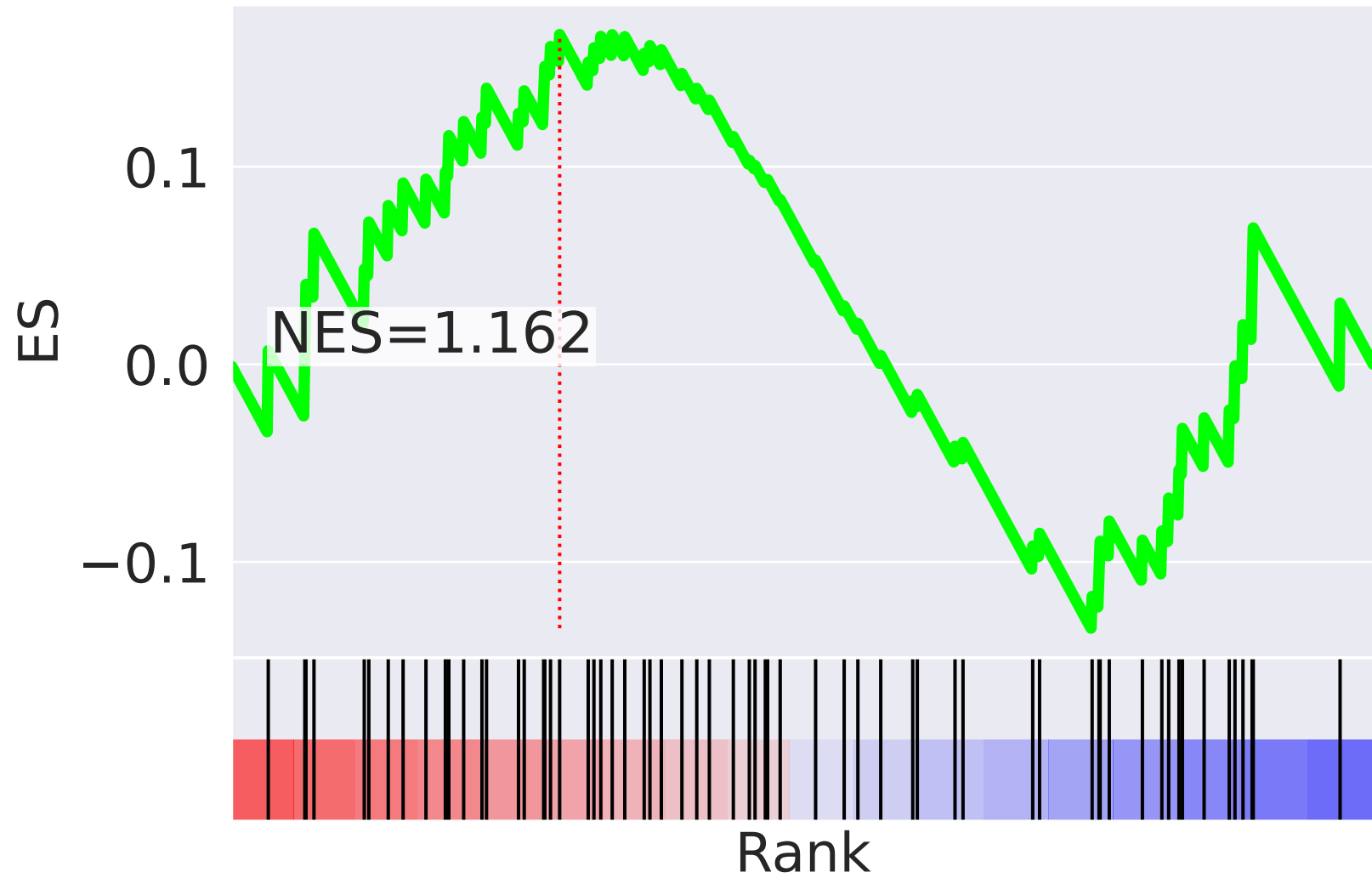






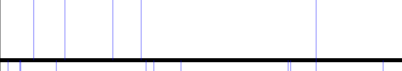

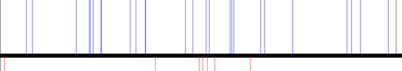
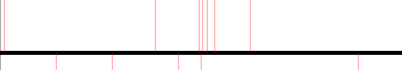


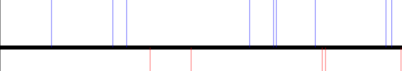
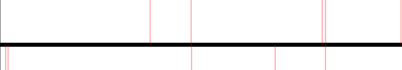


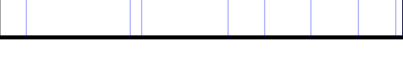
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=1$

mitochondrial translational elongation (GO:0070125)



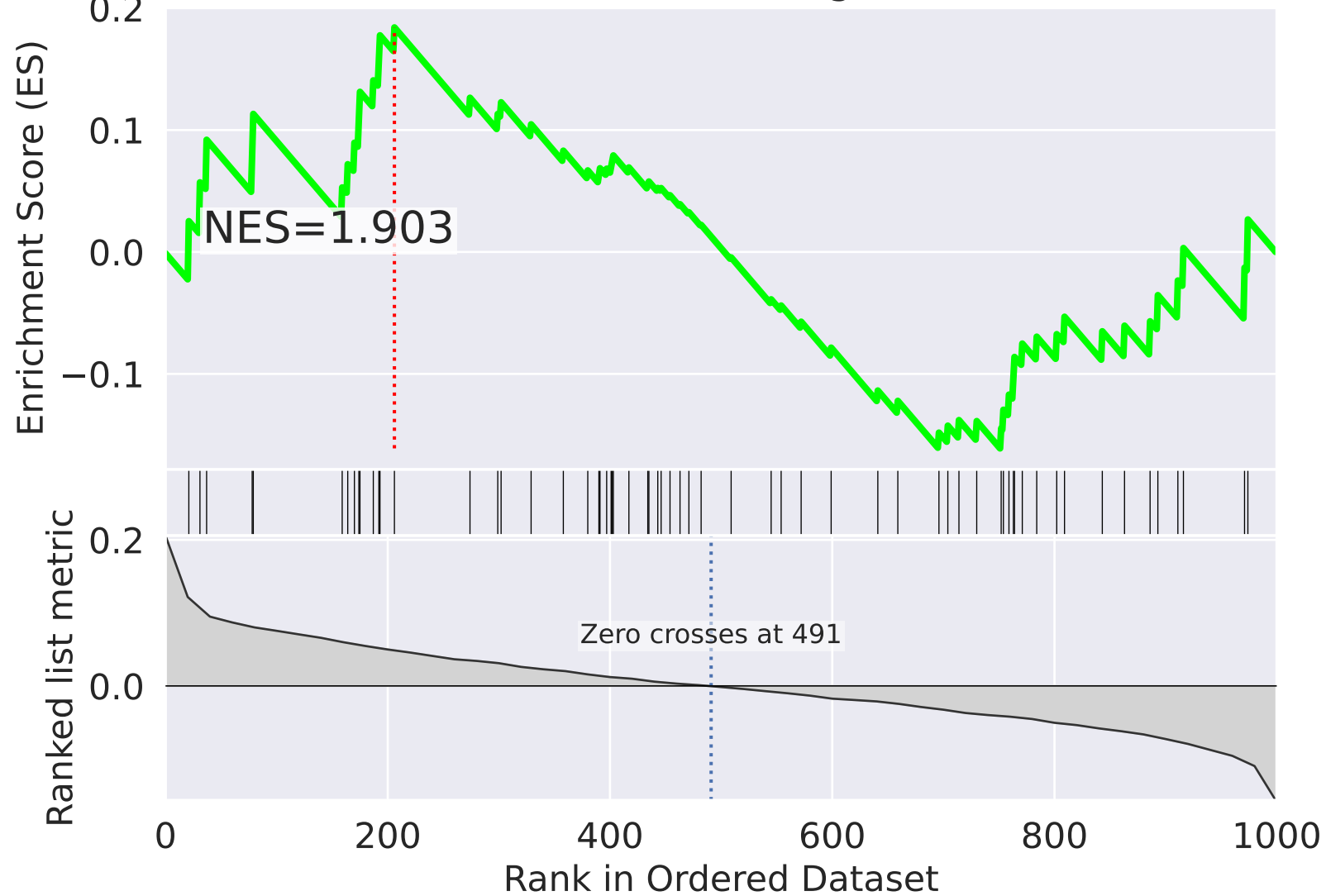
mitochondrial translational elongation (GO:0070125)



NES		SET
-3.017		integrin-mediated signaling pathway (GO:0007229)
-2.962		DNA repair (GO:0006281)
-2.423		retrograde transport, endosome to Golgi (GO:0042147)
2.314		positive regulation of gene expression (GO:0010628)
-2.152		positive regulation of protein catabolic process (GO:0045732)
-2.107		cell migration (GO:0016477)
-2.107		mRNA splicing, via spliceosome (GO:0000398)
2.044		cellular protein modification process (GO:0006464)
2.010		ERK1 and ERK2 cascade (GO:0070371)
1.994		negative regulation of cell proliferation (GO:0008285)
-1.976		double-strand break repair via nonhomologous end joining (GO:0006303)
1.941		inflammatory response (GO:0006954)
1.875		regulation of cell migration (GO:0030334)
-1.864		nervous system development (GO:0007399)
-1.862		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 $z=2$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)


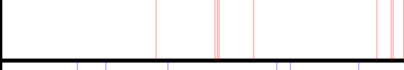
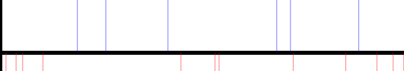





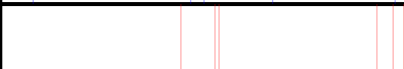
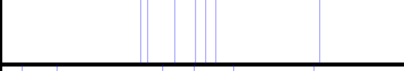


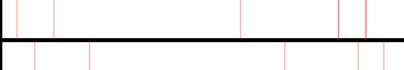
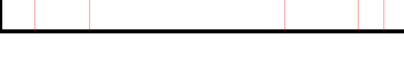

ES

0.2
0.1
0.0
-0.1

NES=1.903

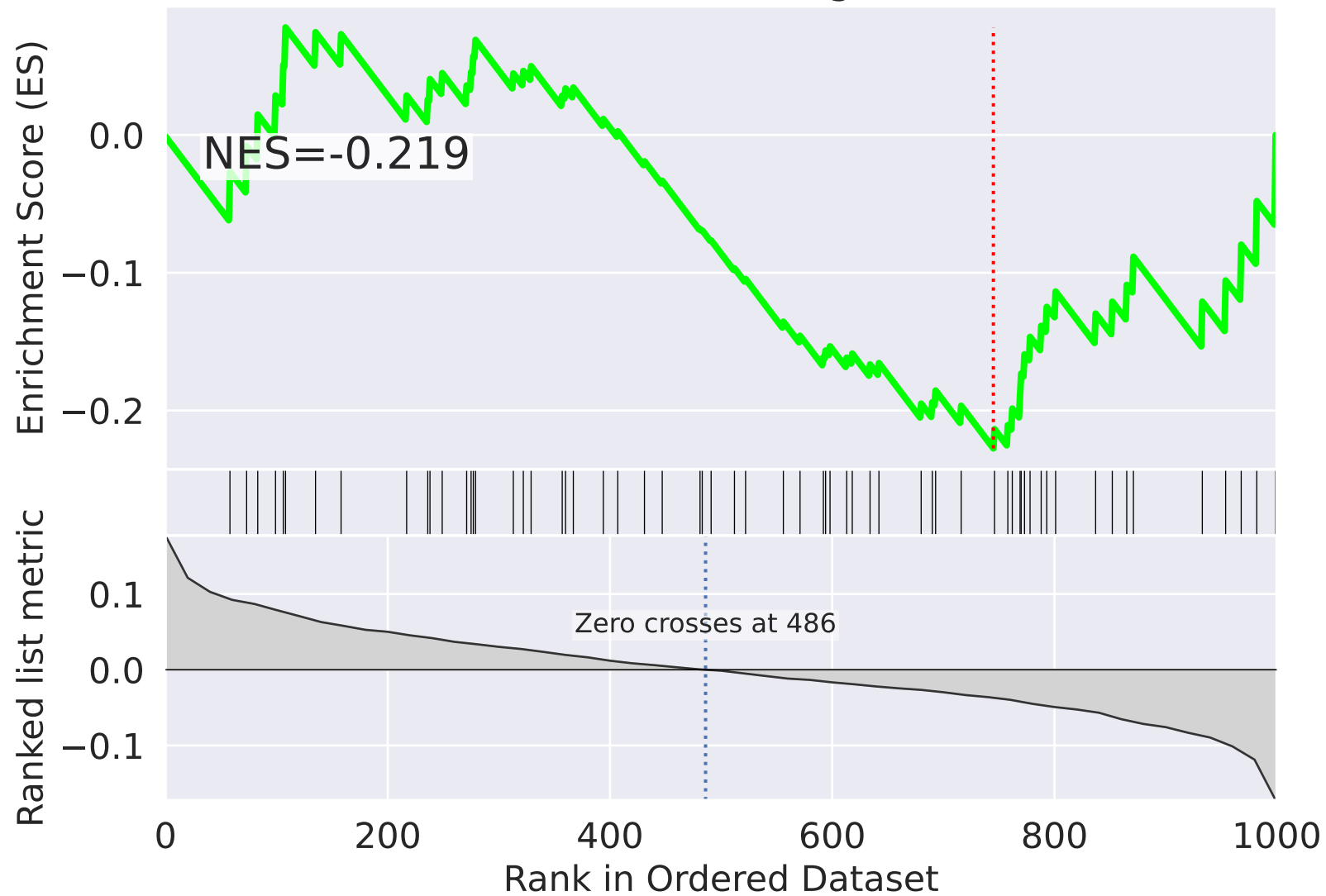
Rank



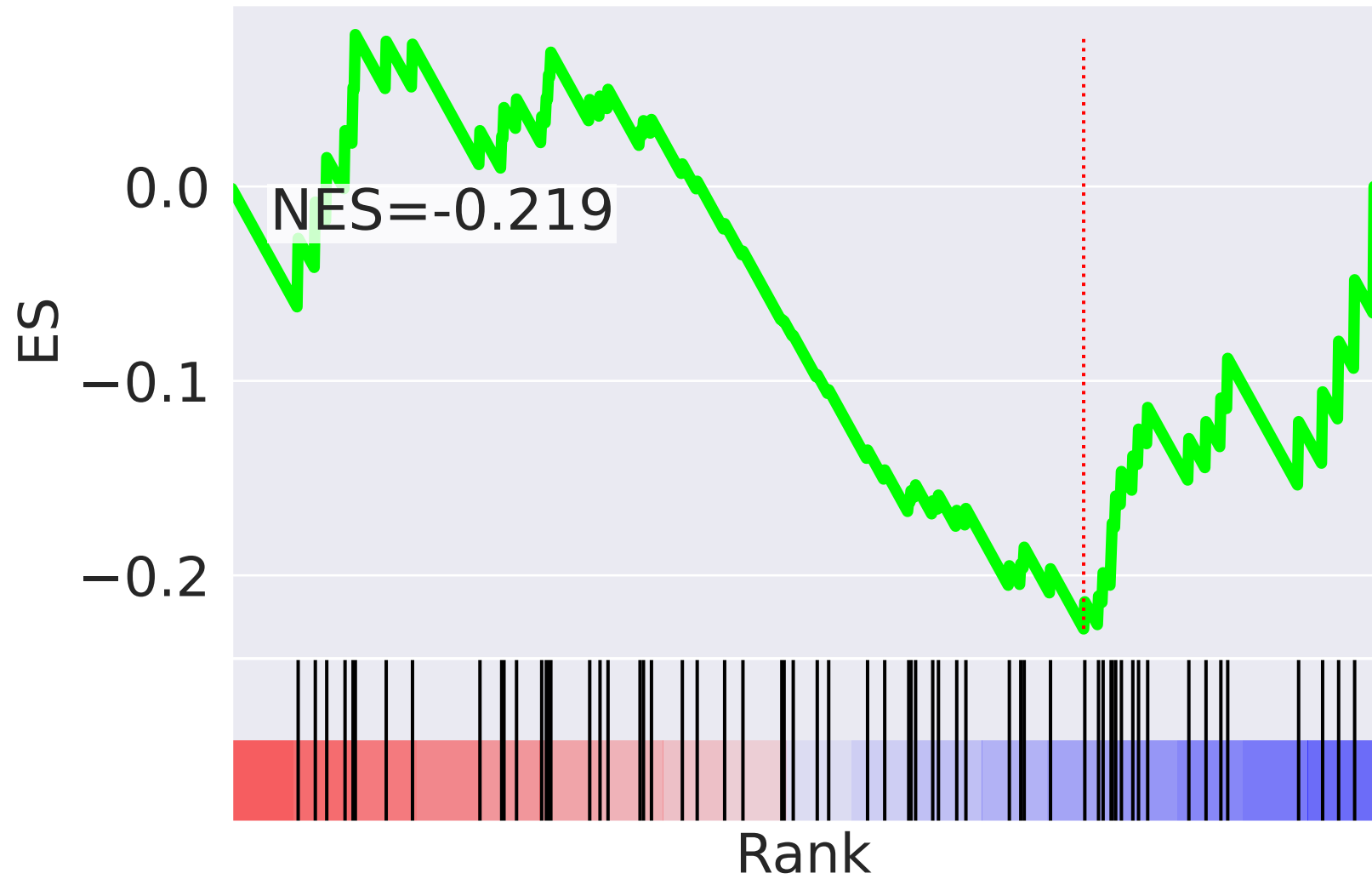
NES		SET
2.814		tricarboxylic acid cycle (GO:0006099)
2.545		positive regulation of TOR signaling (GO:0032008)
-2.513		protein K11-linked ubiquitination (GO:0070979)
2.405		regulation of macroautophagy (GO:0016241)
-2.328		movement of cell or subcellular component (GO:0006928)
-2.298		chromatin remodeling (GO:0006338)
-2.289		interstrand cross-link repair (GO:0036297)
2.258		histone H3-K4 methylation (GO:0051568)
-2.252		mitotic nuclear envelope disassembly (GO:0007077)
2.192		cellular response to amino acid stimulus (GO:0071230)
-2.111		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.110		positive regulation of gene expression, epigenetic (GO:0045815)
-2.105		Fc-epsilon receptor signaling pathway (GO:0038095)
2.087		cell surface receptor signaling pathway (GO:0007166)
2.054		nucleobase-containing small molecule interconversion (GO:0015949)


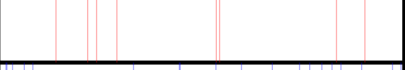





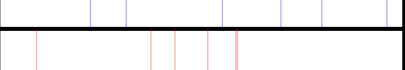
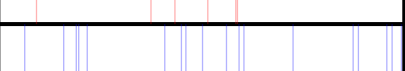
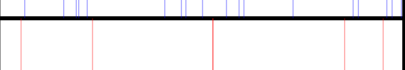





The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=3$

mitochondrial translational elongation (GO:0070125)



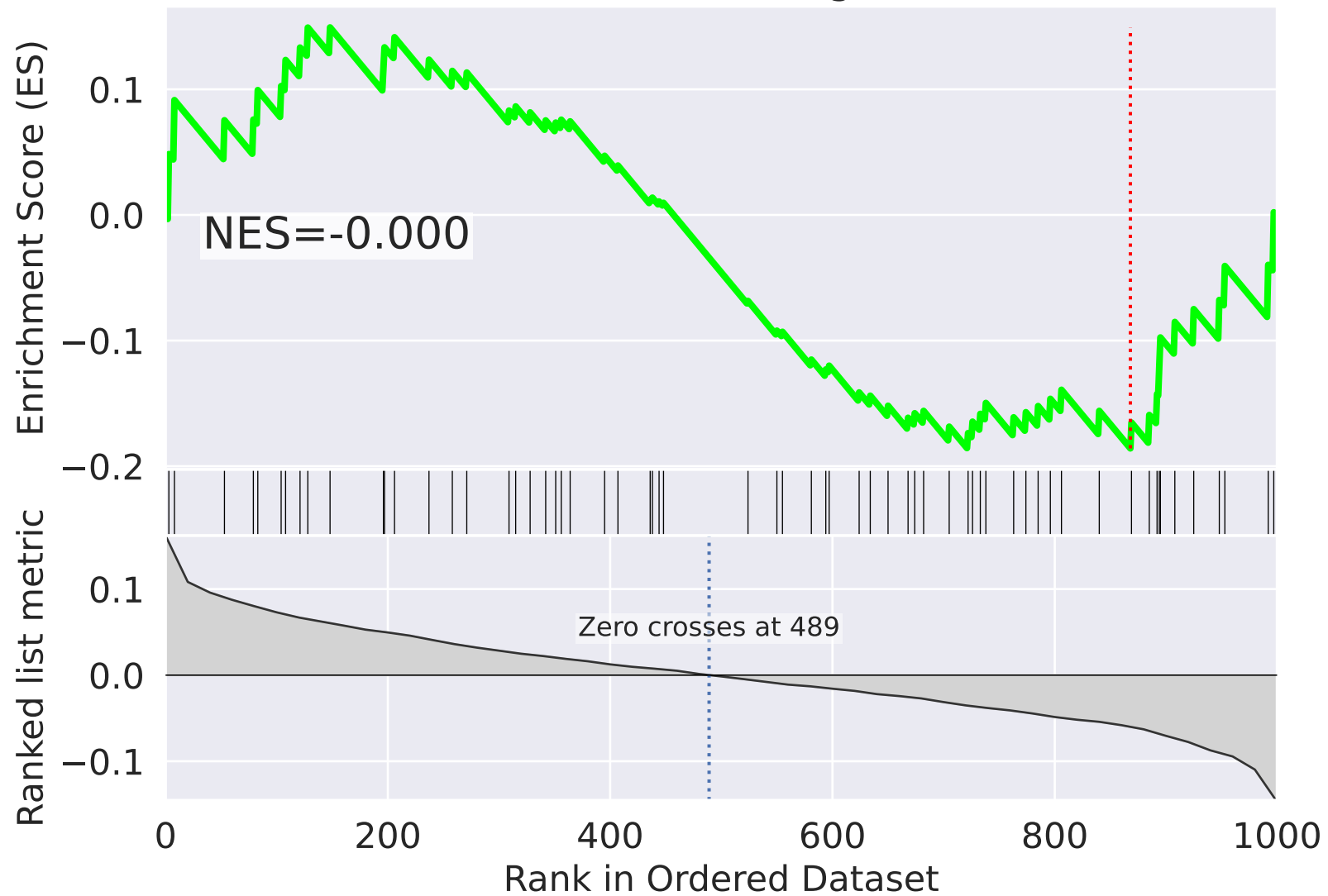
mitochondrial translational elongation (GO:0070125)



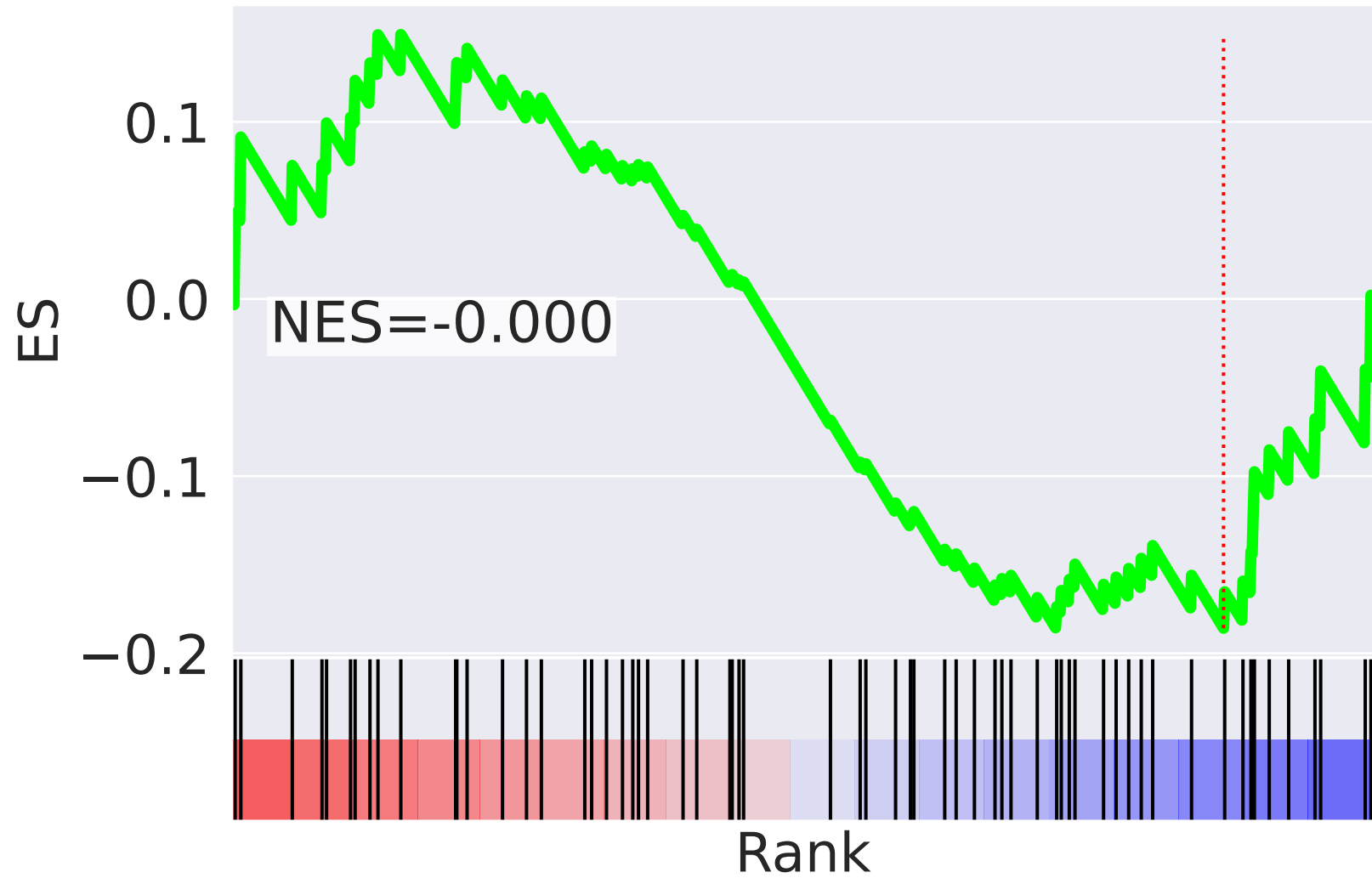
NES		SET
2.474		regulation of apoptotic process (GO:0042981)
2.432		negative regulation of translation (GO:0017148)
-2.254		negative regulation of cell proliferation (GO:0008285)
-2.237		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
-2.173		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-2.111		positive regulation of type I interferon production (GO:0032481)
-2.105		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.078		heart development (GO:0007507)
2.005		phosphatidylinositol biosynthetic process (GO:0006661)
-1.990		transcription from RNA polymerase II promoter (GO:0006366)
1.953		chromosome segregation (GO:0007059)
-1.939		cell differentiation (GO:0030154)
-1.938		peptidyl-serine phosphorylation (GO:0018105)
-1.920		positive regulation of TOR signaling (GO:0032008)
1.918		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)

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

mitochondrial translational elongation (GO:0070125)



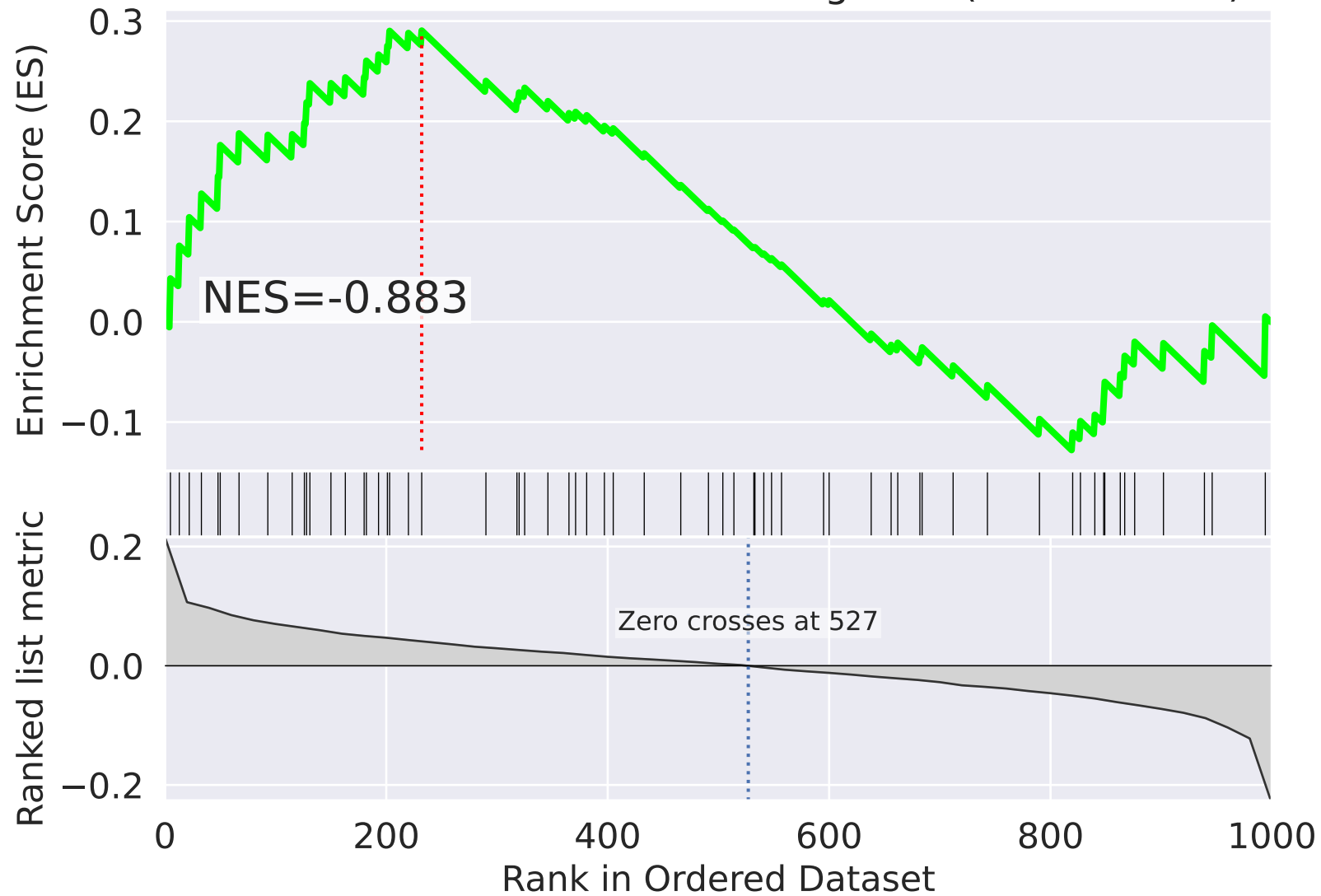
mitochondrial translational elongation (GO:0070125)



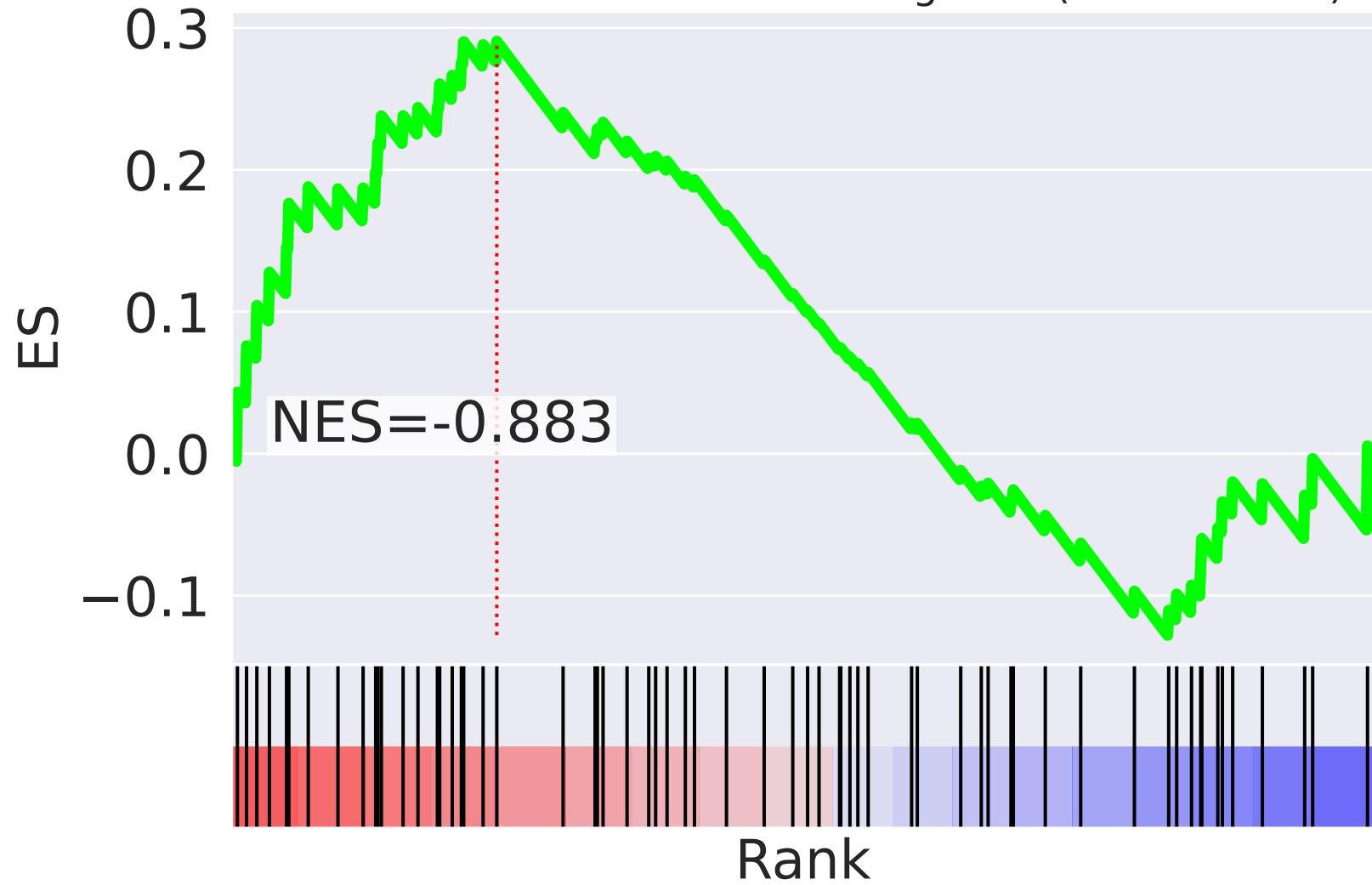
NES		SET
3.030		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-2.419		nucleobase-containing small molecule interconversion (GO:0015949)
2.394		response to endoplasmic reticulum stress (GO:0034976)
2.394		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.382		regulation of cholesterol biosynthetic process (GO:0045540)
-2.366		cholesterol biosynthetic process (GO:0006695)
2.346		positive regulation by host of viral transcription (GO:0043923)
2.345		endocytosis (GO:0006897)
2.288		positive regulation of gene expression (GO:0010628)
2.239		Wnt signaling pathway (GO:0016055)
2.201		double-strand break repair (GO:0006302)
2.168		tricarboxylic acid cycle (GO:0006099)
-2.136		regulation of defense response to virus by virus (GO:0050690)
-2.018		Fc-epsilon receptor signaling pathway (GO:0038095)
-1.979		T cell costimulation (GO:0031295)


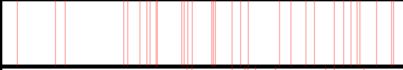
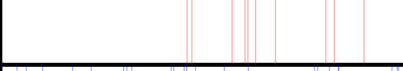
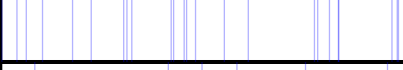


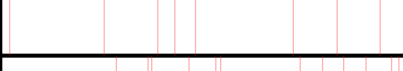
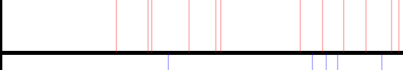
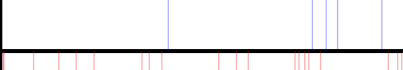
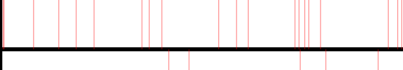

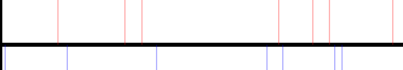
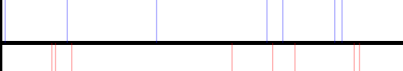
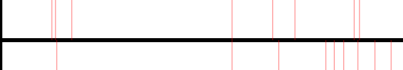
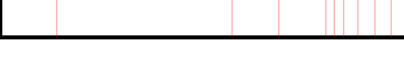
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=5$

mitochondrial translational elongation (GO:0070125)



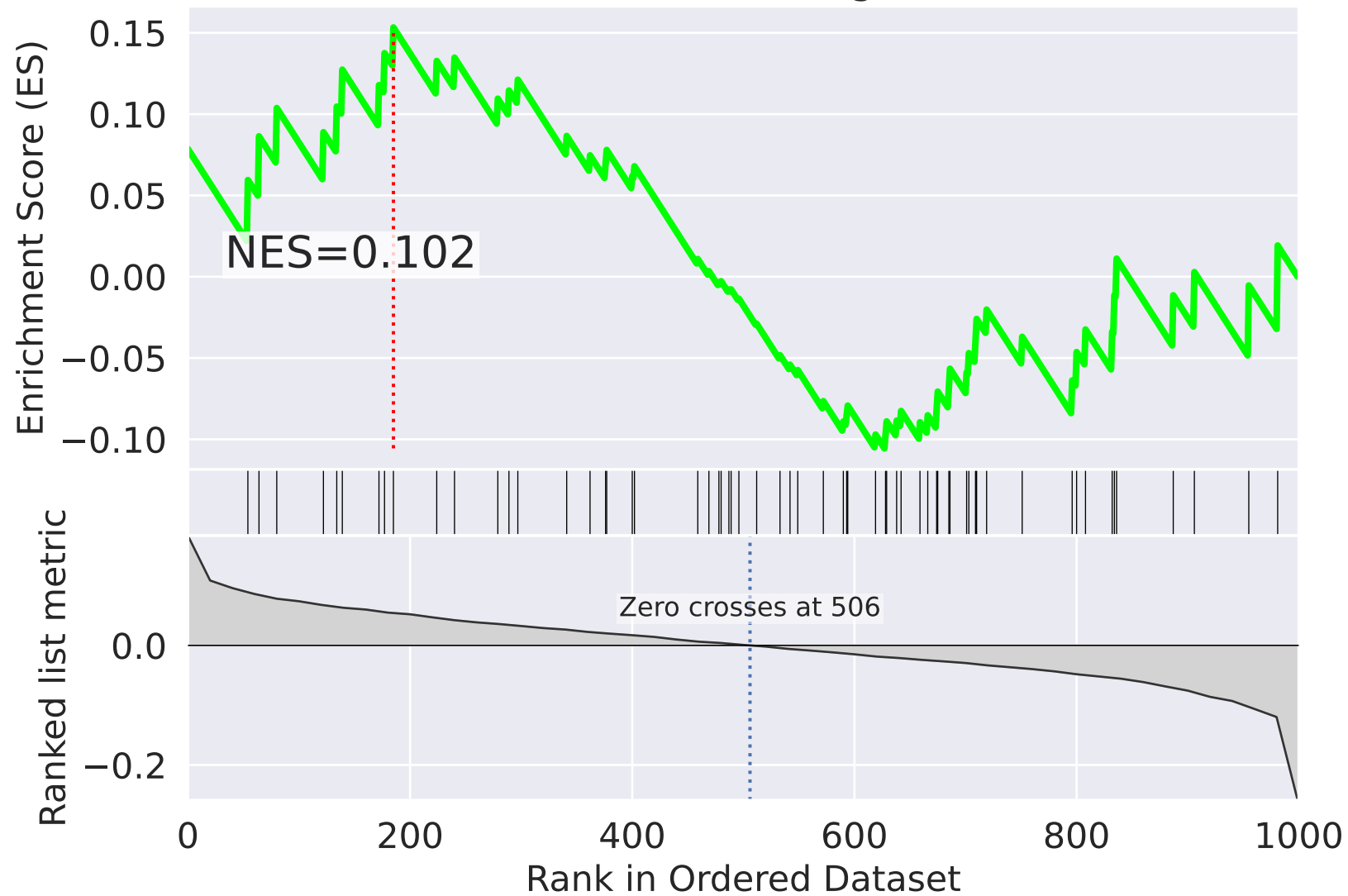
mitochondrial translational elongation (GO:0070125)



NES		SET
3.305		epidermal growth factor receptor signaling pathway (GO:0007173)
3.070		positive regulation of cell proliferation (GO:0008284)
2.779		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.634		regulation of transcription, DNA-templated (GO:0006355)
-2.353		cellular protein modification process (GO:0006464)
2.295		sister chromatid cohesion (GO:0007062)
2.287		ciliary basal body docking (GO:0097711)
2.285		mitotic metaphase plate congression (GO:0007080)
-2.218		lipid metabolic process (GO:0006629)
2.114		cellular response to DNA damage stimulus (GO:0006974)
2.101		cell division (GO:0051301)
2.062		Wnt signaling pathway (GO:0016055)
-2.061		protein N-linked glycosylation via asparagine (GO:0018279)
1.993		regulation of cell proliferation (GO:0042127)
1.988		integrin-mediated signaling pathway (GO:0007229)

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)



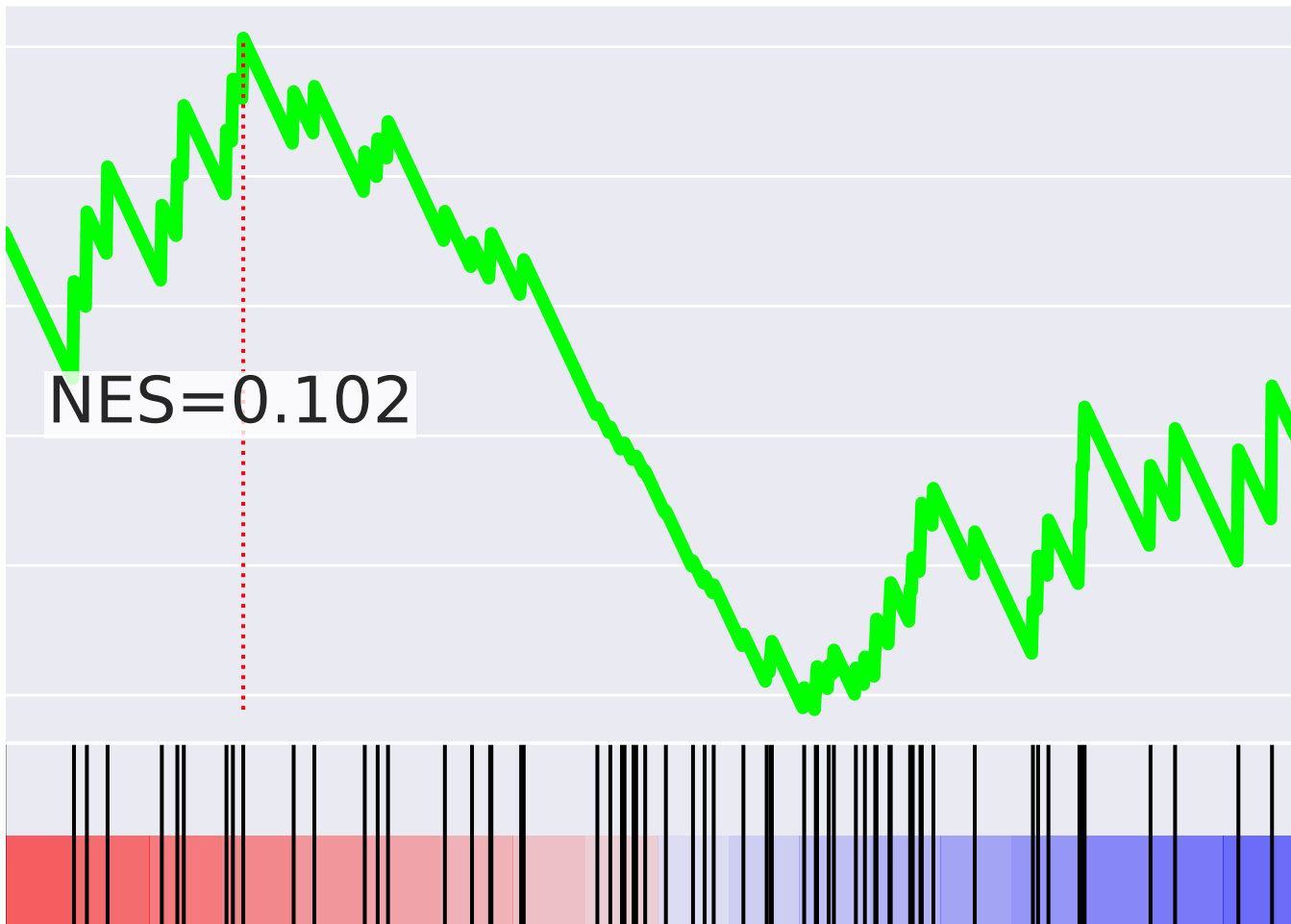
mitochondrial translational elongation (GO:0070125)

ES

0.15
0.10
0.05
0.00
-0.05
-0.10

NES=0.102

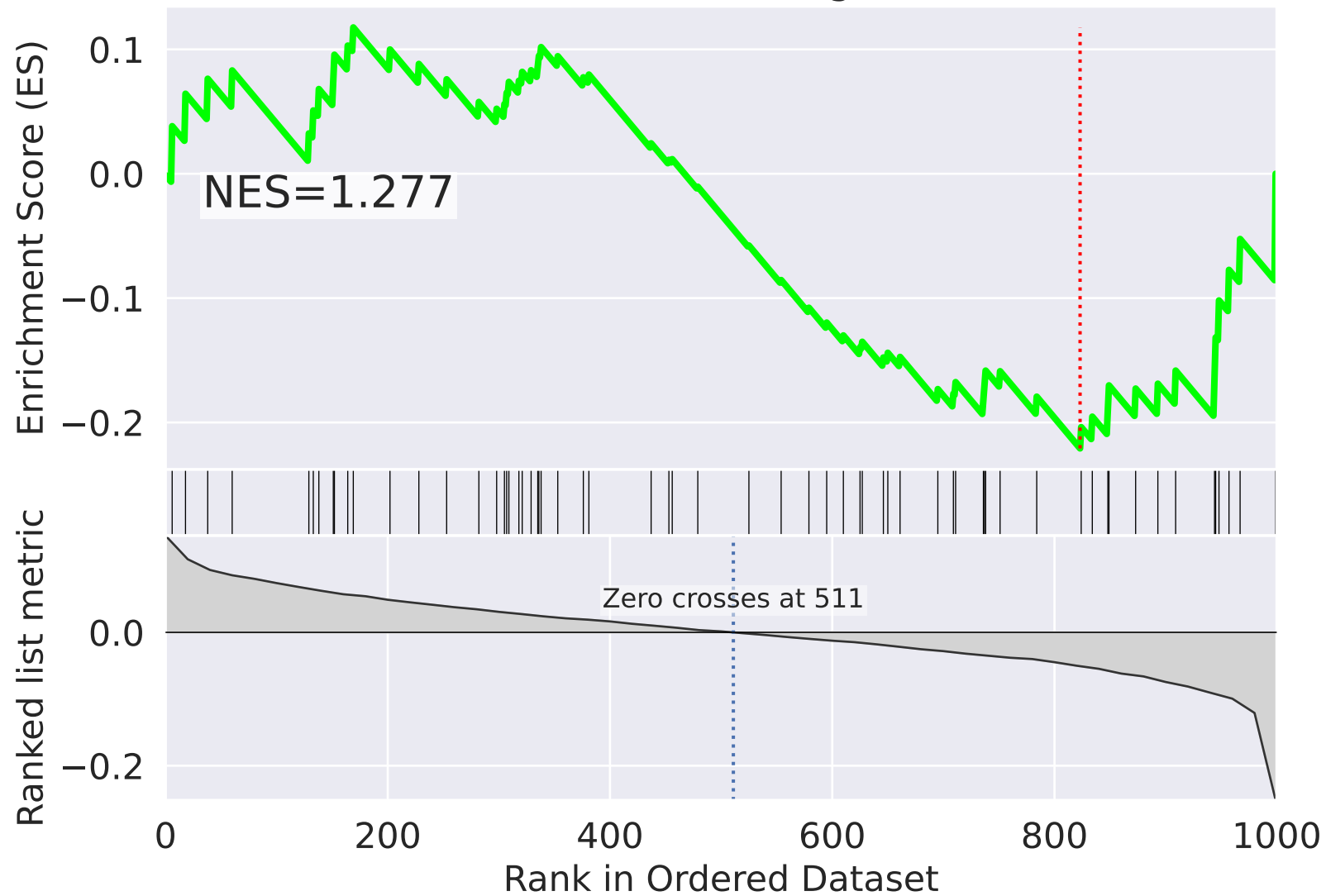
Rank



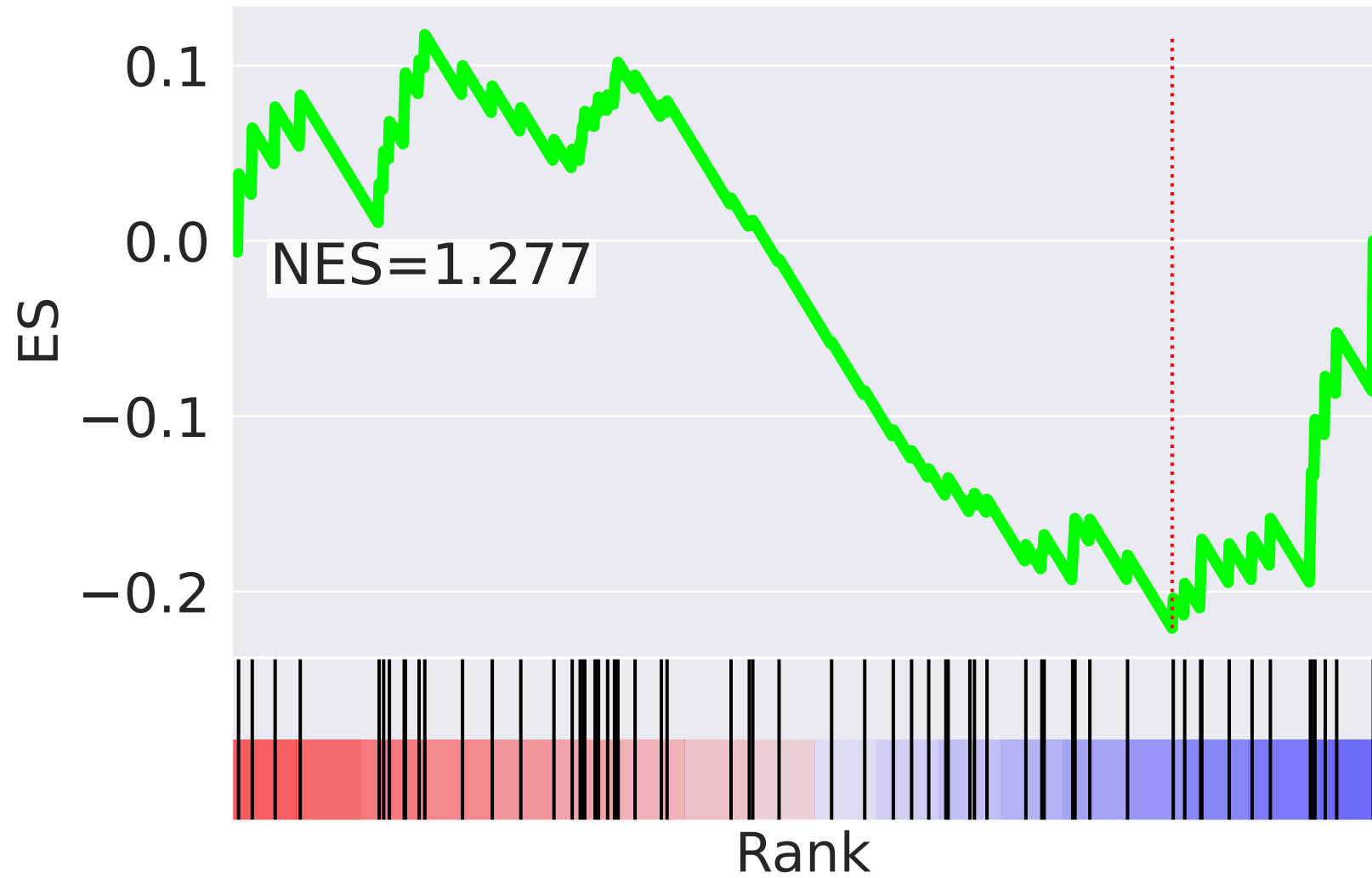
NES		SET
3.071		positive regulation of cell proliferation (GO:0008284)
2.573		G2/M transition of mitotic cell cycle (GO:0000086)
2.495		sister chromatid cohesion (GO:0007062)
-2.437		positive regulation of gene expression, epigenetic (GO:0045815)
-2.401		positive regulation of TOR signaling (GO:0032008)
2.289		mitotic metaphase plate congression (GO:0007080)
2.135		protein homooligomerization (GO:0051260)
-2.066		cell cycle arrest (GO:0007050)
-2.029		protein stabilization (GO:0050821)
1.987		cell-matrix adhesion (GO:0007160)
-1.972		protein N-linked glycosylation via asparagine (GO:0018279)
1.963		viral budding via host ESCRT complex (GO:0039702)
1.940		G1/S transition of mitotic cell cycle (GO:0000082)
-1.904		transcription-coupled nucleotide-excision repair (GO:0006283)
1.882		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)

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

mitochondrial translational elongation (GO:0070125)

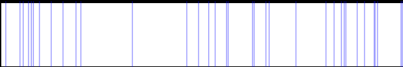
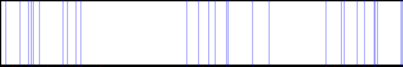



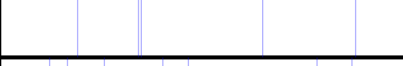

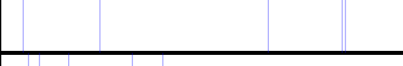


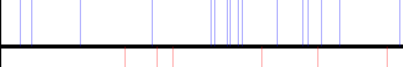
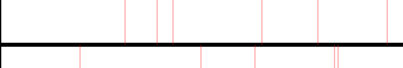

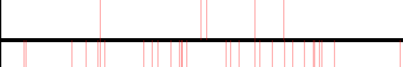
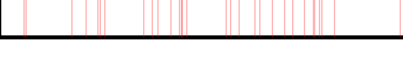


mitochondrial translational elongation (GO:0070125)



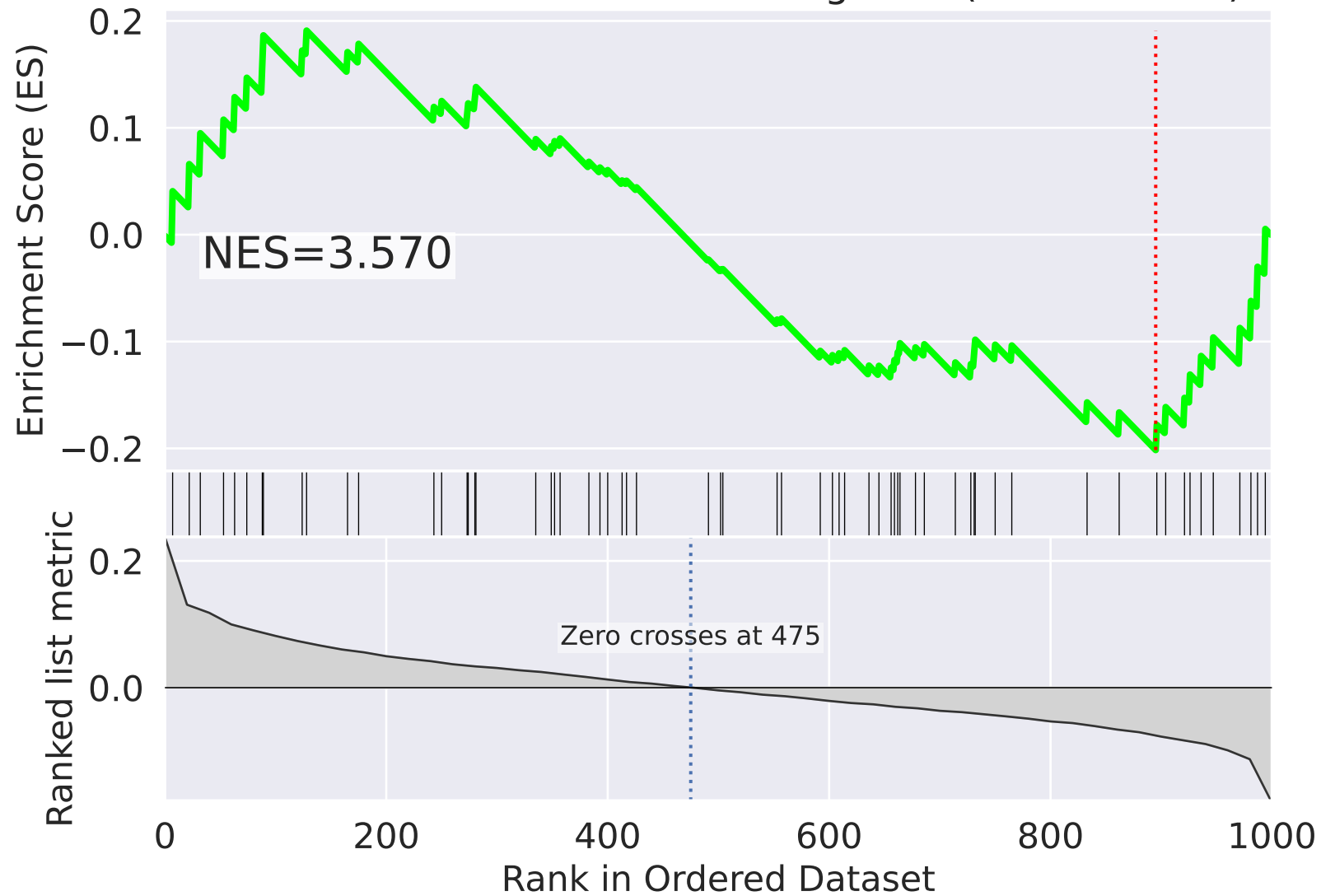
NES

SET

-4.374		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.535		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.527		positive regulation of apoptotic process (GO:0043065)
2.525		platelet aggregation (GO:0070527)
2.207		multicellular organism development (GO:0007275)
-2.092		lipid metabolic process (GO:0006629)
-2.061		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.051		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.014		cellular respiration (GO:0045333)
-2.006		regulation of cell cycle (GO:0051726)
-1.995		transcription initiation from RNA polymerase II promoter (GO:0006367)
1.991		protein K48-linked ubiquitination (GO:0070936)
1.926		positive regulation by host of viral transcription (GO:0043923)
1.911		beta-catenin-TCF complex assembly (GO:1904837)
1.869		negative regulation of transcription, DNA-templated (GO:0045892)




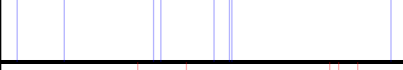

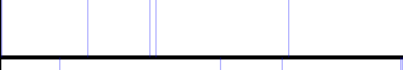









The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=8$

mitochondrial translational elongation (GO:0070125)



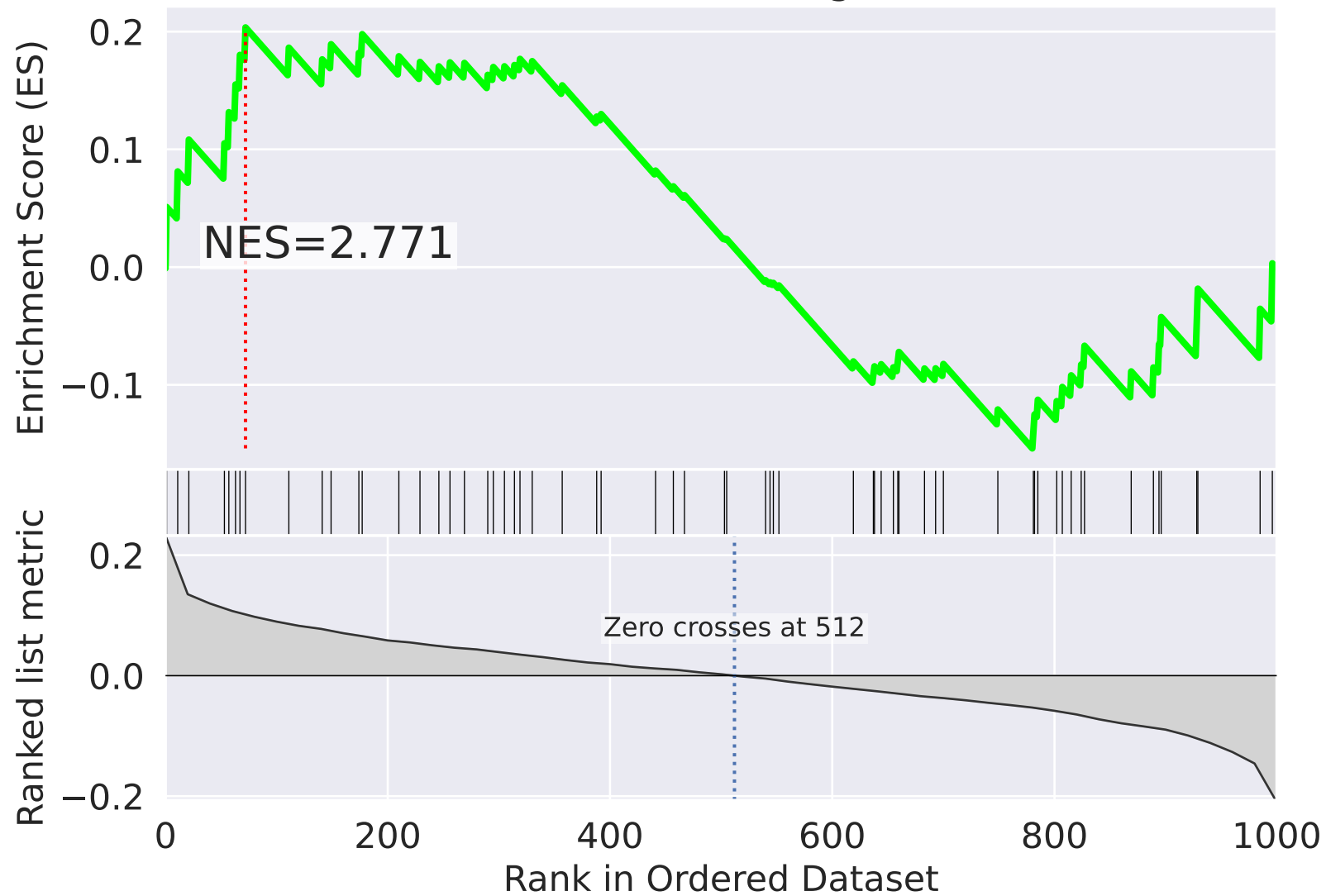
mitochondrial translational elongation (GO:0070125)



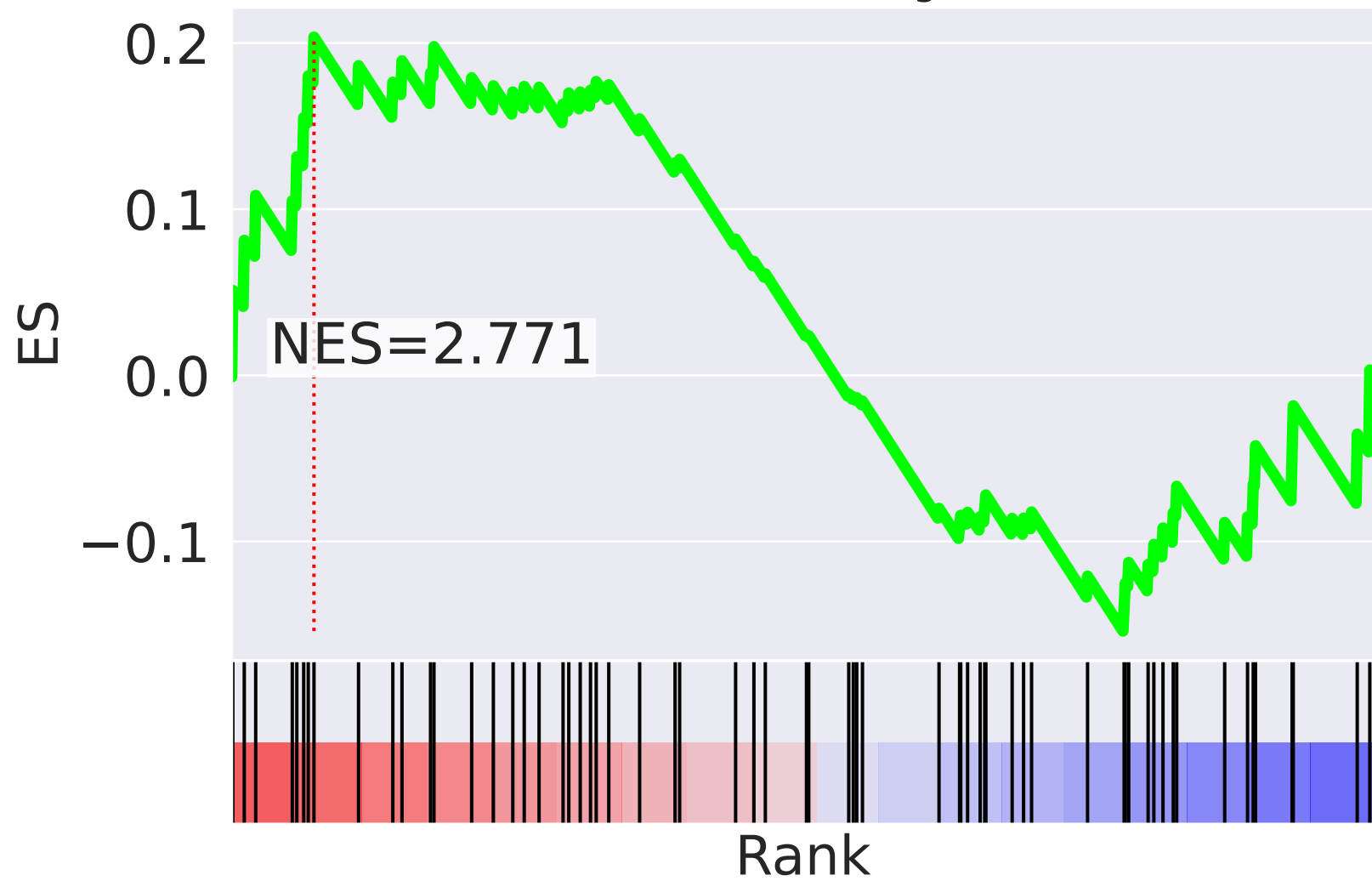
NES		SET
3.570		mitochondrial translational elongation (GO:0070125)
3.517		mitochondrial translational termination (GO:0070126)
-2.407		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.398		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.313		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.205		inflammatory response (GO:0006954)
-2.196		endocytosis (GO:0006897)
-2.142		IRE1-mediated unfolded protein response (GO:0036498)
-2.101		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.031		small molecule metabolic process (GO:0044281)
-2.021		sister chromatid cohesion (GO:0007062)
-2.021		rRNA processing (GO:0006364)
-2.017		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
1.994		transcription from mitochondrial promoter (GO:0006390)
-1.994		lipid metabolic process (GO:0006629)

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)

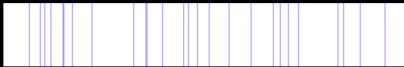
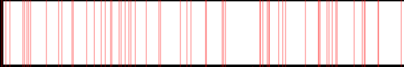
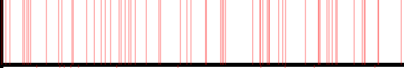







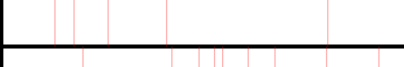
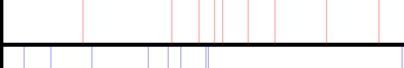


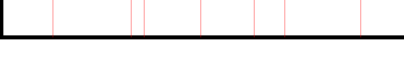


mitochondrial translational elongation (GO:0070125)



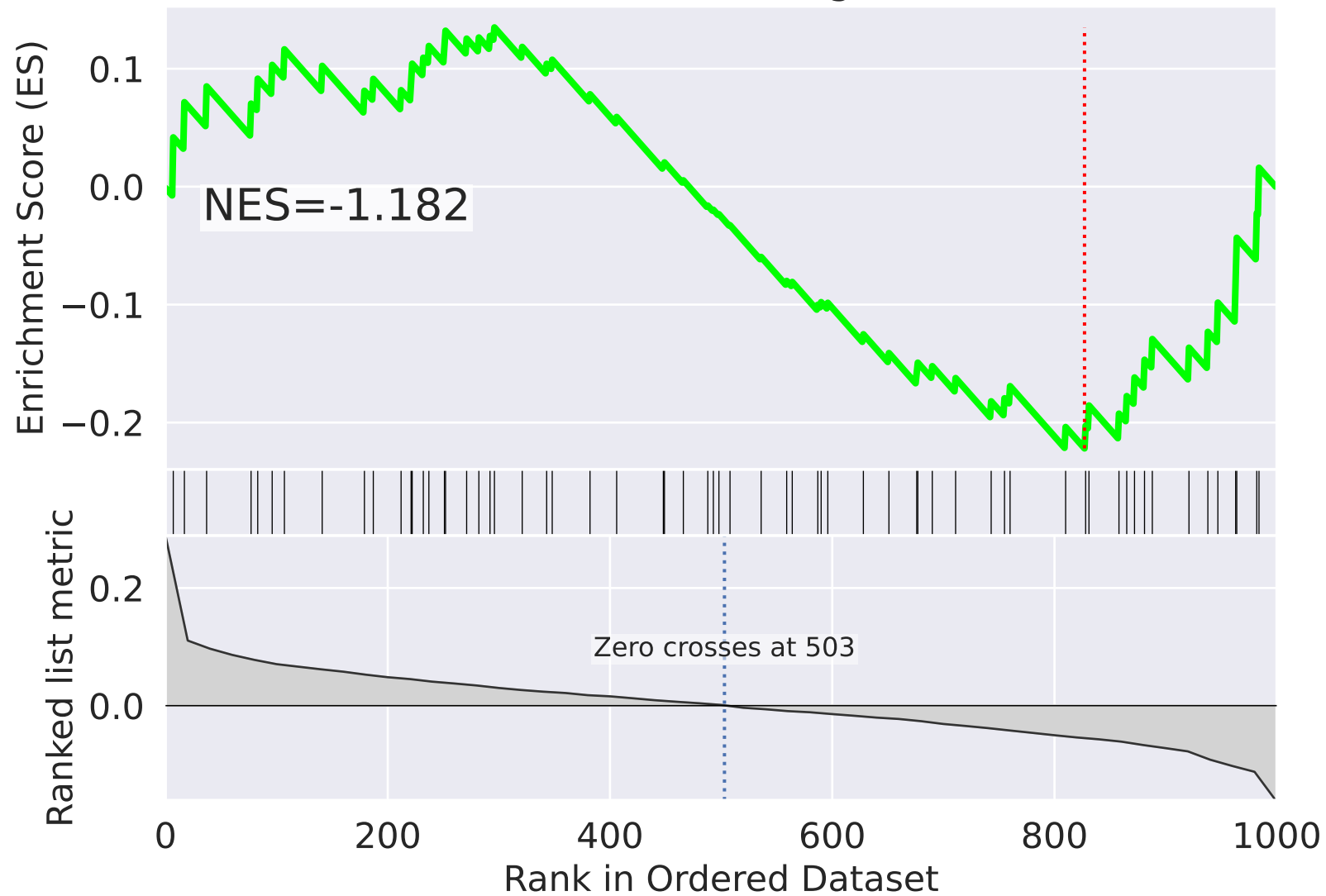
NES

SET

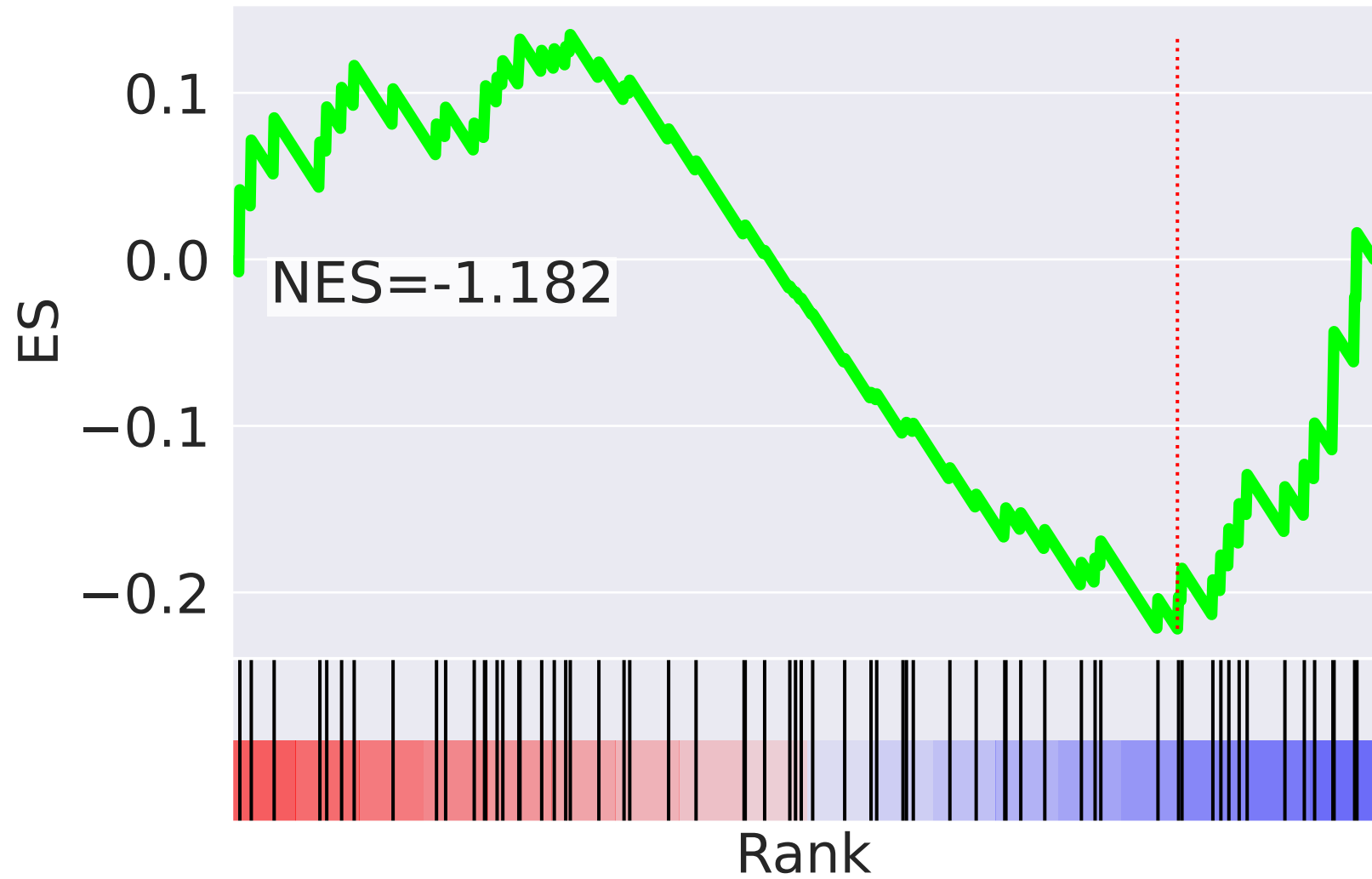
-2.850		protein deubiquitination (GO:0016579)
2.806		mitochondrial translational termination (GO:0070126)
2.771		mitochondrial translational elongation (GO:0070125)
2.465		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.389		rRNA processing (GO:0006364)
-2.369		mitotic nuclear envelope disassembly (GO:0007077)
2.368		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-2.273		regulation of cell motility (GO:2000145)
-2.269		nervous system development (GO:0007399)
2.251		transcription initiation from RNA polymerase II promoter (GO:0006367)
2.248		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.243		positive regulation of TOR signaling (GO:0032008)
-2.182		strand displacement (GO:0000732)
-2.169		apoptotic process (GO:0006915)
2.156		response to virus (GO:0009615)

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

mitochondrial translational elongation (GO:0070125)



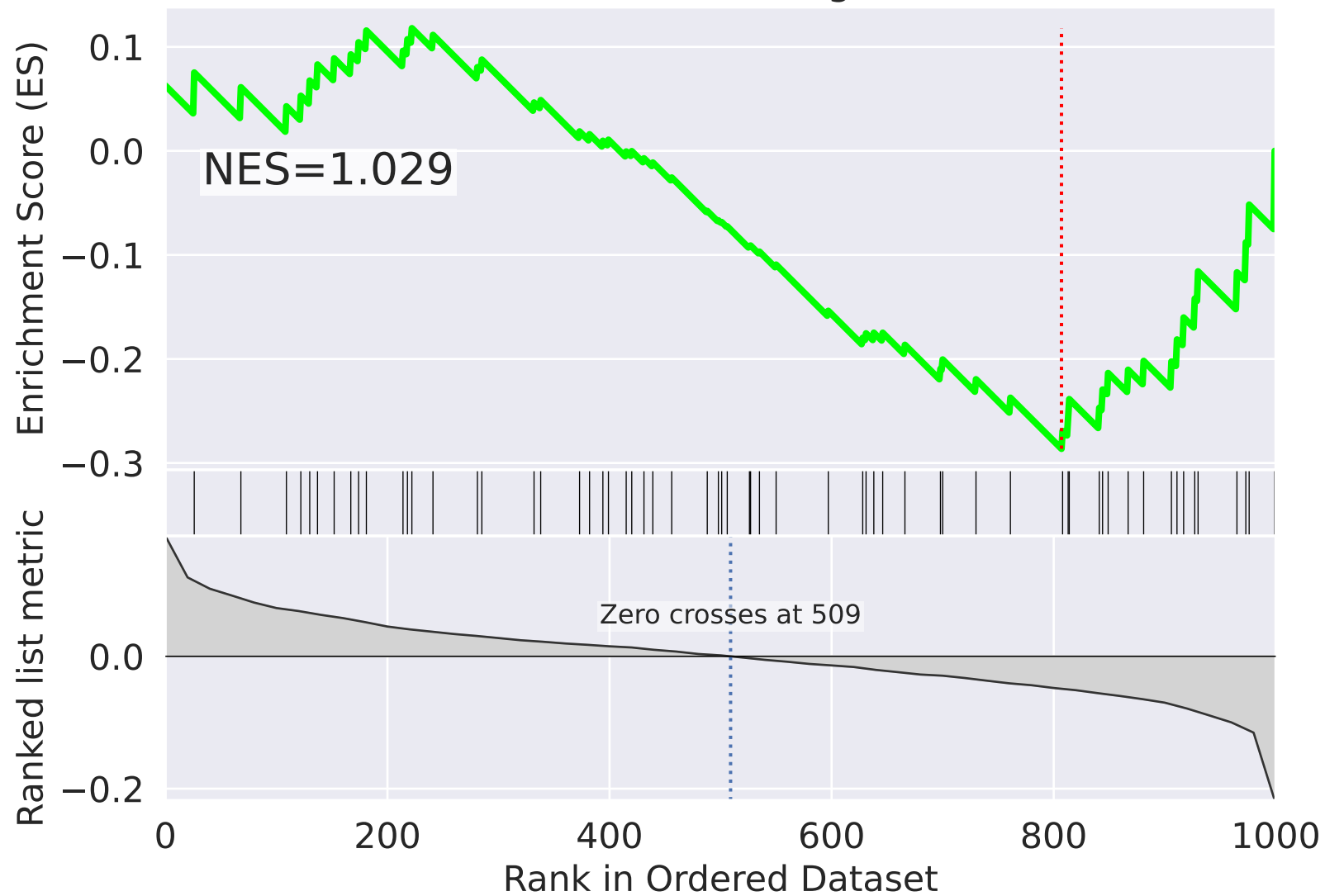
mitochondrial translational elongation (GO:0070125)



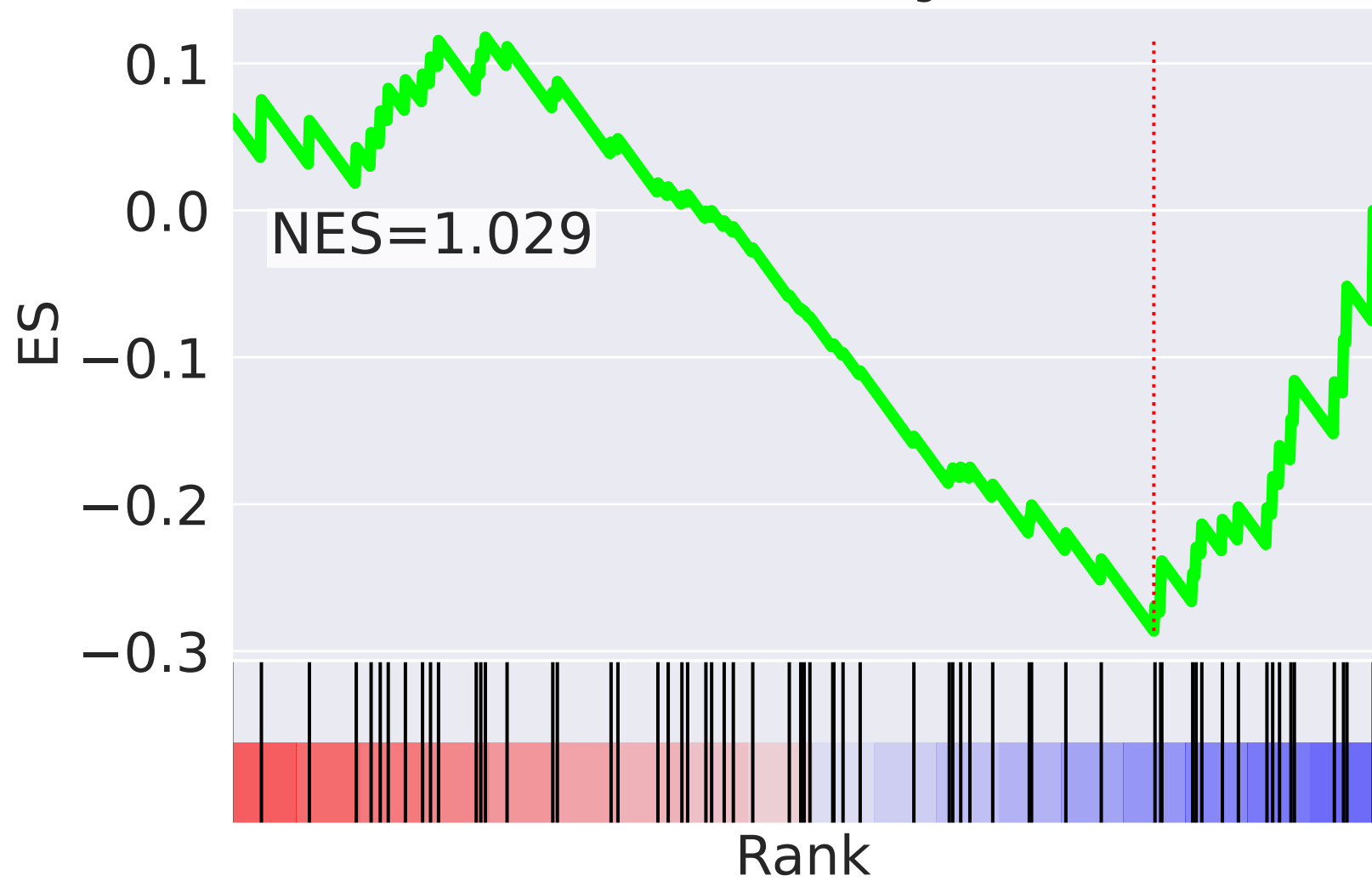
NES		SET
2.681		positive regulation of apoptotic process (GO:0043065)
-2.614		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.518		integrin-mediated signaling pathway (GO:0007229)
2.332		cell-matrix adhesion (GO:0007160)
2.275		cell migration (GO:0016477)
2.254		negative regulation of cell growth (GO:0030308)
2.239		small molecule metabolic process (GO:0044281)
-2.203		chromatin remodeling (GO:0006338)
2.112		telomere capping (GO:0016233)
-2.056		transcription from RNA polymerase II promoter (GO:0006366)
-2.024		positive regulation of viral genome replication (GO:0045070)
-2.016		positive regulation of gene expression (GO:0010628)
-2.002		positive regulation of protein ubiquitination (GO:0031398)
1.987		intracellular signal transduction (GO:0035556)
1.953		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)

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

mitochondrial translational elongation (GO:0070125)



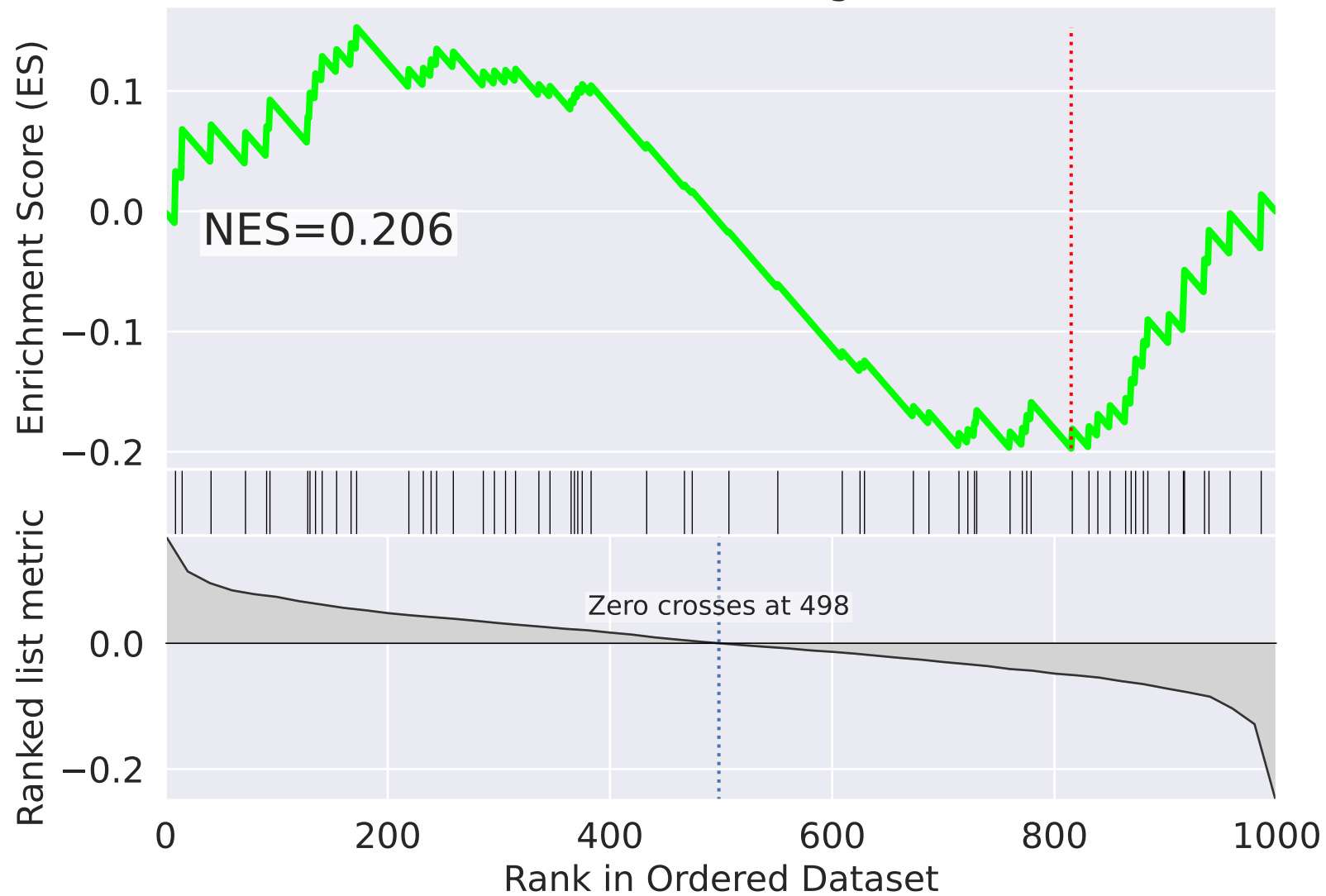
mitochondrial translational elongation (GO:0070125)



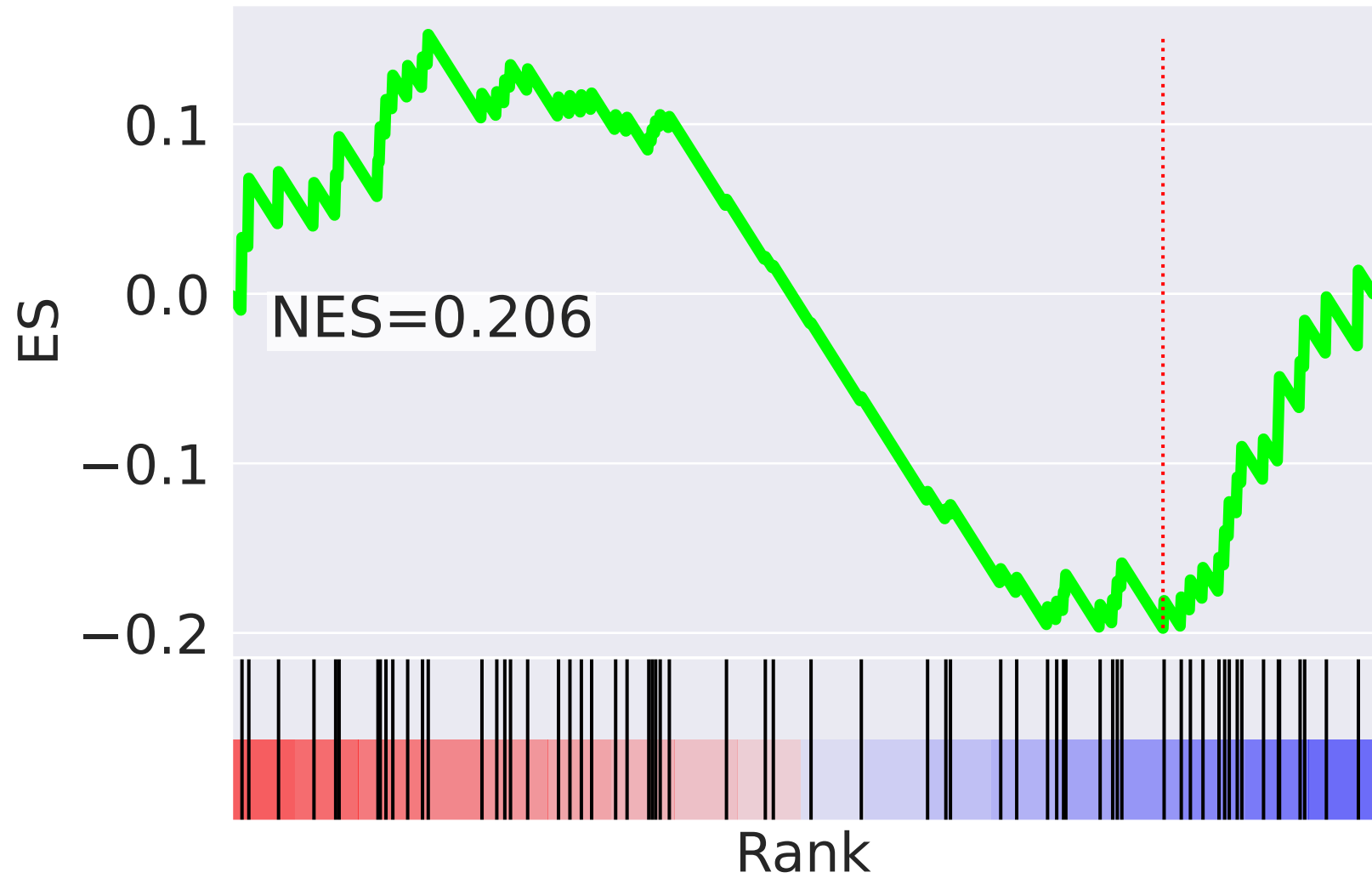
NES		SET
3.165		epidermal growth factor receptor signaling pathway (GO:0007173)
2.914		MAPK cascade (GO:0000165)
2.533		positive regulation of protein phosphorylation (GO:0001934)
2.520		sister chromatid cohesion (GO:0007062)
2.398		regulation of protein stability (GO:0031647)
2.381		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.377		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.361		tricarboxylic acid cycle (GO:0006099)
-2.345		protein N-linked glycosylation (GO:0006487)
-2.130		protein K48-linked ubiquitination (GO:0070936)
-2.117		nucleosome disassembly (GO:0006337)
-2.079		positive regulation by host of viral transcription (GO:0043923)
2.072		substrate adhesion-dependent cell spreading (GO:0034446)
2.059		positive regulation of apoptotic process (GO:0043065)
2.007		regulation of cell proliferation (GO:0042127)



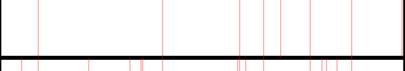
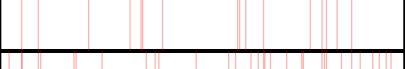
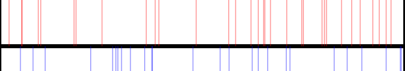





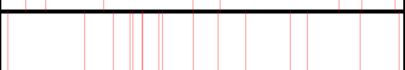

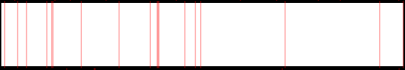


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=12$

mitochondrial translational elongation (GO:0070125)



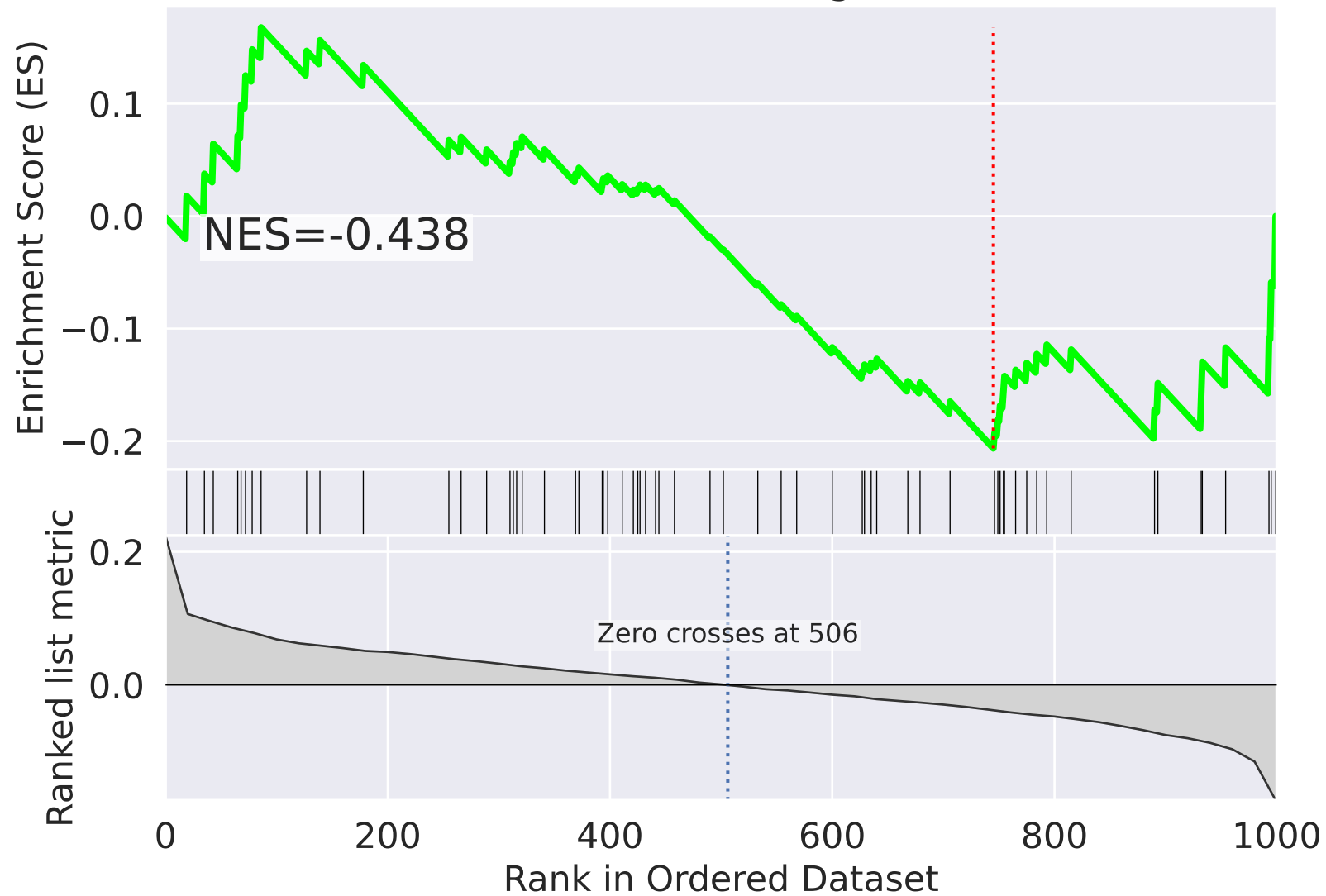
mitochondrial translational elongation (GO:0070125)



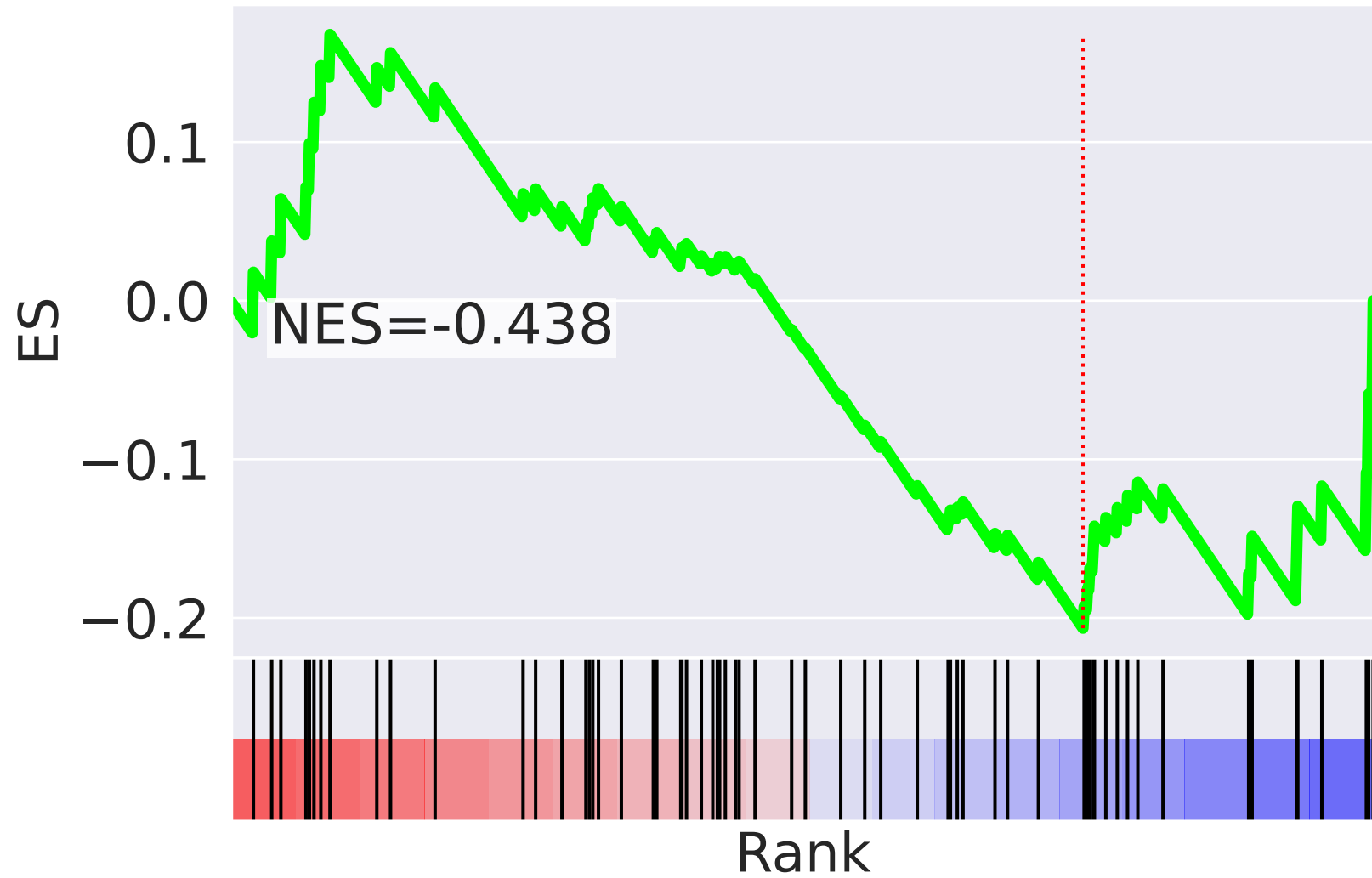
NES		SET
2.770		multicellular organism development (GO:0007275)
2.502		epidermal growth factor receptor signaling pathway (GO:0007173)
2.364		axon guidance (GO:0007411)
2.291		MAPK cascade (GO:0000165)
2.291		positive regulation of cell proliferation (GO:0008284)
-2.249		protein deubiquitination (GO:0016579)
-2.235		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.171		protein polyubiquitination (GO:0000209)
-2.140		ubiquitin-dependent protein catabolic process (GO:0006511)
2.123		ERBB2 signaling pathway (GO:0038128)
2.108		regulation of cell cycle (GO:0051726)
2.077		protein phosphorylation (GO:0006468)
2.000		multivesicular body assembly (GO:0036258)
1.973		G2/M transition of mitotic cell cycle (GO:0000086)
1.874		mitotic nuclear envelope disassembly (GO:0007077)





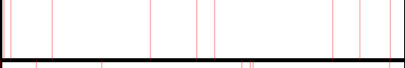
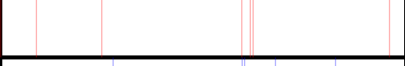




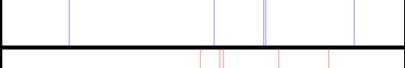
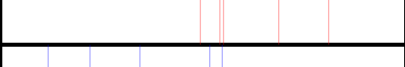


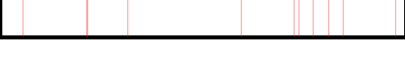
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=13$

mitochondrial translational elongation (GO:0070125)



