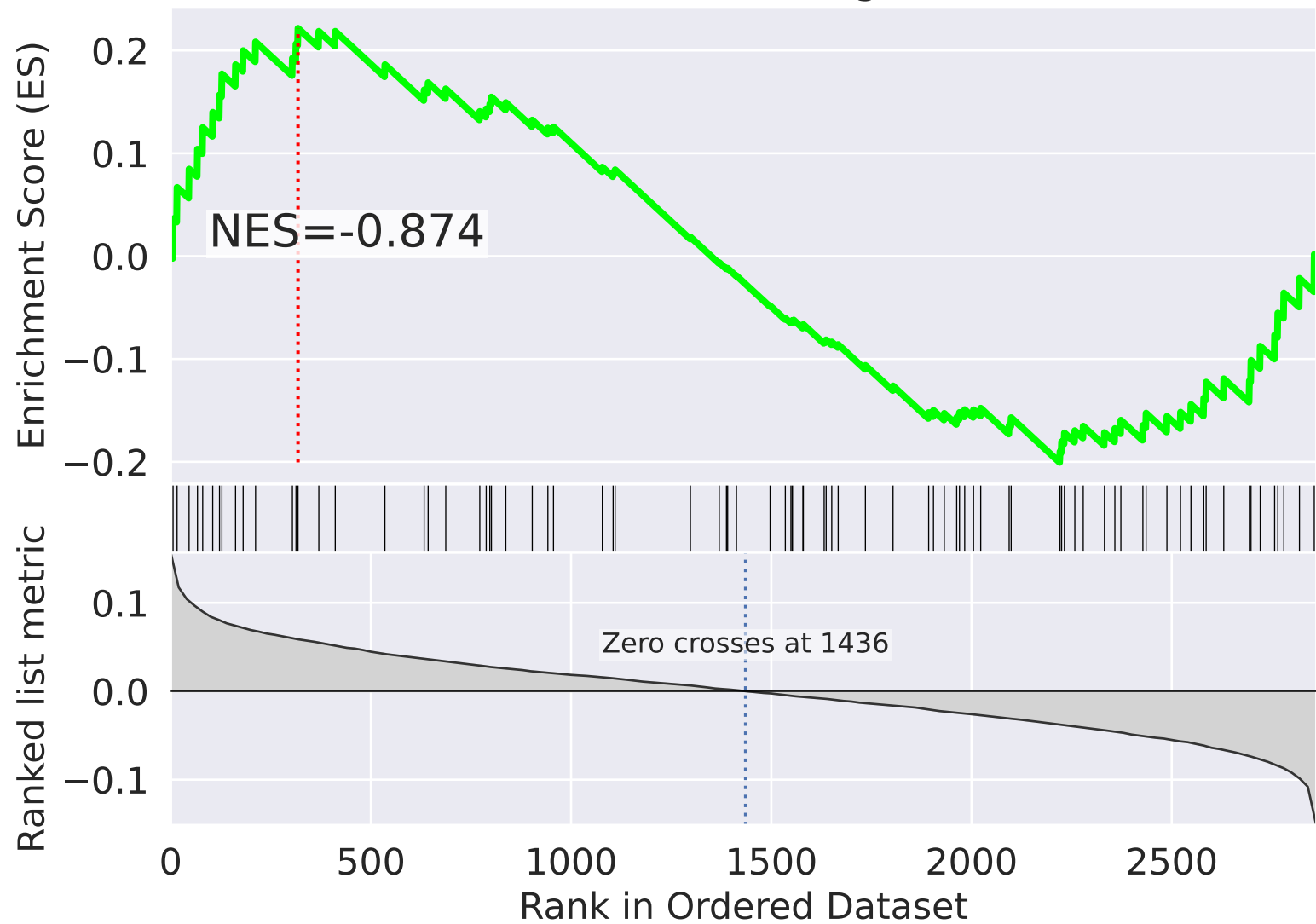
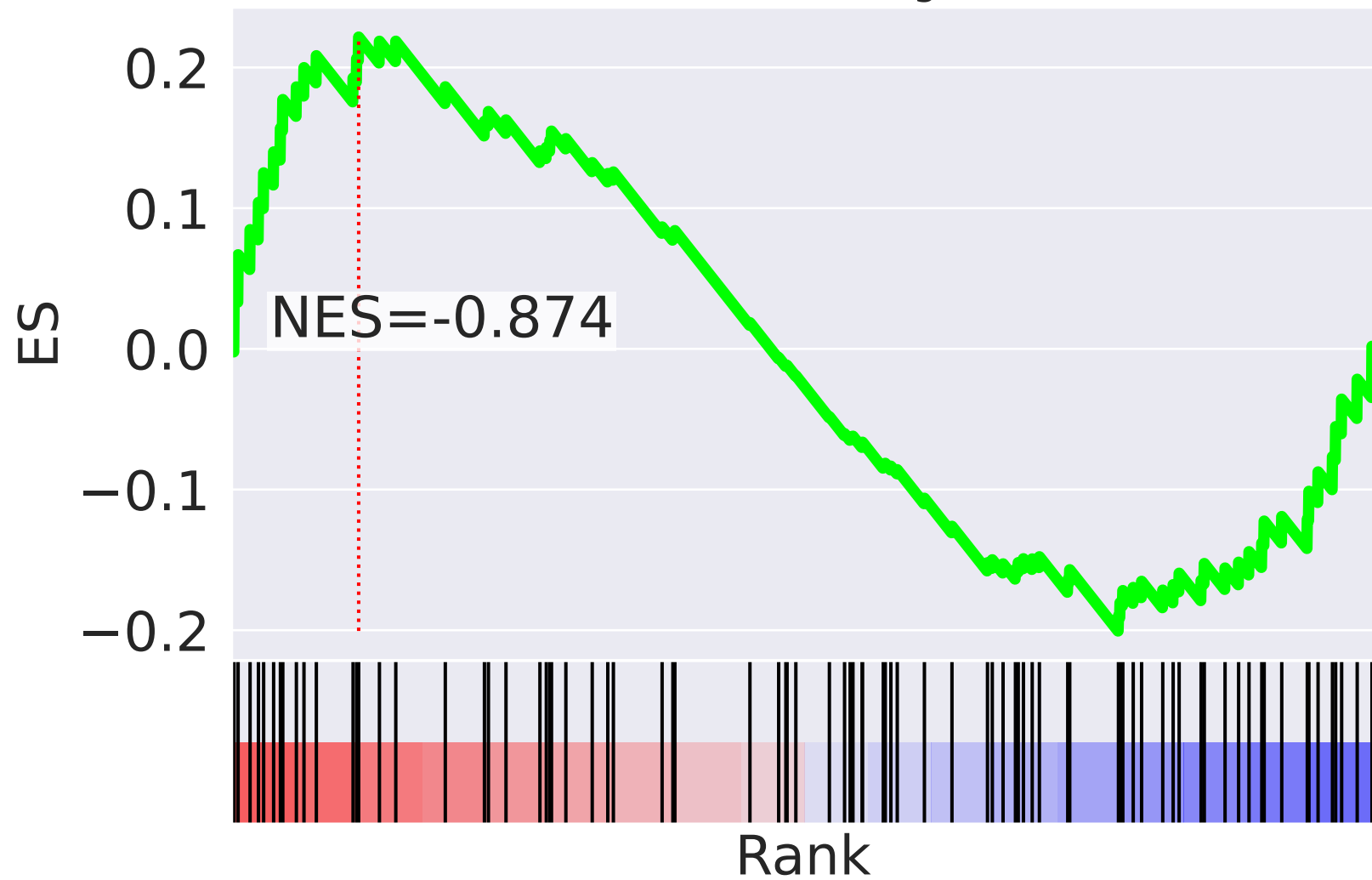


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=1$

# mitochondrial translational elongation (GO:0070125)

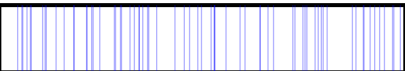


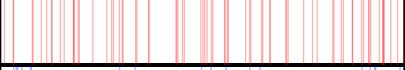
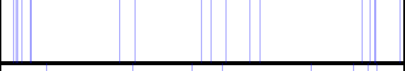

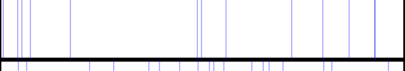
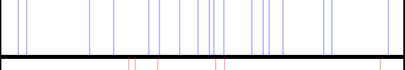
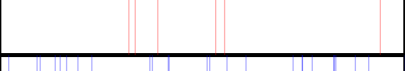


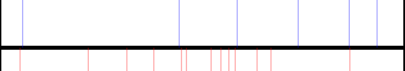


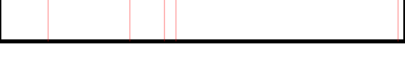


mitochondrial translational elongation (GO:0070125)