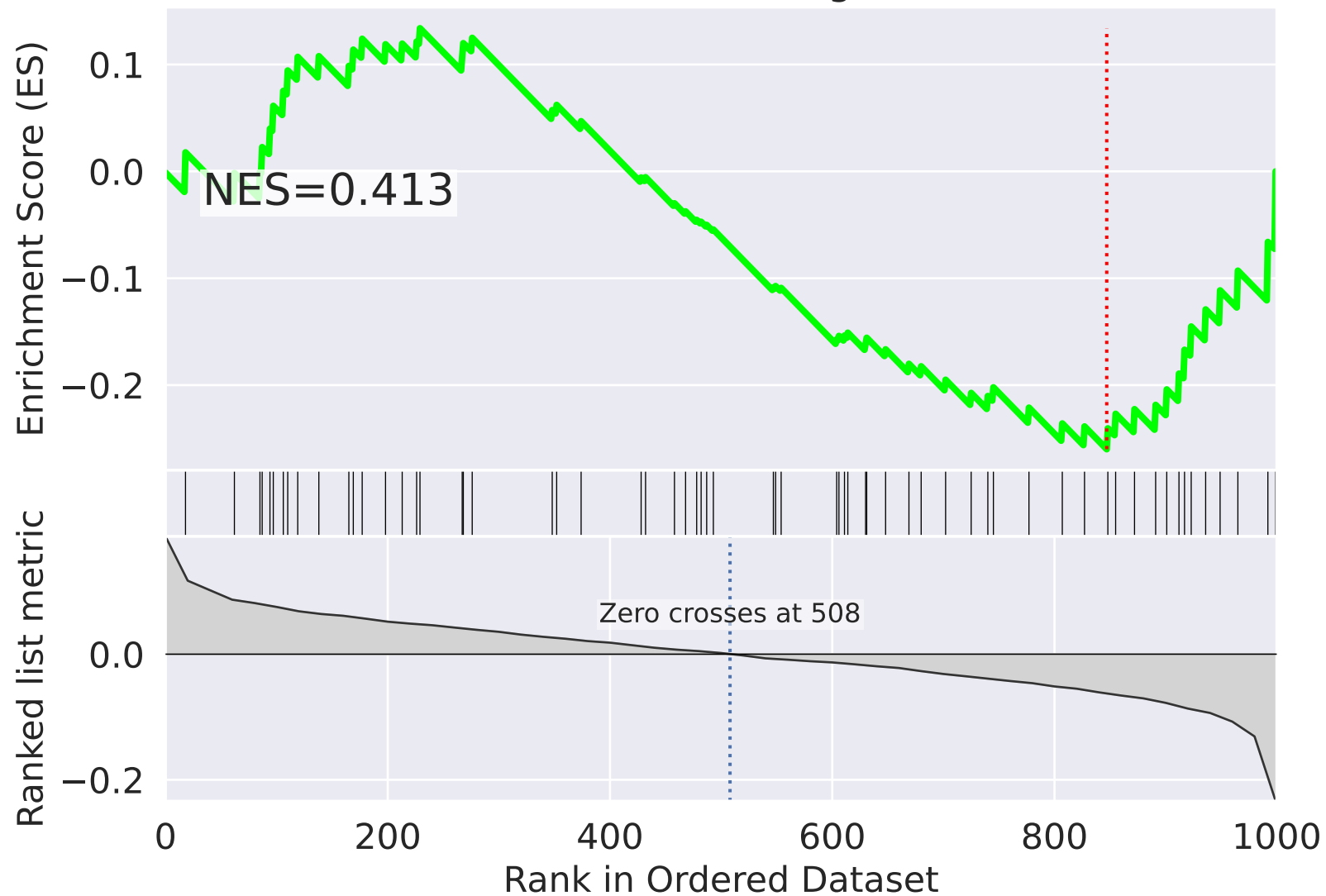
mitochondrial translational elongation (GO:0070125)



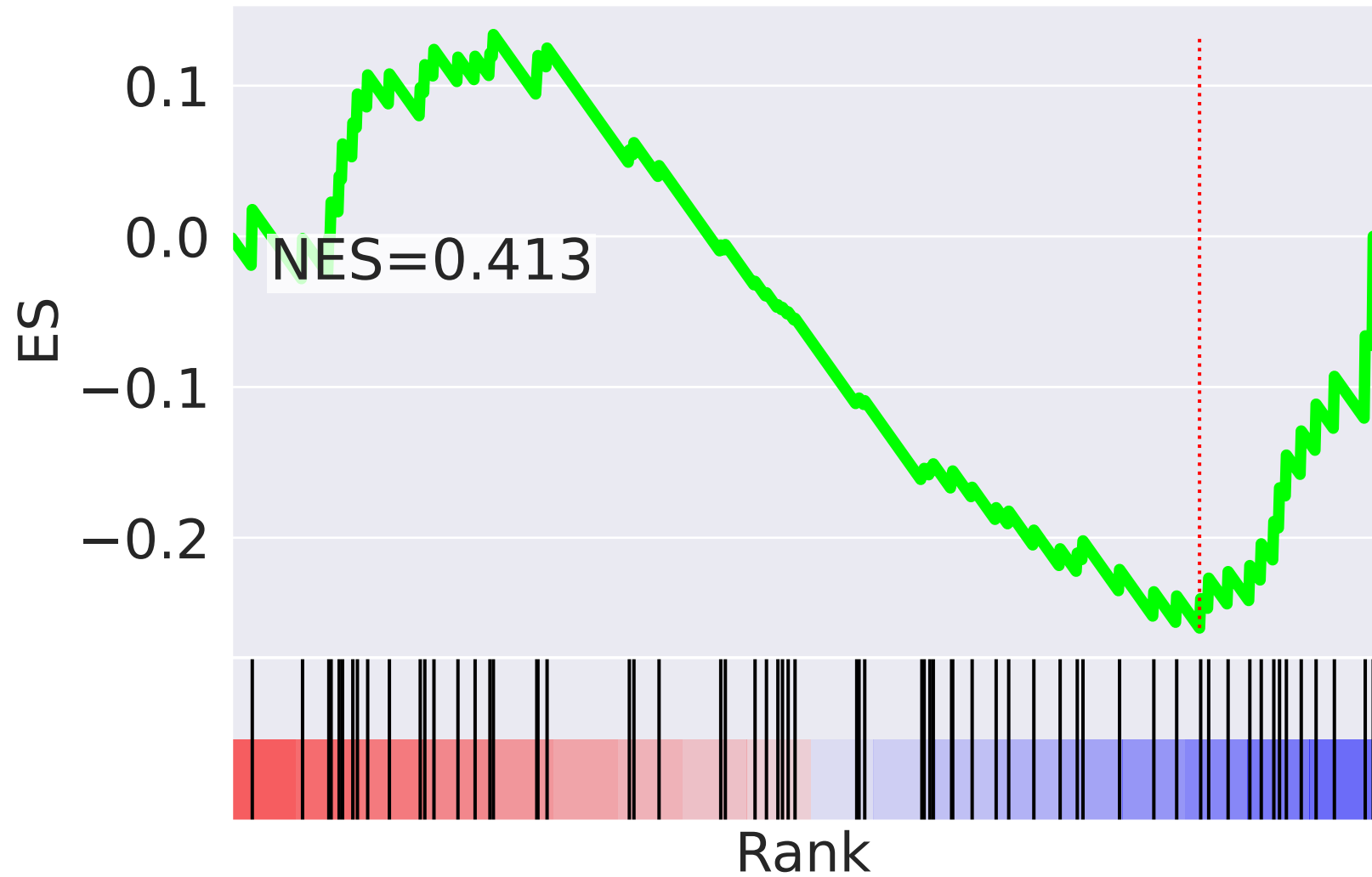
NES		SET
2.493		microtubule-based movement (GO:0007018)
2.387		mitotic metaphase plate congression (GO:0007080)
2.320		protein polyubiquitination (GO:0000209)
2.309		regulation of cellular response to heat (GO:1900034)
2.306		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.212		double-strand break repair (GO:0006302)
-2.174		regulation of cell growth (GO:0001558)
2.152		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-2.147		protein phosphorylation (GO:0006468)
-2.143		peptidyl-serine phosphorylation (GO:0018105)
-2.052		protein N-linked glycosylation (GO:0006487)
2.001		positive regulation by host of viral transcription (GO:0043923)
-1.991		lipid metabolic process (GO:0006629)
-1.973		peptidyl-threonine phosphorylation (GO:0018107)
1.872		snRNA transcription from RNA polymerase II promoter (GO:0042795)





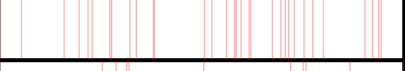


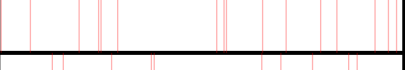

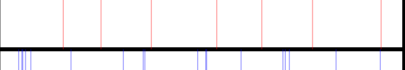
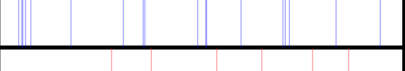
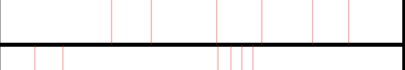
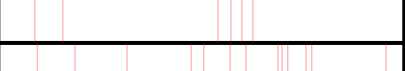


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=14$

mitochondrial translational elongation (GO:0070125)



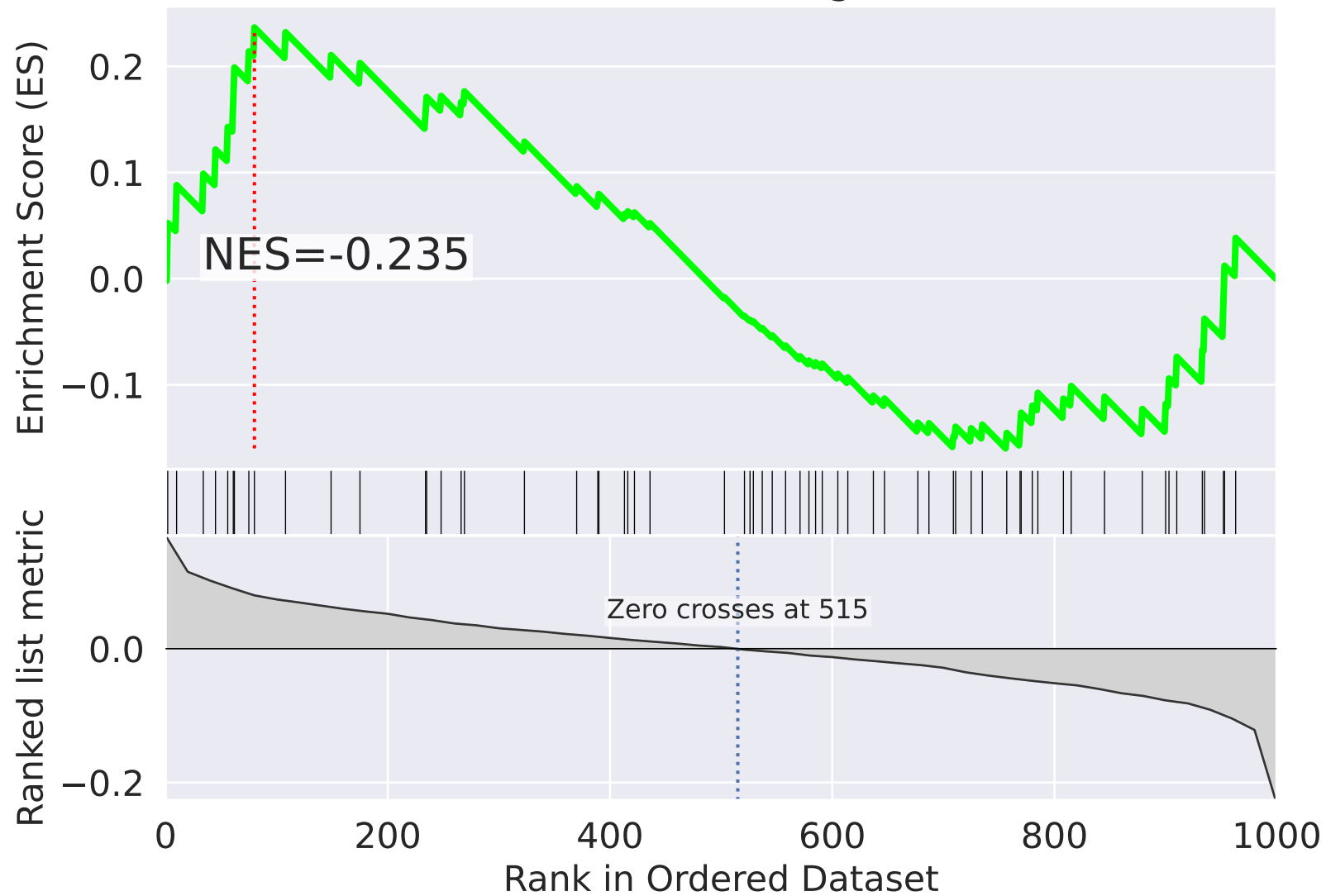
mitochondrial translational elongation (GO:0070125)



NES		SET
3.091		negative regulation of apoptotic process (GO:0043066)
2.701		double-strand break repair via nonhomologous end joining (GO:0006303)
2.669		Fc-epsilon receptor signaling pathway (GO:0038095)
2.668		axon guidance (GO:0007411)
2.634		positive regulation of cell proliferation (GO:0008284)
2.554		sister chromatid cohesion (GO:0007062)
2.482		apoptotic process (GO:0006915)
2.437		protein phosphorylation (GO:0006468)
2.427		epidermal growth factor receptor signaling pathway (GO:0007173)
2.399		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-2.332		transcription from RNA polymerase II promoter (GO:0006366)
2.289		ERBB2 signaling pathway (GO:0038128)
2.250		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.234		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.209		positive regulation of gene expression (GO:0010628)

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)



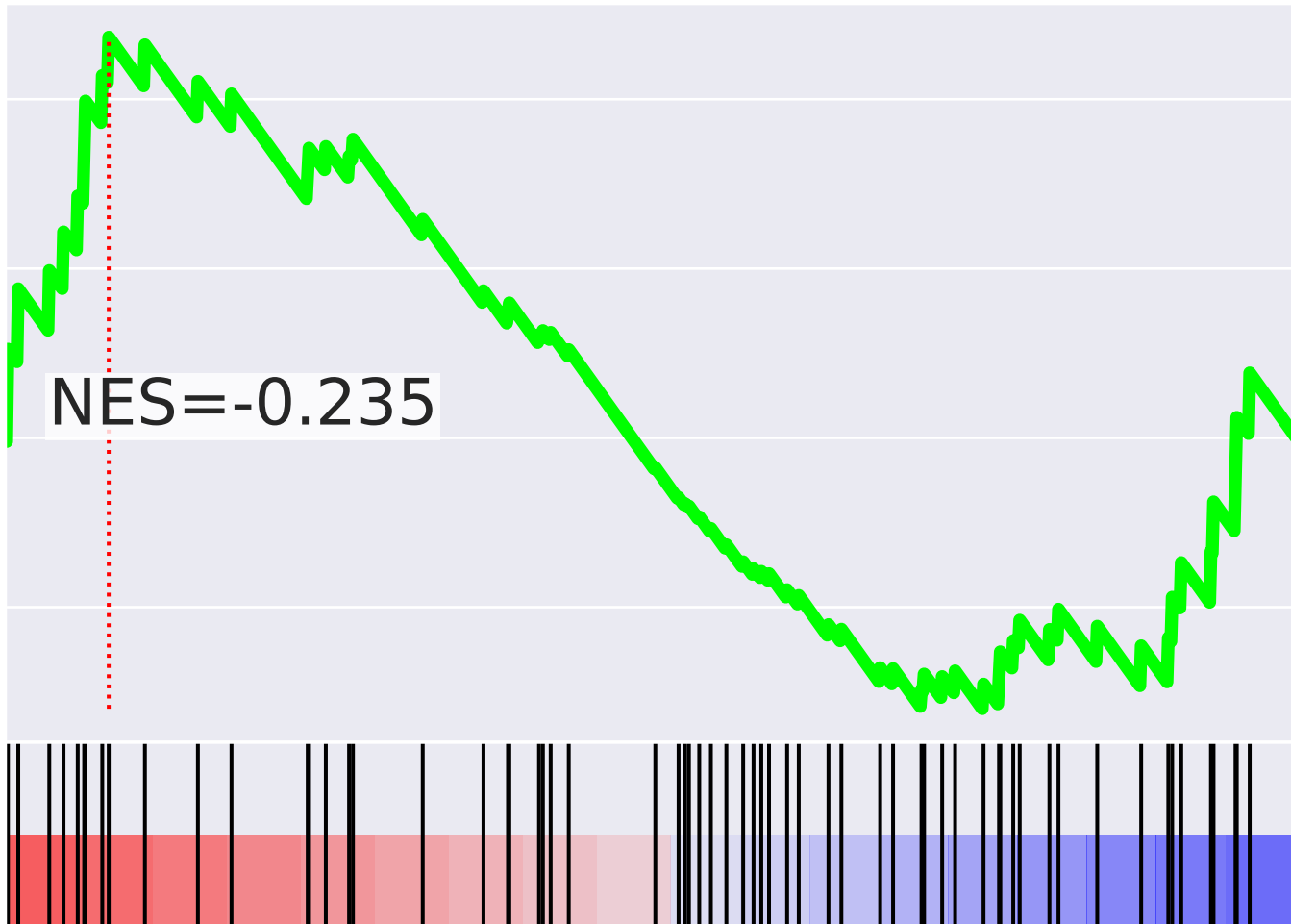
mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1



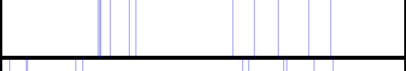



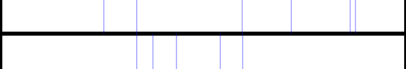

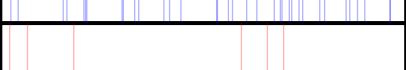


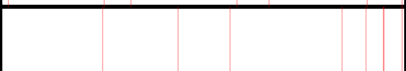



NES=-0.235

Rank



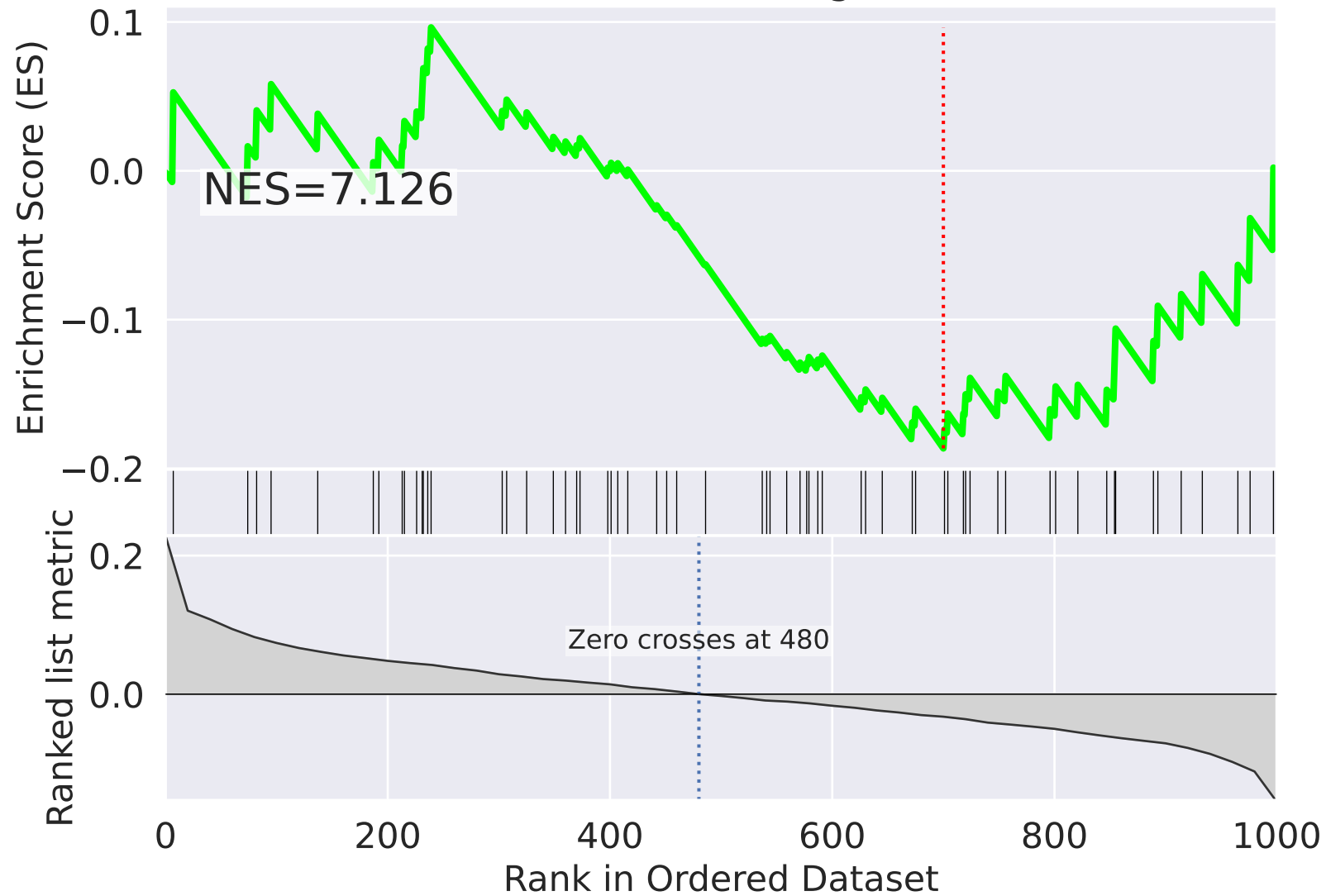
NES

SET

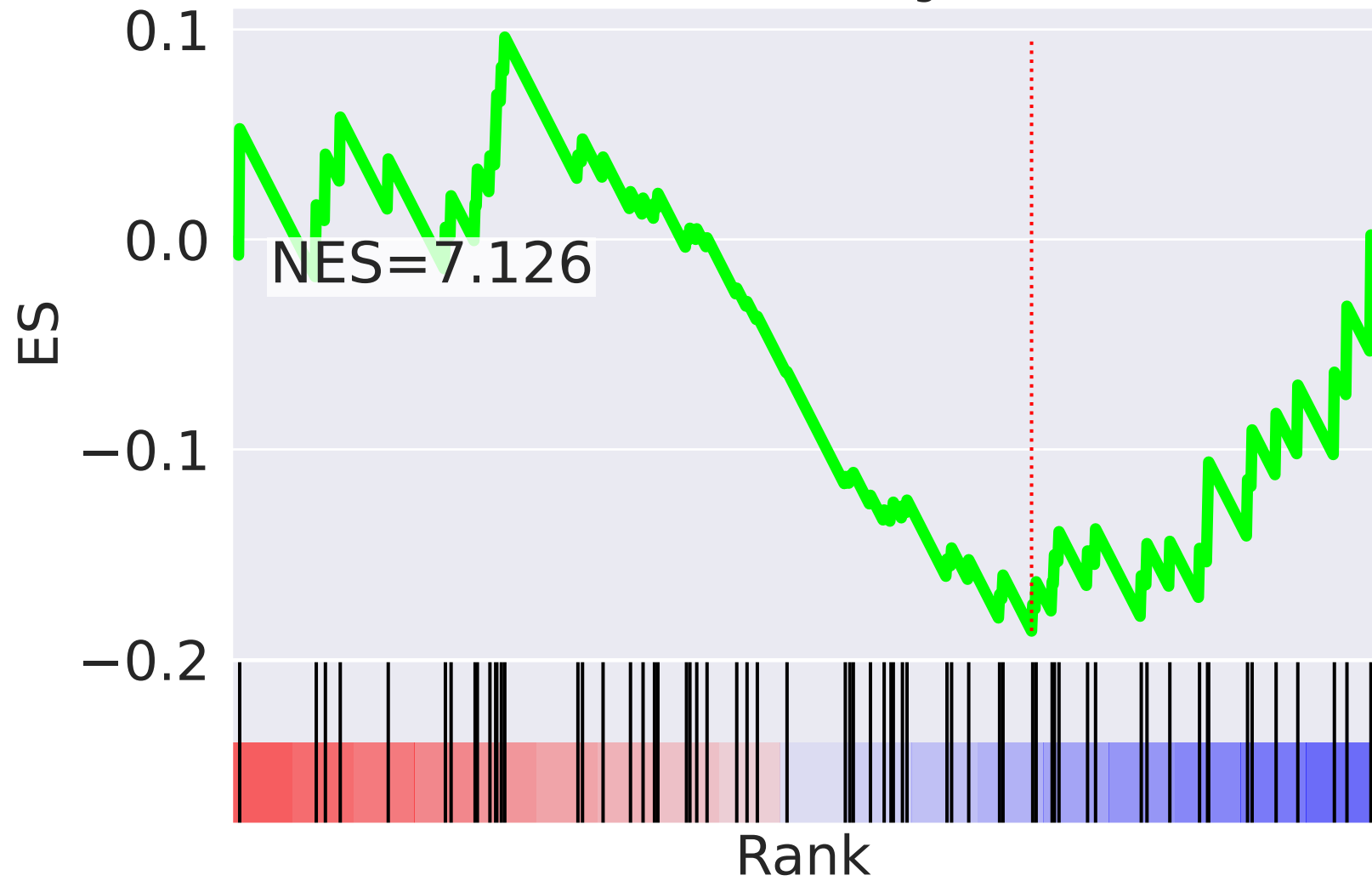
-2.894		positive regulation of transcription, DNA-templated (GO:0045893)
-2.415		protein ubiquitination (GO:0016567)
-2.379		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.241		positive regulation of protein phosphorylation (GO:0001934)
2.240		leukocyte migration (GO:0050900)
-2.218		positive regulation of gene expression (GO:0010628)
-2.004		cellular response to amino acid starvation (GO:0034198)
-1.913		ERK1 and ERK2 cascade (GO:0070371)
-1.825		mitochondrial respiratory chain complex I assembly (GO:0032981)
1.798		ERBB2 signaling pathway (GO:0038128)
1.761		response to endoplasmic reticulum stress (GO:0034976)
1.749		cytokinesis (GO:0000910)
1.744		vesicle-mediated transport (GO:0016192)
-1.743		negative regulation of cell cycle arrest (GO:0071157)
-1.736		histone H3-K4 methylation (GO:0051568)

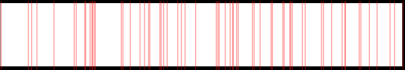
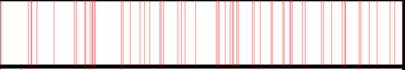

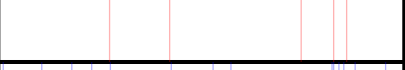

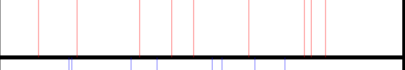


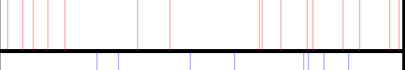

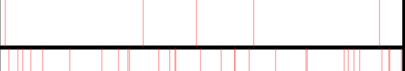
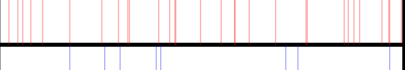
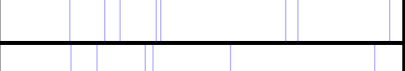
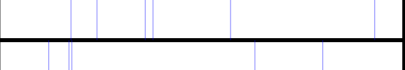
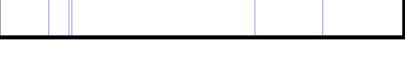
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=16$

mitochondrial translational elongation (GO:0070125)



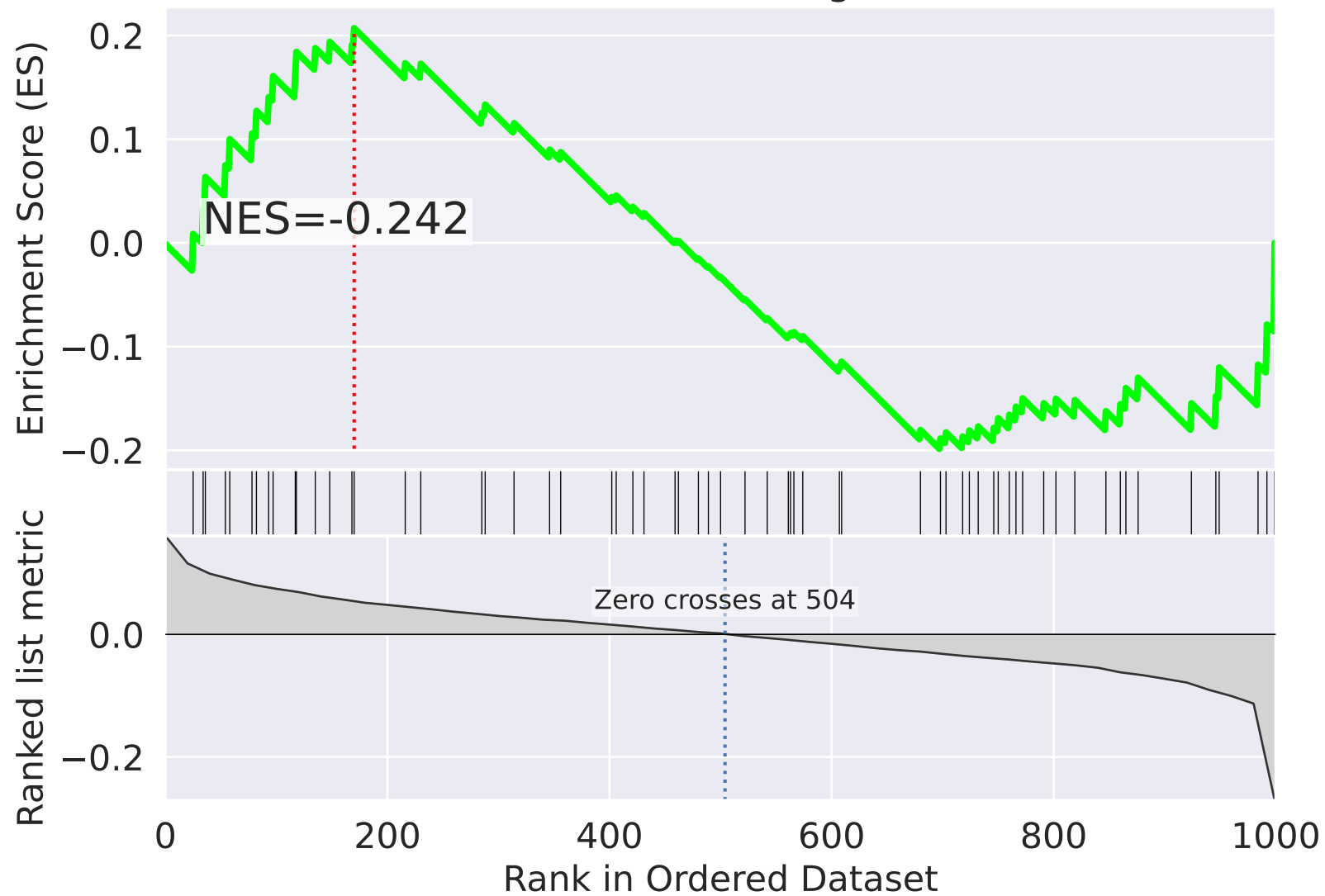
mitochondrial translational elongation (GO:0070125)



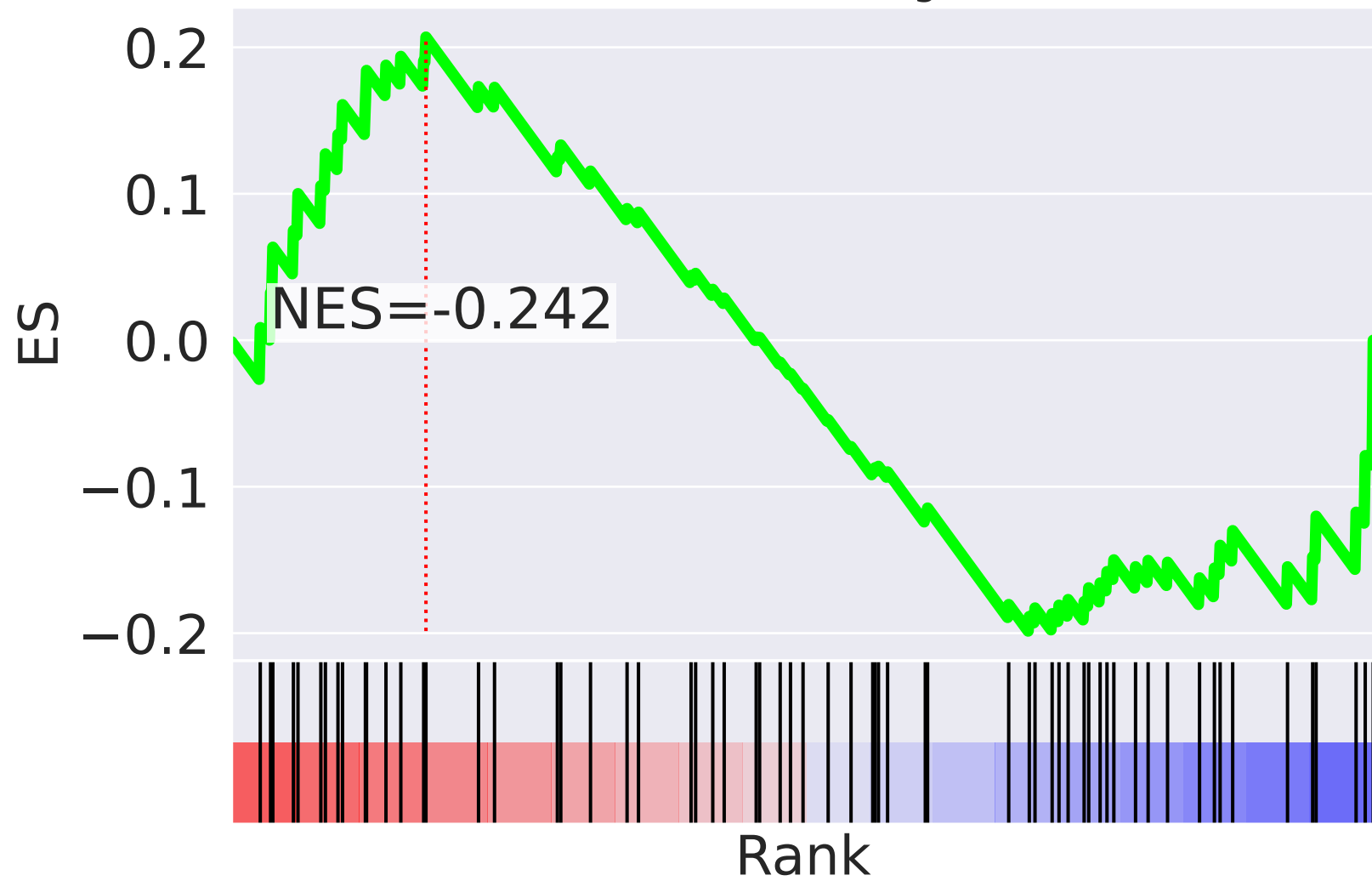
NES		SET
7.126		mitochondrial translational elongation (GO:0070125)
6.961		mitochondrial translational termination (GO:0070126)
2.610		transcription from mitochondrial promoter (GO:0006390)
2.569		telomere maintenance via telomerase (GO:0007004)
-2.456		DNA repair (GO:0006281)
2.358		tRNA aminoacylation for protein translation (GO:0006418)
-2.306		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
2.225		cellular response to amino acid stimulus (GO:0071230)
2.139		cell cycle arrest (GO:0007050)
-2.079		ciliary basal body docking (GO:0097711)
2.058		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.015		neutrophil degranulation (GO:0043312)
-2.012		intracellular signal transduction (GO:0035556)
-2.002		IRE1-mediated unfolded protein response (GO:0036498)
-1.974		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 $z=17$

mitochondrial translational elongation (GO:0070125)



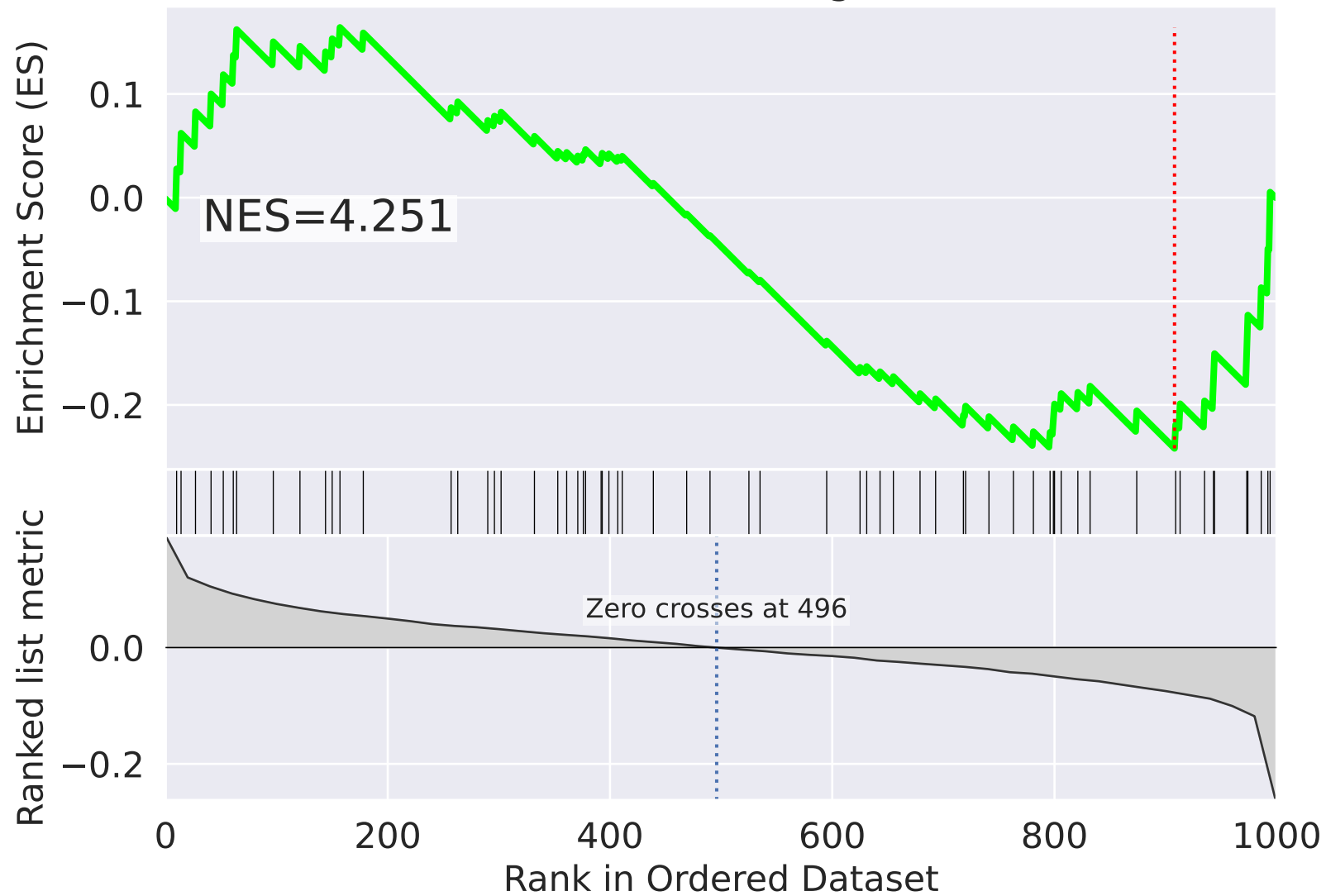
mitochondrial translational elongation (GO:0070125)



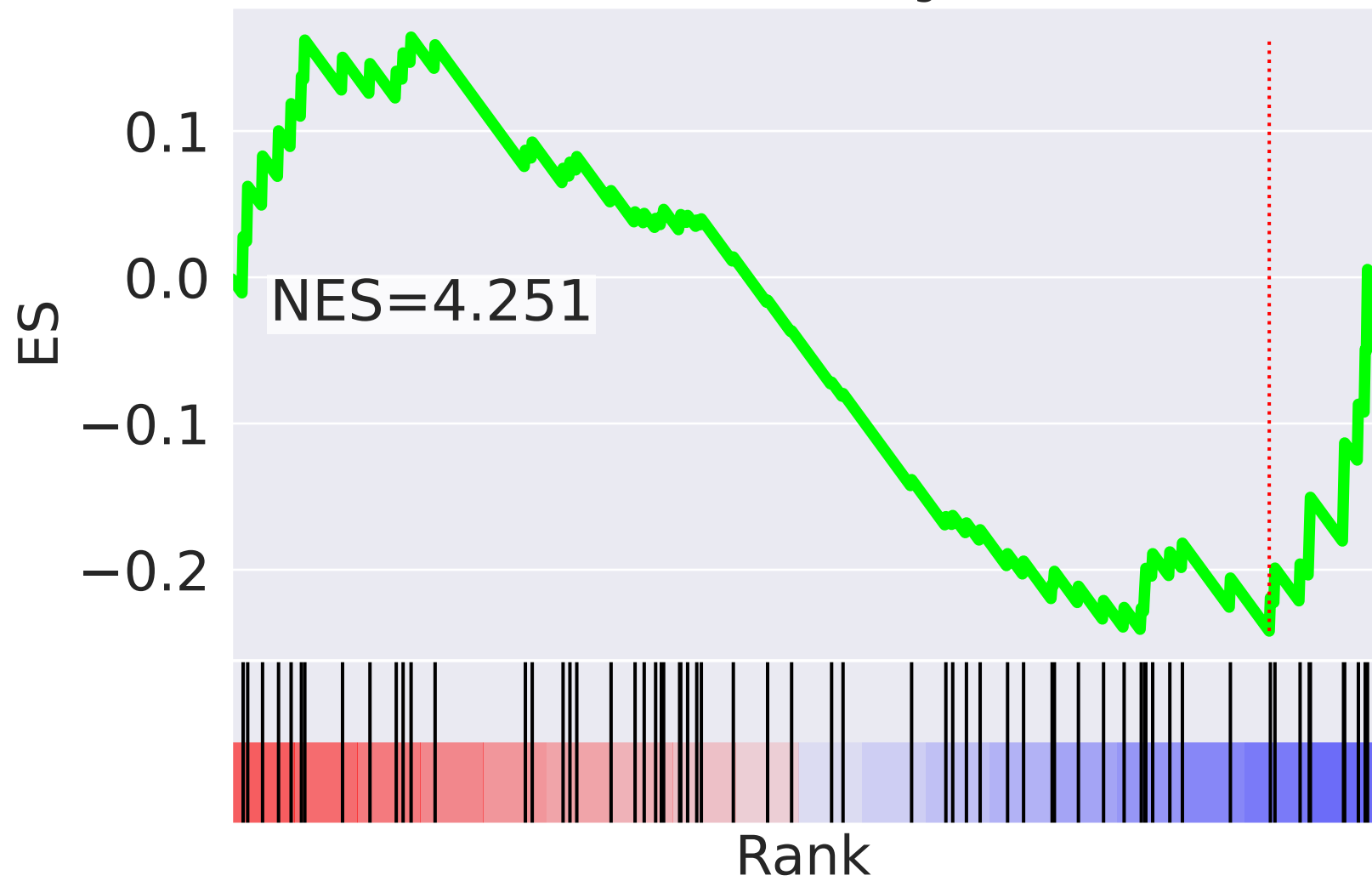
NES		SET
2.696		regulation of cell proliferation (GO:0042127)
2.673		negative regulation of cell cycle arrest (GO:0071157)
2.623		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.573		protein autophosphorylation (GO:0046777)
2.378		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.307		epidermal growth factor receptor signaling pathway (GO:0007173)
2.301		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.261		positive regulation of cell proliferation (GO:0008284)
-2.234		protein stabilization (GO:0050821)
2.190		protein phosphorylation (GO:0006468)
-2.172		cell cycle arrest (GO:0007050)
2.160		Ras protein signal transduction (GO:0007265)
-2.062		protein N-linked glycosylation (GO:0006487)
2.061		Wnt signaling pathway (GO:0016055)
-2.027		ubiquitin-dependent ERAD pathway (GO:0030433)

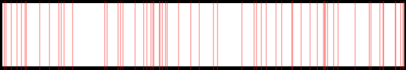
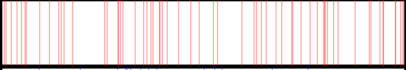
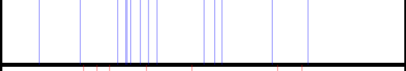
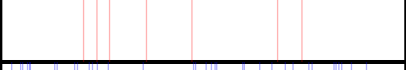
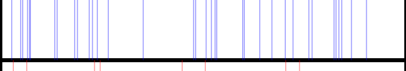
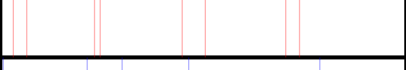
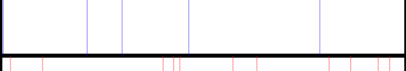
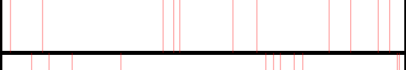
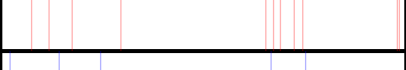


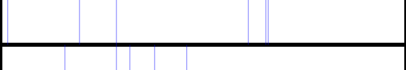



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=18$

mitochondrial translational elongation (GO:0070125)



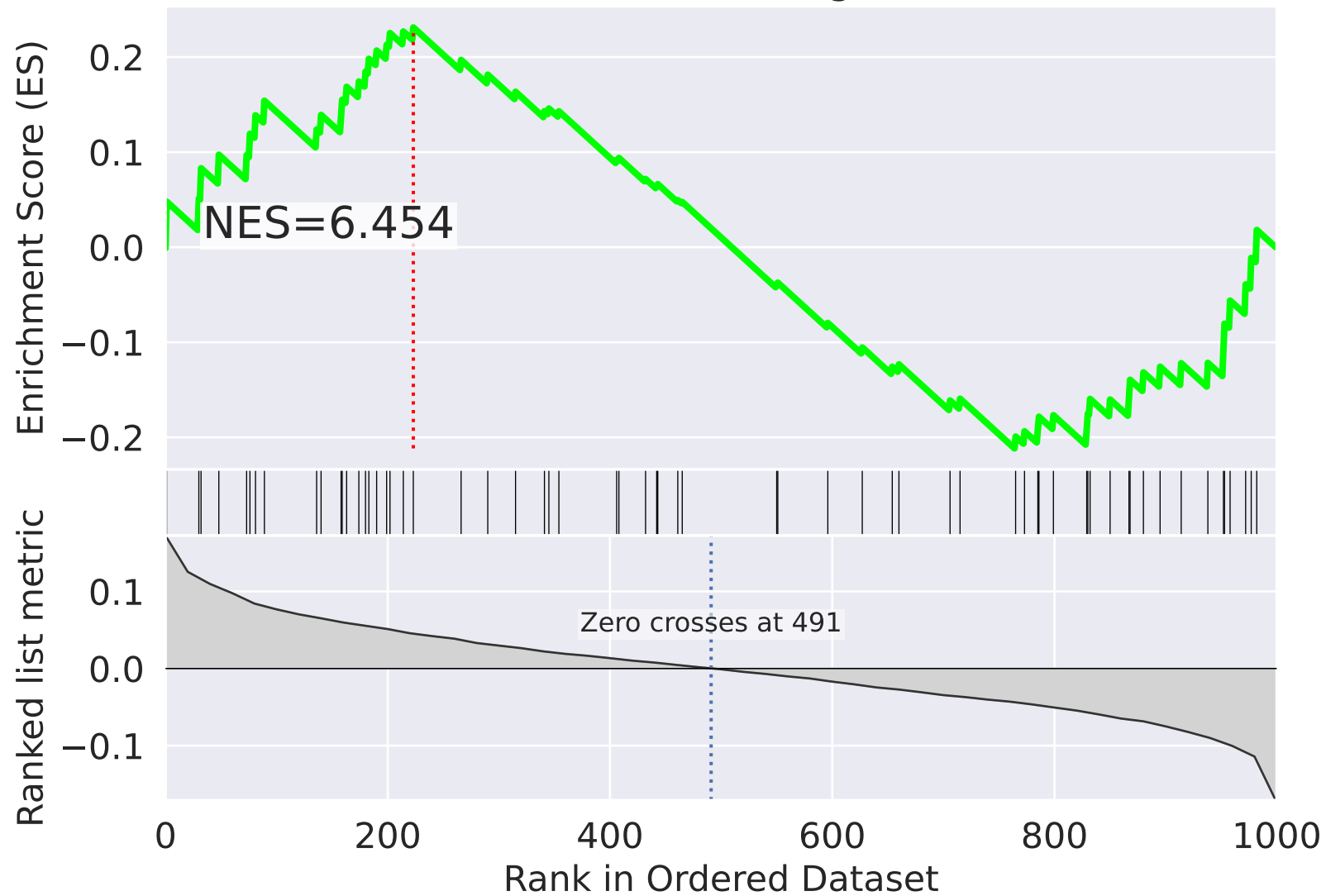
mitochondrial translational elongation (GO:0070125)



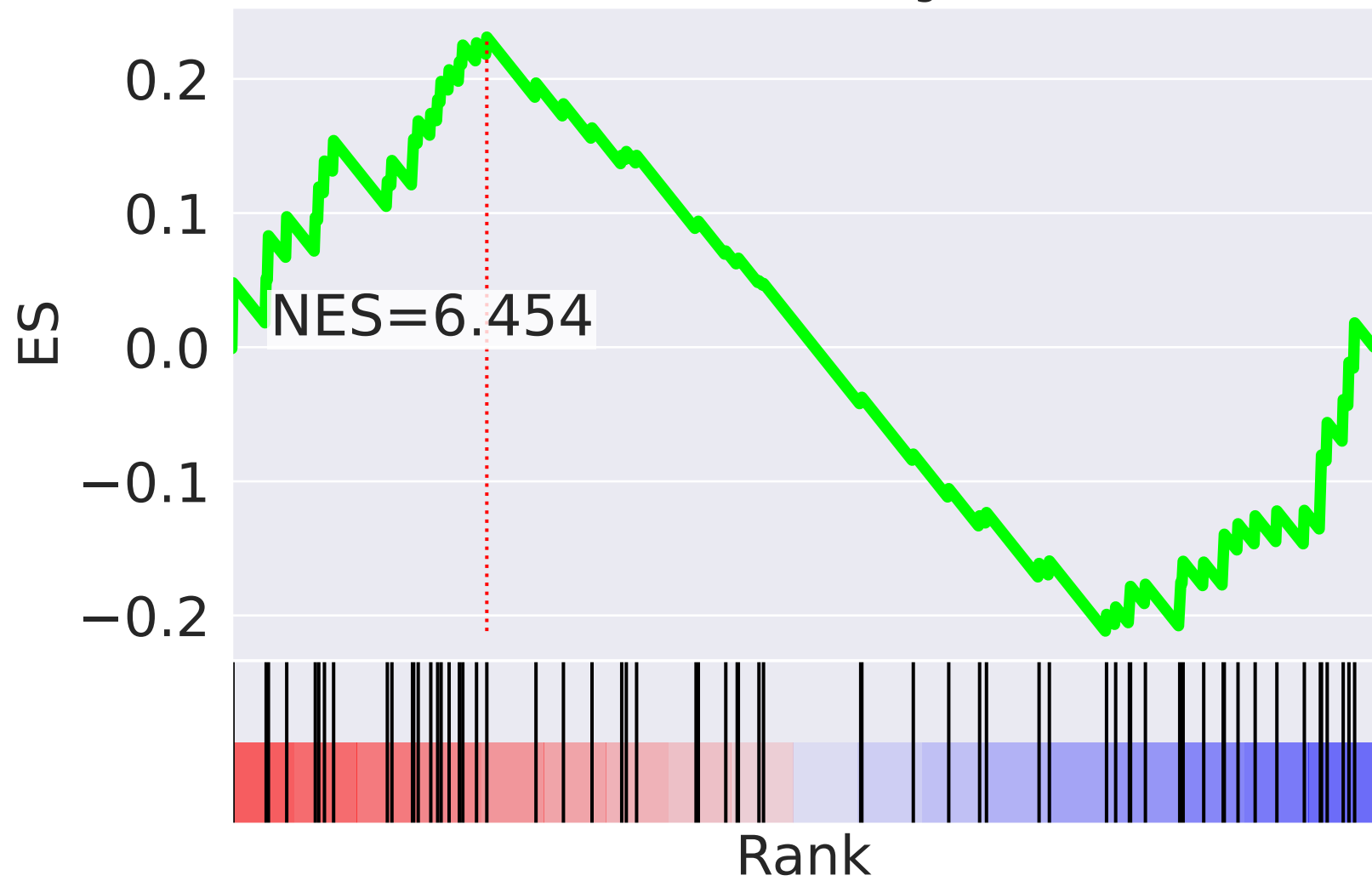
NES		SET
4.251		mitochondrial translational elongation (GO:0070125)
3.531		mitochondrial translational termination (GO:0070126)
-2.802		DNA repair (GO:0006281)
2.427		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.400		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.374		intracellular signal transduction (GO:0035556)
-2.357		protein N-linked glycosylation (GO:0006487)
2.309		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.269		positive regulation of gene expression (GO:0010628)
-2.267		lipid metabolic process (GO:0006629)
-2.170		double-strand break repair via homologous recombination (GO:0000724)
-2.062		protein autoubiquitination (GO:0051865)
-2.056		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
1.929		response to endoplasmic reticulum stress (GO:0034976)
-1.903		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 $z=19$

mitochondrial translational elongation (GO:0070125)

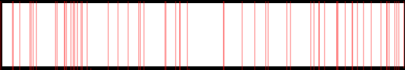
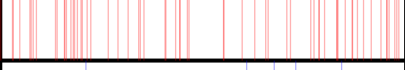
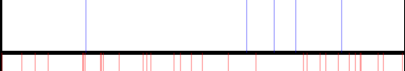
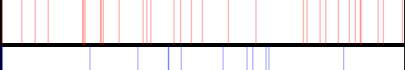

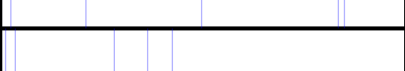

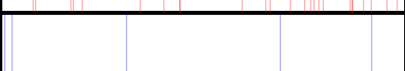

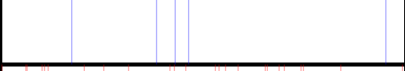
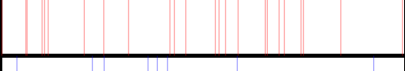






mitochondrial translational elongation (GO:0070125)



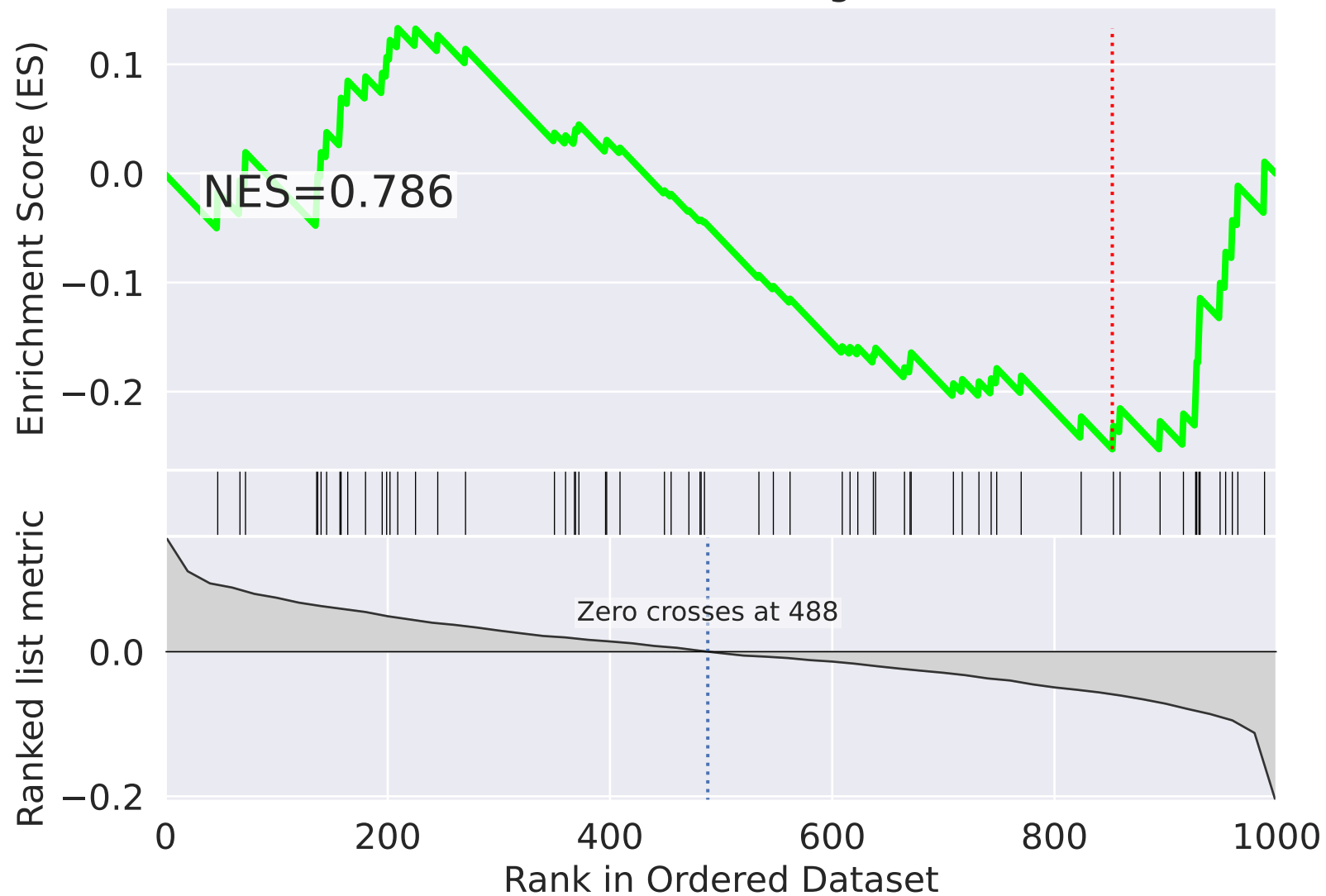
NES

SET

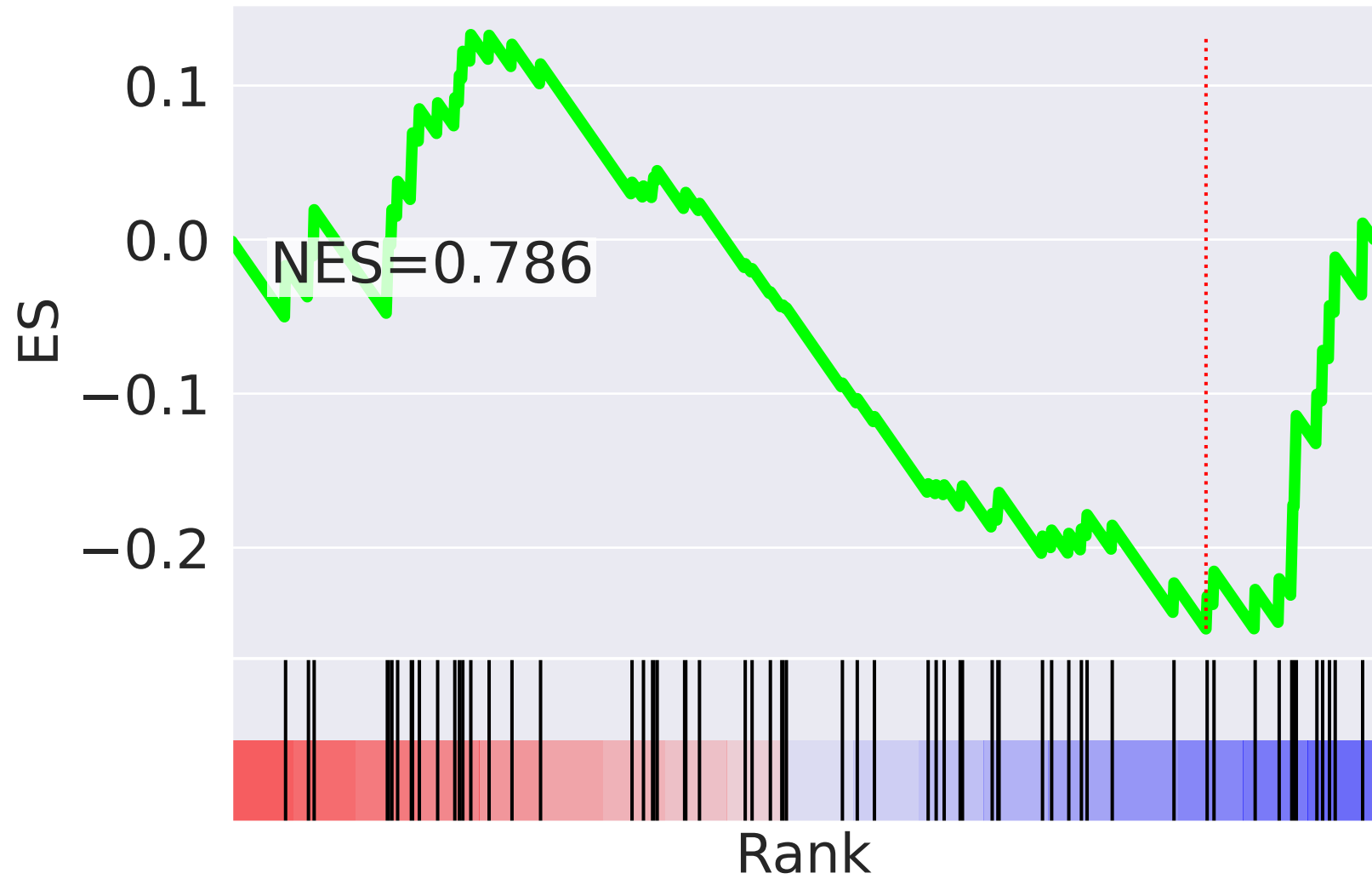
6.471		mitochondrial translational termination (GO:0070126)
6.454		mitochondrial translational elongation (GO:0070125)
-2.362		positive regulation of viral genome replication (GO:0045070)
2.343		positive regulation of cell proliferation (GO:0008284)
-2.197		macroautophagy (GO:0016236)
-2.151		regulation of cell motility (GO:2000145)
-2.088		positive regulation of protein catabolic process (GO:0045732)
2.017		mitochondrial translation (GO:0032543)
-1.987		mitochondrial respiratory chain complex IV assembly (GO:0033617)
1.930		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-1.913		nucleobase-containing small molecule interconversion (GO:0015949)
1.859		regulation of transcription, DNA-templated (GO:0006355)
-1.849		response to ionizing radiation (GO:0010212)
-1.845		intracellular signal transduction (GO:0035556)
1.836		positive regulation of TOR signaling (GO:0032008)

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)





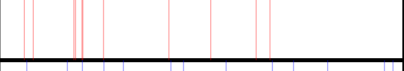
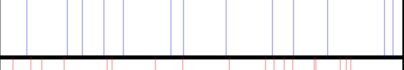


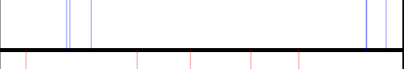




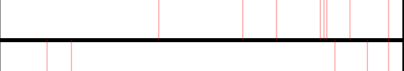
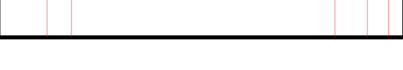


mitochondrial translational elongation (GO:0070125)



NES

SET

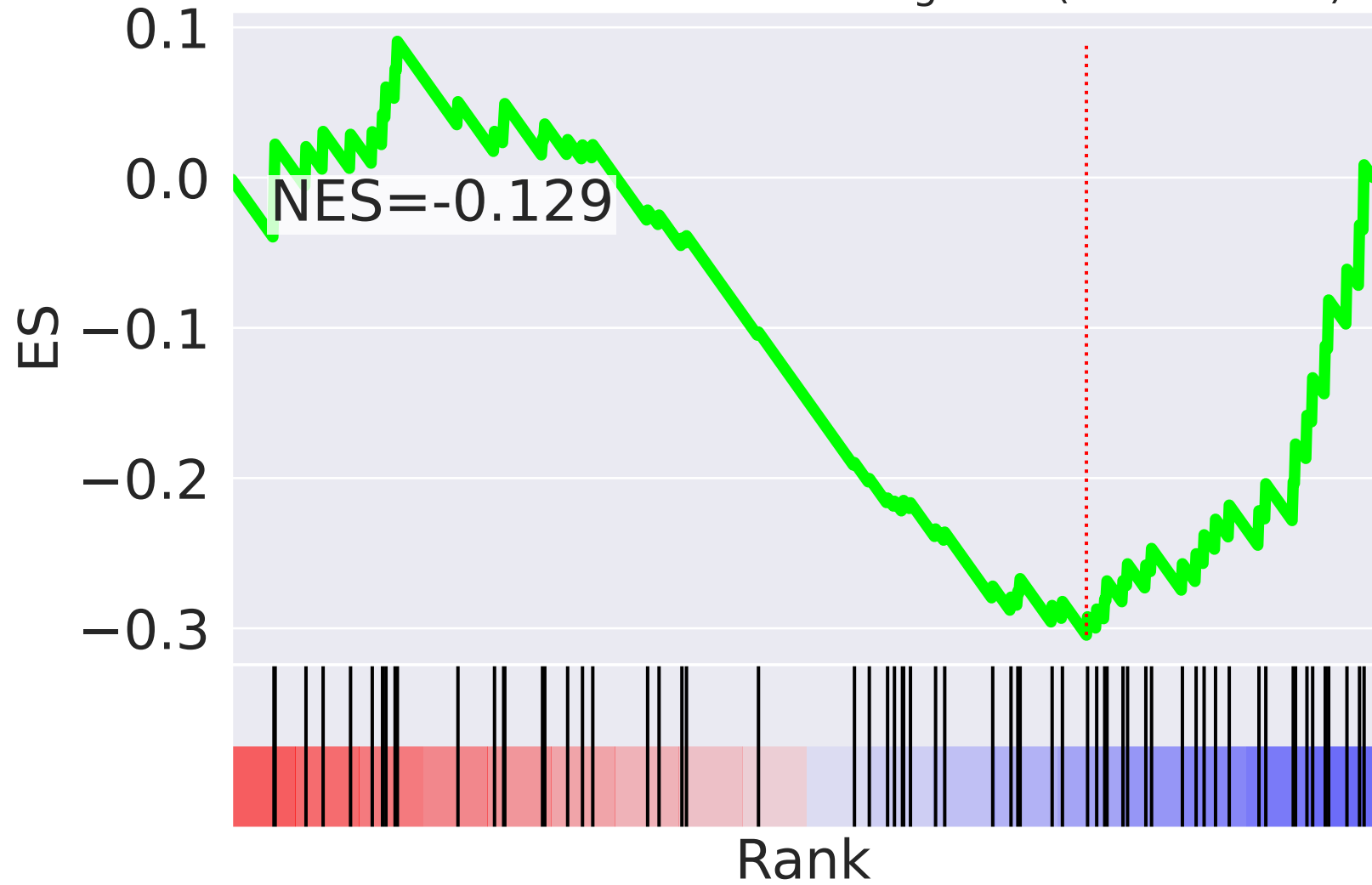
-2.398		transcription-coupled nucleotide-excision repair (GO:0006283)
2.263		ciliary basal body docking (GO:0097711)
2.187		MAPK cascade (GO:0000165)
2.186		DNA damage response, detection of DNA damage (GO:0042769)
2.048		COPII vesicle coating (GO:0048208)
-2.004		histone H3 acetylation (GO:0043966)
1.919		G2/M transition of mitotic cell cycle (GO:0000086)
1.916		inflammatory response (GO:0006954)
-1.880		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
1.858		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
1.839		chromosome segregation (GO:0007059)
-1.793		nucleosome disassembly (GO:0006337)
-1.786		rRNA processing (GO:0006364)
1.717		protein homooligomerization (GO:0051260)
1.671		transcription from mitochondrial promoter (GO:0006390)




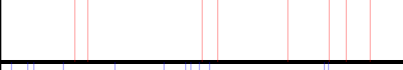
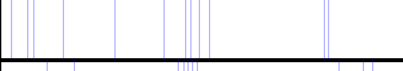
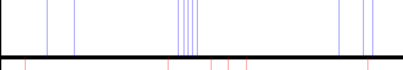




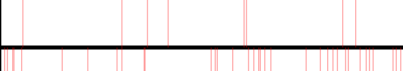
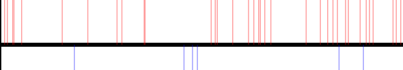
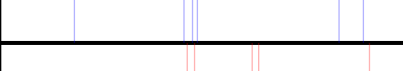


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=21$

mitochondrial translational elongation (GO:0070125)



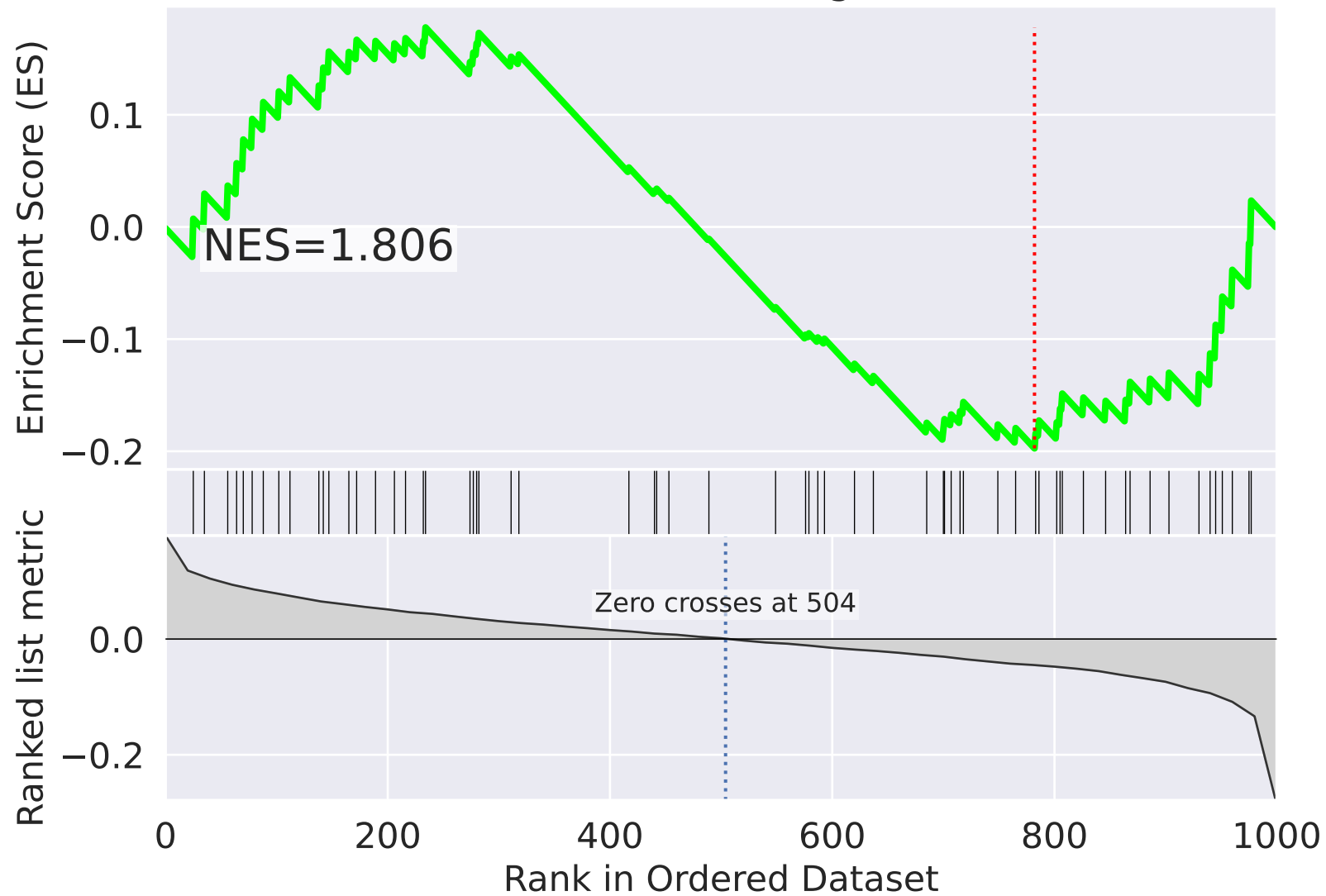
mitochondrial translational elongation (GO:0070125)



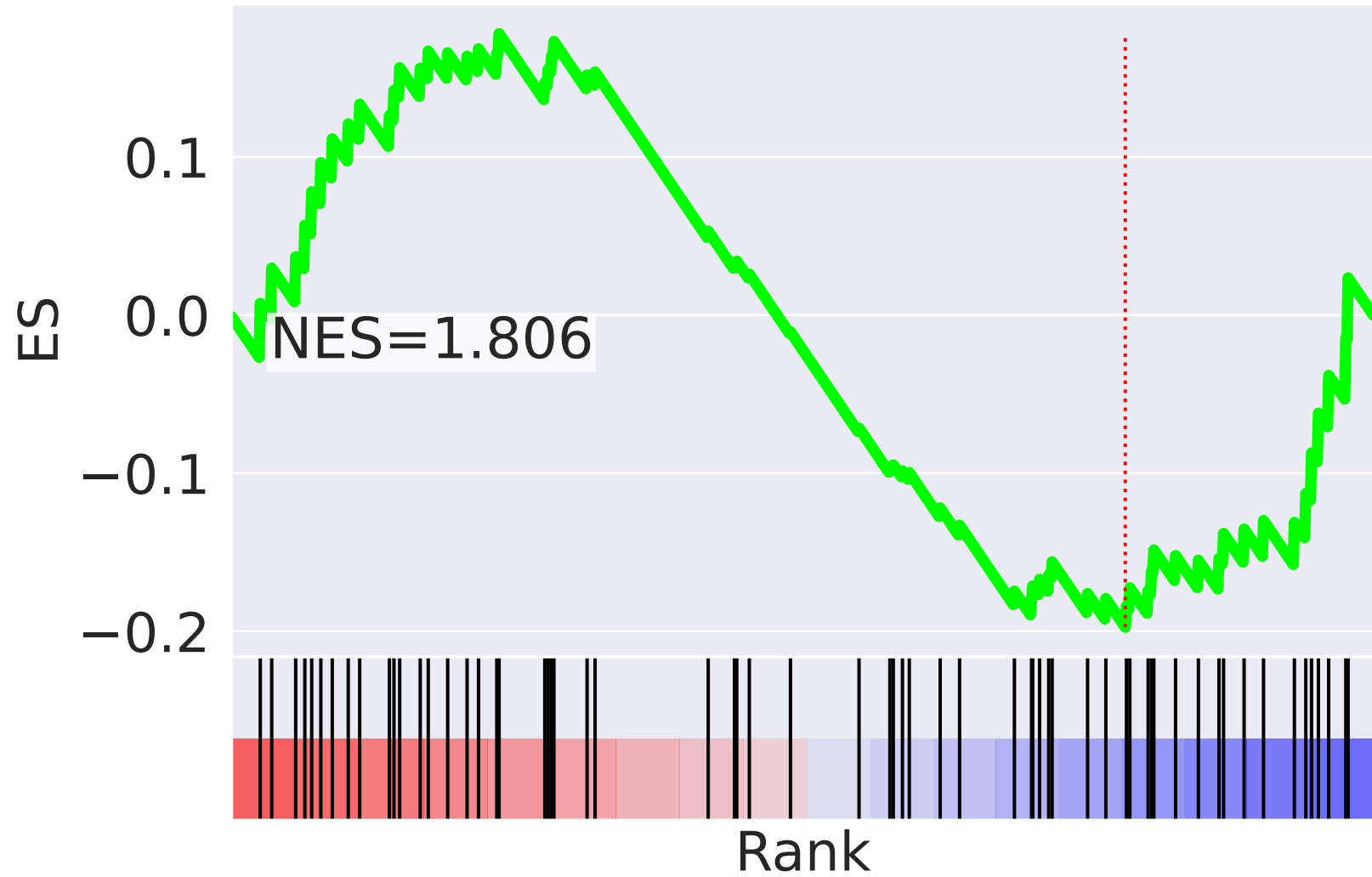
NES		SET
2.641		mitotic cell cycle (GO:0000278)
-2.498		MAPK cascade (GO:0000165)
2.131		microtubule-based movement (GO:0007018)
2.041		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.022		regulation of cholesterol biosynthetic process (GO:0045540)
-1.810		multivesicular body assembly (GO:0036258)
1.749		protein K48-linked ubiquitination (GO:0070936)
1.719		DNA-dependent DNA replication (GO:0006261)
-1.690		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-1.667		protein N-linked glycosylation via asparagine (GO:0018279)
1.656		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
1.653		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-1.644		ESCRT III complex disassembly (GO:1904903)
1.627		inflammatory response (GO:0006954)
1.625		chromosome segregation (GO:0007059)

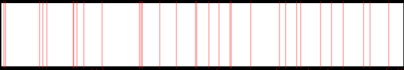


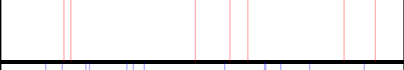

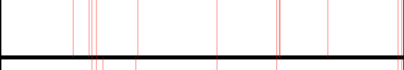


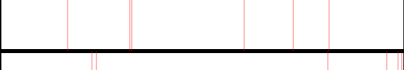
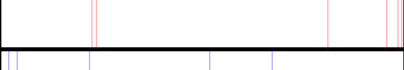





The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=22$

mitochondrial translational elongation (GO:0070125)



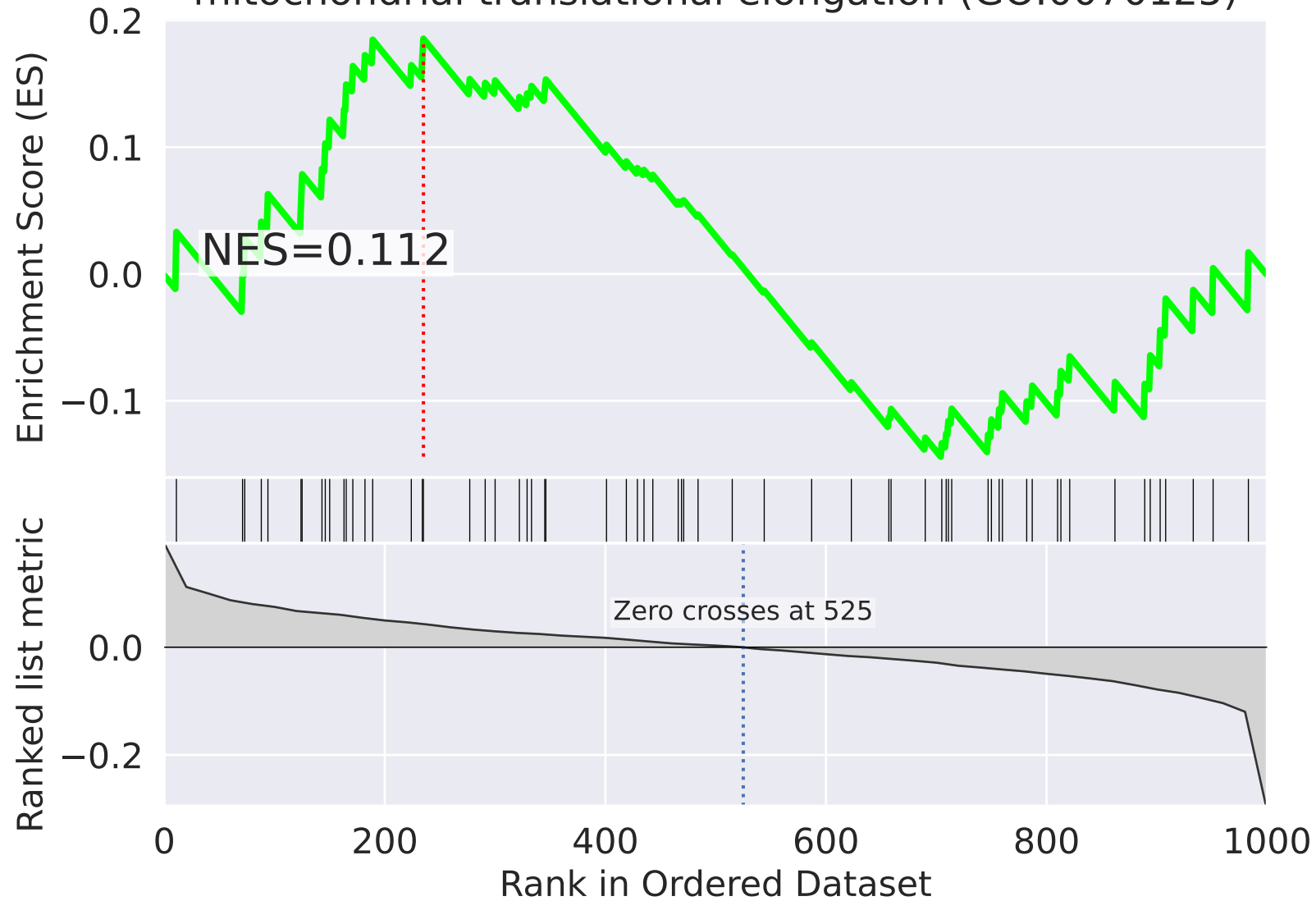
mitochondrial translational elongation (GO:0070125)



NES		SET
3.062		positive regulation of cell proliferation (GO:0008284)
2.723		multivesicular body assembly (GO:0036258)
2.587		axon guidance (GO:0007411)
2.437		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-2.399		protein stabilization (GO:0050821)
2.390		mitotic metaphase plate congression (GO:0007080)
2.291		viral life cycle (GO:0019058)
-2.280		nervous system development (GO:0007399)
2.262		iron-sulfur cluster assembly (GO:0016226)
2.236		ESCRT III complex disassembly (GO:1904903)
-2.220		positive regulation by host of viral transcription (GO:0043923)
2.084		viral budding via host ESCRT complex (GO:0039702)
2.062		small molecule metabolic process (GO:0044281)
2.061		nucleus organization (GO:0006997)
-2.041		RNA splicing (GO:0008380)

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)



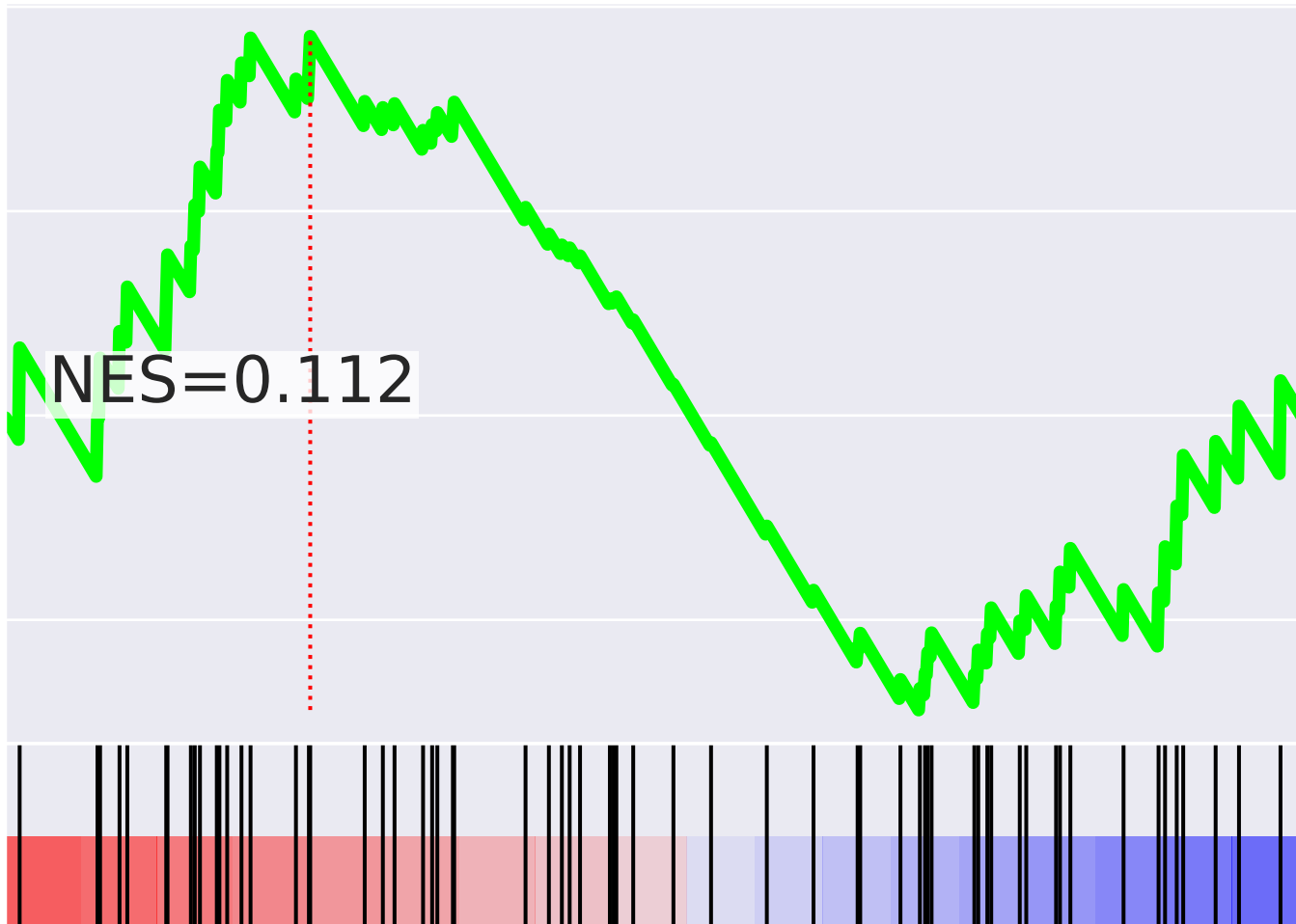
mitochondrial translational elongation (GO:0070125)




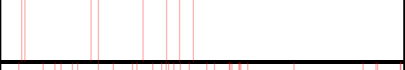
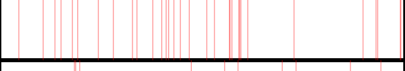
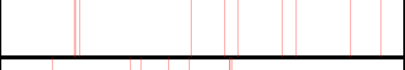
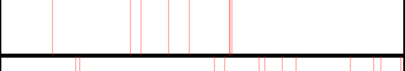
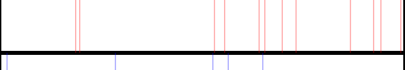
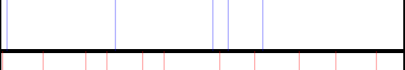
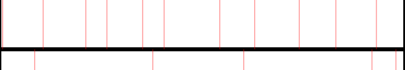
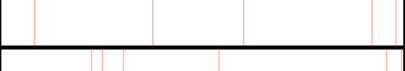
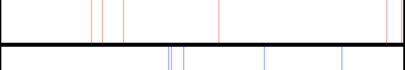
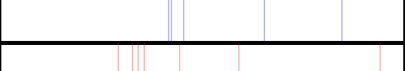
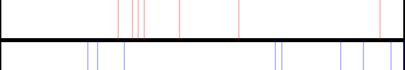
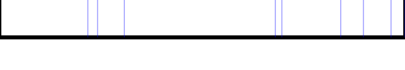
ES

0.2
0.1
0.0
-0.1

NES=0.112

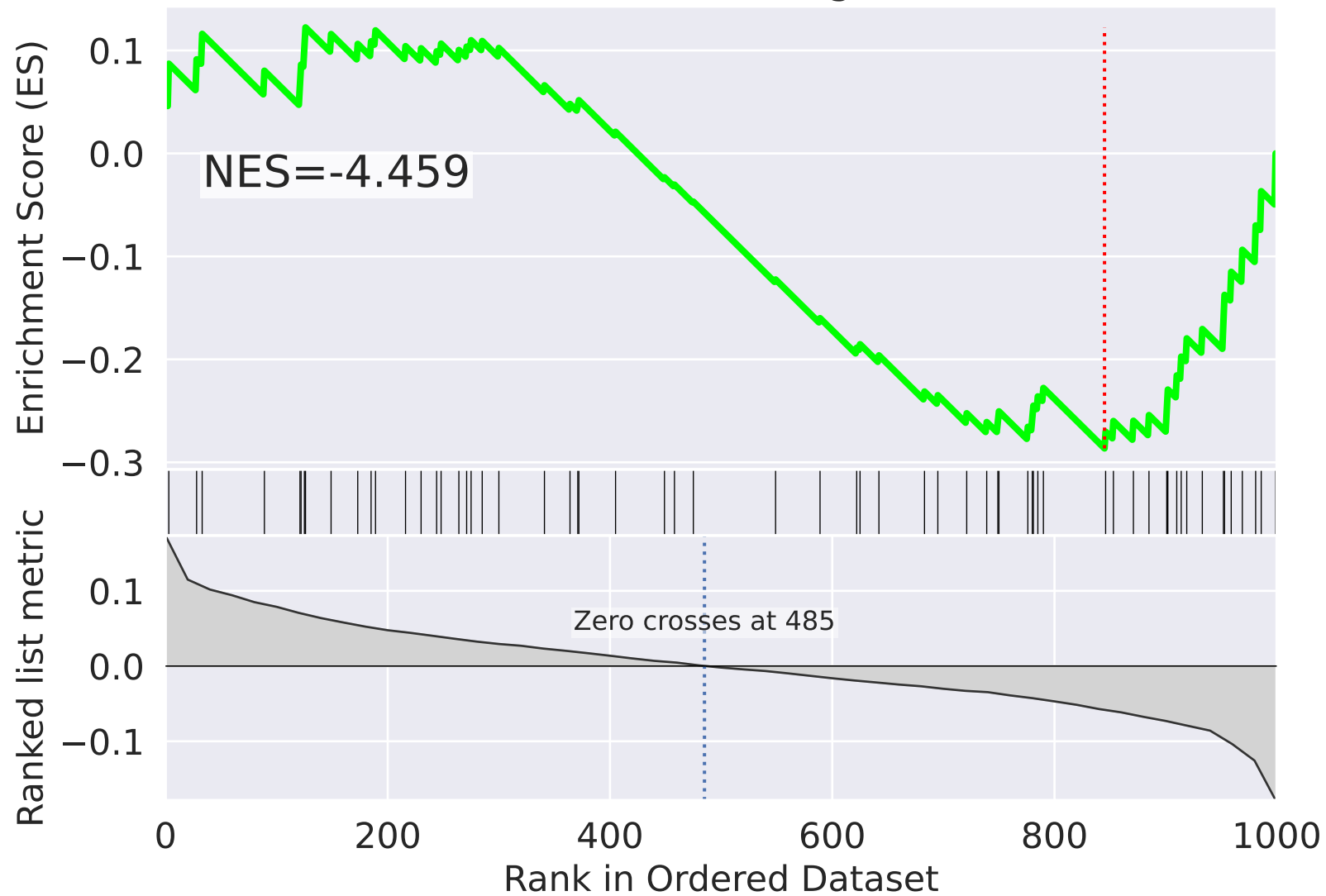
Rank



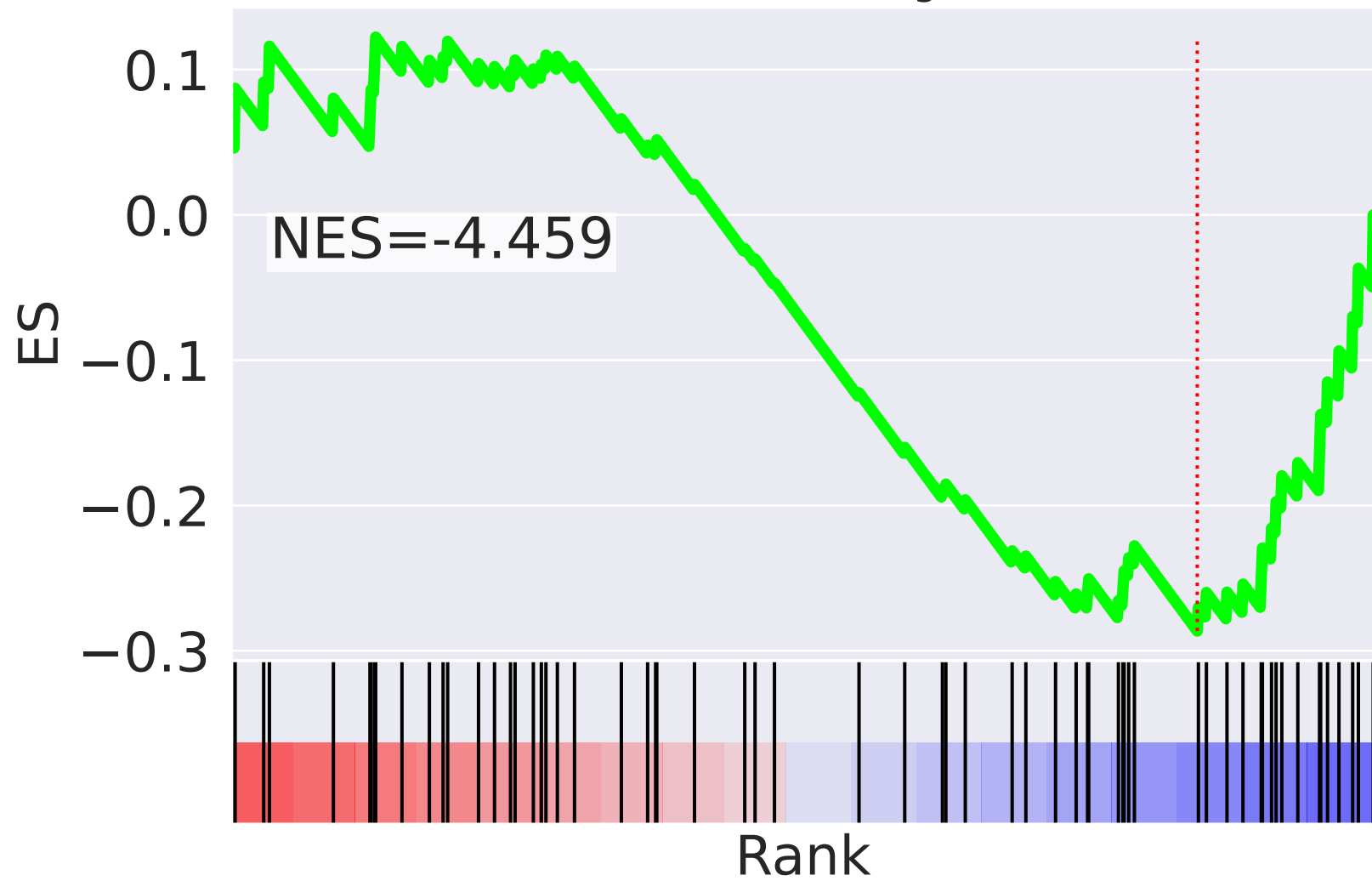
NES		SET
-2.600		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.573		protein targeting to mitochondrion (GO:0006626)
2.510		ESCRT III complex disassembly (GO:1904903)
2.473		cell-matrix adhesion (GO:0007160)
2.439		positive regulation of cell proliferation (GO:0008284)
2.408		multivesicular body assembly (GO:0036258)
2.366		positive regulation of cell migration (GO:0030335)
2.326		mitotic metaphase plate congression (GO:0007080)
-2.269		protein N-linked glycosylation (GO:0006487)
2.234		positive regulation of gene expression (GO:0010628)
2.215		small molecule metabolic process (GO:0044281)
2.172		protein K11-linked ubiquitination (GO:0070979)
-2.164		regulation of cell motility (GO:2000145)
2.091		multicellular organism development (GO:0007275)
-2.046		positive regulation of TOR signaling (GO:0032008)

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)


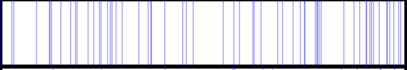


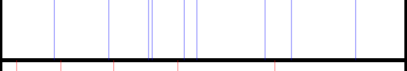
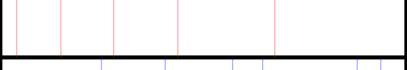



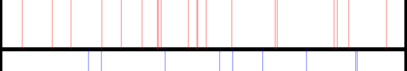

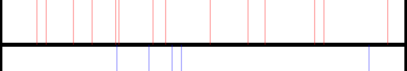
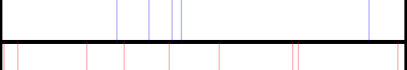
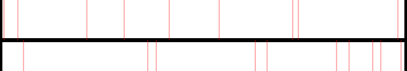
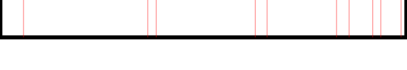


mitochondrial translational elongation (GO:0070125)



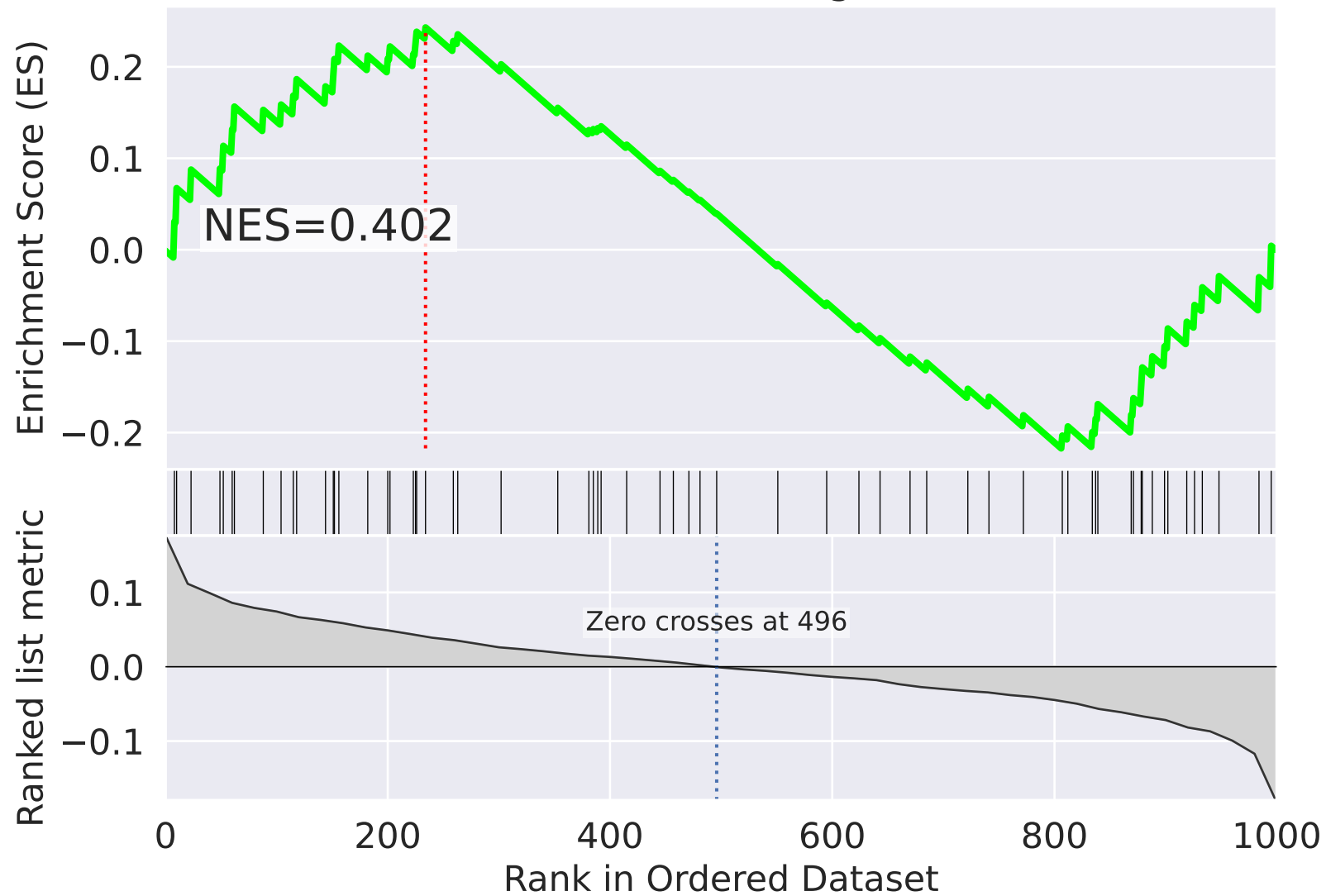
NES

SET

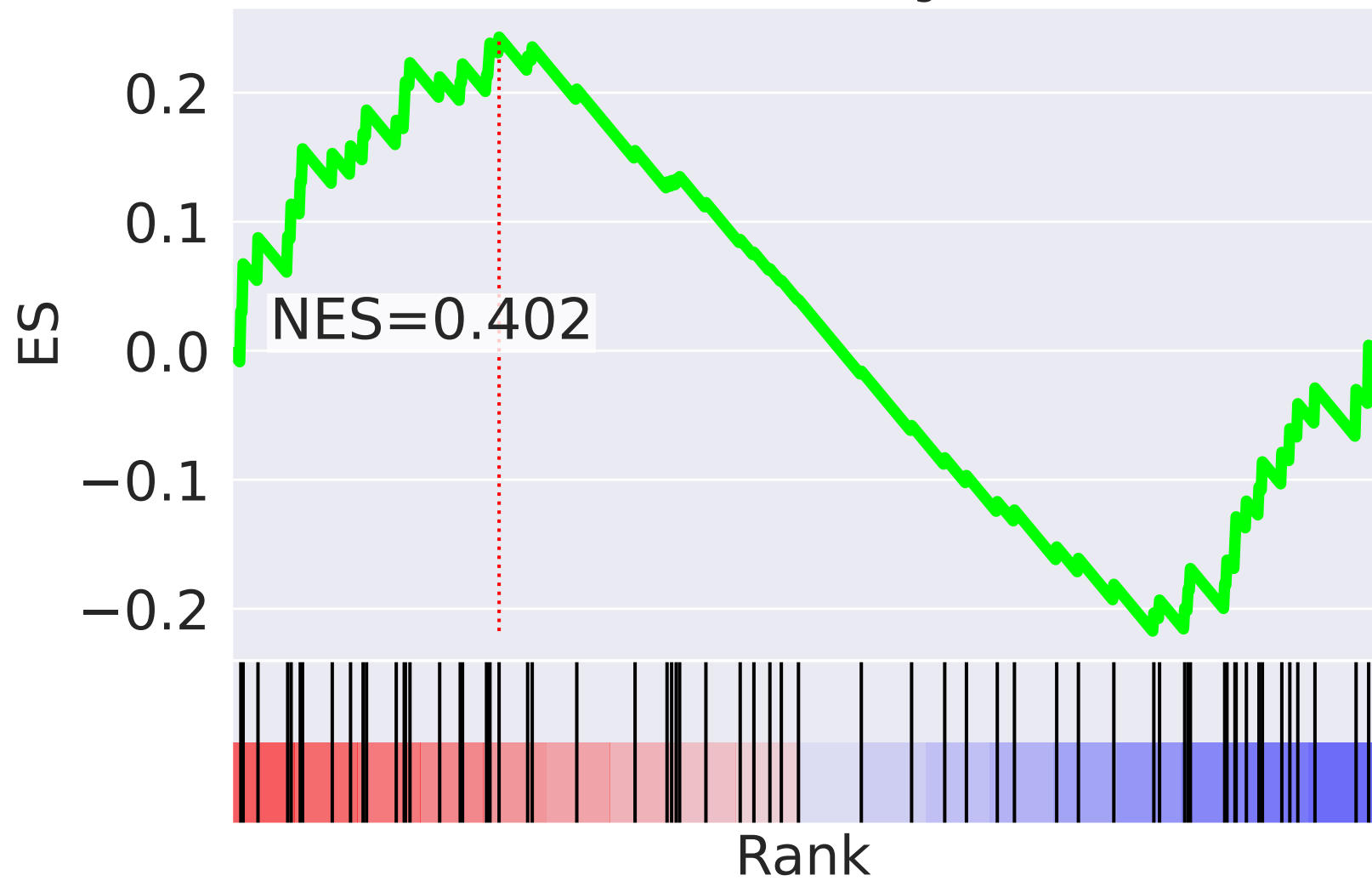
-4.459		mitochondrial translational elongation (GO:0070125)
-4.262		mitochondrial translational termination (GO:0070126)
-2.626		regulation of macroautophagy (GO:0016241)
-2.336		regulation of lipid metabolic process (GO:0019216)
-2.235		peptidyl-serine phosphorylation (GO:0018105)
2.147		apoptotic signaling pathway (GO:0097190)
-2.039		cellular response to amino acid stimulus (GO:0071230)
2.036		apoptotic process (GO:0006915)
1.935		COPII vesicle coating (GO:0048208)
1.894		cellular response to DNA damage stimulus (GO:0006974)
-1.877		positive regulation of TOR signaling (GO:0032008)
1.865		mitotic cell cycle (GO:0000278)
-1.854		carbohydrate metabolic process (GO:0005975)
1.840		regulation of mRNA stability (GO:0043488)
1.814		RNA splicing (GO:0008380)





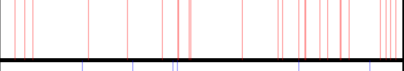



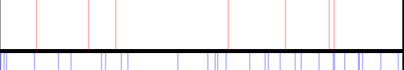
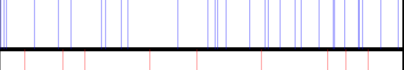




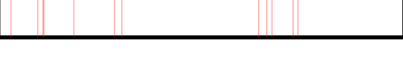
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=25$

mitochondrial translational elongation (GO:0070125)