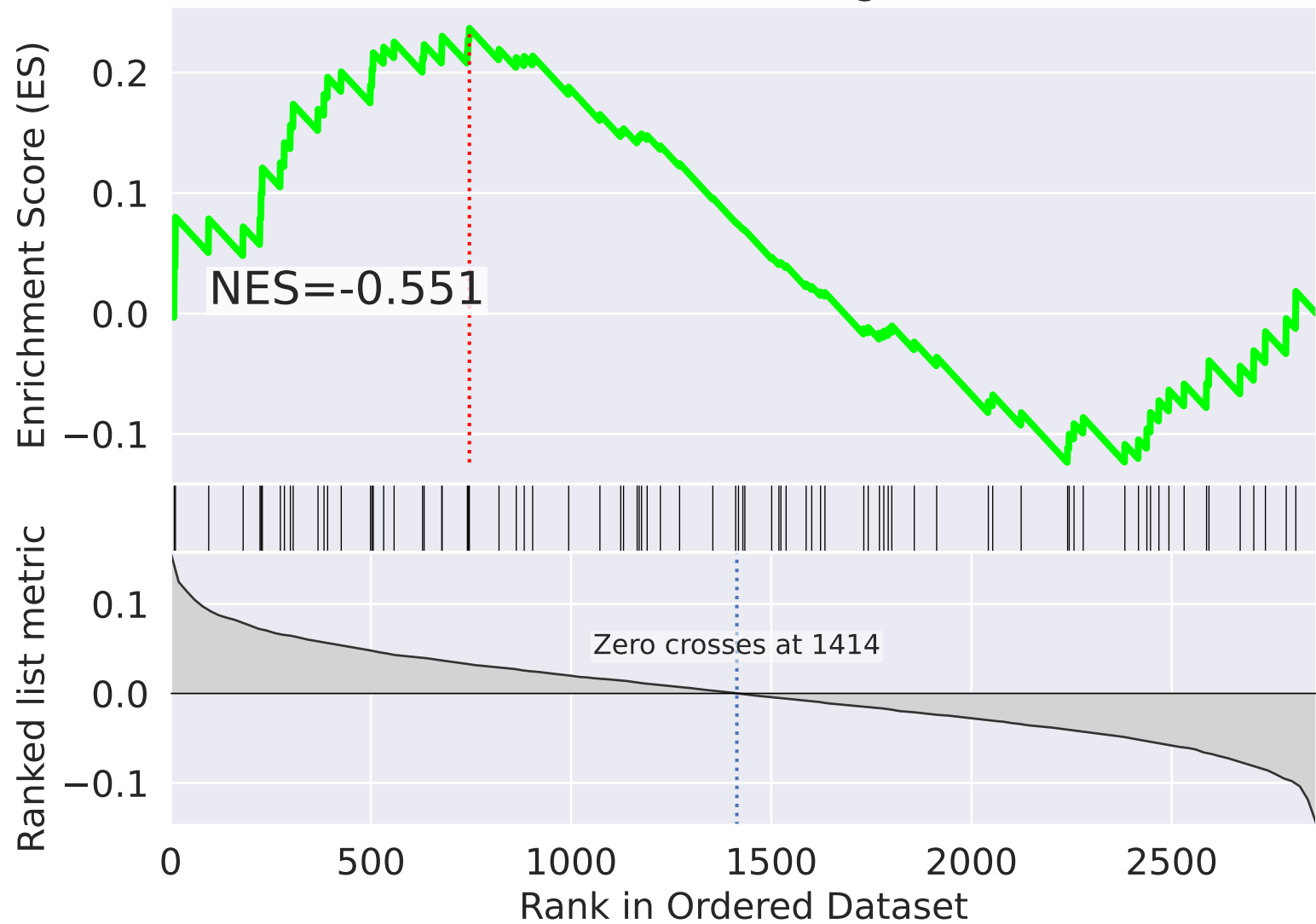
NES

SET

-3.372		transcription initiation from RNA polymerase II promoter (GO:0006367)
-3.032		transcription initiation from RNA polymerase I promoter (GO:0006361)
-3.032		transcription elongation from RNA polymerase I promoter (GO:0006362)
2.950		regulation of transcription, DNA-templated (GO:0006355)
-2.922		termination of RNA polymerase I transcription (GO:0006363)
-2.911		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
-2.807		nucleotide-excision repair, preincision complex assembly (GO:0006294)
-2.661		CENP-A containing nucleosome assembly (GO:0034080)
2.600		humoral immune response (GO:0006959)
-2.594		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.521		negative regulation of cell cycle arrest (GO:0071157)
-2.507		mitotic DNA replication checkpoint (GO:0033314)
2.473		transcription from RNA polymerase III promoter (GO:0006383)
2.385		heart development (GO:0007507)
2.362		regulation of telomere maintenance (GO:0032204)

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

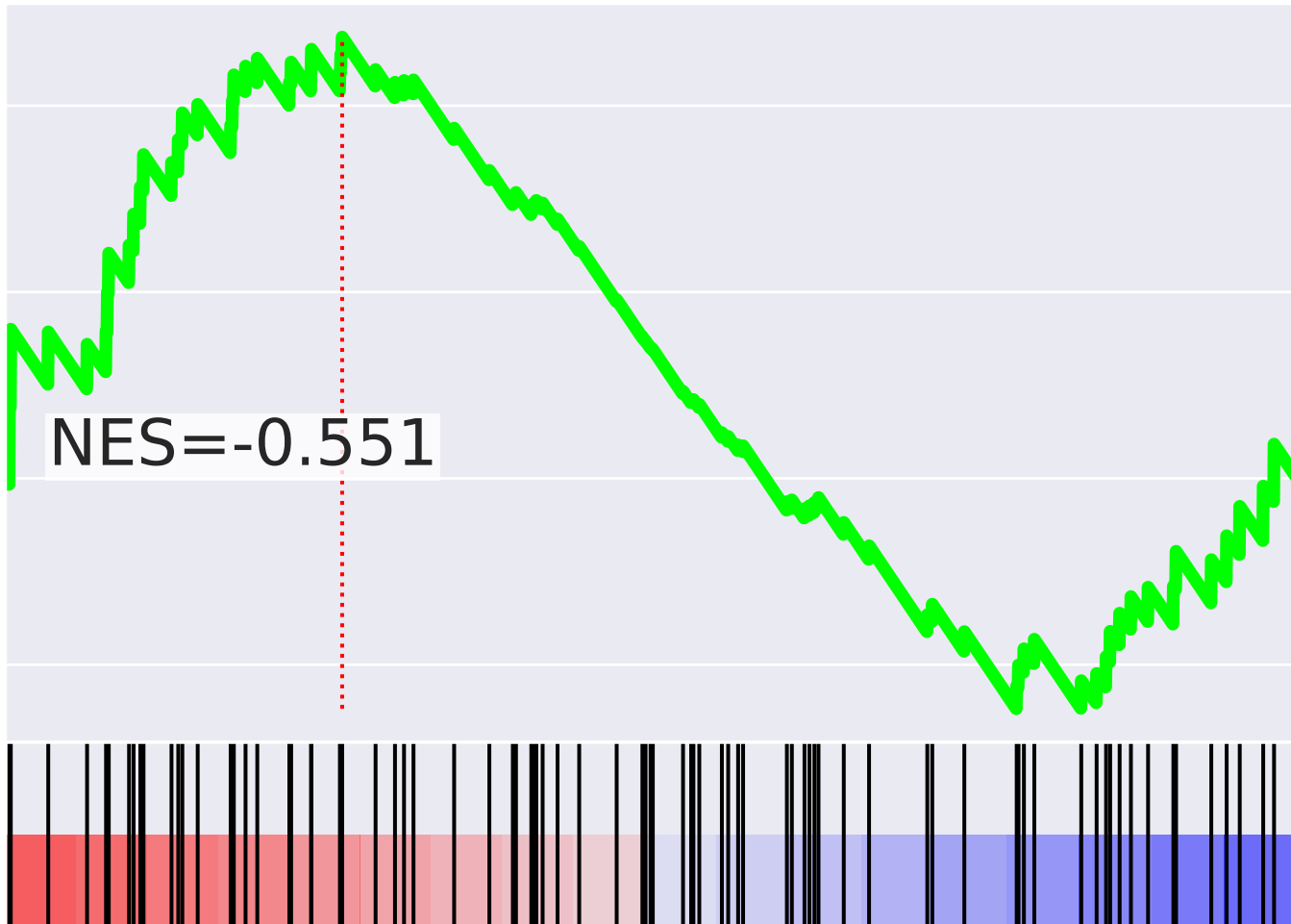
0.1

0.0

-0.1

NES=-0.551

Rank

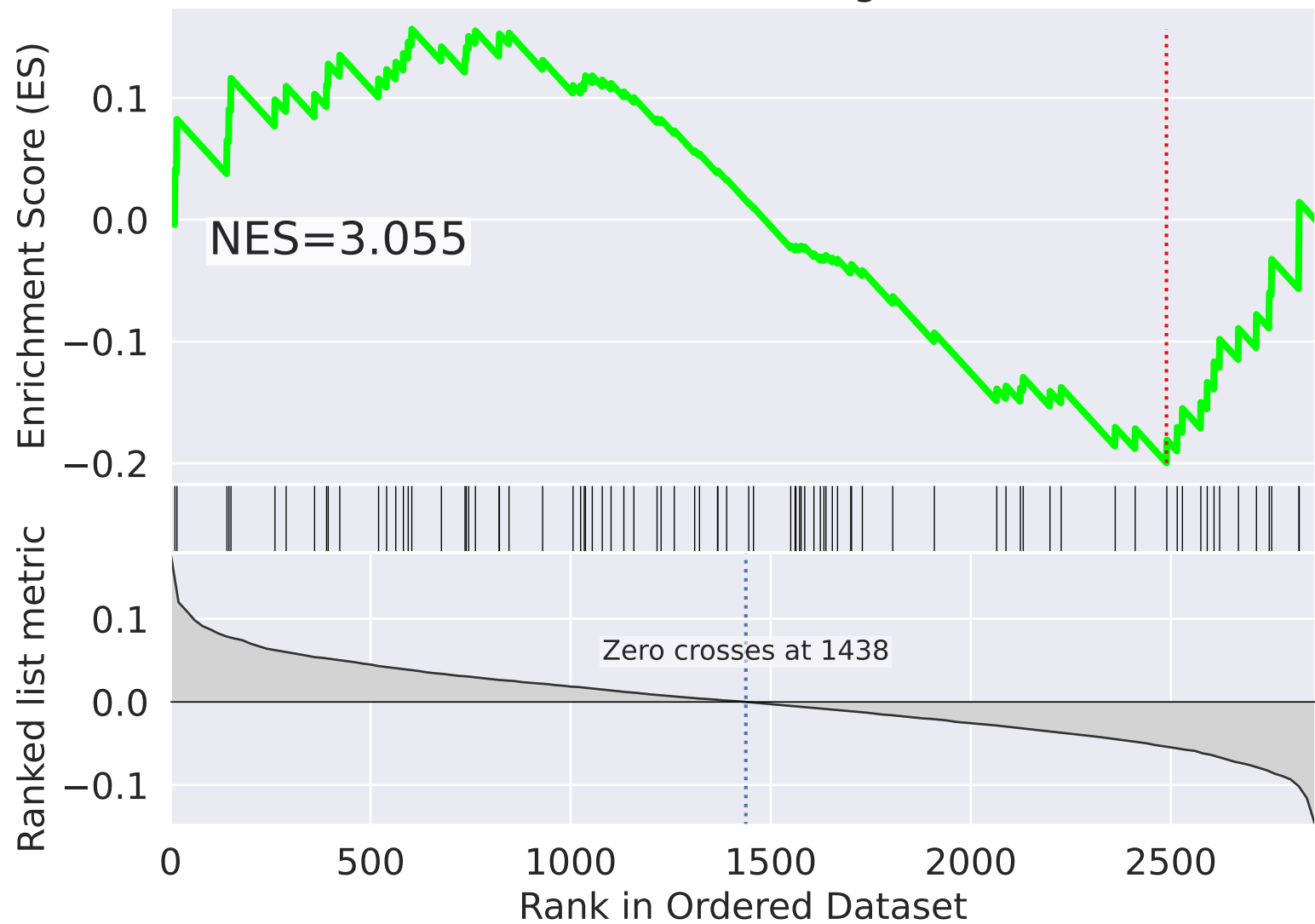


NES	SET
4.369	post-translational protein modification (GO:0043687)
4.295	regulation of cellular amino acid metabolic process (GO:0006521)
4.185	transmembrane transport (GO:0055085)
4.179	negative regulation of canonical Wnt signaling pathway (GO:0090090)
4.016	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
4.004	anaphase-promoting complex-dependent catabolic process (GO:0031145)
3.952	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
3.940	protein polyubiquitination (GO:0000209)
3.929	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
3.839	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
3.721	RNA splicing (GO:0008380)
3.692	regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
3.659	proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
3.610	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
3.603	mRNA export from nucleus (GO:0006406)

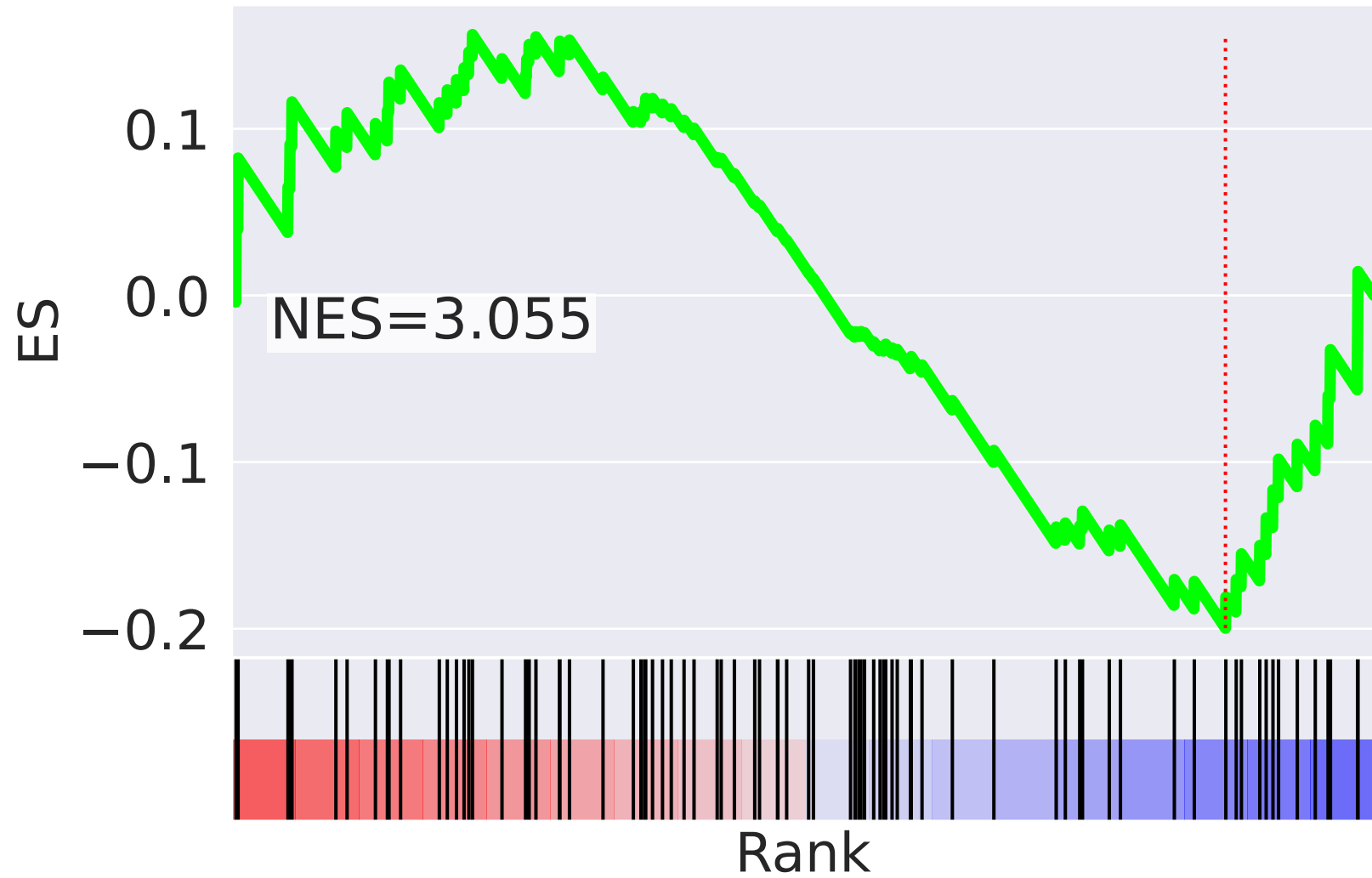


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=3$

# mitochondrial translational elongation (GO:0070125)



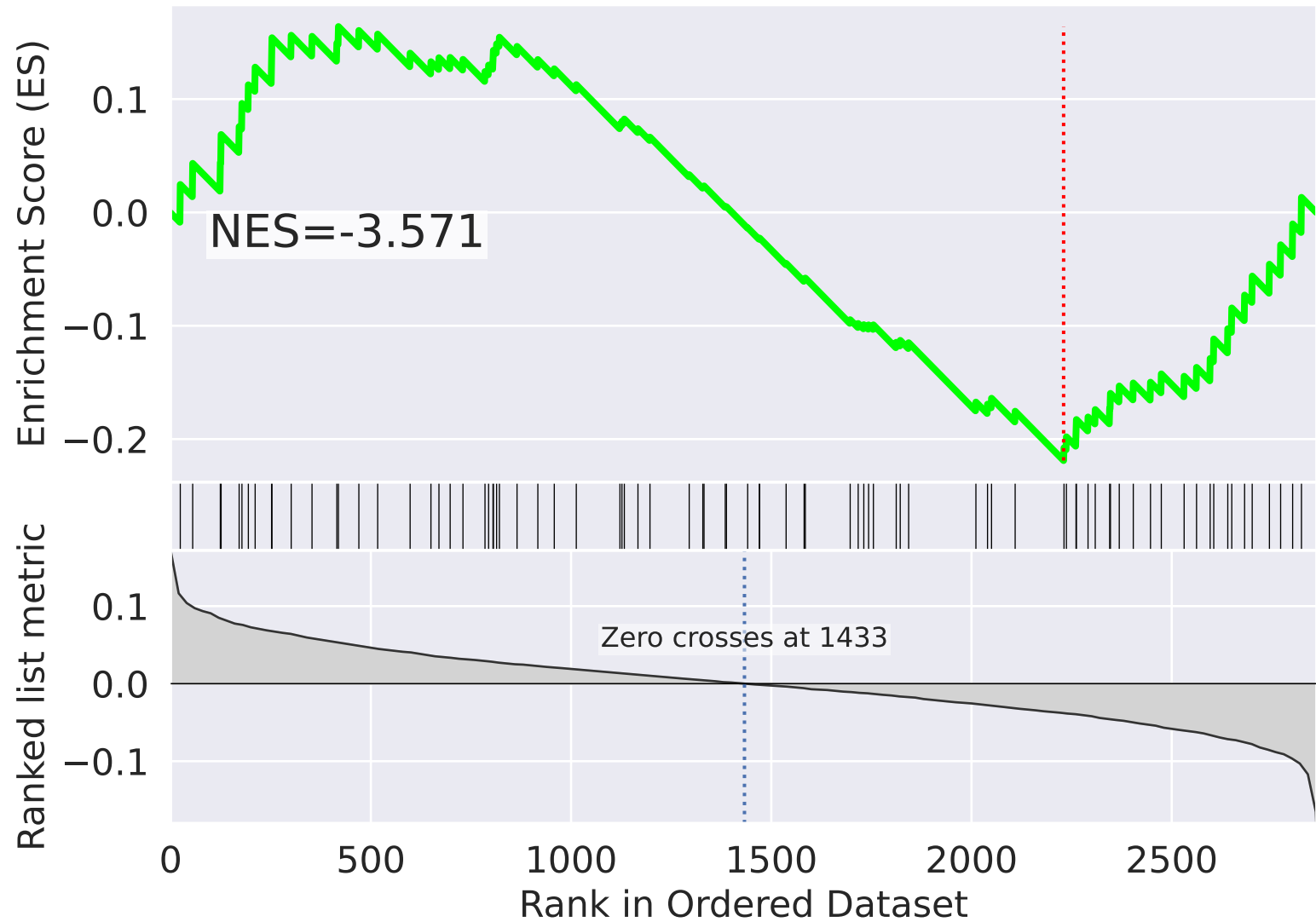
mitochondrial translational elongation (GO:0070125)