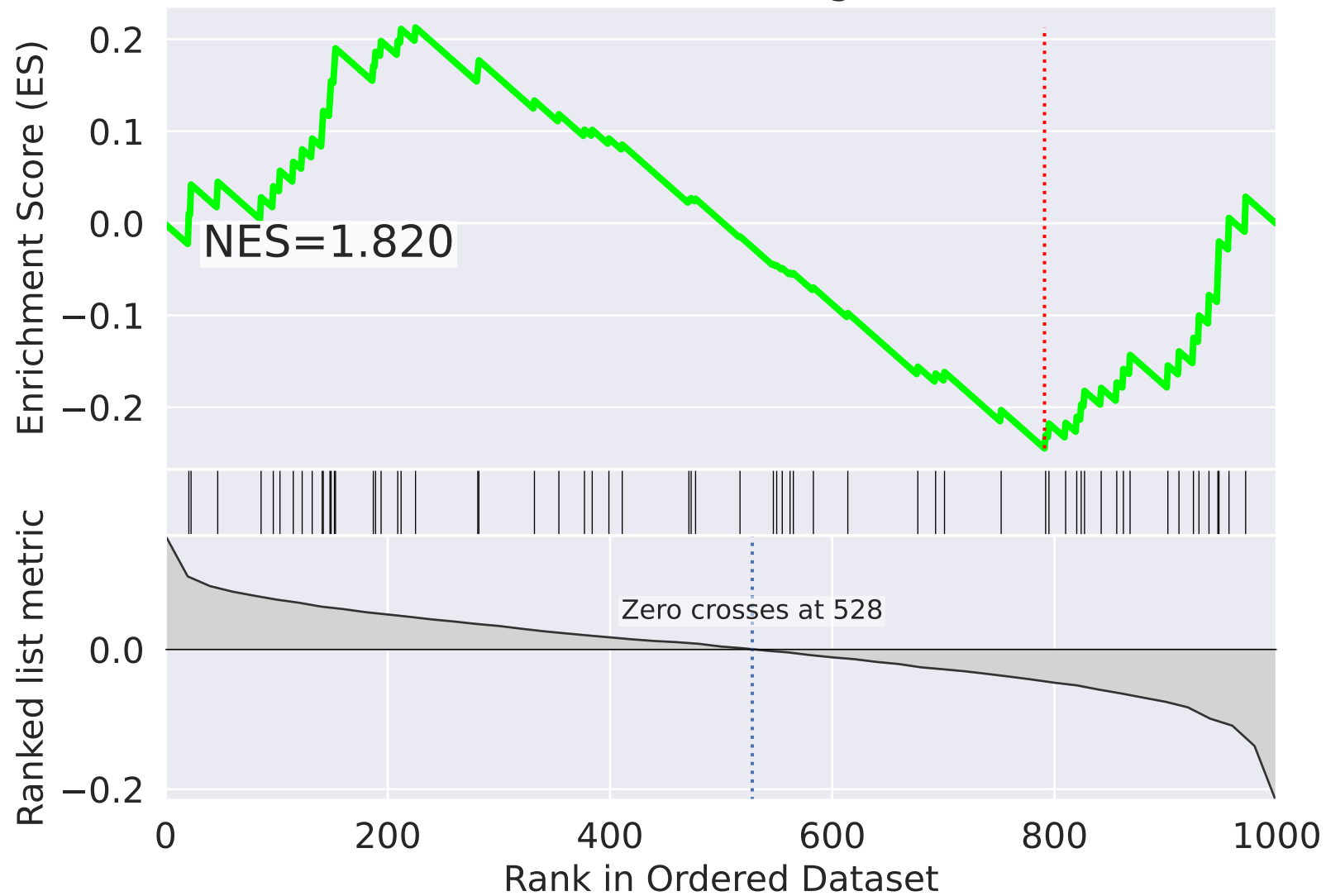
mitochondrial translational elongation (GO:0070125)



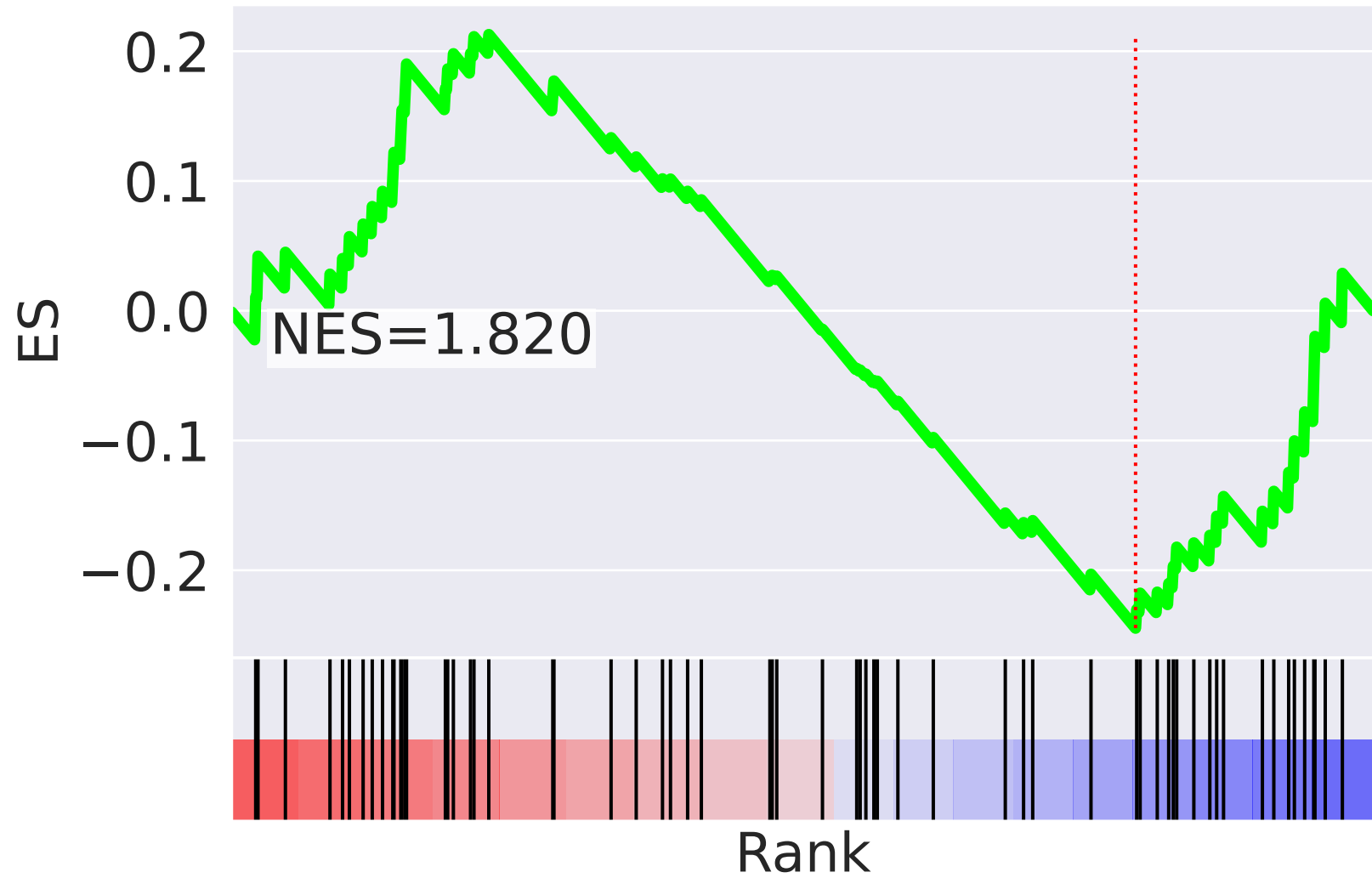
NES		SET
-2.481		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
2.395		chromosome segregation (GO:0007059)
2.371		DNA-dependent DNA replication (GO:0006261)
2.354		regulation of apoptotic process (GO:0042981)
2.270		protein deubiquitination (GO:0016579)
-2.219		regulation of DNA replication (GO:0006275)
-2.057		protein autophosphorylation (GO:0046777)
1.997		macroautophagy (GO:0016236)
1.864		response to endoplasmic reticulum stress (GO:0034976)
-1.780		neutrophil degranulation (GO:0043312)
1.747		strand displacement (GO:0000732)
-1.744		regulation of protein stability (GO:0031647)
-1.724		regulation of macroautophagy (GO:0016241)
-1.641		mitochondrial translation (GO:0032543)
1.608		mitochondrion organization (GO:0007005)

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

mitochondrial translational elongation (GO:0070125)



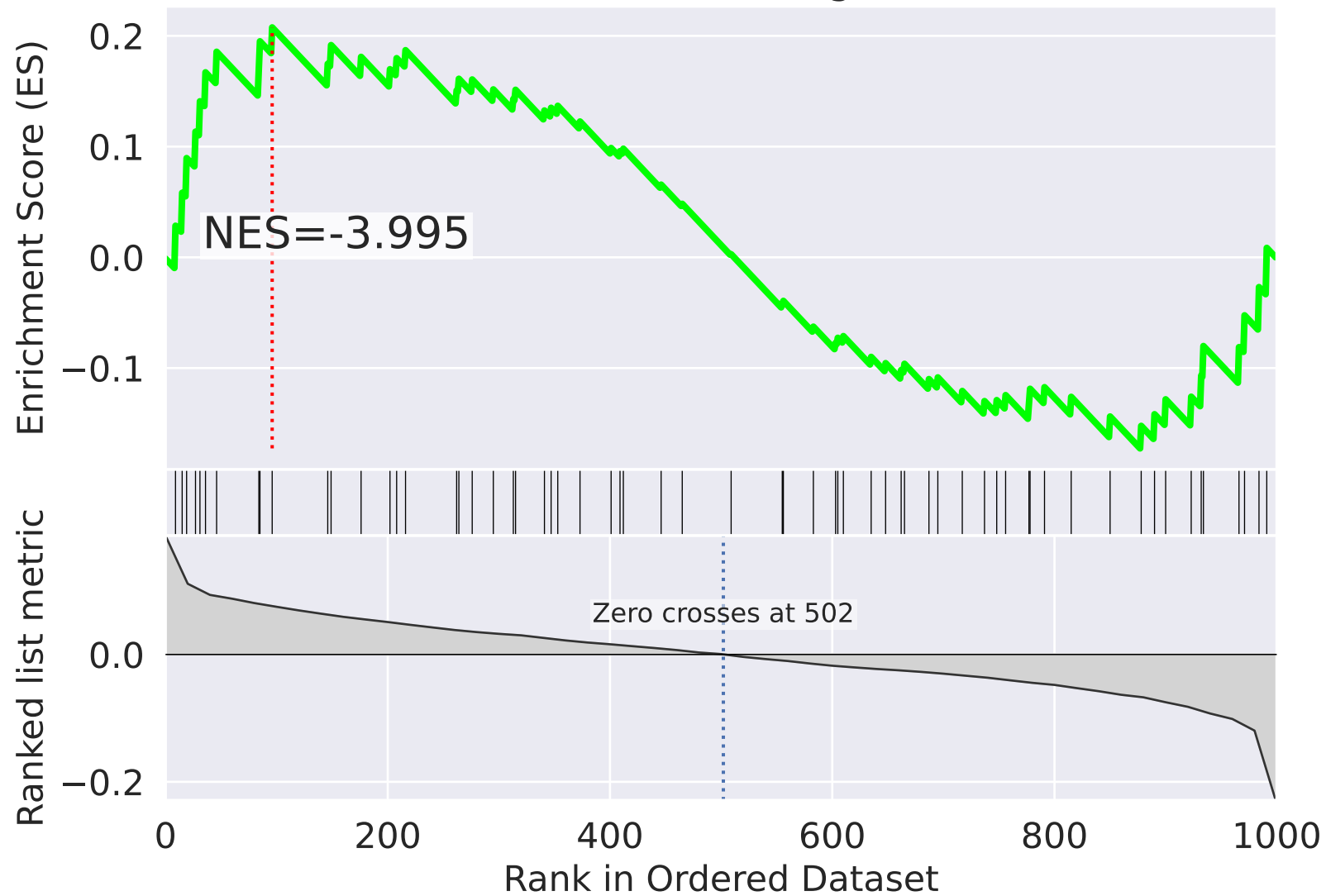
mitochondrial translational elongation (GO:0070125)



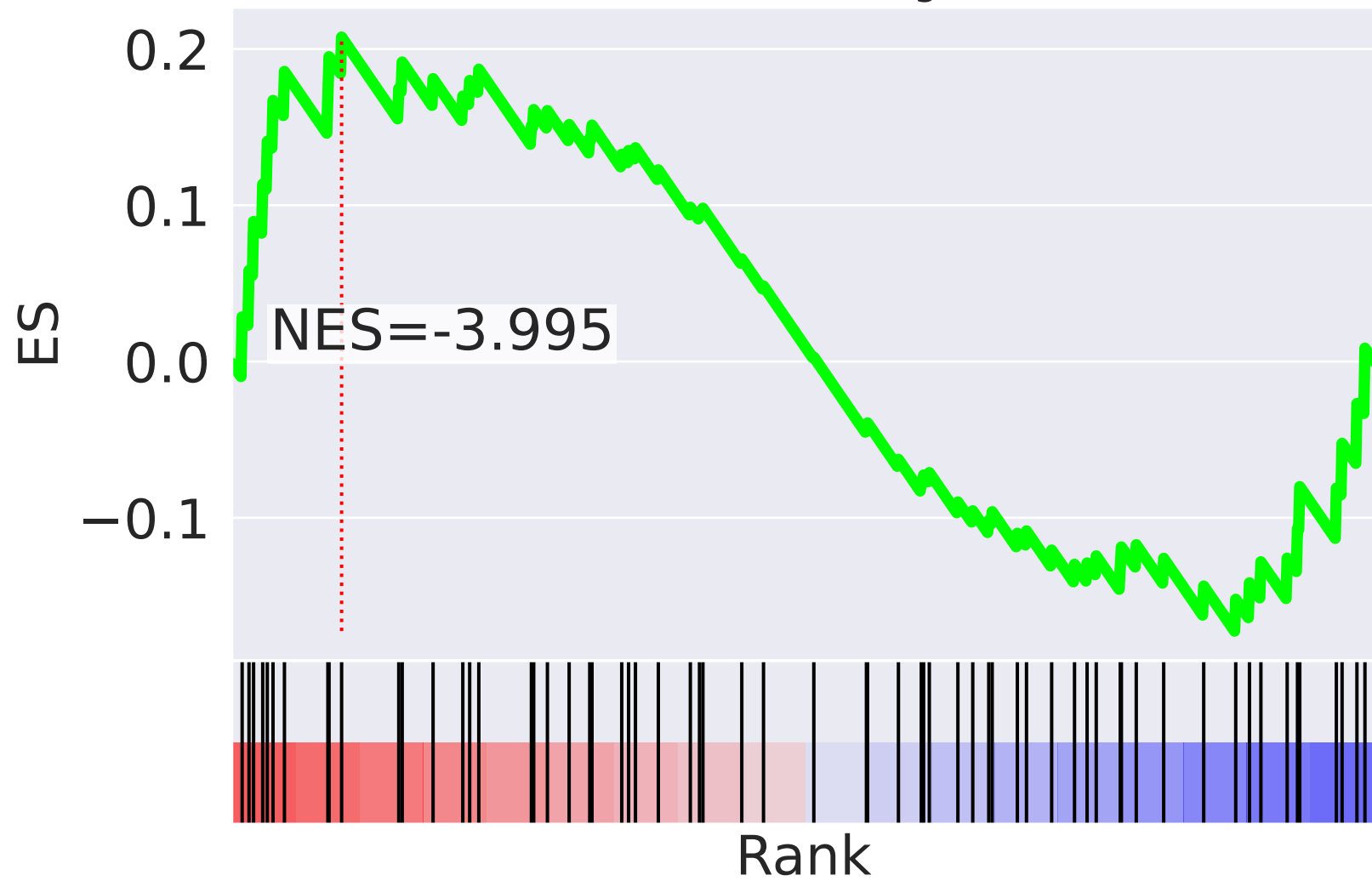
NES		SET
3.207		positive regulation of cell proliferation (GO:0008284)
2.567		multicellular organism development (GO:0007275)
2.521		positive regulation of gene expression (GO:0010628)
2.517		axon guidance (GO:0007411)
2.474		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.334		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.242		cellular protein modification process (GO:0006464)
2.165		Fc-epsilon receptor signaling pathway (GO:0038095)
2.126		intracellular protein transport (GO:0006886)
-2.101		protein polyubiquitination (GO:0000209)
2.089		negative regulation of apoptotic process (GO:0043066)
2.066		execution phase of apoptosis (GO:0097194)
2.058		positive regulation of protein phosphorylation (GO:0001934)
2.057		MAPK cascade (GO:0000165)
-2.051		fibroblast growth factor receptor signaling pathway (GO:0008543)

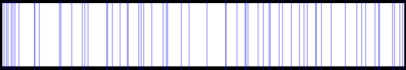
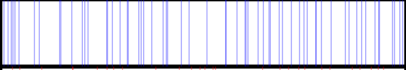
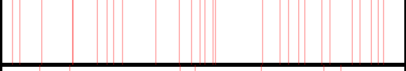
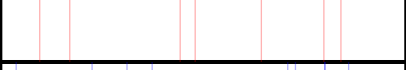

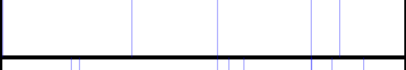



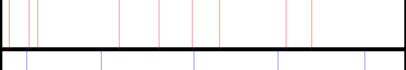


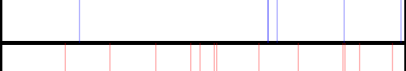
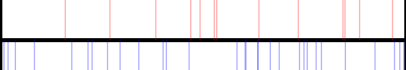

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=27$

mitochondrial translational elongation (GO:0070125)



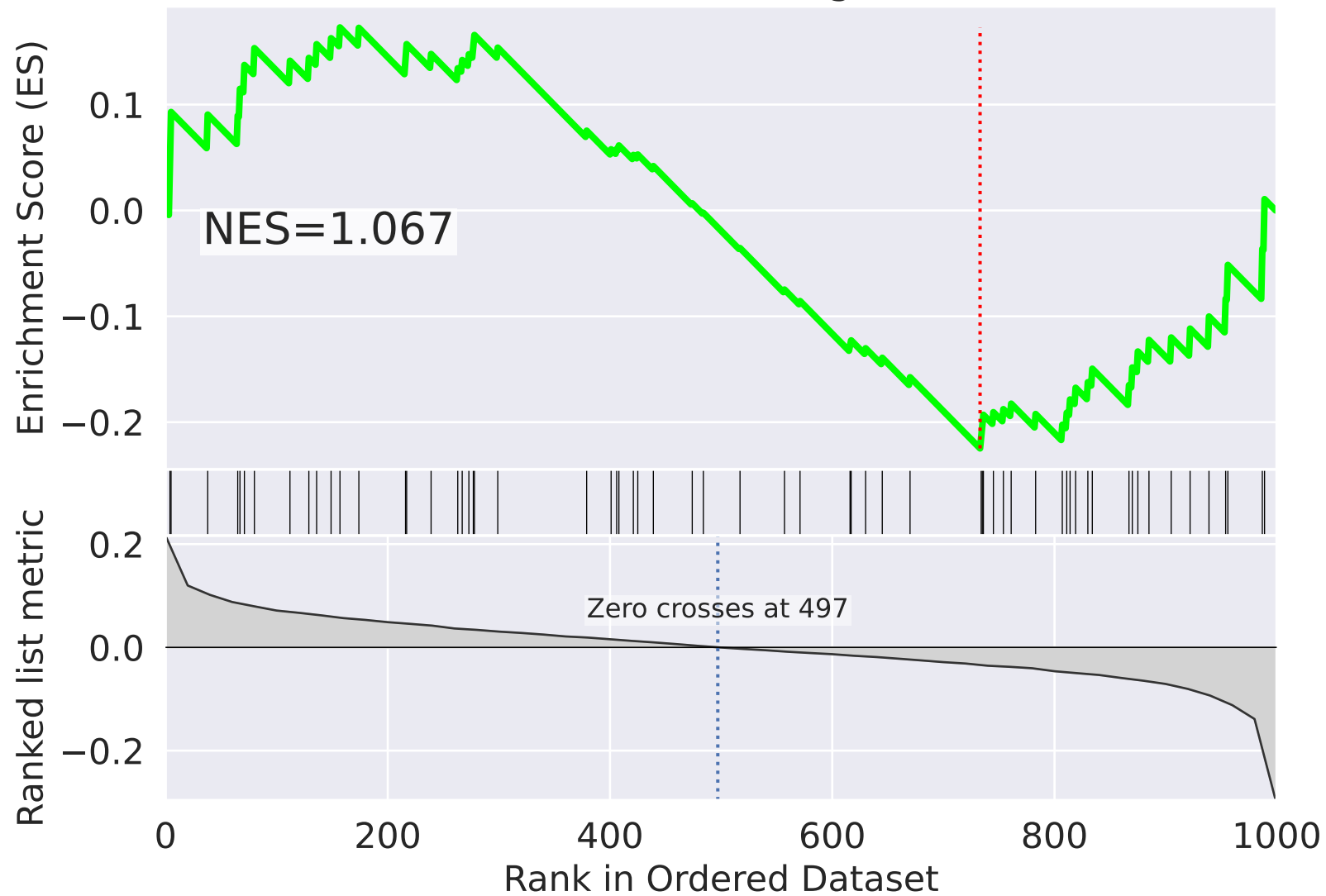
mitochondrial translational elongation (GO:0070125)



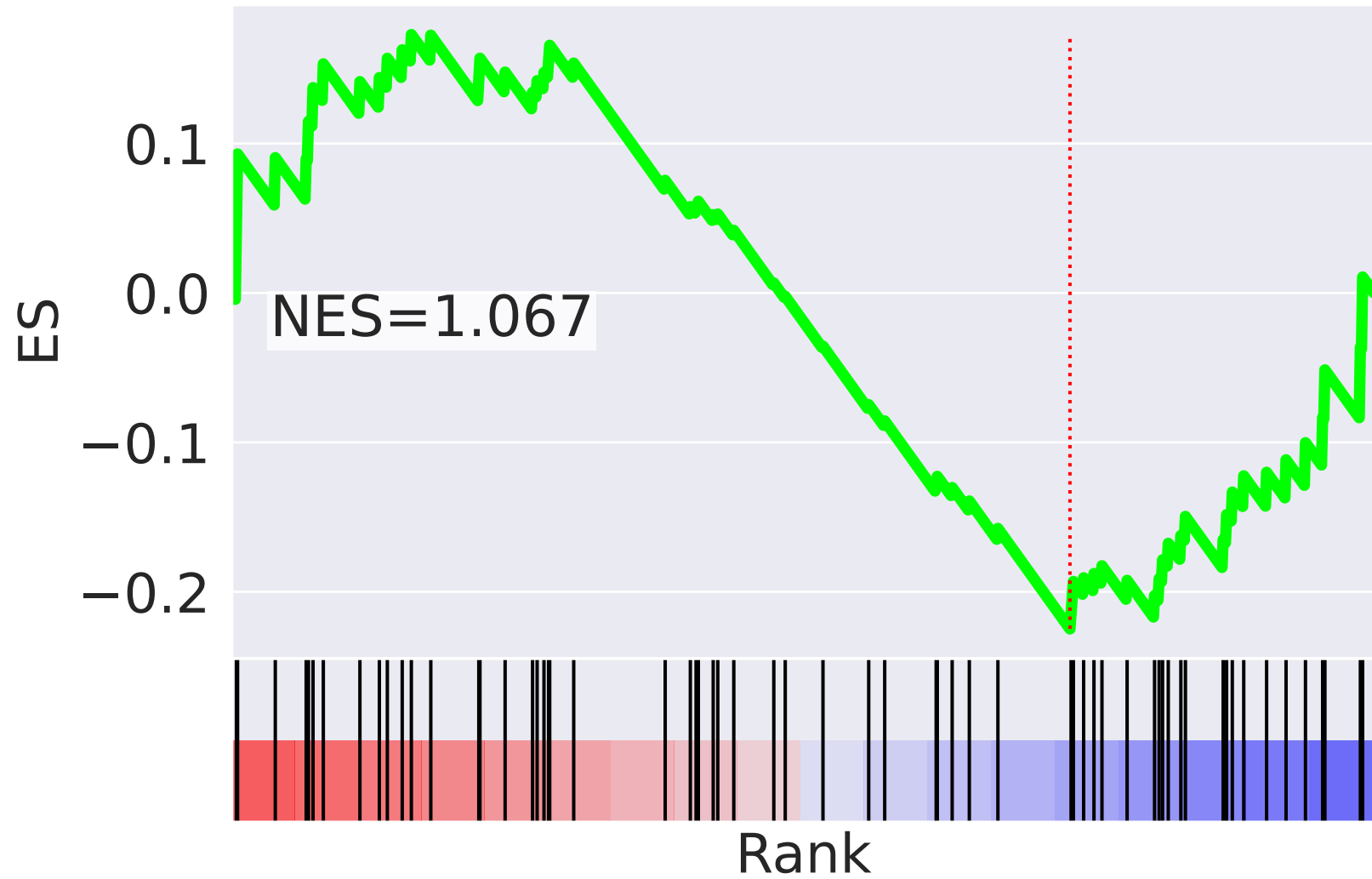
NES		SET
-3.995		mitochondrial translational elongation (GO:0070125)
-3.477		mitochondrial translational termination (GO:0070126)
2.859		negative regulation of apoptotic process (GO:0043066)
2.700		cellular nitrogen compound metabolic process (GO:0034641)
-2.599		tRNA aminoacylation for protein translation (GO:0006418)
-2.517		positive regulation of GTPase activity (GO:0043547)
-2.457		retrograde transport, endosome to Golgi (GO:0042147)
2.342		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.307		positive regulation of viral genome replication (GO:0045070)
2.255		regulation of protein stability (GO:0031647)
-2.121		post-Golgi vesicle-mediated transport (GO:0006892)
2.108		carbohydrate metabolic process (GO:0005975)
-2.098		IRE1-mediated unfolded protein response (GO:0036498)
2.021		apoptotic process (GO:0006915)
-2.003		translation (GO:0006412)





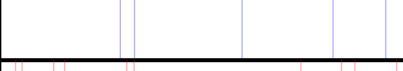

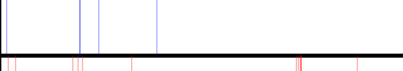



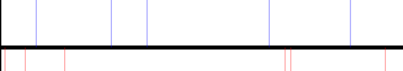
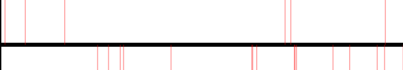
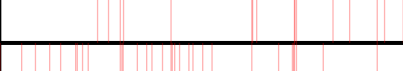
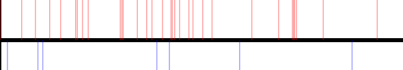

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=28$

mitochondrial translational elongation (GO:0070125)



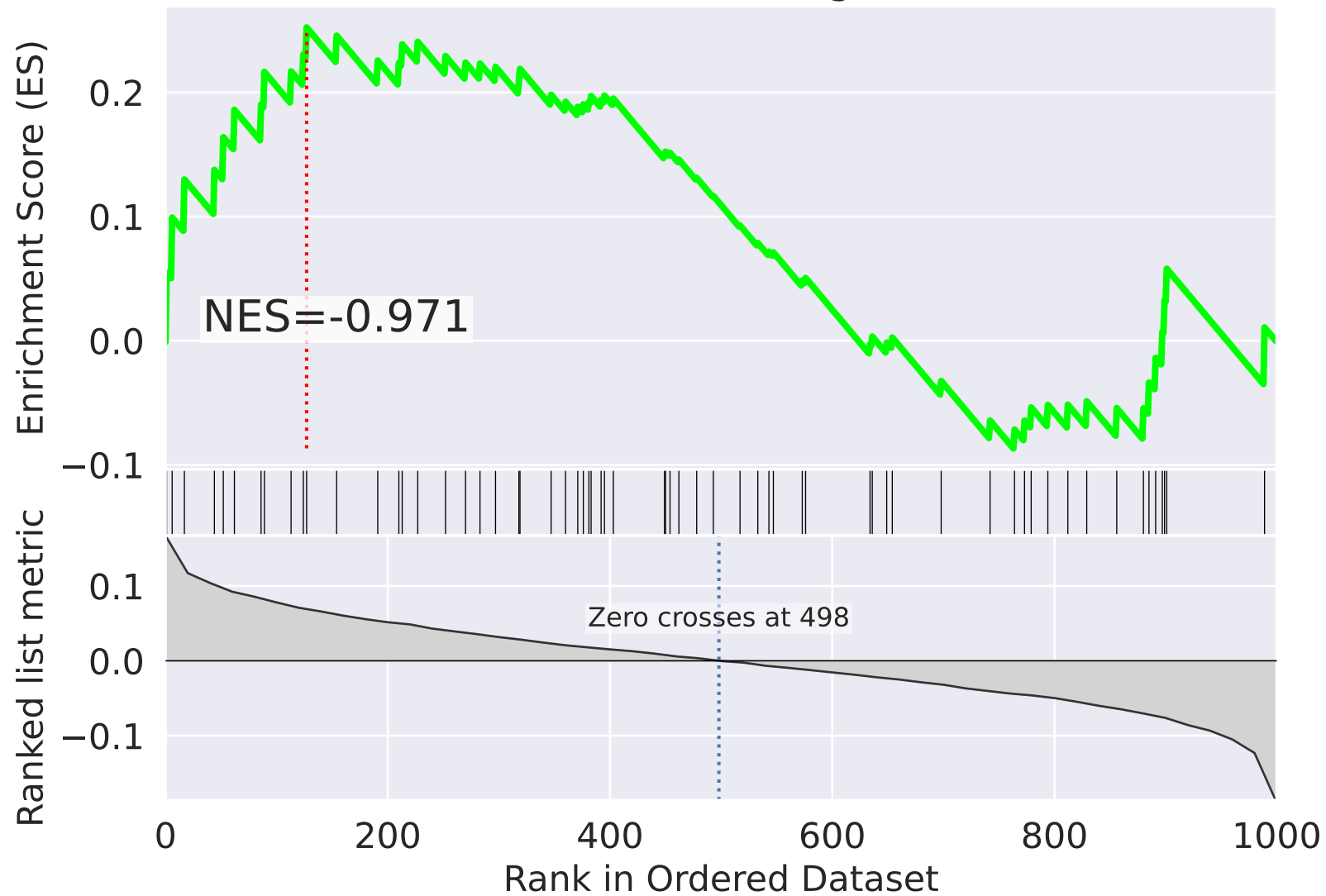
mitochondrial translational elongation (GO:0070125)



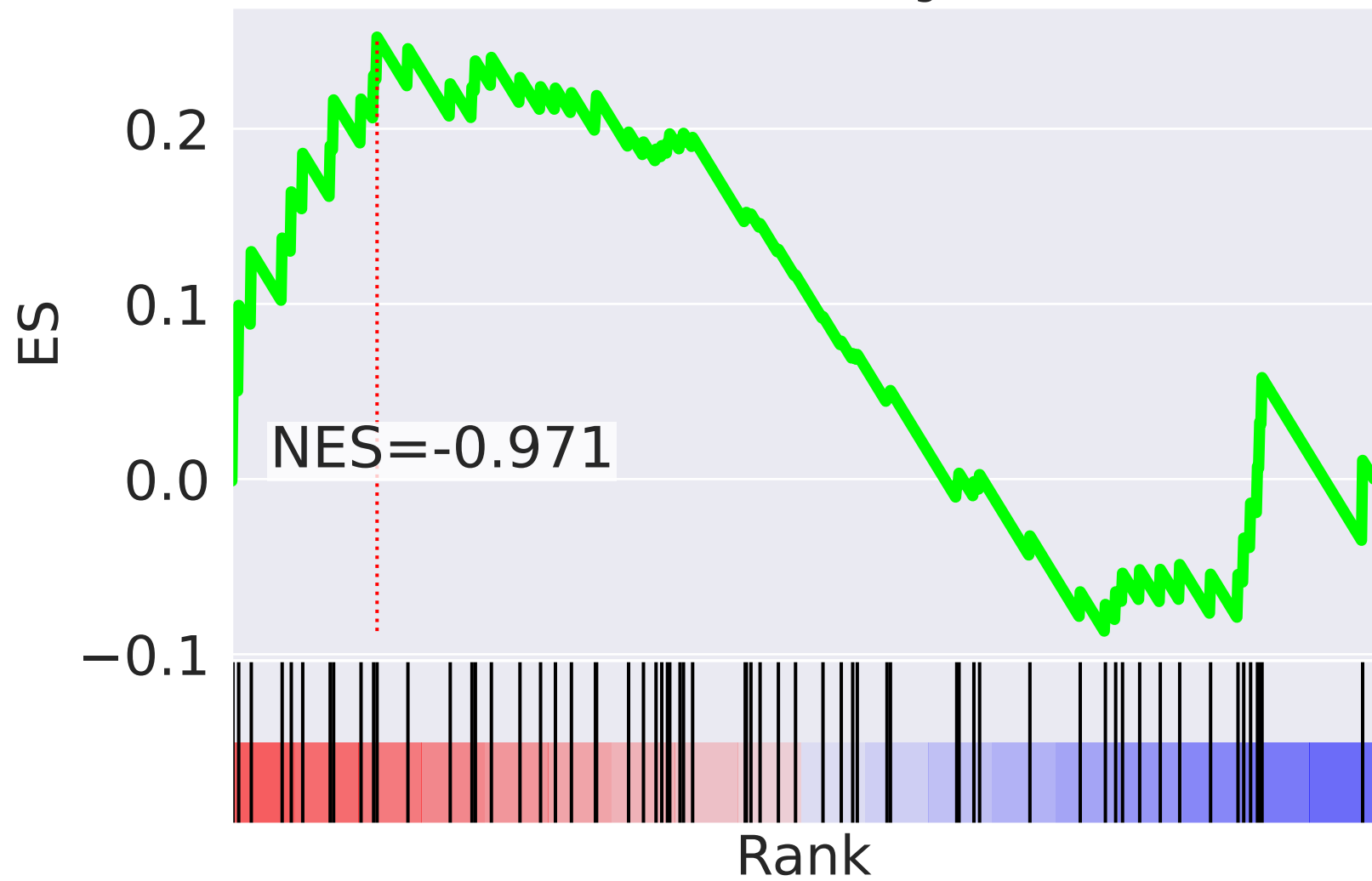
NES		SET
-2.644		protein stabilization (GO:0050821)
2.453		Fc-epsilon receptor signaling pathway (GO:0038095)
2.397		substrate adhesion-dependent cell spreading (GO:0034446)
2.359		cell division (GO:0051301)
-2.349		regulation of cell motility (GO:2000145)
2.286		sister chromatid cohesion (GO:0007062)
-2.278		lipid metabolic process (GO:0006629)
2.267		mitotic metaphase plate congression (GO:0007080)
2.202		epidermal growth factor receptor signaling pathway (GO:0007173)
2.183		negative regulation of cell cycle arrest (GO:0071157)
-2.166		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.101		DNA-dependent DNA replication (GO:0006261)
2.081		MAPK cascade (GO:0000165)
2.074		positive regulation of cell proliferation (GO:0008284)
-2.068		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 $z=29$

mitochondrial translational elongation (GO:0070125)



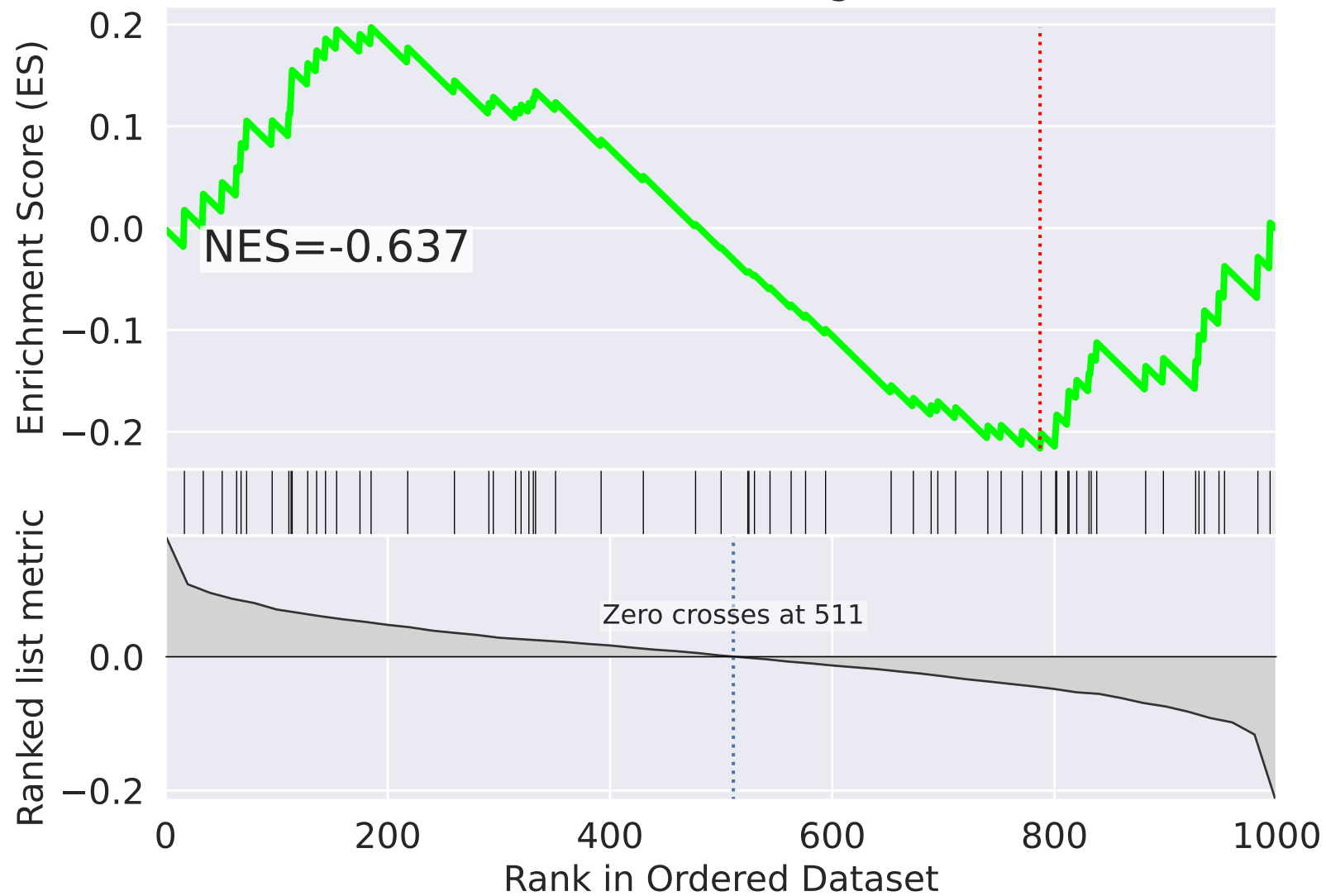
mitochondrial translational elongation (GO:0070125)



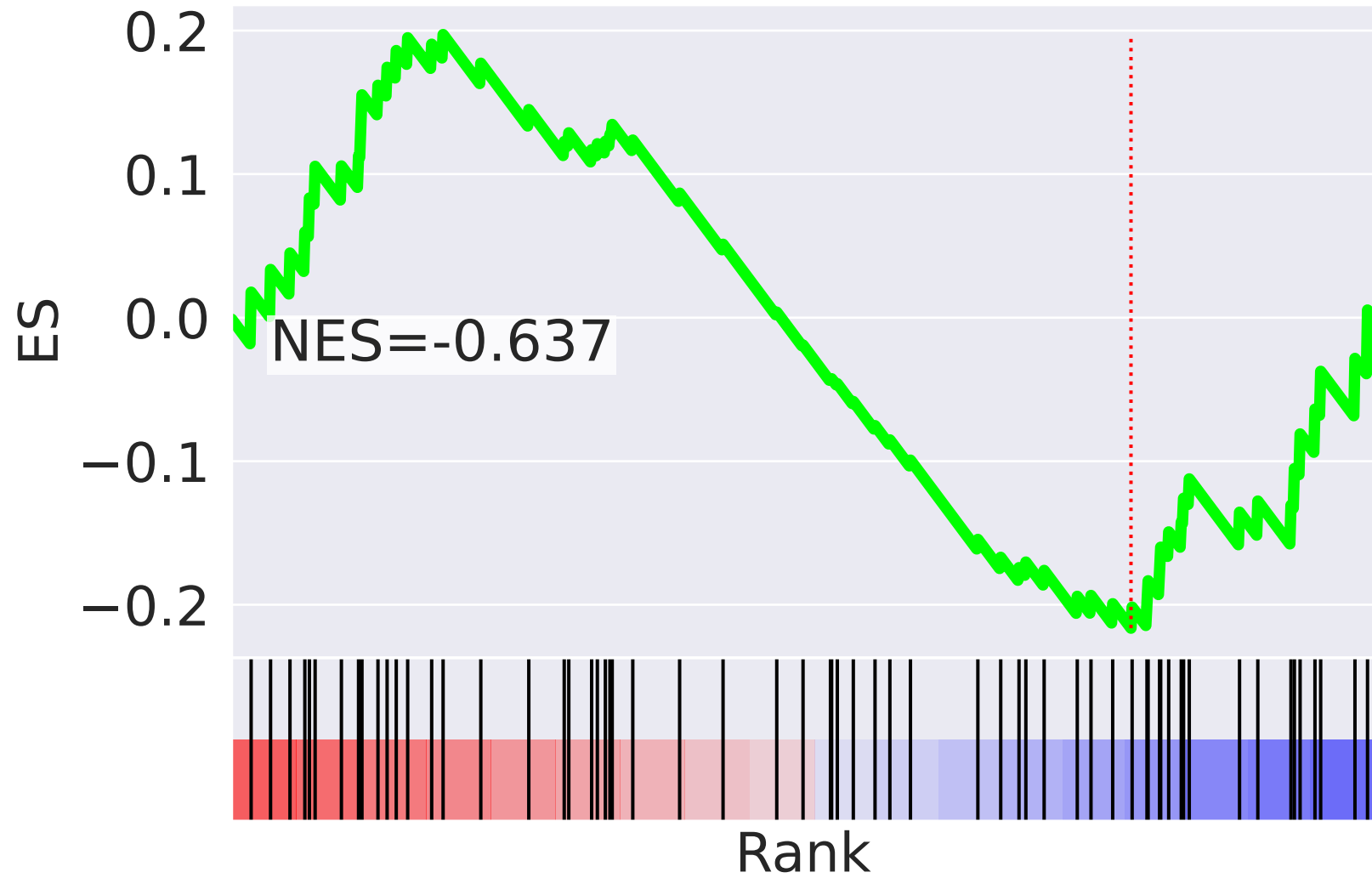
NES		SET
2.329		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.056		positive regulation of cytokinesis (GO:0032467)
-2.020		regulation of mitotic spindle assembly (GO:1901673)
-1.975		double-strand break repair via nonhomologous end joining (GO:0006303)
1.931		execution phase of apoptosis (GO:0097194)
1.900		cellular respiration (GO:0045333)
-1.895		cellular nitrogen compound metabolic process (GO:0034641)
1.884		positive regulation of viral genome replication (GO:0045070)
-1.879		positive regulation of protein ubiquitination (GO:0031398)
-1.872		mitochondrial translation (GO:0032543)
1.851		integrin-mediated signaling pathway (GO:0007229)
-1.830		multivesicular body assembly (GO:0036258)
1.800		endoplasmic reticulum organization (GO:0007029)
1.780		regulation of mRNA stability (GO:0043488)
-1.771		movement of cell or subcellular component (GO:0006928)

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

mitochondrial translational elongation (GO:0070125)



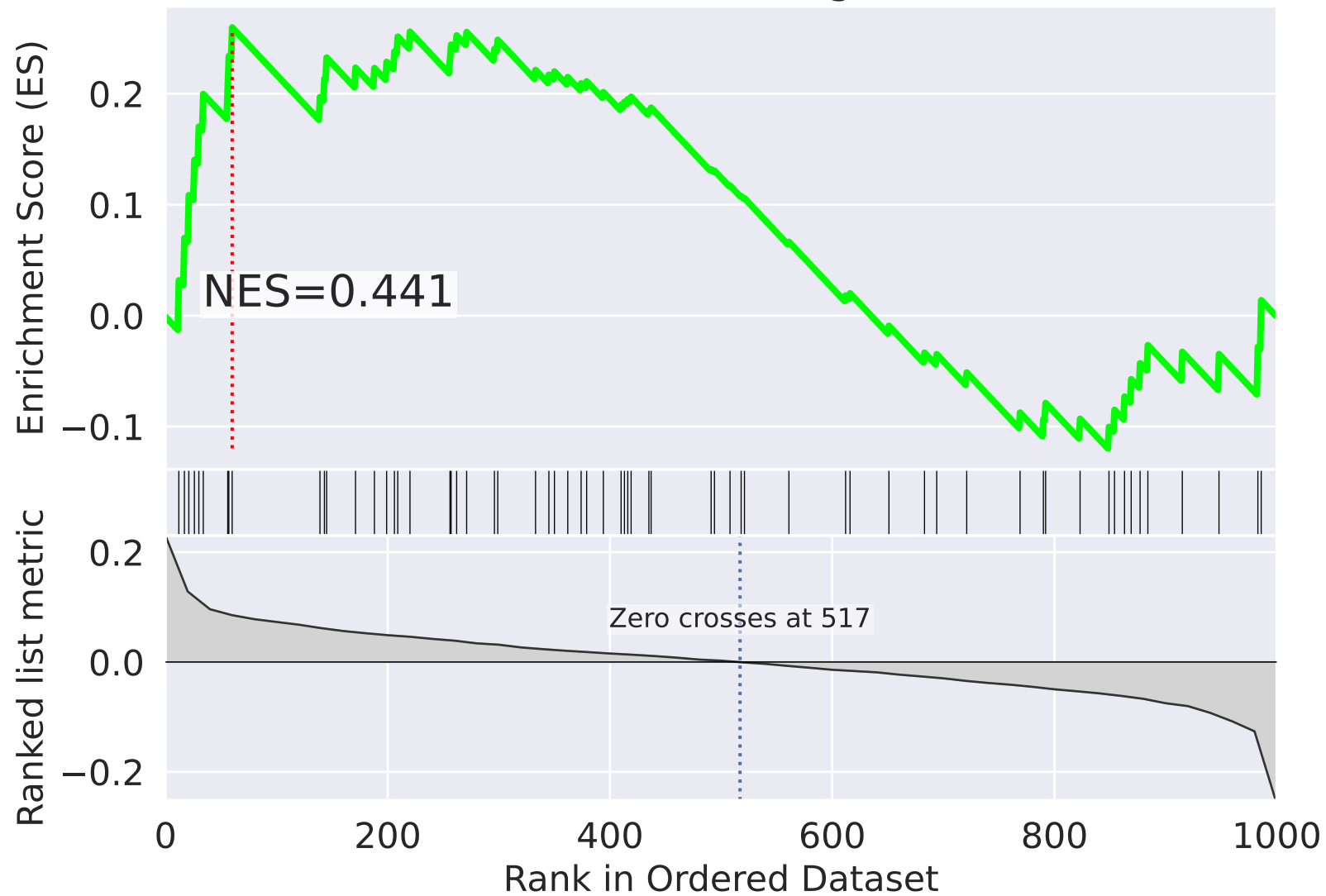
mitochondrial translational elongation (GO:0070125)



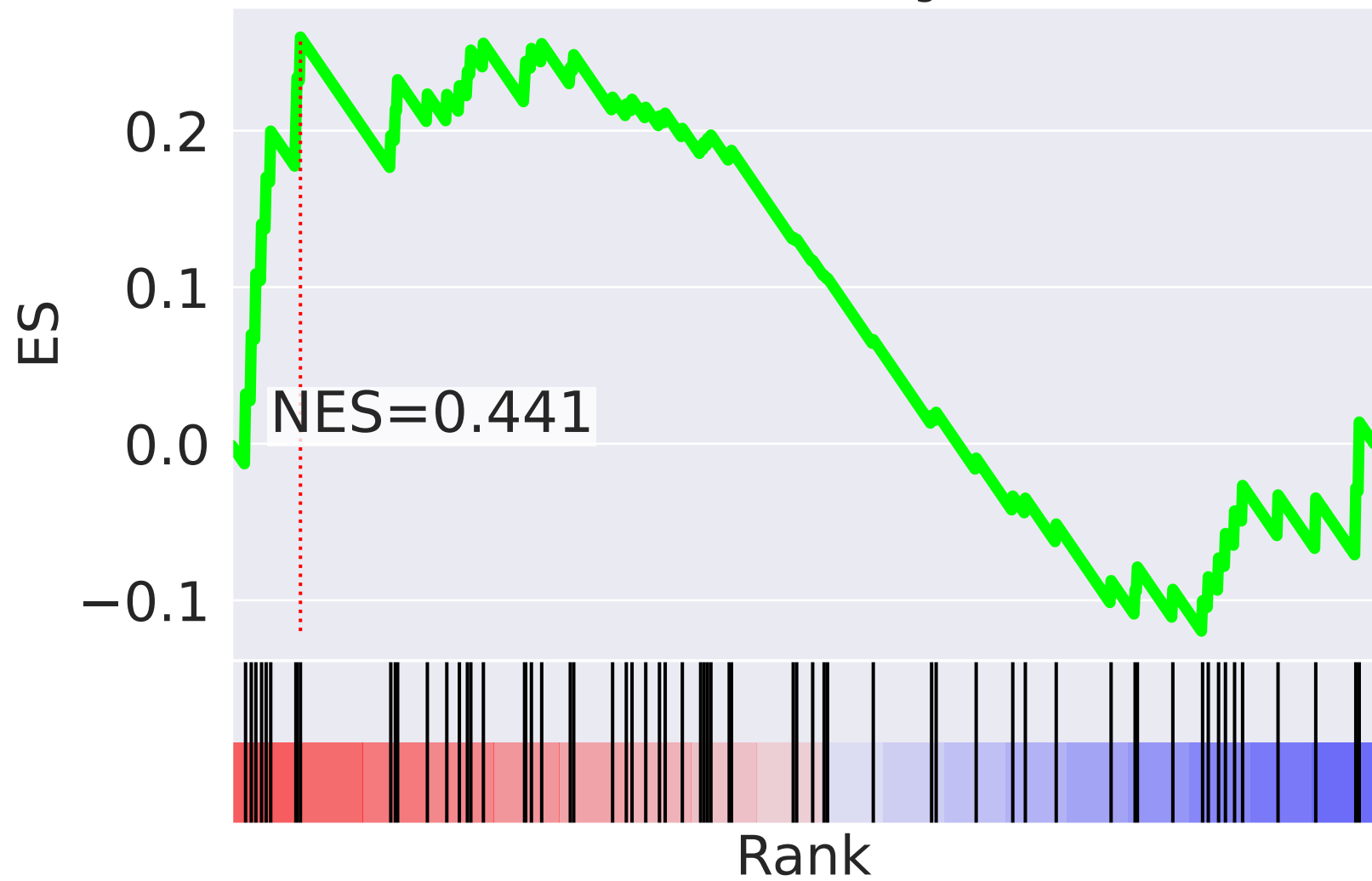
NES		SET
-2.663		positive regulation of transcription, DNA-templated (GO:0045893)
-2.581		regulation of transcription, DNA-templated (GO:0006355)
-2.310		negative regulation of cell growth (GO:0030308)
2.281		mitotic metaphase plate congression (GO:0007080)
-2.152		peptidyl-threonine phosphorylation (GO:0018107)
-2.149		regulation of mRNA stability (GO:0043488)
2.149		cell migration (GO:0016477)
-2.122		cellular response to amino acid starvation (GO:0034198)
2.108		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.047		nervous system development (GO:0007399)
-2.038		ATP-dependent chromatin remodeling (GO:0043044)
-1.969		IRE1-mediated unfolded protein response (GO:0036498)
-1.937		chromatin remodeling (GO:0006338)
-1.923		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.907		ERK1 and ERK2 cascade (GO:0070371)


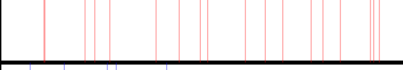
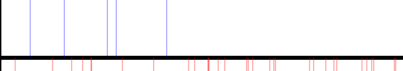
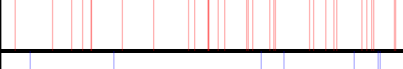
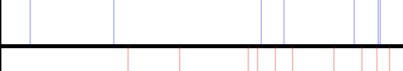
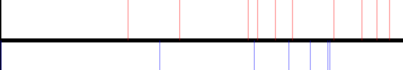
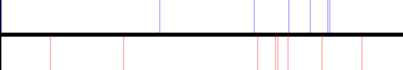

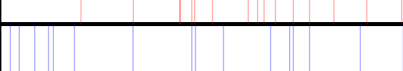

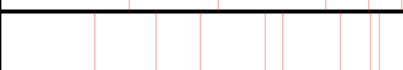


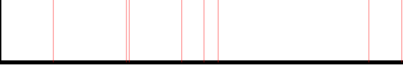

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=31$

mitochondrial translational elongation (GO:0070125)



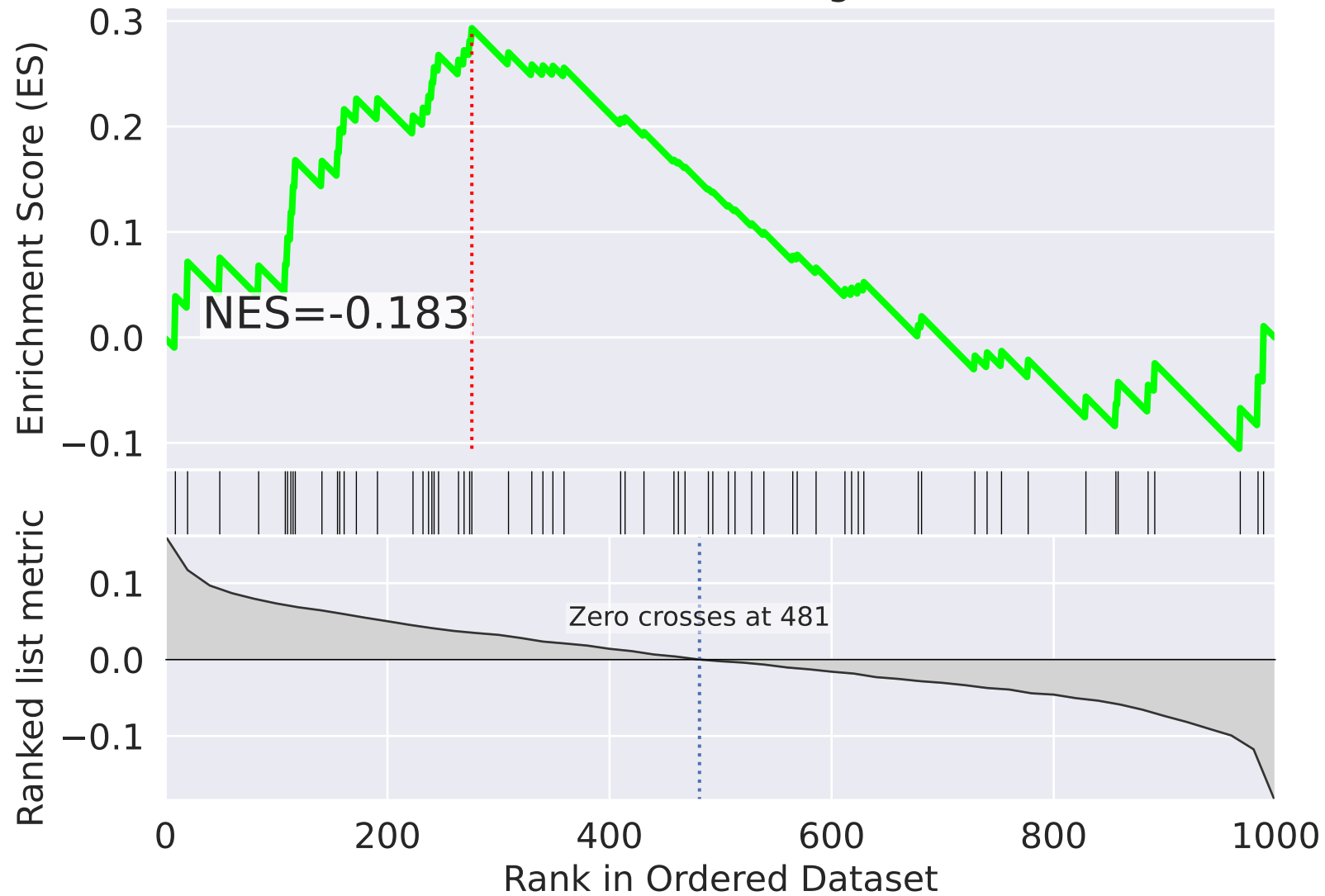
mitochondrial translational elongation (GO:0070125)



NES		SET
-3.069		protein stabilization (GO:0050821)
2.911		G2/M transition of mitotic cell cycle (GO:0000086)
-2.577		lipid metabolic process (GO:0006629)
2.568		positive regulation of cell proliferation (GO:0008284)
-2.402		cellular nitrogen compound metabolic process (GO:0034641)
2.311		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.277		protein N-linked glycosylation via asparagine (GO:0018279)
2.244		regulation of cell proliferation (GO:0042127)
2.230		MAPK cascade (GO:0000165)
-2.223		cell cycle arrest (GO:0007050)
2.176		substrate adhesion-dependent cell spreading (GO:0034446)
2.149		ciliary basal body docking (GO:0097711)
-2.107		ubiquitin-dependent ERAD pathway (GO:0030433)
2.080		positive regulation of cell growth (GO:0030307)
2.076		cell-matrix adhesion (GO:0007160)









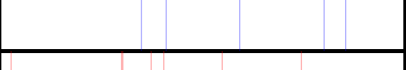
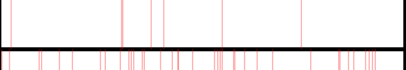
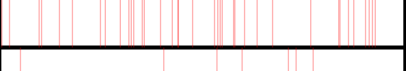
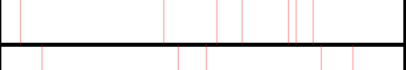


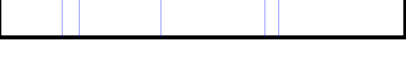
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=32$

mitochondrial translational elongation (GO:0070125)



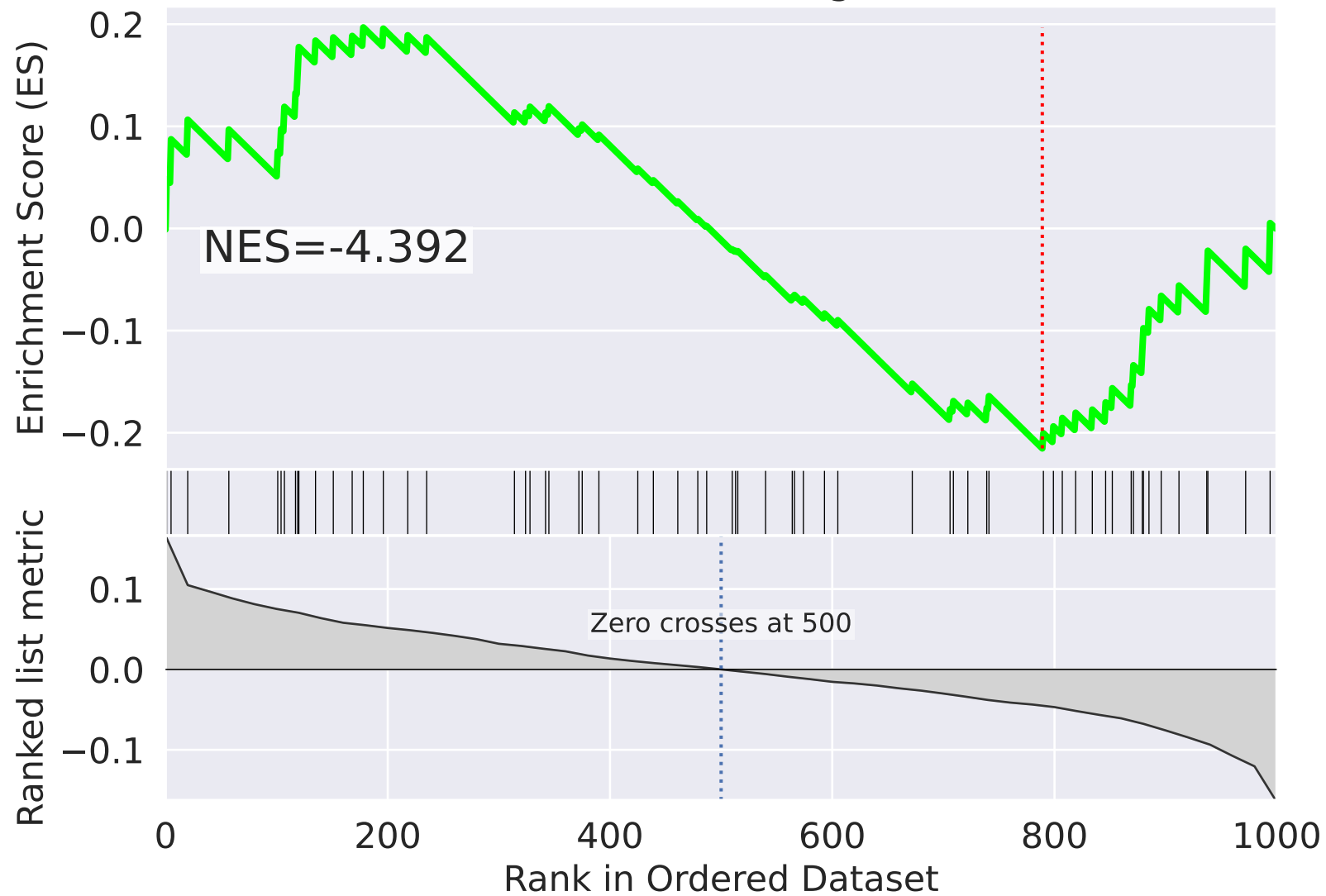
mitochondrial translational elongation (GO:0070125)



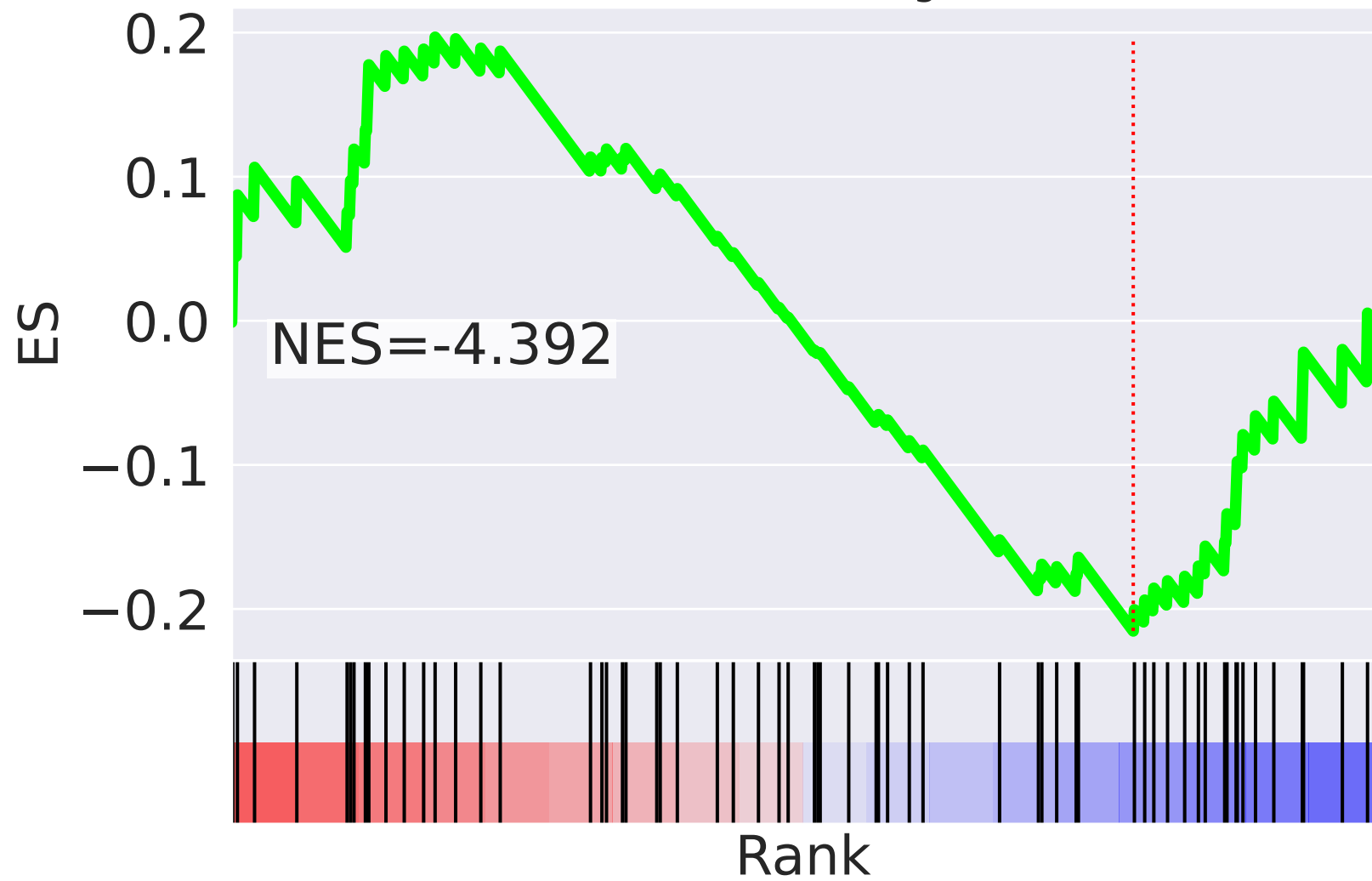
NES		SET
2.341		IRE1-mediated unfolded protein response (GO:0036498)
2.304		protein N-linked glycosylation via asparagine (GO:0018279)
2.237		regulation of cell motility (GO:2000145)
-2.149		small molecule metabolic process (GO:0044281)
-2.047		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.042		regulation of lipid metabolic process (GO:0019216)
-2.033		telomere capping (GO:0016233)
-2.029		cellular response to DNA damage stimulus (GO:0006974)
-2.023		intracellular transport of virus (GO:0075733)
2.020		blood coagulation (GO:0007596)
1.978		regulation of transcription from RNA polymerase II promoter (GO:0006357)
1.960		movement of cell or subcellular component (GO:0006928)
1.932		lipid metabolic process (GO:0006629)
-1.862		cellular respiration (GO:0045333)
-1.813		transcription from mitochondrial promoter (GO:0006390)

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

mitochondrial translational elongation (GO:0070125)

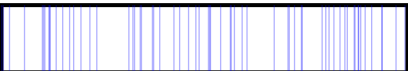




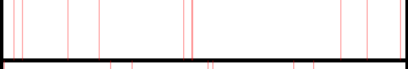
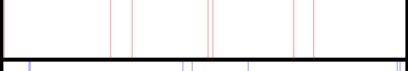
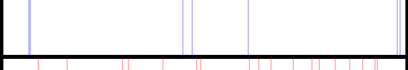
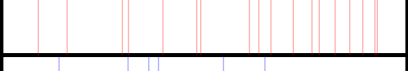





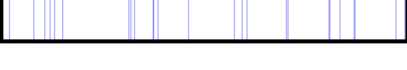


mitochondrial translational elongation (GO:0070125)



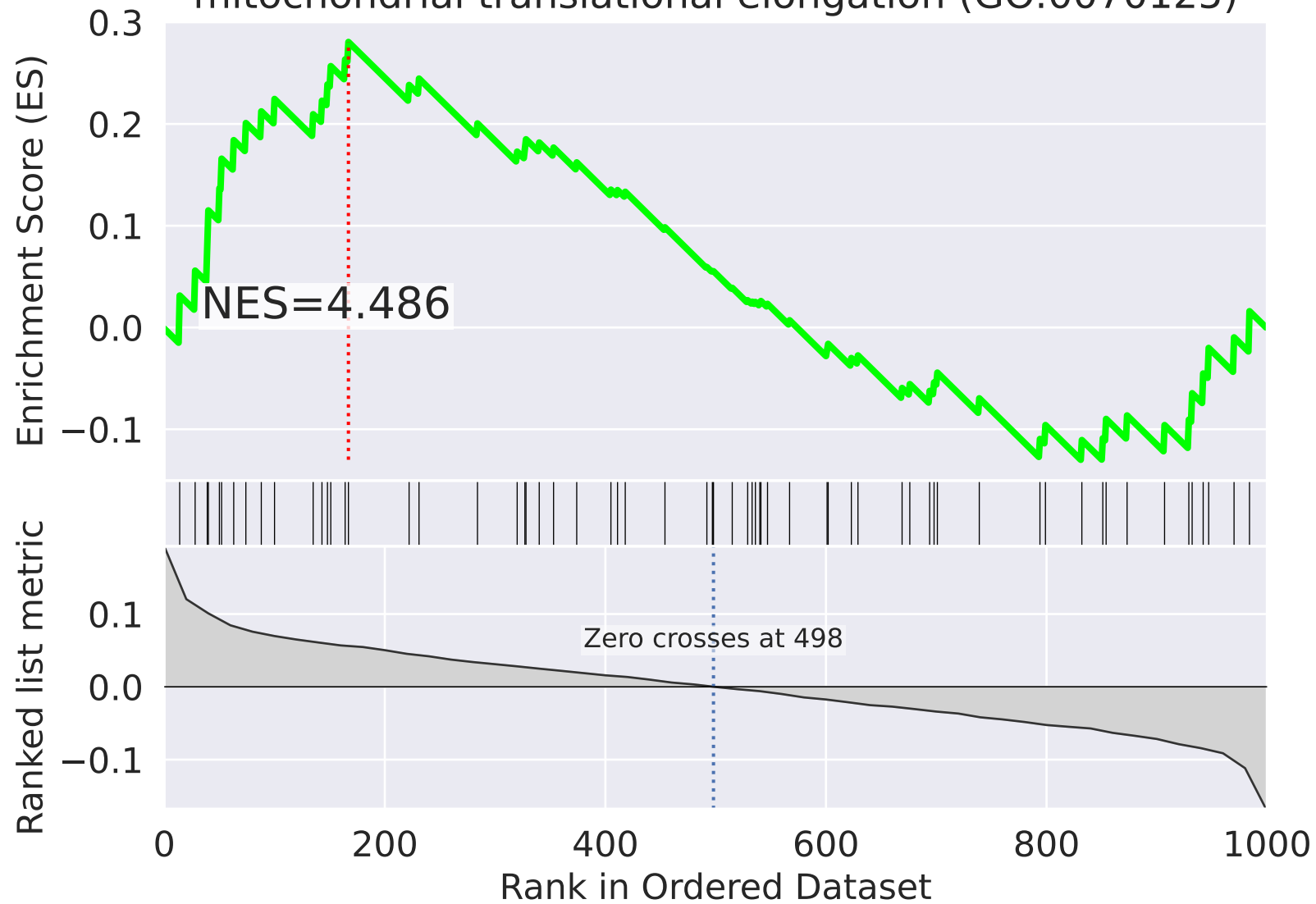
NES

SET

-4.392		mitochondrial translational elongation (GO:0070125)
-3.941		mitochondrial translational termination (GO:0070126)
-2.957		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.601		regulation of protein stability (GO:0031647)
-2.273		peptidyl-threonine phosphorylation (GO:0018107)
2.261		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.137		double-strand break repair (GO:0006302)
-2.130		cellular nitrogen compound metabolic process (GO:0034641)
2.049		G2/M transition of mitotic cell cycle (GO:0000086)
-1.963		heart development (GO:0007507)
-1.923		regulation of transcription from RNA polymerase II promoter (GO:0006357)
1.910		negative regulation of telomere maintenance via telomerase (GO:0032211)
-1.910		insulin receptor signaling pathway (GO:0008286)
-1.908		protein N-linked glycosylation via asparagine (GO:0018279)
-1.904		mitochondrial translation (GO:0032543)

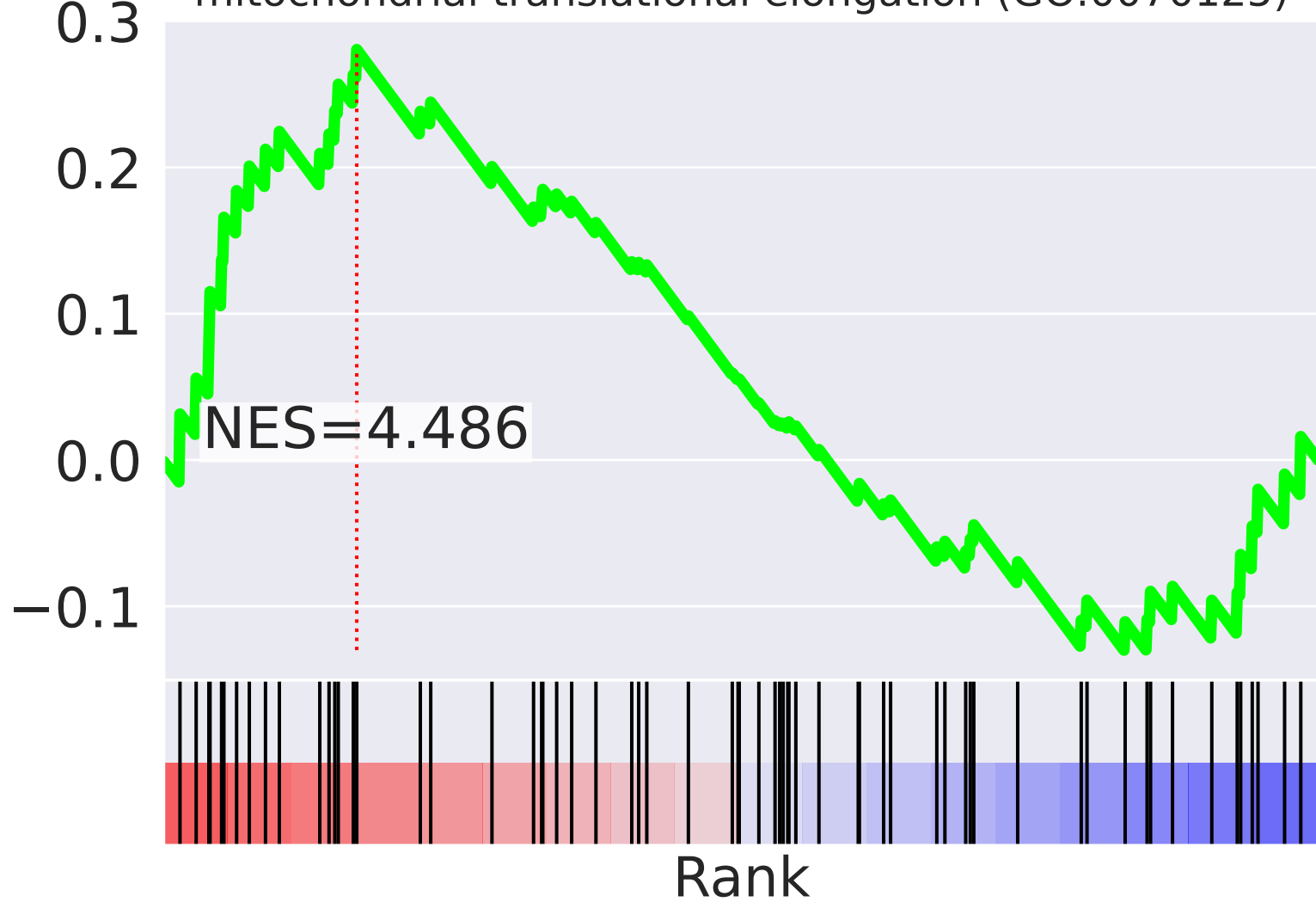
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=34$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

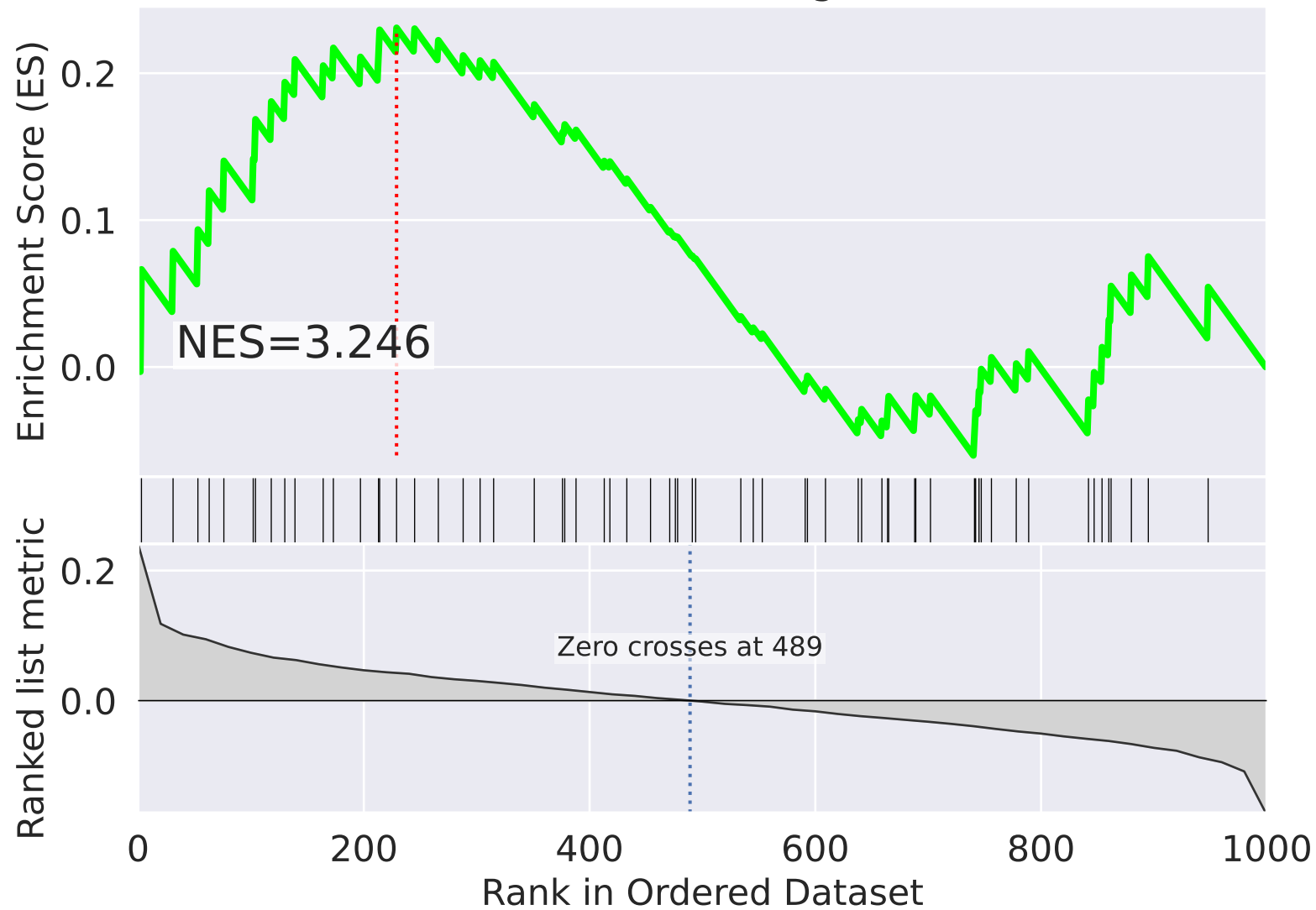
ES



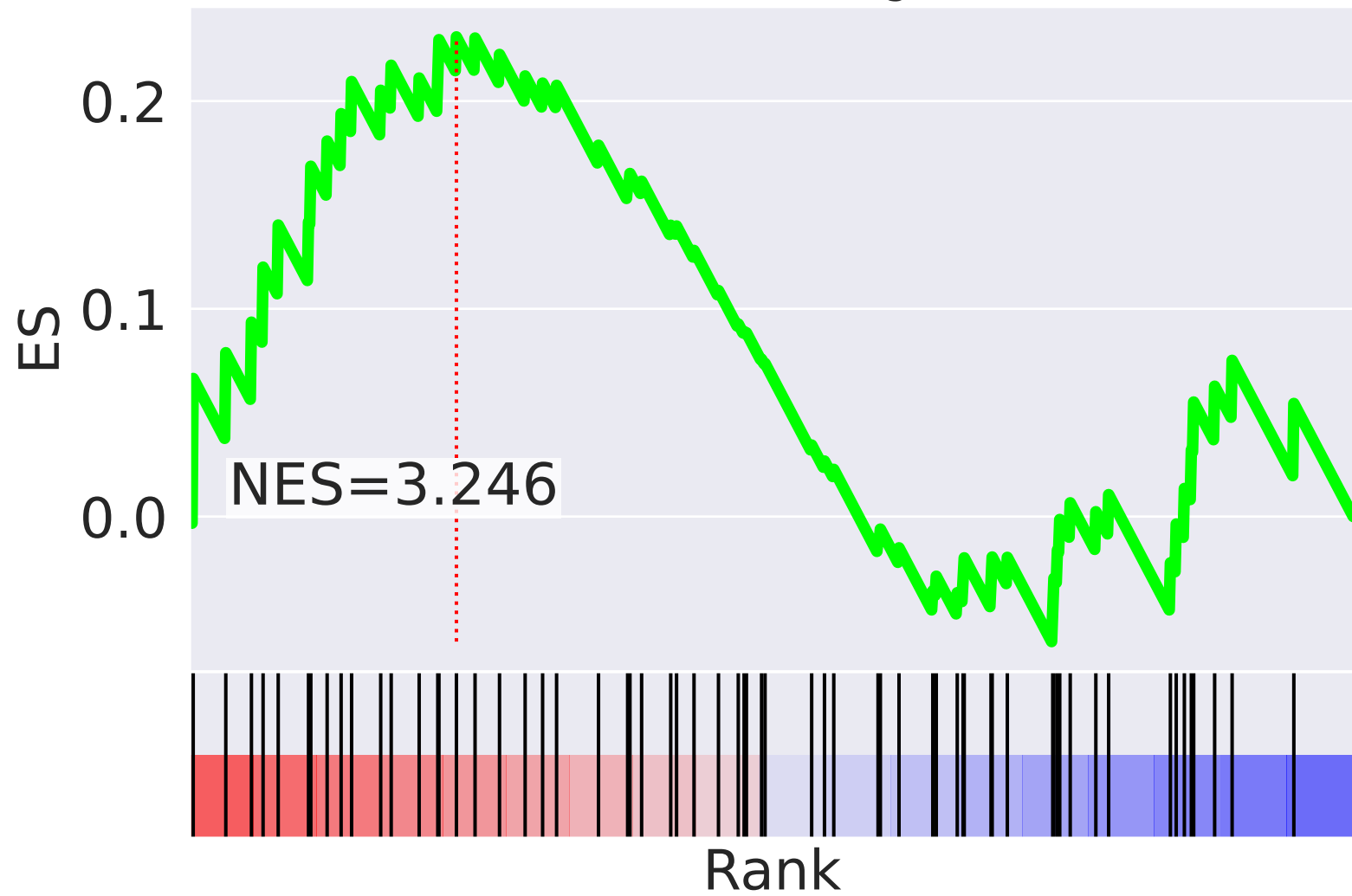
NES		SET
4.486		mitochondrial translational elongation (GO:0070125)
4.347		mitochondrial translational termination (GO:0070126)
3.050		translation (GO:0006412)
2.597		mitochondrial translation (GO:0032543)
-2.385		integrin-mediated signaling pathway (GO:0007229)
-2.329		negative regulation of cell cycle arrest (GO:0071157)
-2.241		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.232		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
-2.219		nervous system development (GO:0007399)
2.167		generation of precursor metabolites and energy (GO:0006091)
-2.119		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.110		cell migration (GO:0016477)
-2.044		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.025		RNA splicing (GO:0008380)
-1.927		mRNA export from nucleus (GO:0006406)

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)

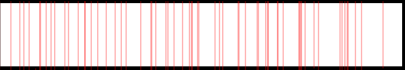
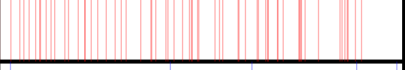


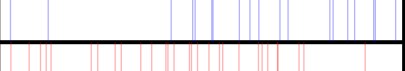
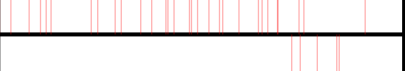

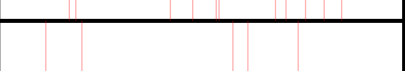
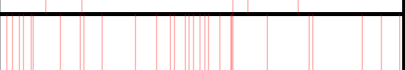








mitochondrial translational elongation (GO:0070125)



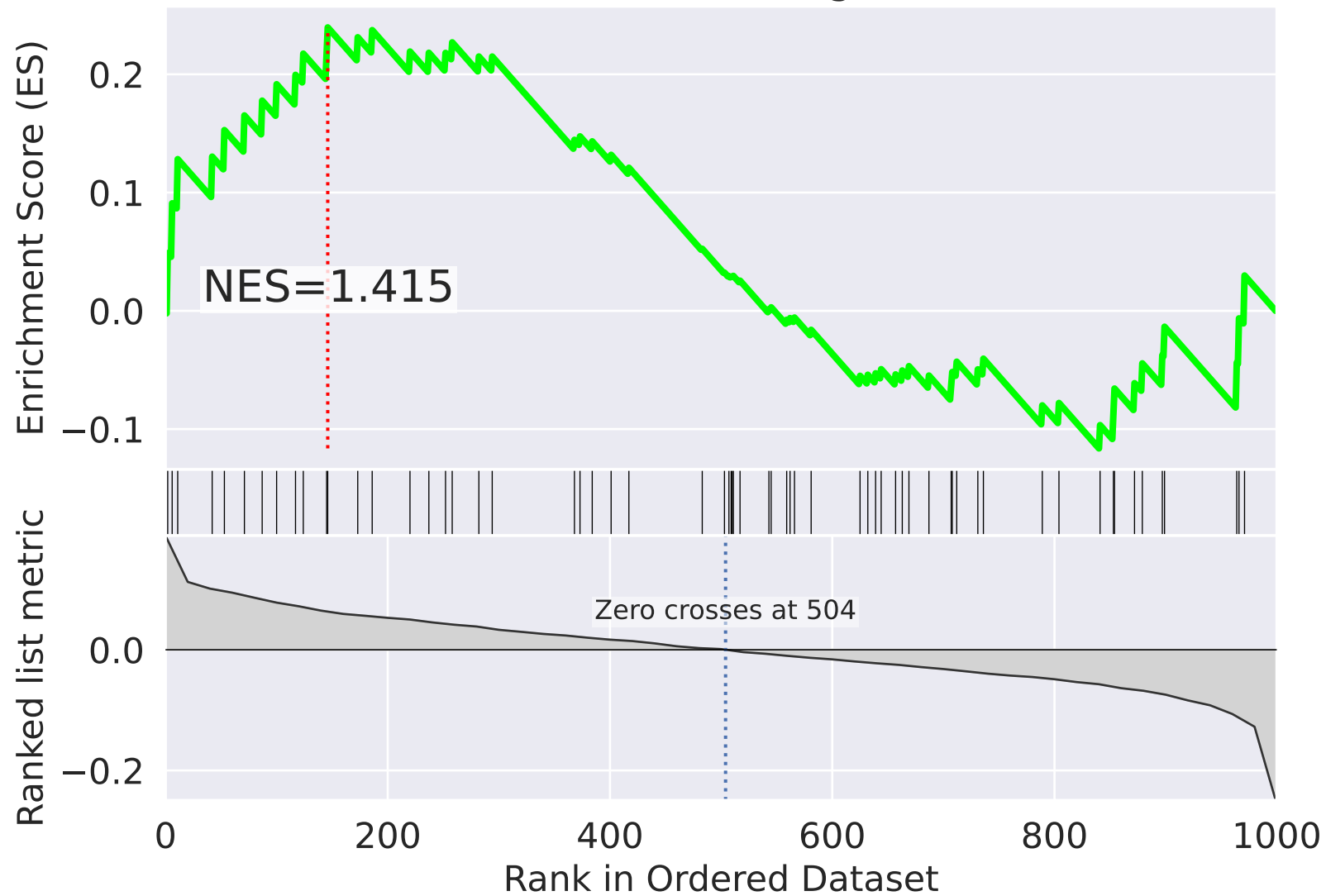
NES

SET

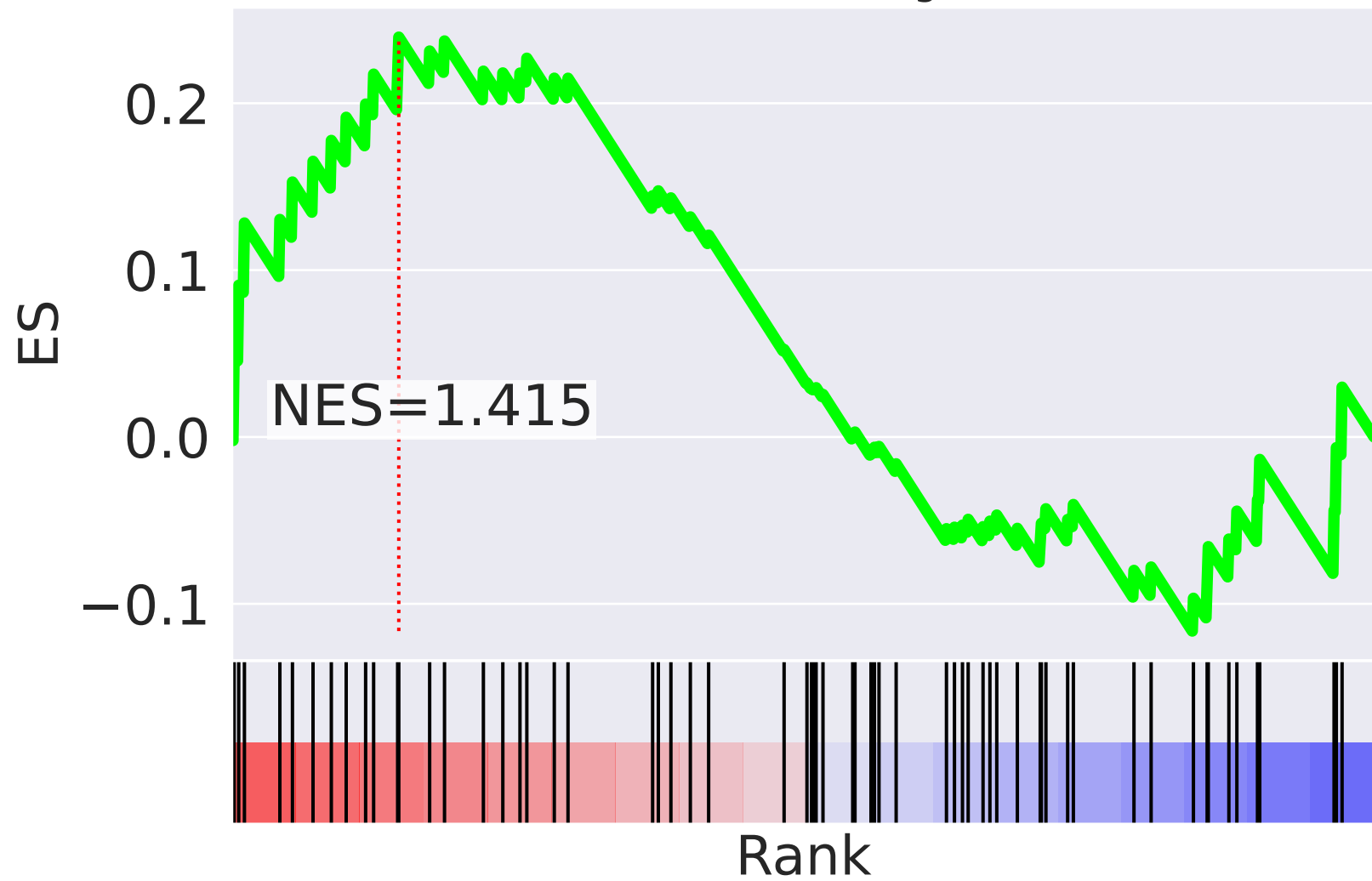
3.246		mitochondrial translational elongation (GO:0070125)
3.108		mitochondrial translational termination (GO:0070126)
-2.479		peptidyl-threonine phosphorylation (GO:0018107)
-2.448		execution phase of apoptosis (GO:0097194)
-2.415		negative regulation of cell proliferation (GO:0008285)
2.278		translation (GO:0006412)
2.237		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.160		positive regulation of gene expression (GO:0010628)
2.138		brain development (GO:0007420)
2.072		neutrophil degranulation (GO:0043312)
-2.015		intracellular signal transduction (GO:0035556)
-2.000		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
1.974		Golgi organization (GO:0007030)
-1.874		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.865		endoplasmic reticulum organization (GO:0007029)




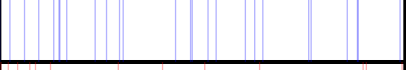
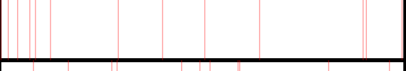


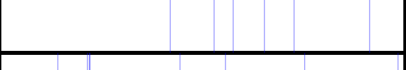

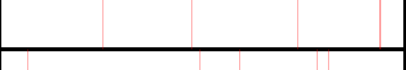



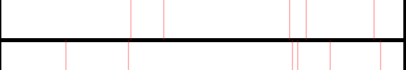
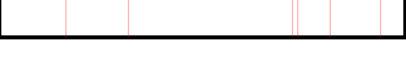
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=36$

mitochondrial translational elongation (GO:0070125)



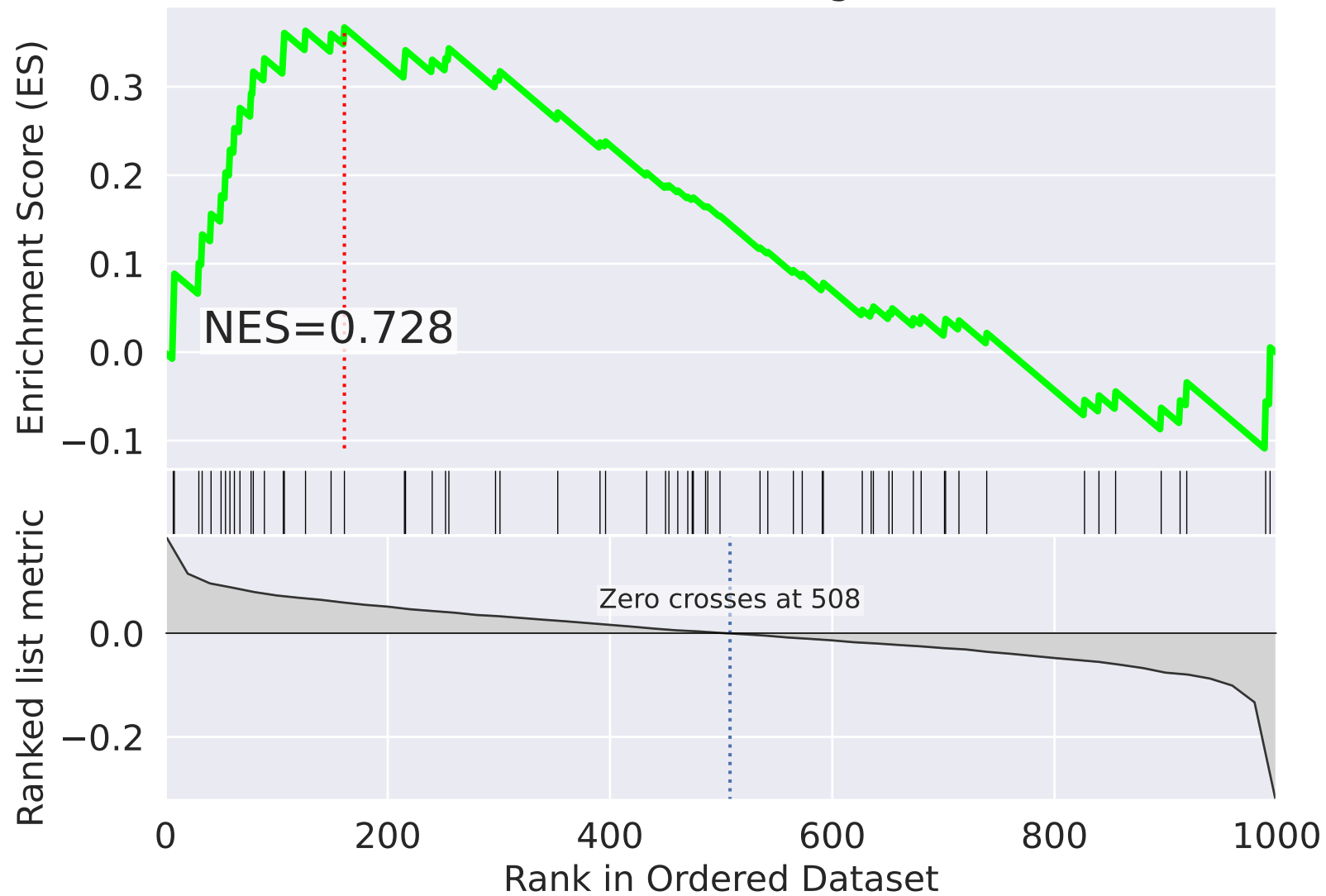
mitochondrial translational elongation (GO:0070125)



NES		SET
3.136		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.335		chromatin remodeling (GO:0006338)
-2.318		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
-2.241		mRNA splicing, via spliceosome (GO:0000398)
2.153		histone H3 acetylation (GO:0043966)
2.095		phosphatidylinositol-mediated signaling (GO:0048015)
2.085		ESCRT III complex disassembly (GO:1904903)
-1.993		iron-sulfur cluster assembly (GO:0016226)
-1.957		tRNA modification (GO:0006400)
1.957		nucleosome disassembly (GO:0006337)
1.956		regulation of cell motility (GO:2000145)
-1.954		regulation of cellular response to heat (GO:1900034)
1.950		cell migration (GO:0016477)
1.904		inflammatory response (GO:0006954)
1.898		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 $z=37$

mitochondrial translational elongation (GO:0070125)



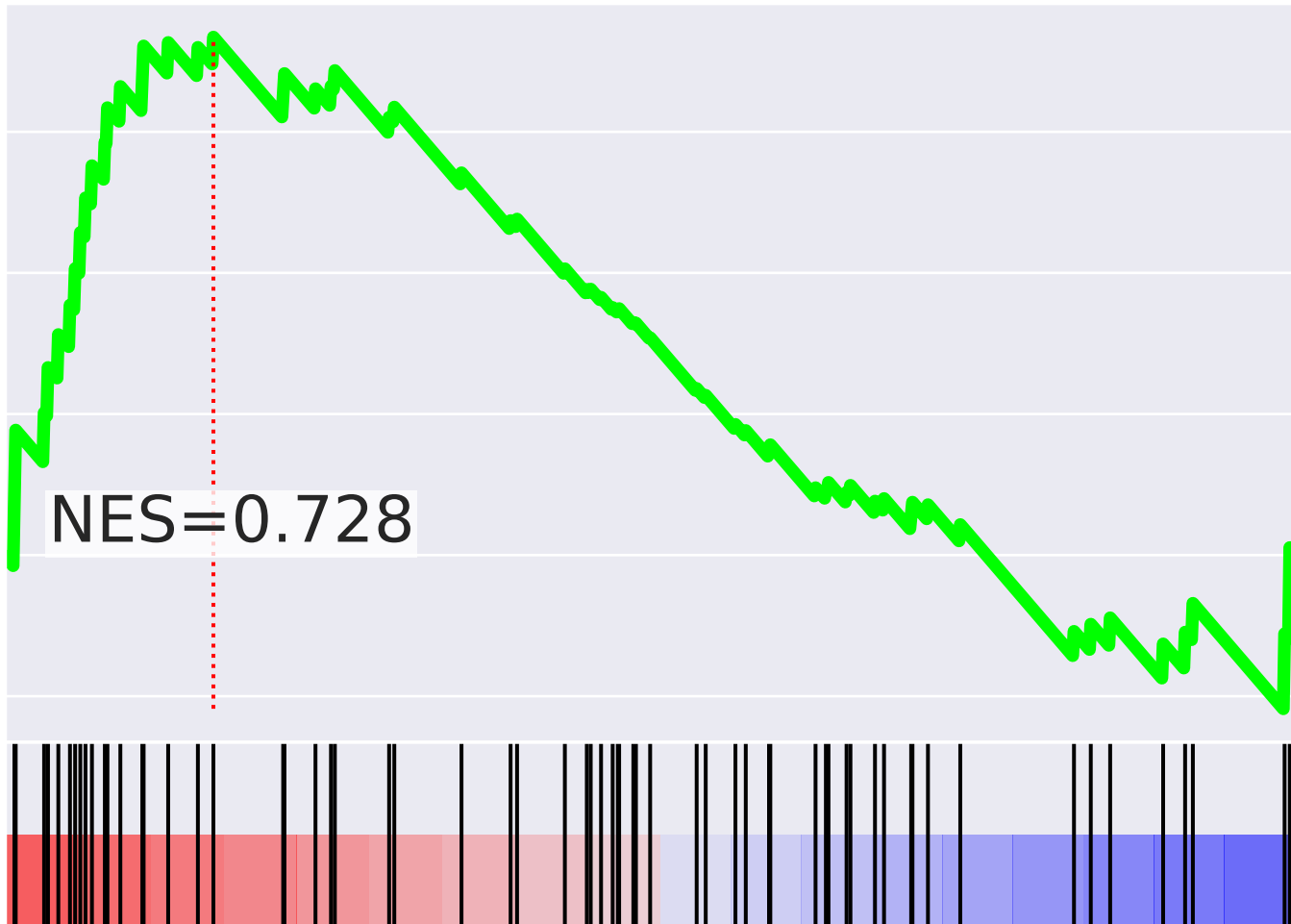
mitochondrial translational elongation (GO:0070125)

ES

0.3
0.2
0.1
0.0
-0.1




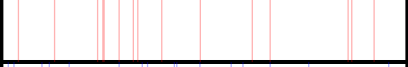


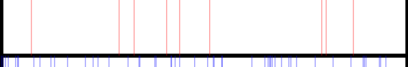
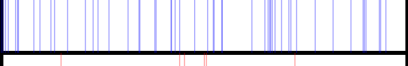
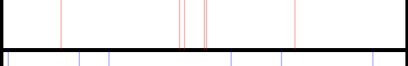
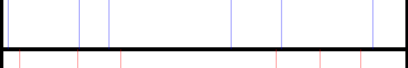


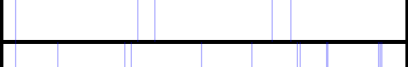

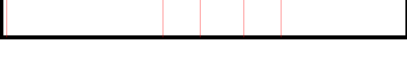
NES=0.728

Rank



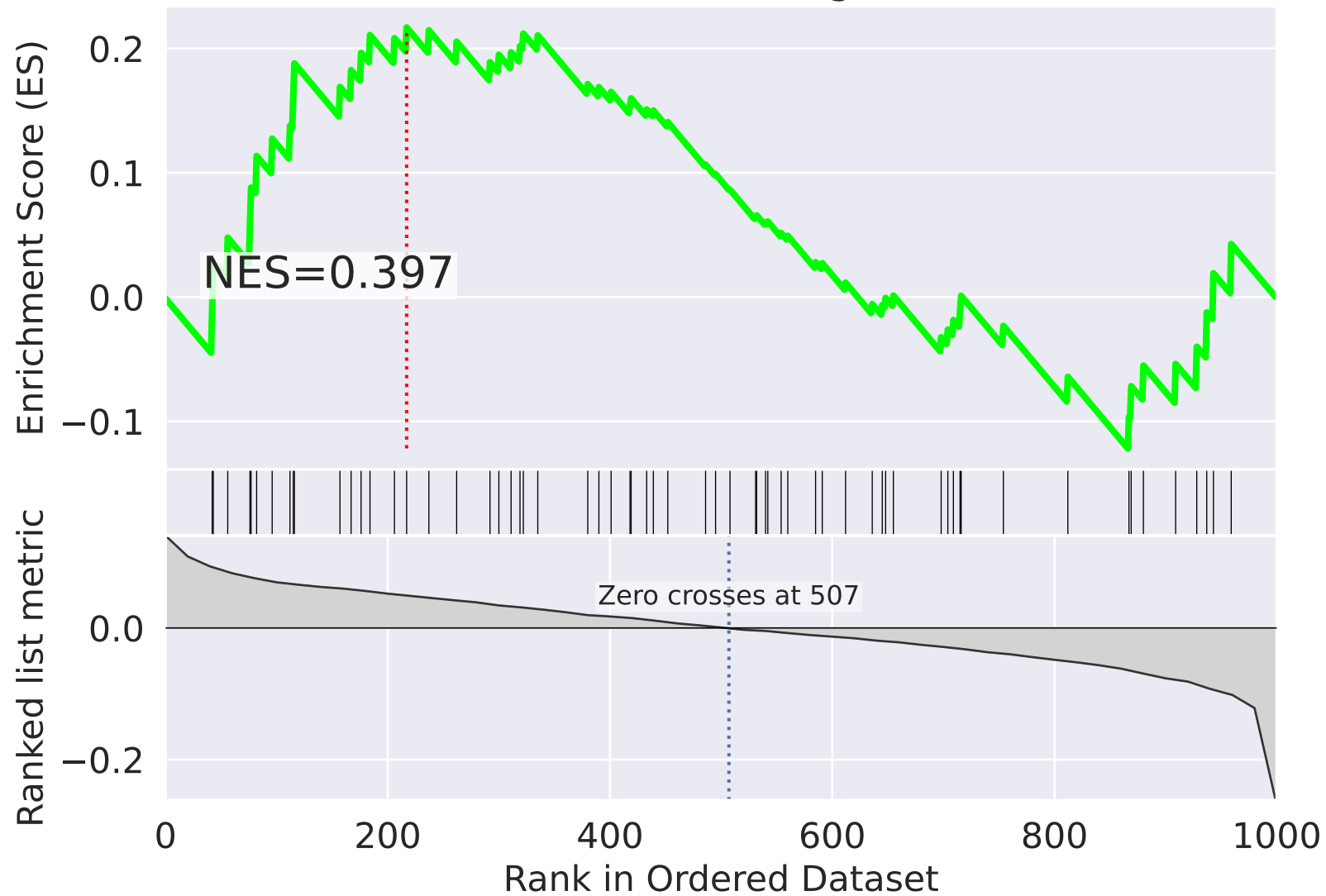
NES

SET

3.056		positive regulation of gene expression (GO:0010628)
-2.980		regulation of transcription, DNA-templated (GO:0006355)
2.640		mitotic metaphase plate congression (GO:0007080)
2.230		positive regulation of apoptotic process (GO:0043065)
-2.223		cell cycle arrest (GO:0007050)
-2.187		nervous system development (GO:0007399)
2.172		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.127		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.124		chromosome segregation (GO:0007059)
-2.121		heart development (GO:0007507)
2.091		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.082		regulation of cell motility (GO:2000145)
-2.047		positive regulation by host of viral transcription (GO:0043923)
-2.035		protein stabilization (GO:0050821)
2.034		regulation of defense response to virus by virus (GO:0050690)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1



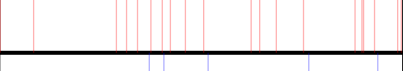




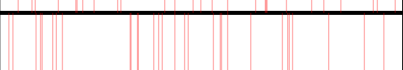


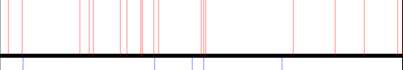
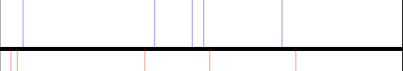
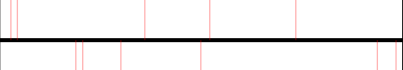
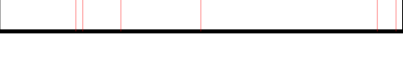

0.0

-0.1

NES=0.397

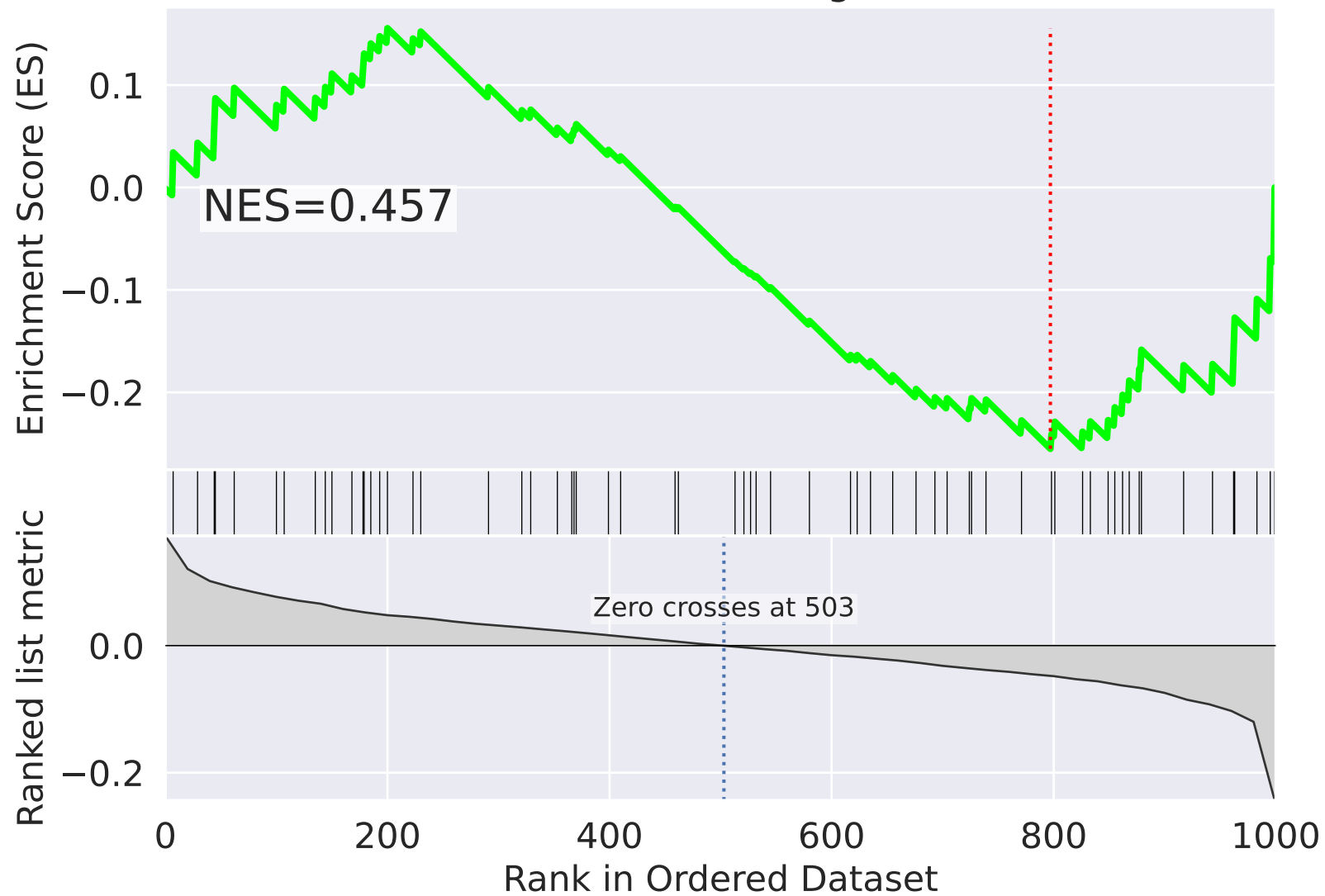
Rank



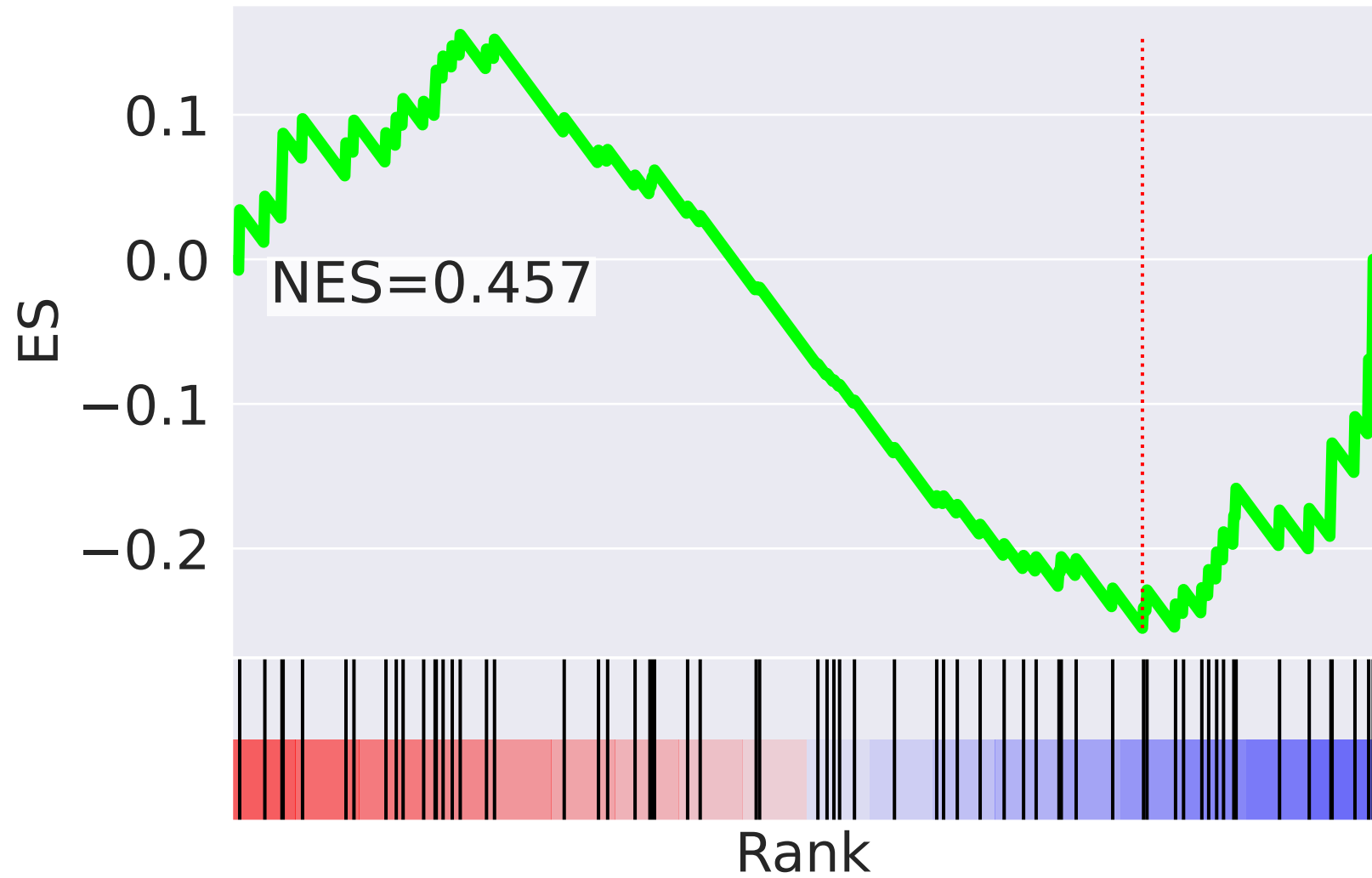
NES		SET
-3.868		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.950		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.533		cellular response to DNA damage stimulus (GO:0006974)
-2.291		cellular respiration (GO:0045333)
2.224		positive regulation of apoptotic process (GO:0043065)
2.171		regulation of signal transduction by p53 class mediator (GO:1901796)
2.040		DNA replication (GO:0006260)
1.977		mRNA splicing, via spliceosome (GO:0000398)
1.935		negative regulation of transcription, DNA-templated (GO:0045892)
1.923		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
1.904		RNA metabolic process (GO:0016070)
1.857		negative regulation of cell proliferation (GO:0008285)
-1.850		peptidyl-threonine phosphorylation (GO:0018107)
1.783		platelet degranulation (GO:0002576)
1.720		mRNA processing (GO:0006397)



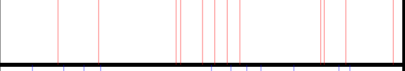


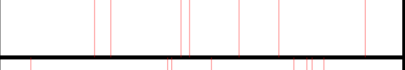
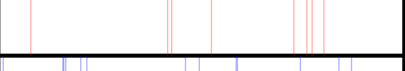
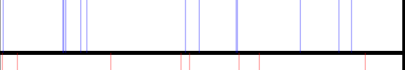

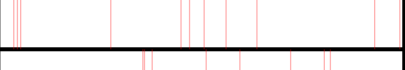



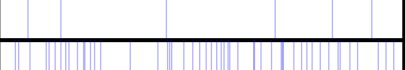
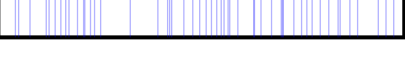
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=39$

mitochondrial translational elongation (GO:0070125)



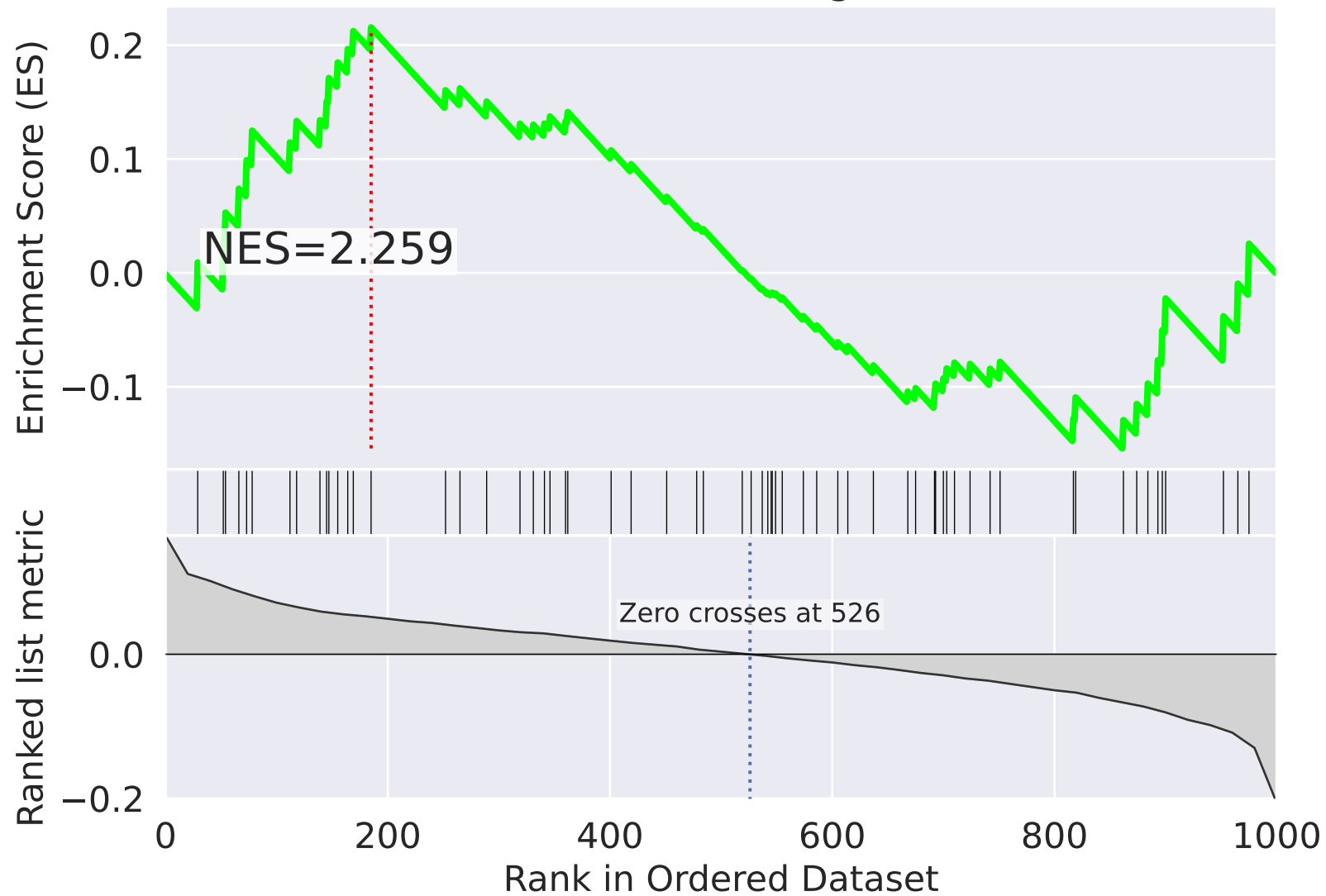
mitochondrial translational elongation (GO:0070125)



NES		SET
2.820		positive regulation of apoptotic process (GO:0043065)
2.658		T cell costimulation (GO:0031295)
2.609		mitotic metaphase plate congression (GO:0007080)
-2.498		chromatin remodeling (GO:0006338)
2.477		multivesicular body assembly (GO:0036258)
2.339		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.296		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
-2.292		histone H3 acetylation (GO:0043966)
2.238		axon guidance (GO:0007411)
2.233		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.161		protein homooligomerization (GO:0051260)
-2.097		protein N-linked glycosylation (GO:0006487)
-2.076		nervous system development (GO:0007399)
-2.031		centrosome cycle (GO:0007098)
-1.979		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)

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)

ES

0.2

0.1

0.0

-0.1

NES=2.259

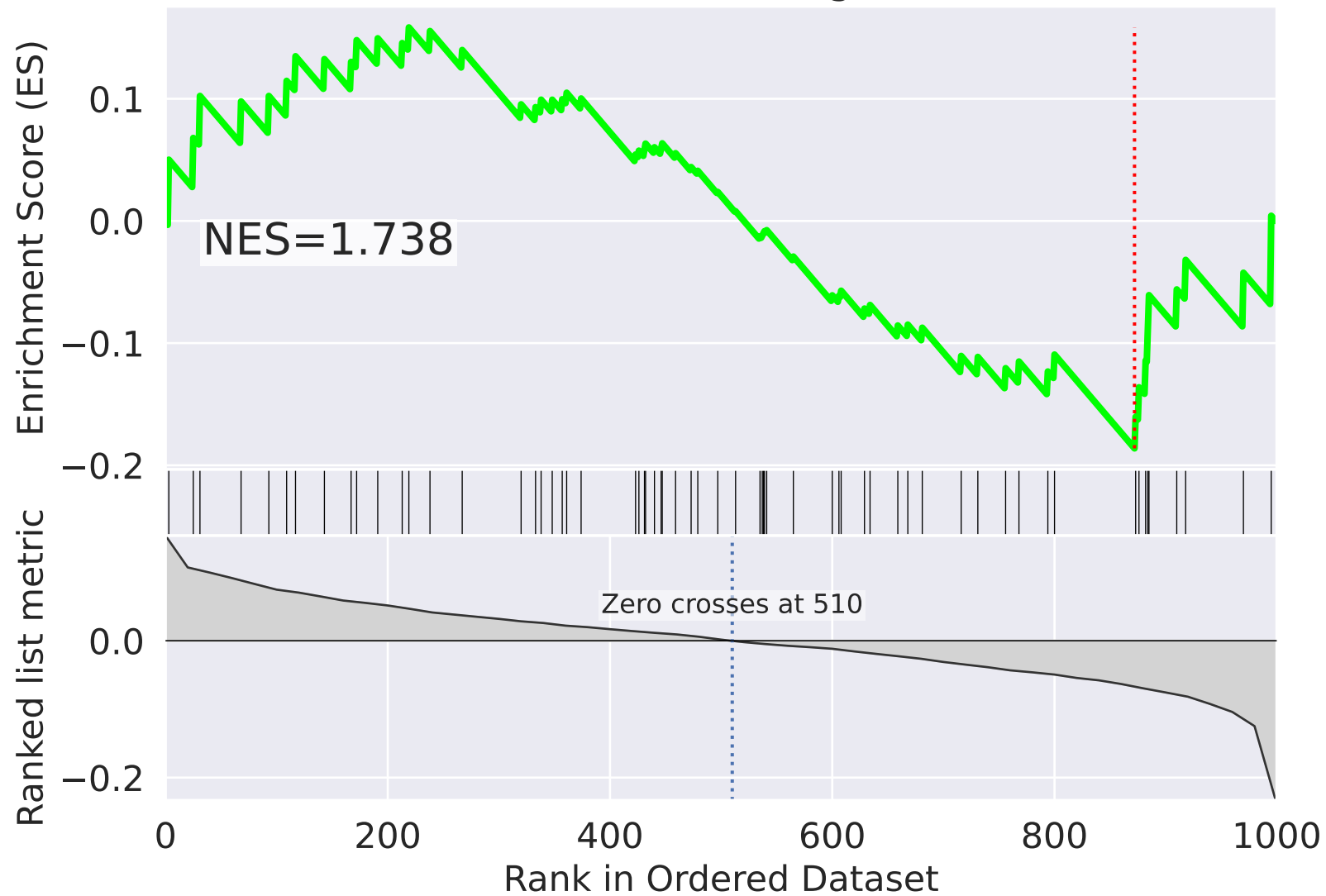
Rank



NES		SET
2.811		mitochondrial translational termination (GO:0070126)
2.663		ESCRT III complex disassembly (GO:1904903)
-2.591		chromatin remodeling (GO:0006338)
2.570		cell division (GO:0051301)
2.518		epidermal growth factor receptor signaling pathway (GO:0007173)
2.389		mitotic metaphase plate congression (GO:0007080)
2.382		execution phase of apoptosis (GO:0097194)
-2.365		positive regulation of protein ubiquitination (GO:0031398)
-2.321		nucleosome disassembly (GO:0006337)
-2.301		cellular nitrogen compound metabolic process (GO:0034641)
2.262		nucleus organization (GO:0006997)
2.259		mitochondrial translational elongation (GO:0070125)
-2.234		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.194		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.164		regulation of cell motility (GO:2000145)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

NES=1.738

Rank

0.1

0.0

-0.1

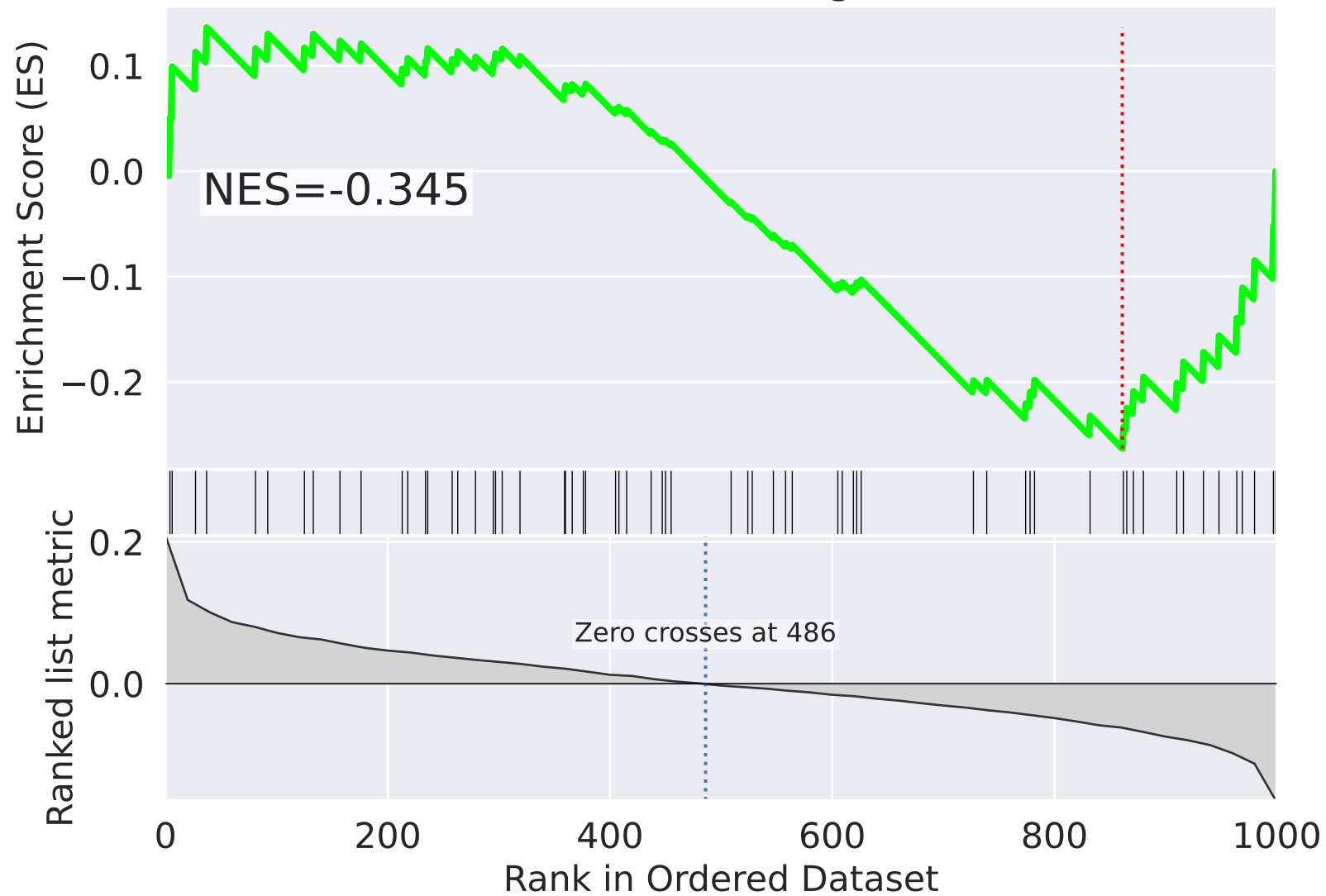
-0.2



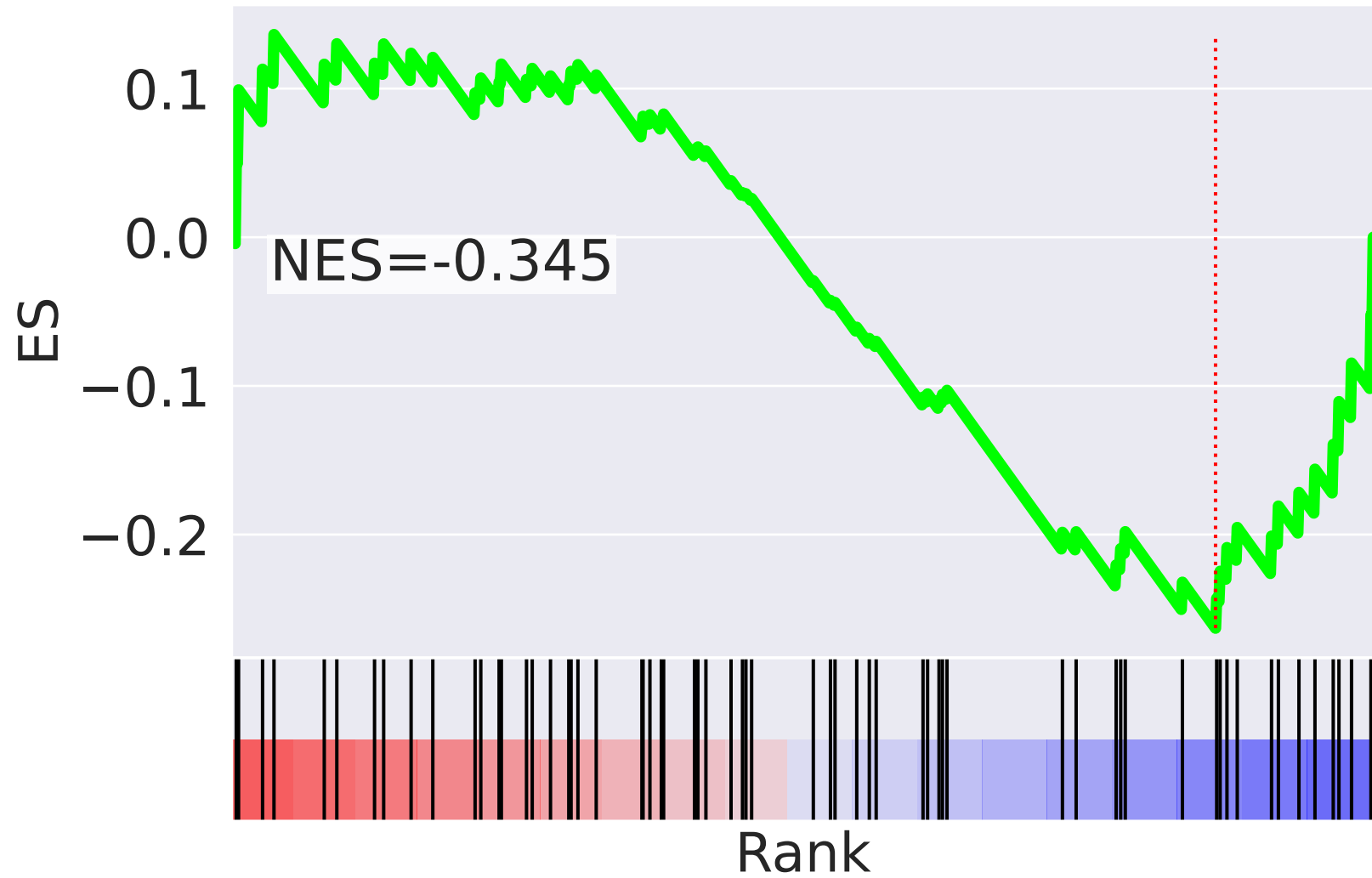
NES		SET
-3.517		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.623		chromatin remodeling (GO:0006338)
-2.619		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.473		platelet aggregation (GO:0070527)
2.357		cell migration (GO:0016477)
-2.317		mRNA export from nucleus (GO:0006406)
2.260		multicellular organism development (GO:0007275)
2.108		ERBB2 signaling pathway (GO:0038128)
2.103		nucleosome disassembly (GO:0006337)
2.053		positive regulation of cell growth (GO:0030307)
-2.015		cellular respiration (GO:0045333)
2.007		negative regulation of translation (GO:0017148)
1.952		cell growth (GO:0016049)
1.913		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
1.876		regulation of transcription from RNA polymerase II promoter (GO:0006357)


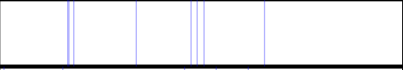


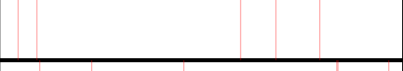



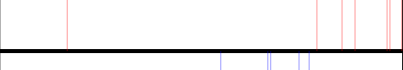


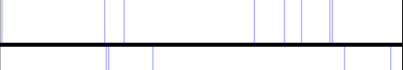
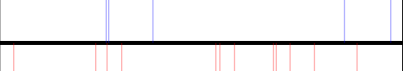
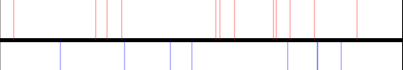

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=42$

mitochondrial translational elongation (GO:0070125)



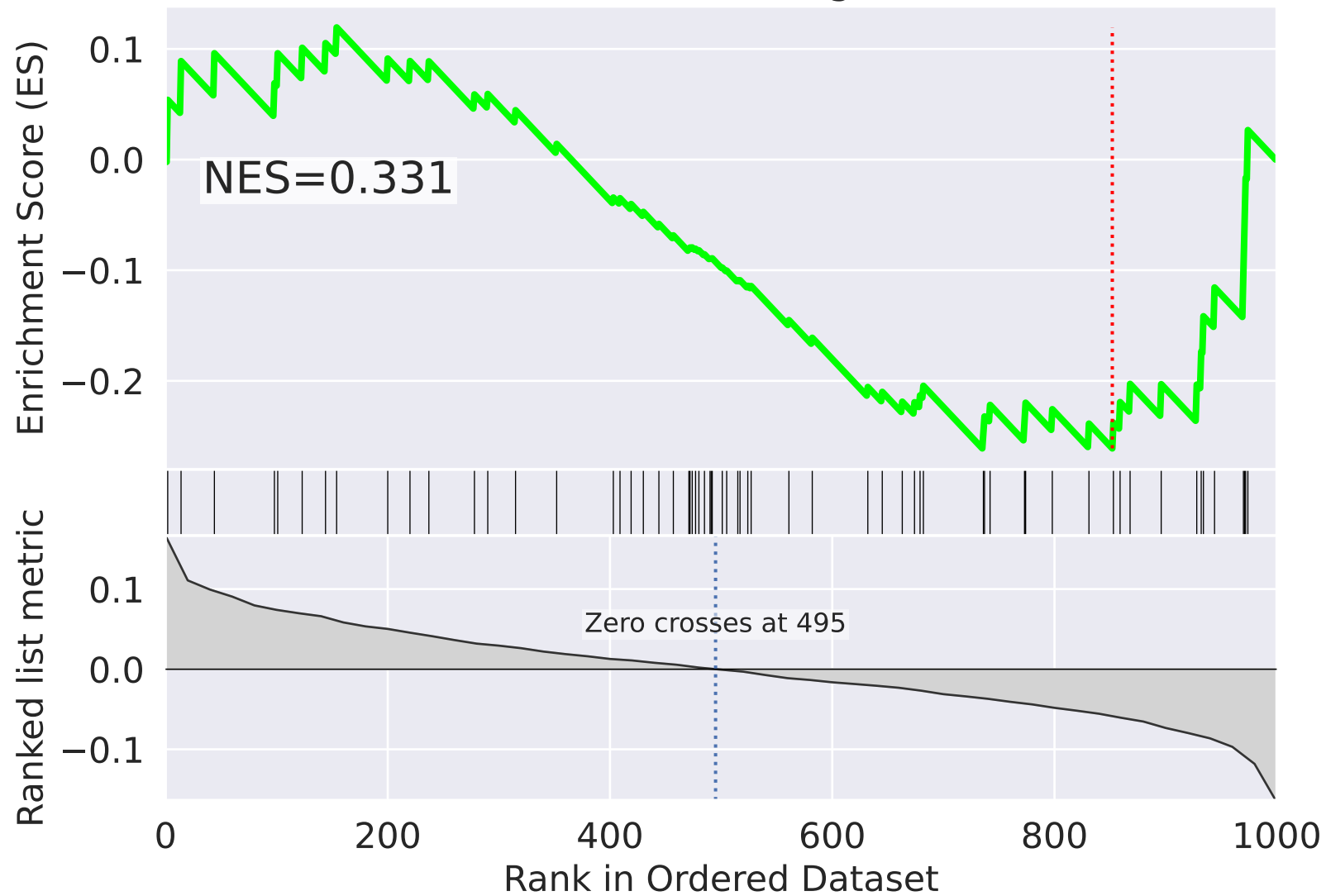
mitochondrial translational elongation (GO:0070125)



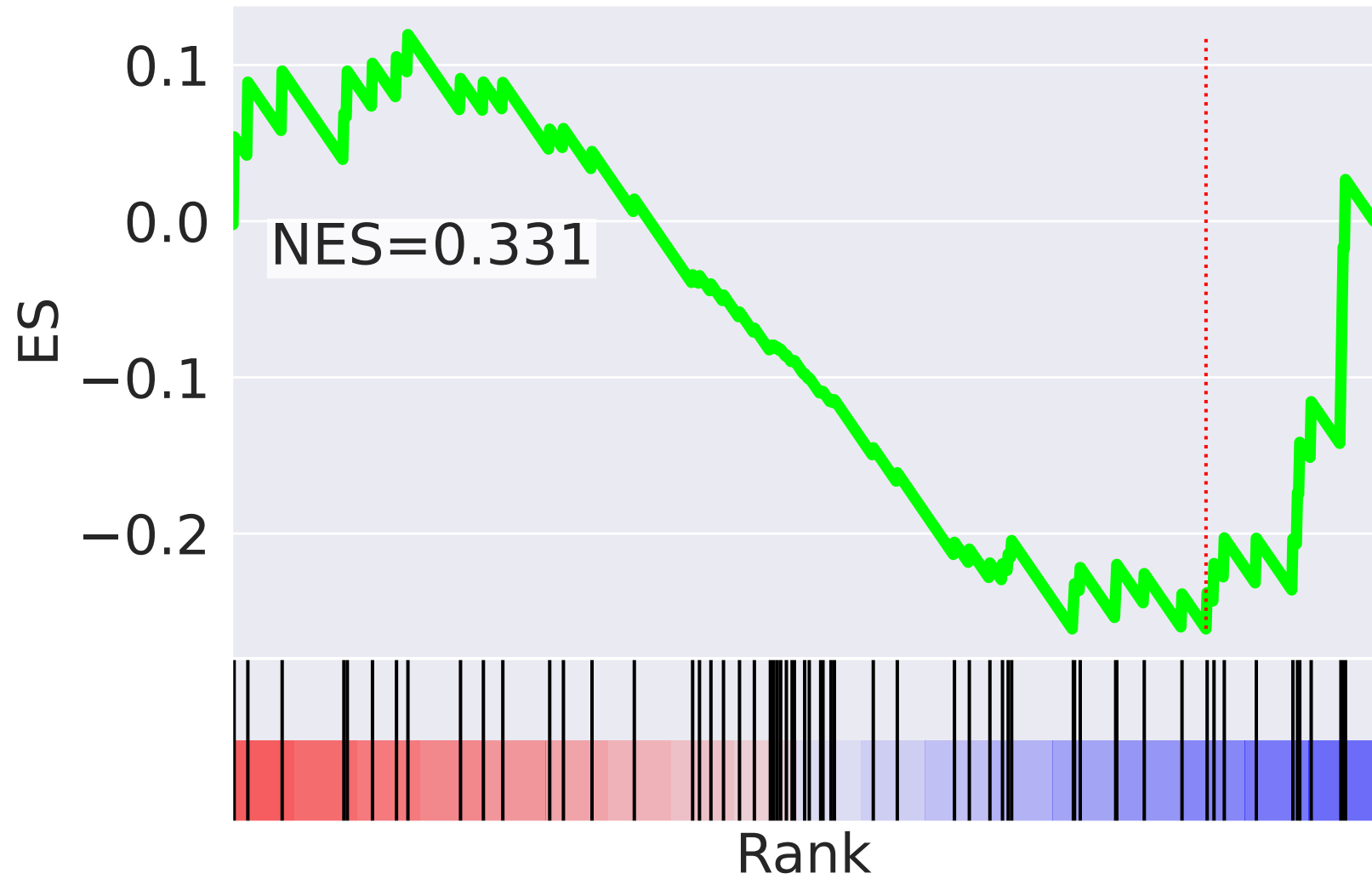
NES		SET
2.105		iron-sulfur cluster assembly (GO:0016226)
-2.051		negative regulation of translation (GO:0017148)
-2.008		intracellular transport of virus (GO:0075733)
-1.995		mitotic cell cycle (GO:0000278)
1.981		positive regulation of GTPase activity (GO:0043547)
1.971		histone H3-K4 methylation (GO:0051568)
1.950		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-1.943		termination of RNA polymerase II transcription (GO:0006369)
1.802		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-1.759		mRNA 3'-end processing (GO:0031124)
1.717		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-1.716		nervous system development (GO:0007399)
-1.707		positive regulation of protein catabolic process (GO:0045732)
1.703		mitotic metaphase plate congression (GO:0007080)
-1.671		intracellular signal transduction (GO:0035556)

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

mitochondrial translational elongation (GO:0070125)



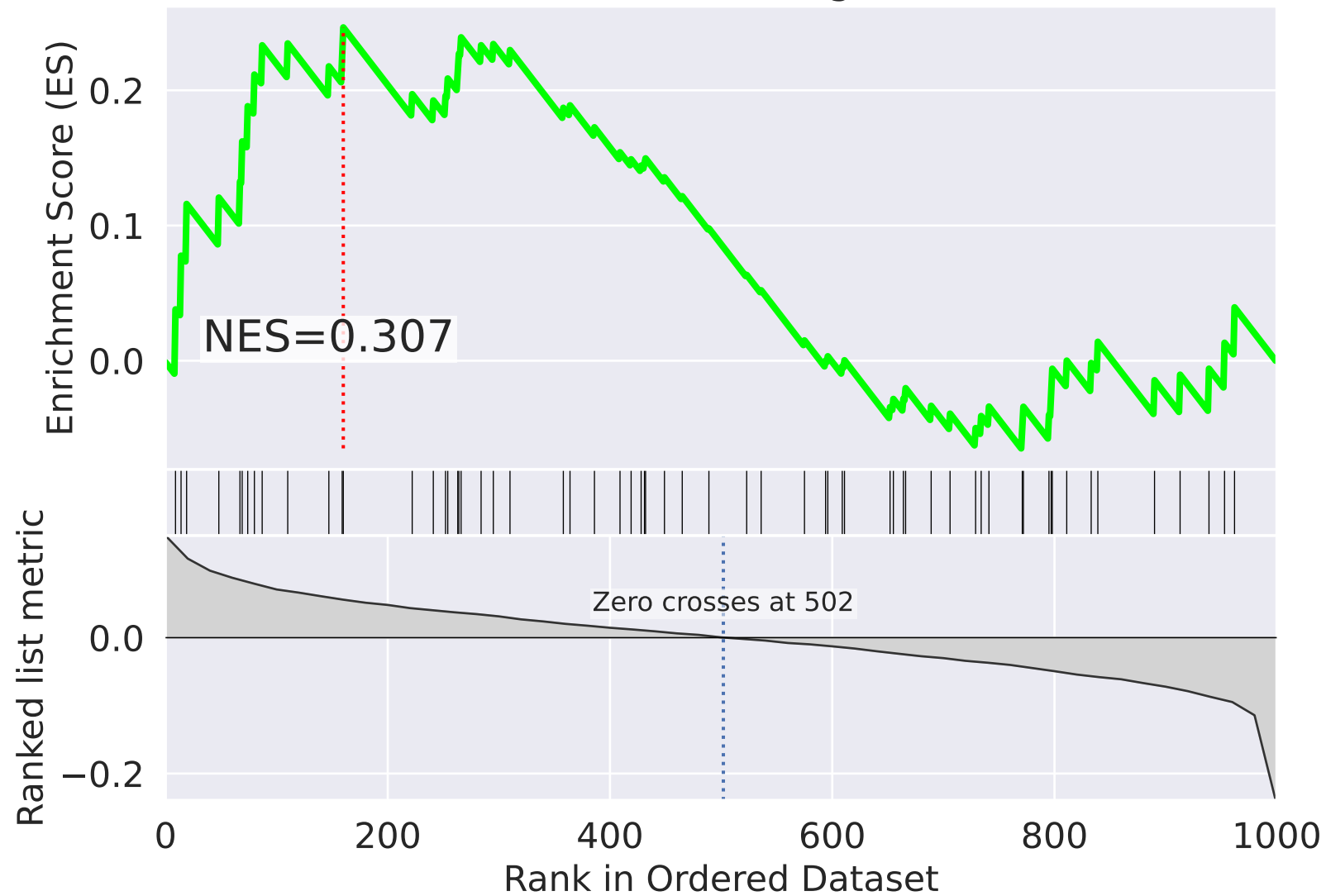
mitochondrial translational elongation (GO:0070125)



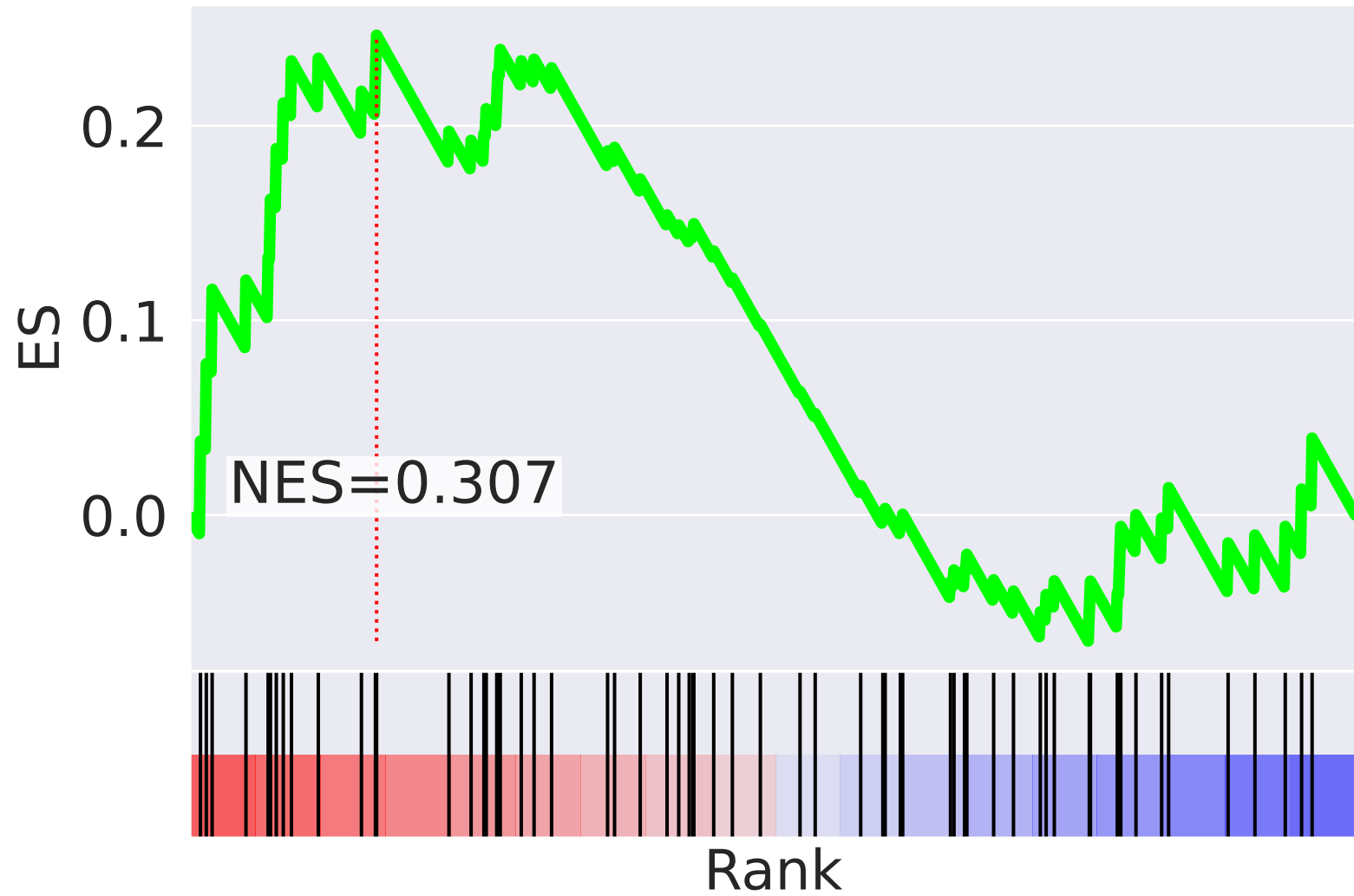
NES		SET
-2.552		mitotic metaphase plate congression (GO:0007080)
-2.494		regulation of macroautophagy (GO:0016241)
-2.464		nucleus organization (GO:0006997)
-2.348		cell separation after cytokinesis (GO:0000920)
2.343		cellular response to DNA damage stimulus (GO:0006974)
-2.143		protein homooligomerization (GO:0051260)
2.143		ubiquitin-dependent protein catabolic process (GO:0006511)
2.126		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.118		multivesicular body assembly (GO:0036258)
-2.098		ESCRT III complex disassembly (GO:1904903)
-2.083		transcription from RNA polymerase II promoter (GO:0006366)
-2.061		cellular response to amino acid stimulus (GO:0071230)
2.045		regulation of mRNA stability (GO:0043488)
-2.033		vesicle-mediated transport (GO:0016192)
-2.004		cell division (GO:0051301)

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)



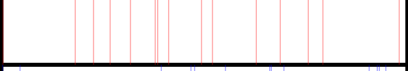
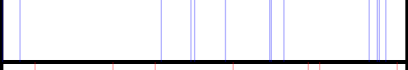

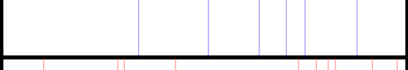



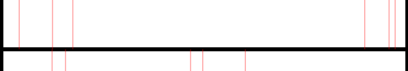
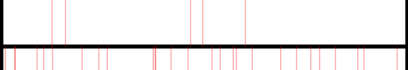
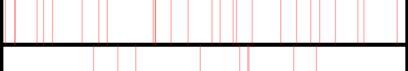





mitochondrial translational elongation (GO:0070125)



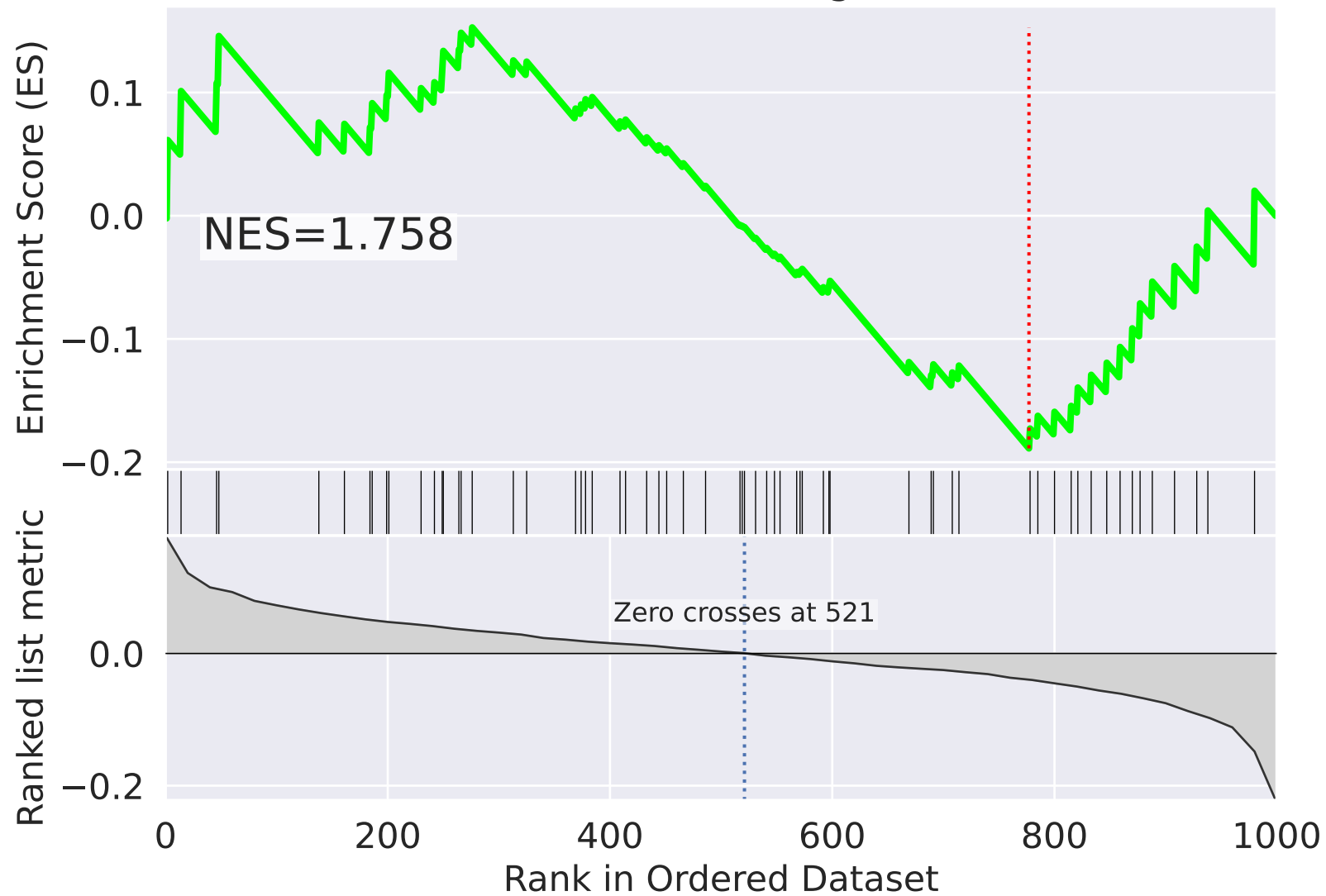
NES

SET

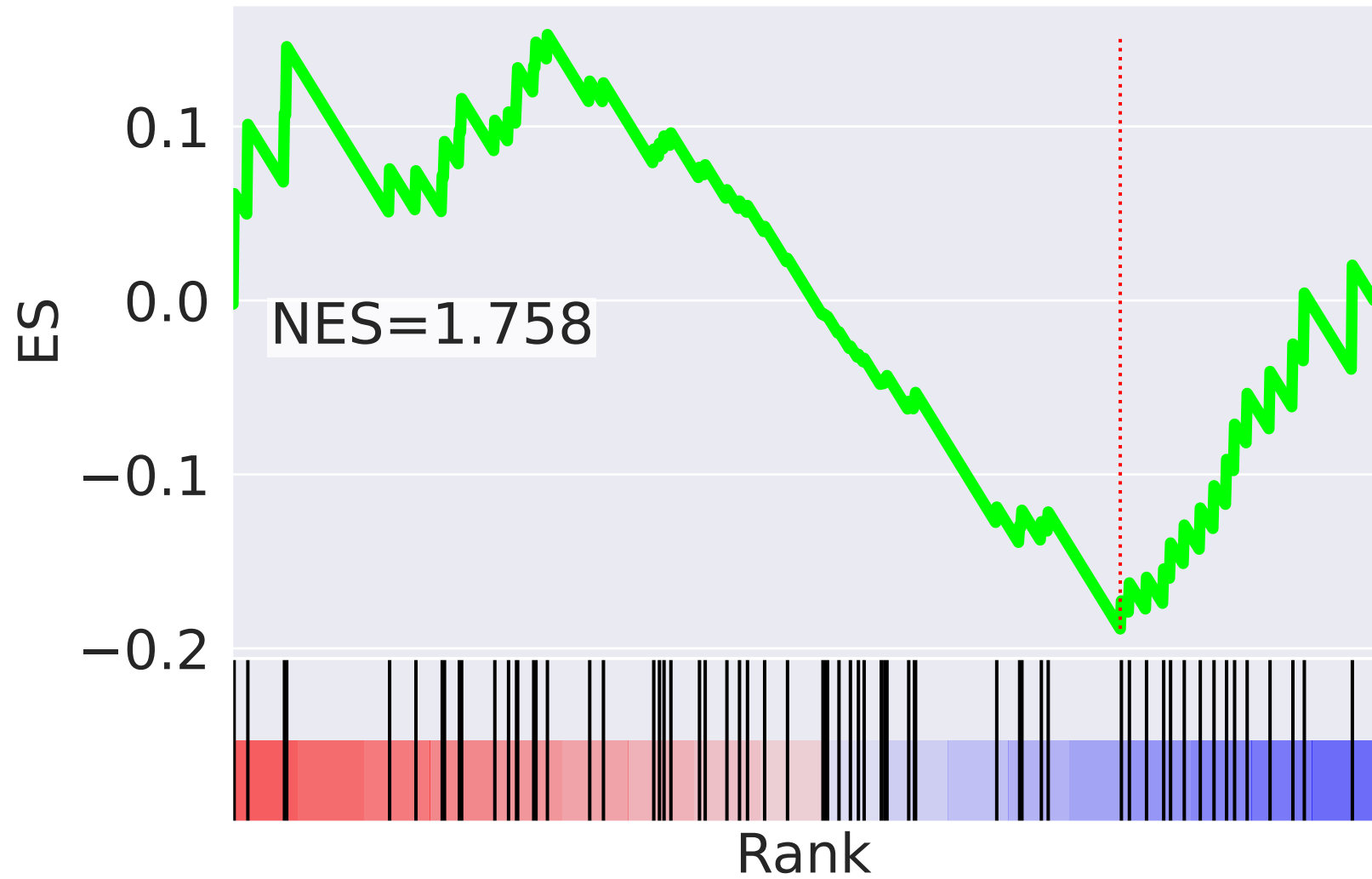
2.953		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.779		axon guidance (GO:0007411)
2.510		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-2.461		histone H3 acetylation (GO:0043966)
2.435		cell surface receptor signaling pathway (GO:0007166)
-2.410		interstrand cross-link repair (GO:0036297)
2.337		epidermal growth factor receptor signaling pathway (GO:0007173)
2.272		negative regulation of translation (GO:0017148)
2.264		mitotic metaphase plate congression (GO:0007080)
2.261		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
2.249		DNA damage checkpoint (GO:0000077)
2.163		signal transduction (GO:0007165)
2.158		integrin-mediated signaling pathway (GO:0007229)
-2.125		nervous system development (GO:0007399)
2.104		regulation of cell proliferation (GO:0042127)


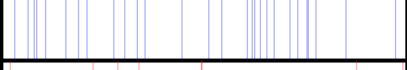




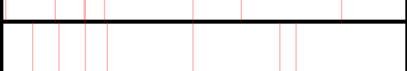





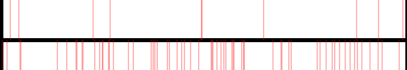
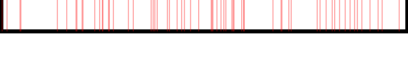

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=45$

mitochondrial translational elongation (GO:0070125)



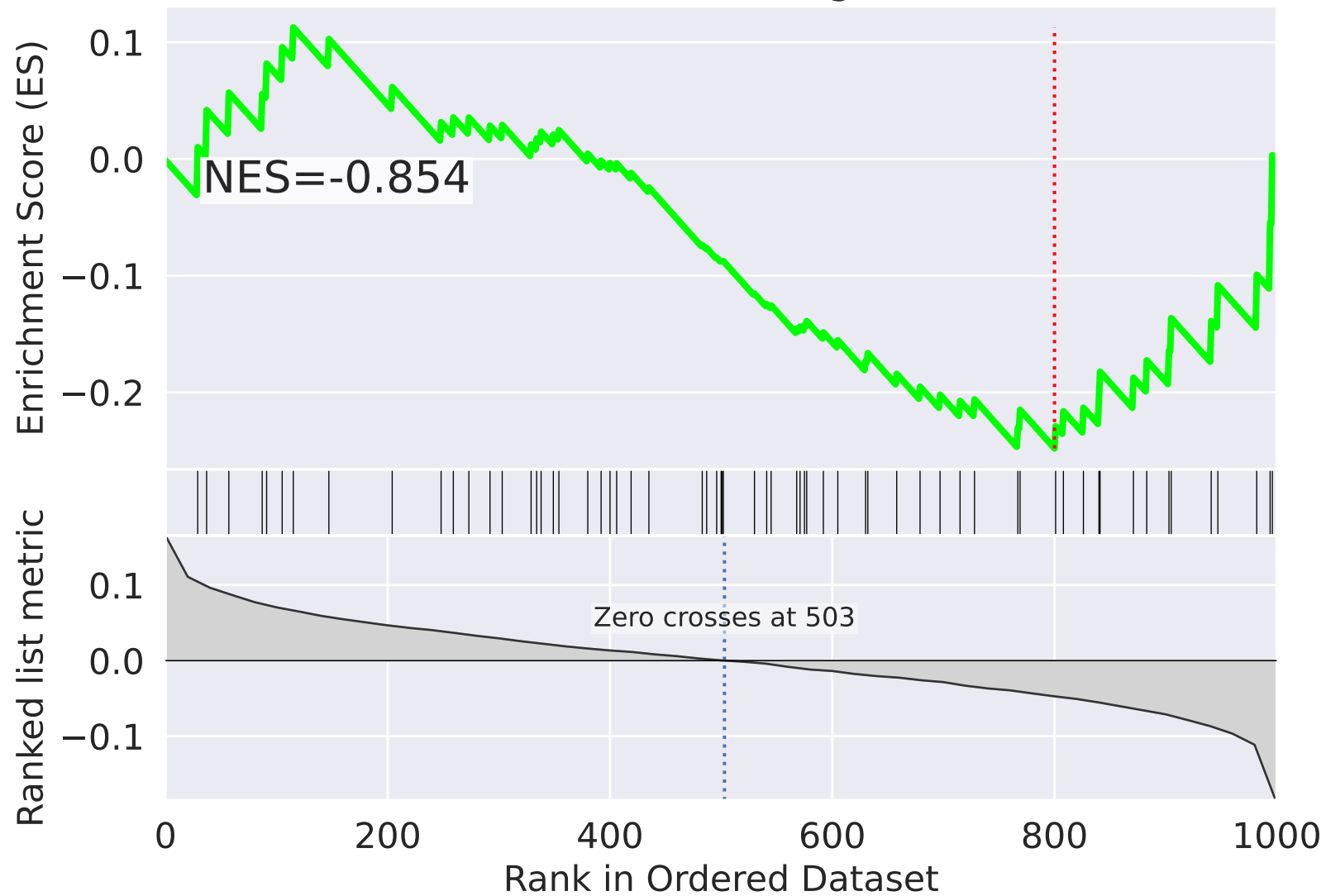
mitochondrial translational elongation (GO:0070125)



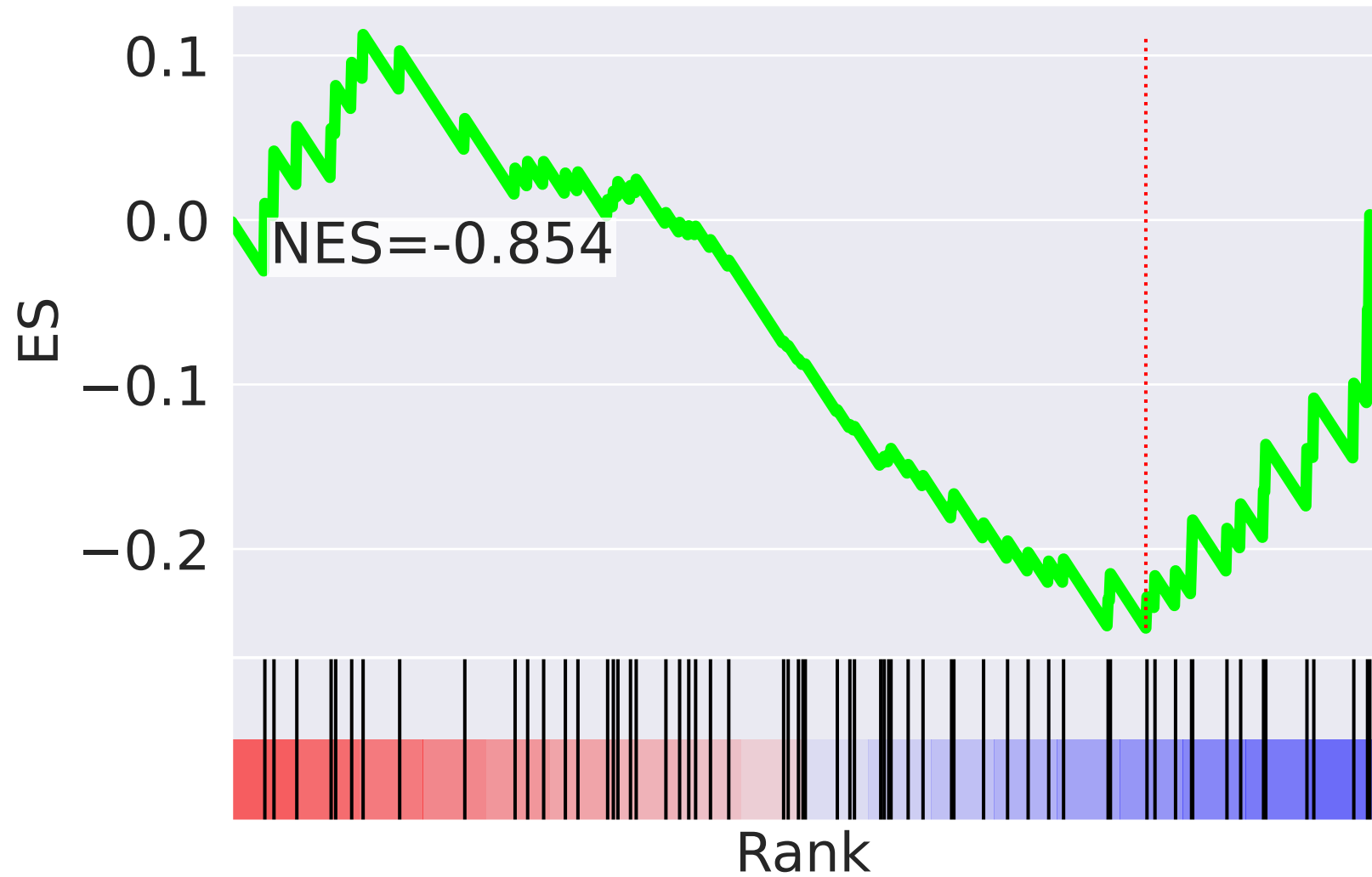
NES		SET
-3.688		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.865		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.550		viral life cycle (GO:0019058)
-2.518		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.267		T cell costimulation (GO:0031295)
-2.235		cellular respiration (GO:0045333)
2.103		axon guidance (GO:0007411)
2.068		insulin receptor signaling pathway (GO:0008286)
2.060		ESCRT III complex disassembly (GO:1904903)
1.995		multivesicular body assembly (GO:0036258)
-1.975		fibroblast growth factor receptor signaling pathway (GO:0008543)
1.930		nucleus organization (GO:0006997)
-1.908		lipid metabolic process (GO:0006629)
1.894		endosomal transport (GO:0016197)
1.758		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 $z=46$

mitochondrial translational elongation (GO:0070125)



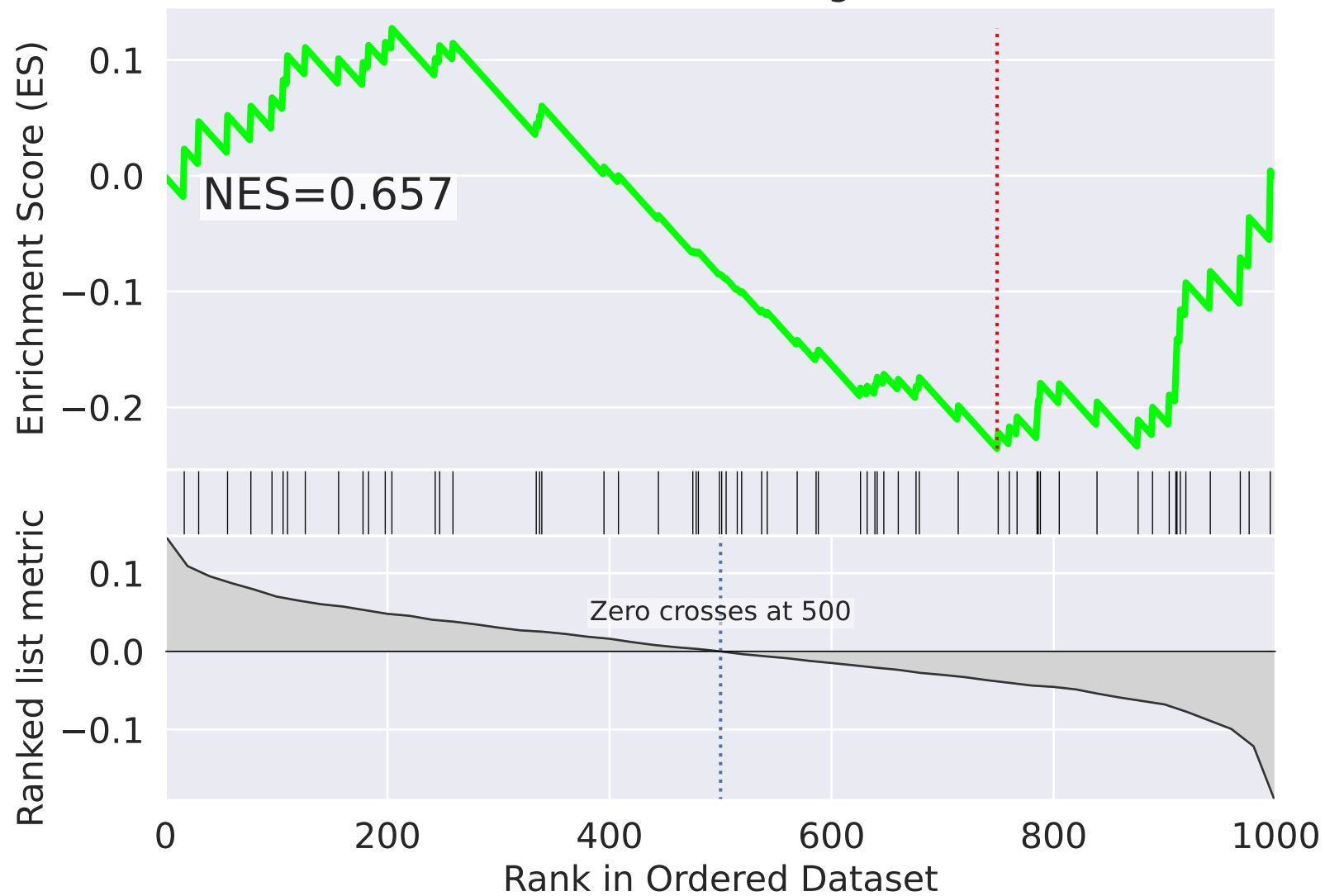
mitochondrial translational elongation (GO:0070125)



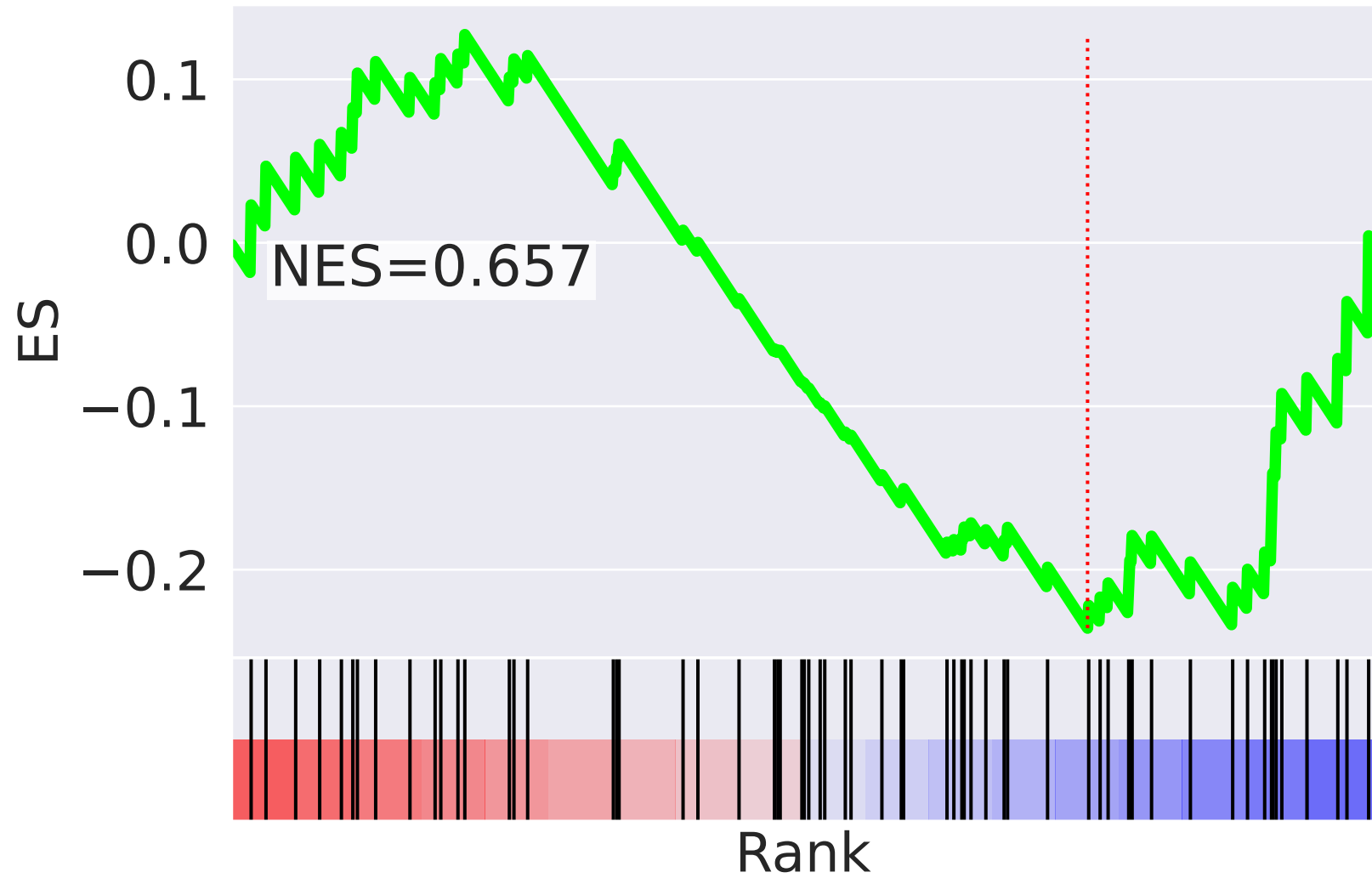
NES		SET
-2.928		transcription initiation from RNA polymerase II promoter (GO:0006367)
2.832		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.710		androgen receptor signaling pathway (GO:0030521)
-2.658		intracellular signal transduction (GO:0035556)
2.238		protein deubiquitination (GO:0016579)
2.218		mitotic cell cycle (GO:0000278)
2.212		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)
2.139		protein dephosphorylation (GO:0006470)
2.013		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.009		positive regulation of GTPase activity (GO:0043547)
1.982		anaphase-promoting complex-dependent catabolic process (GO:0031145)
1.932		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
-1.932		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
-1.894		snRNA transcription from RNA polymerase II promoter (GO:0042795)
1.881		negative regulation of apoptotic process (GO:0043066)

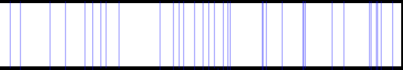
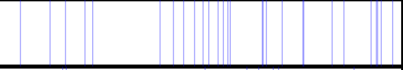



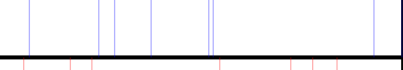
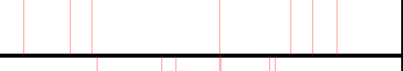
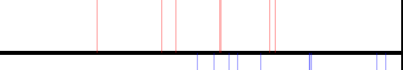

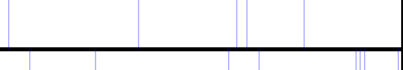

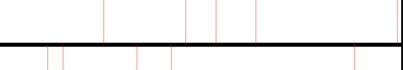
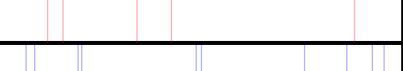
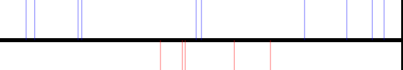

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=47$

mitochondrial translational elongation (GO:0070125)



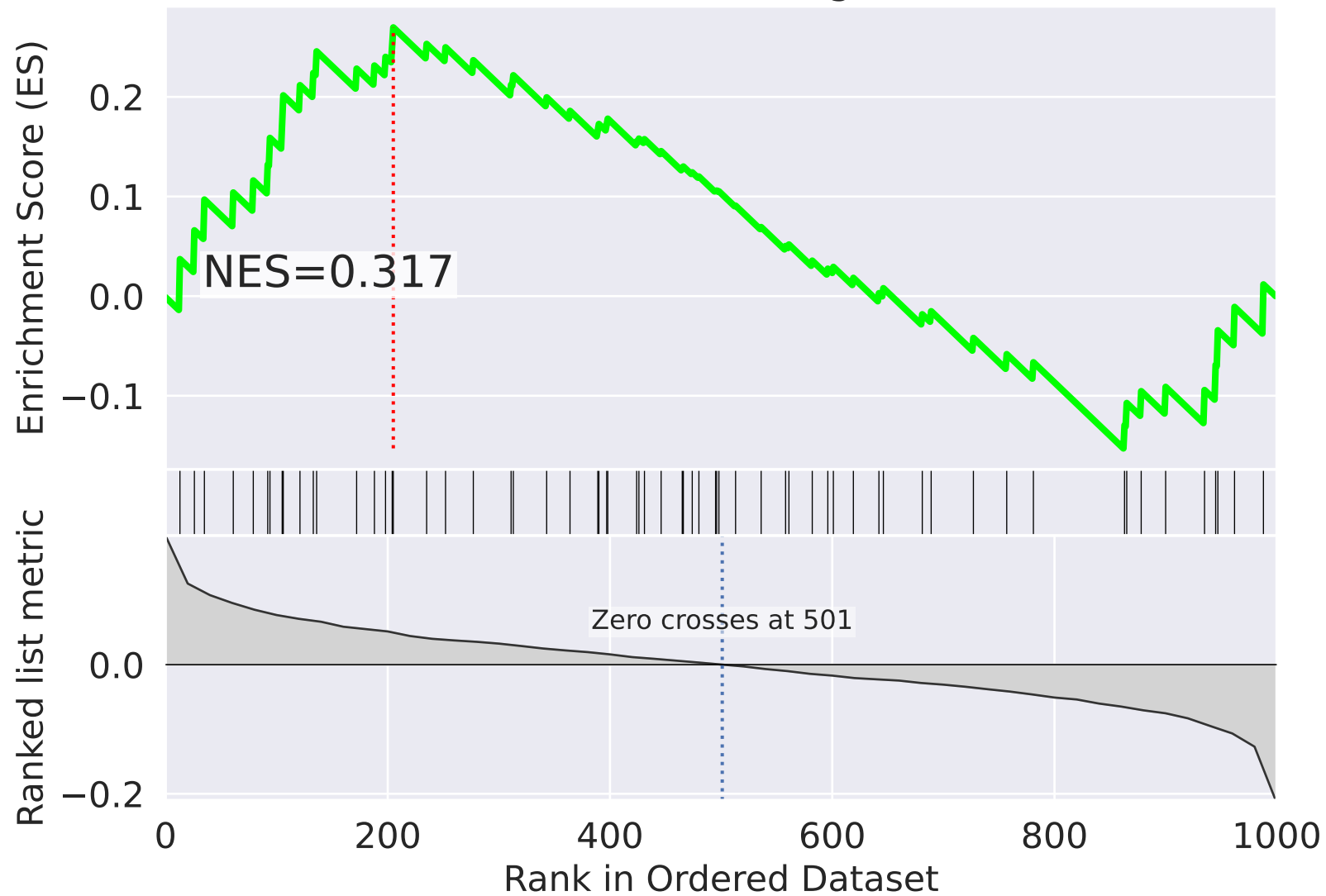
mitochondrial translational elongation (GO:0070125)



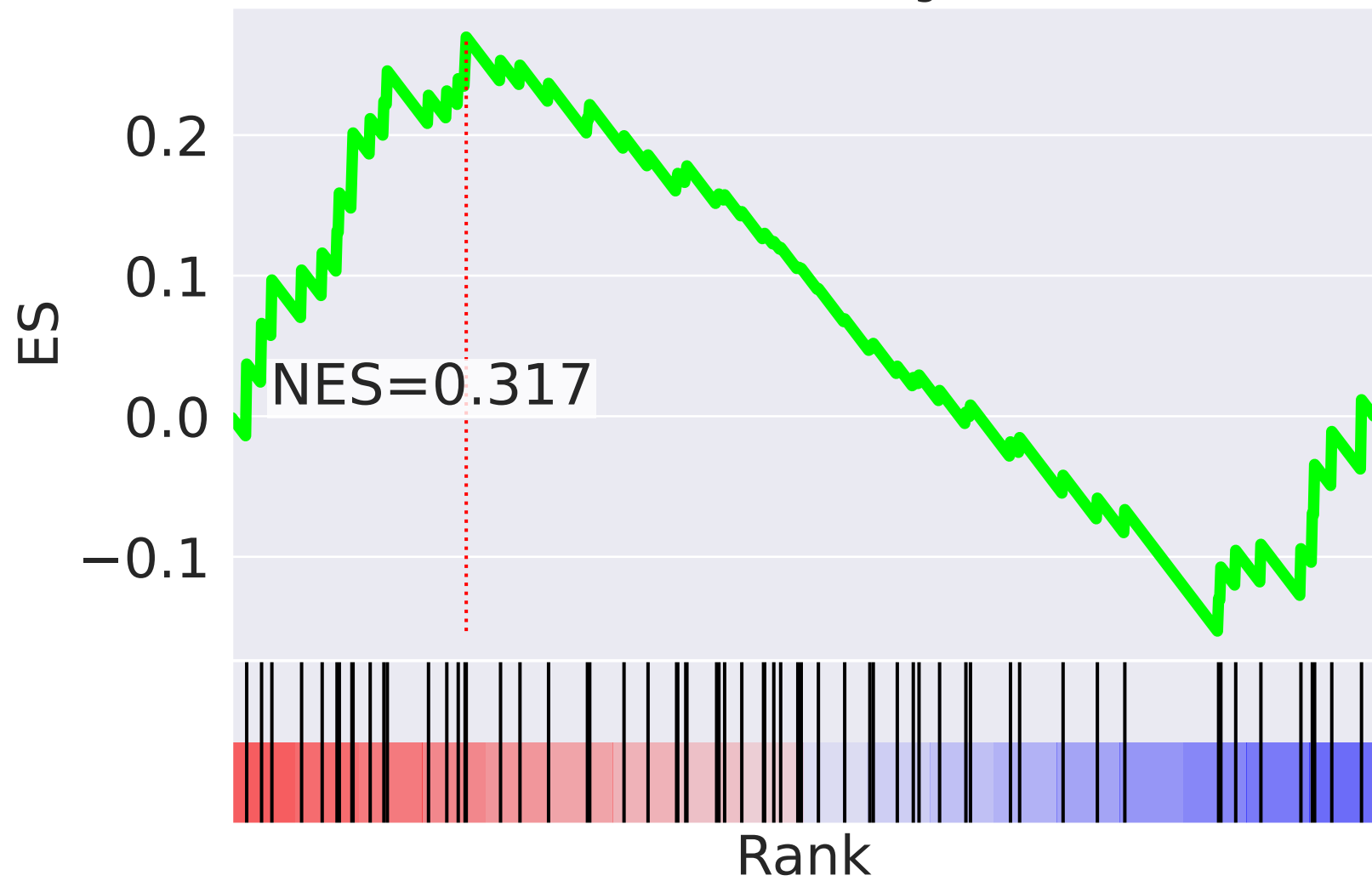
NES		SET
-3.418		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.229		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.218		protein homooligomerization (GO:0051260)
2.198		positive regulation of viral genome replication (GO:0045070)
2.120		phosphatidylinositol biosynthetic process (GO:0006661)
-2.035		nervous system development (GO:0007399)
1.957		double-strand break repair (GO:0006302)
1.954		cell surface receptor signaling pathway (GO:0007166)
-1.831		protein dephosphorylation (GO:0006470)
-1.818		release of cytochrome c from mitochondria (GO:0001836)
-1.765		transforming growth factor beta receptor signaling pathway (GO:0007179)
1.749		nucleobase-containing small molecule interconversion (GO:0015949)
1.707		endocytosis (GO:0006897)
-1.684		intracellular protein transport (GO:0006886)
1.647		nucleosome disassembly (GO:0006337)



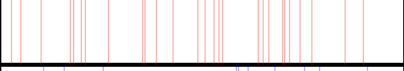



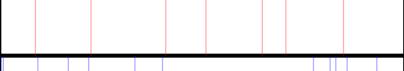
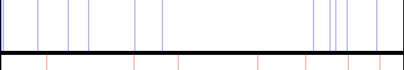
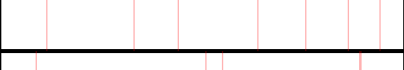
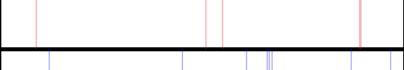
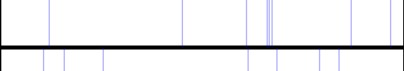
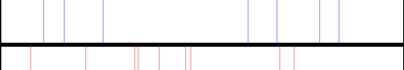
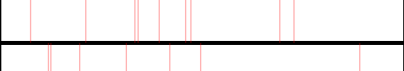
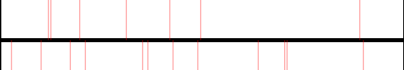

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=48$

mitochondrial translational elongation (GO:0070125)



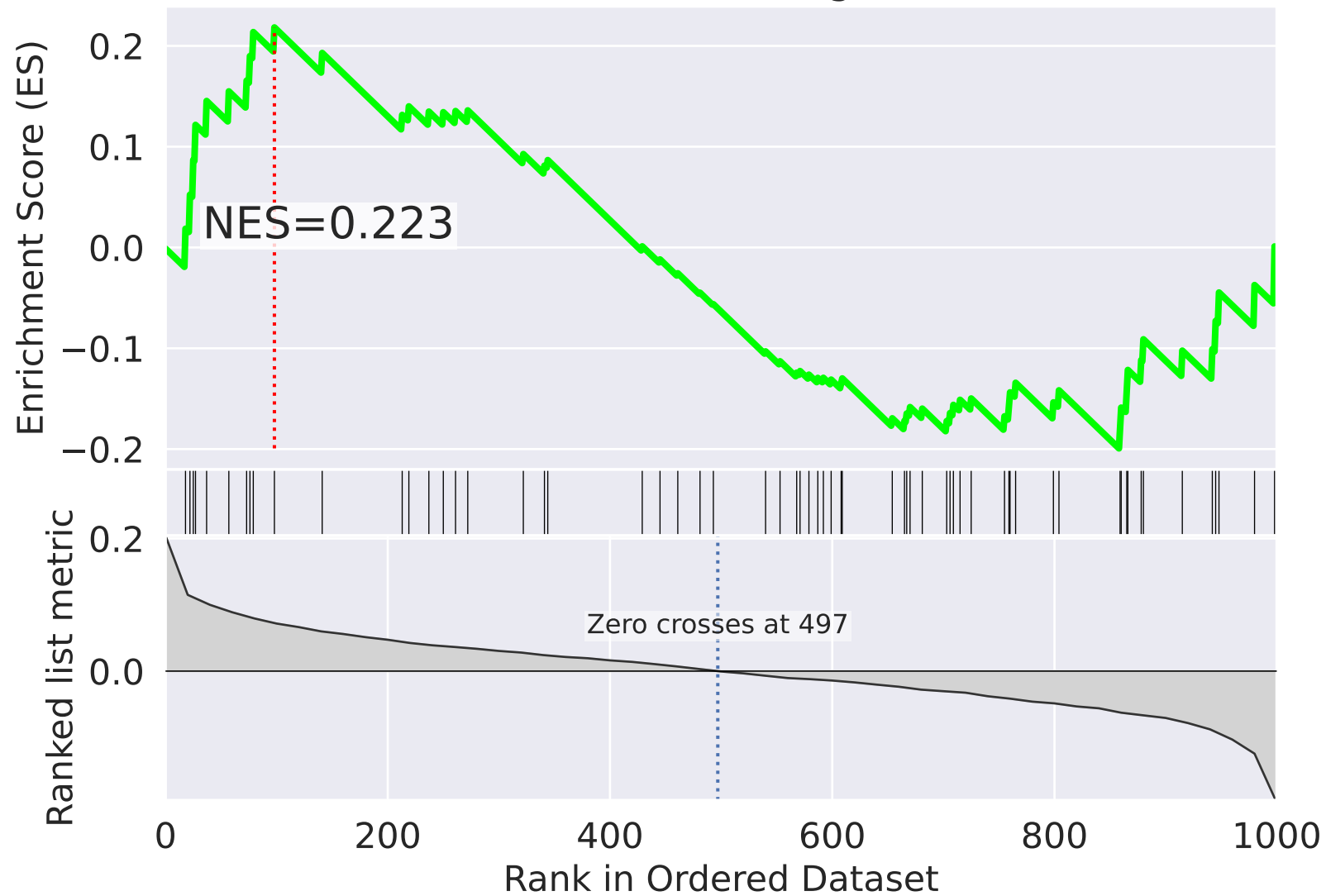
mitochondrial translational elongation (GO:0070125)



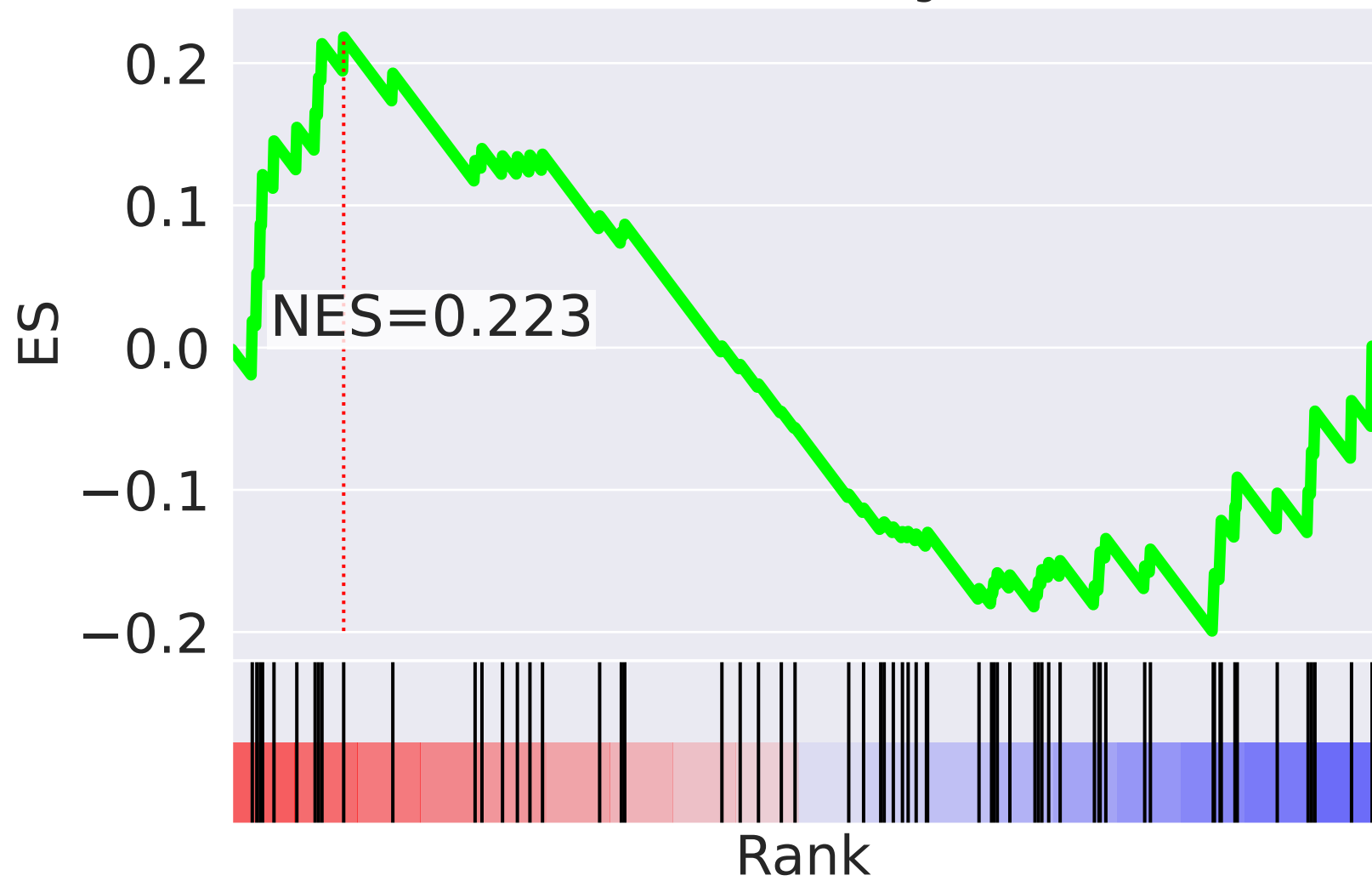
NES		SET
2.646		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.588		cellular response to DNA damage stimulus (GO:0006974)
2.432		protein ubiquitination (GO:0016567)
-2.426		endosomal transport (GO:0016197)
2.304		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.215		small molecule metabolic process (GO:0044281)
2.162		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.097		regulation of cholesterol biosynthetic process (GO:0045540)
2.074		microtubule-based movement (GO:0007018)
2.056		transcription-coupled nucleotide-excision repair (GO:0006283)
-2.038		tRNA modification (GO:0006400)
-2.024		viral budding via host ESCRT complex (GO:0039702)
1.969		regulation of protein stability (GO:0031647)
1.947		DNA damage response, detection of DNA damage (GO:0042769)
1.946		ubiquitin-dependent protein catabolic process (GO:0006511)

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)



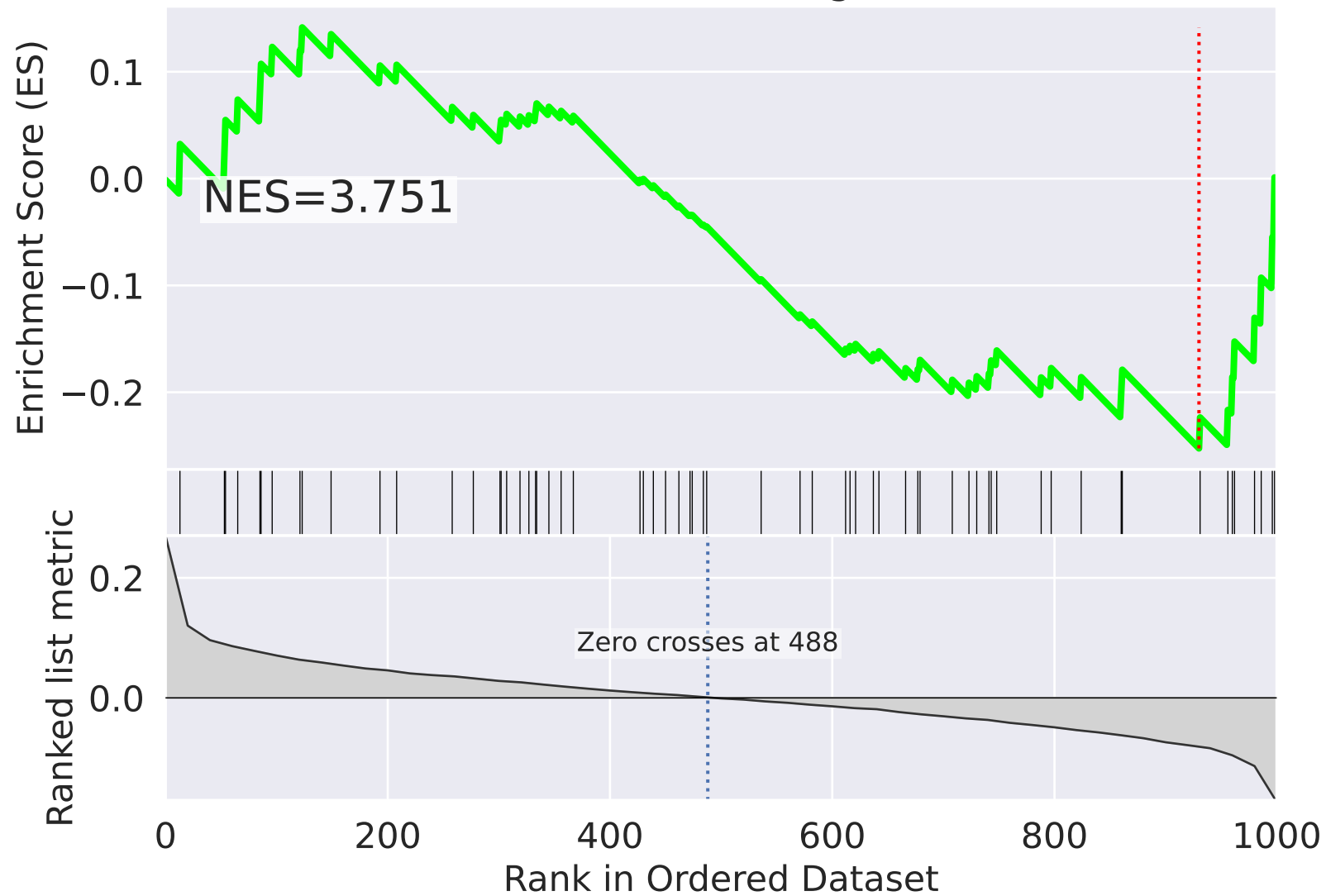
mitochondrial translational elongation (GO:0070125)



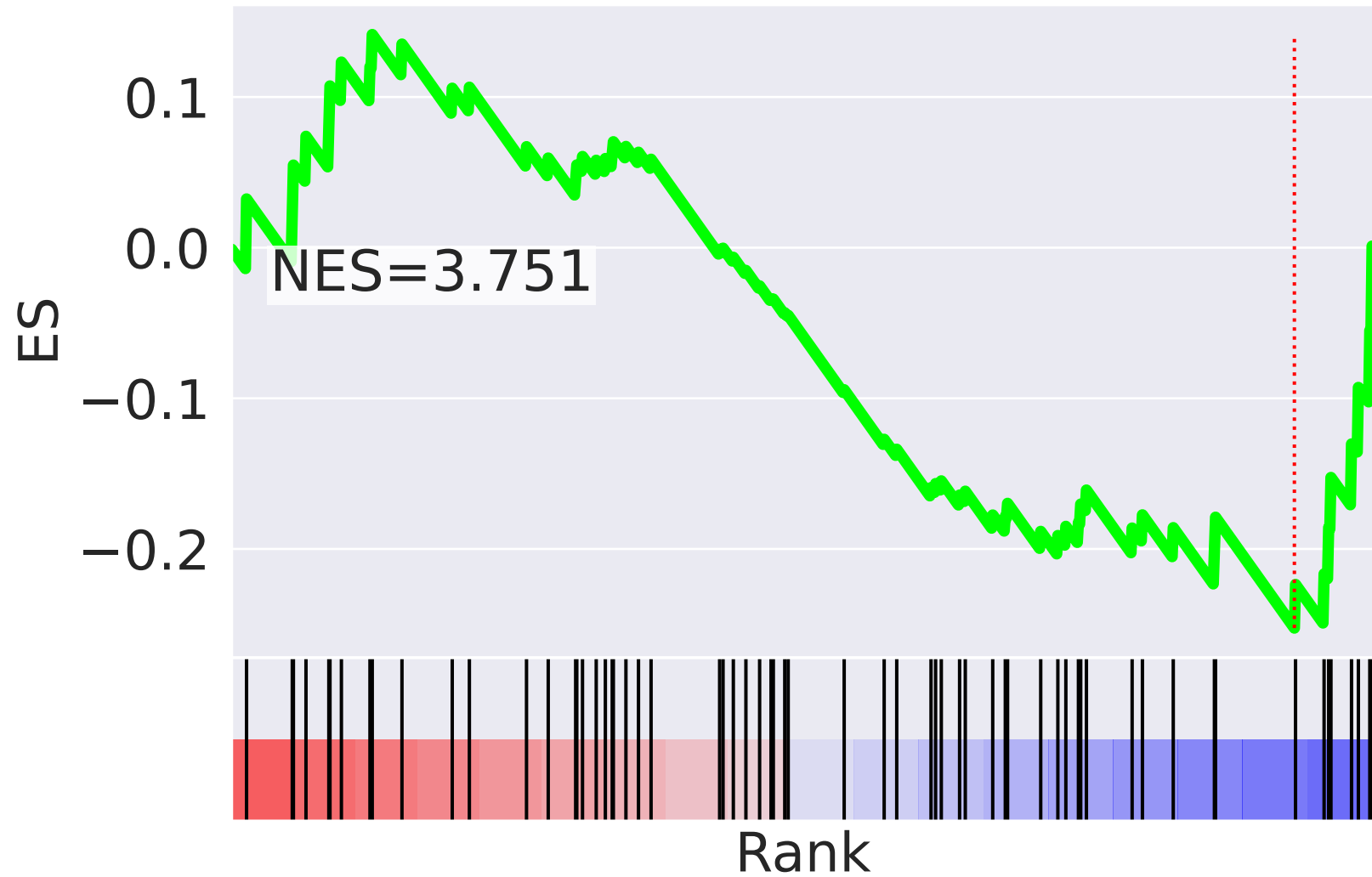
NES		SET
2.622		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.289		positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)
2.251		DNA-dependent DNA replication (GO:0006261)
-2.139		regulation of cell growth (GO:0001558)
2.109		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.076		endosomal transport (GO:0016197)
-2.070		insulin receptor signaling pathway (GO:0008286)
-2.017		cell division (GO:0051301)
1.994		microtubule-based movement (GO:0007018)
-1.904		movement of cell or subcellular component (GO:0006928)
1.897		heme biosynthetic process (GO:0006783)
1.892		protein K48-linked ubiquitination (GO:0070936)
-1.864		regulation of gene expression (GO:0010468)
1.829		positive regulation of protein ubiquitination (GO:0031398)
1.807		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 $z=50$

mitochondrial translational elongation (GO:0070125)



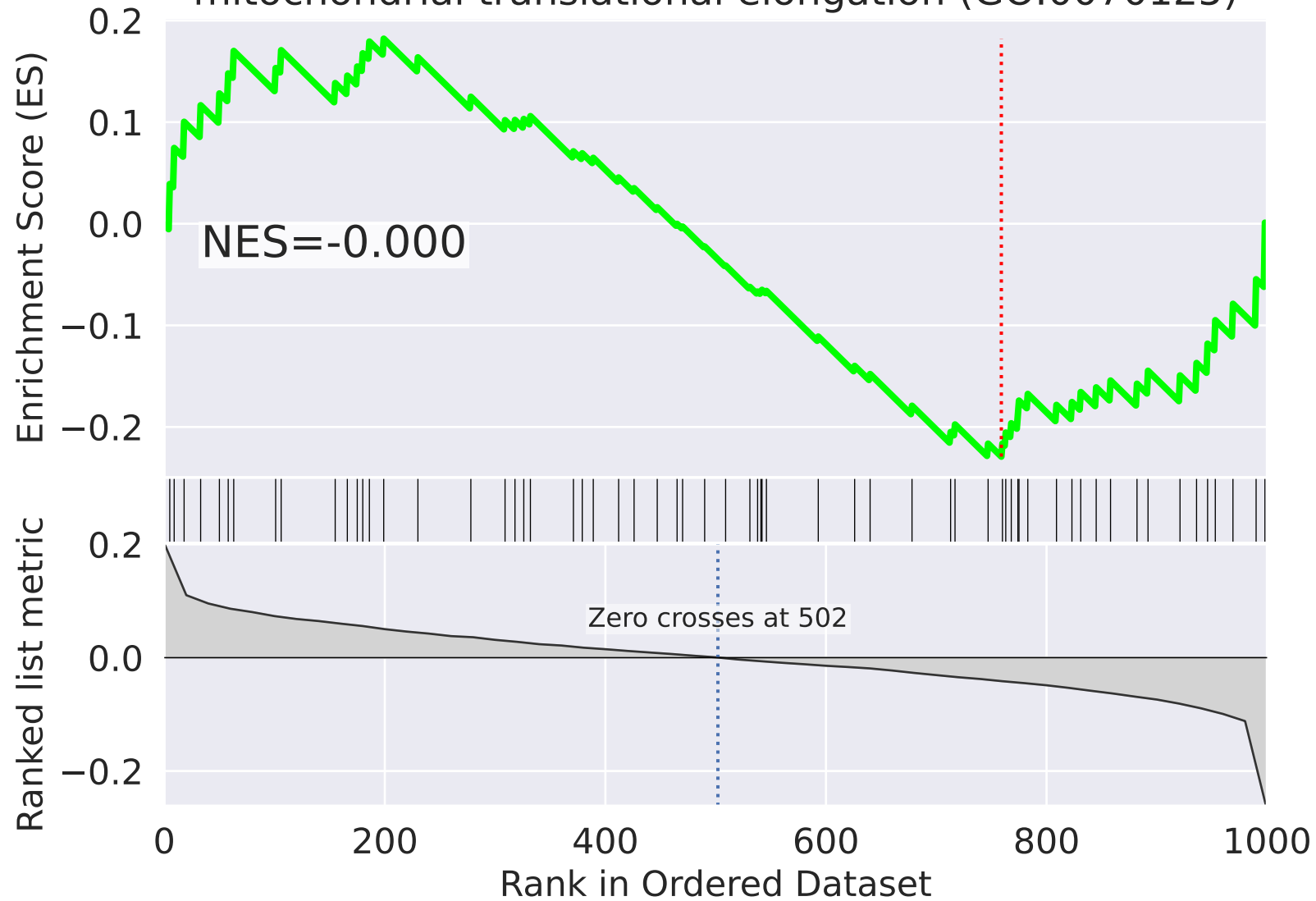
mitochondrial translational elongation (GO:0070125)



NES		SET
3.791		mitochondrial translational termination (GO:0070126)
3.751		mitochondrial translational elongation (GO:0070125)
-2.658		endosomal transport (GO:0016197)
-2.533		multivesicular body assembly (GO:0036258)
-2.399		cellular nitrogen compound metabolic process (GO:0034641)
-2.130		positive regulation of gene expression, epigenetic (GO:0045815)
-2.128		cell separation after cytokinesis (GO:0000920)
2.126		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.119		macroautophagy (GO:0016236)
-2.115		apoptotic process (GO:0006915)
-2.105		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.060		mRNA processing (GO:0006397)
-2.034		viral life cycle (GO:0019058)
2.031		regulation of lipid metabolic process (GO:0019216)
-2.030		execution phase of apoptosis (GO:0097194)

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)