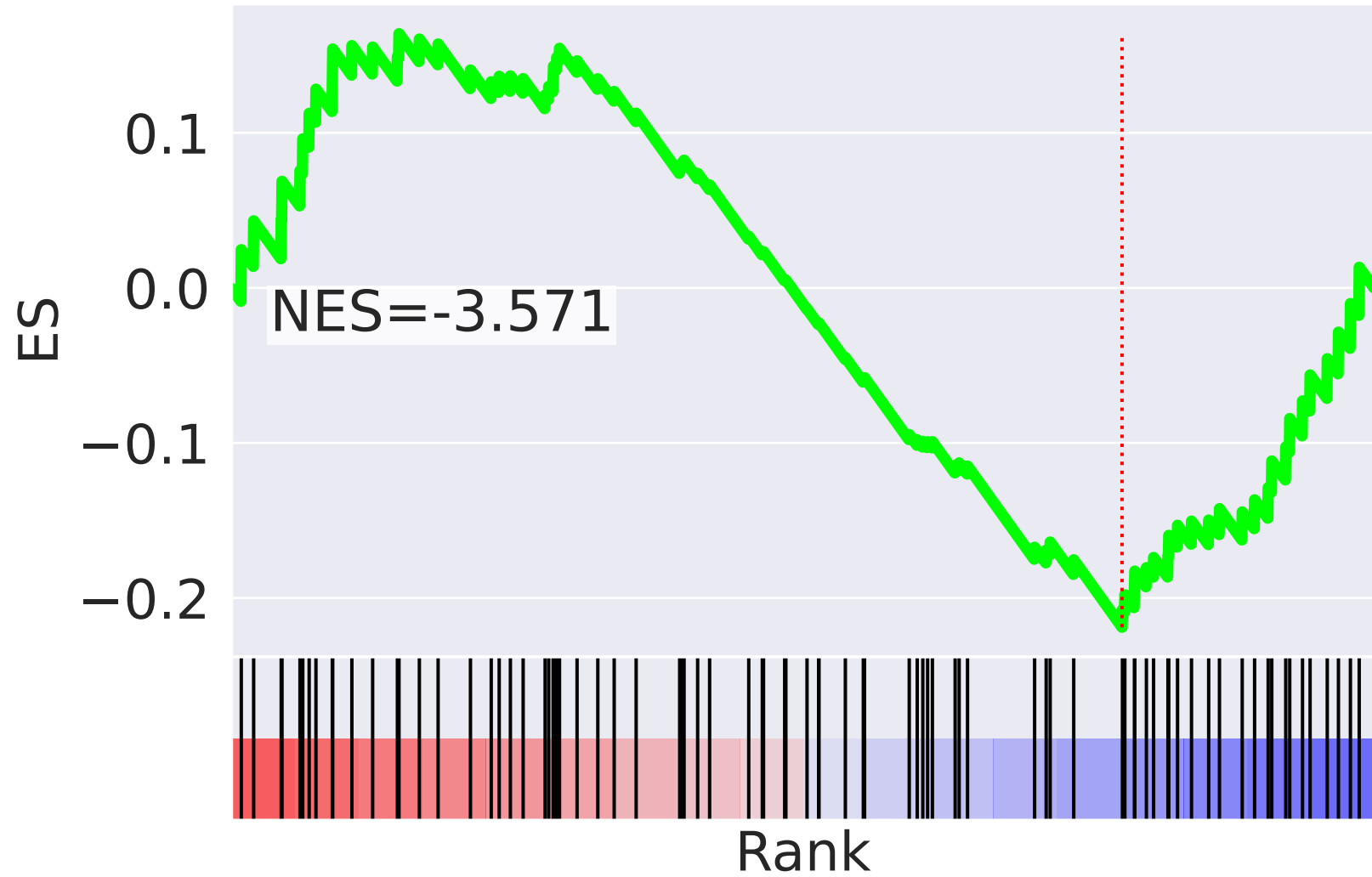
NES		SET
3.654		tricarboxylic acid cycle (GO:0006099)
3.055		mitochondrial translational elongation (GO:0070125)
2.946		positive regulation of TOR signaling (GO:0032008)
-2.872		mitotic metaphase plate congression (GO:0007080)
2.868		mitochondrial translational termination (GO:0070126)
2.866		nucleobase-containing compound metabolic process (GO:0006139)
2.829		cellular nitrogen compound metabolic process (GO:0034641)
2.829		nervous system development (GO:0007399)
-2.762		mitotic cell cycle (GO:0000278)
2.742		humoral immune response (GO:0006959)
-2.722		chromosome segregation (GO:0007059)
-2.707		intra-Golgi vesicle-mediated transport (GO:0006891)
2.693		histone H3 acetylation (GO:0043966)
2.672		cellular response to amino acid stimulus (GO:0071230)
-2.652		single organismal cell-cell adhesion (GO:0016337)

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)

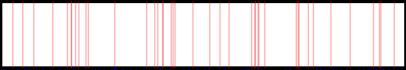
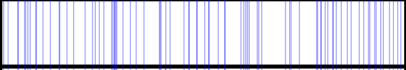
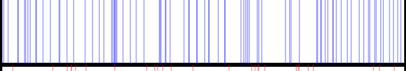
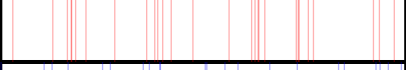
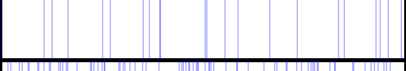
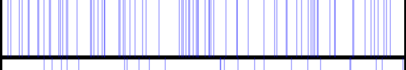
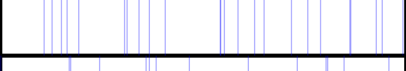

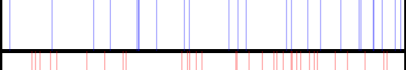
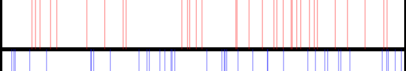
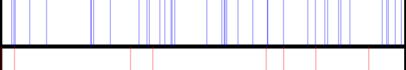
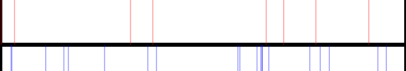





mitochondrial translational elongation (GO:0070125)



NES

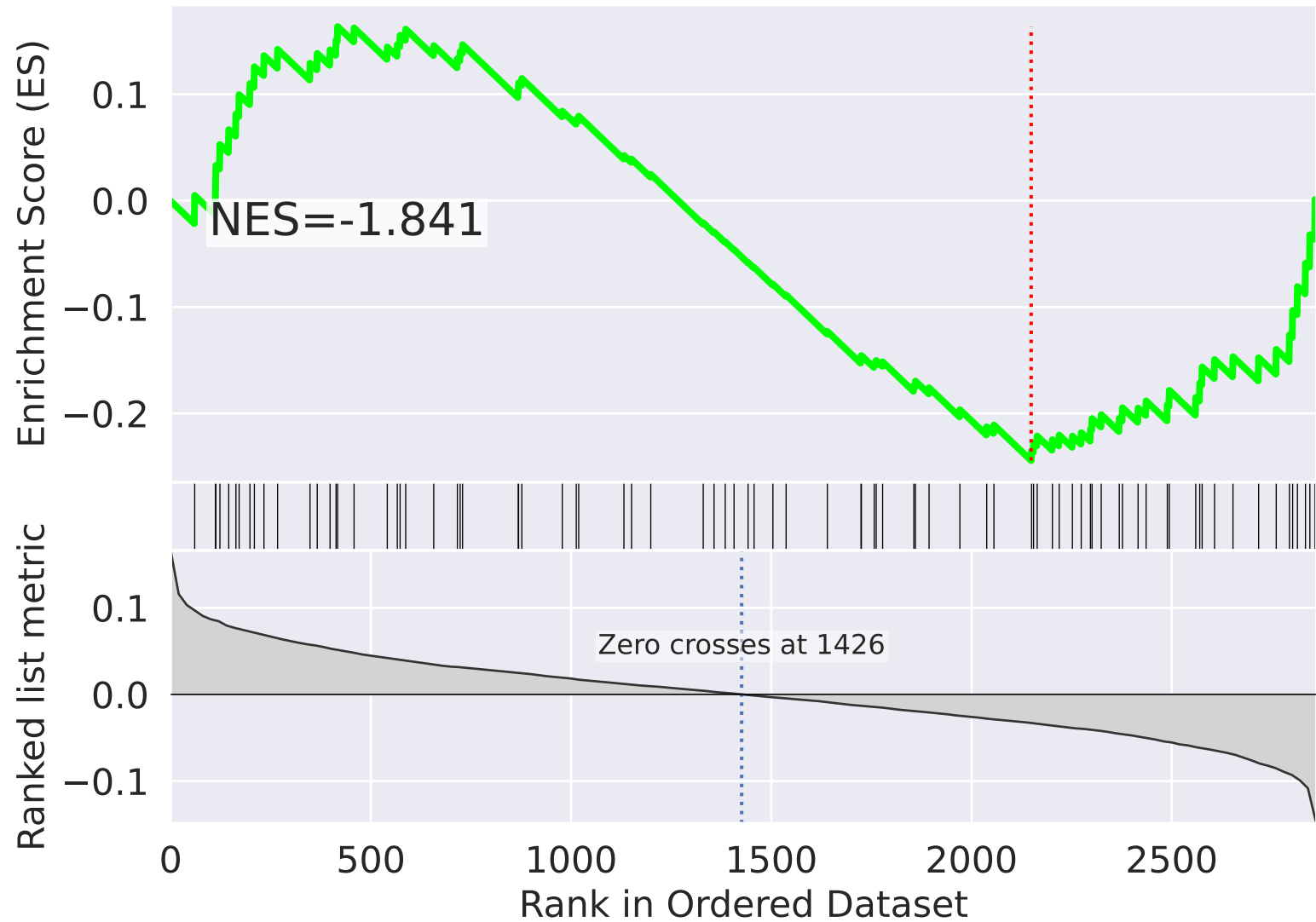
SET

3.863		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.571		mitochondrial translational elongation (GO:0070125)
-3.554		mitochondrial translational termination (GO:0070126)
3.542		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.069		Golgi organization (GO:0007030)
-3.058		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.960		COPII vesicle coating (GO:0048208)
-2.957		autophagy (GO:0006914)
-2.955		intracellular protein transport (GO:0006886)
2.805		double-strand break repair via homologous recombination (GO:0000724)
-2.663		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.629		cellular nitrogen compound metabolic process (GO:0034641)
-2.552		7-methylguanosine mRNA capping (GO:0006370)
2.546		generation of precursor metabolites and energy (GO:0006091)
2.444		response to unfolded protein (GO:0006986)