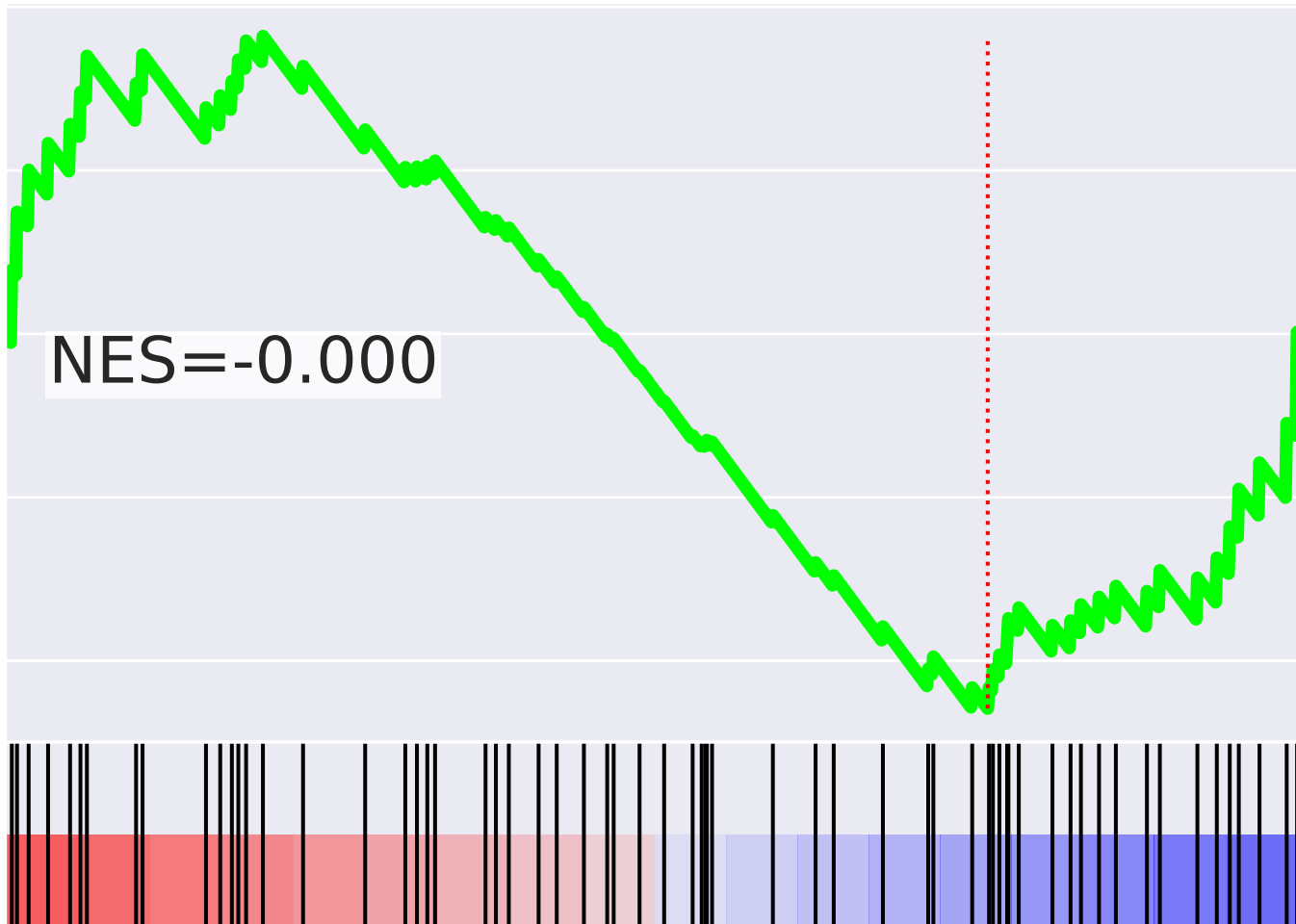
mitochondrial translational elongation (GO:0070125)

ES

NES=-0.000




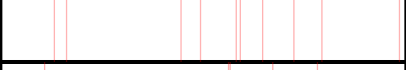


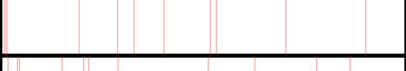


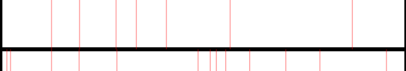
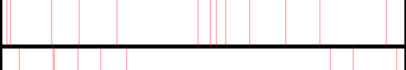


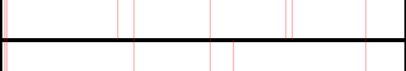

0.2
0.1
0.0
-0.1
-0.2

Rank



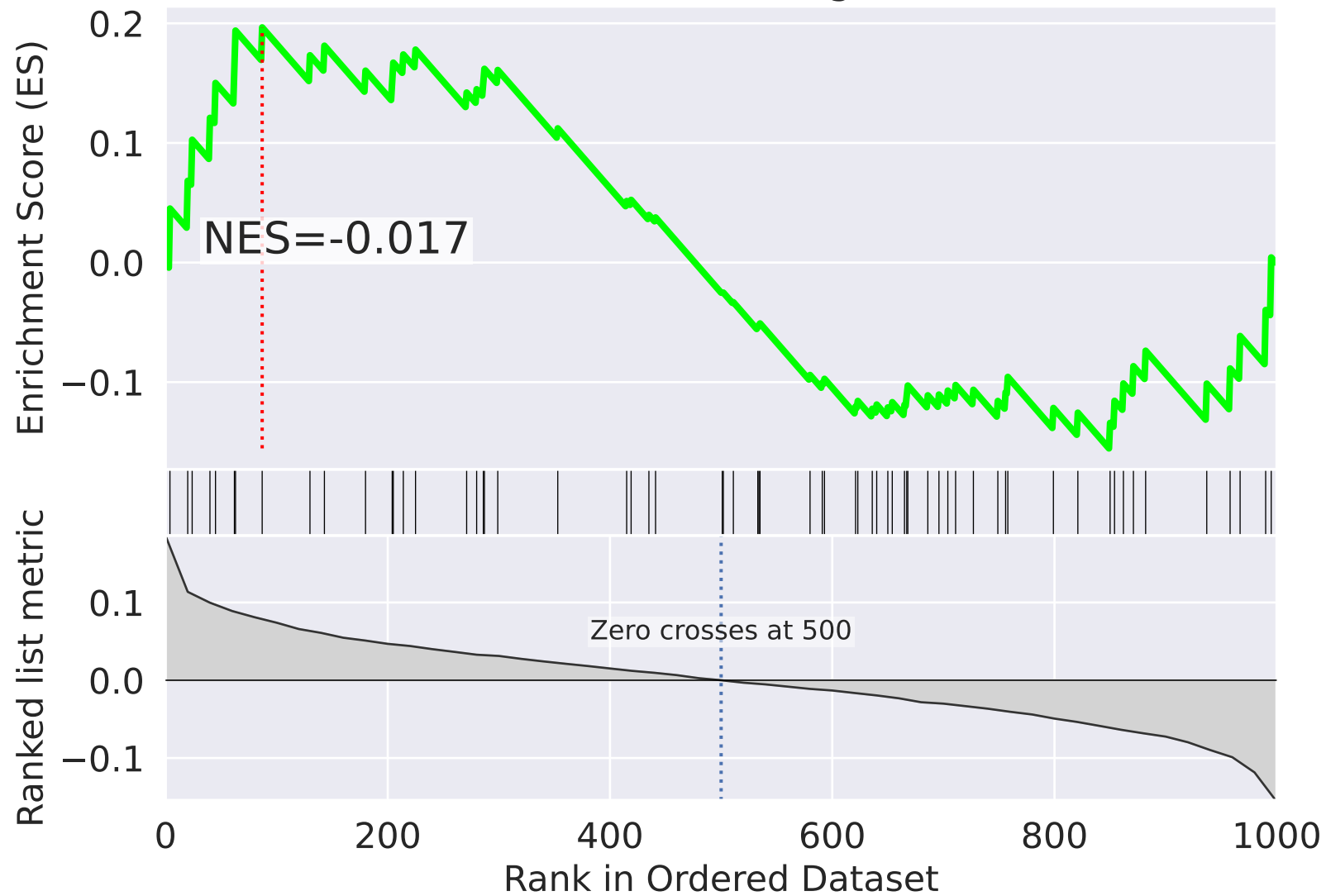
NES

SET

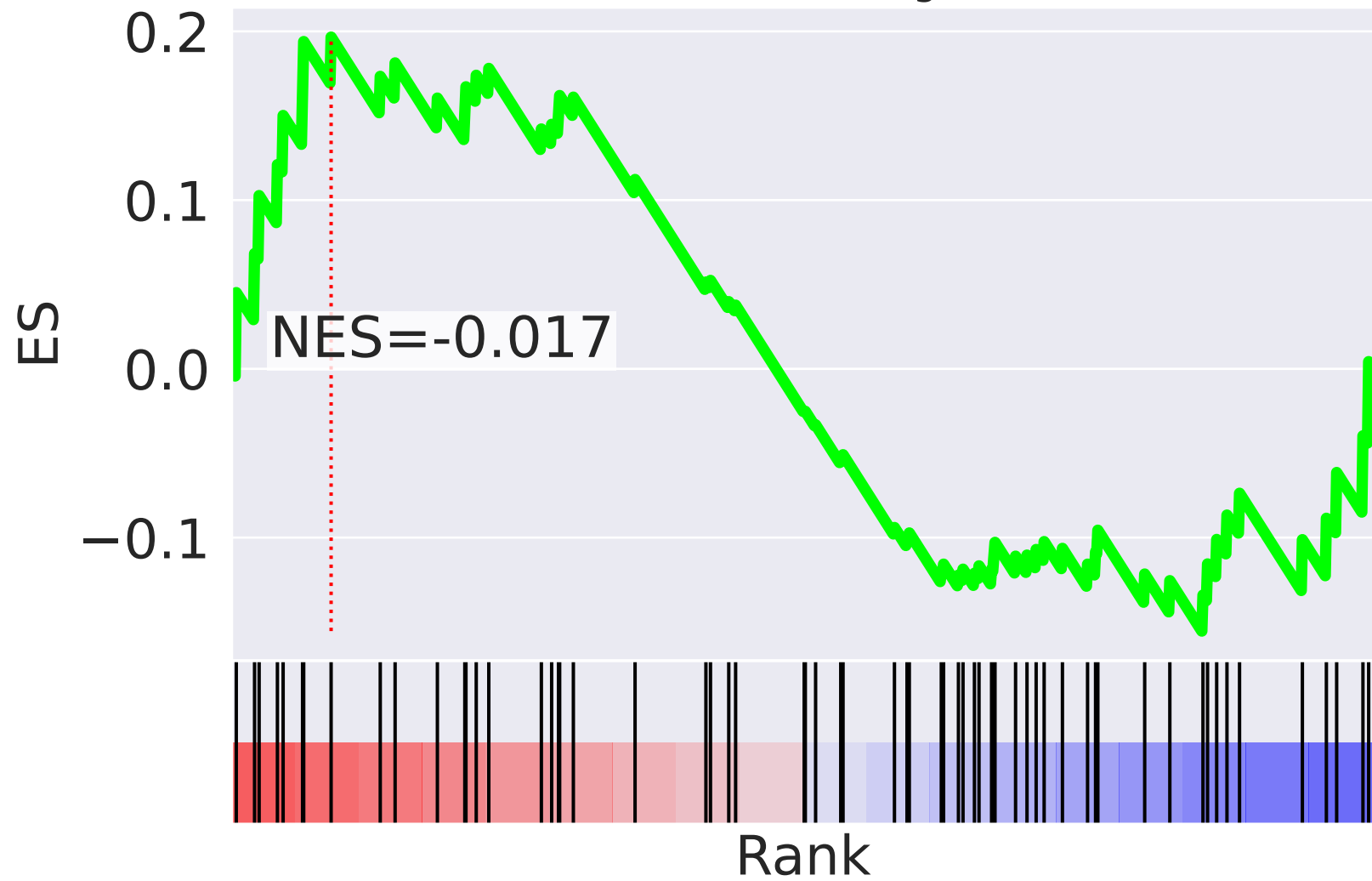
2.681		positive regulation of cell proliferation (GO:0008284)
2.561		viral life cycle (GO:0019058)
2.529		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.485		sister chromatid cohesion (GO:0007062)
2.485		inflammatory response (GO:0006954)
2.453		axon guidance (GO:0007411)
2.450		multivesicular body assembly (GO:0036258)
2.438		positive regulation of gene expression (GO:0010628)
-2.419		protein N-linked glycosylation via asparagine (GO:0018279)
2.350		blood coagulation (GO:0007596)
2.342		macroautophagy (GO:0016236)
2.342		double-strand break repair via nonhomologous end joining (GO:0006303)
2.307		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
2.302		nucleus organization (GO:0006997)
2.171		regulation of centrosome duplication (GO:0010824)







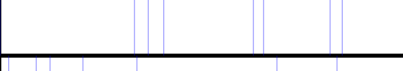


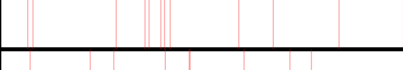


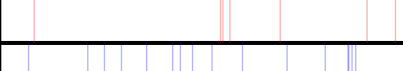

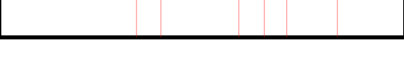
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=52$

mitochondrial translational elongation (GO:0070125)



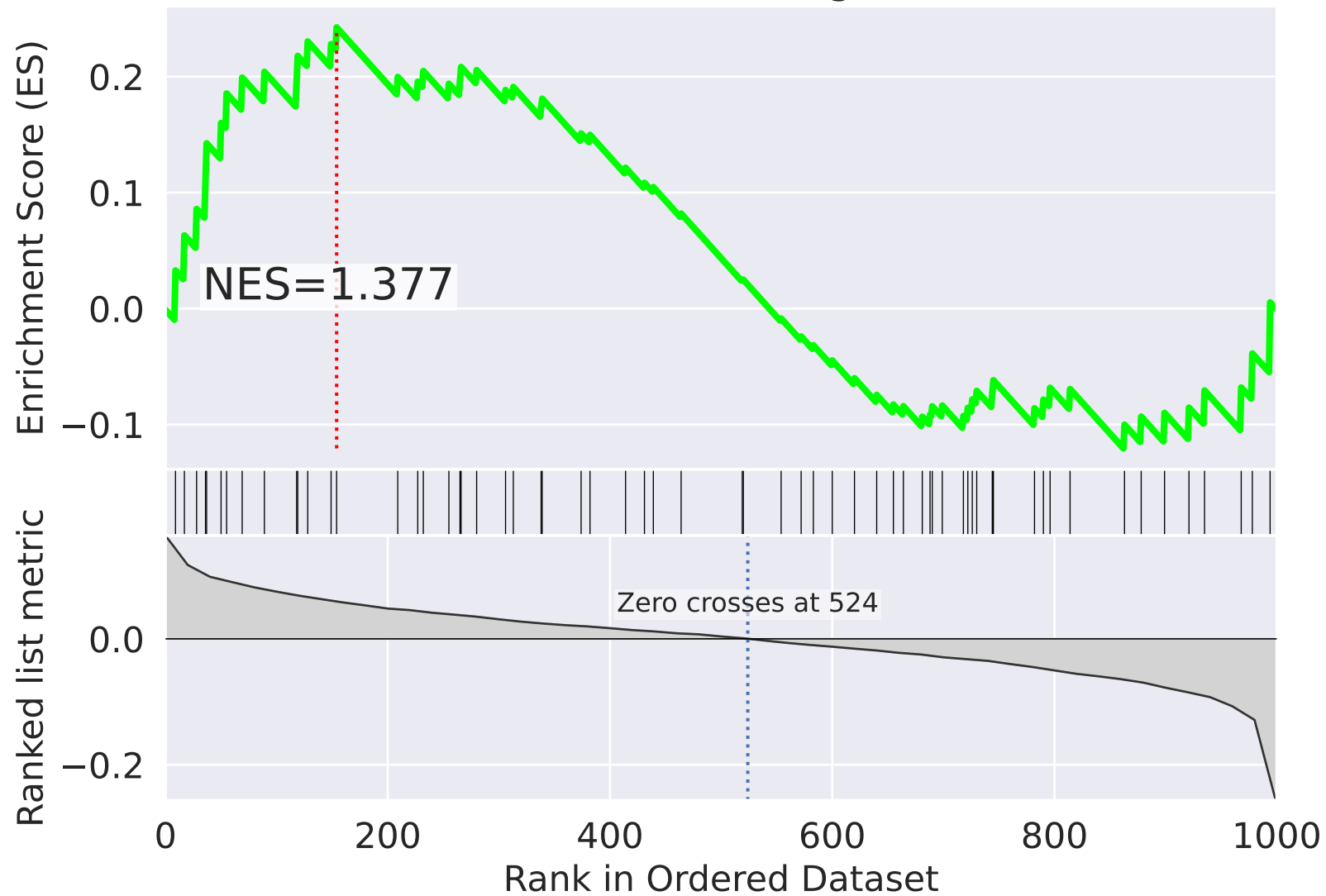
mitochondrial translational elongation (GO:0070125)



NES		SET
2.637		chromosome segregation (GO:0007059)
2.431		substrate adhesion-dependent cell spreading (GO:0034446)
2.406		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.397		mitotic cytokinesis (GO:0000281)
2.387		intracellular signal transduction (GO:0035556)
-2.362		androgen receptor signaling pathway (GO:0030521)
-2.358		nervous system development (GO:0007399)
-2.286		viral life cycle (GO:0019058)
-2.256		regulation of cell growth (GO:0001558)
2.144		ubiquitin-dependent protein catabolic process (GO:0006511)
2.073		Fc-epsilon receptor signaling pathway (GO:0038095)
2.024		blood coagulation (GO:0007596)
2.022		RNA metabolic process (GO:0016070)
-2.022		transcription initiation from RNA polymerase II promoter (GO:0006367)
1.952		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 $z=53$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)


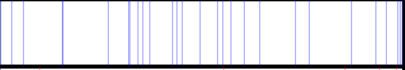


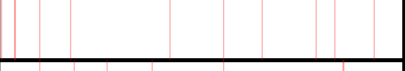

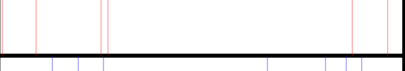
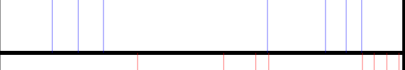


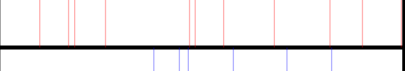

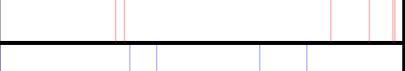
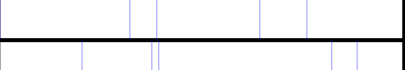
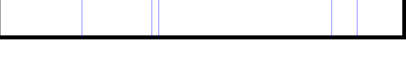
ES

0.2
0.1
0.0
-0.1

NES=1.377

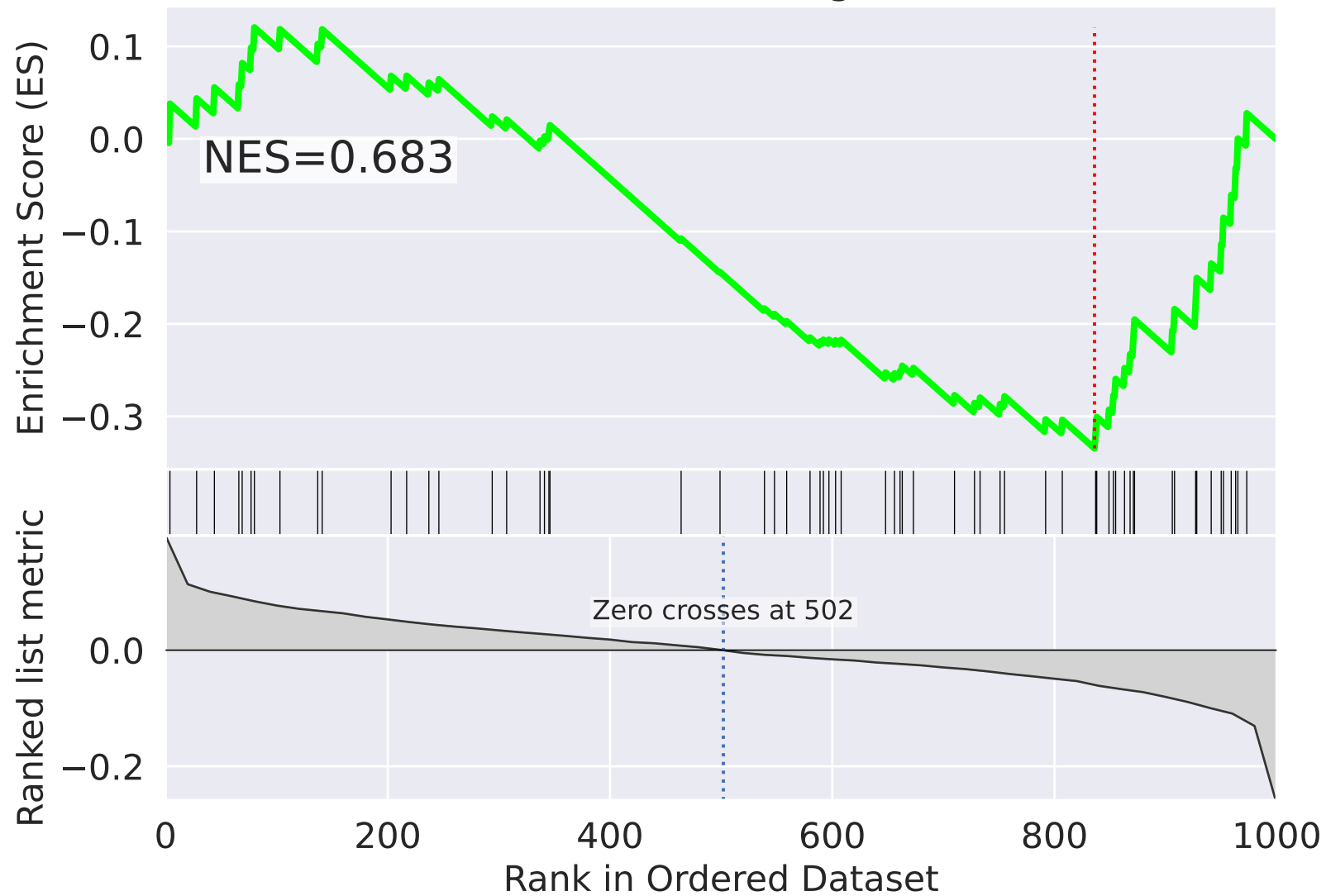
Rank



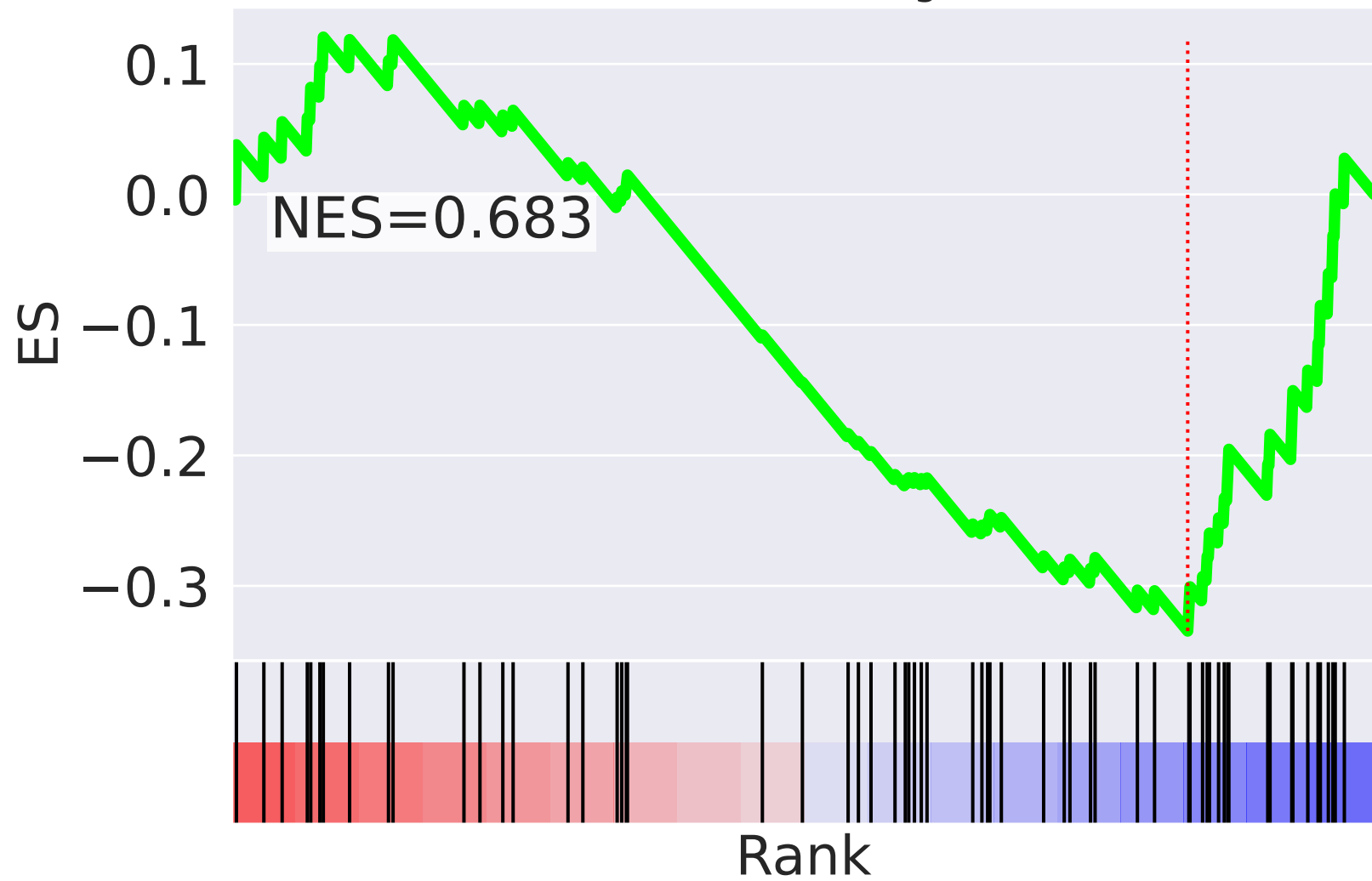
NES		SET
-4.595		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.157		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.554		positive regulation of cell growth (GO:0030307)
2.514		protein homooligomerization (GO:0051260)
2.475		positive regulation of protein phosphorylation (GO:0001934)
2.322		cell surface receptor signaling pathway (GO:0007166)
2.281		ATP-dependent chromatin remodeling (GO:0043044)
-2.202		cytokinesis (GO:0000910)
2.177		positive regulation of cell migration (GO:0030335)
2.112		cell migration (GO:0016477)
2.094		phosphatidylinositol-mediated signaling (GO:0048015)
-2.005		cellular response to amino acid starvation (GO:0034198)
1.984		negative regulation of telomere maintenance via telomerase (GO:0032211)
-1.974		cellular respiration (GO:0045333)
-1.882		regulation of gene expression (GO:0010468)


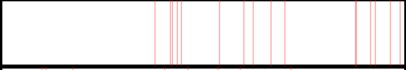



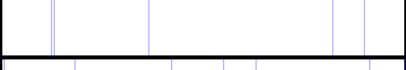


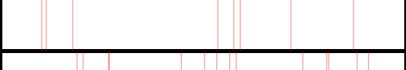
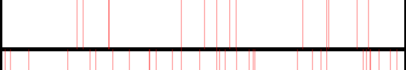
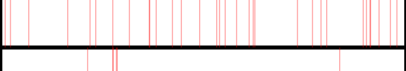




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=54$

mitochondrial translational elongation (GO:0070125)



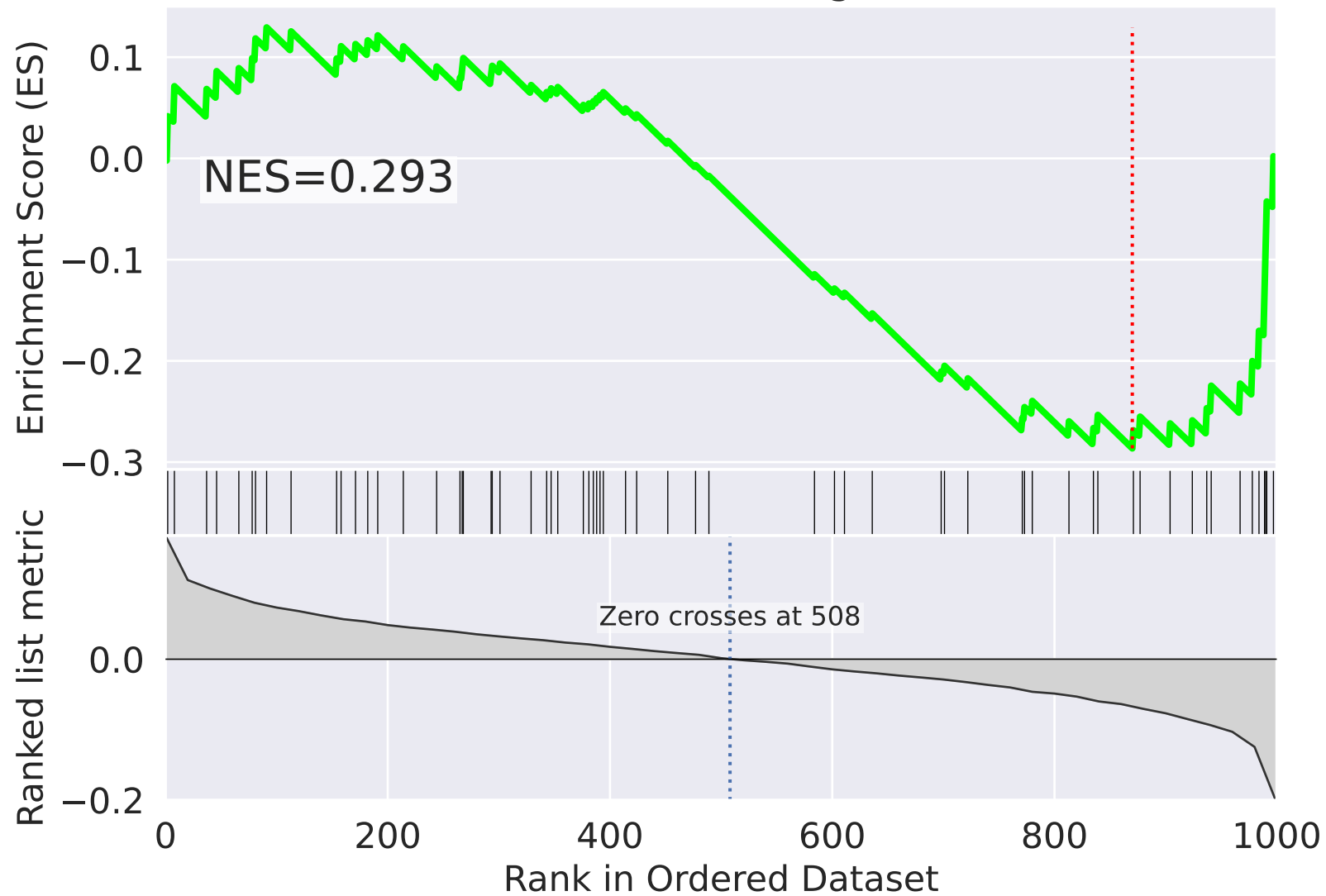
mitochondrial translational elongation (GO:0070125)



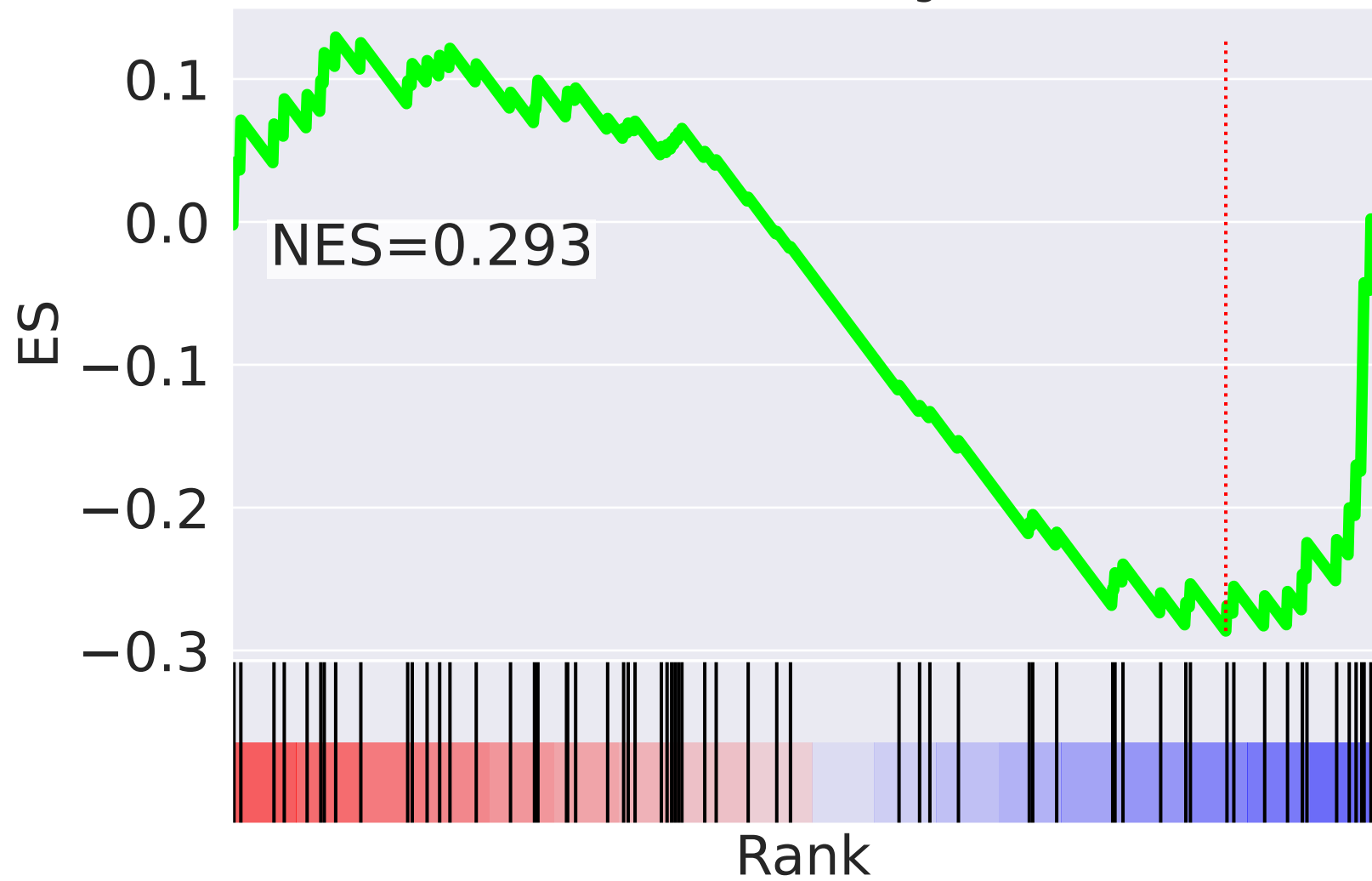
NES		SET
2.823		multivesicular body assembly (GO:0036258)
2.636		MAPK cascade (GO:0000165)
2.600		viral life cycle (GO:0019058)
2.567		protein homooligomerization (GO:0051260)
2.512		ESCRT III complex disassembly (GO:1904903)
-2.256		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.250		negative regulation of cell growth (GO:0030308)
-2.234		histone H3 acetylation (GO:0043966)
2.218		nucleus organization (GO:0006997)
2.102		G1/S transition of mitotic cell cycle (GO:0000082)
2.095		positive regulation of cell proliferation (GO:0008284)
2.009		T cell receptor signaling pathway (GO:0050852)
-1.999		tRNA modification (GO:0006400)
-1.989		mitochondrial respiratory chain complex I assembly (GO:0032981)
-1.985		ciliary basal body docking (GO:0097711)

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

mitochondrial translational elongation (GO:0070125)



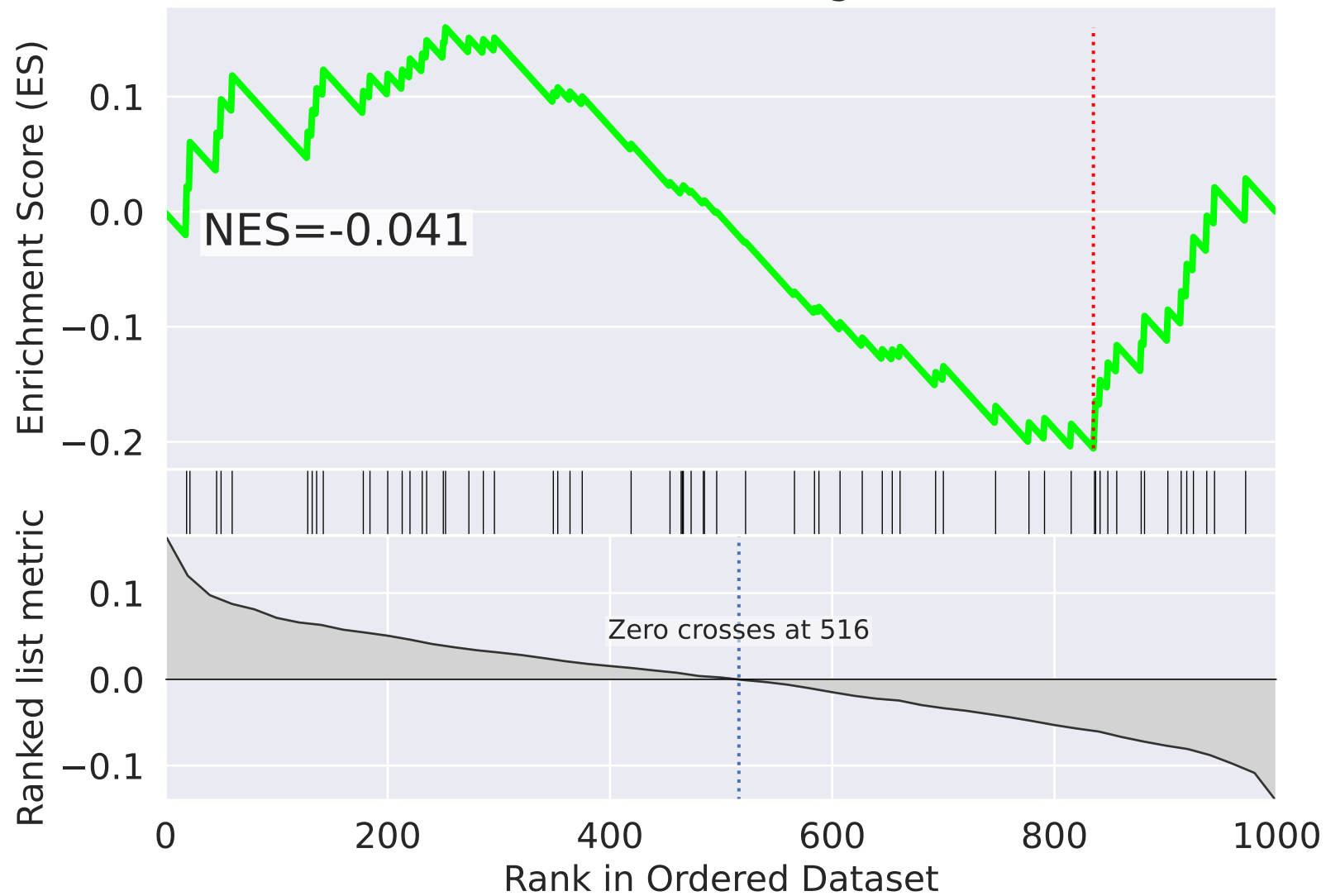
mitochondrial translational elongation (GO:0070125)



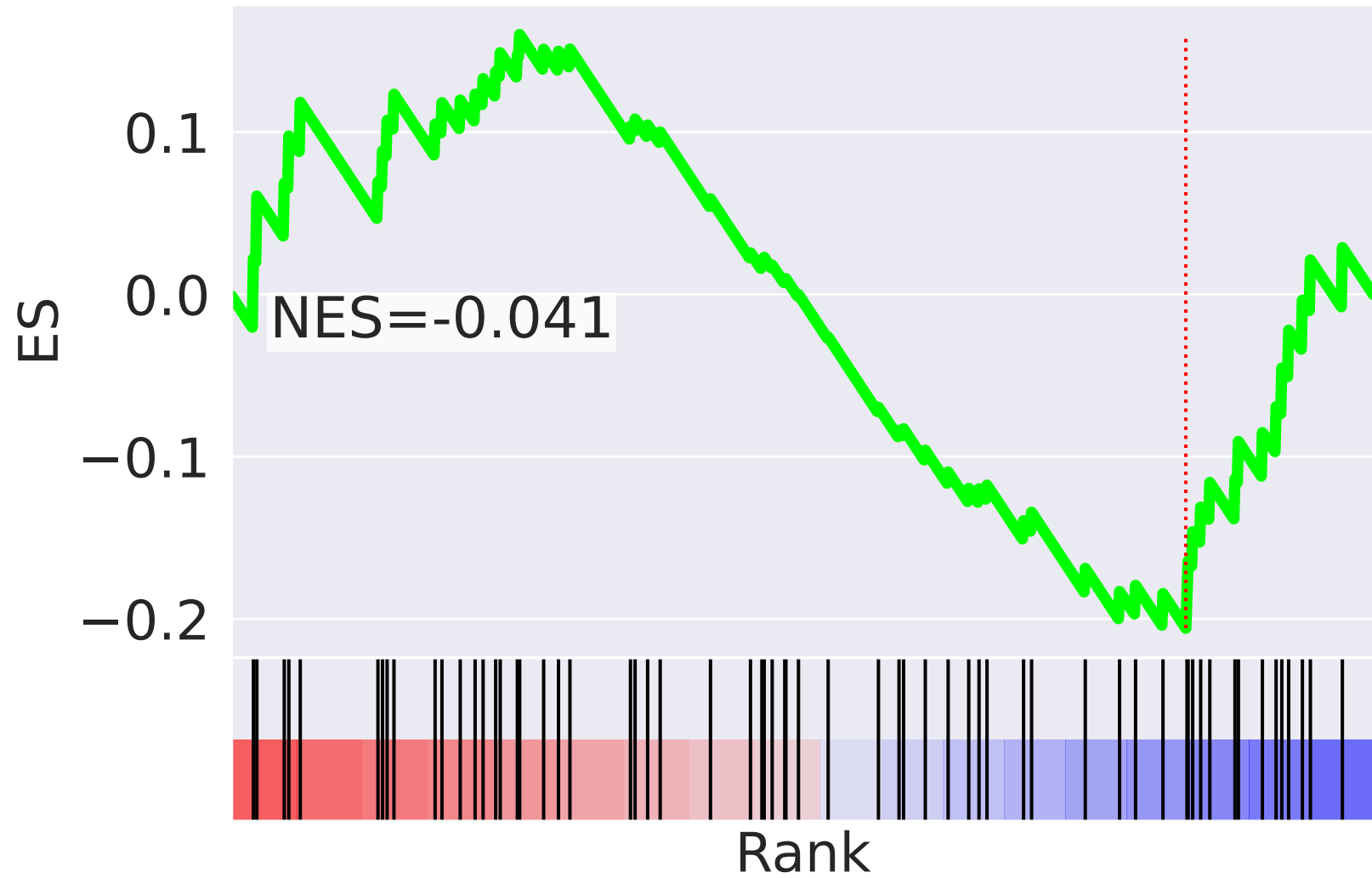
NES		SET
-2.551		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.421		androgen receptor signaling pathway (GO:0030521)
2.350		negative regulation of transcription, DNA-templated (GO:0045892)
2.251		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.103		response to ionizing radiation (GO:0010212)
2.024		intracellular signal transduction (GO:0035556)
2.012		interstrand cross-link repair (GO:0036297)
-2.003		transcription initiation from RNA polymerase II promoter (GO:0006367)
1.960		double-strand break repair via homologous recombination (GO:0000724)
-1.947		cellular respiration (GO:0045333)
1.916		response to virus (GO:0009615)
1.850		strand displacement (GO:0000732)
1.832		innate immune response (GO:0045087)
1.827		aerobic respiration (GO:0009060)
1.825		cellular protein modification process (GO:0006464)


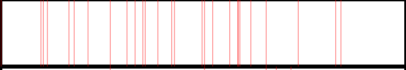

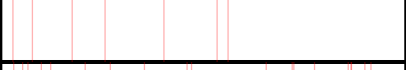


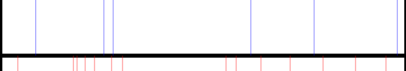



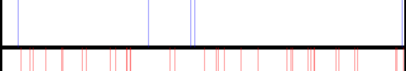
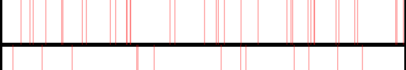
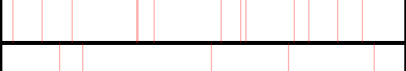
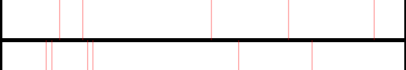
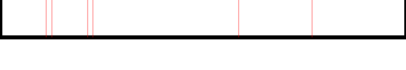
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=56$

mitochondrial translational elongation (GO:0070125)



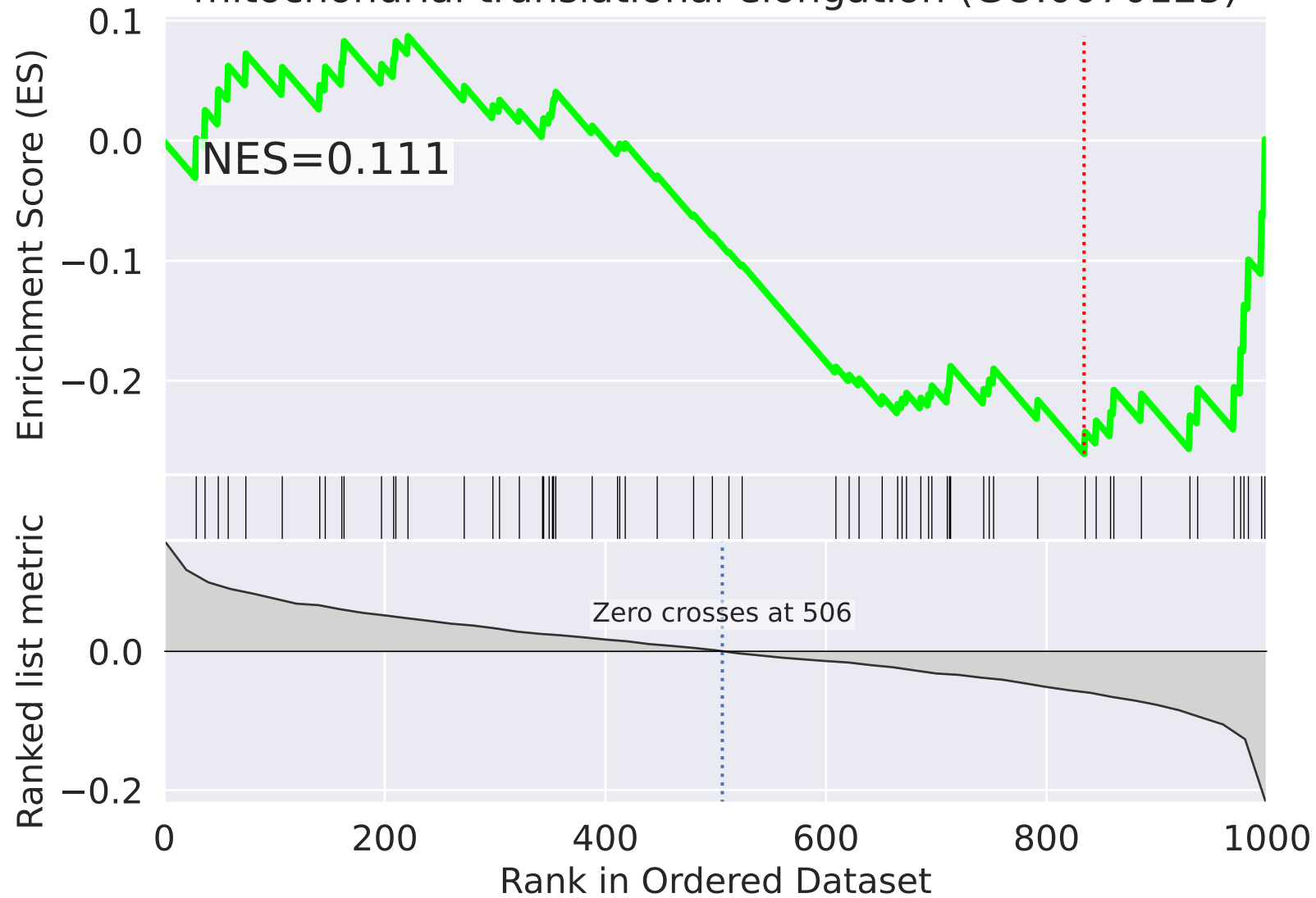
mitochondrial translational elongation (GO:0070125)



NES		SET
2.857		post-translational protein modification (GO:0043687)
2.604		protein ubiquitination (GO:0016567)
2.551		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
2.346		microtubule-based movement (GO:0007018)
2.301		negative regulation of cell proliferation (GO:0008285)
2.266		mRNA processing (GO:0006397)
-2.220		cellular protein localization (GO:0034613)
2.185		DNA repair (GO:0006281)
2.184		DNA damage checkpoint (GO:0000077)
2.158		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.124		protein N-linked glycosylation (GO:0006487)
2.082		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.071		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.063		heme biosynthetic process (GO:0006783)
2.048		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 $z=57$

mitochondrial translational elongation (GO:0070125)

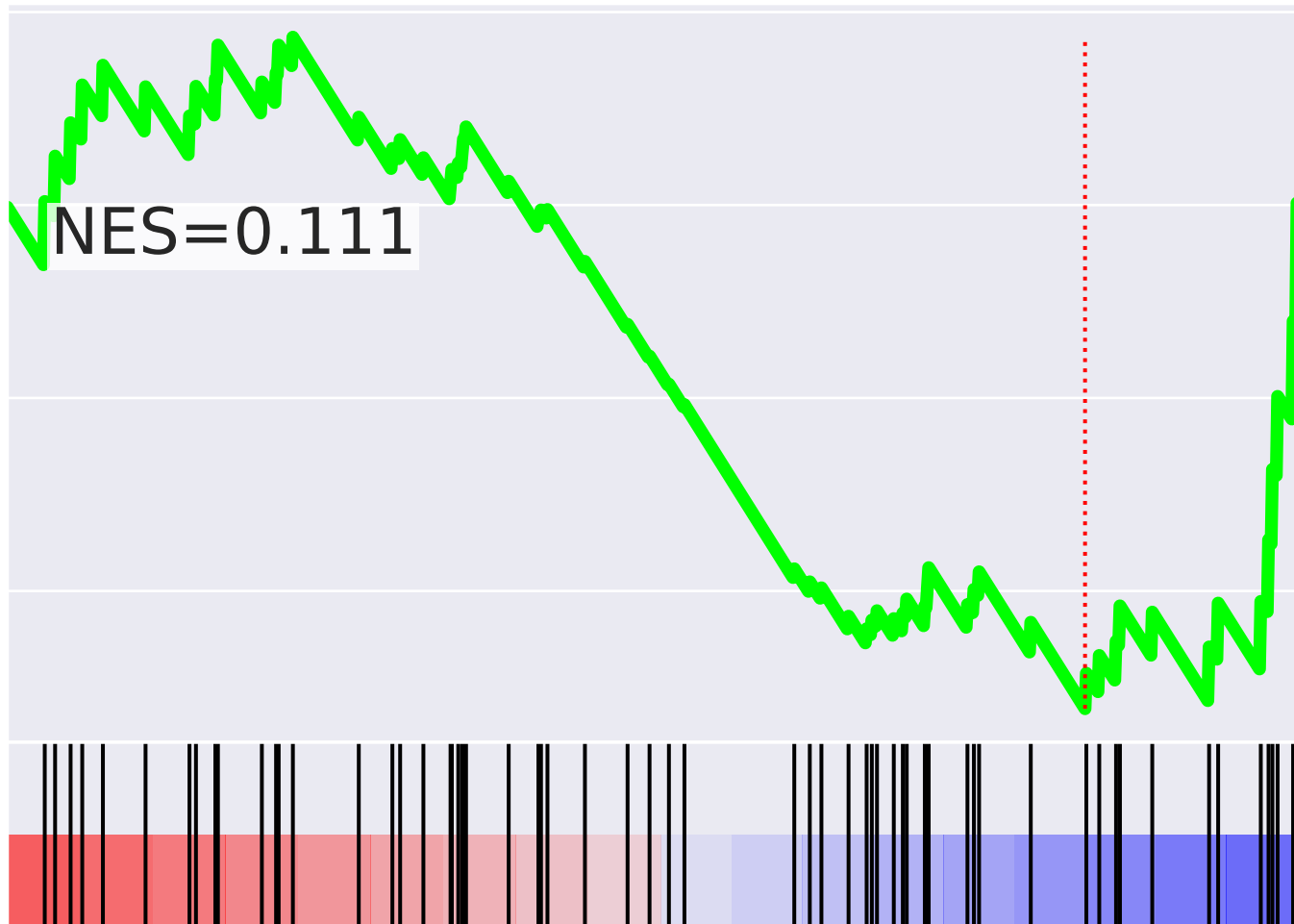




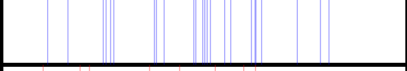
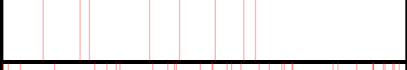
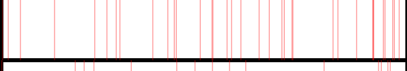
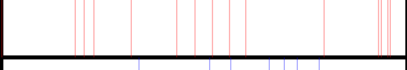
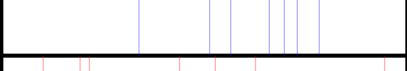
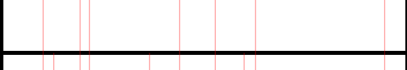


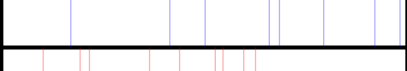

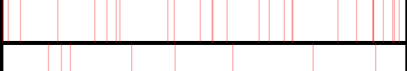
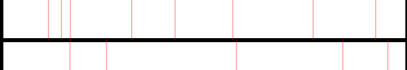
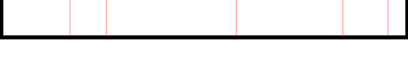
mitochondrial translational elongation (GO:0070125)

ES

NES=0.1111

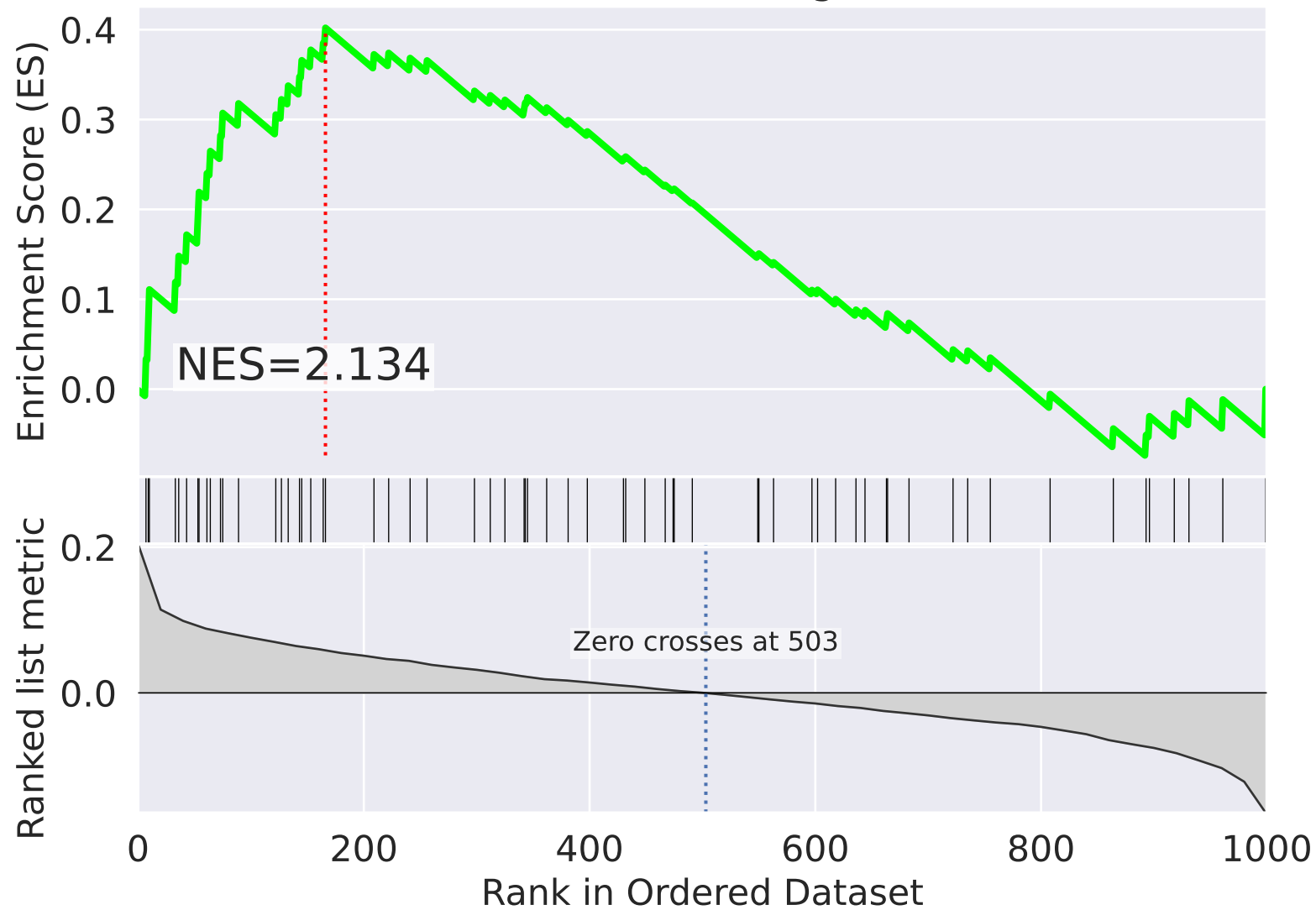
Rank



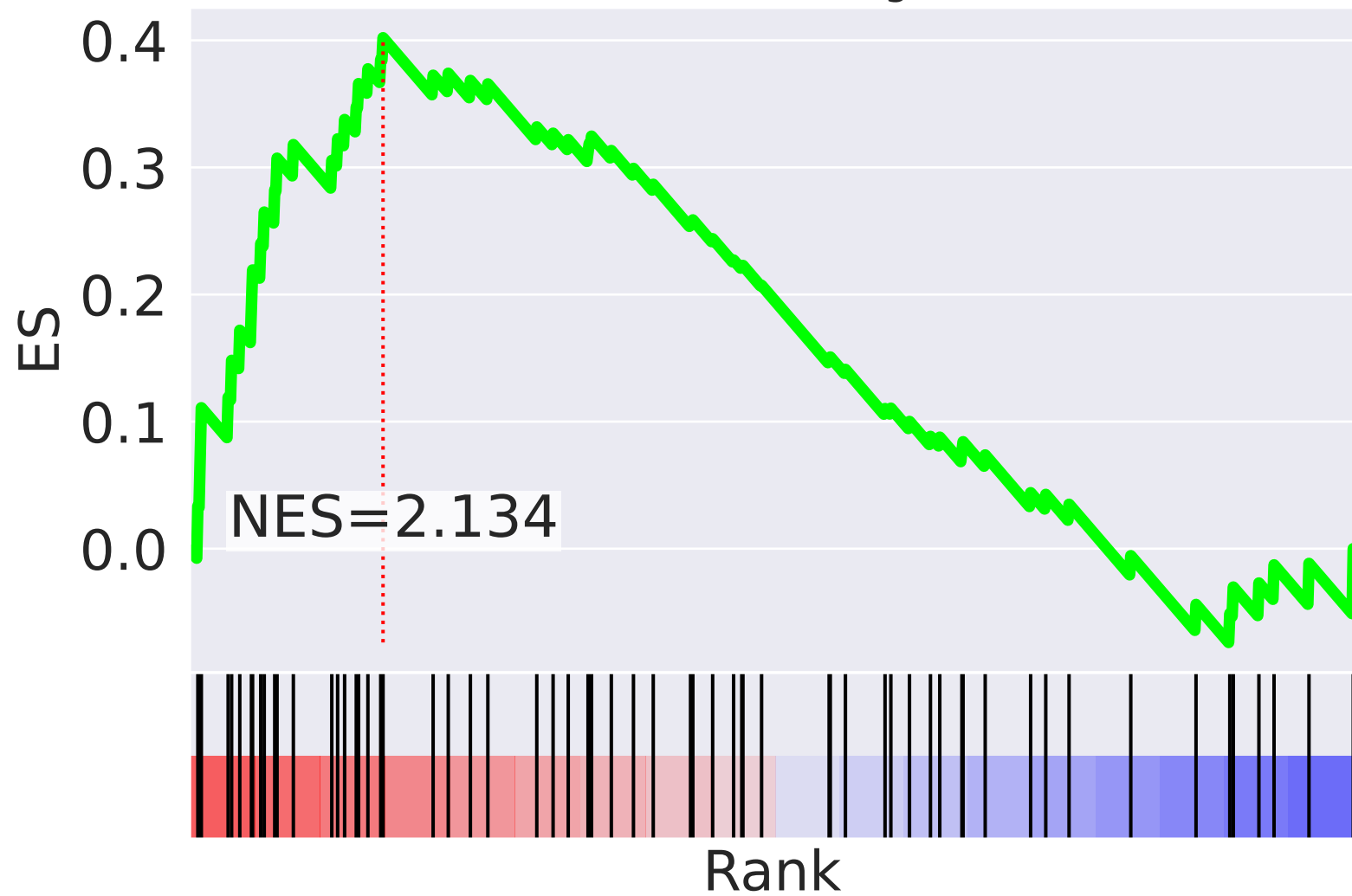
NES		SET
2.856		cell-matrix adhesion (GO:0007160)
2.516		mitotic metaphase plate congression (GO:0007080)
-2.516		regulation of transcription, DNA-templated (GO:0006355)
2.426		nucleus organization (GO:0006997)
2.381		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.310		positive regulation of apoptotic process (GO:0043065)
-2.309		negative regulation of cell growth (GO:0030308)
2.279		viral budding via host ESCRT complex (GO:0039702)
2.237		multivesicular body assembly (GO:0036258)
2.210		intracellular protein transport (GO:0006886)
-2.187		substantia nigra development (GO:0021762)
2.137		cell separation after cytokinesis (GO:0000920)
2.132		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.126		regulation of apoptotic process (GO:0042981)
2.043		substrate adhesion-dependent cell spreading (GO:0034446)




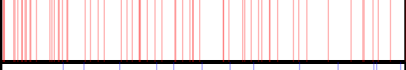


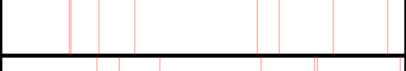



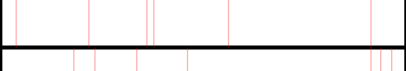
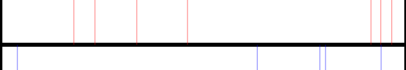
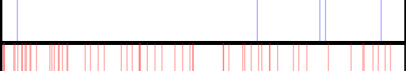
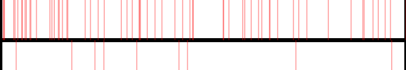

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=58$

mitochondrial translational elongation (GO:0070125)



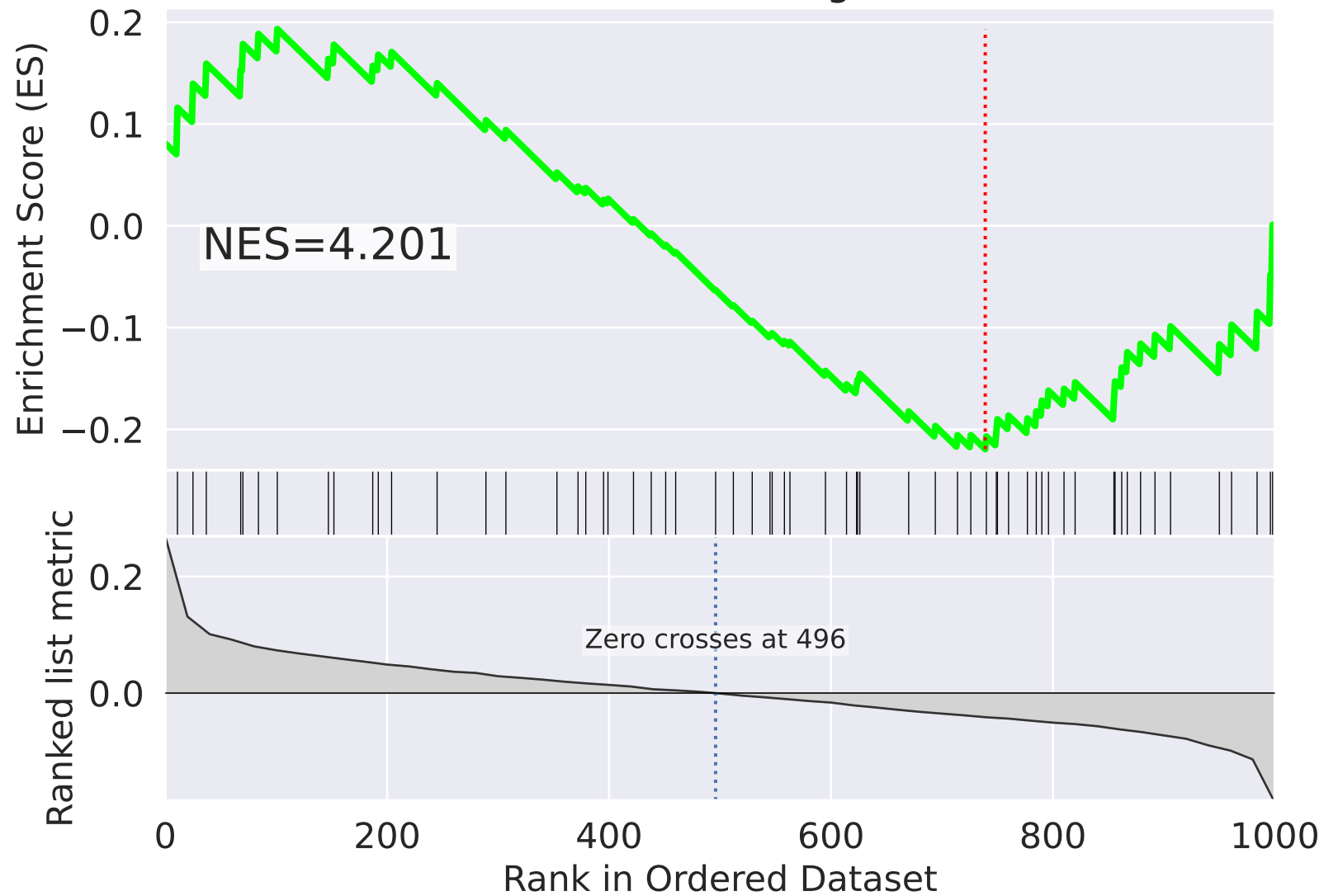
mitochondrial translational elongation (GO:0070125)



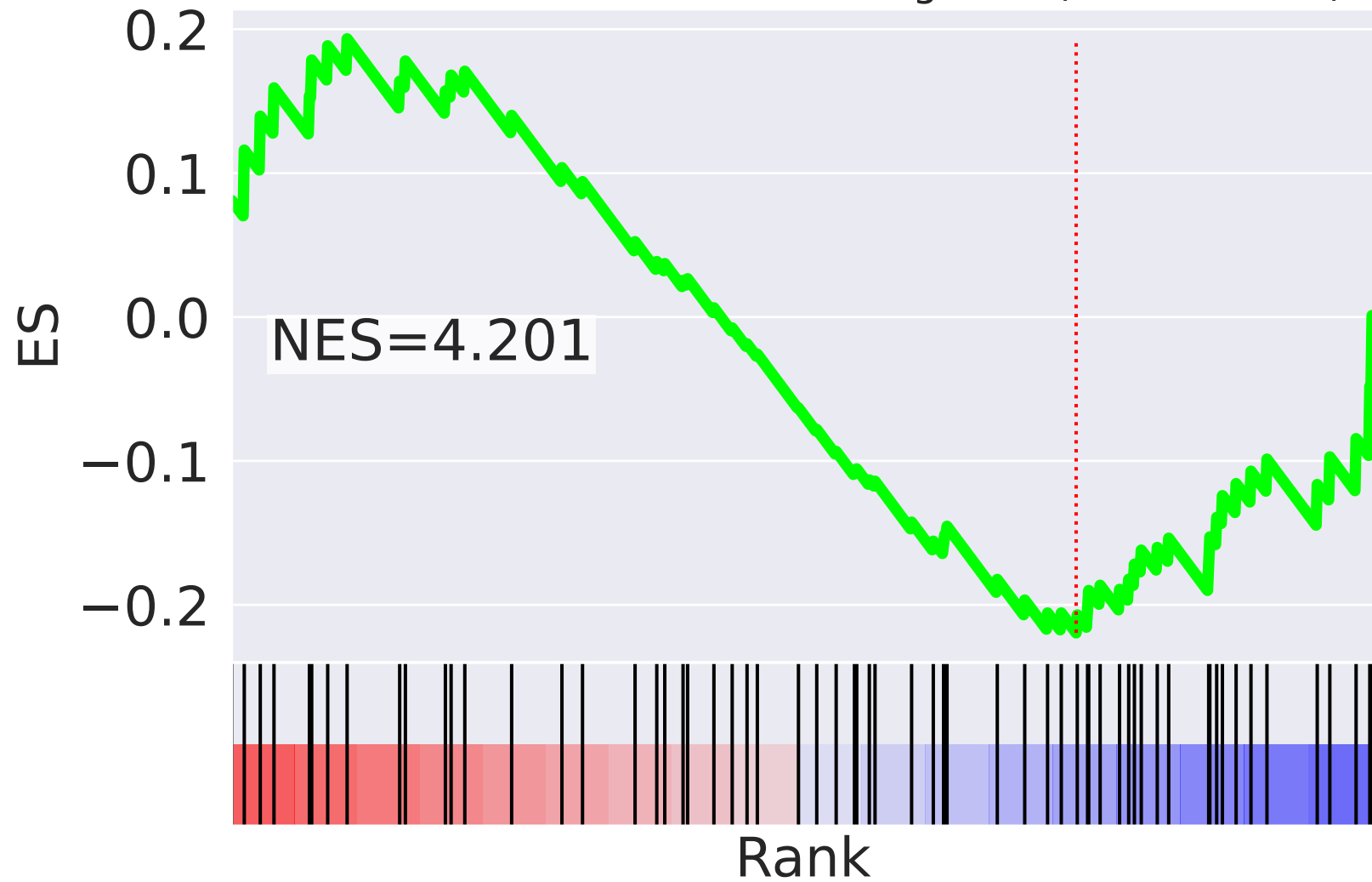
NES		SET
-2.509		endosomal transport (GO:0016197)
2.501		tricarboxylic acid cycle (GO:0006099)
2.322		generation of precursor metabolites and energy (GO:0006091)
2.134		mitochondrial translational elongation (GO:0070125)
-2.098		macroautophagy (GO:0016236)
-2.092		platelet aggregation (GO:0070527)
2.053		intracellular signal transduction (GO:0035556)
2.033		termination of RNA polymerase II transcription (GO:0006369)
-2.022		regulation of gene expression (GO:0010468)
-2.009		protein N-linked glycosylation (GO:0006487)
1.975		interstrand cross-link repair (GO:0036297)
1.964		double-strand break repair (GO:0006302)
-1.921		regulation of defense response to virus by virus (GO:0050690)
1.913		mitochondrial translational termination (GO:0070126)
1.896		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 $z=59$

mitochondrial translational elongation (GO:0070125)

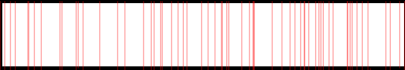
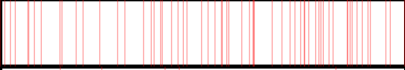
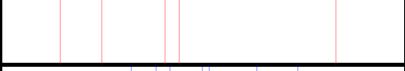

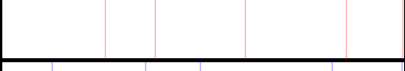



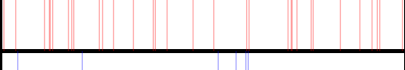

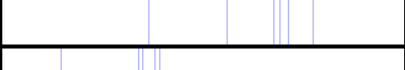
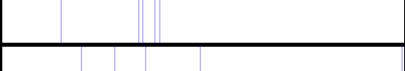


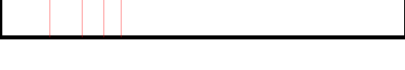


mitochondrial translational elongation (GO:0070125)



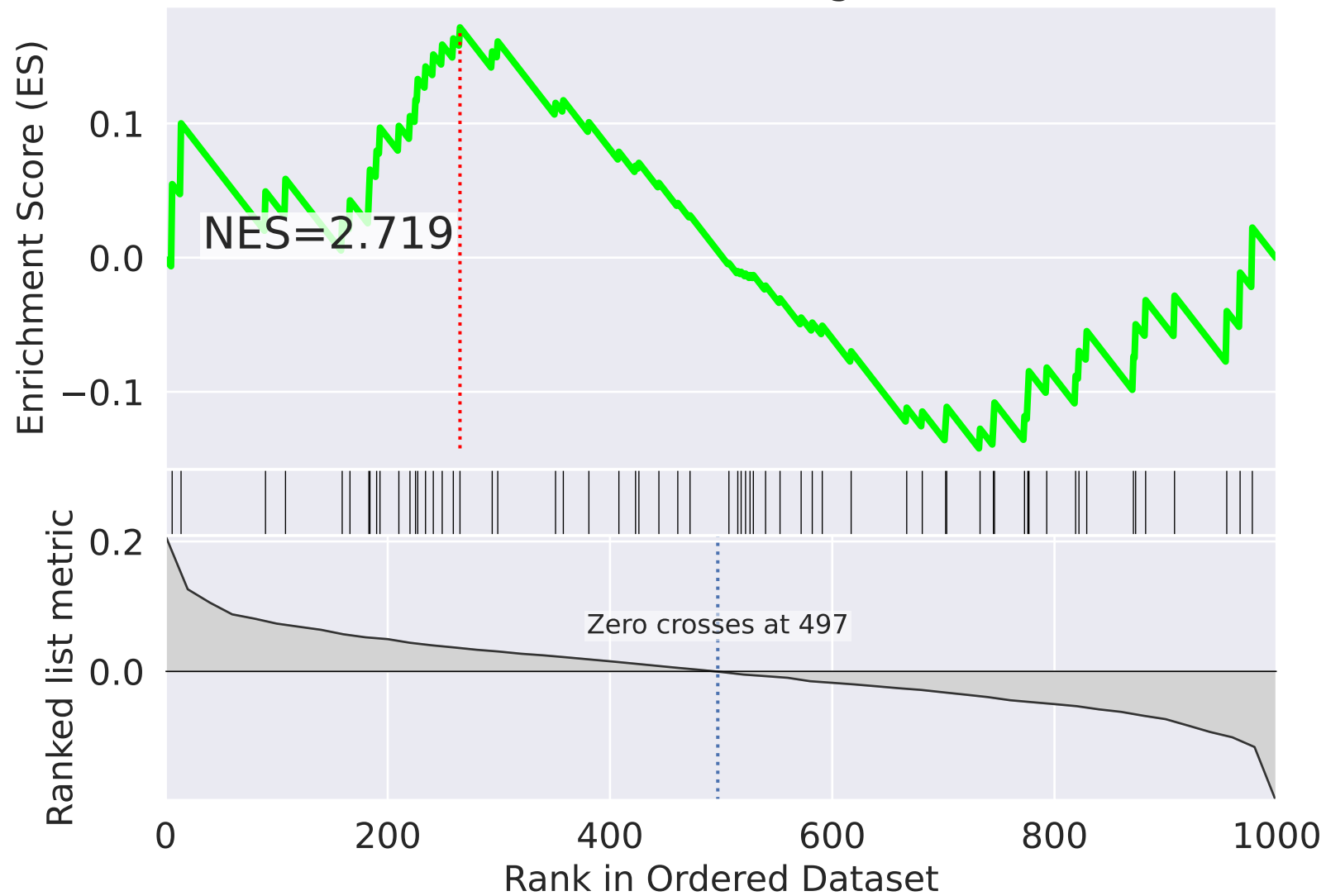
NES

SET

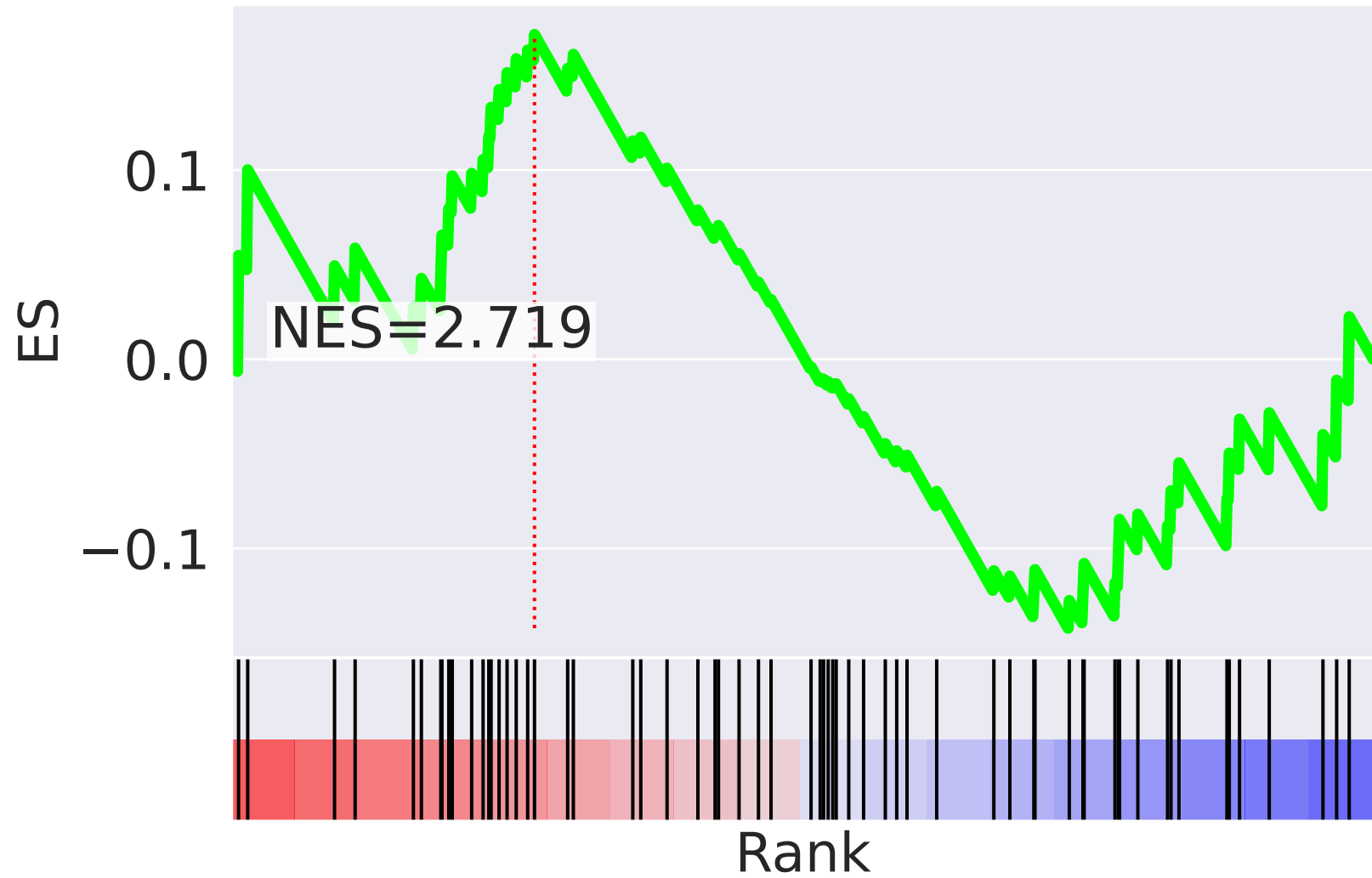
4.201		mitochondrial translational elongation (GO:0070125)
4.133		mitochondrial translational termination (GO:0070126)
2.593		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.495		movement of cell or subcellular component (GO:0006928)
2.347		carbohydrate metabolic process (GO:0005975)
-2.206		mitotic nuclear envelope disassembly (GO:0007077)
-2.185		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.111		transcription from mitochondrial promoter (GO:0006390)
2.040		positive regulation of cell proliferation (GO:0008284)
-2.002		fibroblast growth factor receptor signaling pathway (GO:0008543)
-1.953		execution phase of apoptosis (GO:0097194)
-1.934		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.927		intracellular transport of virus (GO:0075733)
-1.861		platelet degranulation (GO:0002576)
1.811		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)

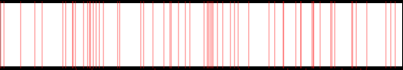

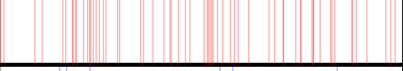

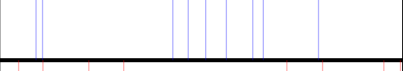

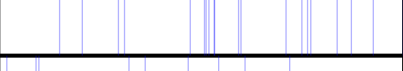







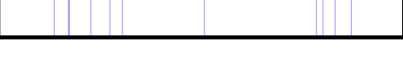
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=60$

mitochondrial translational elongation (GO:0070125)



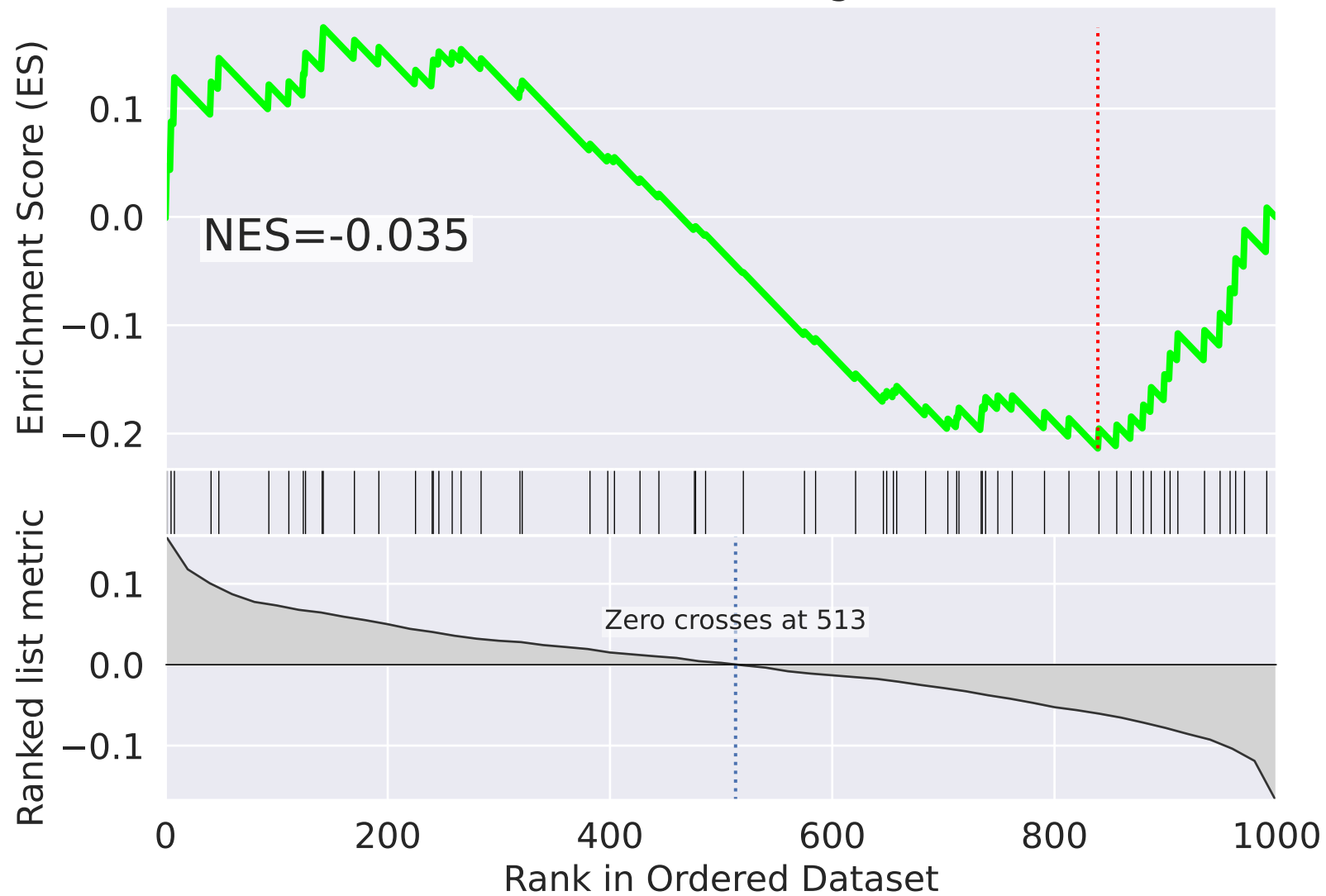
mitochondrial translational elongation (GO:0070125)



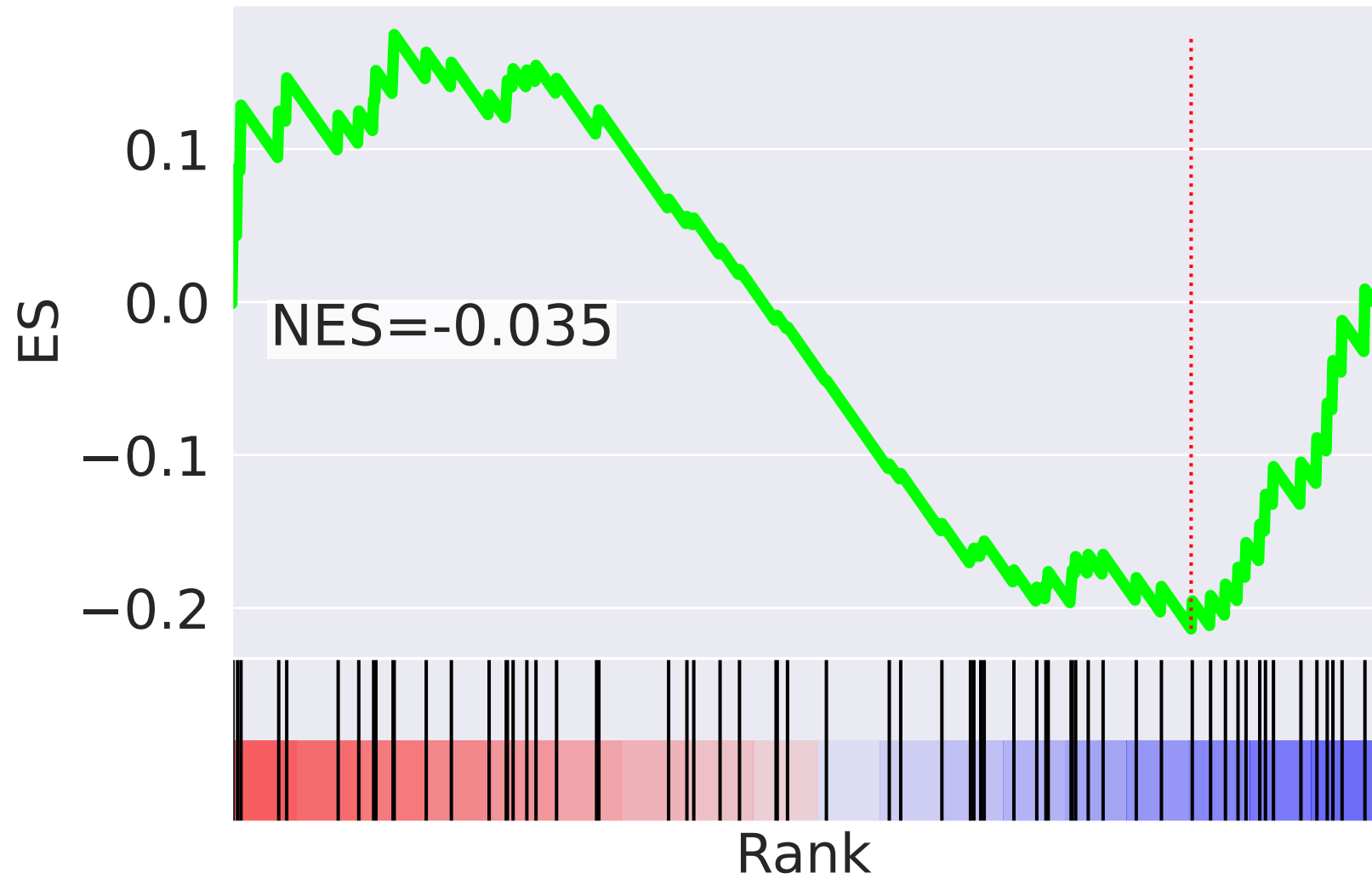
NES		SET
3.049		mitochondrial translational termination (GO:0070126)
2.991		tricarboxylic acid cycle (GO:0006099)
2.719		mitochondrial translational elongation (GO:0070125)
-2.422		interstrand cross-link repair (GO:0036297)
-2.387		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.385		regulation of cell cycle (GO:0051726)
-2.356		cellular response to DNA damage stimulus (GO:0006974)
-2.341		retrograde transport, endosome to Golgi (GO:0042147)
-2.323		mitotic nuclear envelope disassembly (GO:0007077)
-2.279		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.229		response to ionizing radiation (GO:0010212)
-2.182		negative regulation of translation (GO:0017148)
-2.166		DNA synthesis involved in DNA repair (GO:0000731)
-2.162		intracellular signal transduction (GO:0035556)
-2.124		cell migration (GO:0016477)

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

mitochondrial translational elongation (GO:0070125)



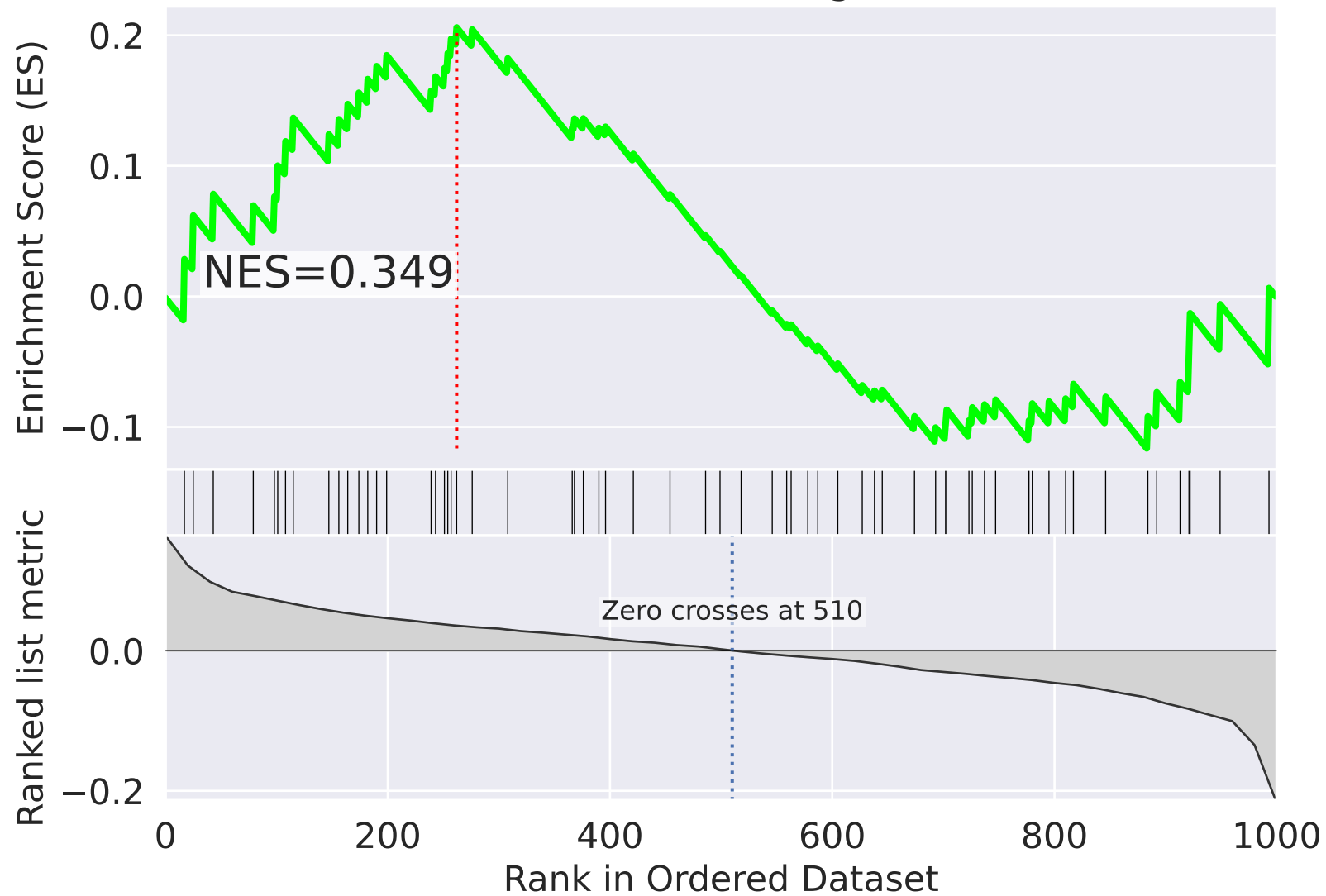
mitochondrial translational elongation (GO:0070125)



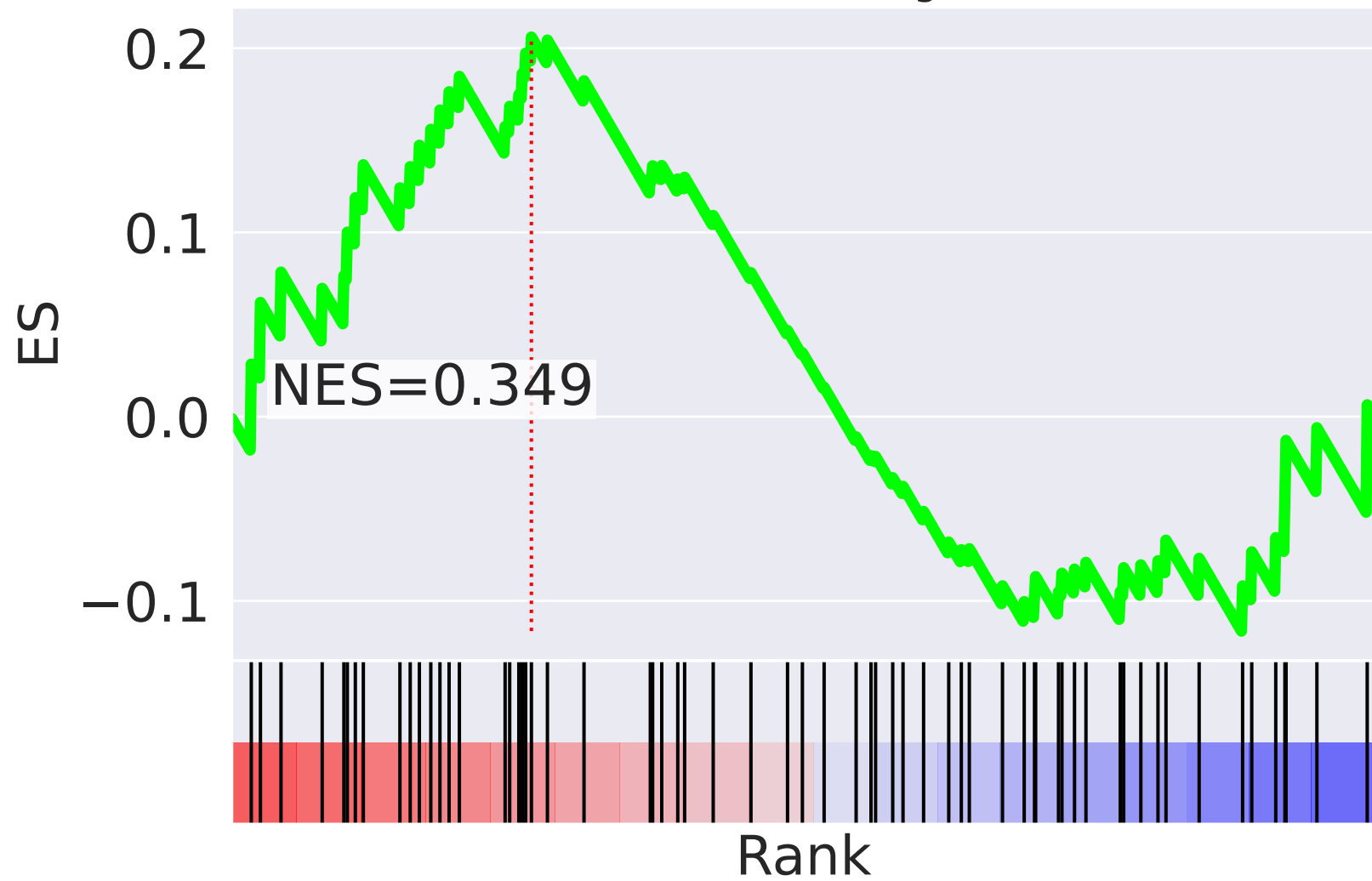
NES		SET
-2.623		protein autoubiquitination (GO:0051865)
2.138		protein deubiquitination (GO:0016579)
2.124		positive regulation of protein catabolic process (GO:0045732)
-2.123		viral life cycle (GO:0019058)
-2.096		transcription from RNA polymerase II promoter (GO:0006366)
2.043		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-1.952		nucleus organization (GO:0006997)
1.950		protein targeting to mitochondrion (GO:0006626)
-1.922		interstrand cross-link repair (GO:0036297)
-1.860		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-1.848		regulation of centrosome duplication (GO:0010824)
1.828		iron-sulfur cluster assembly (GO:0016226)
1.819		ubiquitin-dependent ERAD pathway (GO:0030433)
-1.736		mRNA processing (GO:0006397)
1.730		oxidation-reduction process (GO:0055114)






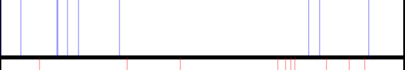
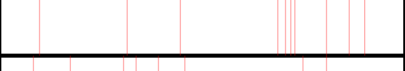
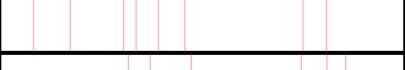

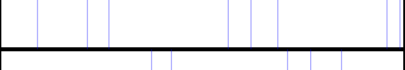
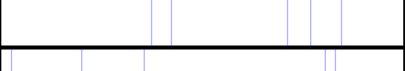
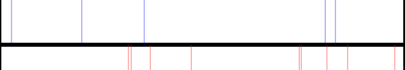

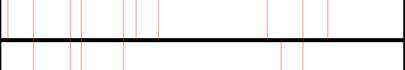
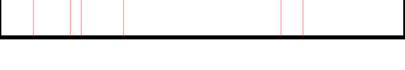
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=62$

mitochondrial translational elongation (GO:0070125)



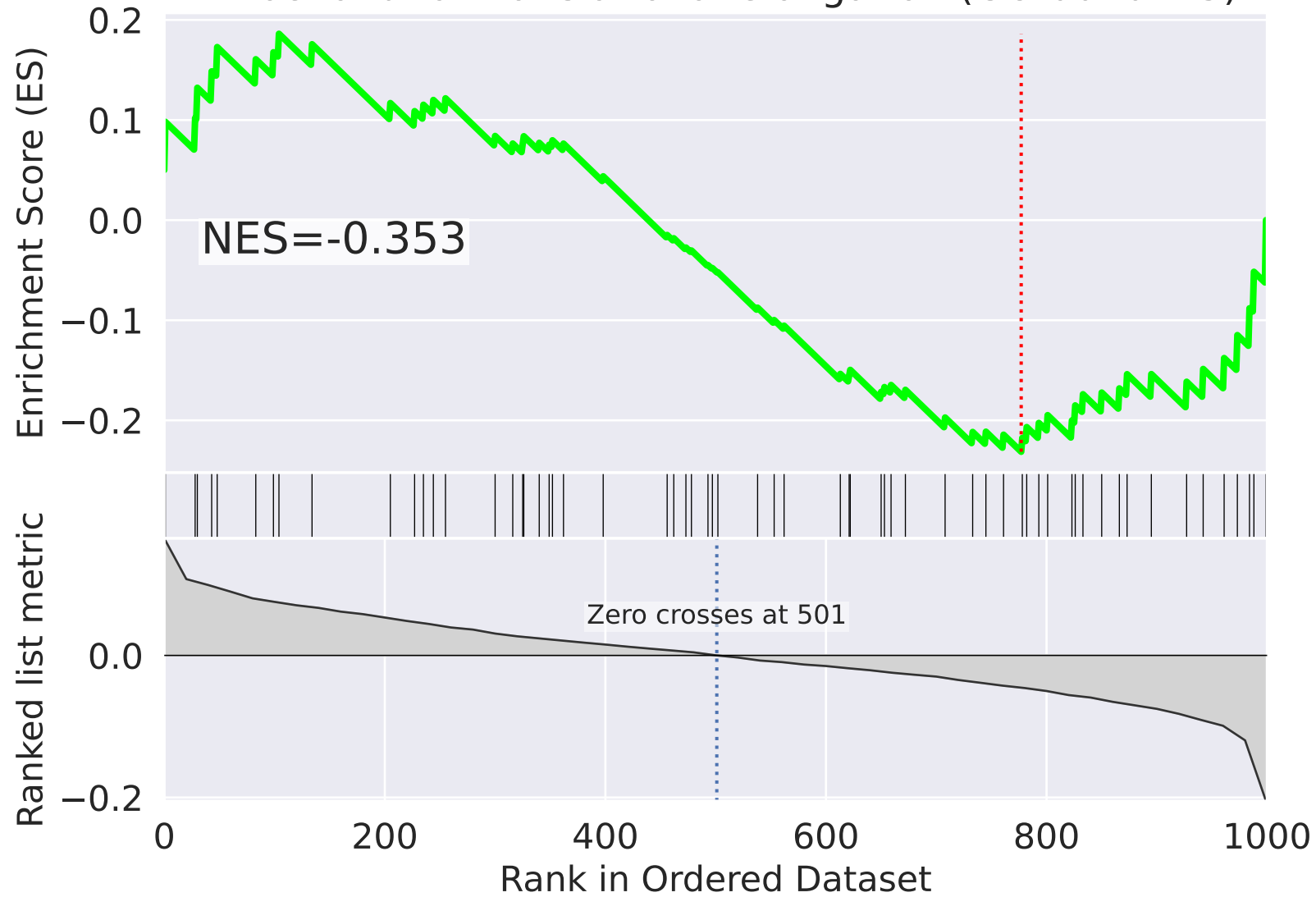
mitochondrial translational elongation (GO:0070125)



NES		SET
2.768		mitotic metaphase plate congression (GO:0007080)
2.593		sister chromatid cohesion (GO:0007062)
-2.437		cell cycle arrest (GO:0007050)
2.434		nucleus organization (GO:0006997)
2.421		mitotic nuclear envelope disassembly (GO:0007077)
-2.306		protein dephosphorylation (GO:0006470)
2.234		regulation of cellular response to heat (GO:1900034)
2.188		axon guidance (GO:0007411)
2.083		ESCRT III complex disassembly (GO:1904903)
-2.076		nervous system development (GO:0007399)
-2.072		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-2.020		ubiquitin-dependent ERAD pathway (GO:0030433)
1.989		cell separation after cytokinesis (GO:0000920)
1.958		epidermal growth factor receptor signaling pathway (GO:0007173)
1.941		ERBB2 signaling pathway (GO:0038128)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1

0.0



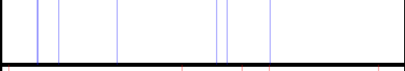

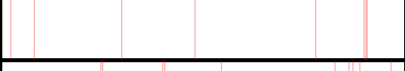

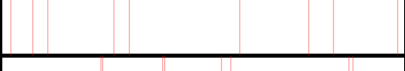
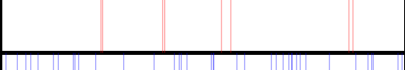
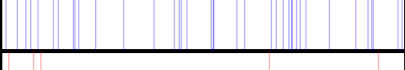




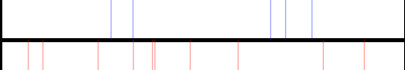
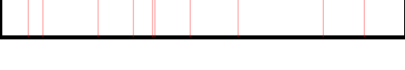
-0.1