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)

ES

0.1

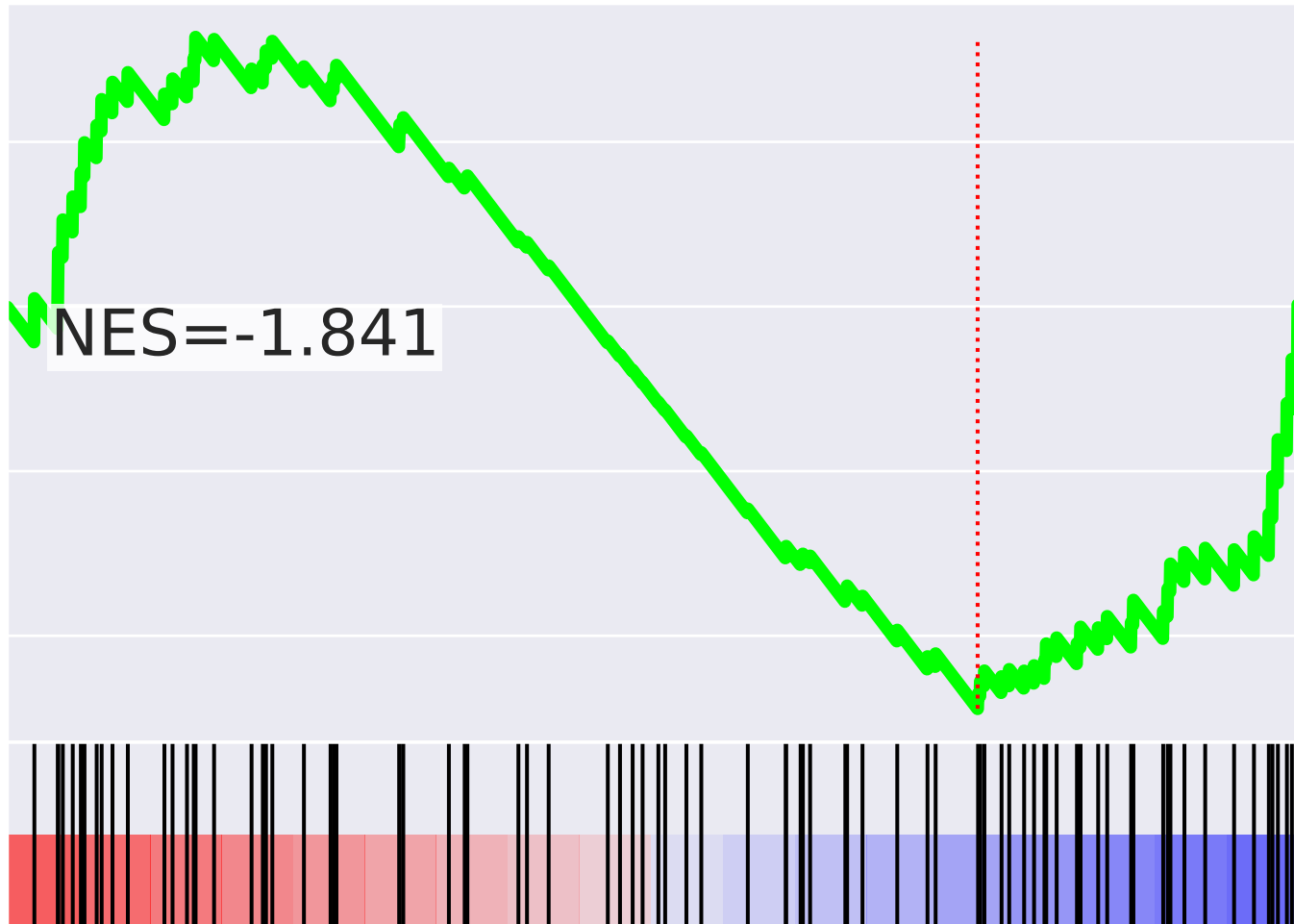
0.0

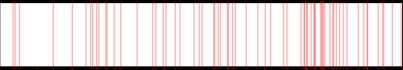
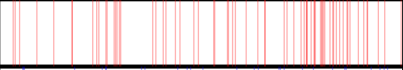
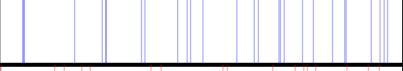
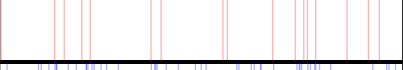
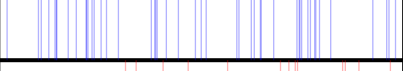
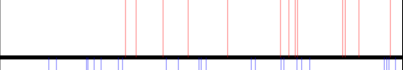
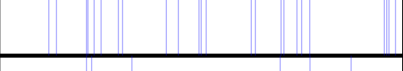
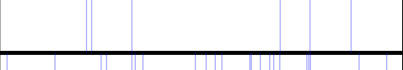
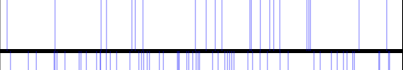
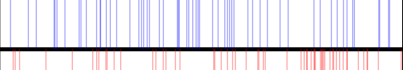
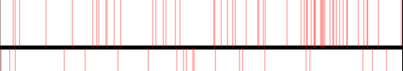
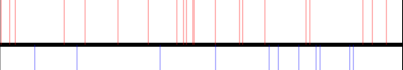
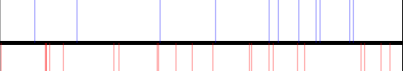

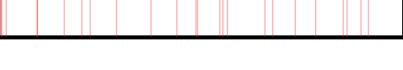
-0.1

-0.2

NES=-1.841

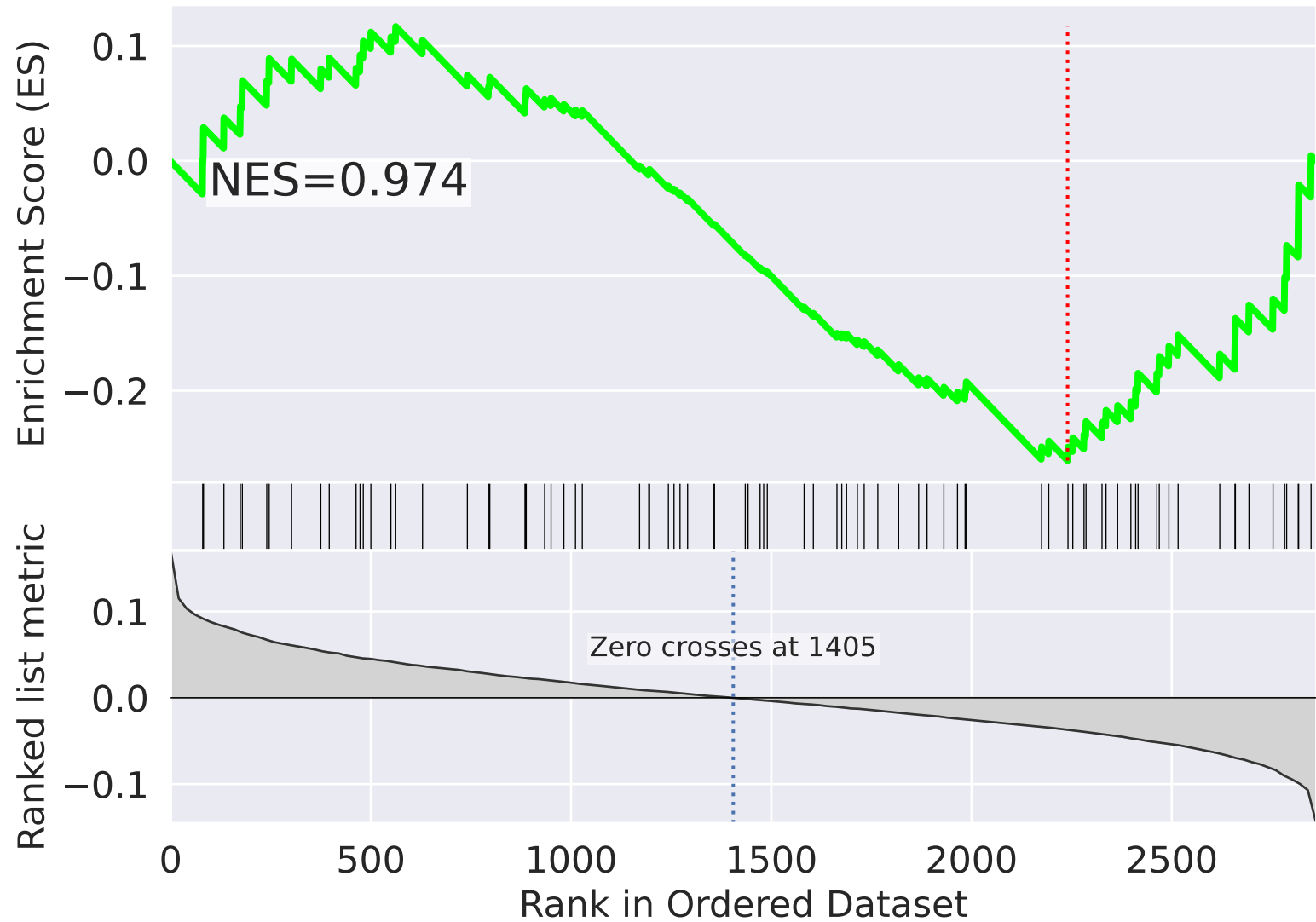
Rank



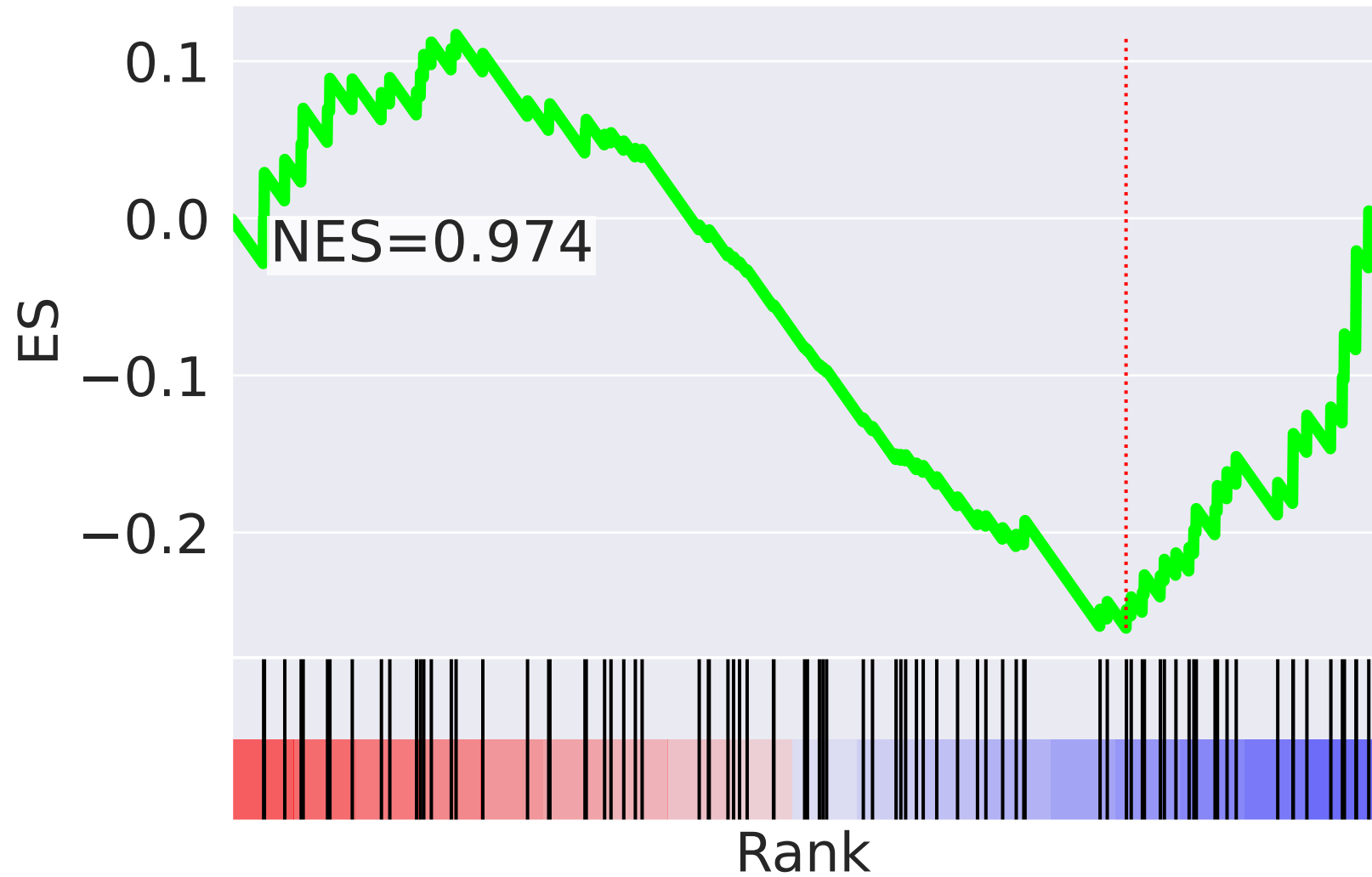
NES		SET
3.528		translational initiation (GO:0006413)
3.329		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-3.108		ciliary basal body docking (GO:0097711)
2.905		I-kappaB kinase/NF-kappaB signaling (GO:0007249)
-2.706		ER to Golgi vesicle-mediated transport (GO:0006888)
2.650		heart development (GO:0007507)
-2.634		COPII vesicle coating (GO:0048208)
-2.615		exocytosis (GO:0006887)
-2.594		Golgi organization (GO:0007030)
-2.562		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.549		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
2.537		positive regulation of type I interferon production (GO:0032481)
-2.518		regulation of defense response to virus by virus (GO:0050690)
2.498		negative regulation of gene expression (GO:0010629)
2.494		positive regulation of NF-kappaB transcription factor activity (GO:0051092)

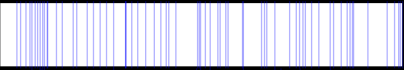

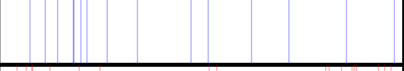
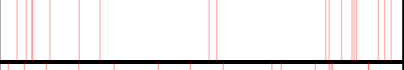
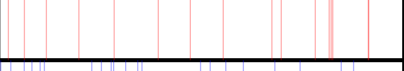
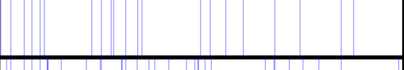
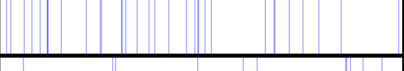
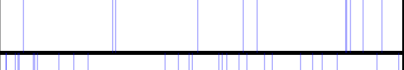
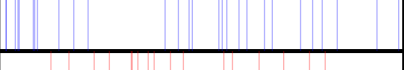
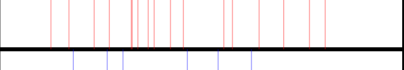

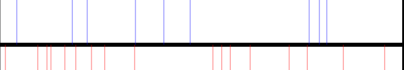
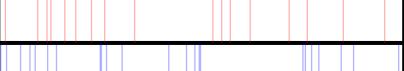
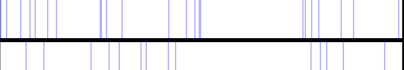

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=6$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