-0.2

NES=-0.353

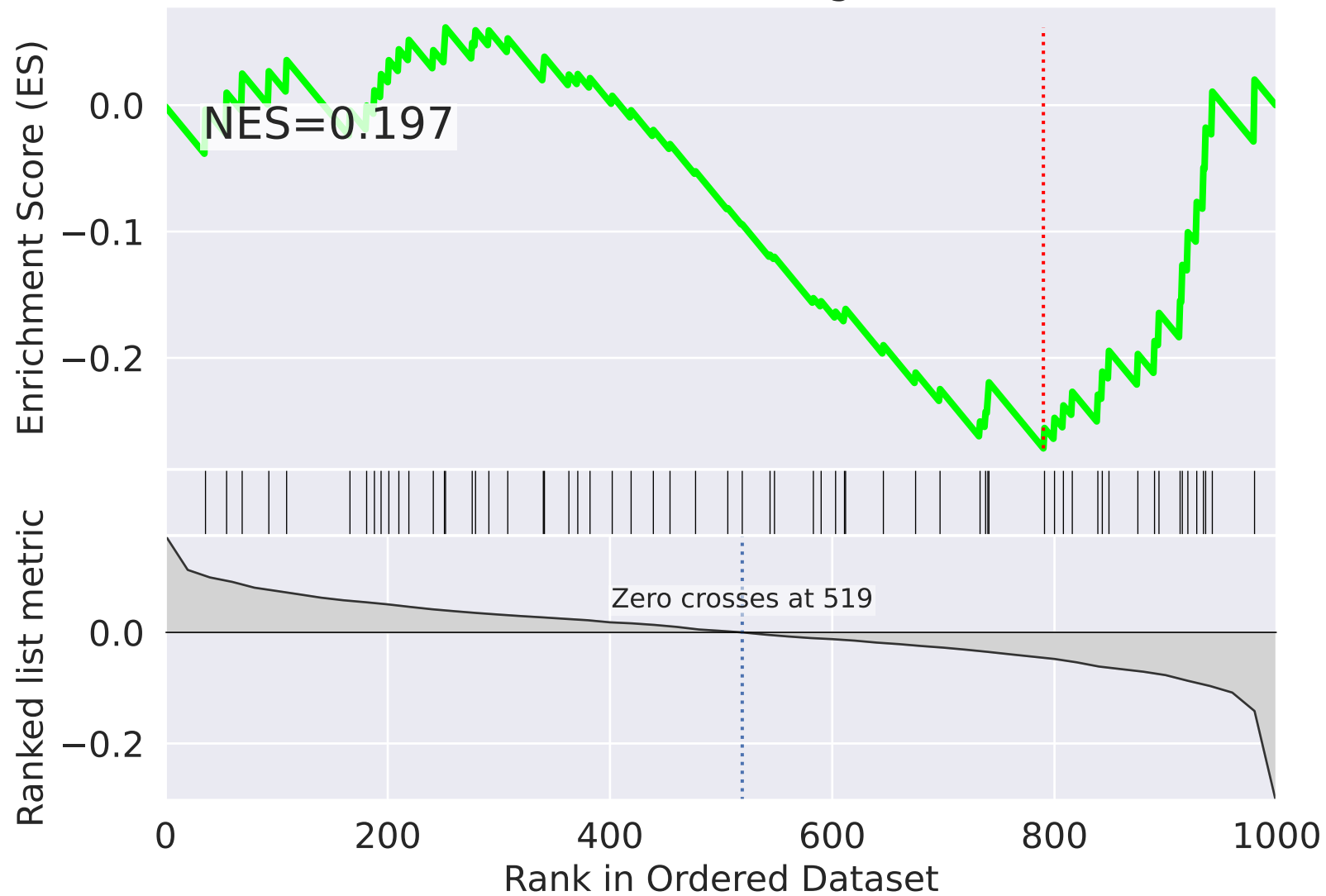
Rank



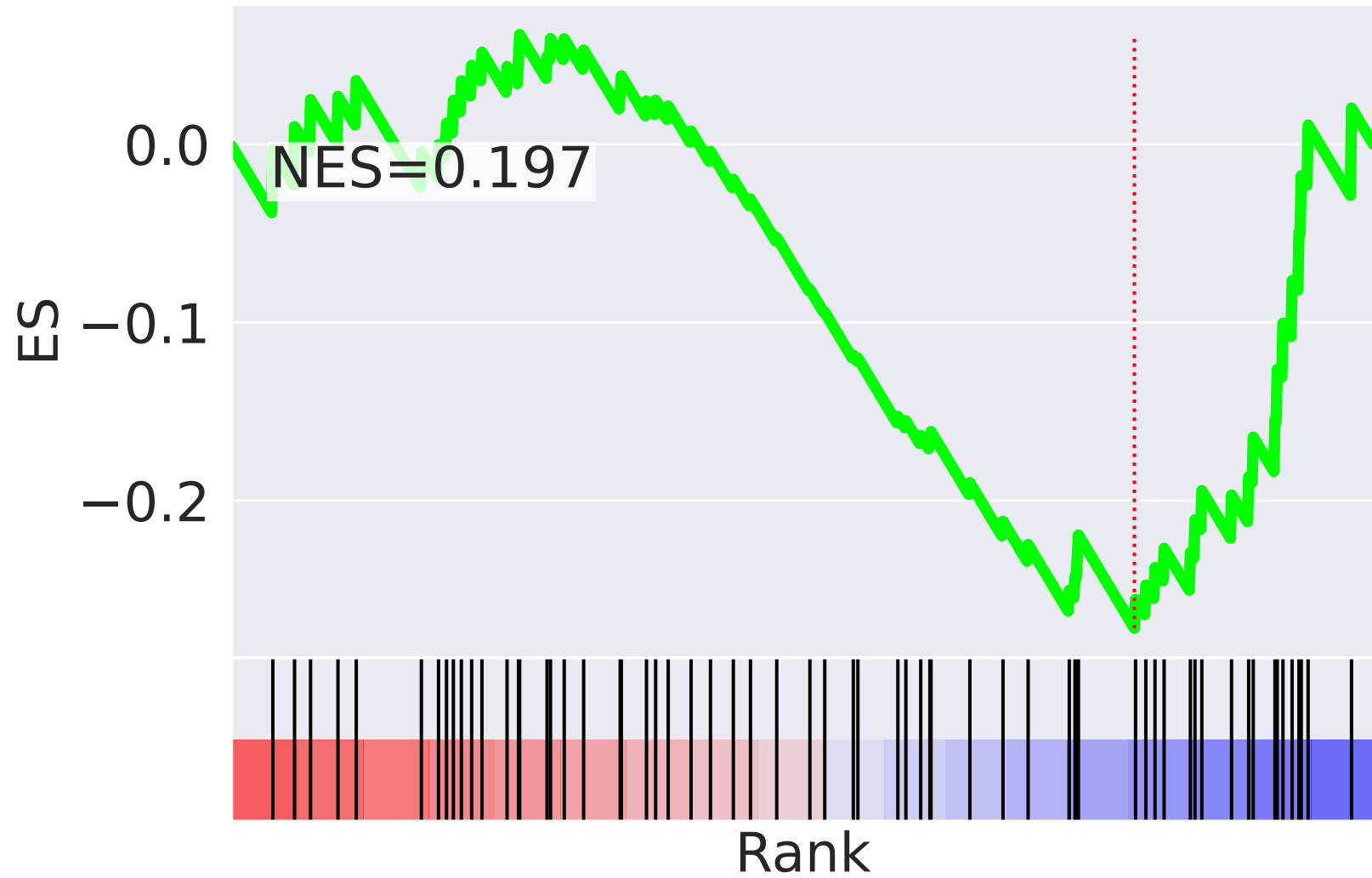
NES		SET
-2.891		protein N-linked glycosylation via asparagine (GO:0018279)
-2.724		IRE1-mediated unfolded protein response (GO:0036498)
-2.724		Wnt signaling pathway (GO:0016055)
2.606		aerobic respiration (GO:0009060)
2.515		negative regulation of translation (GO:0017148)
2.458		multivesicular body assembly (GO:0036258)
2.365		regulation of mRNA stability (GO:0043488)
2.221		nucleus organization (GO:0006997)
-2.199		positive regulation of transcription, DNA-templated (GO:0045893)
2.187		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.143		axon guidance (GO:0007411)
-2.095		cell cycle arrest (GO:0007050)
-2.030		protein stabilization (GO:0050821)
-2.012		peptidyl-threonine phosphorylation (GO:0018107)
2.005		sister chromatid cohesion (GO:0007062)

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

mitochondrial translational elongation (GO:0070125)


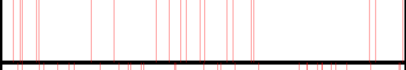
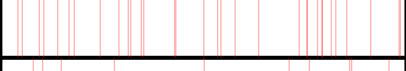



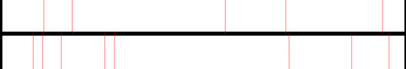
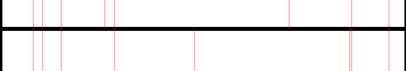
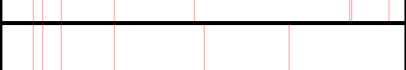
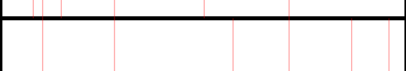
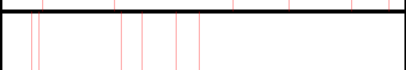
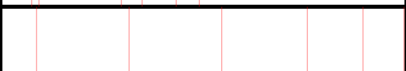

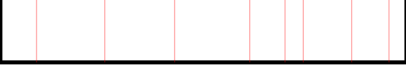



mitochondrial translational elongation (GO:0070125)



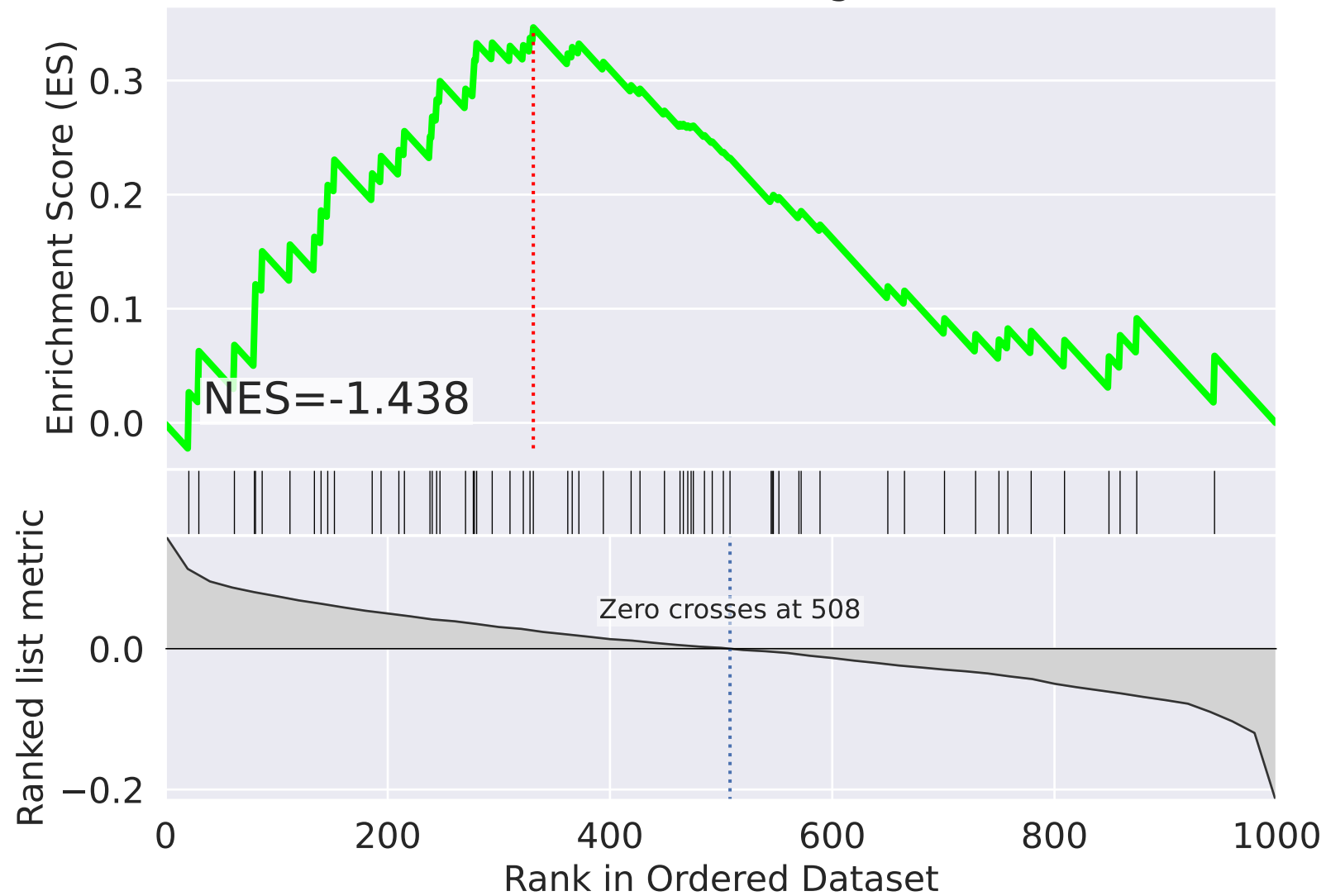
NES

SET

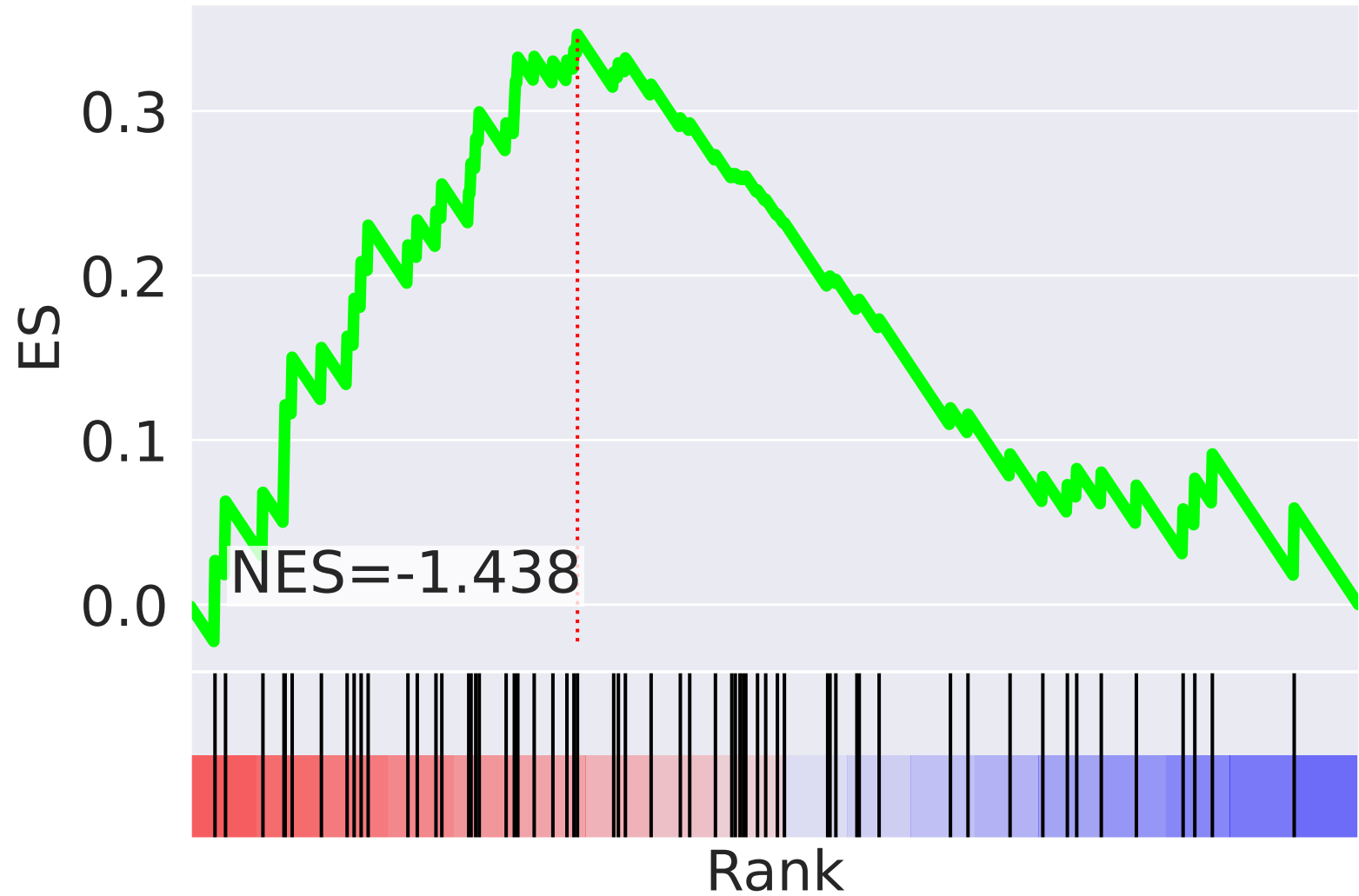
-3.745		regulation of transcription, DNA-templated (GO:0006355)
3.394		cellular response to DNA damage stimulus (GO:0006974)
3.168		positive regulation of cell proliferation (GO:0008284)
3.070		multivesicular body assembly (GO:0036258)
2.746		mitotic metaphase plate congression (GO:0007080)
2.646		protein phosphorylation (GO:0006468)
2.512		inflammatory response (GO:0006954)
2.484		nucleus organization (GO:0006997)
2.465		viral life cycle (GO:0019058)
2.453		ESCRT III complex disassembly (GO:1904903)
2.411		regulation of centrosome duplication (GO:0010824)
2.406		iron-sulfur cluster assembly (GO:0016226)
2.404		execution phase of apoptosis (GO:0097194)
2.392		negative regulation of apoptotic process (GO:0043066)
2.353		mitotic cytokinesis (GO:0000281)






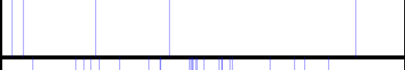
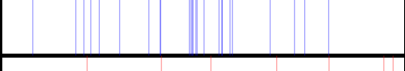


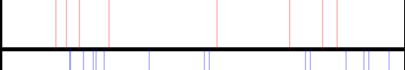

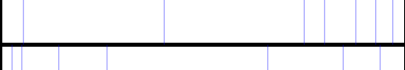
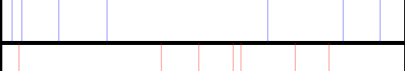
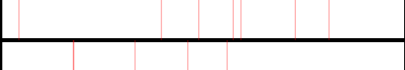
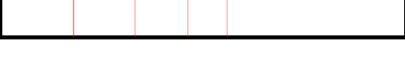
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=65$

mitochondrial translational elongation (GO:0070125)



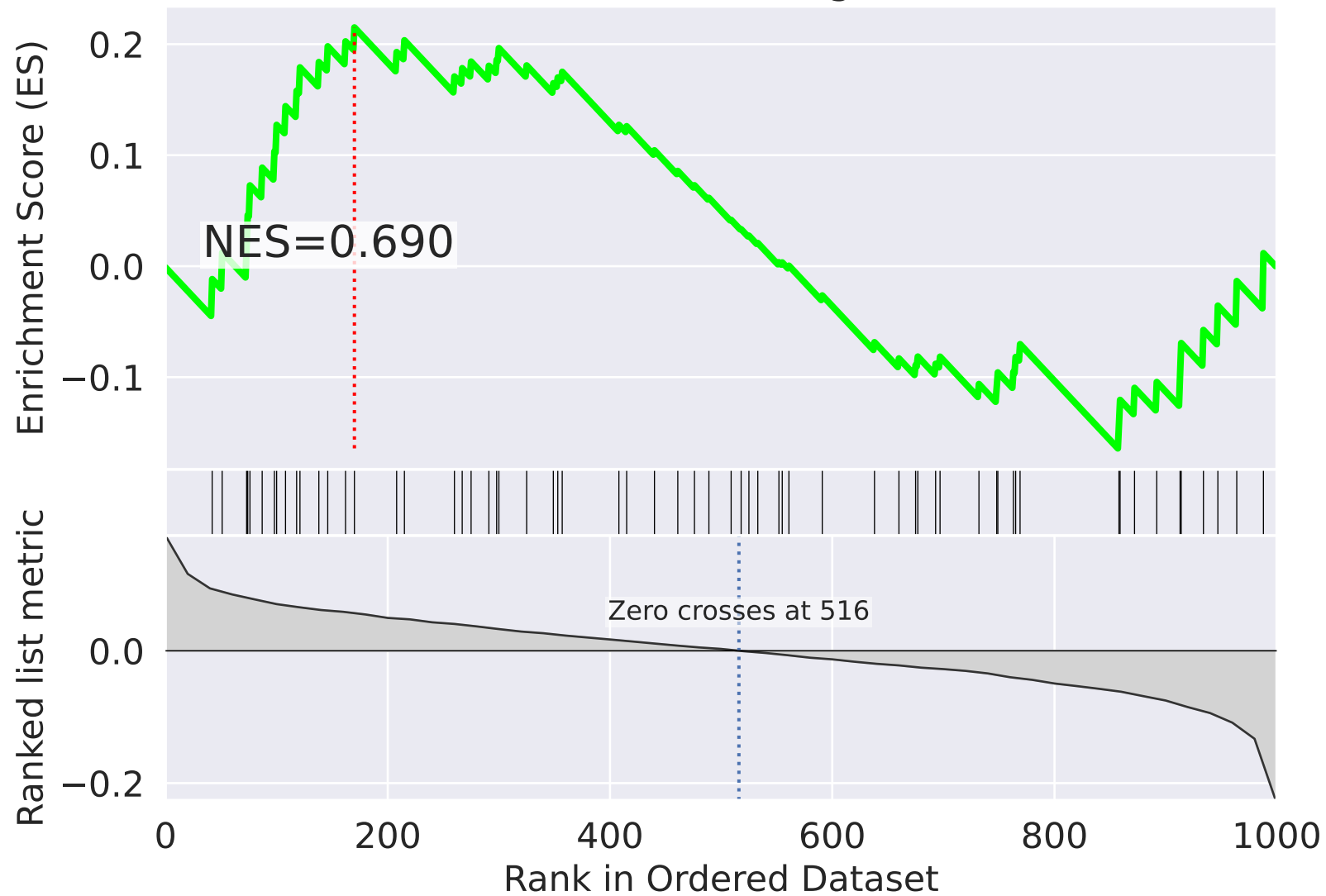
mitochondrial translational elongation (GO:0070125)



NES		SET
2.725		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.512		G2/M transition of mitotic cell cycle (GO:0000086)
2.504		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.394		signal transduction (GO:0007165)
-2.369		regulation of DNA replication (GO:0006275)
-2.320		regulation of cell motility (GO:2000145)
-2.237		mitochondrial translation (GO:0032543)
2.162		axon guidance (GO:0007411)
-2.131		protein phosphorylation (GO:0006468)
2.098		vesicle-mediated transport (GO:0016192)
-2.071		positive regulation of apoptotic process (GO:0043065)
-2.063		cell surface receptor signaling pathway (GO:0007166)
-2.058		response to virus (GO:0009615)
1.914		Ras protein signal transduction (GO:0007265)
1.849		heme biosynthetic process (GO:0006783)

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)

ES

0.2

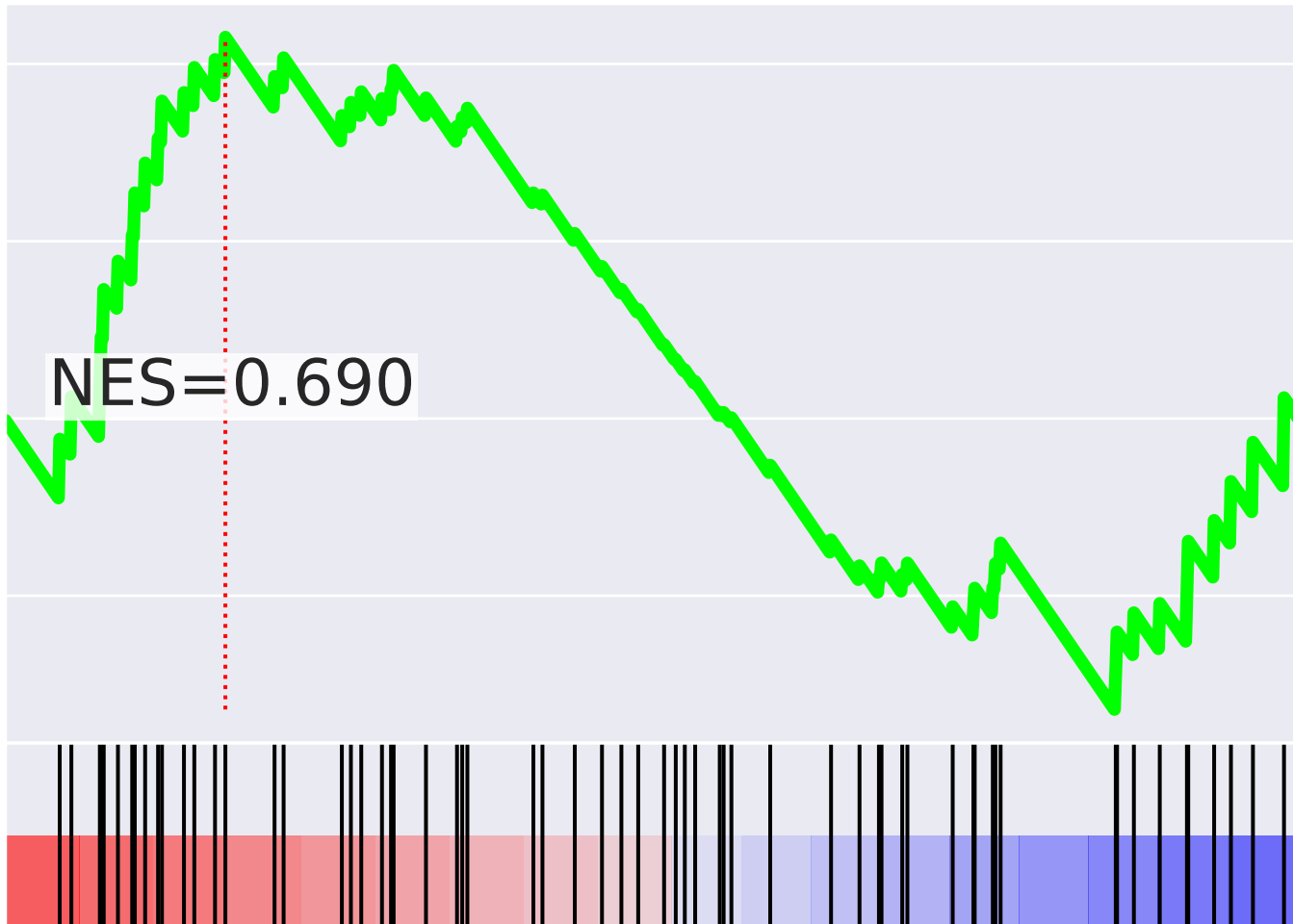
0.1

NES=0.690

0.0






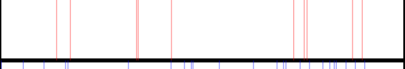
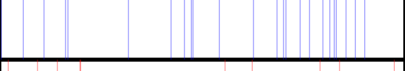
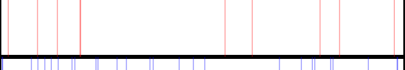
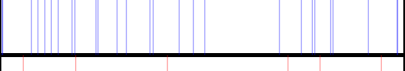
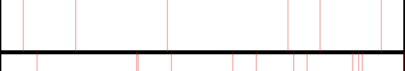
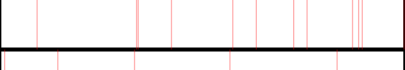



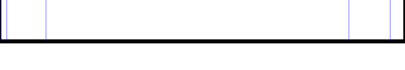
-0.1

Rank



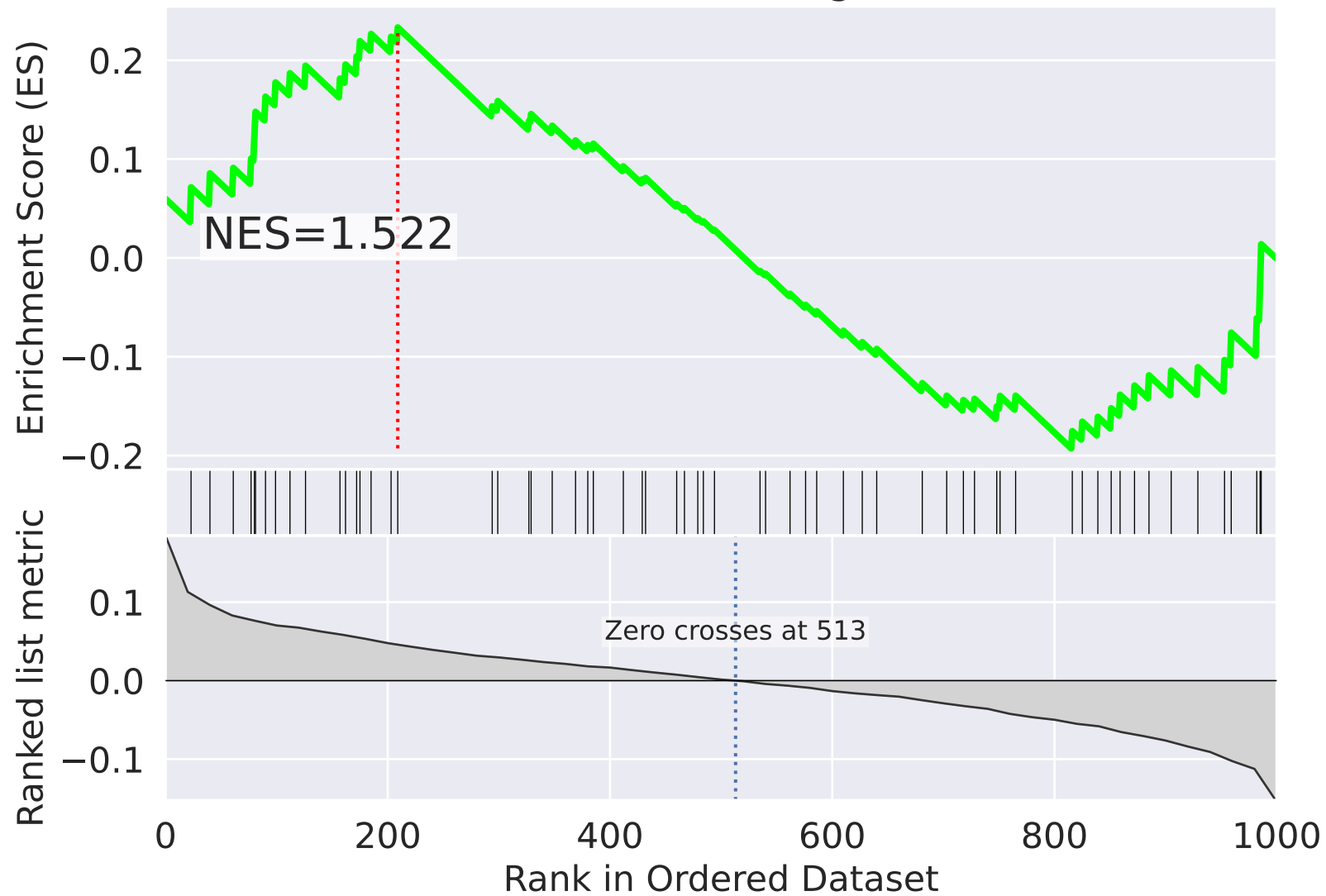
NES

SET

2.591		regulation of cell proliferation (GO:0042127)
2.492		sister chromatid cohesion (GO:0007062)
2.424		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.379		protein stabilization (GO:0050821)
2.343		viral budding via host ESCRT complex (GO:0039702)
2.334		multivesicular body assembly (GO:0036258)
-2.276		regulation of transcription, DNA-templated (GO:0006355)
2.238		positive regulation of gene expression (GO:0010628)
-2.210		mRNA splicing, via spliceosome (GO:0000398)
2.187		chromosome segregation (GO:0007059)
2.137		mitotic metaphase plate congression (GO:0007080)
2.137		small molecule metabolic process (GO:0044281)
-2.121		nucleosome disassembly (GO:0006337)
-2.098		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.068		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 $z=67$

mitochondrial translational elongation (GO:0070125)



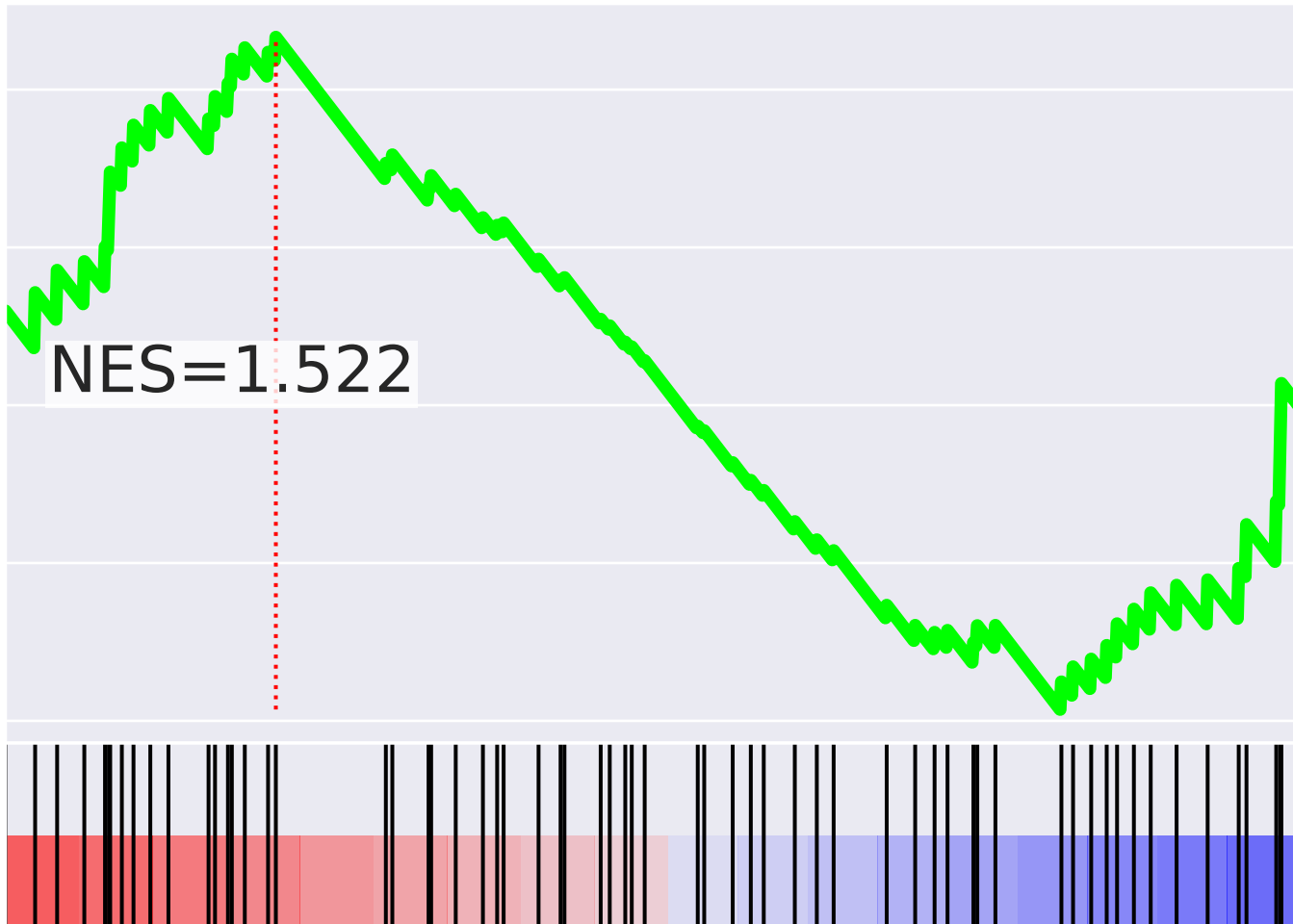
mitochondrial translational elongation (GO:0070125)

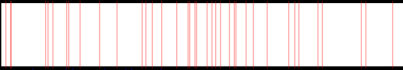





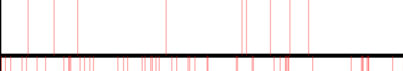
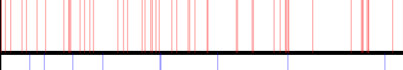


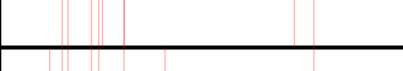



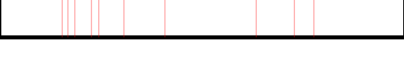
ES

NES=1.522

0.2
0.1
0.0
-0.1
-0.2

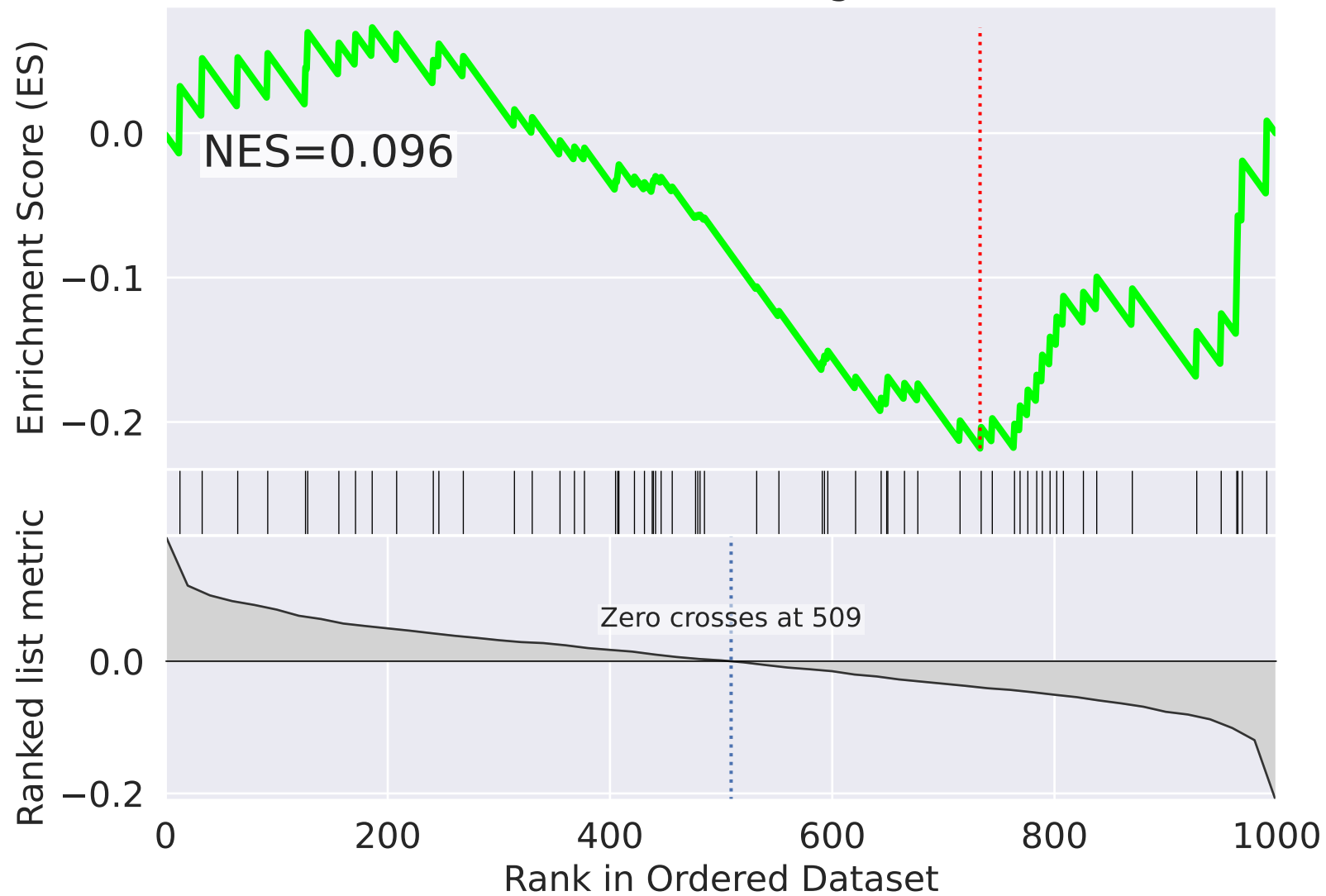
Rank



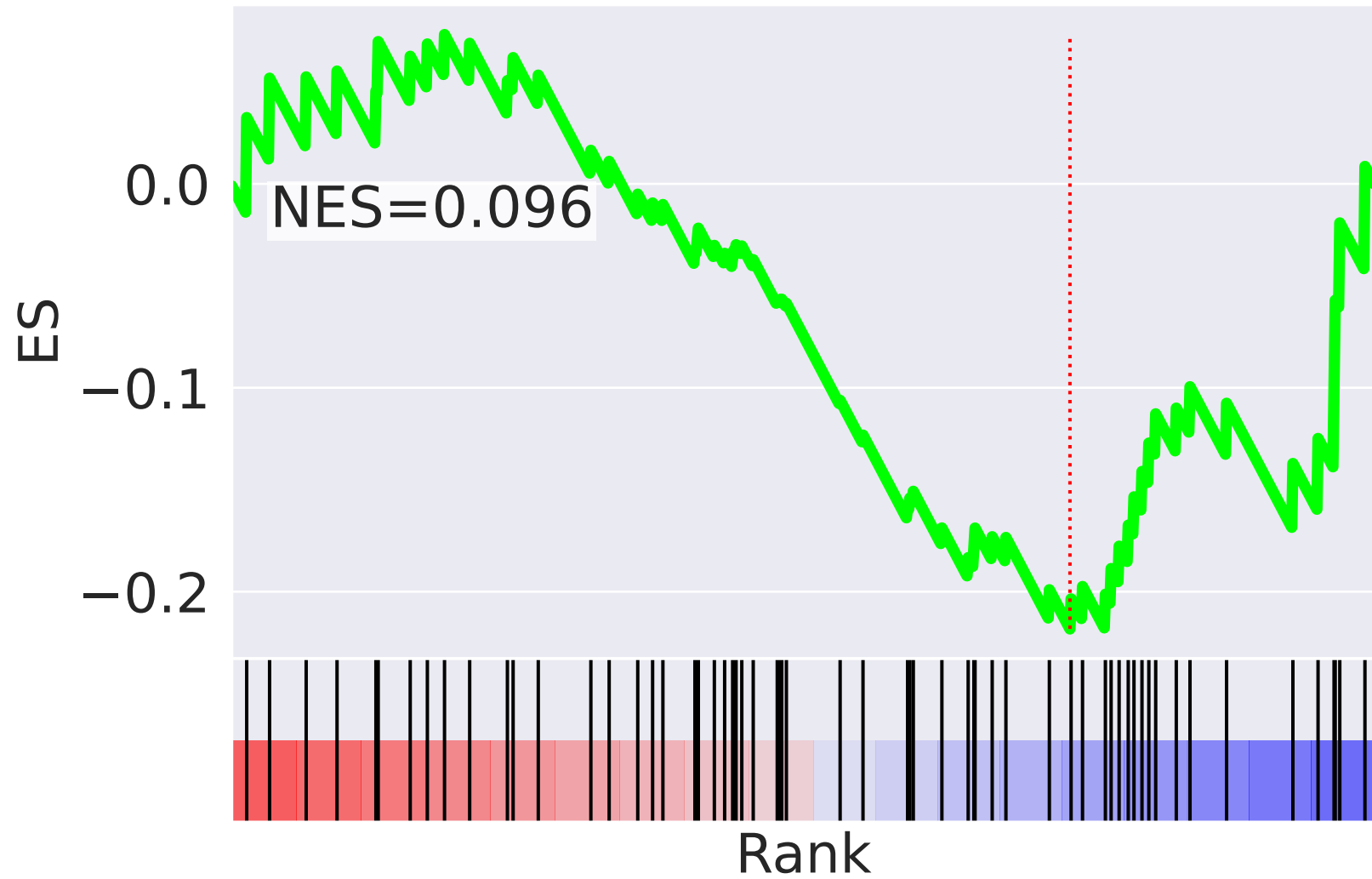
NES		SET
3.154		positive regulation of transcription, DNA-templated (GO:0045893)
-2.931		T cell costimulation (GO:0031295)
-2.827		regulation of mRNA stability (GO:0043488)
-2.697		response to ionizing radiation (GO:0010212)
-2.534		membrane organization (GO:0061024)
-2.491		positive regulation of protein catabolic process (GO:0045732)
2.455		tricarboxylic acid cycle (GO:0006099)
2.376		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.364		peptidyl-serine phosphorylation (GO:0018105)
-2.344		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
2.311		cell separation after cytokinesis (GO:0000920)
2.282		viral life cycle (GO:0019058)
-2.279		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-2.233		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.231		multivesicular body assembly (GO:0036258)


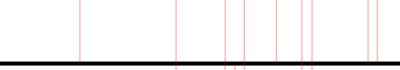
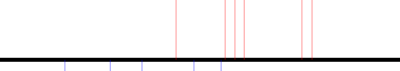
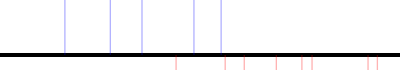
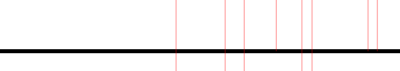
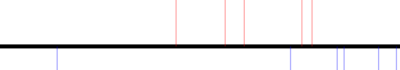
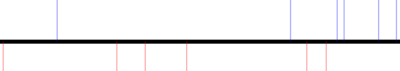
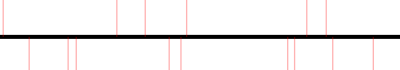



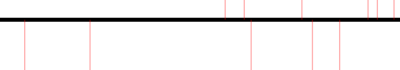



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=68$

mitochondrial translational elongation (GO:0070125)



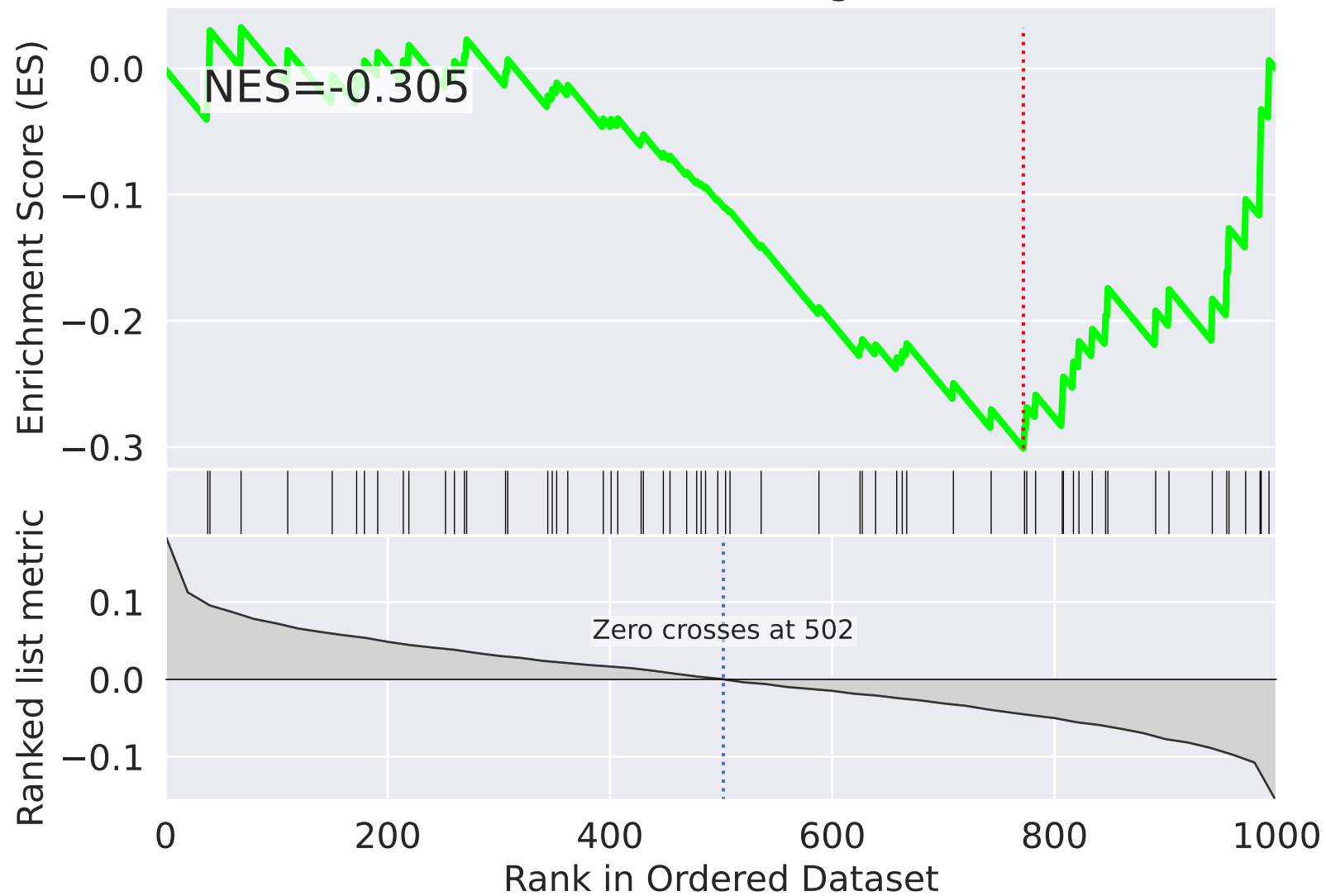
mitochondrial translational elongation (GO:0070125)



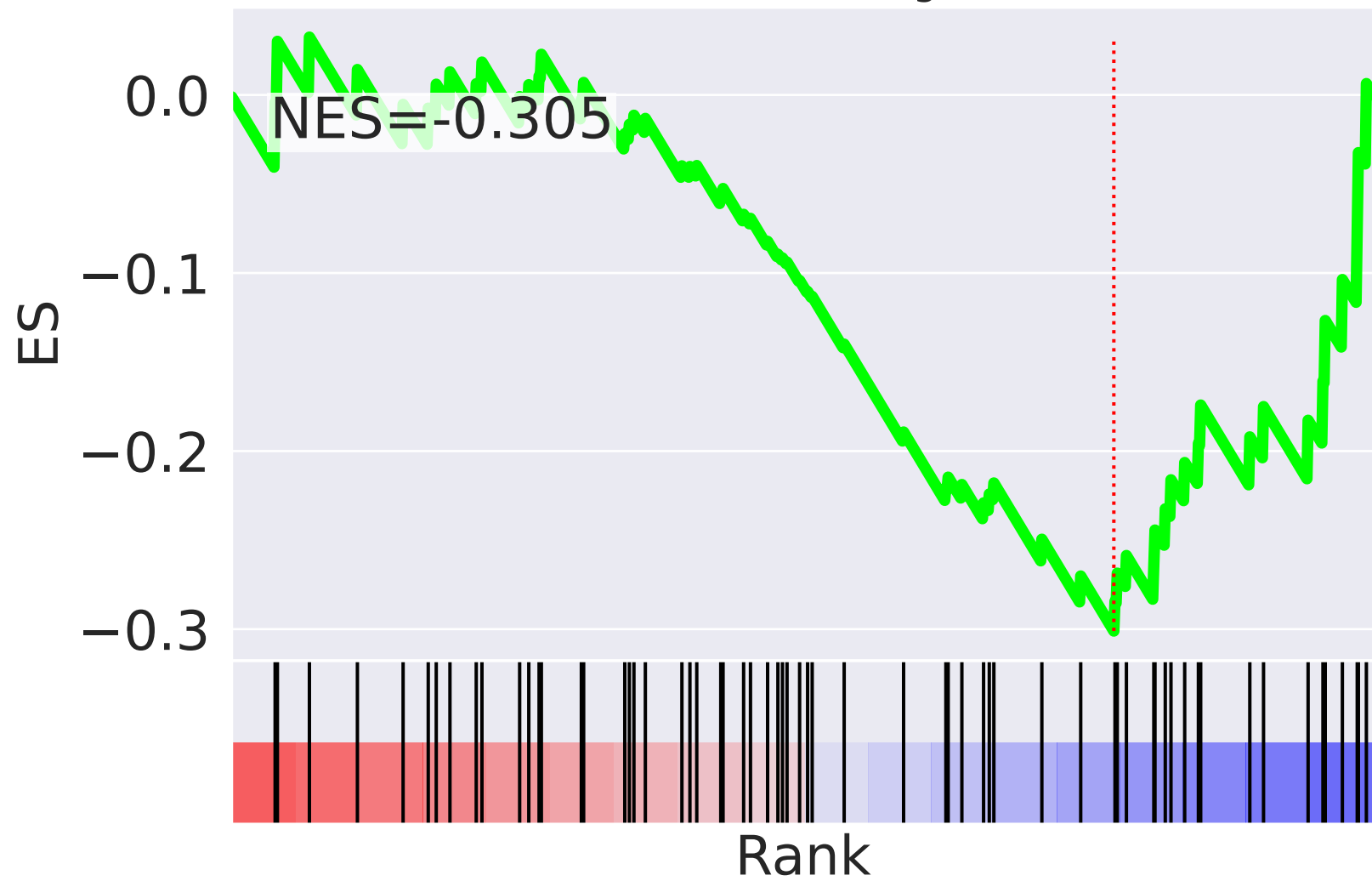
NES		SET
2.677		epidermal growth factor receptor signaling pathway (GO:0007173)
2.577		cell separation after cytokinesis (GO:0000920)
2.486		regulation of centrosome duplication (GO:0010824)
-2.469		transcription-coupled nucleotide-excision repair (GO:0006283)
2.434		nucleus organization (GO:0006997)
2.386		regulation of mitotic spindle assembly (GO:1901673)
-2.319		histone H3-K4 methylation (GO:0051568)
2.178		protein targeting to mitochondrion (GO:0006626)
2.155		generation of precursor metabolites and energy (GO:0006091)
2.105		regulation of cell proliferation (GO:0042127)
-2.084		post-Golgi vesicle-mediated transport (GO:0006892)
1.970		ESCRT III complex disassembly (GO:1904903)
1.895		nucleobase-containing small molecule interconversion (GO:0015949)
-1.887		DNA repair (GO:0006281)
1.887		iron-sulfur cluster assembly (GO:0016226)

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

mitochondrial translational elongation (GO:0070125)



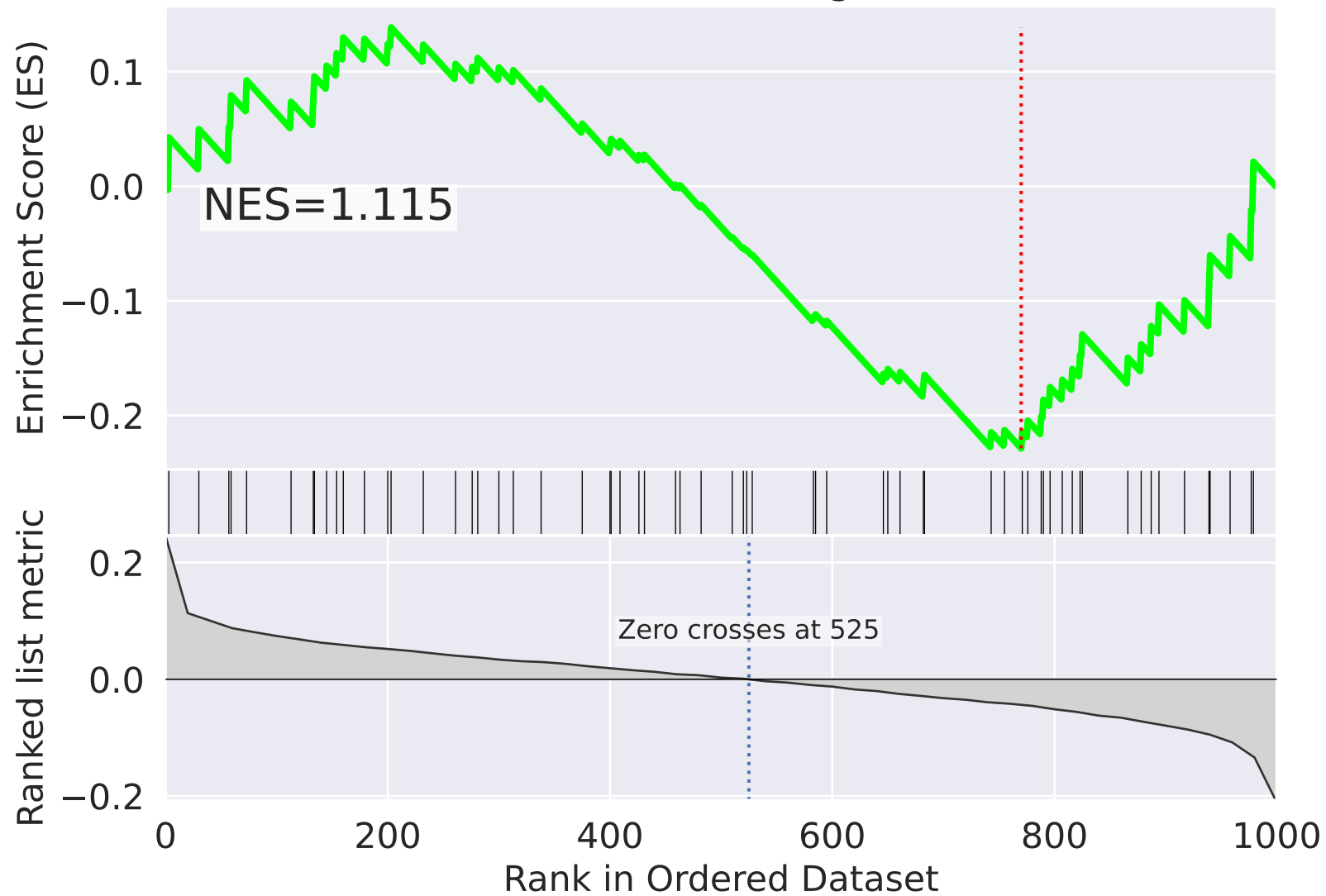
mitochondrial translational elongation (GO:0070125)



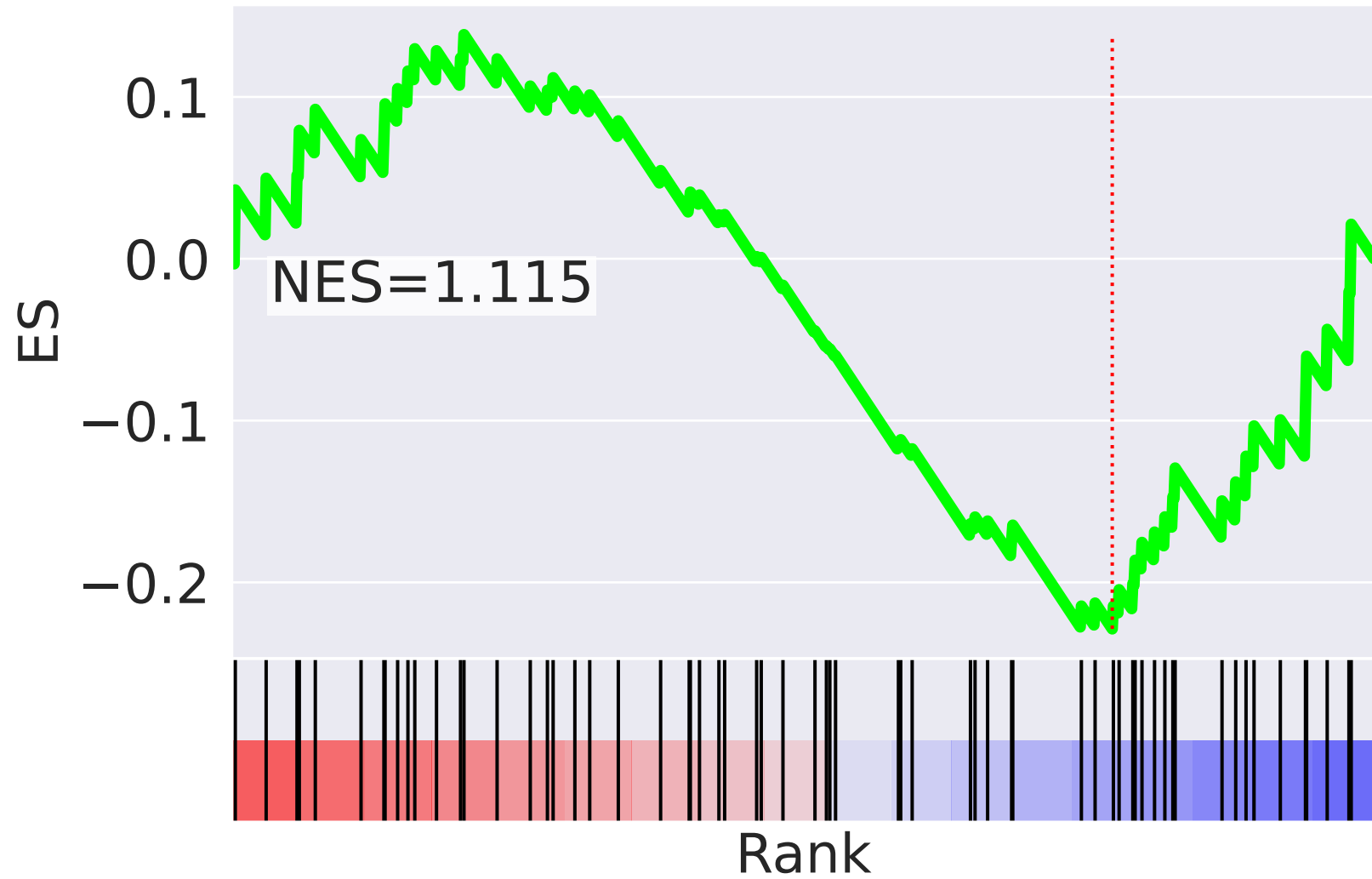
NES		SET
2.417		chromosome segregation (GO:0007059)
-2.395		transcription, DNA-templated (GO:0006351)
2.355		double-strand break repair via nonhomologous end joining (GO:0006303)
2.267		regulation of apoptotic process (GO:0042981)
2.065		termination of RNA polymerase II transcription (GO:0006369)
2.047		protein N-linked glycosylation (GO:0006487)
2.002		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
1.950		strand displacement (GO:0000732)
1.924		ciliary basal body docking (GO:0097711)
1.866		cellular response to DNA damage stimulus (GO:0006974)
-1.752		positive regulation of transcription, DNA-templated (GO:0045893)
-1.722		regulation of macroautophagy (GO:0016241)
-1.716		cellular protein localization (GO:0034613)
1.712		protein ubiquitination (GO:0016567)
1.657		DNA synthesis involved in DNA repair (GO:0000731)

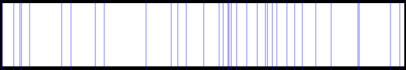
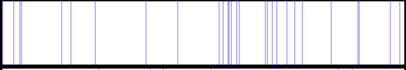


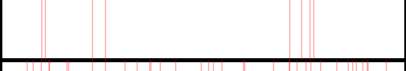
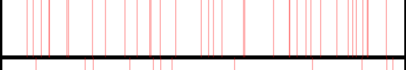




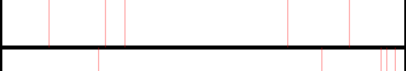

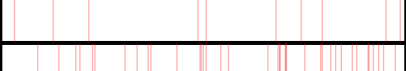
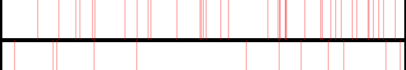
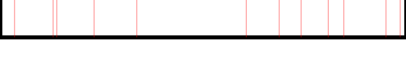
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=70$

mitochondrial translational elongation (GO:0070125)



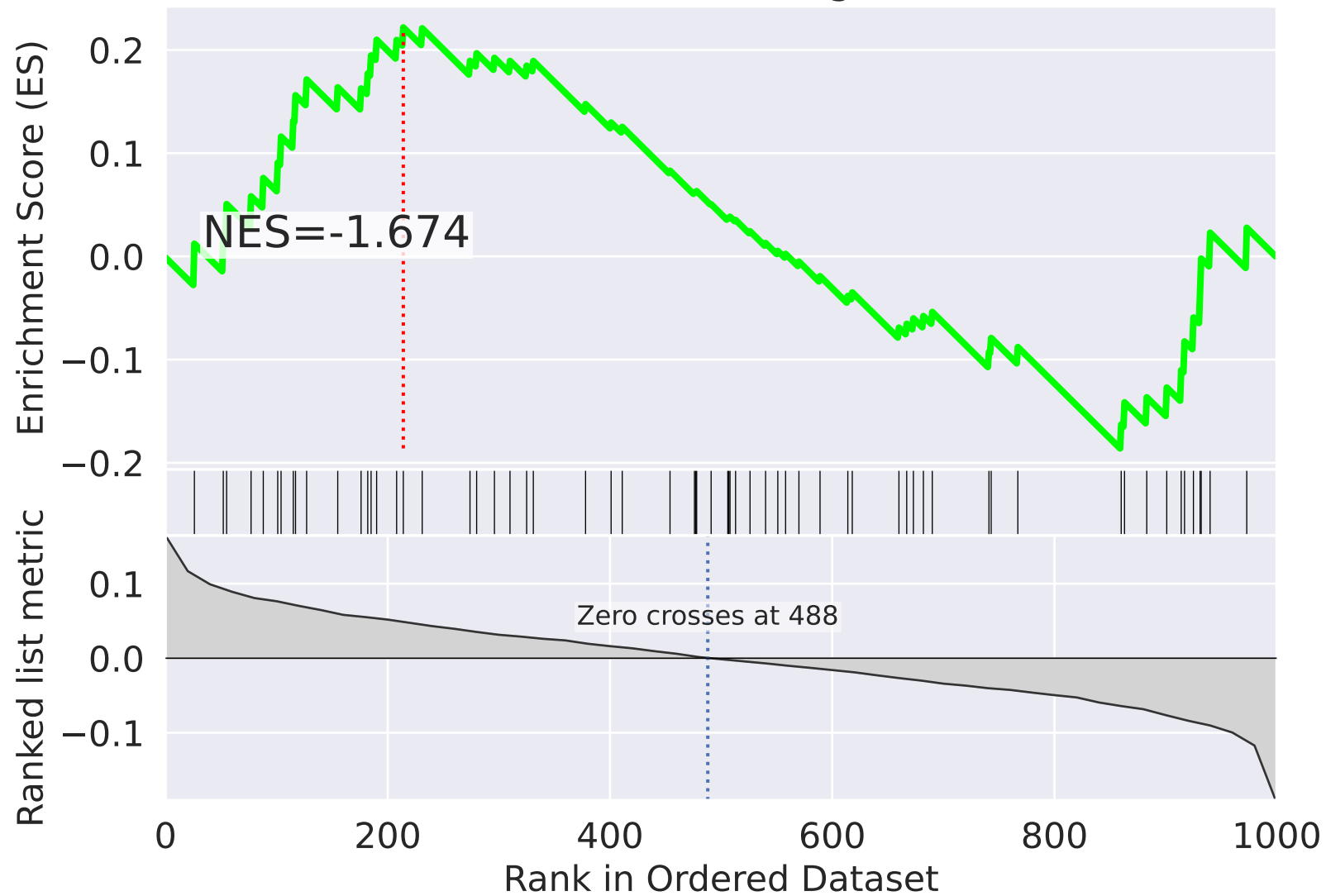
mitochondrial translational elongation (GO:0070125)



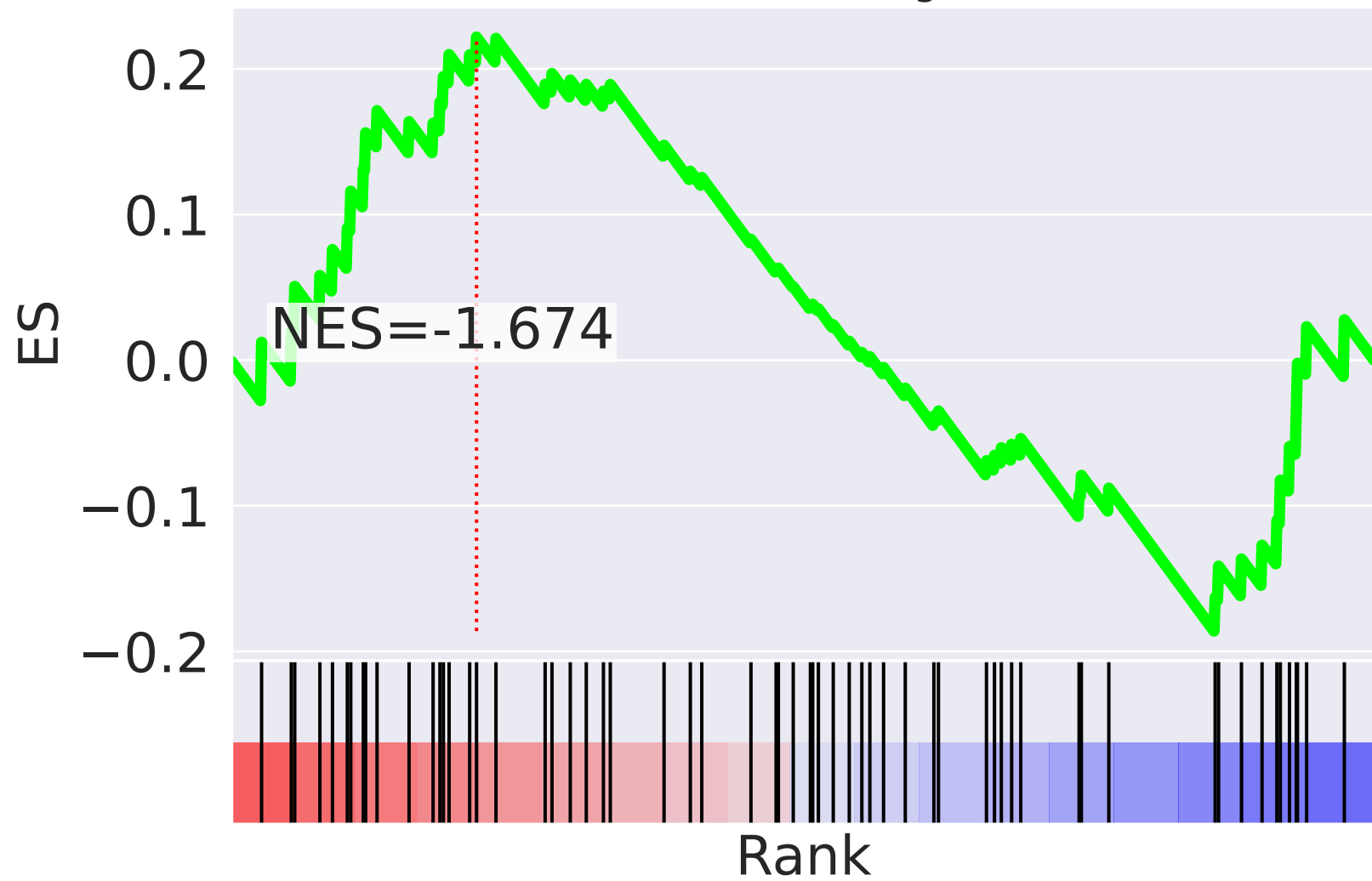
NES		SET
-3.265		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.519		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.429		histone H3-K4 methylation (GO:0051568)
-2.351		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.273		regulation of cell cycle (GO:0051726)
2.191		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.167		regulation of macroautophagy (GO:0016241)
2.085		cellular response to epidermal growth factor stimulus (GO:0071364)
2.078		platelet aggregation (GO:0070527)
2.067		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.043		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
1.960		transcription, DNA-templated (GO:0006351)
1.932		epidermal growth factor receptor signaling pathway (GO:0007173)
1.925		positive regulation of transcription, DNA-templated (GO:0045893)
1.909		leukocyte migration (GO:0050900)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=71$

mitochondrial translational elongation (GO:0070125)



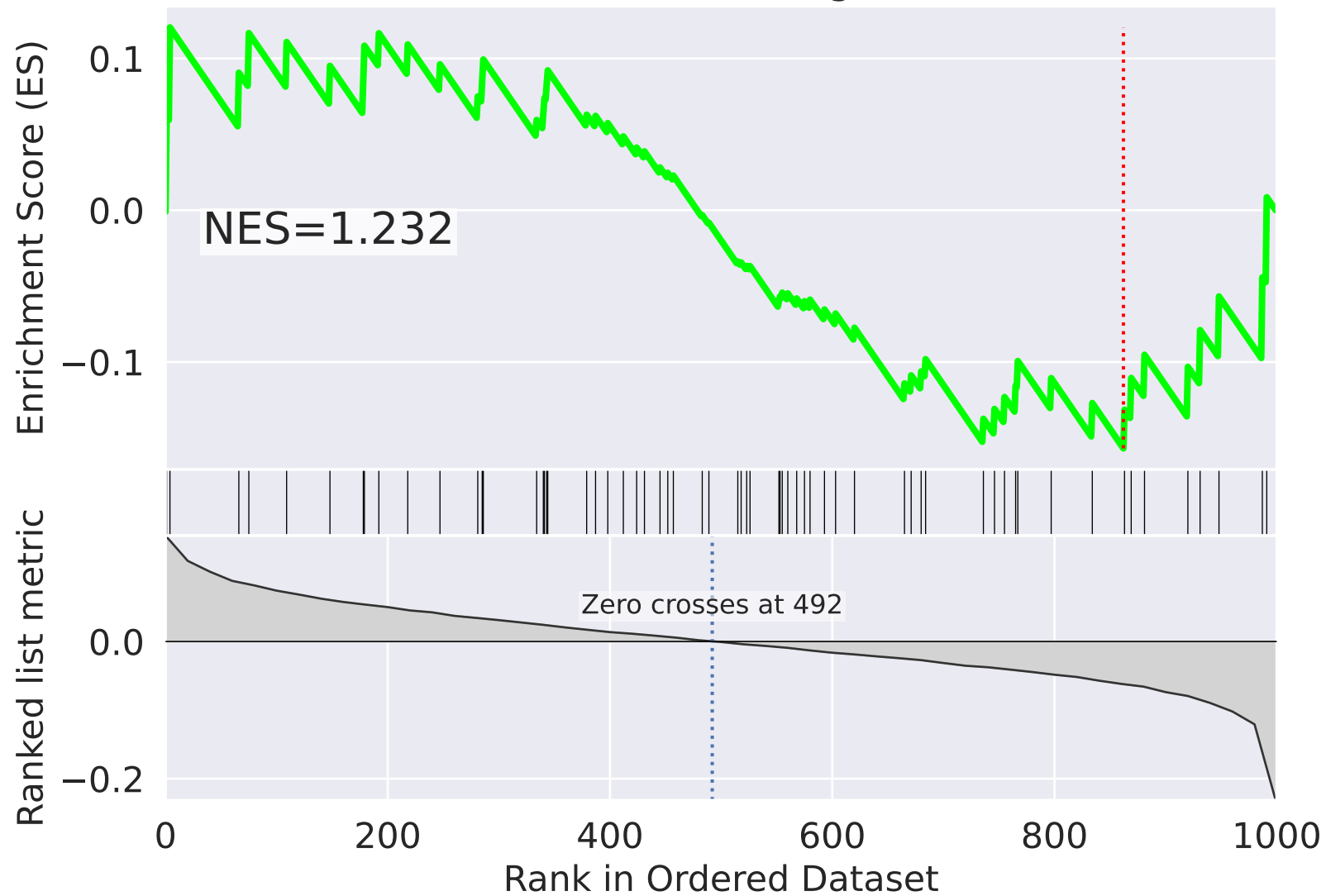
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.858		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.495		DNA replication (GO:0006260)
2.491		chromosome segregation (GO:0007059)
2.381		DNA damage checkpoint (GO:0000077)
2.313		DNA repair (GO:0006281)
2.304		DNA synthesis involved in DNA repair (GO:0000731)
-2.299		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.291		cellular response to DNA damage stimulus (GO:0006974)
2.261		negative regulation of translation (GO:0017148)
-2.260		ephrin receptor signaling pathway (GO:0048013)
-2.252		brain development (GO:0007420)
-2.225		regulation of lipid metabolic process (GO:0019216)
2.222		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-2.189		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
2.113		regulation of apoptotic process (GO:0042981)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=72$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.1

0.0

-0.1

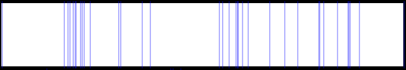




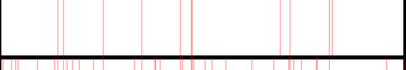
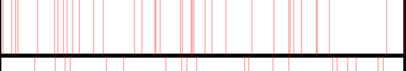
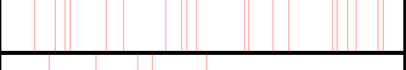
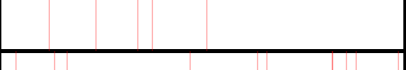

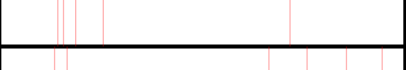
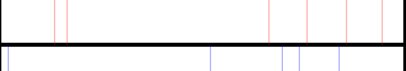

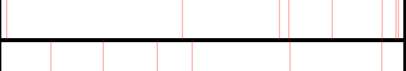
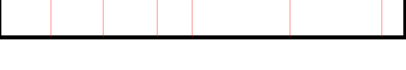
NES=1.232

Rank



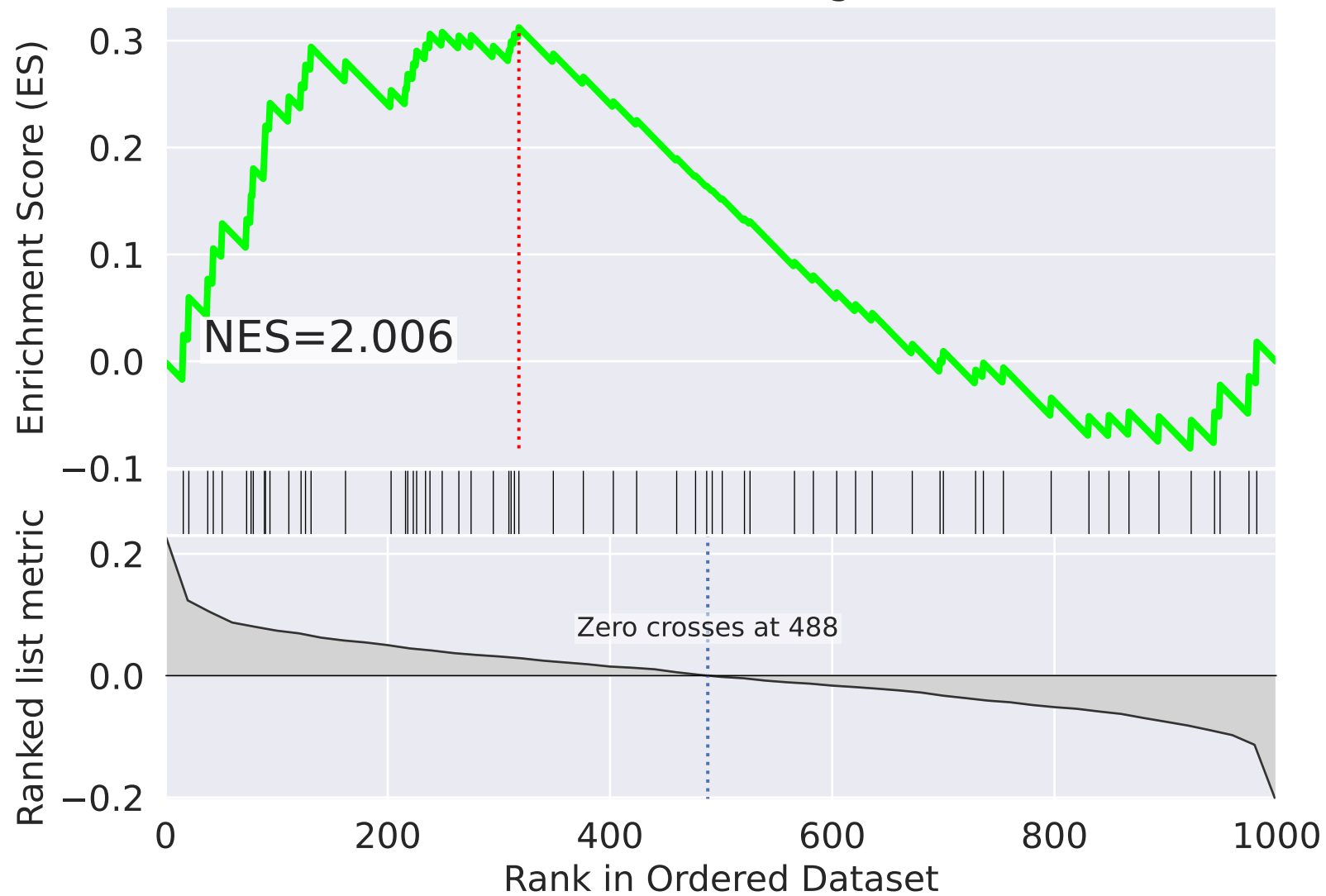
NES

SET

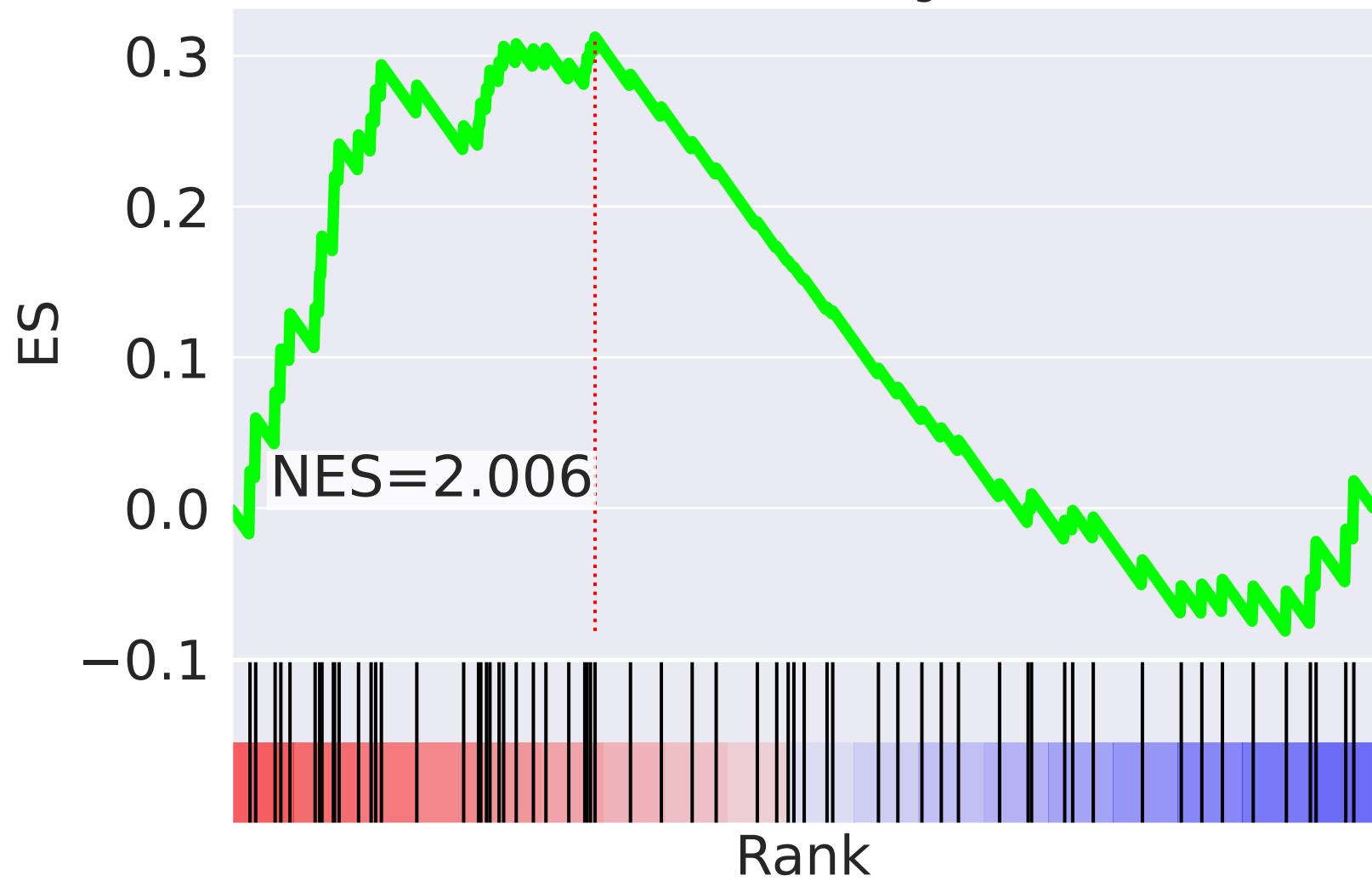
-2.760		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.721		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.638		cell migration (GO:0016477)
2.489		negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.387		cell surface receptor signaling pathway (GO:0007166)
2.332		chromatin remodeling (GO:0006338)
2.287		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.233		cellular response to DNA damage stimulus (GO:0006974)
2.226		transcription from mitochondrial promoter (GO:0006390)
2.174		positive regulation of protein phosphorylation (GO:0001934)
2.156		nucleosome disassembly (GO:0006337)
2.143		ERBB2 signaling pathway (GO:0038128)
-2.136		post-Golgi vesicle-mediated transport (GO:0006892)
2.087		regulation of cell proliferation (GO:0042127)
2.033		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 $z=73$

mitochondrial translational elongation (GO:0070125)


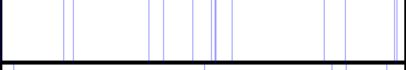


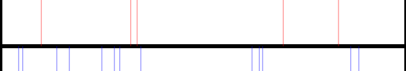


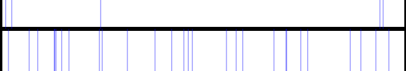




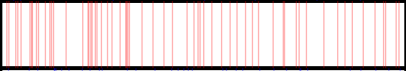
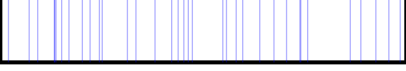



mitochondrial translational elongation (GO:0070125)



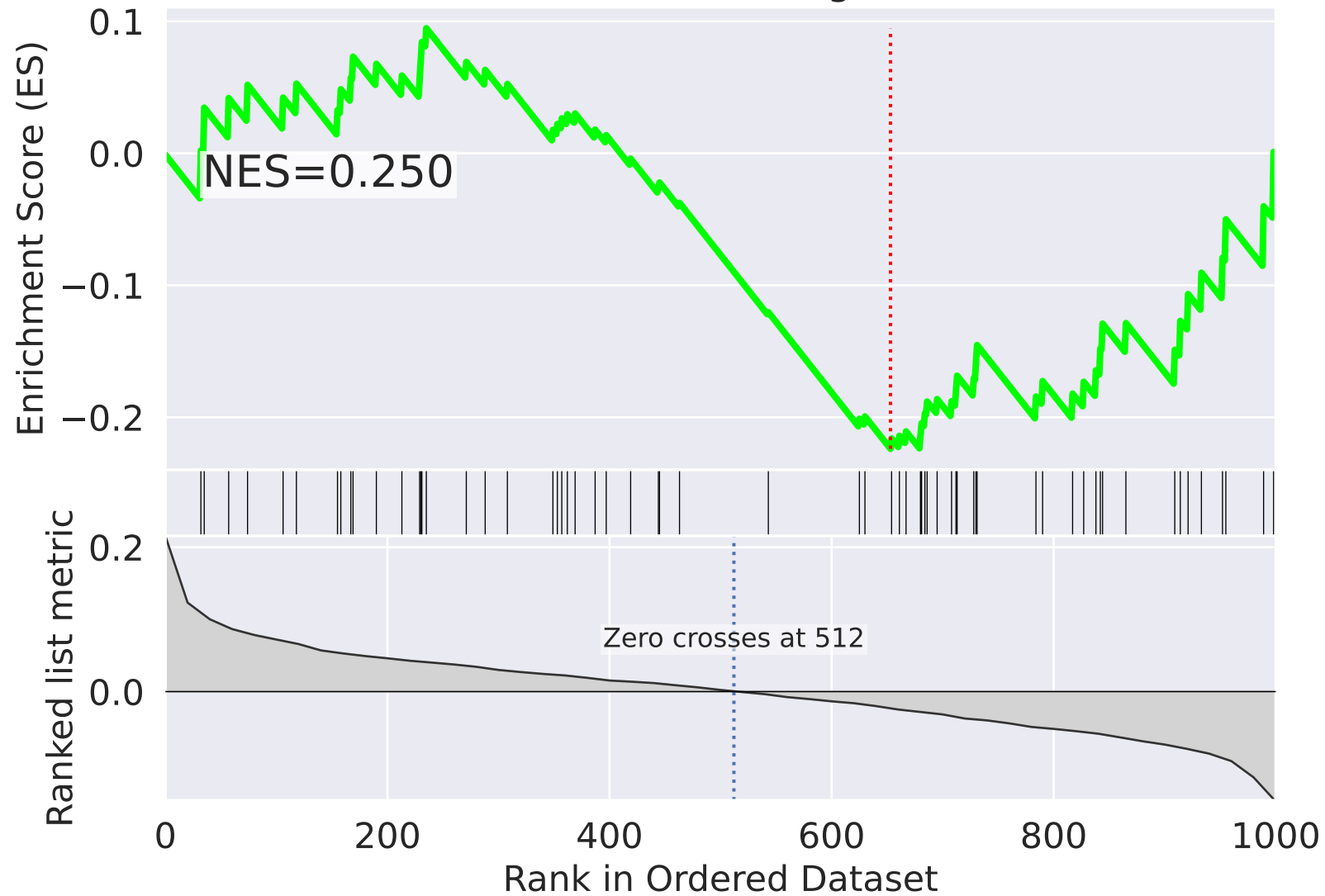
NES

SET

-3.041		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-2.651		DNA repair (GO:0006281)
-2.635		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.569		intracellular transport of virus (GO:0075733)
2.478		transcription from mitochondrial promoter (GO:0006390)
-2.438		macroautophagy (GO:0016236)
-2.415		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.349		endoplasmic reticulum organization (GO:0007029)
-2.349		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.328		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.297		telomere maintenance via recombination (GO:0000722)
-2.221		T cell costimulation (GO:0031295)
-2.152		protein N-linked glycosylation via asparagine (GO:0018279)
2.097		mitochondrial translational termination (GO:0070126)
-2.037		mitochondrial respiratory chain complex I assembly (GO:0032981)








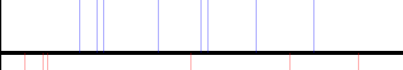

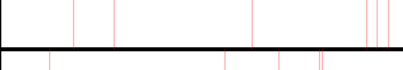
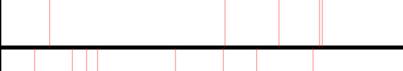
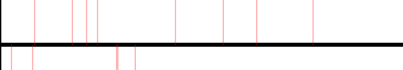

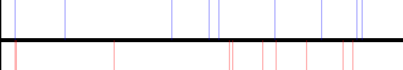

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=74$

mitochondrial translational elongation (GO:0070125)



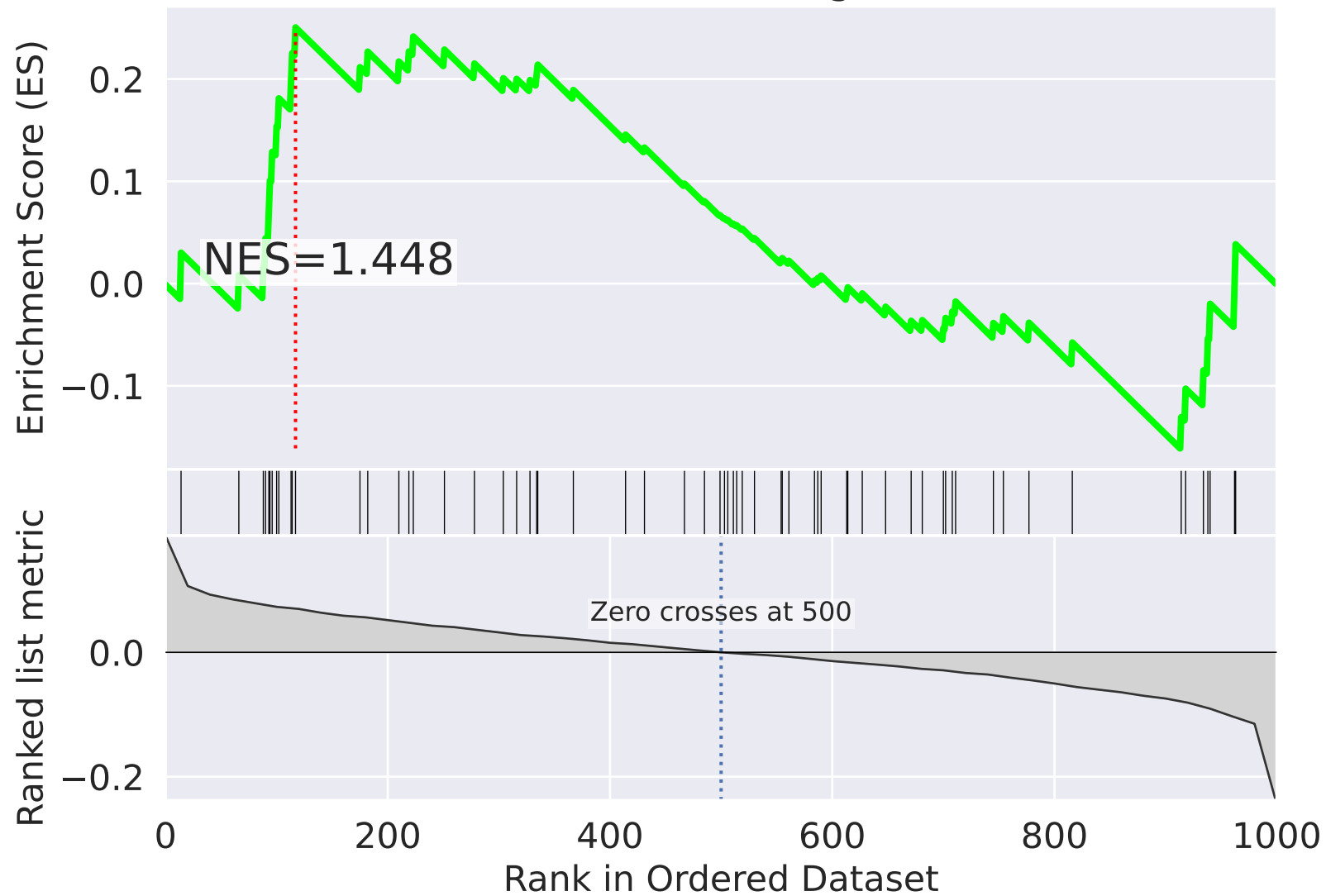
mitochondrial translational elongation (GO:0070125)



NES		SET
2.805		chromosome segregation (GO:0007059)
-2.478		Golgi organization (GO:0007030)
2.252		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.137		telomere maintenance via recombination (GO:0000722)
2.088		apoptotic process (GO:0006915)
-2.073		ER to Golgi vesicle-mediated transport (GO:0006888)
1.956		intracellular transport of virus (GO:0075733)
-1.920		protein homooligomerization (GO:0051260)
1.904		protein K48-linked ubiquitination (GO:0070936)
1.895		phosphatidylinositol biosynthetic process (GO:0006661)
1.863		positive regulation of protein ubiquitination (GO:0031398)
1.862		transcription elongation from RNA polymerase II promoter (GO:0006368)
1.856		mitotic nuclear envelope disassembly (GO:0007077)
-1.811		peptidyl-serine phosphorylation (GO:0018105)
1.755		vascular endothelial growth factor receptor signaling pathway (GO:0048010)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=75$

mitochondrial translational elongation (GO:0070125)



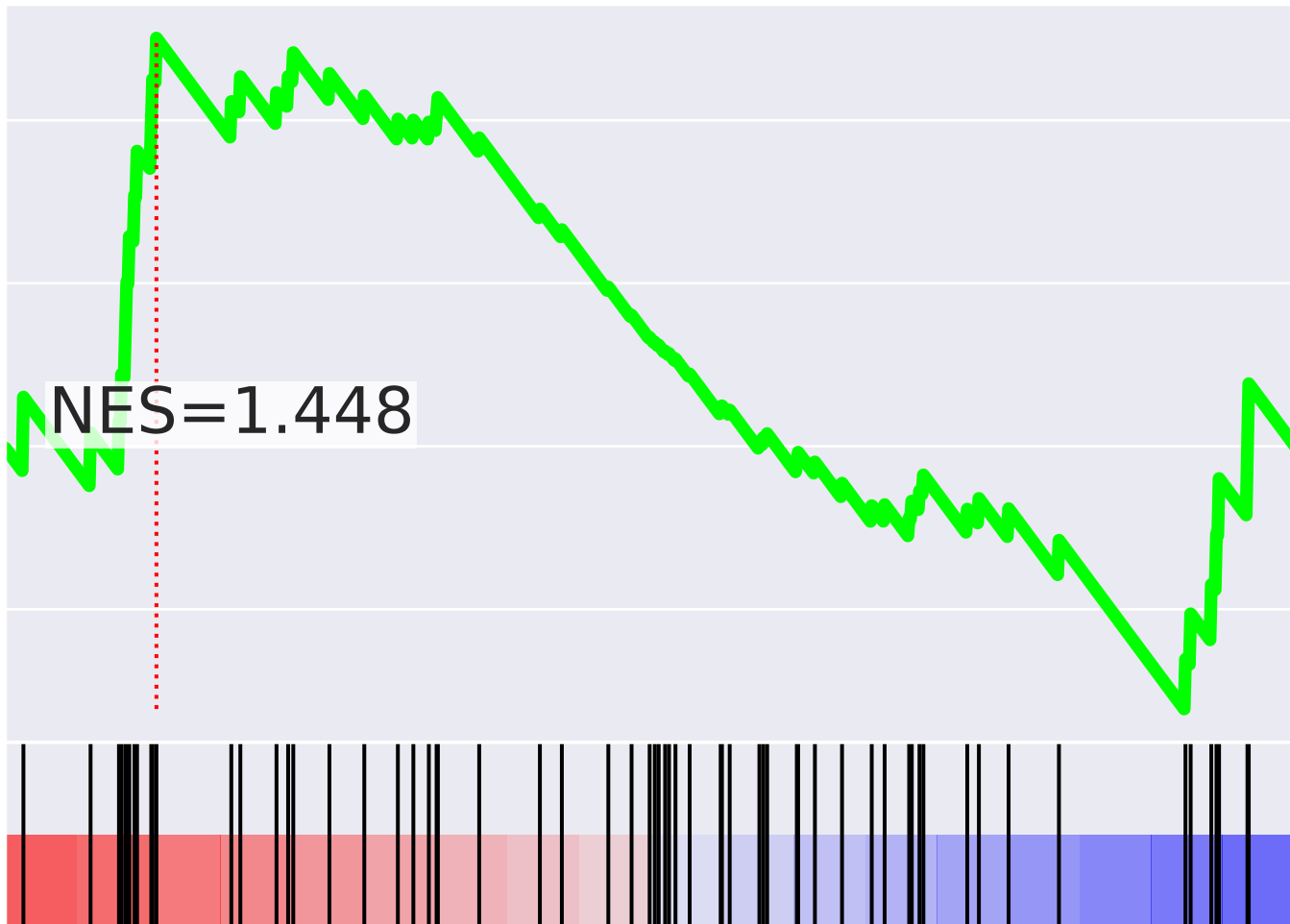
mitochondrial translational elongation (GO:0070125)

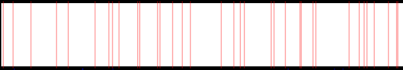



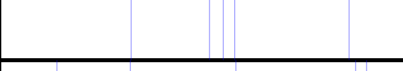


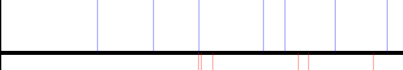
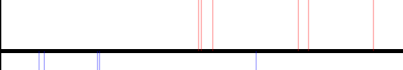
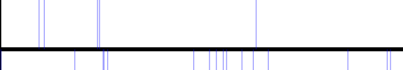
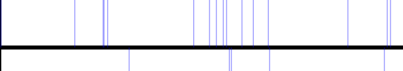
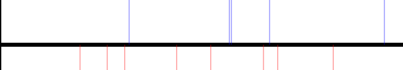
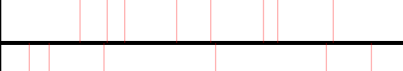
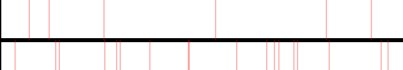

ES

0.2
0.1
0.0
-0.1

NES=1.448

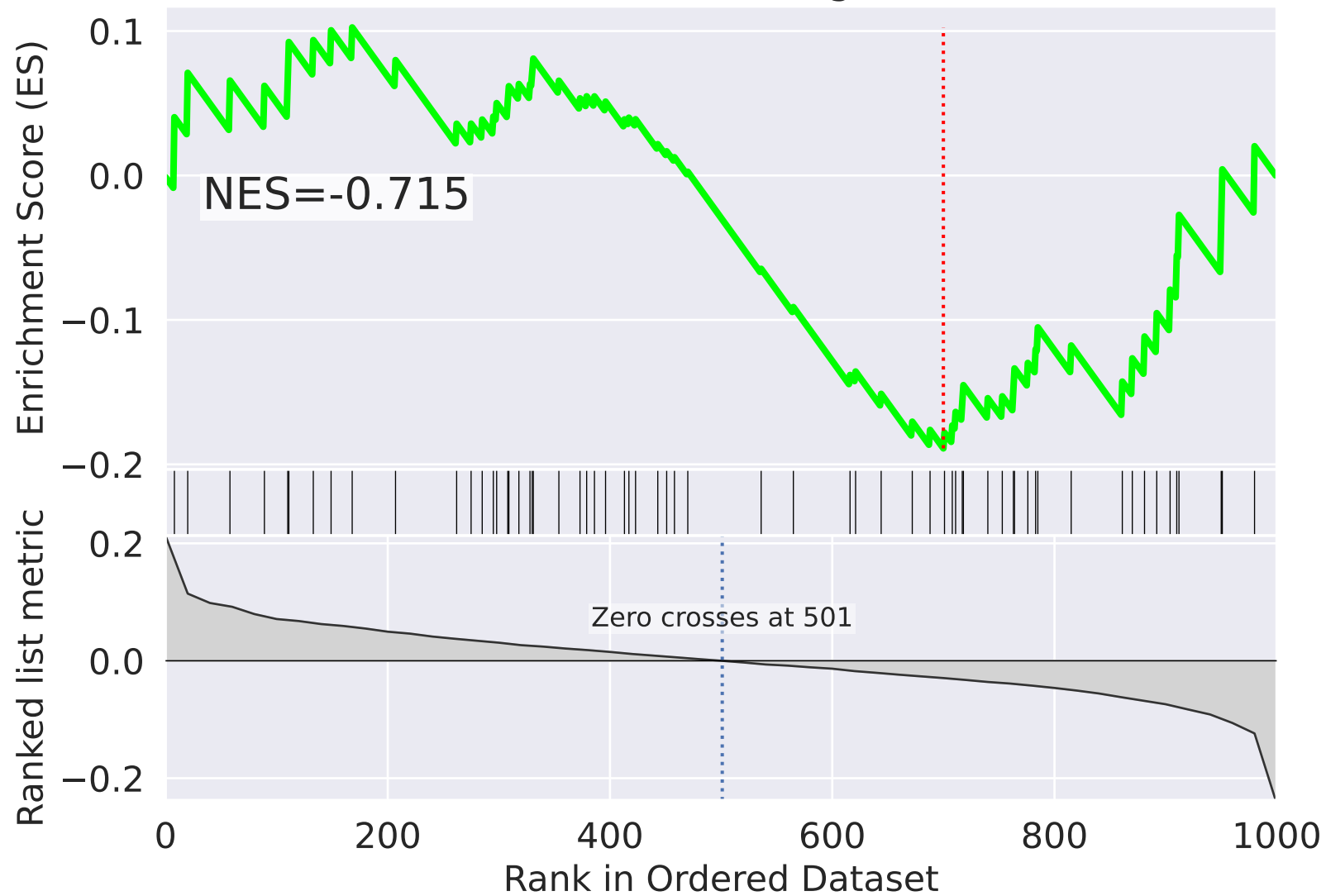
Rank



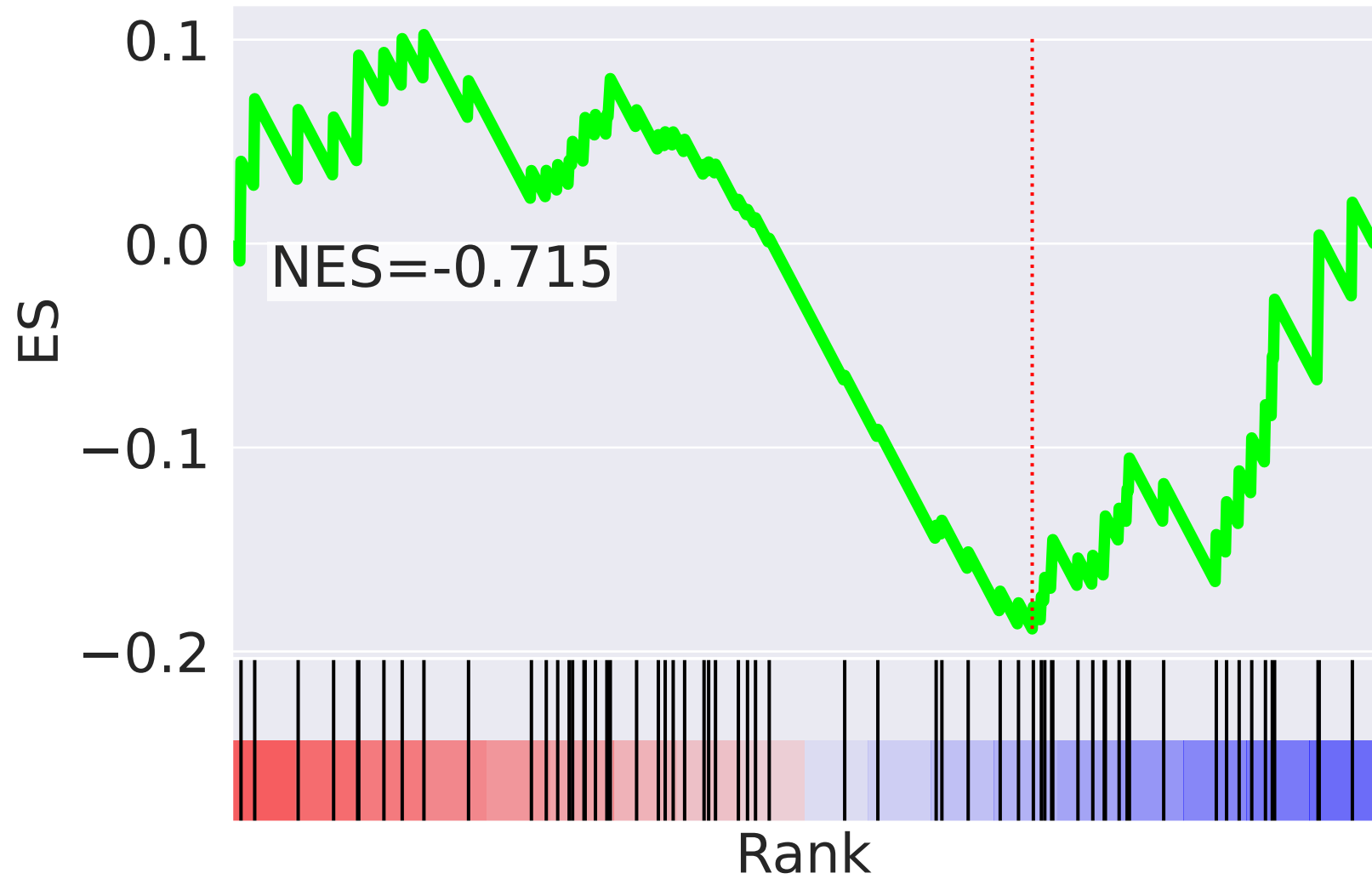
NES		SET
2.661		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.656		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.601		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.392		ATP-dependent chromatin remodeling (GO:0043044)
-2.385		positive regulation of protein catabolic process (GO:0045732)
-2.356		ubiquitin-dependent ERAD pathway (GO:0030433)
2.271		sister chromatid cohesion (GO:0007062)
-2.268		cell differentiation (GO:0030154)
2.202		protein K11-linked ubiquitination (GO:0070979)
-2.195		nucleosome disassembly (GO:0006337)
-2.176		cell cycle arrest (GO:0007050)
-2.166		regulation of cell migration (GO:0030334)
2.057		axon guidance (GO:0007411)
1.997		protein targeting to mitochondrion (GO:0006626)
1.987		G2/M transition of mitotic cell cycle (GO:0000086)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=76$

mitochondrial translational elongation (GO:0070125)