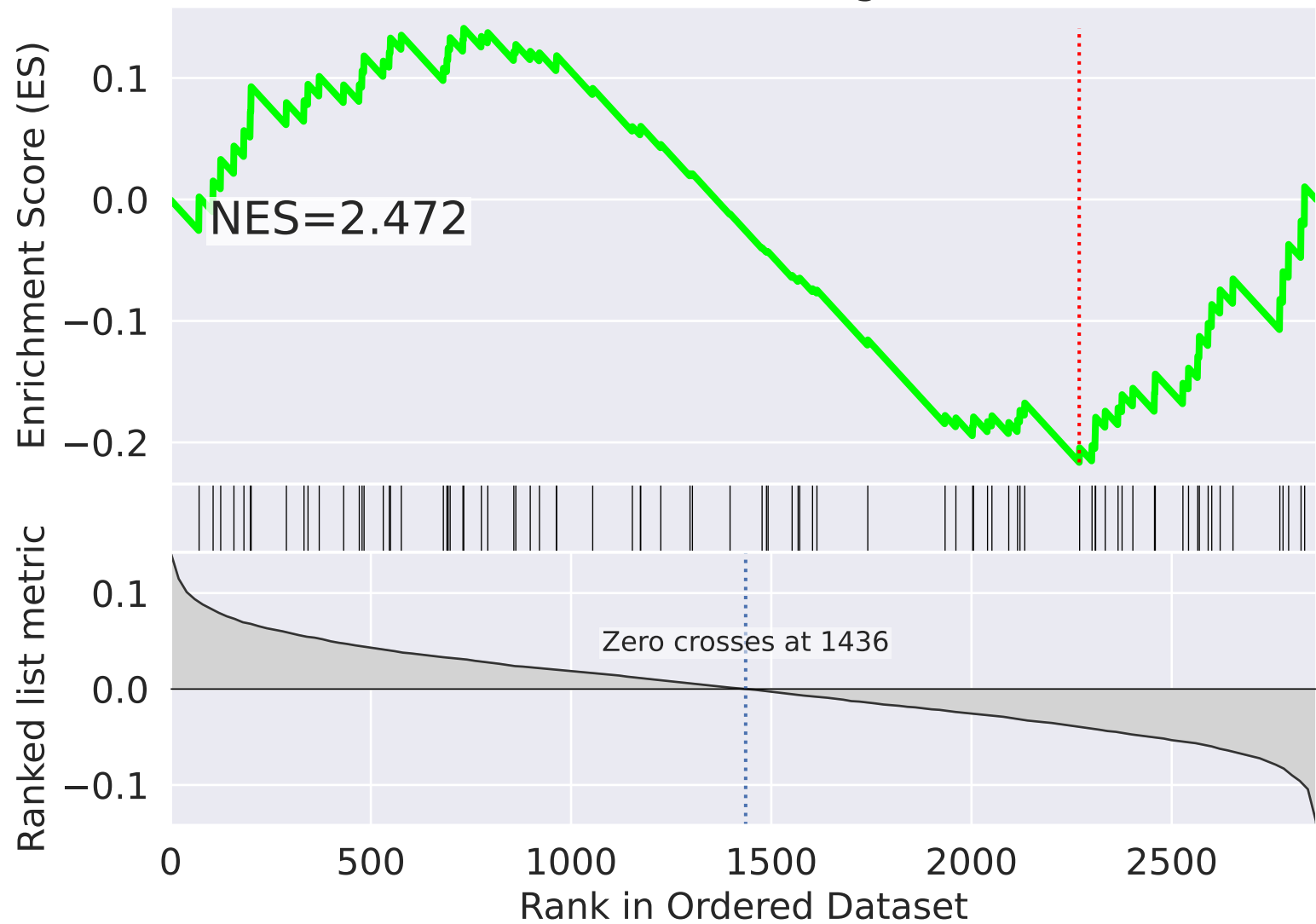


NES		SET
-2.908		DNA replication (GO:0006260)
-2.863		error-prone translesion synthesis (GO:0042276)
-2.777		positive regulation of protein catabolic process (GO:0045732)
2.774		cell differentiation (GO:0030154)
2.667		nervous system development (GO:0007399)
-2.658		telomere maintenance via recombination (GO:0000722)
-2.651		double-strand break repair via homologous recombination (GO:0000724)
-2.621		cilium assembly (GO:0060271)
-2.618		chromosome segregation (GO:0007059)
2.616		positive regulation of TOR signaling (GO:0032008)
-2.614		beta-catenin destruction complex disassembly (GO:1904886)
-2.609		DNA-templated transcription, initiation (GO:0006352)
2.598		platelet activation (GO:0030168)
-2.576		DNA synthesis involved in DNA repair (GO:0000731)
-2.491		negative regulation of protein kinase activity (GO:0006469)

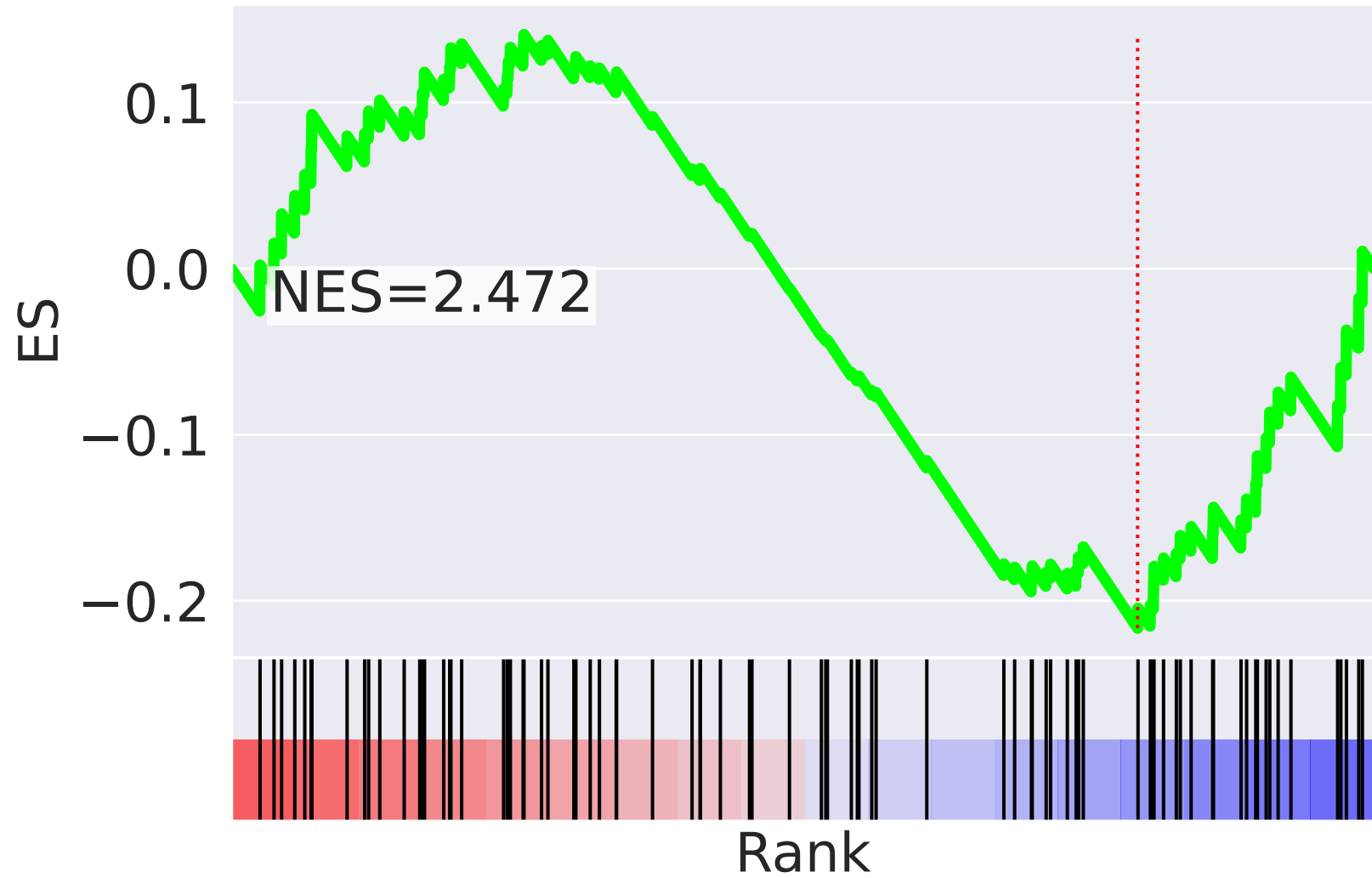


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=7$

# mitochondrial translational elongation (GO:0070125)



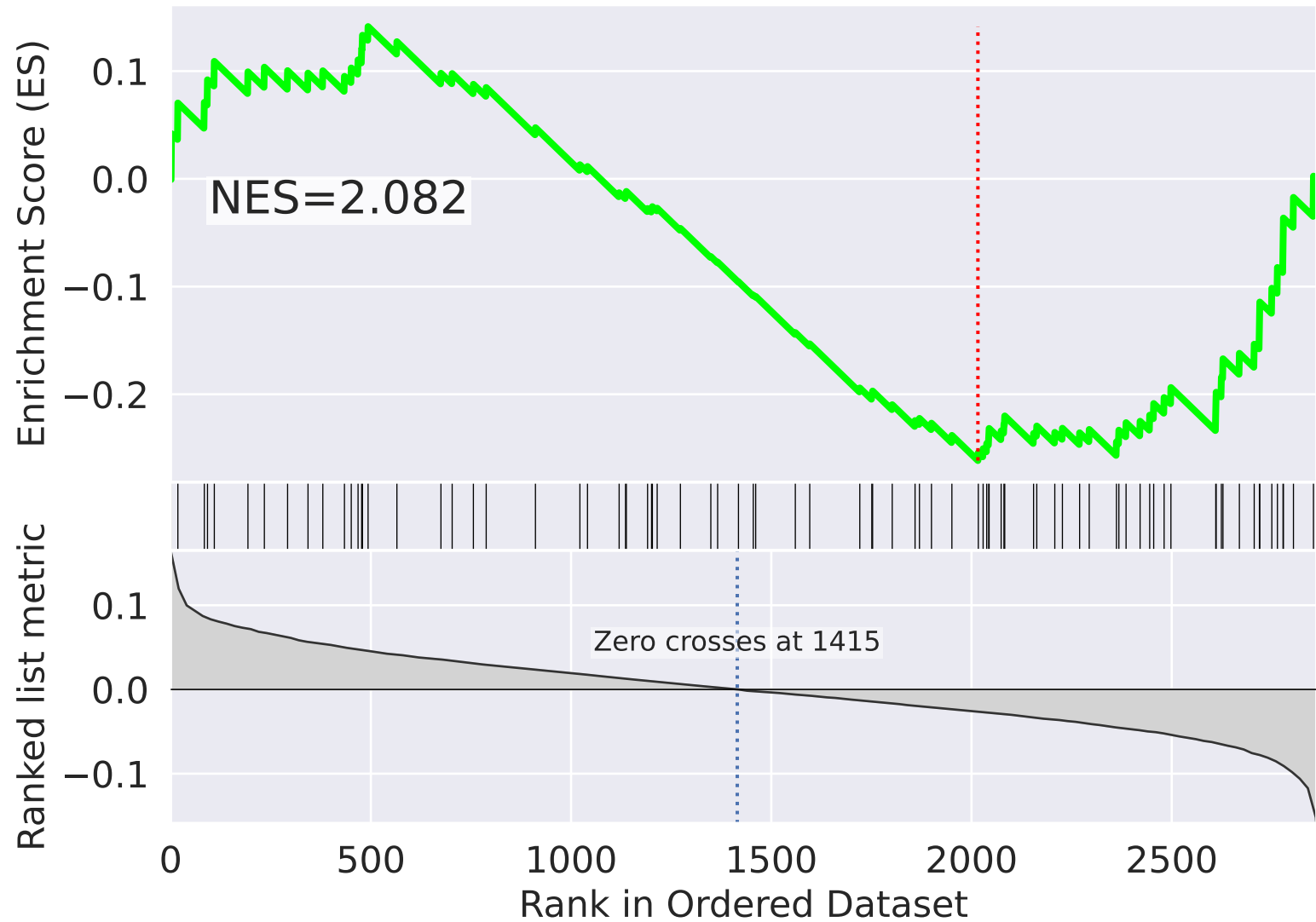
# mitochondrial translational elongation (GO:0070125)