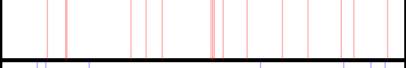

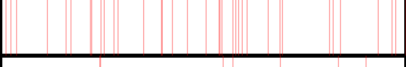
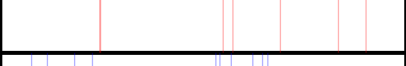
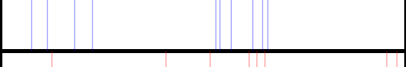

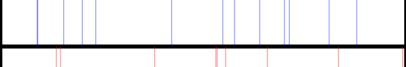
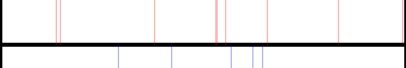
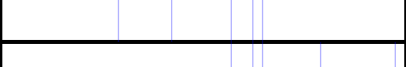
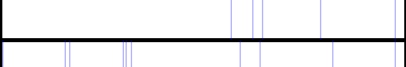
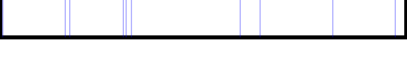


mitochondrial translational elongation (GO:0070125)



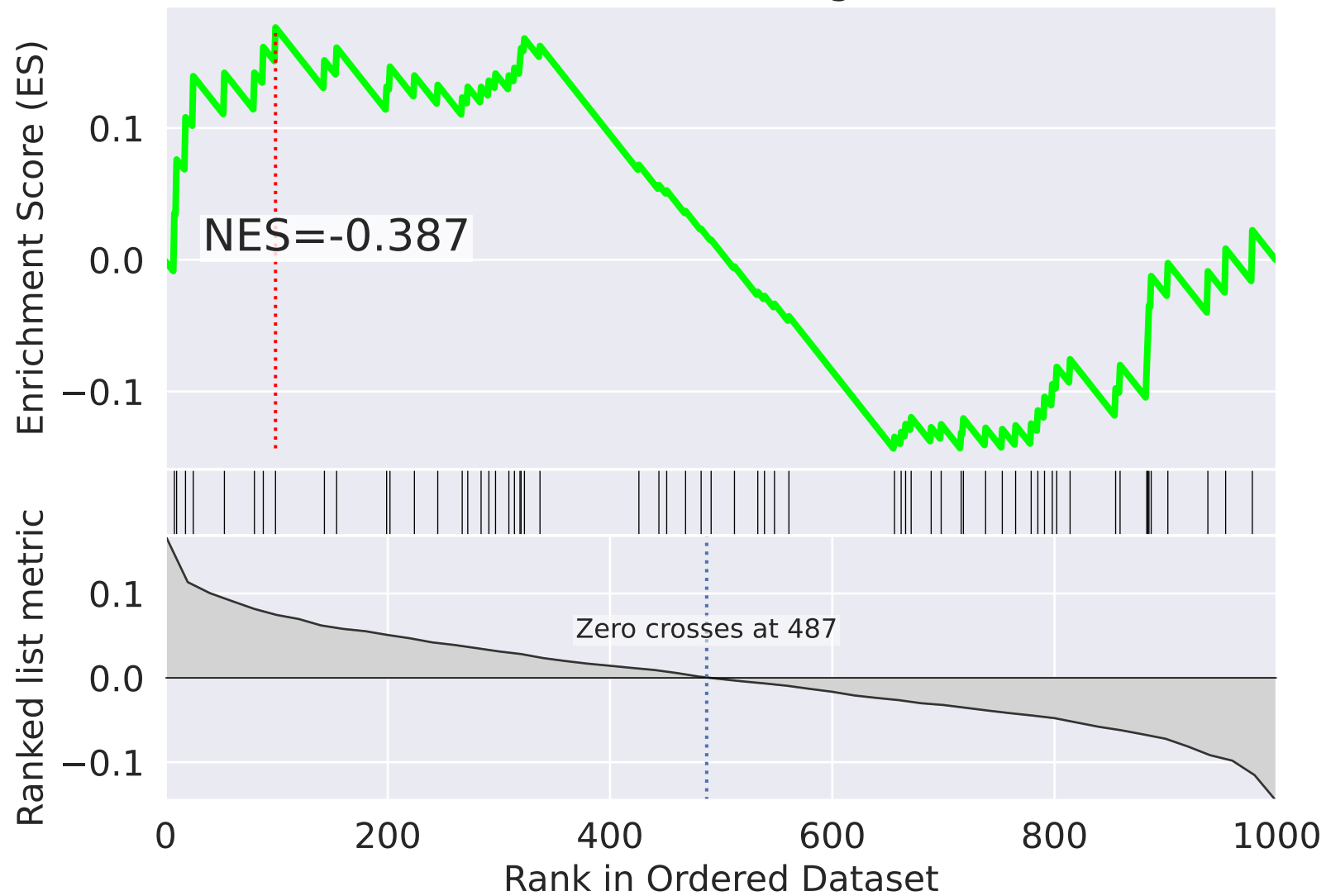
NES

SET

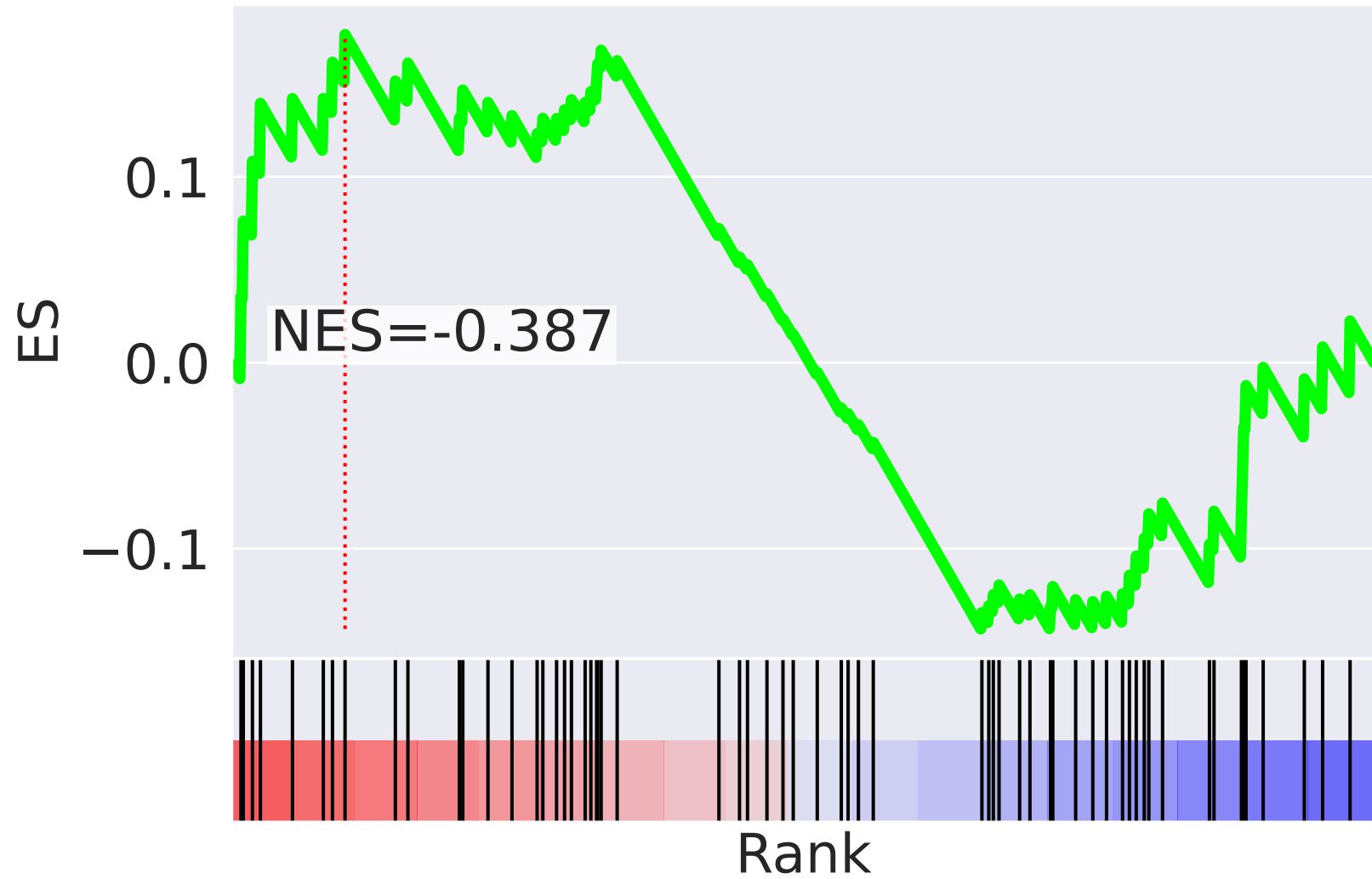
-2.464		heart development (GO:0007507)
-2.403		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.313		brain development (GO:0007420)
2.276		negative regulation of apoptotic process (GO:0043066)
2.259		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.169		cytokinesis (GO:0000910)
2.161		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.124		multicellular organism development (GO:0007275)
-2.103		regulation of cellular response to heat (GO:1900034)
2.095		positive regulation of cell migration (GO:0030335)
-2.079		macroautophagy (GO:0016236)
1.973		regulation of mRNA stability (GO:0043488)
-1.960		intracellular transport of virus (GO:0075733)
-1.945		mitotic nuclear envelope disassembly (GO:0007077)
-1.933		protein dephosphorylation (GO:0006470)

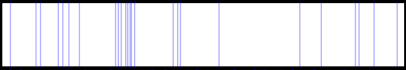

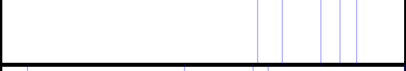


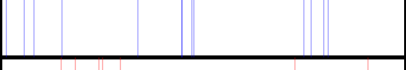
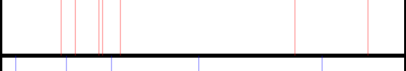



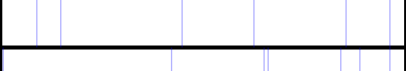

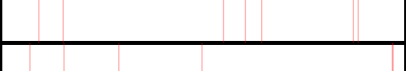


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=77$

mitochondrial translational elongation (GO:0070125)



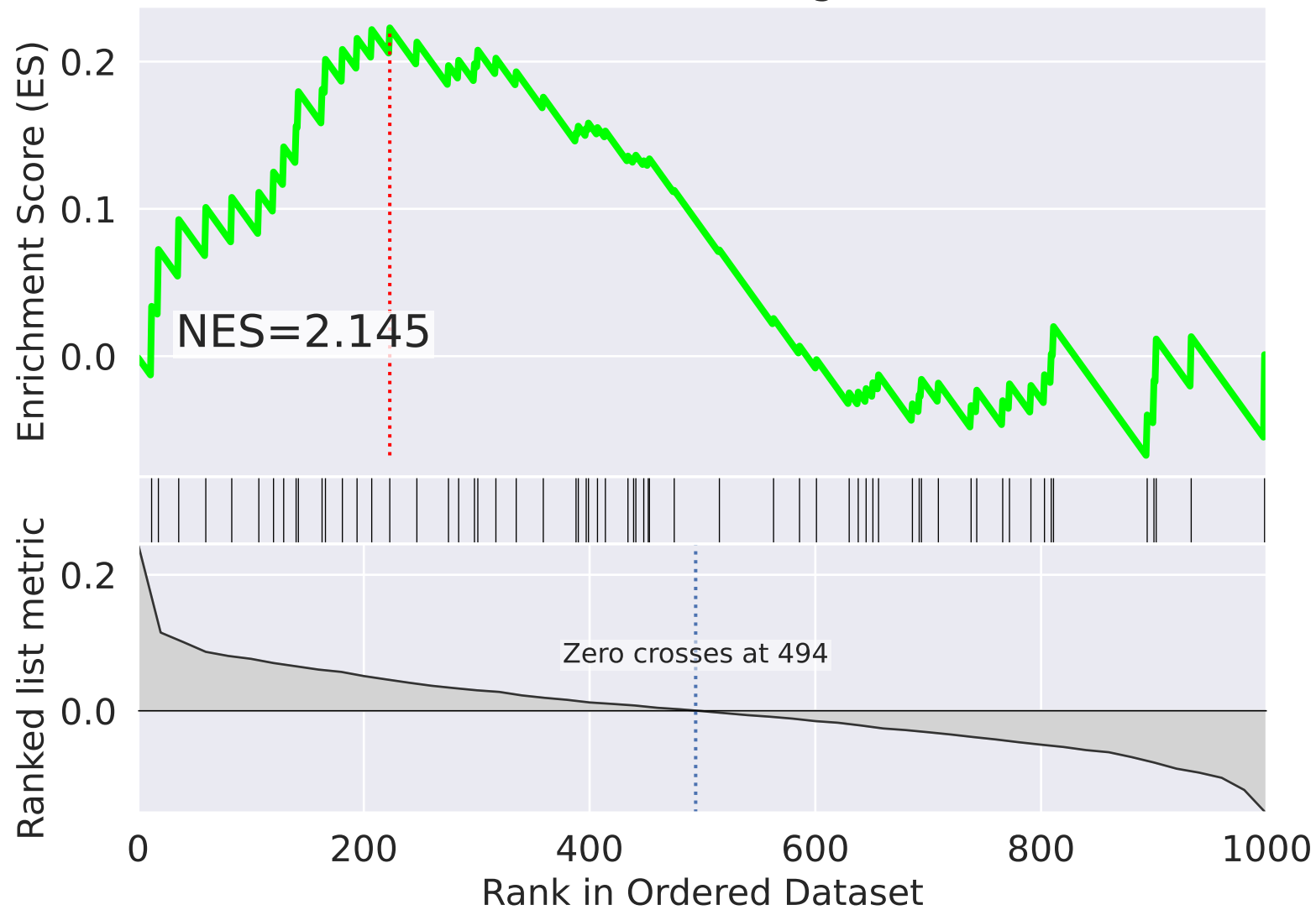
mitochondrial translational elongation (GO:0070125)



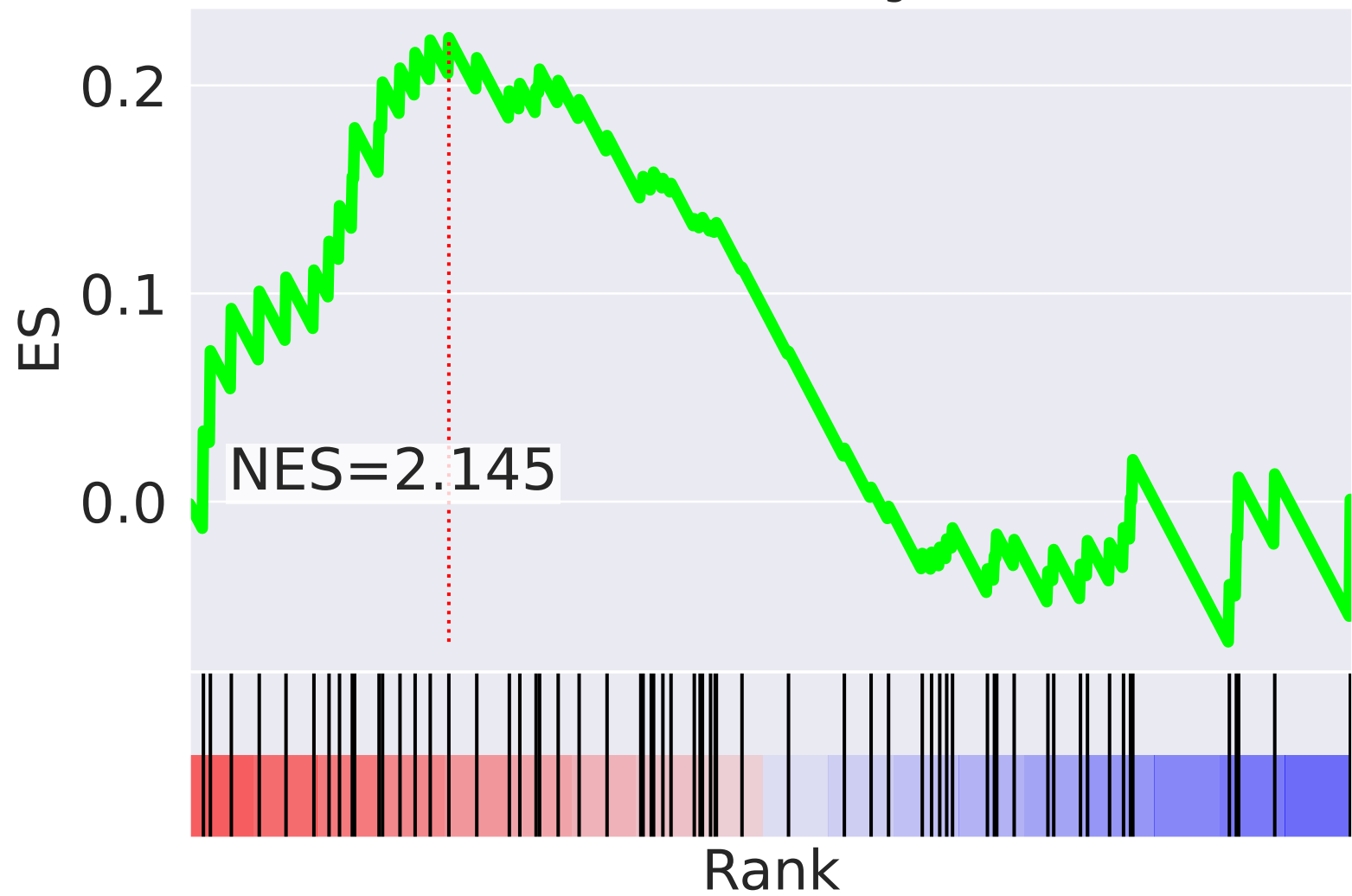
NES		SET
-2.524		mitochondrial translation (GO:0032543)
-2.273		protein phosphorylation (GO:0006468)
-2.218		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
-2.069		DNA damage checkpoint (GO:0000077)
-2.040		double-strand break repair via homologous recombination (GO:0000724)
-2.010		protein stabilization (GO:0050821)
2.002		microtubule-based movement (GO:0007018)
-1.945		release of cytochrome c from mitochondria (GO:0001836)
-1.936		small molecule metabolic process (GO:0044281)
-1.935		regulation of centrosome duplication (GO:0010824)
-1.901		histone H4 acetylation (GO:0043967)
-1.881		double-strand break repair (GO:0006302)
1.868		movement of cell or subcellular component (GO:0006928)
1.794		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-1.785		regulation of alternative mRNA splicing, via spliceosome (GO:0000381)






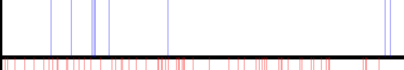
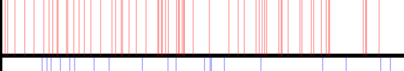
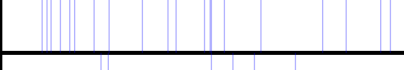
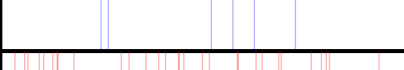
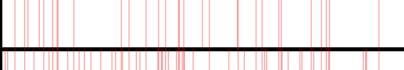
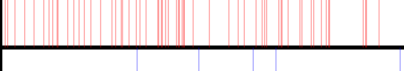


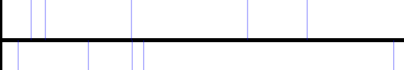
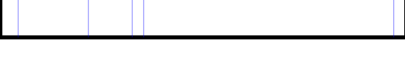
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=78$

mitochondrial translational elongation (GO:0070125)



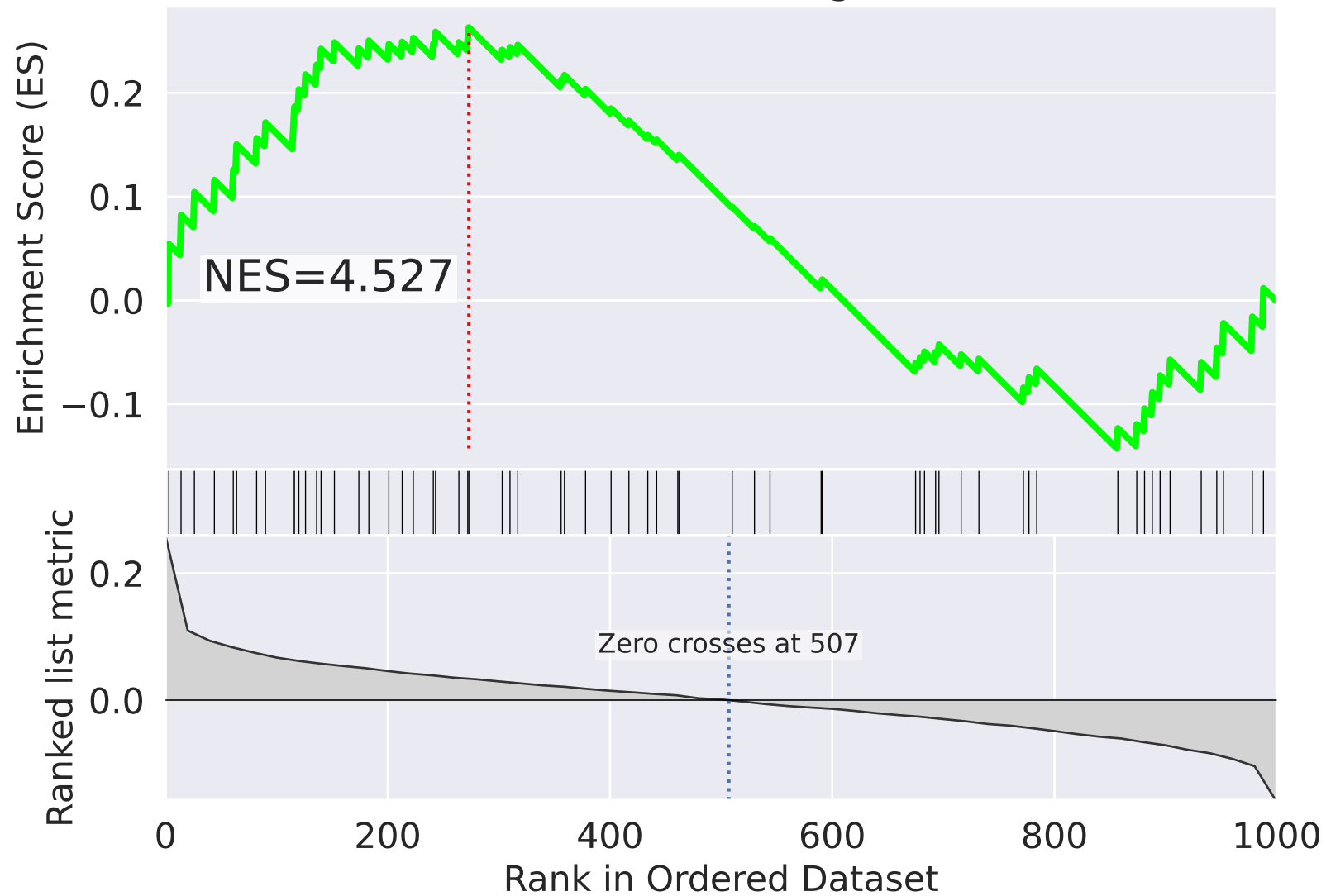
mitochondrial translational elongation (GO:0070125)



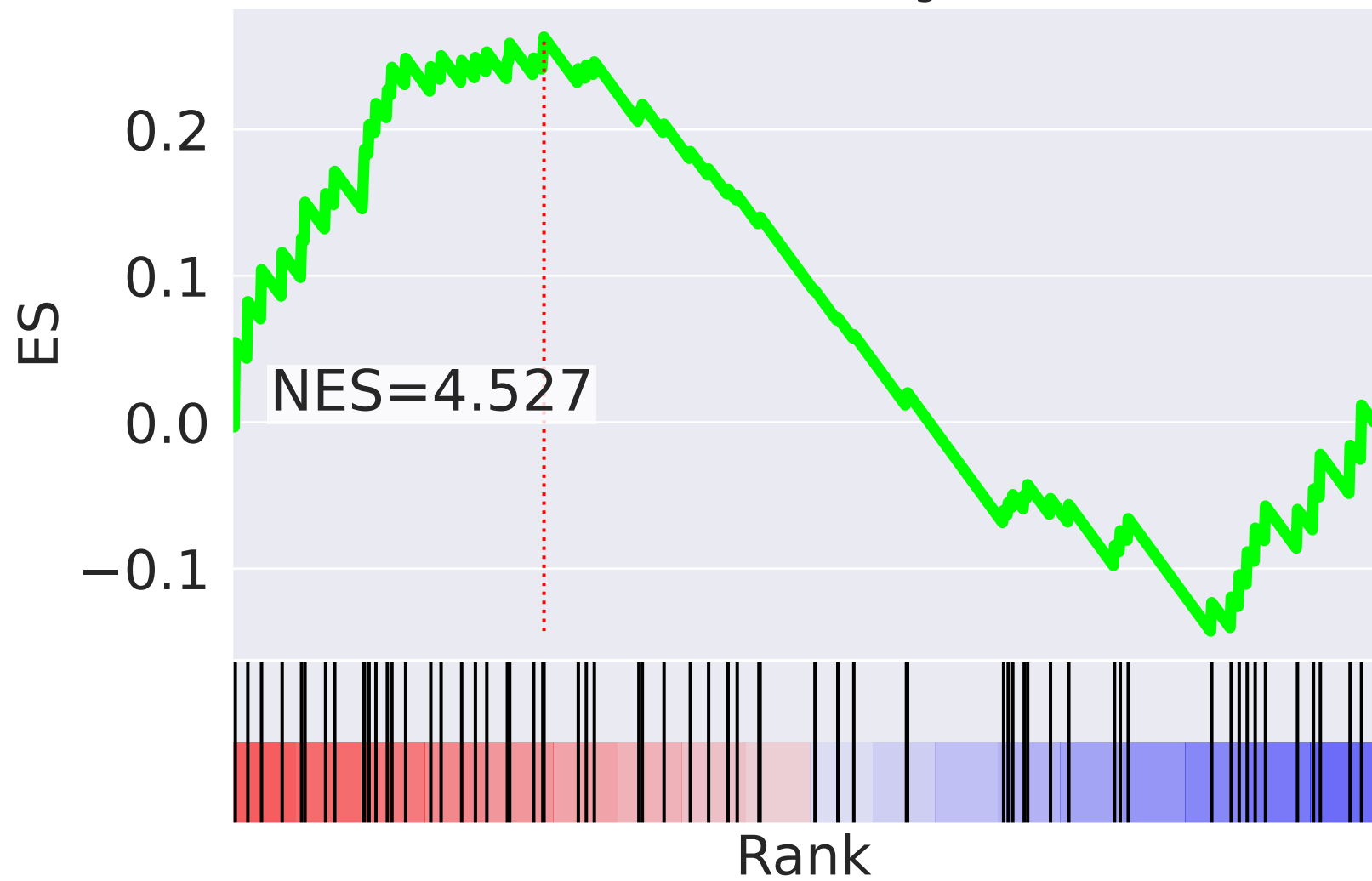
NES		SET
2.841		mitochondrial translation (GO:0032543)
-2.799		peptidyl-serine phosphorylation (GO:0018105)
-2.461		protein N-linked glycosylation (GO:0006487)
-2.460		T cell costimulation (GO:0031295)
-2.203		rRNA processing (GO:0006364)
-2.171		double-strand break repair via nonhomologous end joining (GO:0006303)
2.145		mitochondrial translational elongation (GO:0070125)
-2.141		cellular response to DNA damage stimulus (GO:0006974)
-2.129		regulation of centrosome duplication (GO:0010824)
2.054		translation (GO:0006412)
2.038		mitochondrial translational termination (GO:0070126)
-1.985		platelet degranulation (GO:0002576)
-1.932		mRNA splicing, via spliceosome (GO:0000398)
-1.907		ubiquitin-dependent ERAD pathway (GO:0030433)
-1.906		carbohydrate metabolic process (GO:0005975)

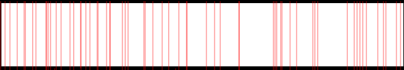
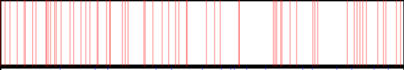

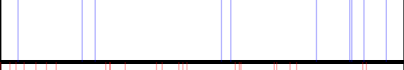
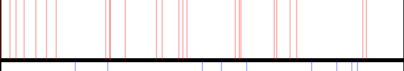

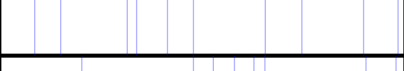
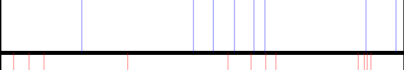



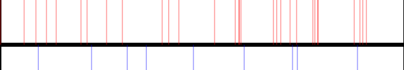

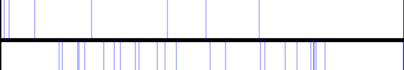

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=79$

mitochondrial translational elongation (GO:0070125)



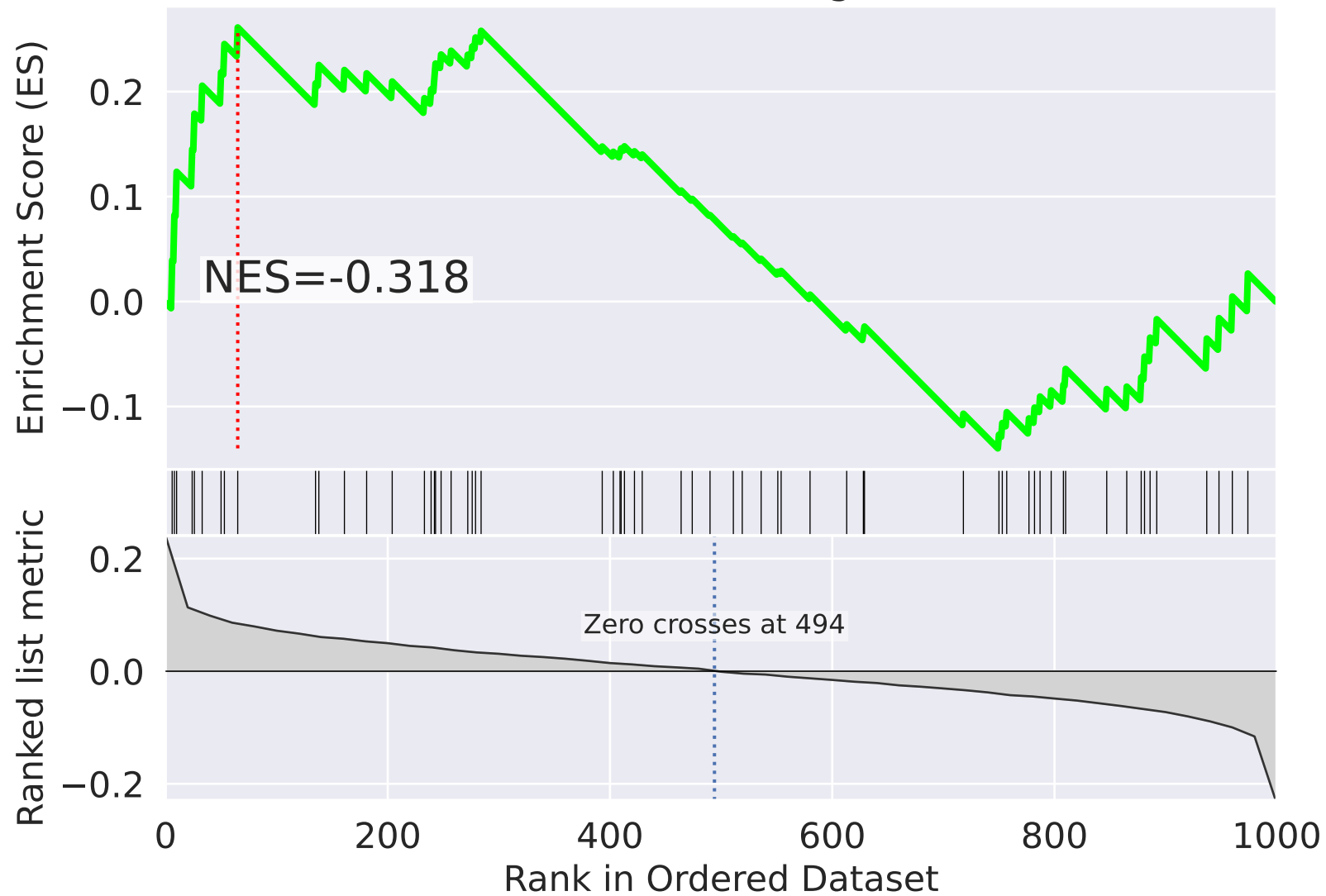
mitochondrial translational elongation (GO:0070125)



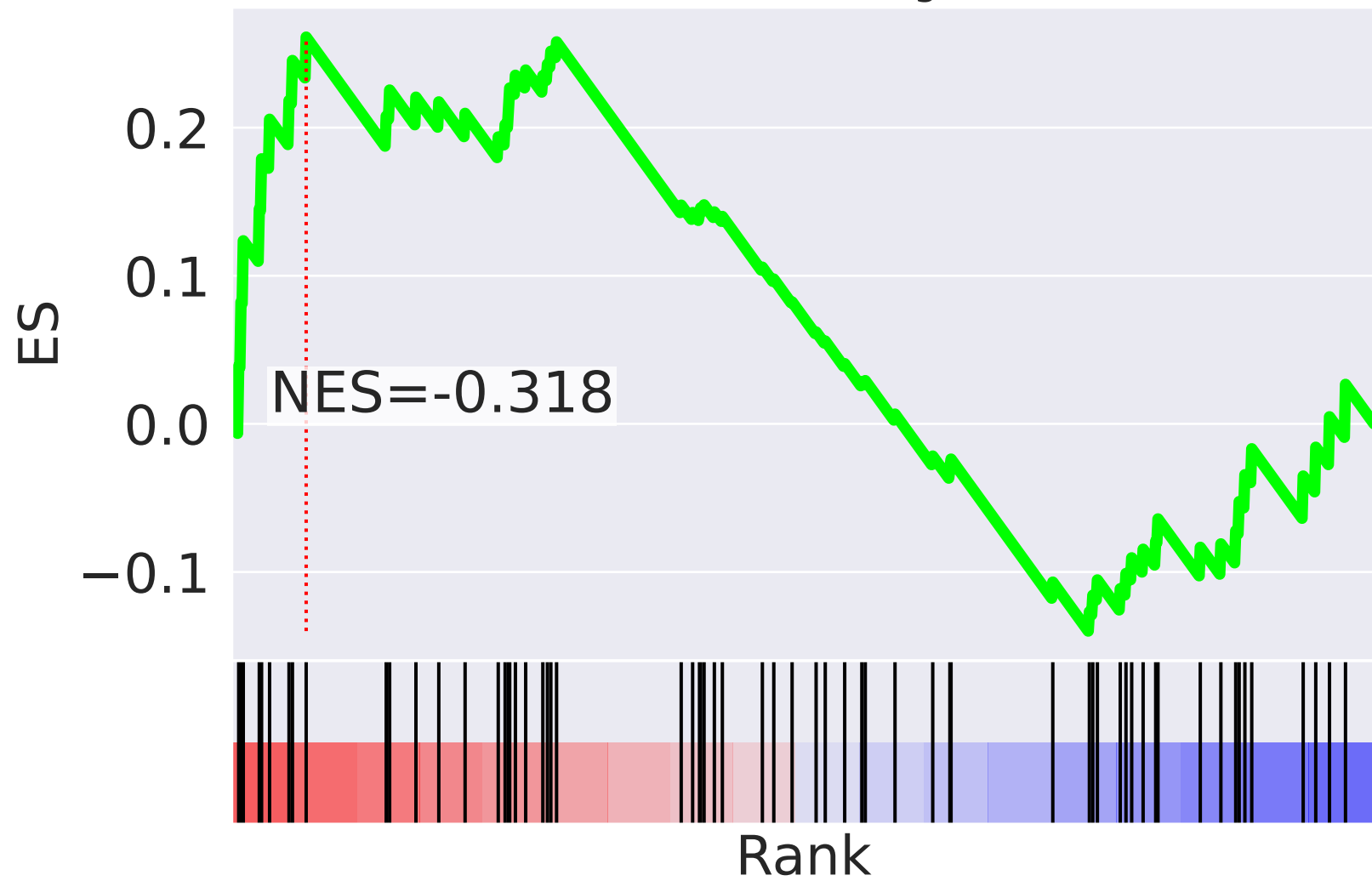
NES		SET
4.625		mitochondrial translational termination (GO:0070126)
4.527		mitochondrial translational elongation (GO:0070125)
-2.842		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.791		intracellular protein transport (GO:0006886)
2.789		mitochondrial translation (GO:0032543)
-2.738		Golgi organization (GO:0007030)
-2.674		protein autophosphorylation (GO:0046777)
-2.617		nervous system development (GO:0007399)
2.457		mitotic metaphase plate congression (GO:0007080)
-2.370		cell surface receptor signaling pathway (GO:0007166)
2.205		release of cytochrome c from mitochondria (GO:0001836)
2.166		translation (GO:0006412)
-2.139		peptidyl-serine phosphorylation (GO:0018105)
-2.132		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-2.120		protein deubiquitination (GO:0016579)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=80$

mitochondrial translational elongation (GO:0070125)



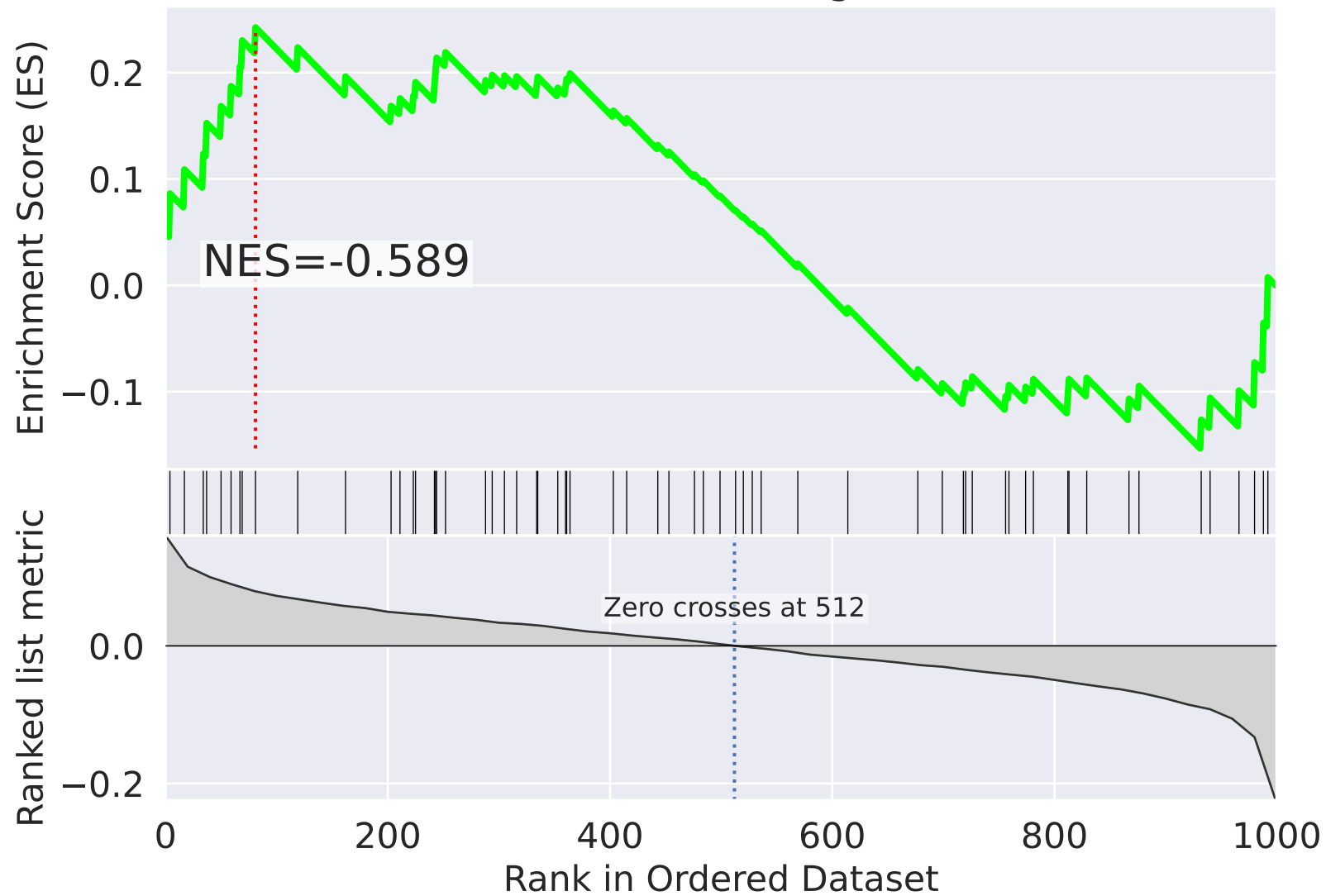
mitochondrial translational elongation (GO:0070125)



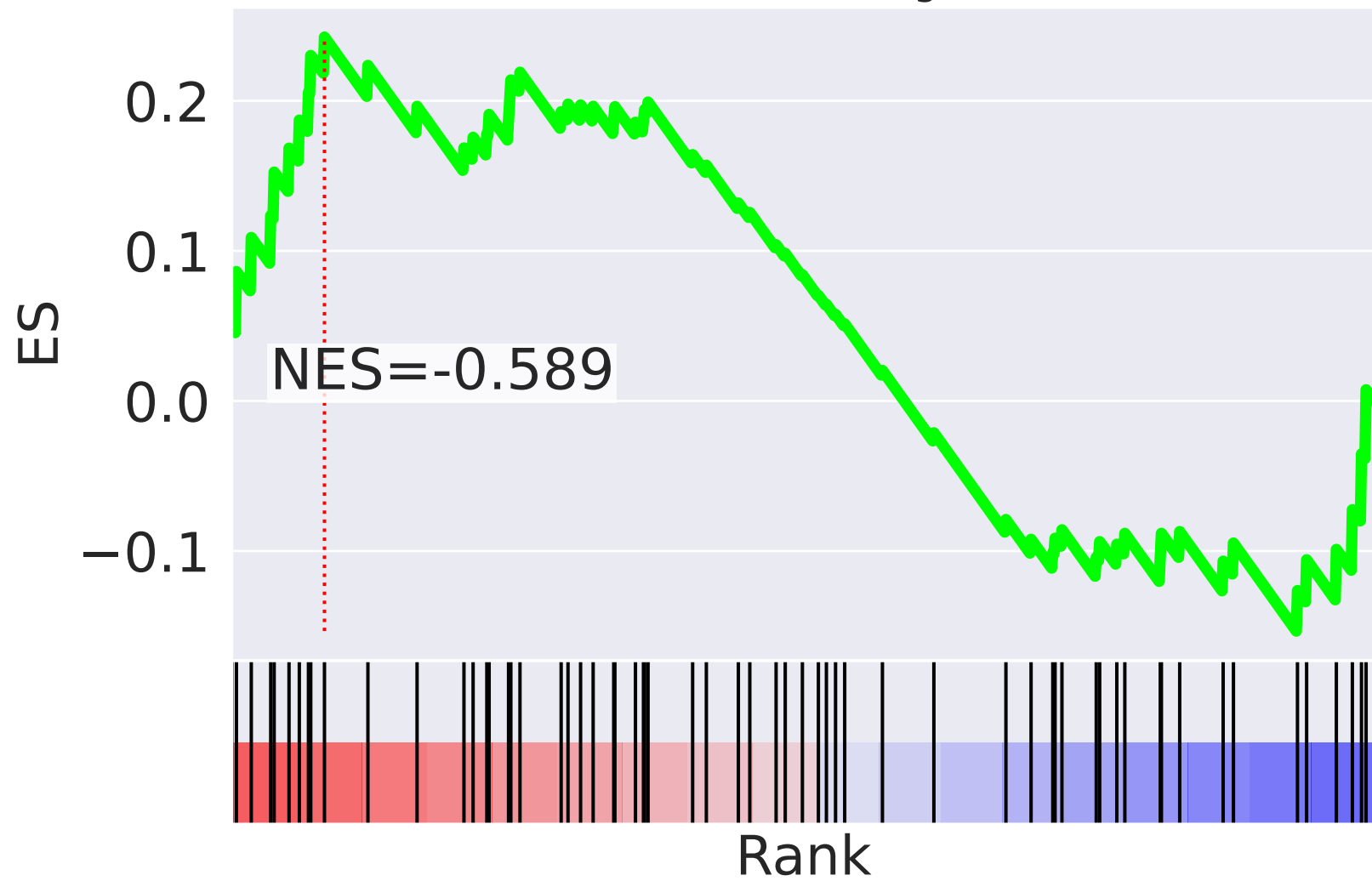
NES		SET
-2.446		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
2.322		nucleosome disassembly (GO:0006337)
2.229		intracellular transport of virus (GO:0075733)
-2.020		inflammatory response (GO:0006954)
-1.968		protein N-linked glycosylation via asparagine (GO:0018279)
-1.960		negative regulation of translation (GO:0017148)
-1.947		ERK1 and ERK2 cascade (GO:0070371)
-1.919		protein dephosphorylation (GO:0006470)
-1.900		histone H4 acetylation (GO:0043967)
1.880		response to endoplasmic reticulum stress (GO:0034976)
1.779		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-1.761		positive regulation of type I interferon production (GO:0032481)
-1.723		positive regulation of protein targeting to mitochondrion (GO:1903955)
-1.721		brain development (GO:0007420)
-1.688		positive regulation of protein ubiquitination (GO:0031398)

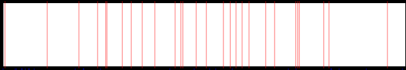
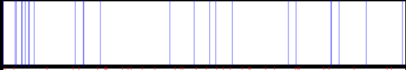
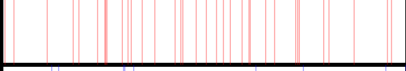
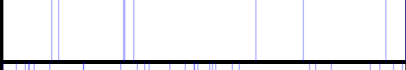
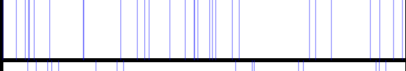
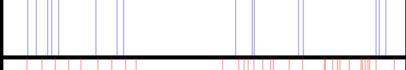


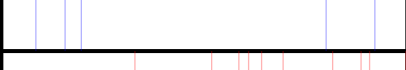




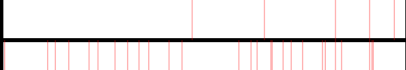

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=81$

mitochondrial translational elongation (GO:0070125)



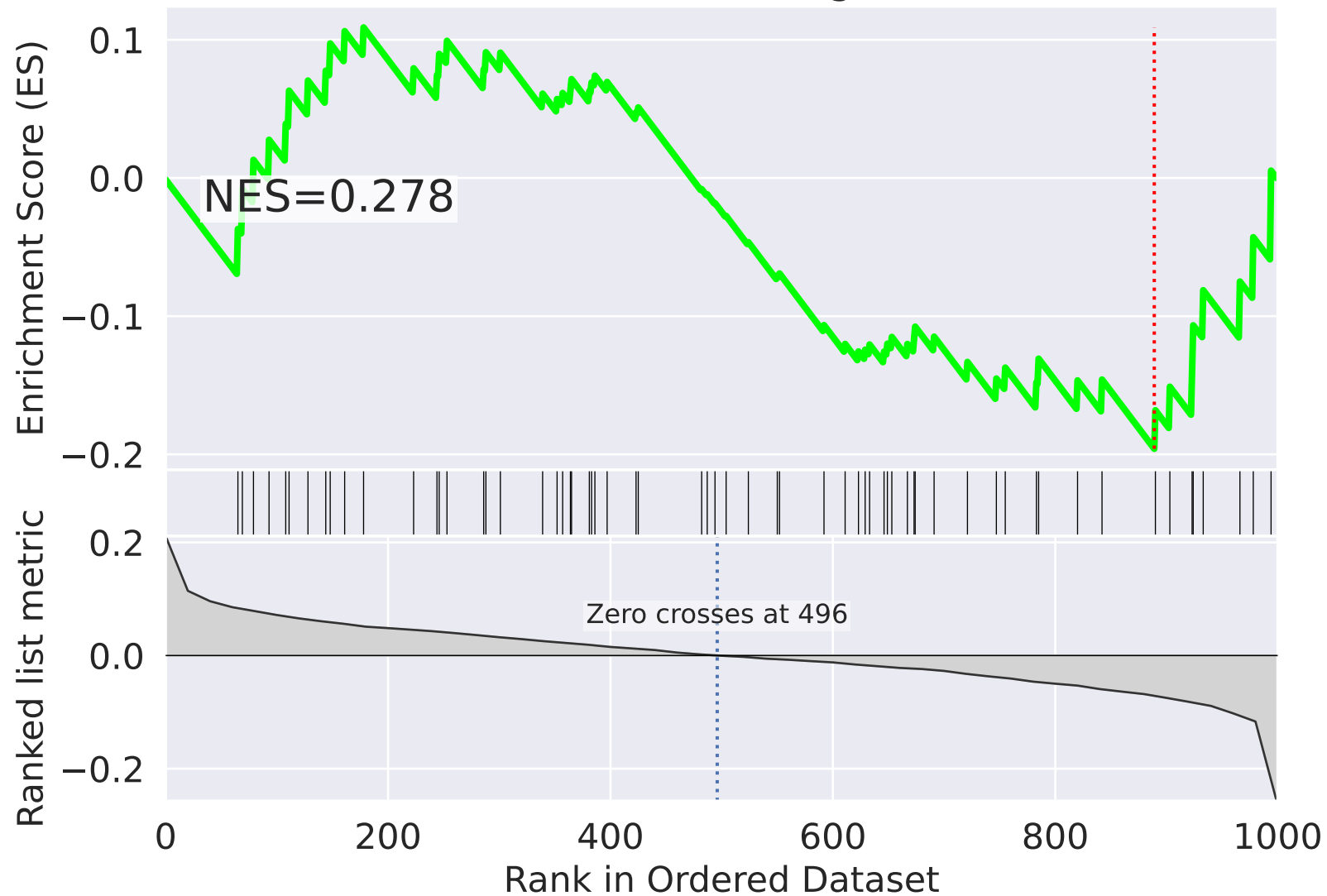
mitochondrial translational elongation (GO:0070125)



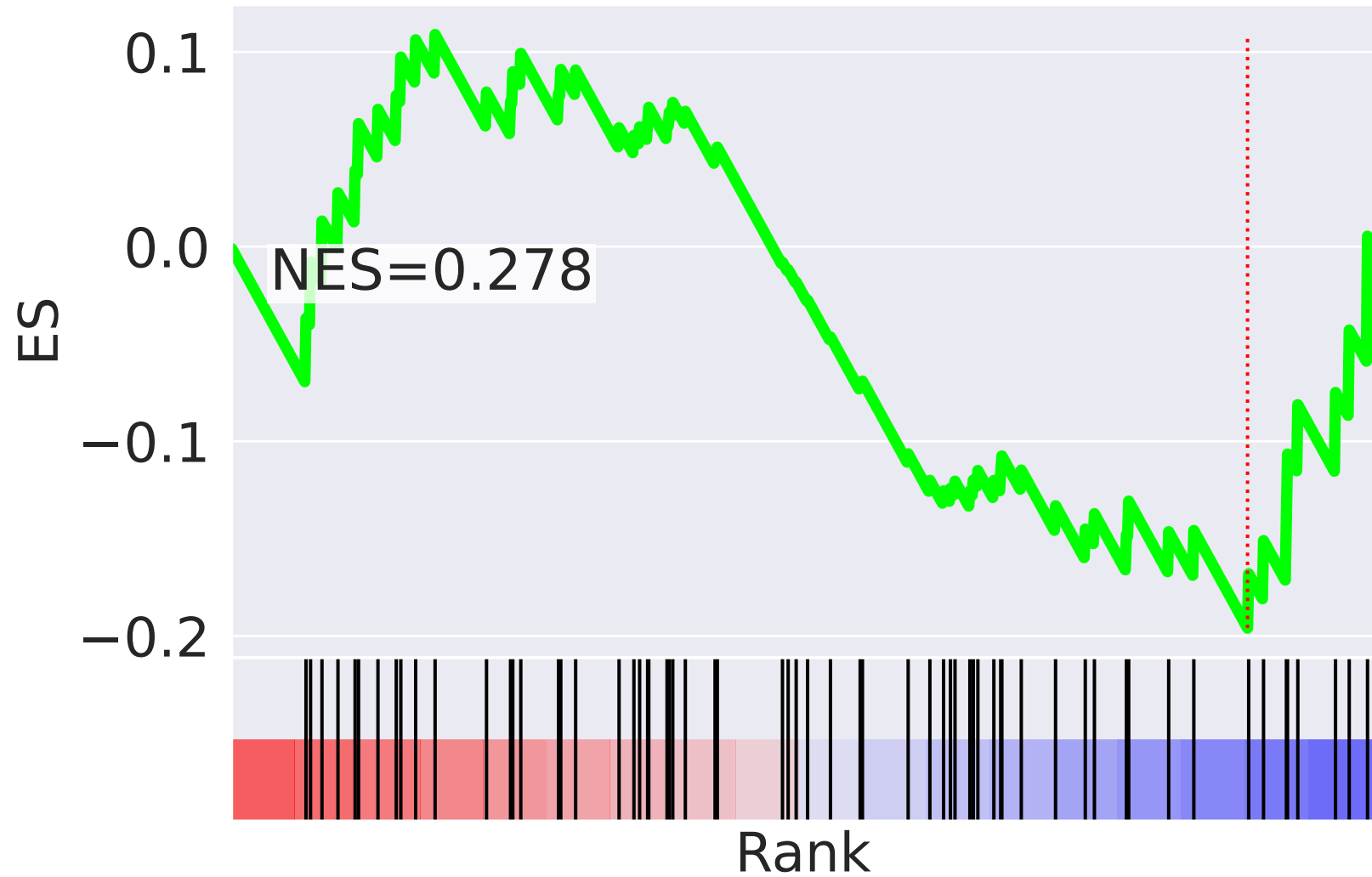
NES		SET
3.735		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.550		mitochondrial translation (GO:0032543)
3.501		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.517		positive regulation of TOR signaling (GO:0032008)
-2.516		translation (GO:0006412)
-2.468		cell cycle arrest (GO:0007050)
2.410		positive regulation of cell proliferation (GO:0008284)
2.321		regulation of DNA replication (GO:0006275)
-2.304		nucleosome disassembly (GO:0006337)
2.297		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.229		chromatin remodeling (GO:0006338)
2.193		regulation of cell proliferation (GO:0042127)
-2.184		negative regulation of cell proliferation (GO:0008285)
2.133		ERK1 and ERK2 cascade (GO:0070371)
2.132		signal transduction (GO:0007165)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=82$

mitochondrial translational elongation (GO:0070125)


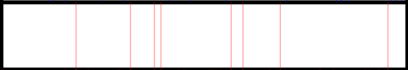
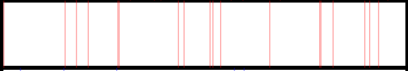



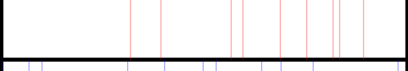


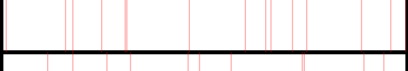

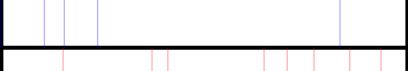
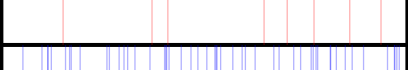
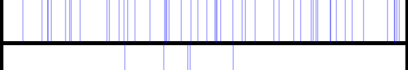



mitochondrial translational elongation (GO:0070125)



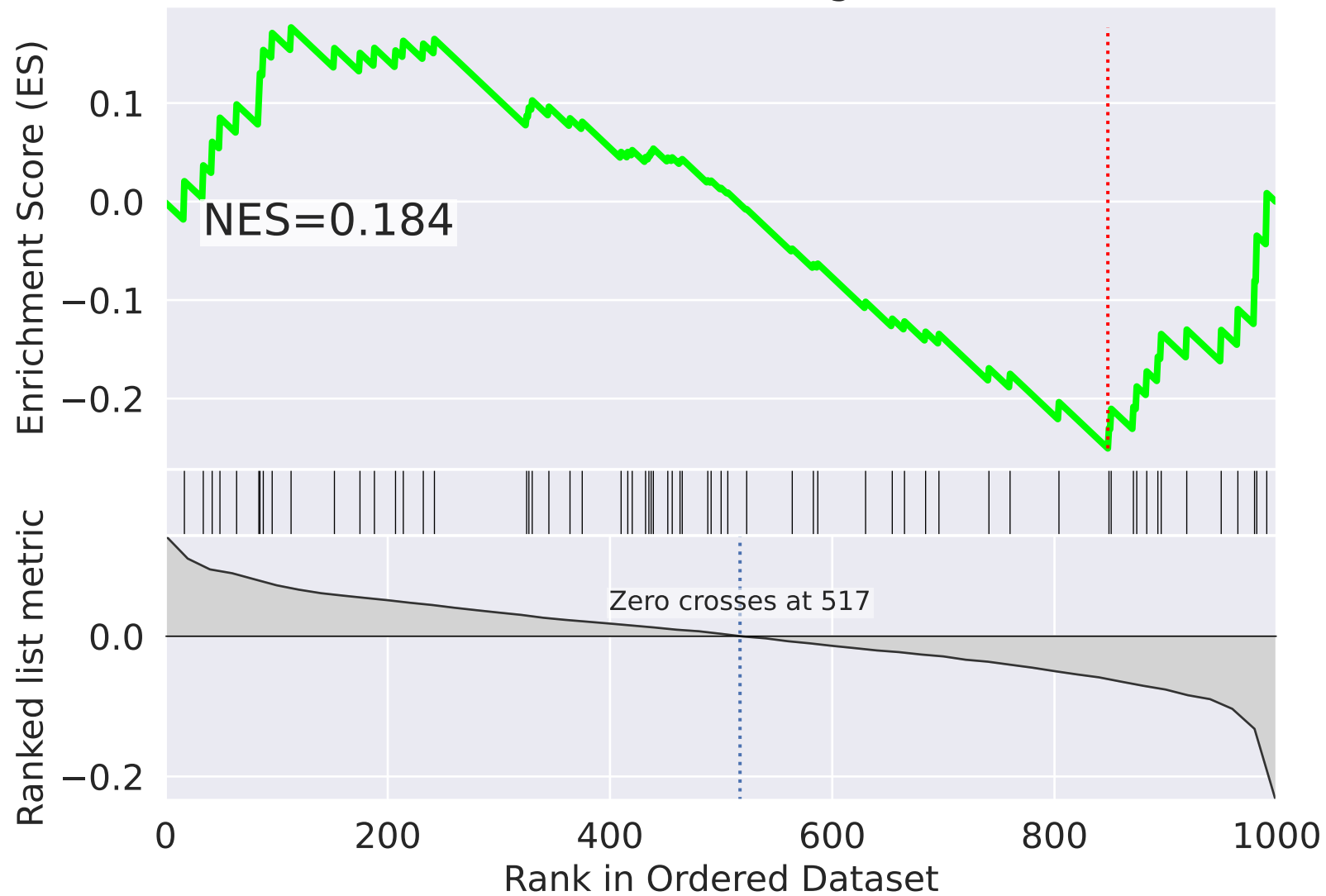
NES

SET

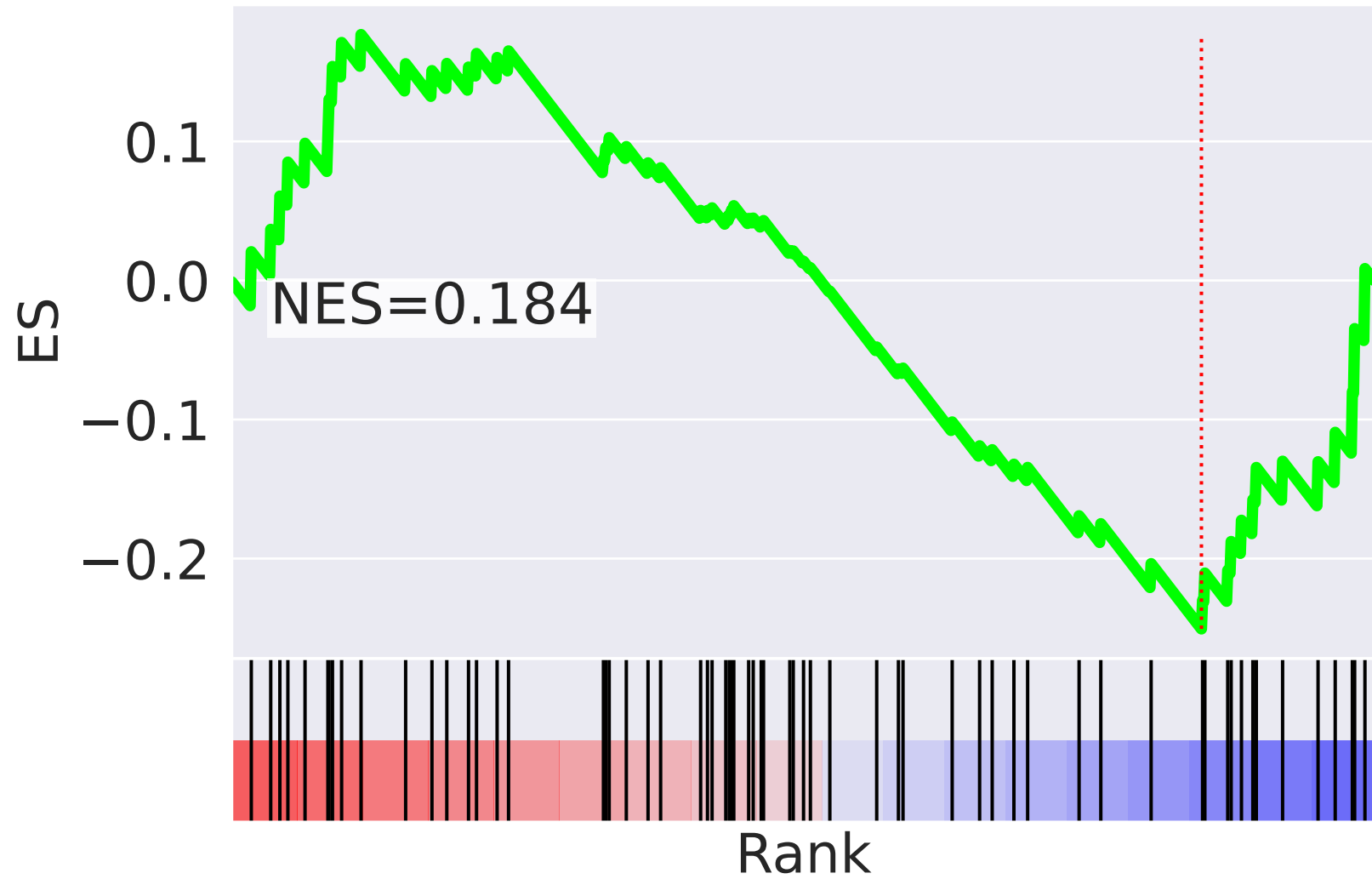
-2.882		cell cycle arrest (GO:0007050)
2.538		axon guidance (GO:0007411)
2.442		G2/M transition of mitotic cell cycle (GO:0000086)
-2.415		protein N-linked glycosylation (GO:0006487)
-2.414		protein N-linked glycosylation via asparagine (GO:0018279)
2.399		epidermal growth factor receptor signaling pathway (GO:0007173)
2.398		Fc-epsilon receptor signaling pathway (GO:0038095)
-2.281		chromatin remodeling (GO:0006338)
-2.278		nervous system development (GO:0007399)
2.247		positive regulation of apoptotic process (GO:0043065)
2.186		positive regulation of gene expression (GO:0010628)
-2.132		positive regulation of cytokinesis (GO:0032467)
2.127		negative regulation of translation (GO:0017148)
-2.107		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-2.092		endocytosis (GO:0006897)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=83$

mitochondrial translational elongation (GO:0070125)




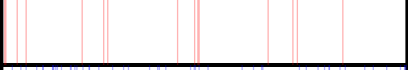
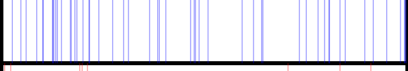






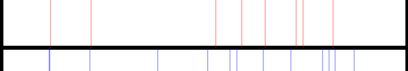
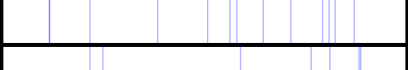
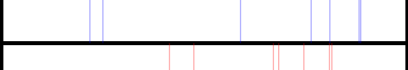



mitochondrial translational elongation (GO:0070125)



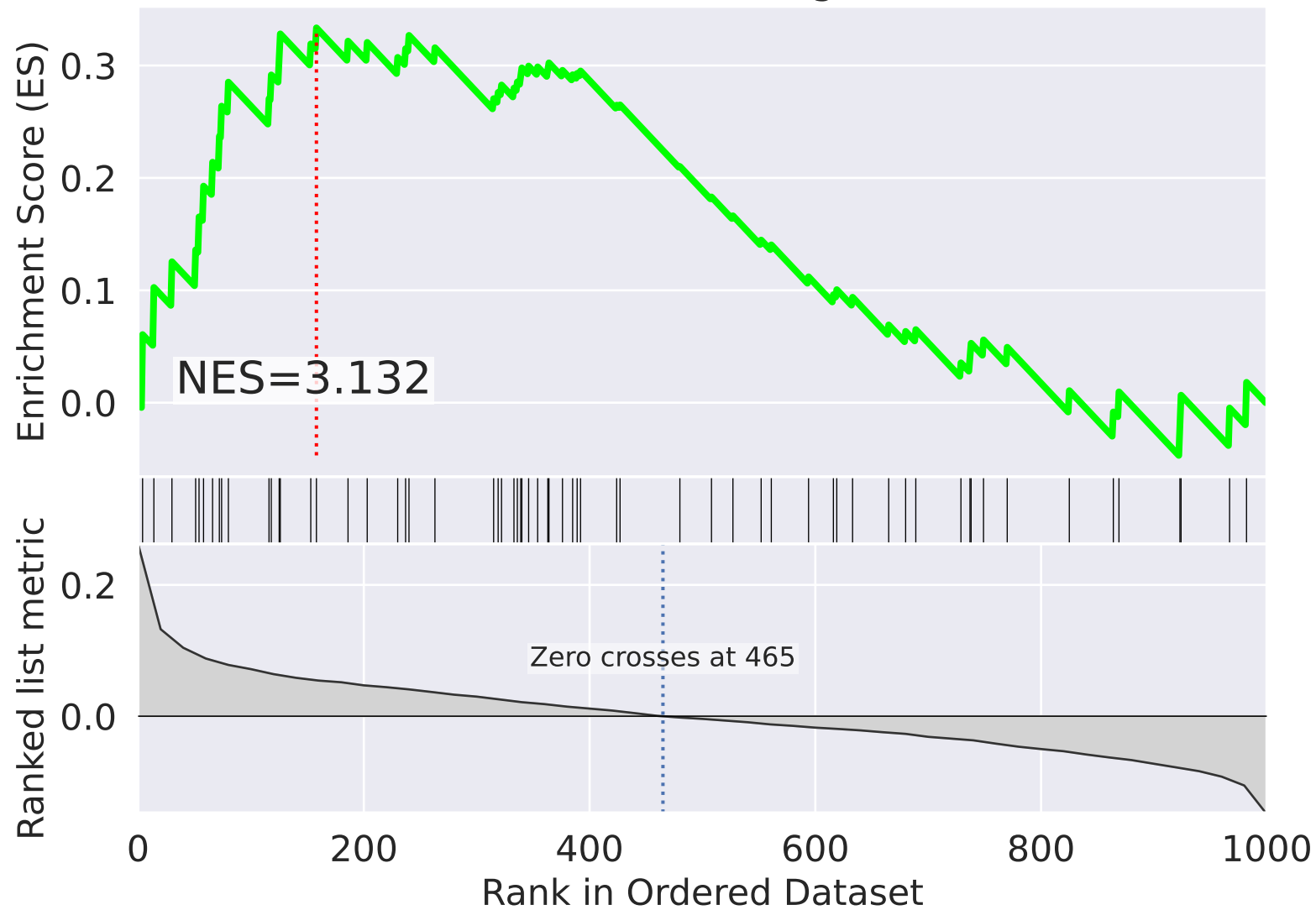
NES

SET

3.088		protein complex assembly (GO:0006461)
-2.466		regulation of transcription, DNA-templated (GO:0006355)
2.461		cell surface receptor signaling pathway (GO:0007166)
2.329		positive regulation of apoptotic process (GO:0043065)
-2.318		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
2.309		cell-matrix adhesion (GO:0007160)
-2.181		mitochondrion organization (GO:0007005)
-2.068		nervous system development (GO:0007399)
-2.056		protein N-linked glycosylation (GO:0006487)
-2.043		post-Golgi vesicle-mediated transport (GO:0006892)
-2.042		IRE1-mediated unfolded protein response (GO:0036498)
2.041		negative regulation of translation (GO:0017148)
-2.038		protein stabilization (GO:0050821)
-2.008		protein N-linked glycosylation via asparagine (GO:0018279)
2.007		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)

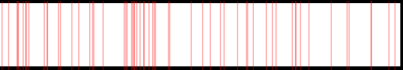
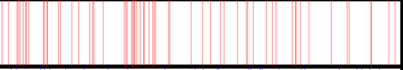
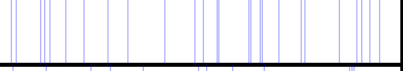
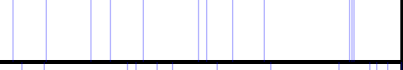
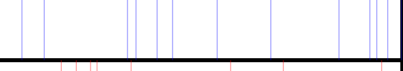
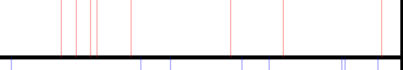

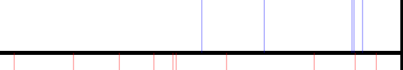


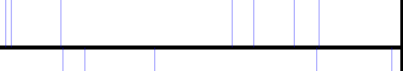
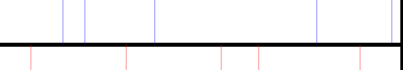



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=84$

mitochondrial translational elongation (GO:0070125)



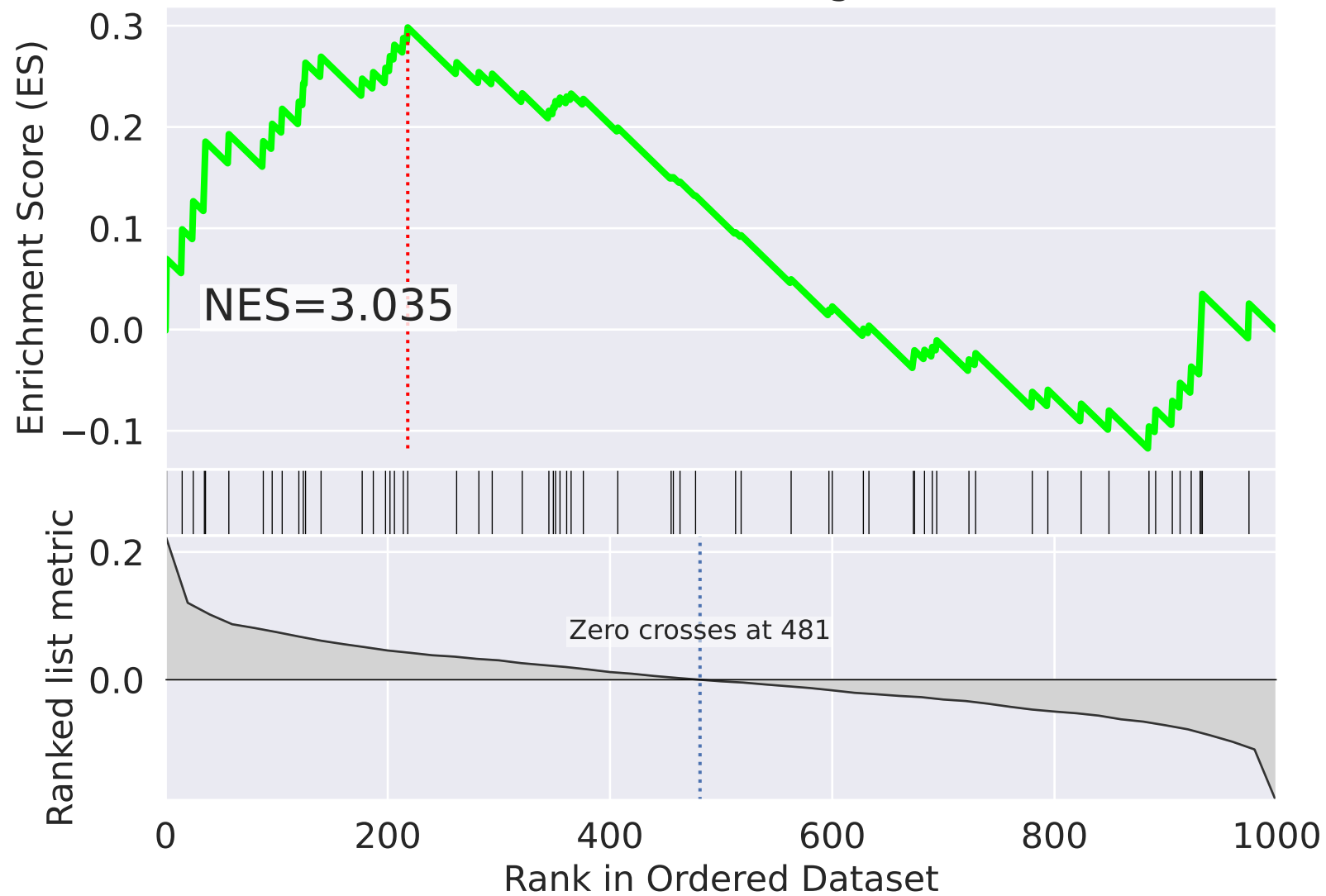
mitochondrial translational elongation (GO:0070125)



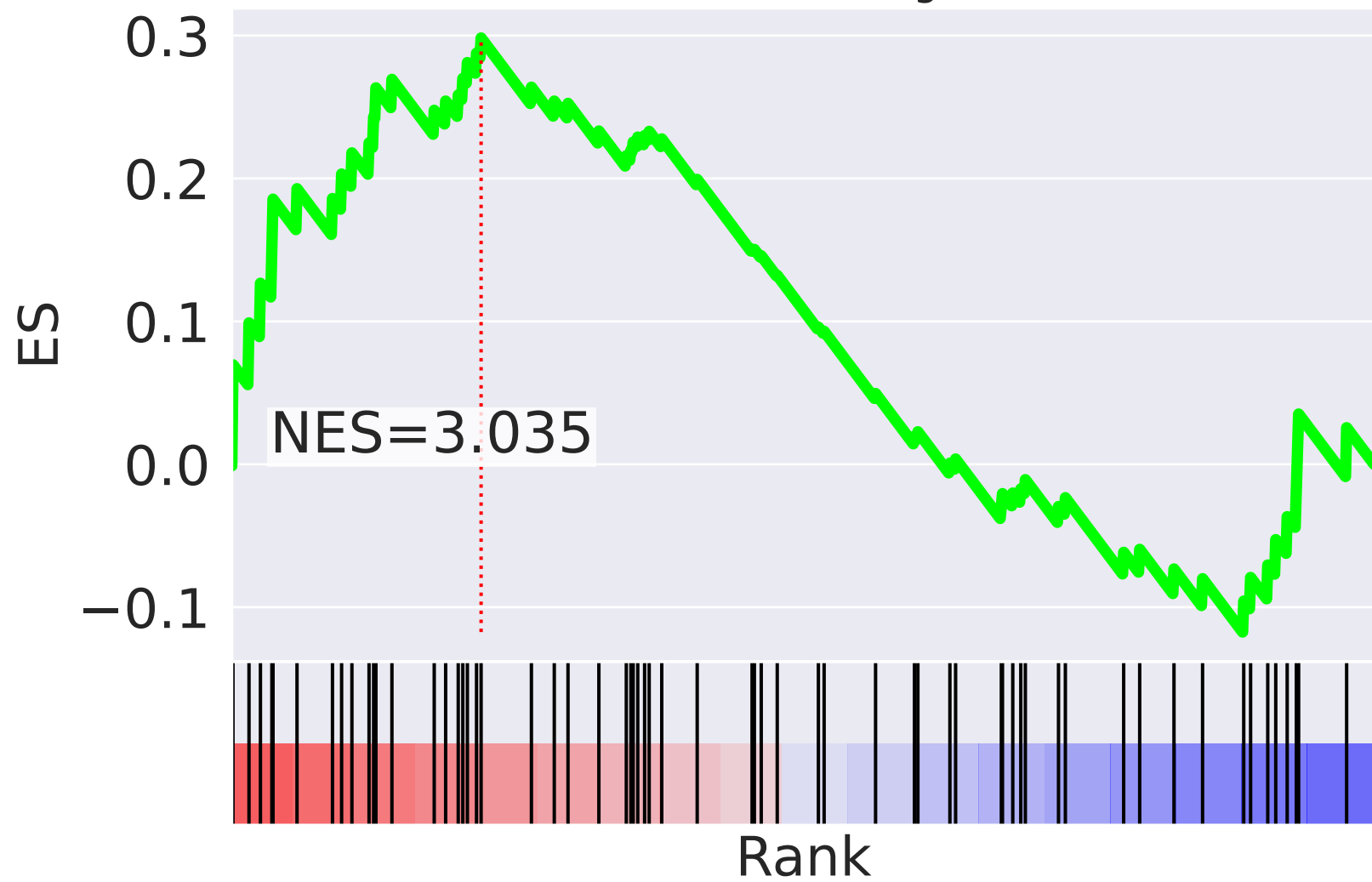
NES		SET
3.337		mitochondrial translational termination (GO:0070126)
3.132		mitochondrial translational elongation (GO:0070125)
-2.854		protein deubiquitination (GO:0016579)
-2.270		mRNA export from nucleus (GO:0006406)
-2.223		apoptotic process (GO:0006915)
2.207		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.199		protein homooligomerization (GO:0051260)
-2.158		mitotic nuclear envelope disassembly (GO:0007077)
2.087		sister chromatid cohesion (GO:0007062)
2.082		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-2.054		Wnt signaling pathway (GO:0016055)
-2.049		cellular respiration (GO:0045333)
2.032		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.029		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-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 $z=85$

mitochondrial translational elongation (GO:0070125)



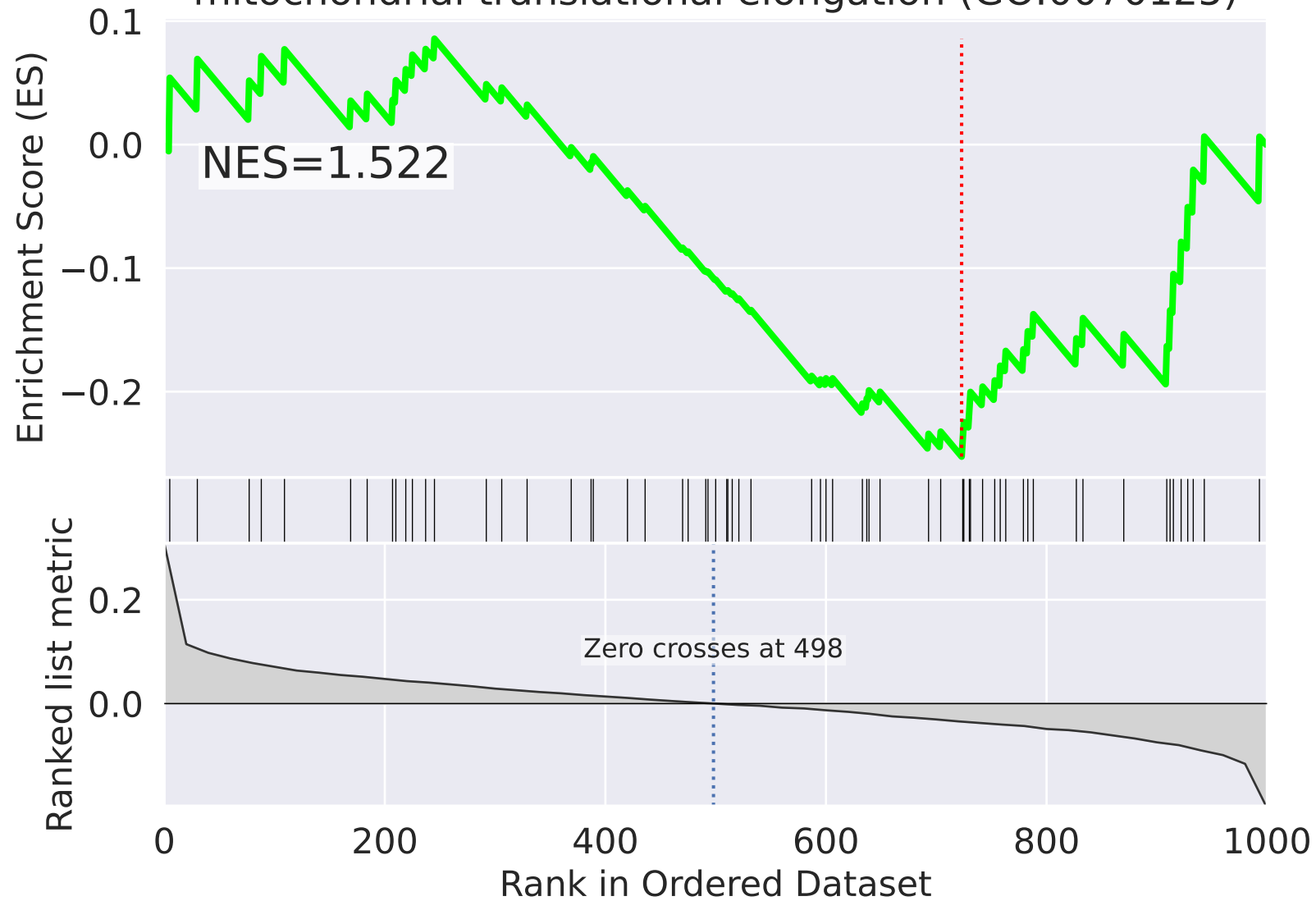
mitochondrial translational elongation (GO:0070125)



NES		SET
3.088		mitochondrial translational termination (GO:0070126)
3.035		mitochondrial translational elongation (GO:0070125)
2.838		mitochondrial translation (GO:0032543)
2.465		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.265		intracellular transport of virus (GO:0075733)
2.262		positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)
2.249		tRNA aminoacylation for protein translation (GO:0006418)
-2.247		regulation of cholesterol biosynthetic process (GO:0045540)
-2.225		protein K48-linked ubiquitination (GO:0070936)
-2.190		strand displacement (GO:0000732)
2.186		ATP-dependent chromatin remodeling (GO:0043044)
-2.156		double-strand break repair via homologous recombination (GO:0000724)
-2.128		DNA synthesis involved in DNA repair (GO:0000731)
2.110		regulation of transcription, DNA-templated (GO:0006355)
2.096		mitochondrion organization (GO:0007005)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=86$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)


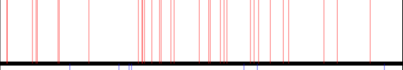





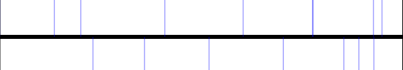
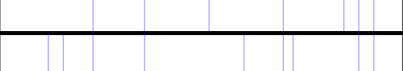
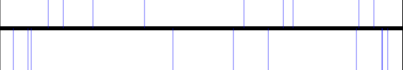

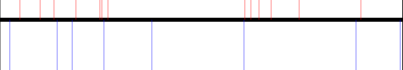
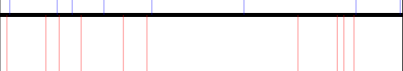
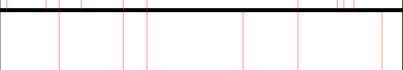
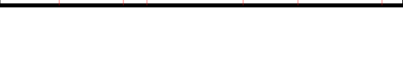
ES

NES=1.522

0.1
0.0
-0.1
-0.2

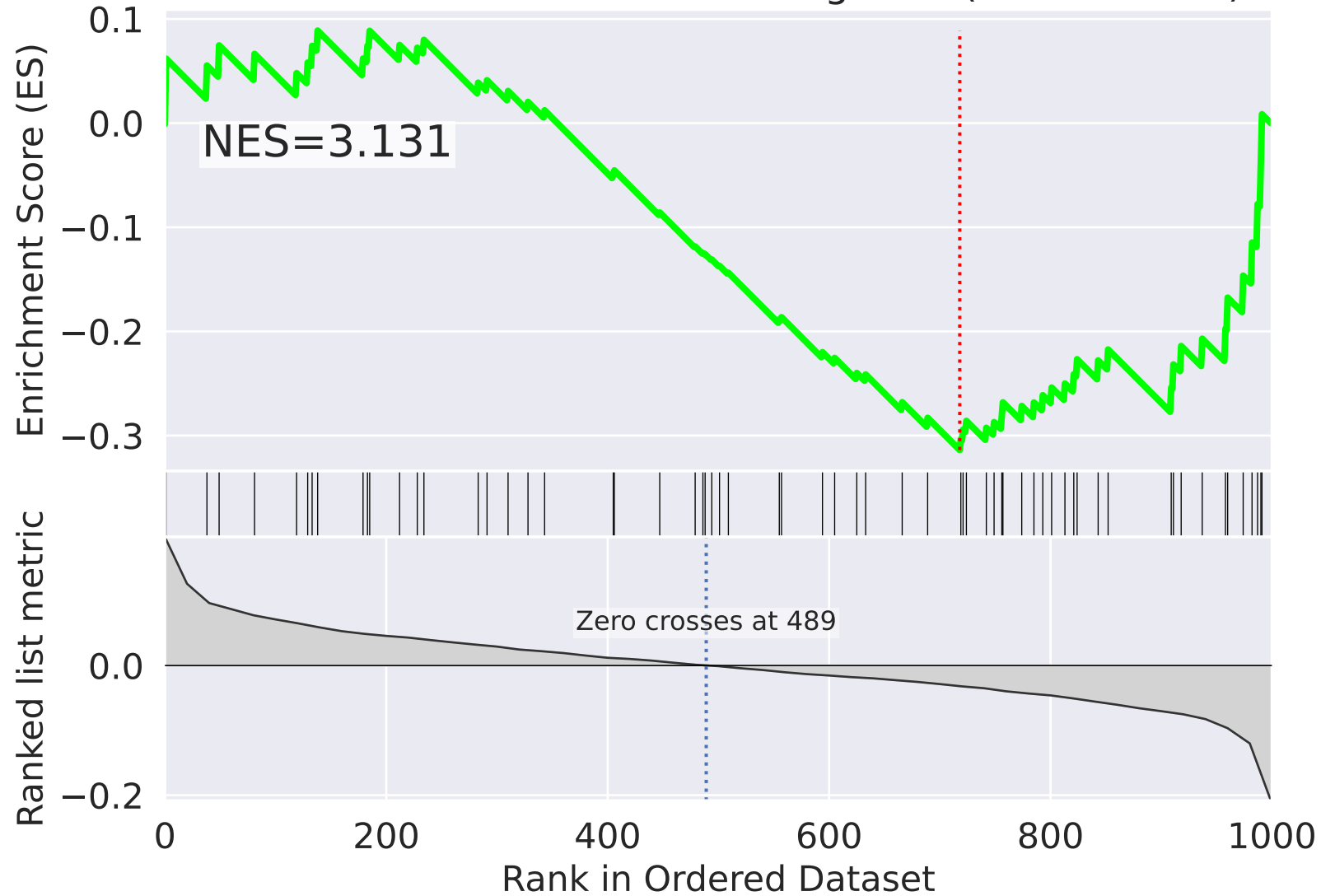
Rank



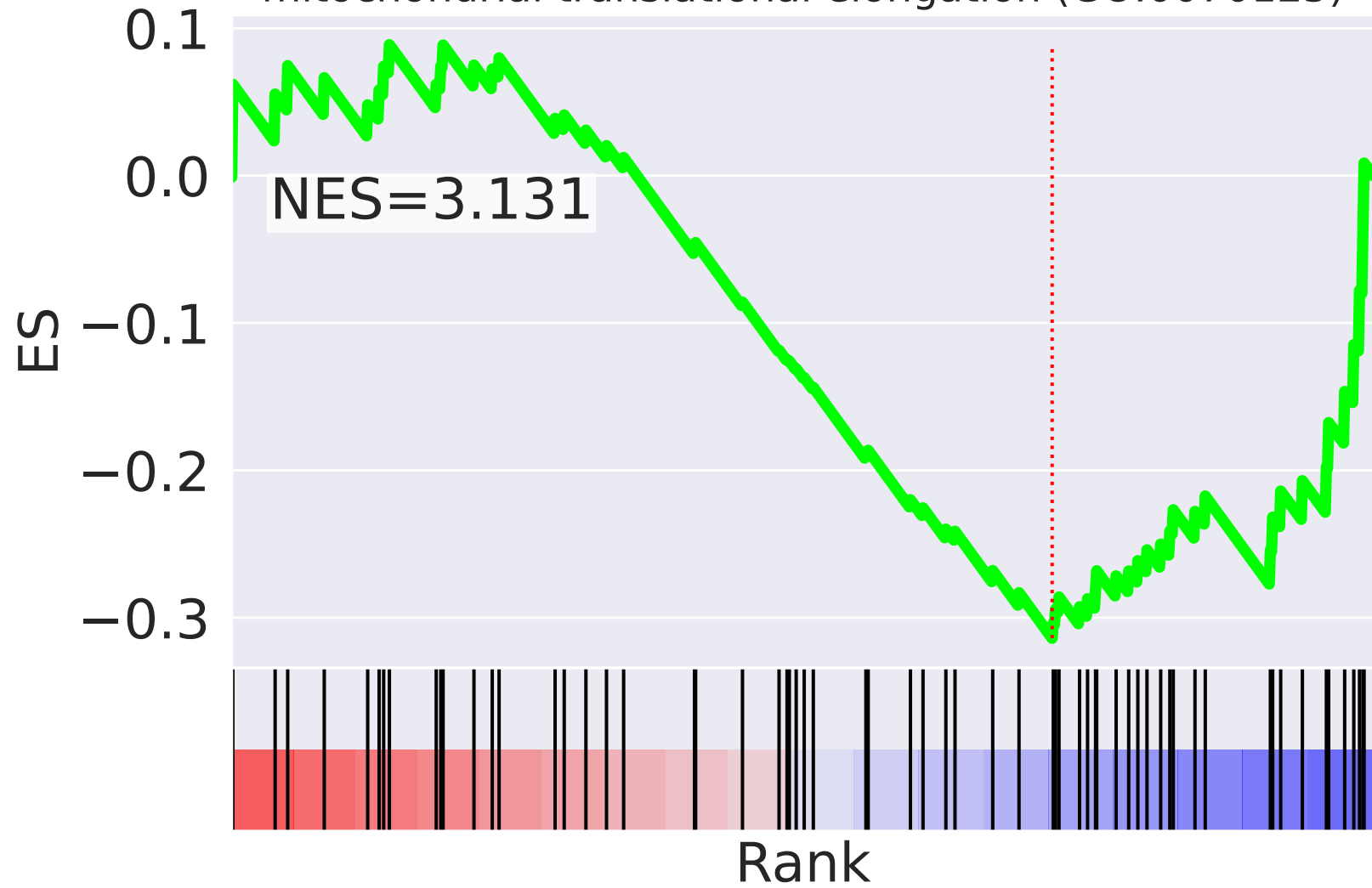
NES		SET
-2.627		Wnt signaling pathway (GO:0016055)
2.571		positive regulation of cell proliferation (GO:0008284)
-2.567		movement of cell or subcellular component (GO:0006928)
-2.545		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-2.378		T cell costimulation (GO:0031295)
-2.315		phosphatidylinositol biosynthetic process (GO:0006661)
-2.190		positive regulation of TOR signaling (GO:0032008)
-2.189		regulation of mRNA stability (GO:0043488)
-2.166		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-2.137		Fc-epsilon receptor signaling pathway (GO:0038095)
-2.105		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.037		histone H3 acetylation (GO:0043966)
-2.011		intracellular signal transduction (GO:0035556)
1.992		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
1.991		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 $z=87$

mitochondrial translational elongation (GO:0070125)


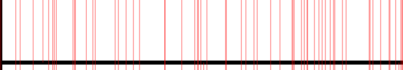
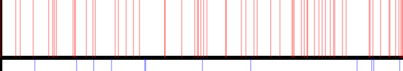


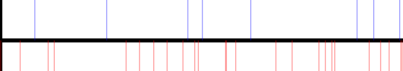
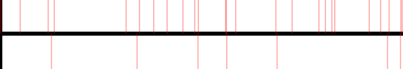
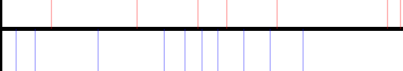



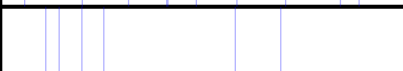





mitochondrial translational elongation (GO:0070125)



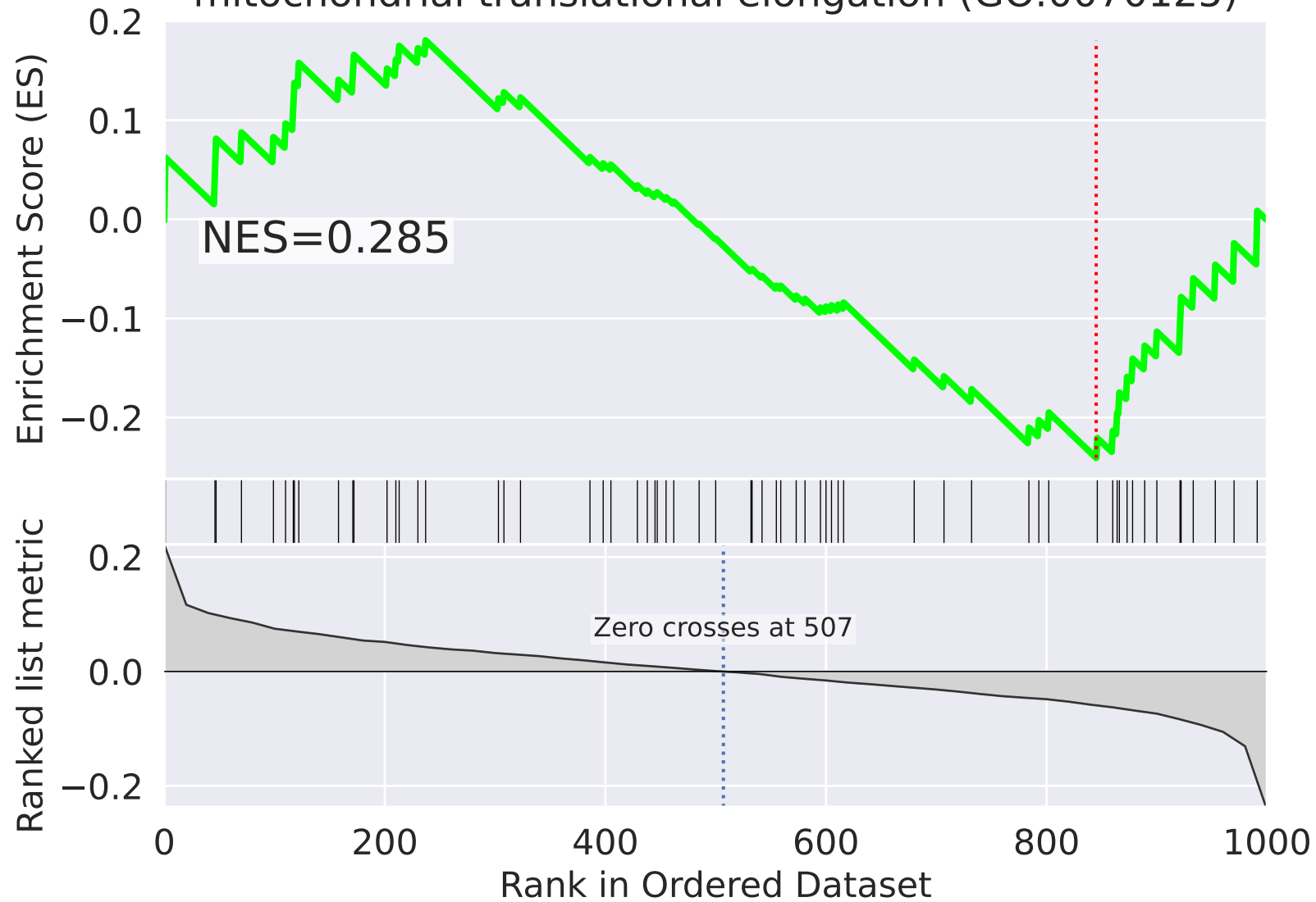
NES

SET

3.191		positive regulation of cell proliferation (GO:0008284)
3.149		mitochondrial translational termination (GO:0070126)
3.131		mitochondrial translational elongation (GO:0070125)
-2.402		mRNA export from nucleus (GO:0006406)
-2.376		DNA-dependent DNA replication (GO:0006261)
-2.126		RNA export from nucleus (GO:0006405)
2.094		mitochondrial translation (GO:0032543)
2.068		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.033		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
-1.902		protein K11-linked ubiquitination (GO:0070979)
-1.865		mRNA processing (GO:0006397)
-1.862		endosomal transport (GO:0016197)
-1.797		protein K48-linked ubiquitination (GO:0070936)
1.769		cell-matrix adhesion (GO:0007160)
-1.765		chromatin remodeling (GO:0006338)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=88$

mitochondrial translational elongation (GO:0070125)



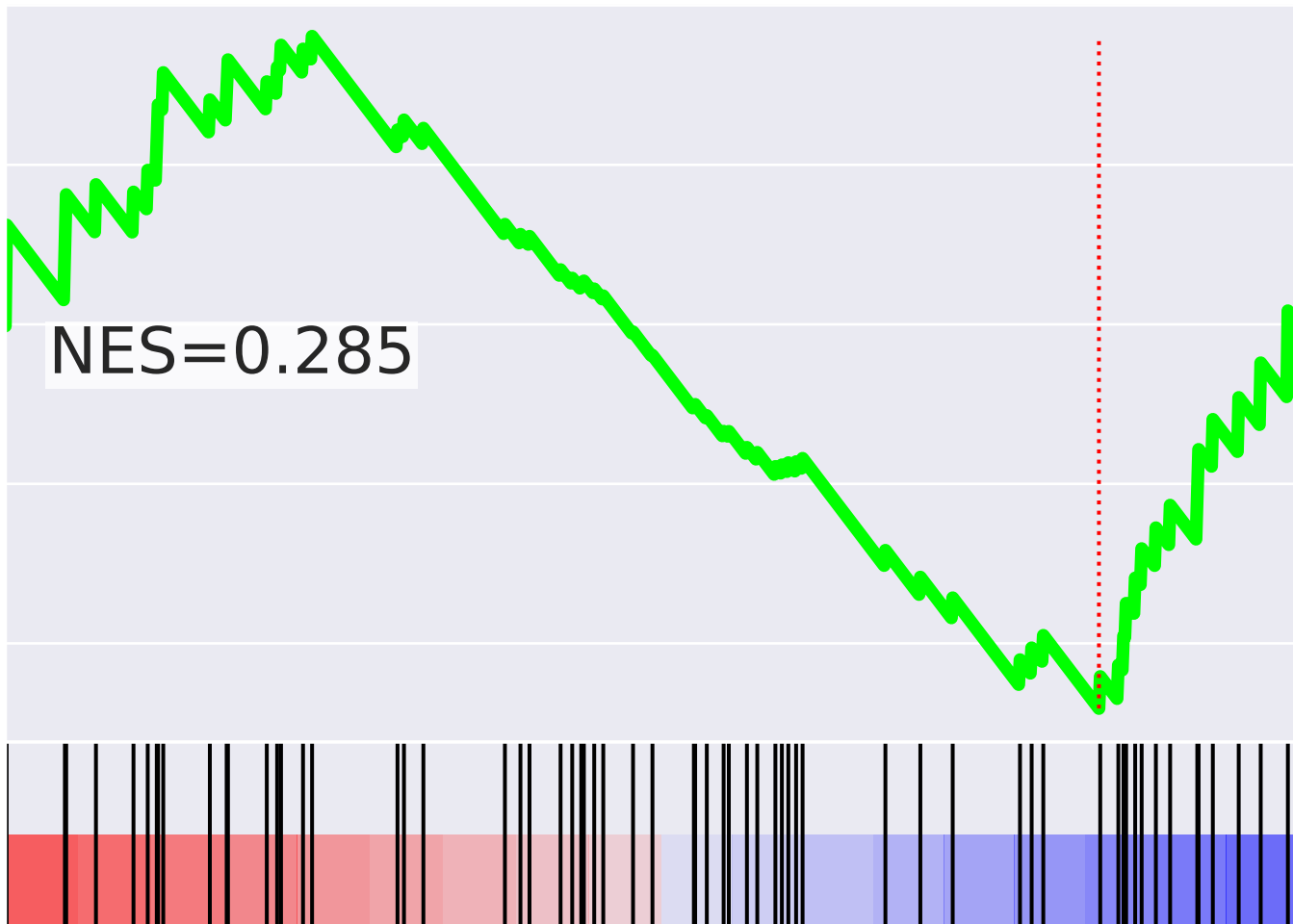
mitochondrial translational elongation (GO:0070125)

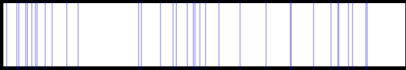


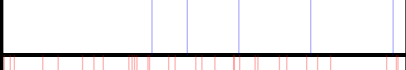
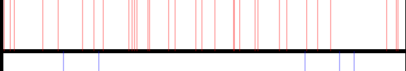
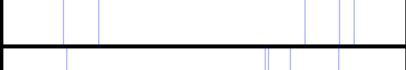


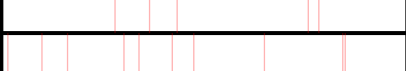
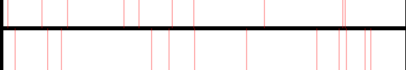
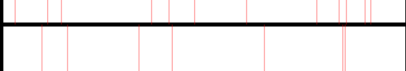
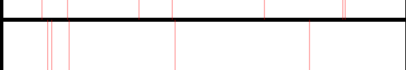
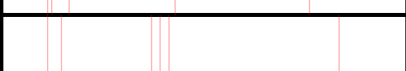
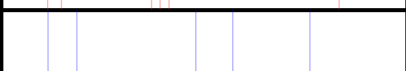
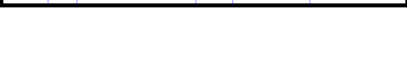
ES

0.2
0.1
0.0
-0.1
-0.2

NES=0.285

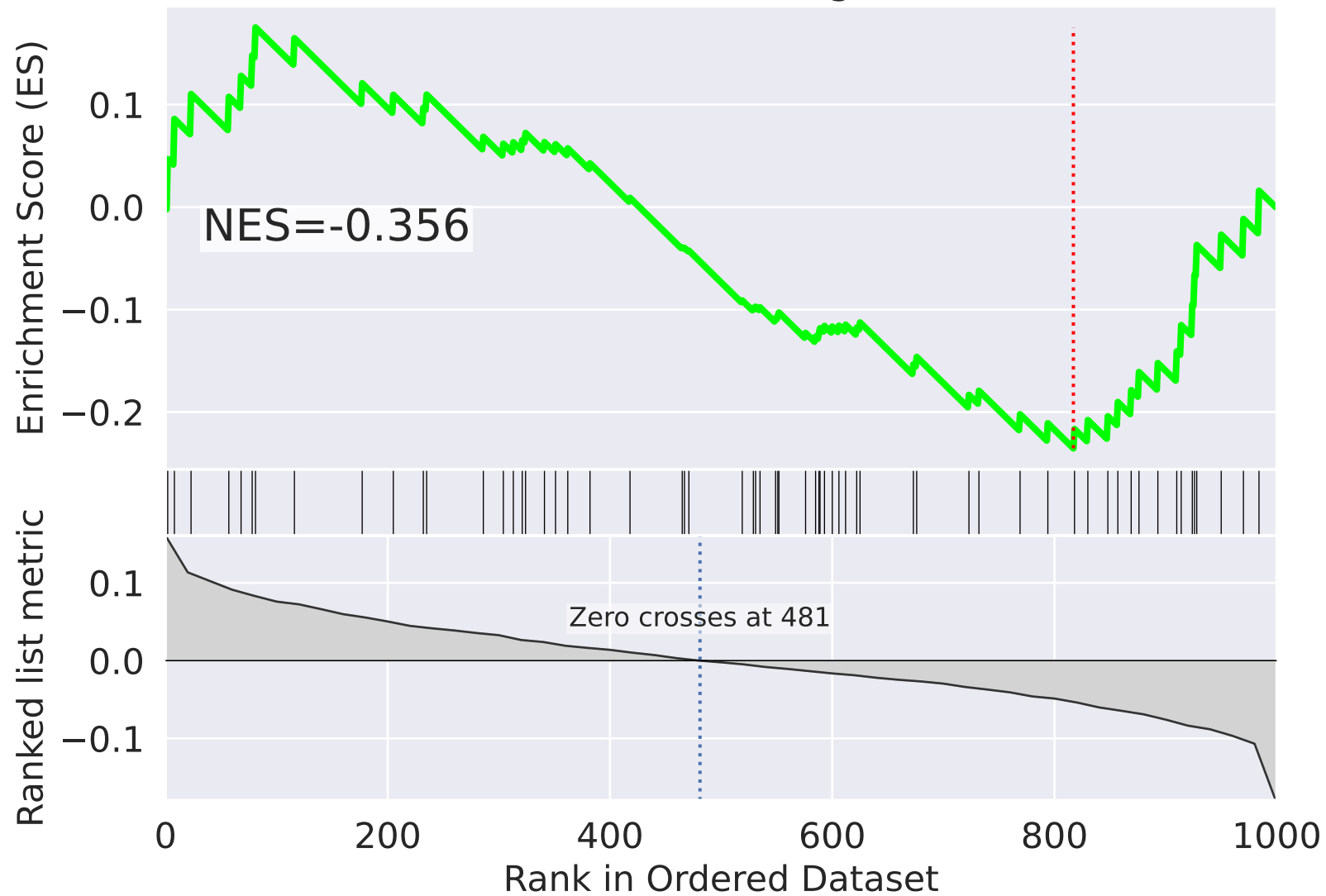
Rank



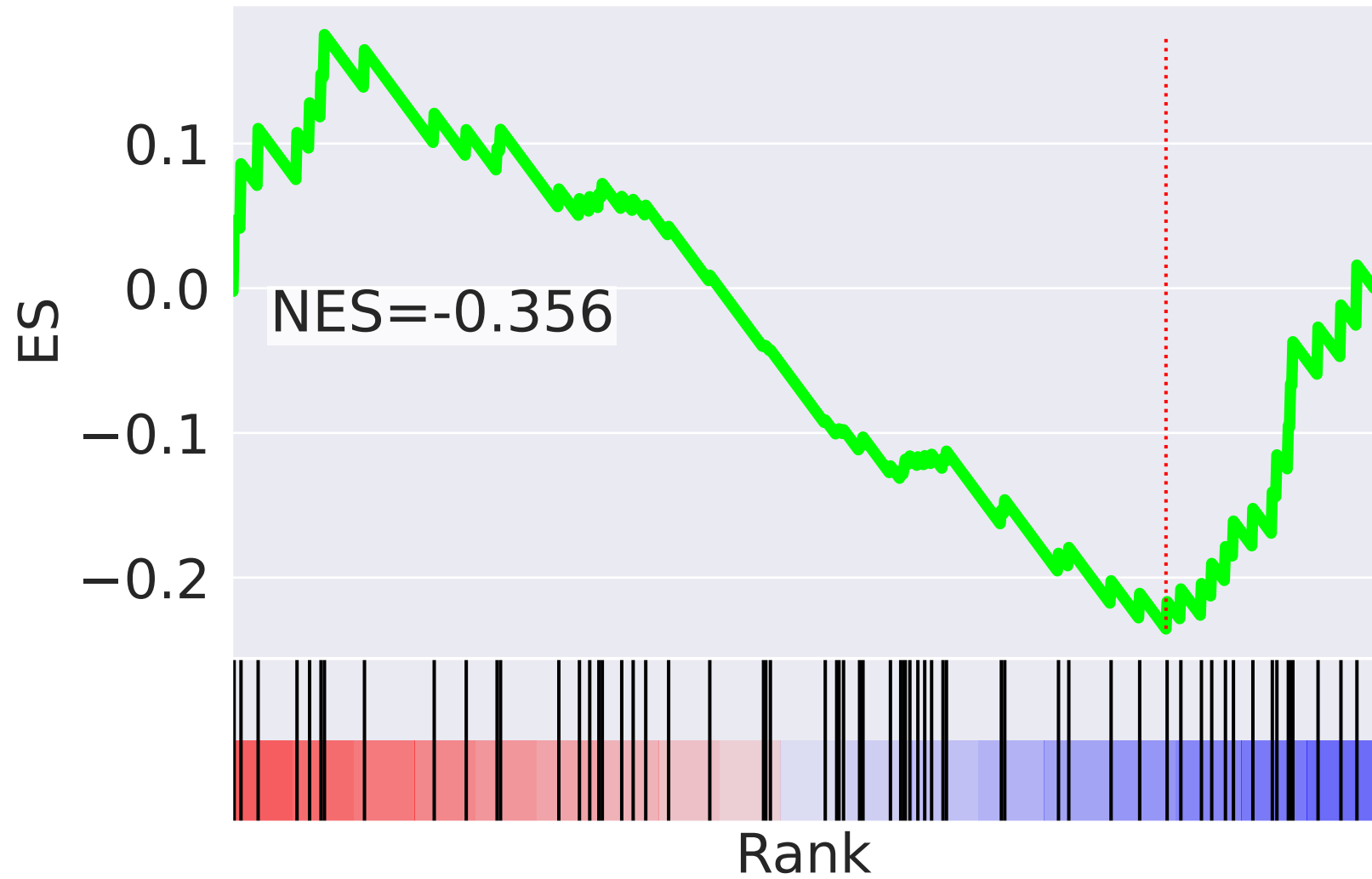
NES		SET
-4.267		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.807		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.742		multicellular organism development (GO:0007275)
-2.728		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.197		positive regulation of cell proliferation (GO:0008284)
-2.177		release of cytochrome c from mitochondria (GO:0001836)
-2.166		cellular respiration (GO:0045333)
-2.153		axon guidance (GO:0007411)
2.152		inflammatory response (GO:0006954)
2.140		multivesicular body assembly (GO:0036258)
2.029		regulation of macroautophagy (GO:0016241)
1.977		viral budding via host ESCRT complex (GO:0039702)
1.879		transcription, DNA-templated (GO:0006351)
1.829		cellular protein localization (GO:0034613)
-1.827		negative regulation of protein kinase activity (GO:0006469)






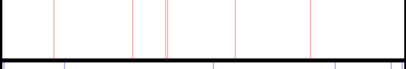


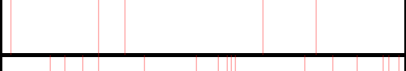
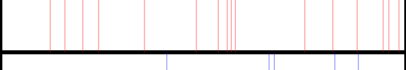
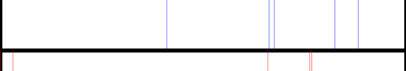
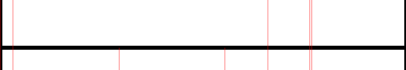
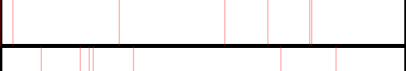

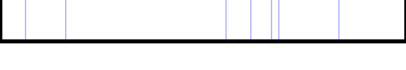
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=89$

mitochondrial translational elongation (GO:0070125)



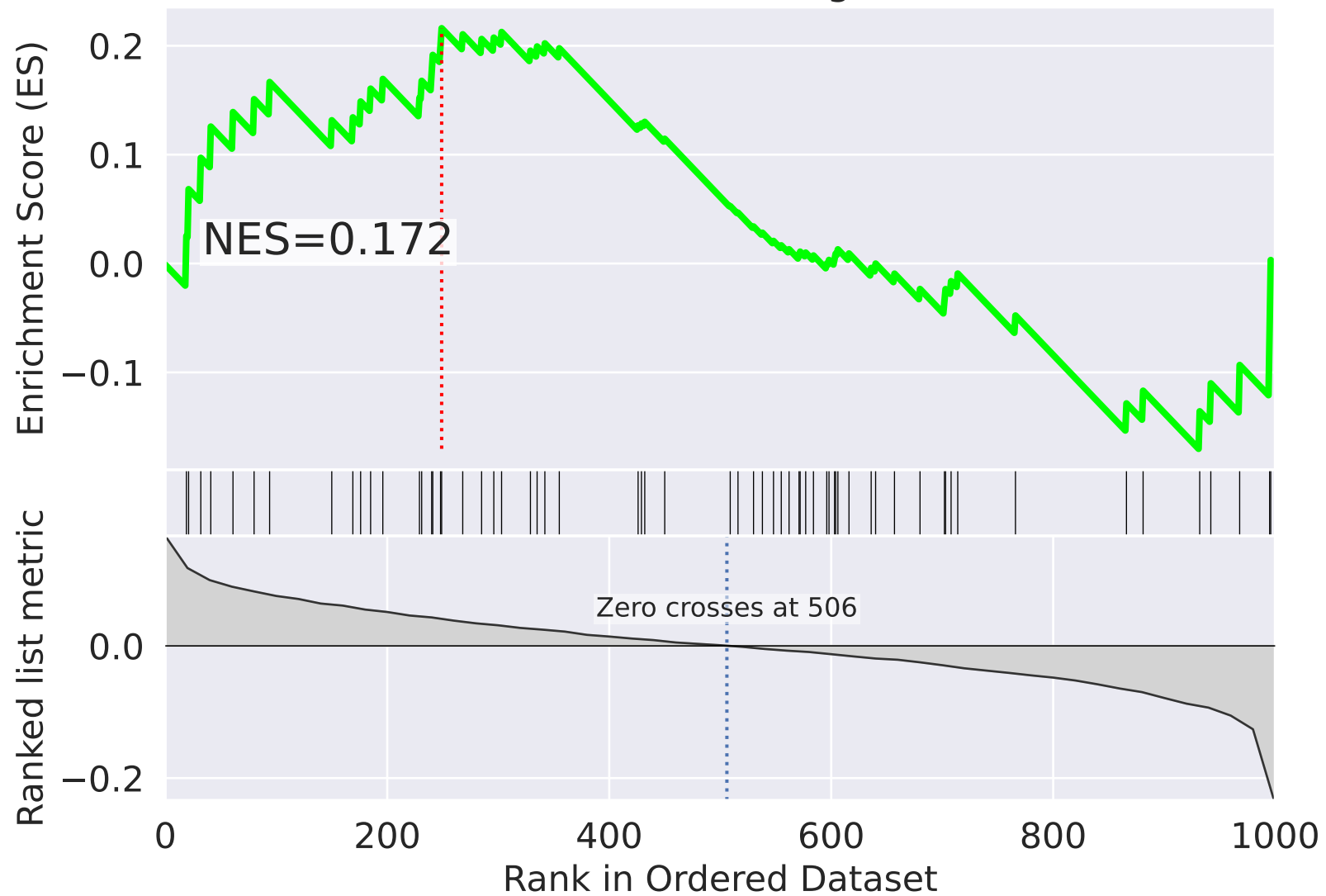
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.401		post-Golgi vesicle-mediated transport (GO:0006892)
-2.290		cell growth (GO:0016049)
-2.228		mitotic cytokinesis (GO:0000281)
-2.172		phosphatidylinositol biosynthetic process (GO:0006661)
2.155		strand displacement (GO:0000732)
2.126		chromosome segregation (GO:0007059)
-2.055		cellular protein localization (GO:0034613)
2.055		peptidyl-threonine phosphorylation (GO:0018107)
2.002		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
1.994		regulation of signal transduction by p53 class mediator (GO:1901796)
-1.967		lipid metabolic process (GO:0006629)
1.956		mRNA 3'-end processing (GO:0031124)
1.932		termination of RNA polymerase II transcription (GO:0006369)
1.909		response to virus (GO:0009615)
-1.905		negative regulation of canonical Wnt signaling pathway (GO:0090090)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=90$

mitochondrial translational elongation (GO:0070125)



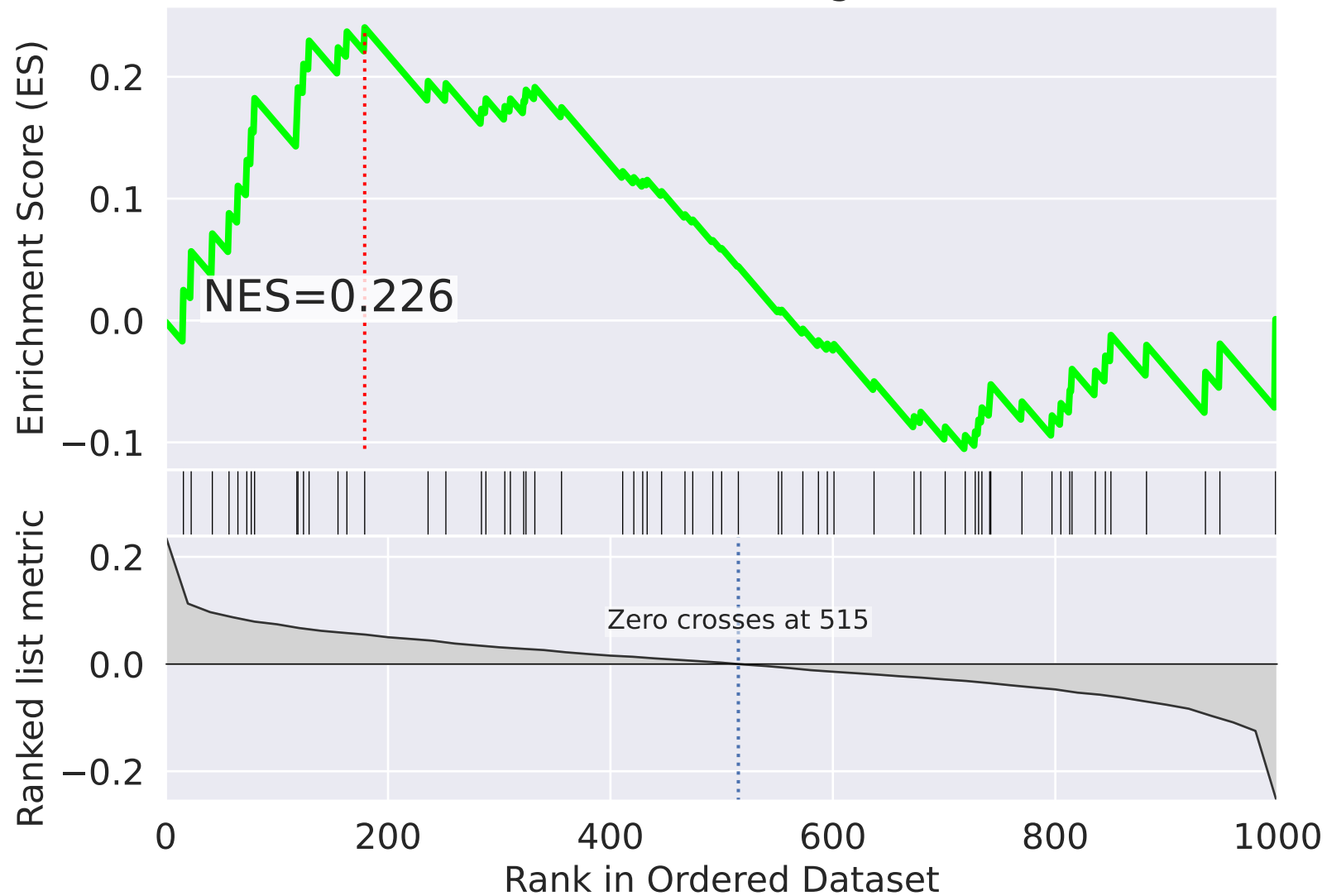
mitochondrial translational elongation (GO:0070125)



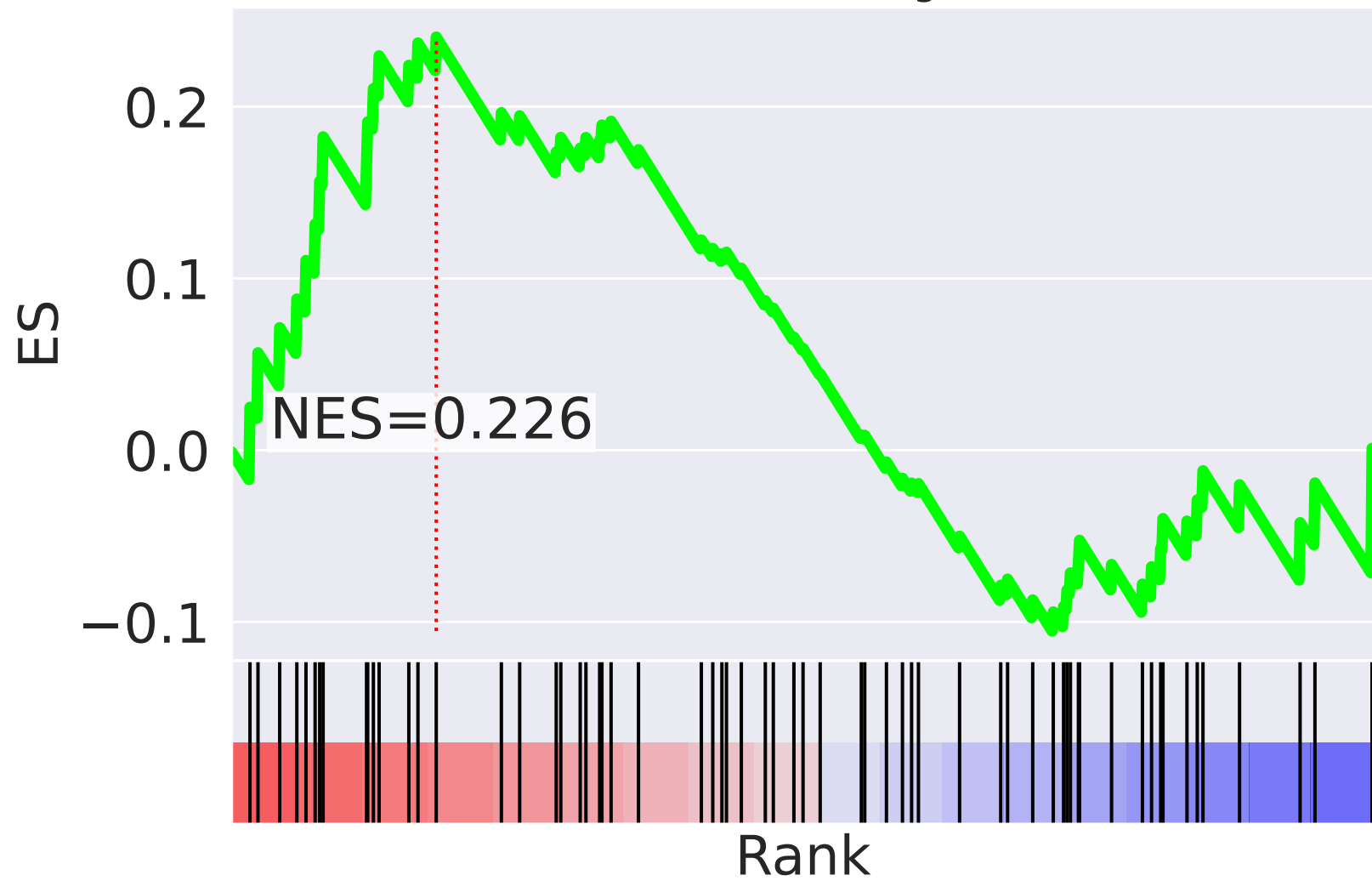
NES		SET
-2.705		cellular nitrogen compound metabolic process (GO:0034641)
2.610		macroautophagy (GO:0016236)
2.515		axon guidance (GO:0007411)
-2.465		cellular protein modification process (GO:0006464)
2.326		G2/M transition of mitotic cell cycle (GO:0000086)
2.153		T cell costimulation (GO:0031295)
-2.093		protein N-linked glycosylation via asparagine (GO:0018279)
2.025		epidermal growth factor receptor signaling pathway (GO:0007173)
1.998		Wnt signaling pathway (GO:0016055)
-1.965		tRNA aminoacylation for protein translation (GO:0006418)
-1.935		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
1.931		multicellular organism development (GO:0007275)
1.929		positive regulation of cell proliferation (GO:0008284)
1.923		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
-1.892		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 $z=91$

mitochondrial translational elongation (GO:0070125)



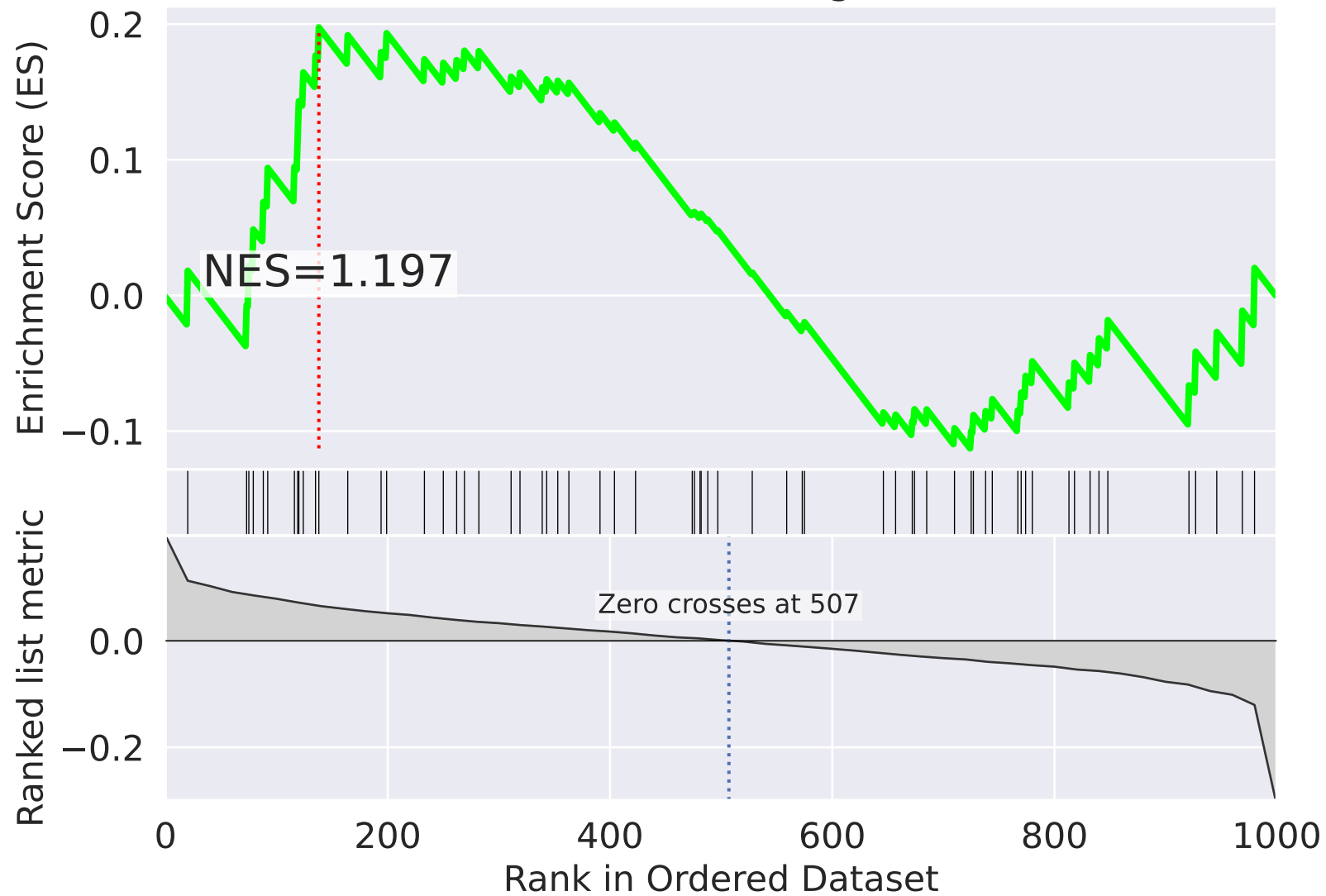
mitochondrial translational elongation (GO:0070125)



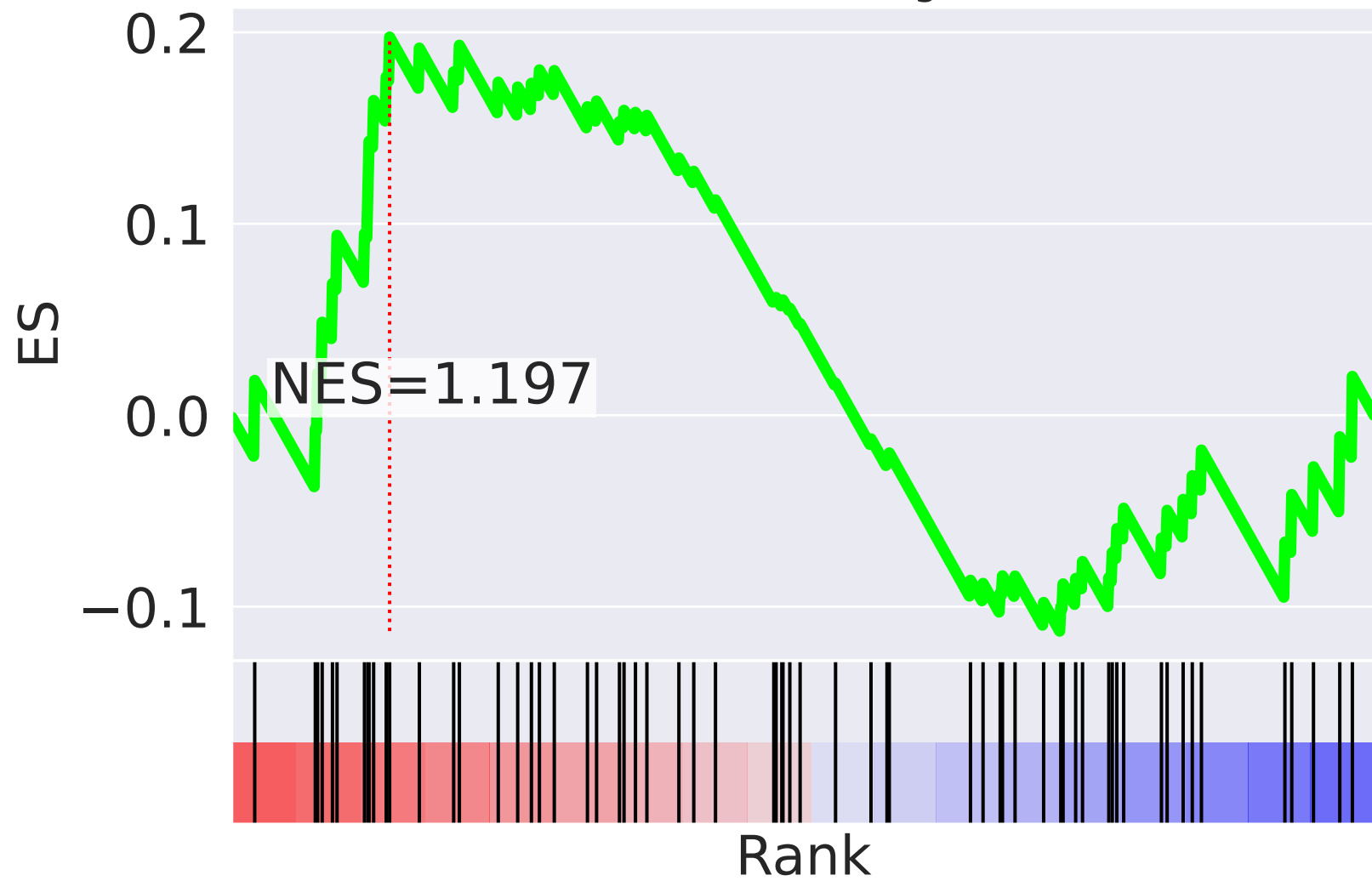
NES		SET
2.451		positive regulation of cell proliferation (GO:0008284)
2.255		Wnt signaling pathway (GO:0016055)
2.253		multivesicular body assembly (GO:0036258)
-2.239		nervous system development (GO:0007399)
2.237		sister chromatid cohesion (GO:0007062)
2.225		MAPK cascade (GO:0000165)
-2.213		cellular nitrogen compound metabolic process (GO:0034641)
-2.150		transcription-coupled nucleotide-excision repair (GO:0006283)
2.144		execution phase of apoptosis (GO:0097194)
-2.112		ubiquitin-dependent ERAD pathway (GO:0030433)
2.098		chromosome segregation (GO:0007059)
2.063		ESCRT III complex disassembly (GO:1904903)
2.048		axon guidance (GO:0007411)
2.035		positive regulation of gene expression (GO:0010628)
-2.031		nucleosome disassembly (GO:0006337)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=92$

mitochondrial translational elongation (GO:0070125)



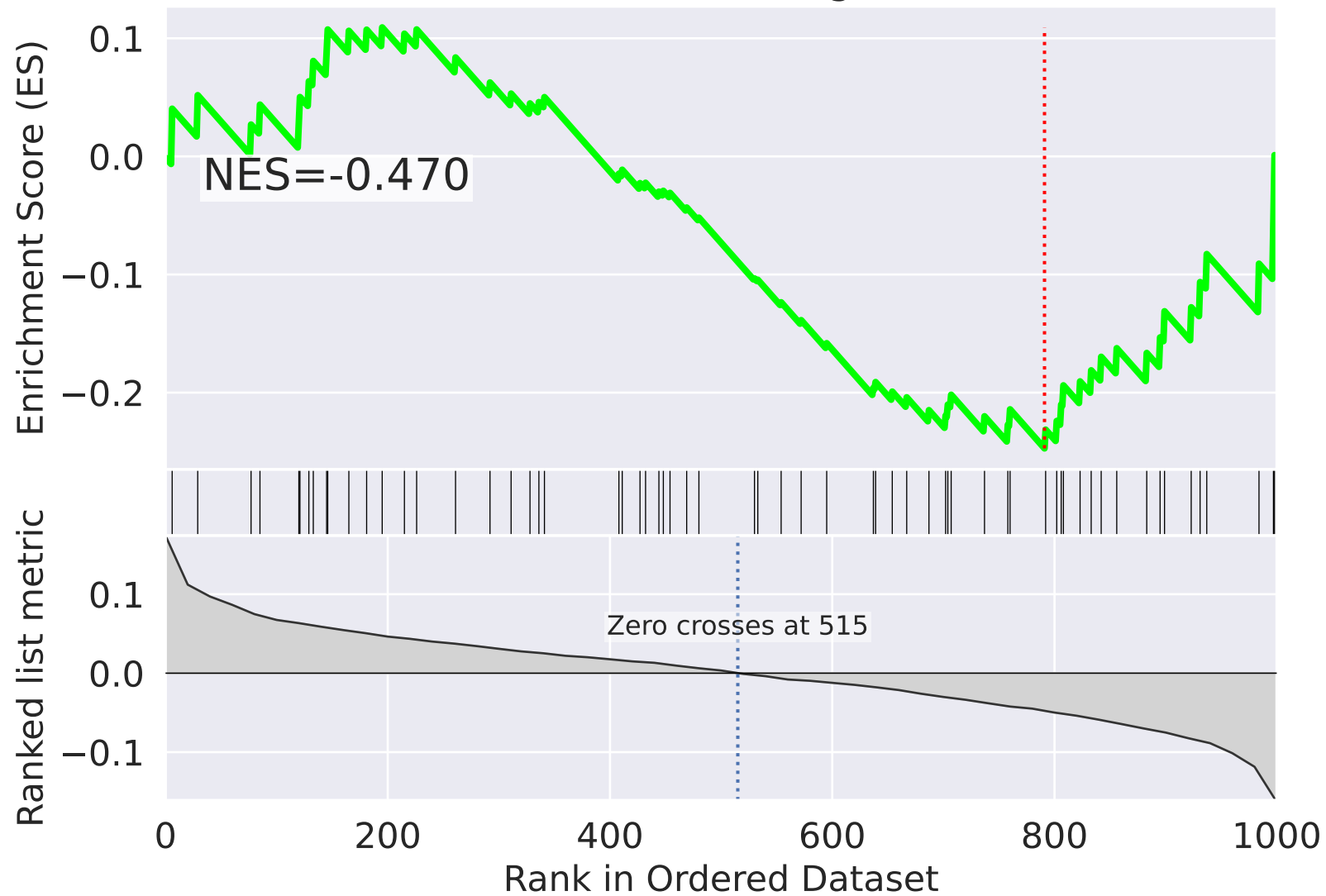
mitochondrial translational elongation (GO:0070125)



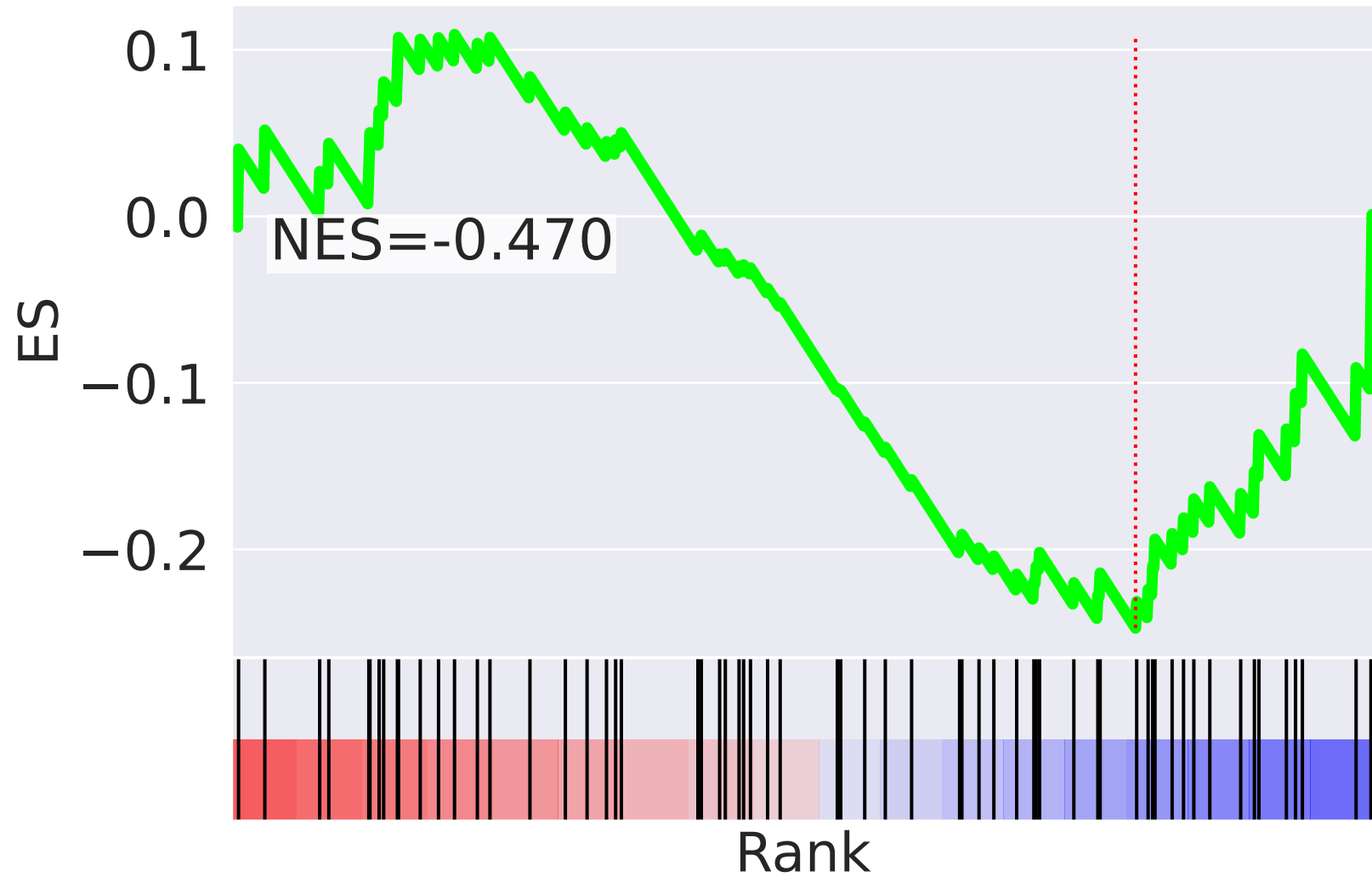
NES		SET
2.759		MAPK cascade (GO:0000165)
2.639		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.625		protein N-linked glycosylation via asparagine (GO:0018279)
2.620		regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
2.600		positive regulation of cell proliferation (GO:0008284)
2.516		multivesicular body assembly (GO:0036258)
2.512		regulation of apoptotic process (GO:0042981)
-2.492		cellular protein modification process (GO:0006464)
2.427		axon guidance (GO:0007411)
2.346		positive regulation of gene expression (GO:0010628)
2.343		mitotic metaphase plate congression (GO:0007080)
2.319		protein phosphorylation (GO:0006468)
2.275		regulation of cellular response to heat (GO:1900034)
2.272		viral budding via host ESCRT complex (GO:0039702)
-2.246		RNA metabolic process (GO:0016070)





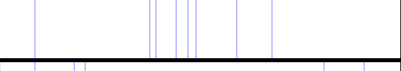

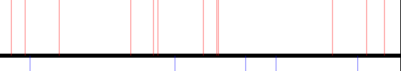

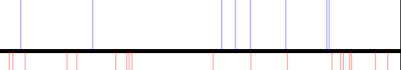
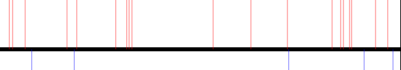




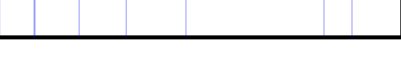
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=93$

mitochondrial translational elongation (GO:0070125)



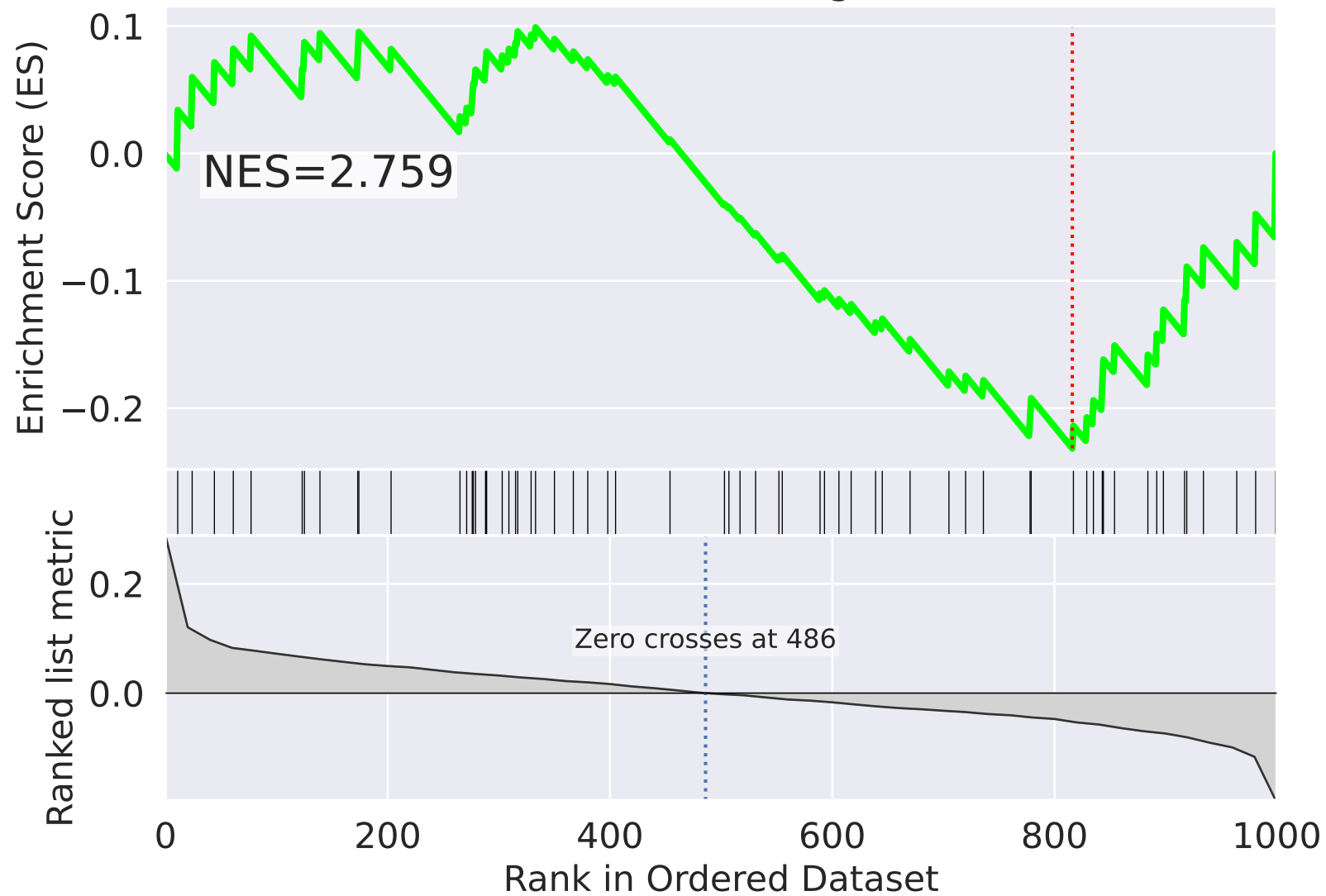
mitochondrial translational elongation (GO:0070125)



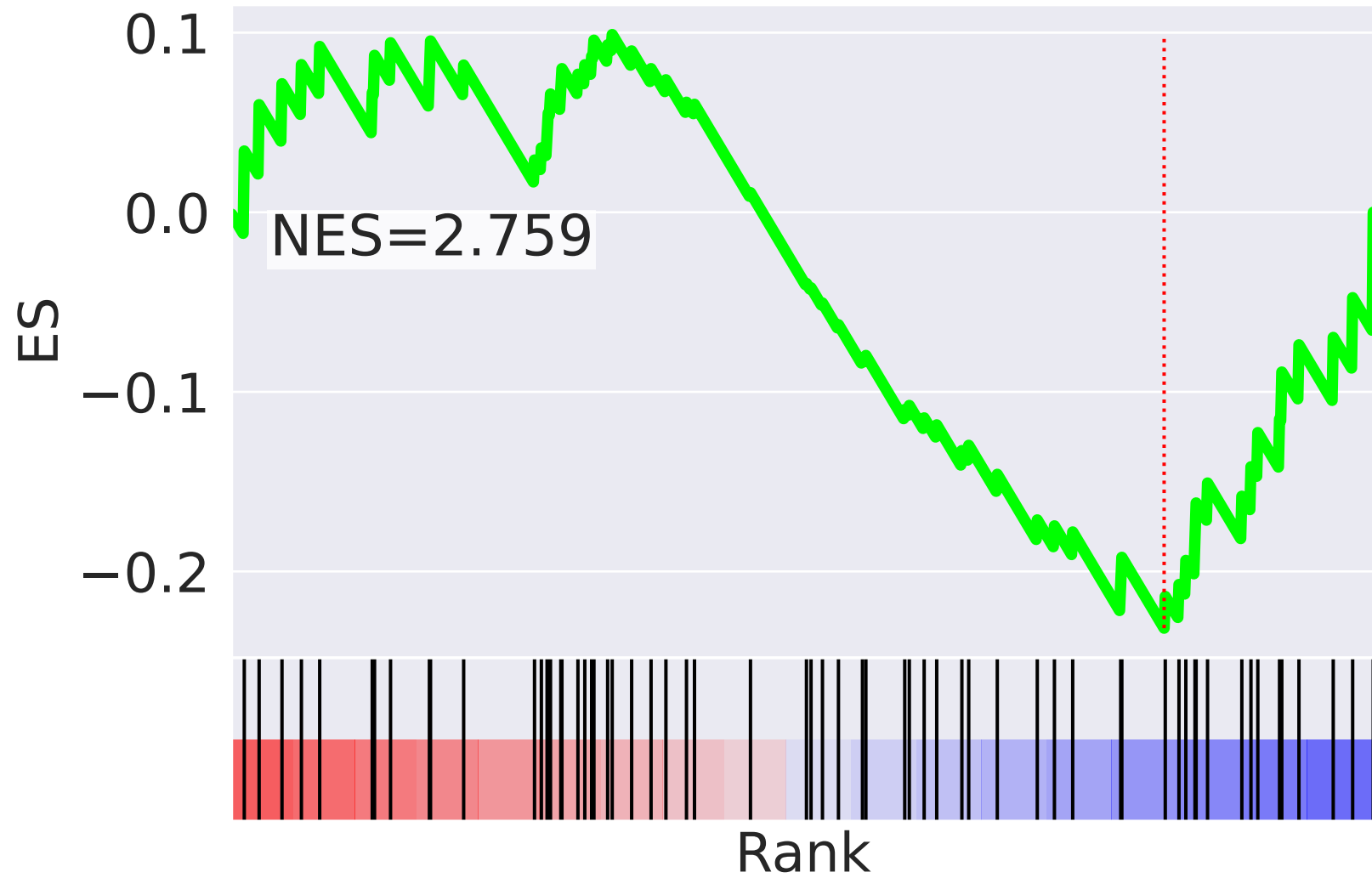
NES		SET
2.725		Golgi organization (GO:0007030)
2.701		ER to Golgi vesicle-mediated transport (GO:0006888)
2.635		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.477		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.246		regulation of cell proliferation (GO:0042127)
-2.245		ERBB2 signaling pathway (GO:0038128)
2.170		mitochondrion organization (GO:0007005)
-2.132		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-2.110		cell-matrix adhesion (GO:0007160)
2.049		negative regulation of cell proliferation (GO:0008285)
-2.024		positive regulation of cell growth (GO:0030307)
-1.971		protein autophosphorylation (GO:0046777)
1.920		DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
-1.903		positive regulation of protein phosphorylation (GO:0001934)
-1.897		Ras protein signal transduction (GO:0007265)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=94$

mitochondrial translational elongation (GO:0070125)



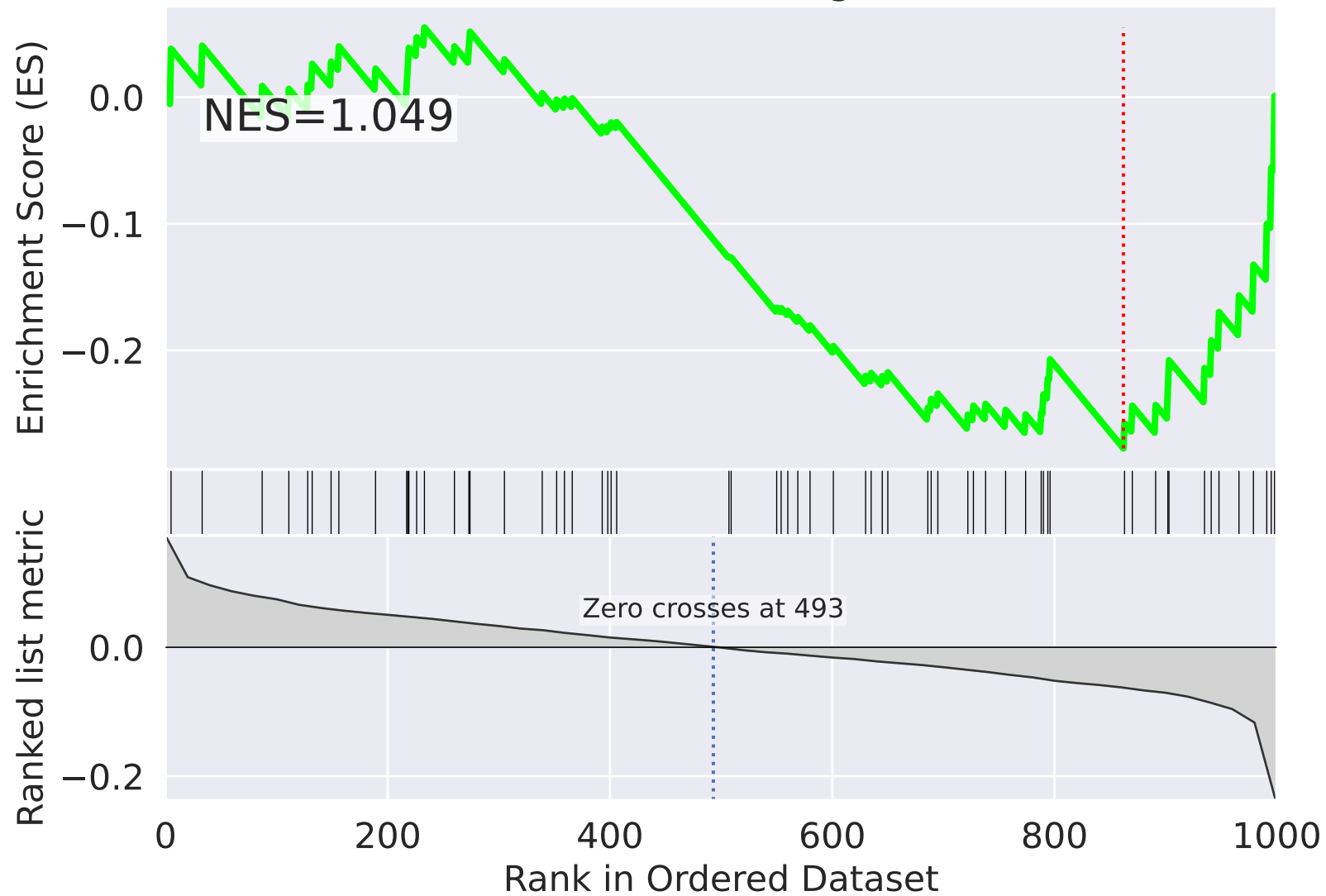
mitochondrial translational elongation (GO:0070125)



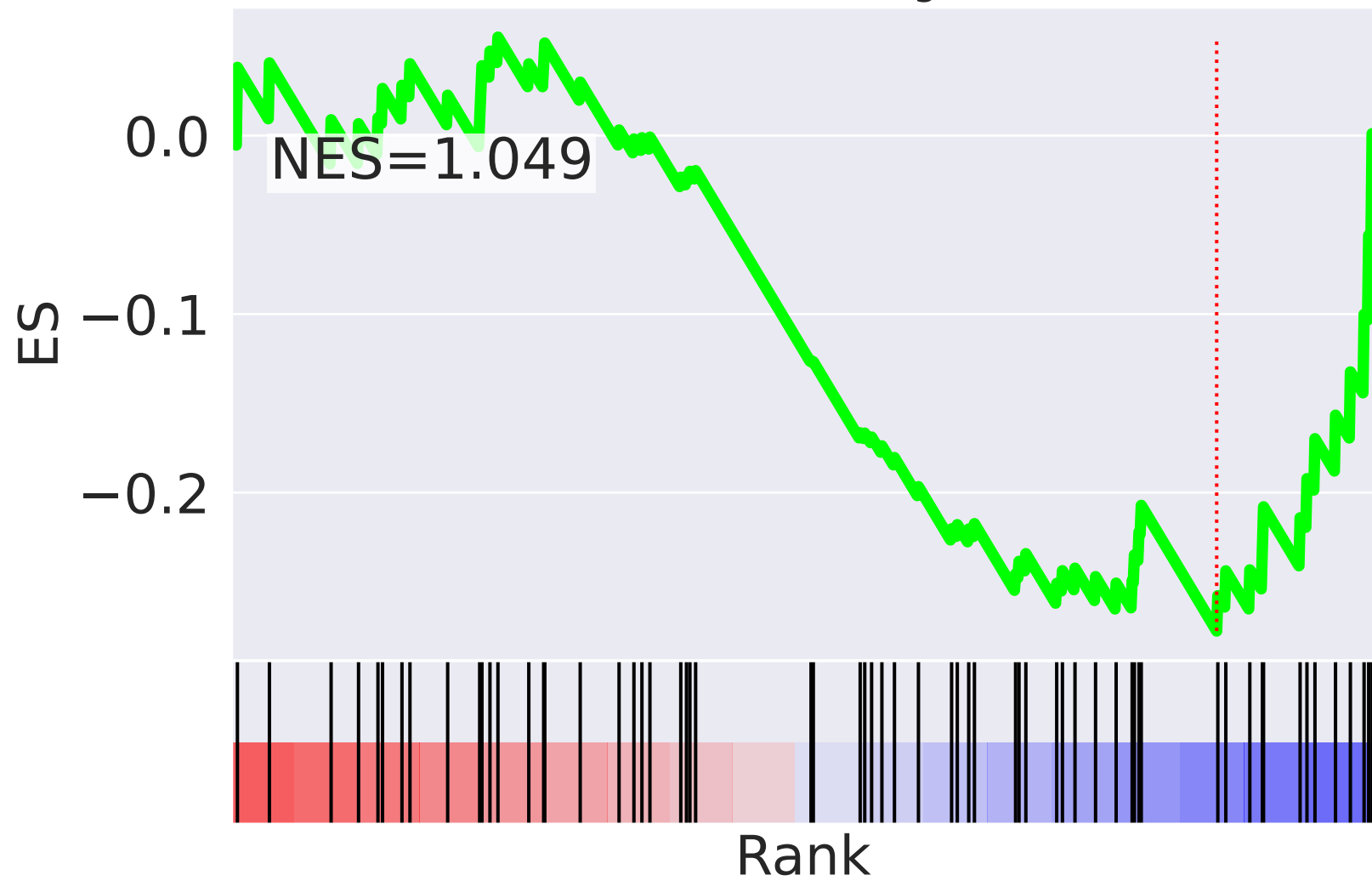
NES		SET
2.759		mitochondrial translational elongation (GO:0070125)
2.637		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.578		mitochondrial translational termination (GO:0070126)
-2.156		cellular respiration (GO:0045333)
-2.007		intracellular transport of virus (GO:0075733)
-1.974		mitochondrial respiratory chain complex IV assembly (GO:0033617)
-1.952		inflammatory response (GO:0006954)
1.863		tricarboxylic acid cycle (GO:0006099)
1.857		positive regulation of cytokinesis (GO:0032467)
-1.833		mRNA export from nucleus (GO:0006406)
1.831		substantia nigra development (GO:0021762)
-1.824		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-1.801		apoptotic process (GO:0006915)
-1.793		RNA export from nucleus (GO:0006405)
-1.778		protein deubiquitination (GO:0016579)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=95$

mitochondrial translational elongation (GO:0070125)

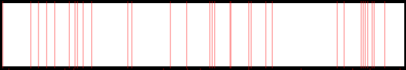



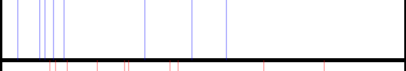
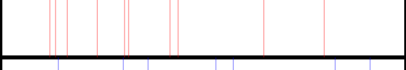
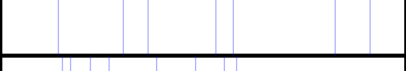
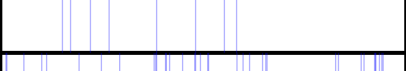
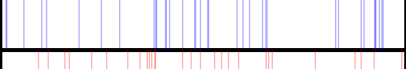
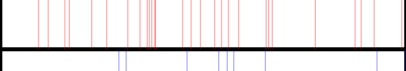
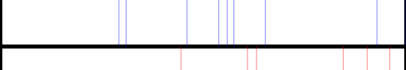
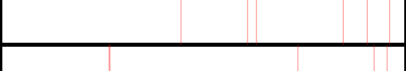

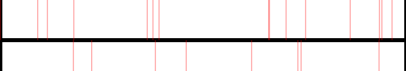
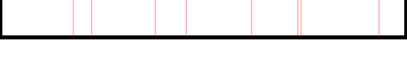


mitochondrial translational elongation (GO:0070125)



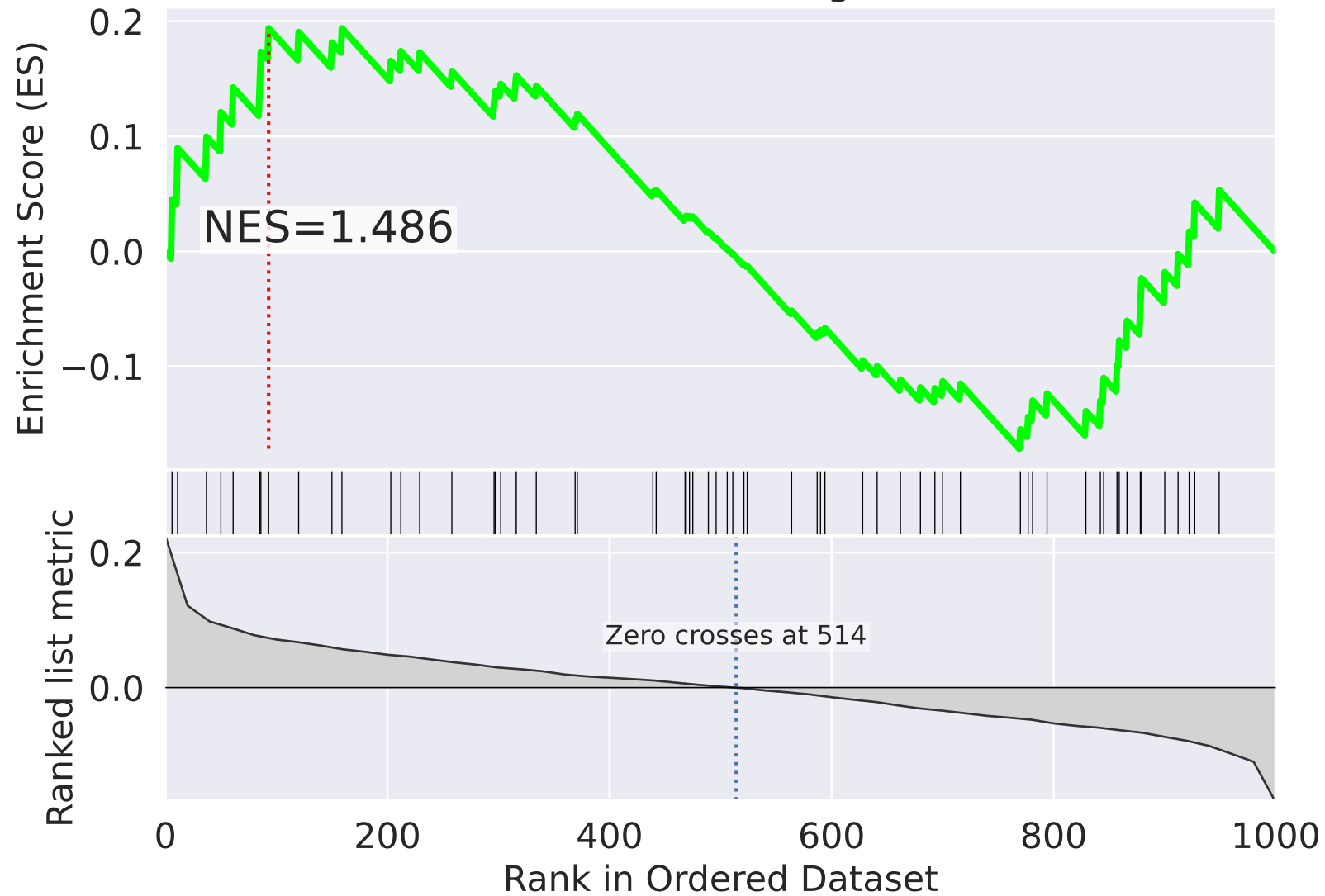
NES

SET

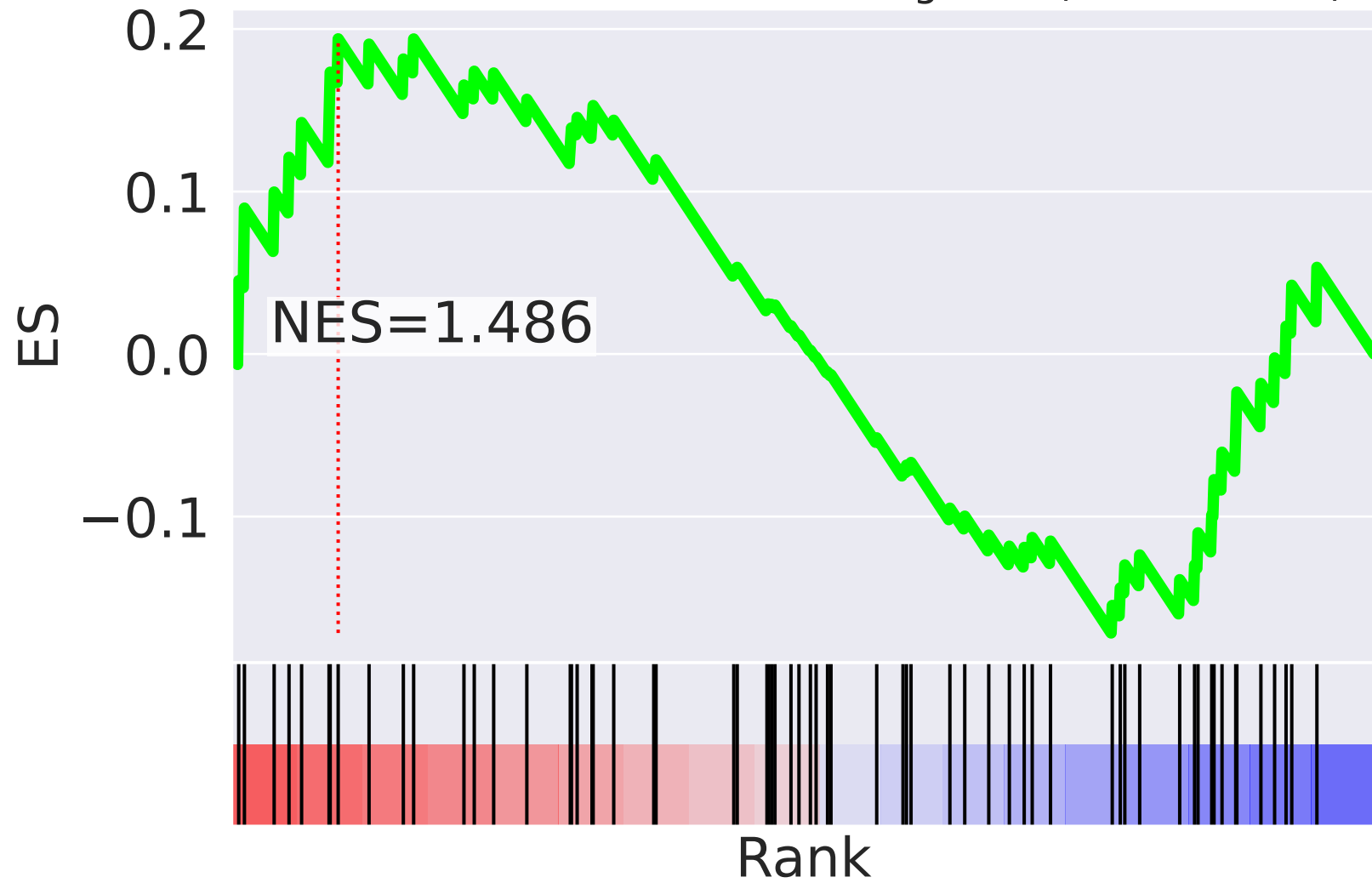
3.605		positive regulation of cell proliferation (GO:0008284)
2.609		positive regulation of gene expression (GO:0010628)
2.433		small molecule metabolic process (GO:0044281)
-2.417		regulation of cell motility (GO:2000145)
-2.357		substantia nigra development (GO:0021762)
2.212		multivesicular body assembly (GO:0036258)
-2.200		fibroblast growth factor receptor signaling pathway (GO:0008543)
-2.176		nervous system development (GO:0007399)
-2.149		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
2.138		negative regulation of apoptotic process (GO:0043066)
-2.053		tRNA aminoacylation for protein translation (GO:0006418)
2.004		iron-sulfur cluster assembly (GO:0016226)
1.989		regulation of cell growth (GO:0001558)
1.939		positive regulation of apoptotic process (GO:0043065)
1.883		regulation of apoptotic process (GO:0042981)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=96$

mitochondrial translational elongation (GO:0070125)





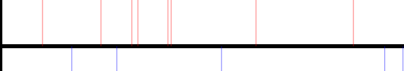
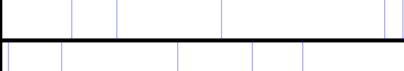

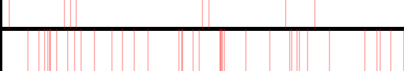
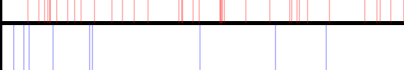


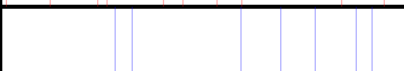





mitochondrial translational elongation (GO:0070125)



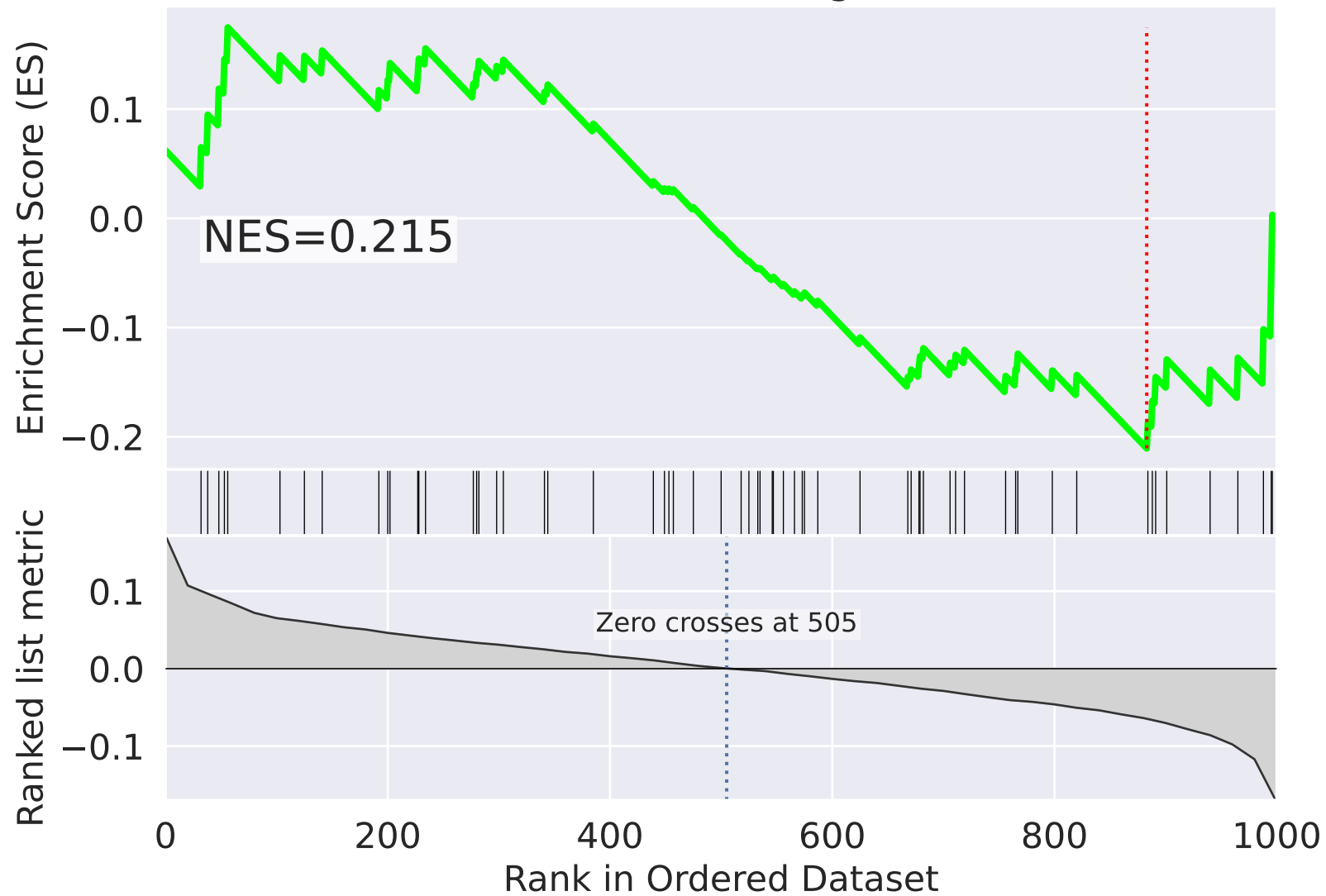
NES

SET

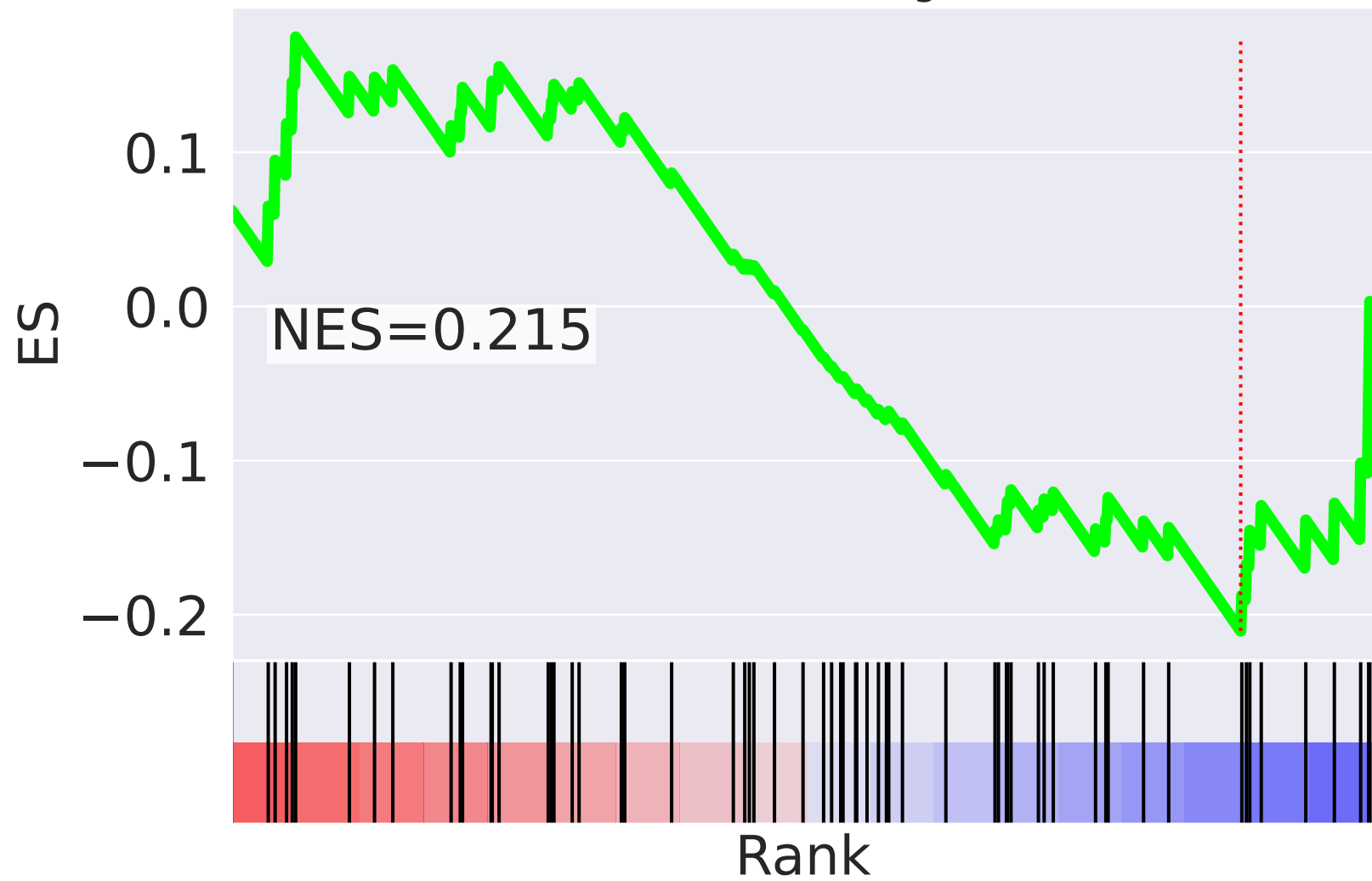
-2.803		ciliary basal body docking (GO:0097711)
-2.774		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.457		peptidyl-serine phosphorylation (GO:0018105)
2.300		protein K48-linked ubiquitination (GO:0070936)
2.278		nucleus organization (GO:0006997)
-2.256		rRNA processing (GO:0006364)
-2.246		peptidyl-threonine phosphorylation (GO:0018107)
2.218		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.192		positive regulation of transcription, DNA-templated (GO:0045893)
-2.186		retrograde transport, endosome to Golgi (GO:0042147)
-2.184		T cell costimulation (GO:0031295)
2.175		protein polyubiquitination (GO:0000209)
-2.158		movement of cell or subcellular component (GO:0006928)
-2.150		nervous system development (GO:0007399)
2.141		regulation of lipid metabolic process (GO:0019216)




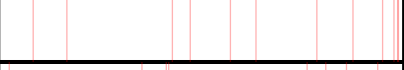


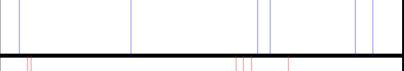


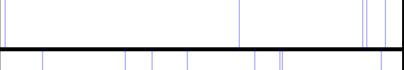
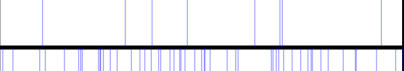
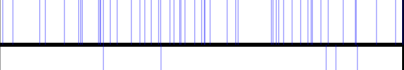
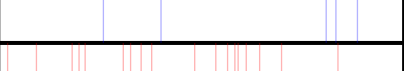
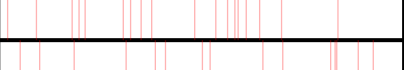

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=97$

mitochondrial translational elongation (GO:0070125)



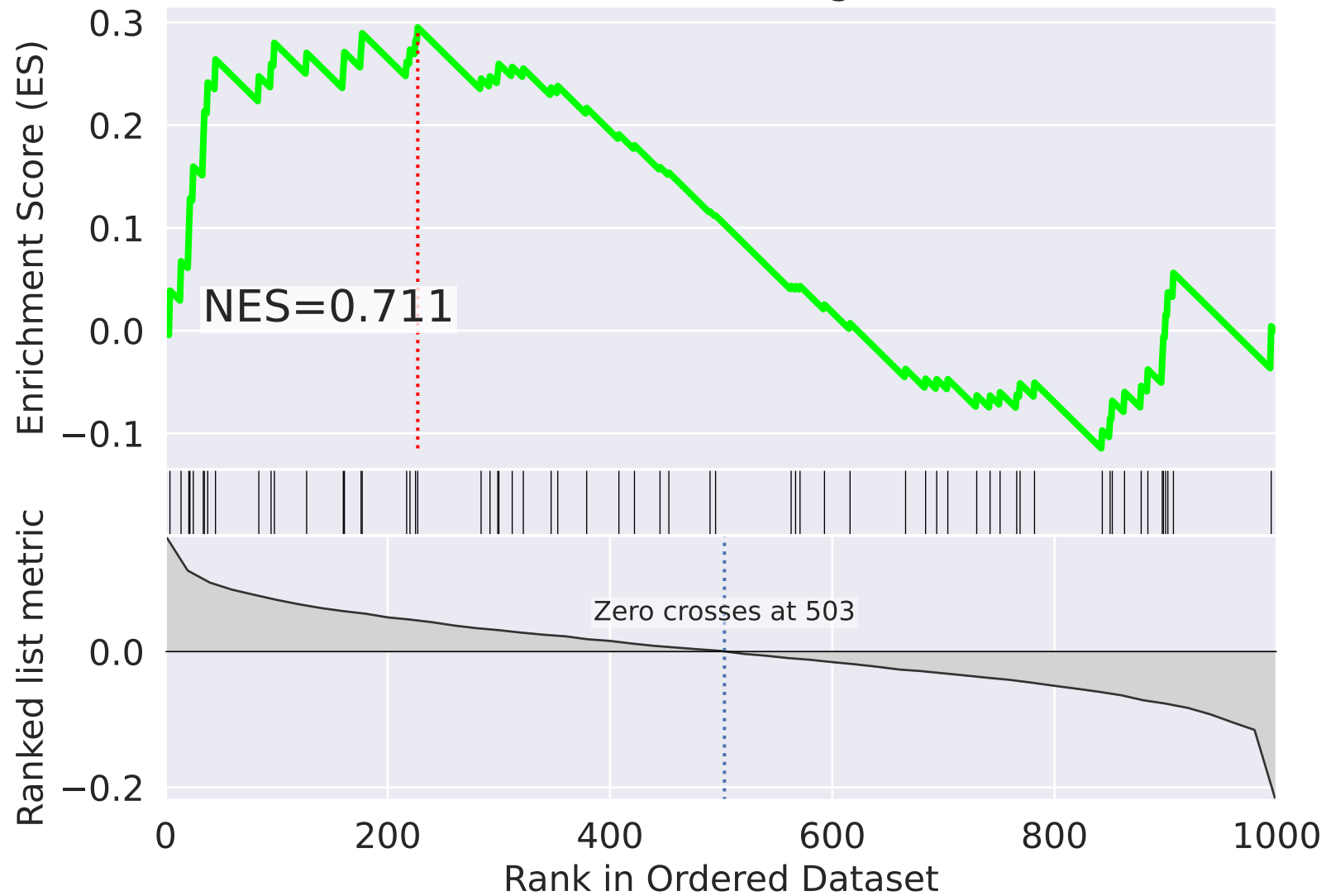
mitochondrial translational elongation (GO:0070125)



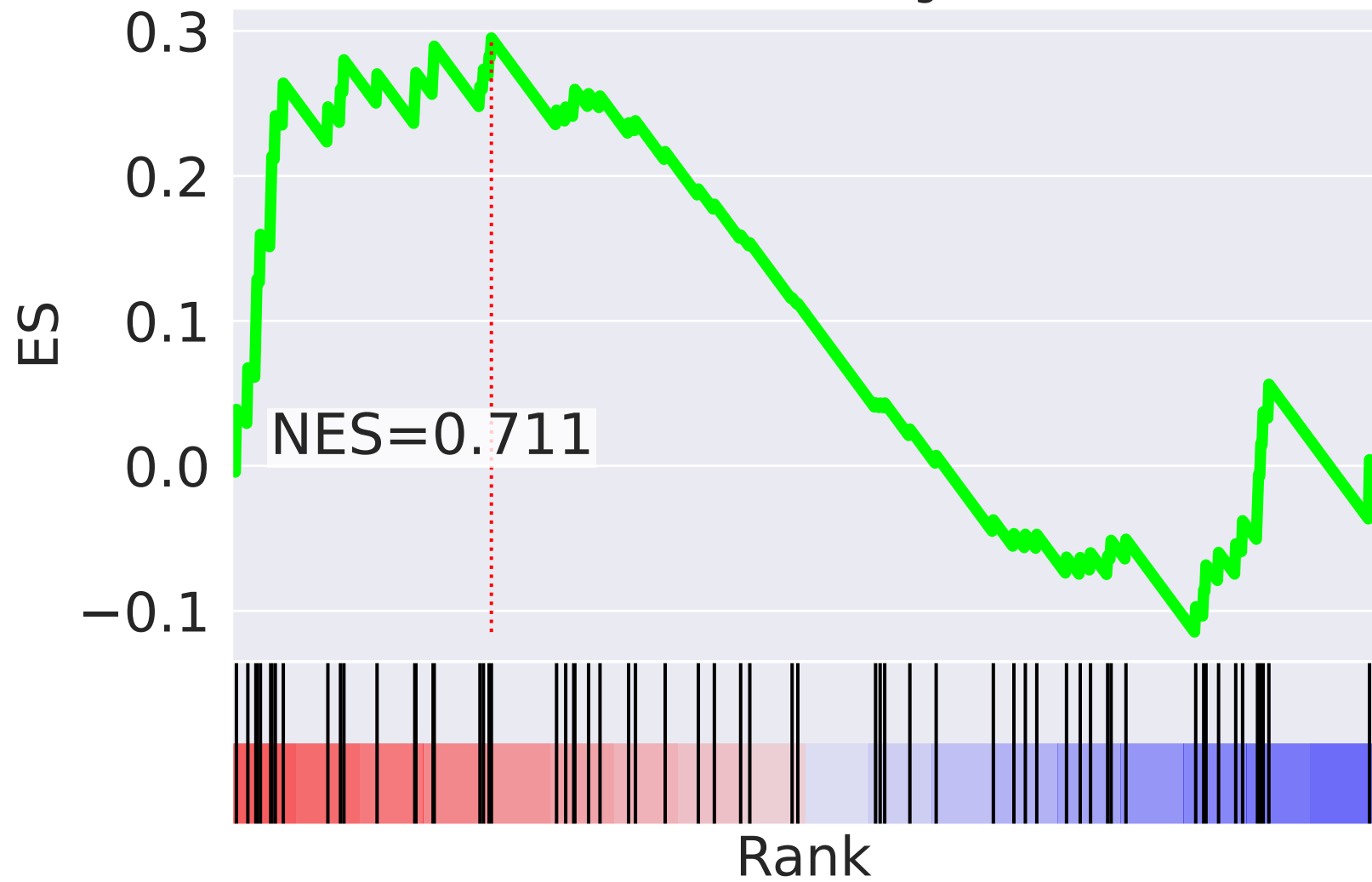
NES		SET
2.577		mitotic metaphase plate congression (GO:0007080)
-2.451		protein polyubiquitination (GO:0000209)
2.362		ESCRT III complex disassembly (GO:1904903)
2.185		regulation of macroautophagy (GO:0016241)
2.098		nucleus organization (GO:0006997)
2.071		positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)
-2.040		positive regulation of gene expression, epigenetic (GO:0045815)
2.032		protein targeting to mitochondrion (GO:0006626)
-2.002		regulation of cell motility (GO:2000145)
-2.002		protein N-linked glycosylation (GO:0006487)
-1.954		tRNA modification (GO:0006400)
-1.950		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-1.944		DNA damage checkpoint (GO:0000077)
1.907		G2/M transition of mitotic cell cycle (GO:0000086)
1.906		positive regulation of apoptotic process (GO:0043065)





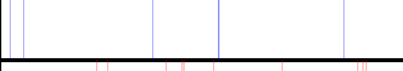
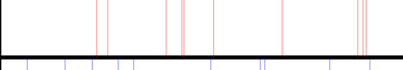

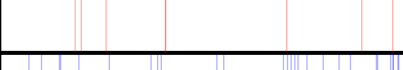
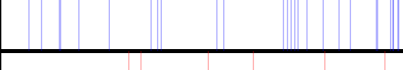


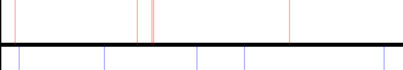


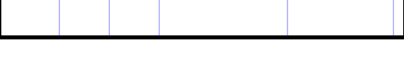
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=98$

mitochondrial translational elongation (GO:0070125)



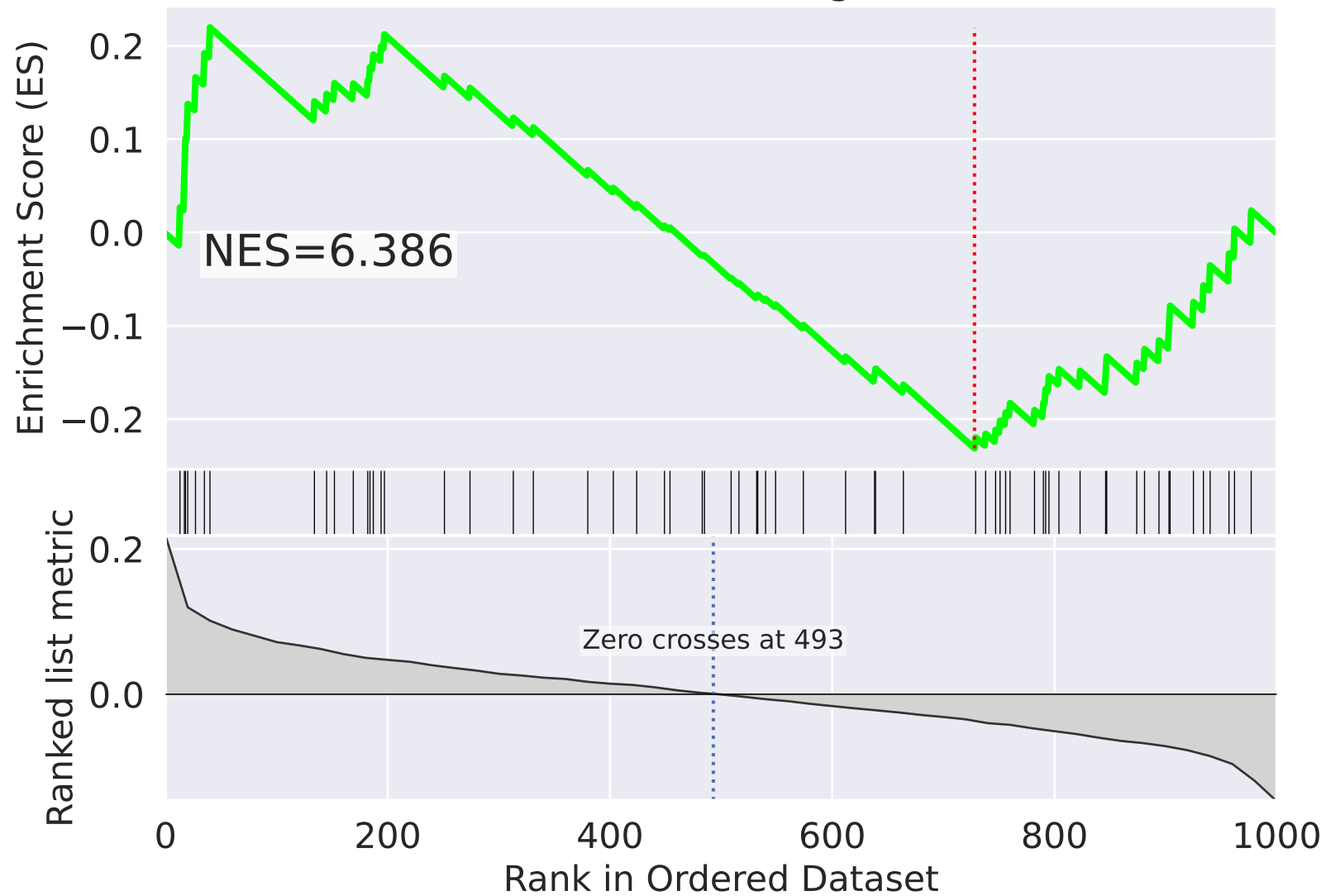
mitochondrial translational elongation (GO:0070125)



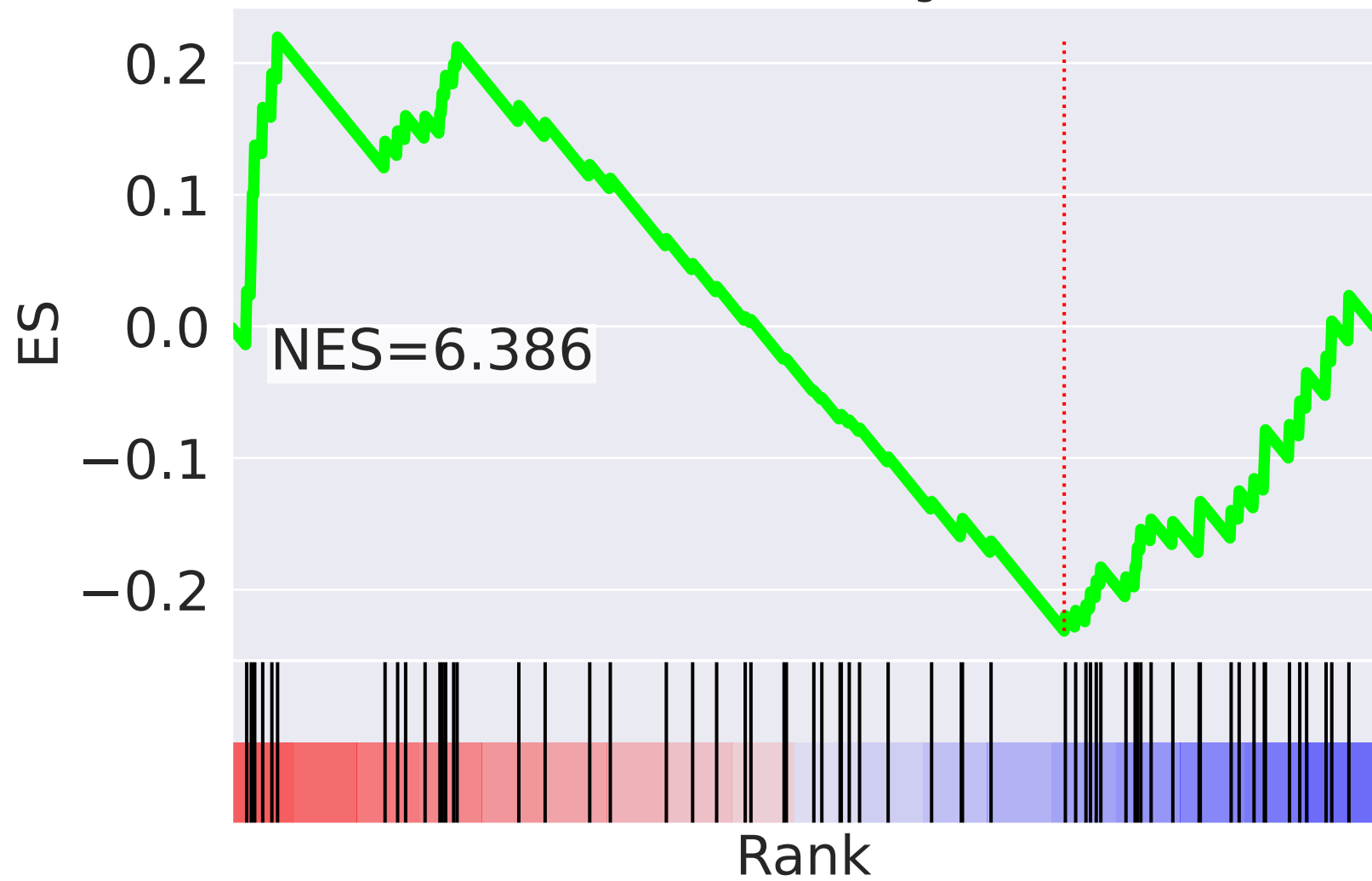
NES		SET
2.346		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-2.245		protein homooligomerization (GO:0051260)
-2.224		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
2.218		leukocyte migration (GO:0050900)
-2.119		mRNA processing (GO:0006397)
2.083		endosomal transport (GO:0016197)
-1.993		protein dephosphorylation (GO:0006470)
1.983		Ras protein signal transduction (GO:0007265)
-1.950		signal transduction (GO:0007165)
1.945		protein K11-linked ubiquitination (GO:0070979)
-1.919		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
1.918		positive regulation of type I interferon production (GO:0032481)
-1.917		small molecule metabolic process (GO:0044281)
-1.867		positive regulation of viral genome replication (GO:0045070)
-1.848		regulation of cell motility (GO:2000145)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=99$

mitochondrial translational elongation (GO:0070125)

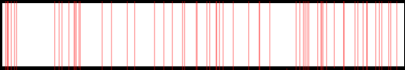
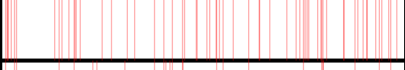
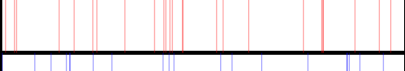
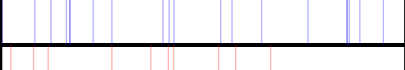
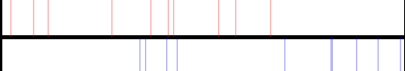






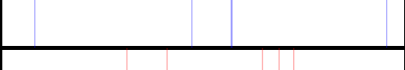





mitochondrial translational elongation (GO:0070125)



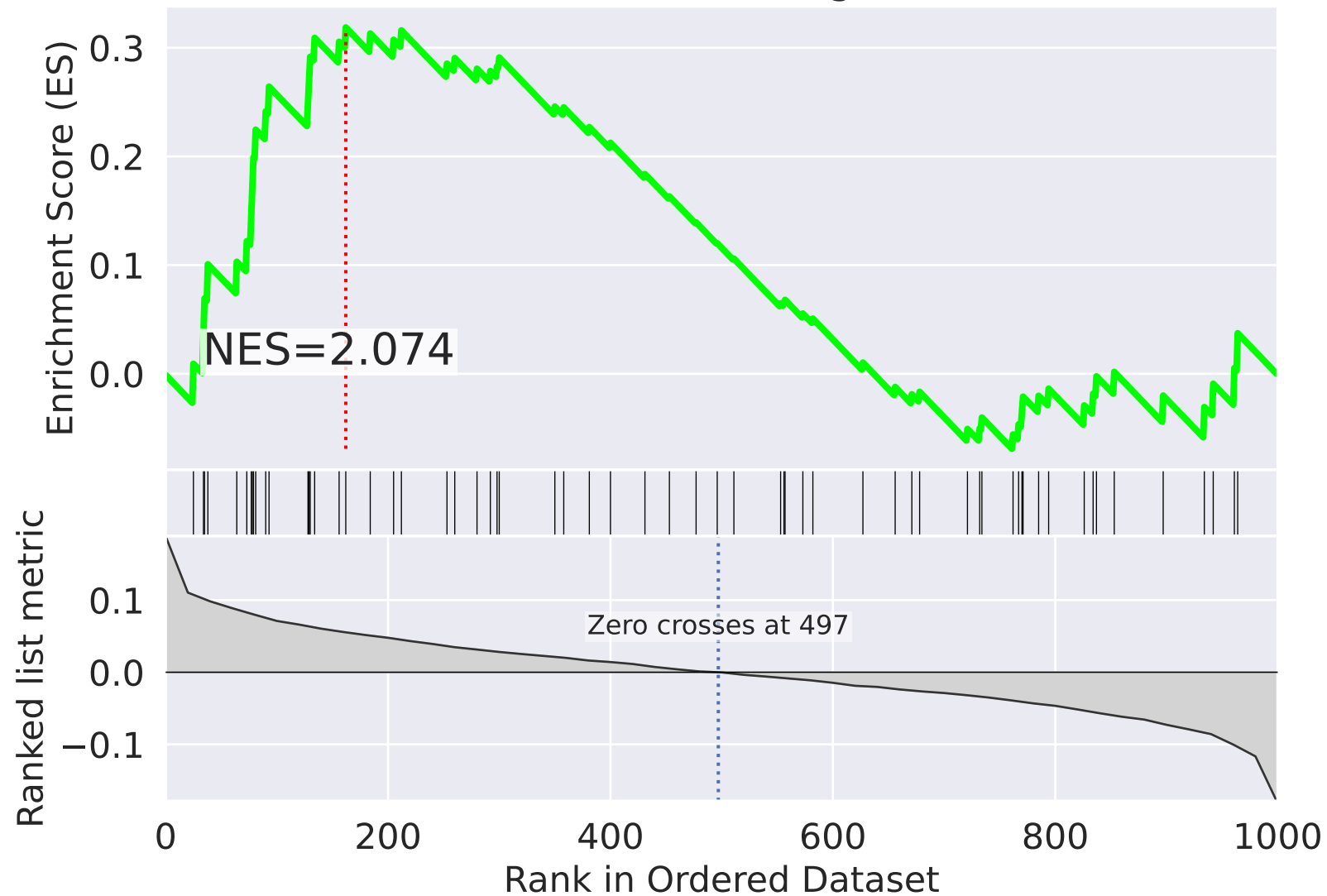
NES

SET

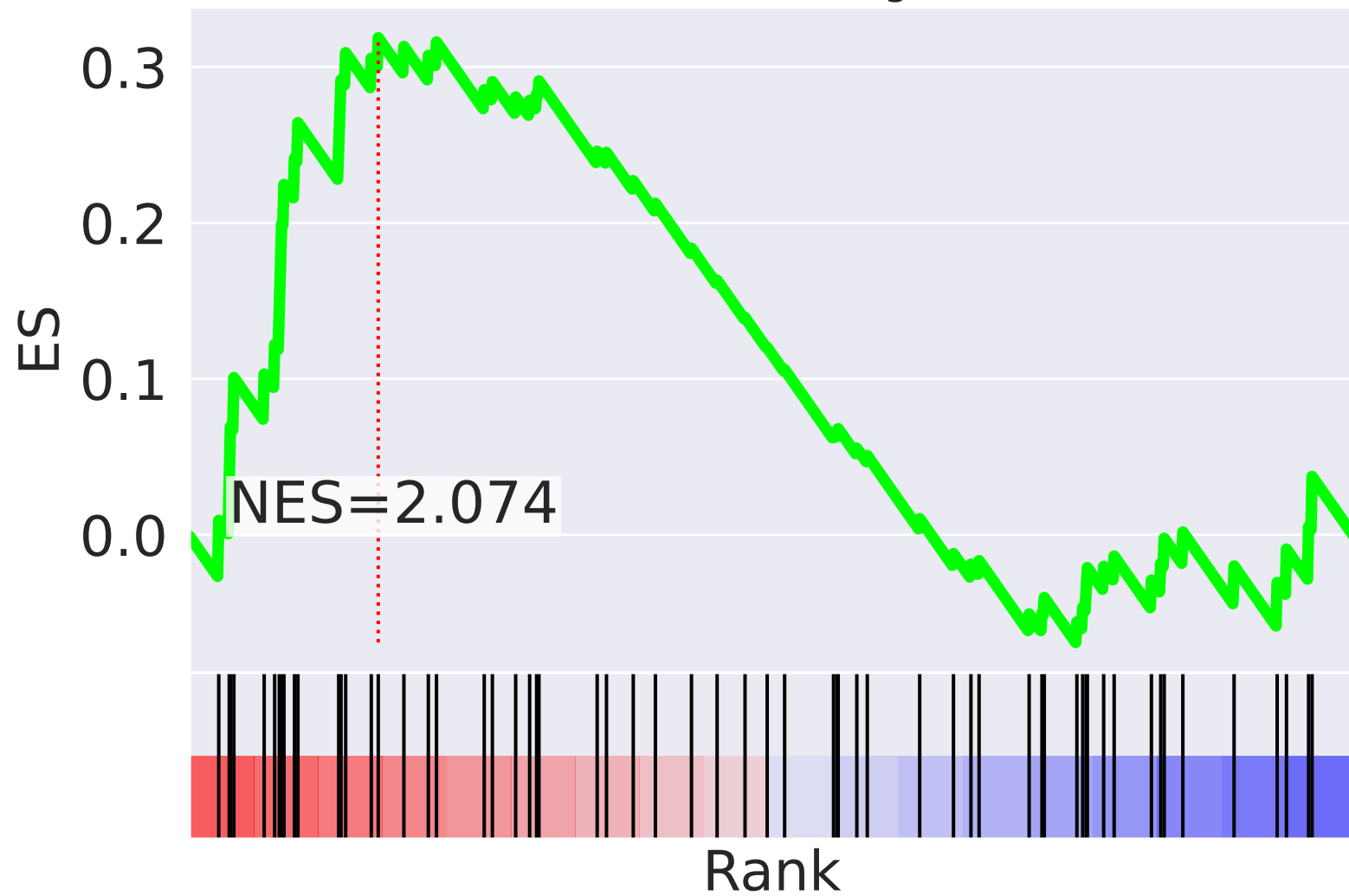
6.386		mitochondrial translational elongation (GO:0070125)
6.243		mitochondrial translational termination (GO:0070126)
2.787		mitochondrial translation (GO:0032543)
-2.584		cellular response to DNA damage stimulus (GO:0006974)
2.532		protein polyubiquitination (GO:0000209)
-2.316		endosomal transport (GO:0016197)
-2.238		positive regulation of cell growth (GO:0030307)
2.104		negative regulation of protein kinase activity (GO:0006469)
-2.087		mitochondrial respiratory chain complex IV assembly (GO:0033617)
2.058		transcription from mitochondrial promoter (GO:0006390)
-2.044		response to ionizing radiation (GO:0010212)
-2.033		nervous system development (GO:0007399)
-2.030		telomere maintenance via recombination (GO:0000722)
1.980		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-1.979		heart development (GO:0007507)

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=100$

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)



NES		SET
2.953		cellular response to DNA damage stimulus (GO:0006974)
2.860		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)
-2.704		Golgi organization (GO:0007030)
2.266		positive regulation of protein catabolic process (GO:0045732)
2.235		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.152		phosphatidylinositol biosynthetic process (GO:0006661)
2.119		execution phase of apoptosis (GO:0097194)
-2.096		positive regulation of cell proliferation (GO:0008284)
2.086		double-strand break repair via nonhomologous end joining (GO:0006303)
2.074		mitochondrial translational elongation (GO:0070125)
-2.019		ERBB2 signaling pathway (GO:0038128)
-1.991		phosphatidylinositol-mediated signaling (GO:0048015)
1.960		ephrin receptor signaling pathway (GO:0048013)
-1.908		insulin receptor signaling pathway (GO:0008286)
1.897		negative regulation of translation (GO:0017148)