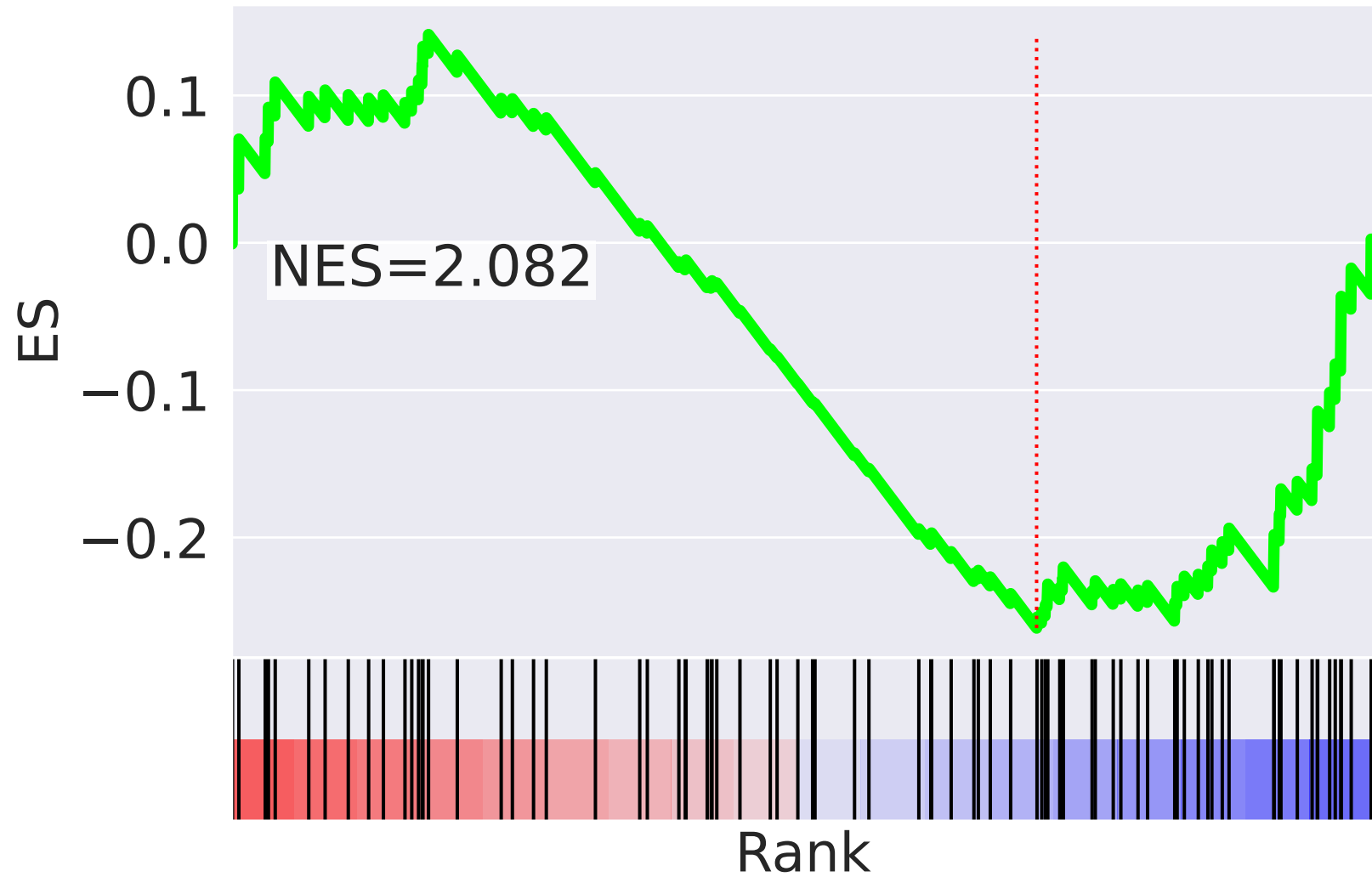
NES		SET
4.550		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.399		protein phosphorylation (GO:0006468)
-3.326		transforming growth factor beta receptor signaling pathway (GO:0007179)
3.287		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.250		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-3.244		MAPK cascade (GO:0000165)
-3.187		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-3.081		tumor necrosis factor-mediated signaling pathway (GO:0033209)
-2.936		negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
-2.936		membrane fusion (GO:0061025)
2.915		mitochondrial respiratory chain complex III assembly (GO:0034551)
-2.911		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
2.842		tricarboxylic acid cycle (GO:0006099)
-2.833		post-translational protein modification (GO:0043687)
-2.750		nucleotide-excision repair, DNA damage recognition (GO:0000715)

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)

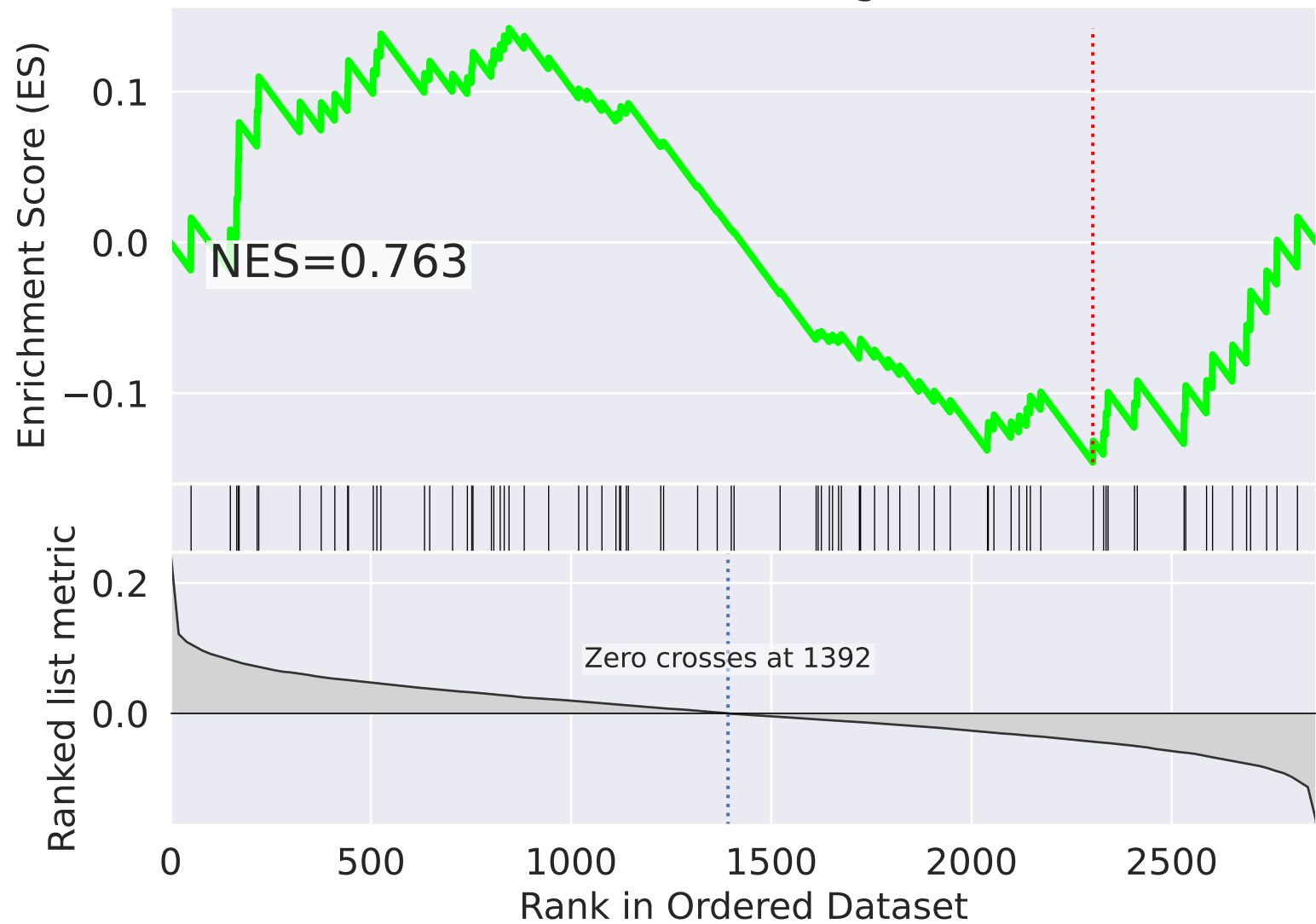


NES		SET
3.766		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
3.679		transmembrane transport (GO:0055085)
3.563		mRNA export from nucleus (GO:0006406)
-3.517		interstrand cross-link repair (GO:0036297)
3.487		regulation of cellular amino acid metabolic process (GO:0006521)
-3.475		transcription from RNA polymerase III promoter (GO:0006383)
3.446		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
3.393		protein polyubiquitination (GO:0000209)
3.389		negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
3.381		ubiquitin-dependent ERAD pathway (GO:0030433)
3.299		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
3.291		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.187		NIK/NF-kappaB signaling (GO:0038061)
3.168		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
3.164		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  $z=9$

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

ES

0.1

0.0

-0.1

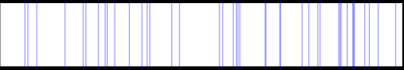
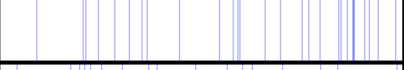
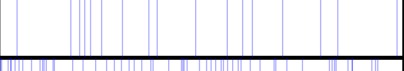
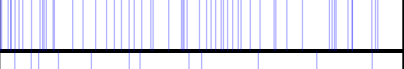
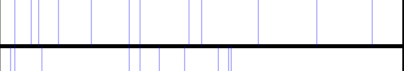
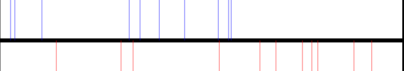

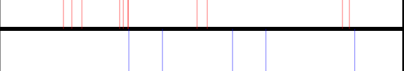
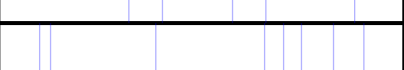
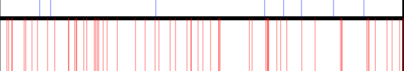





NES=0.763

Rank



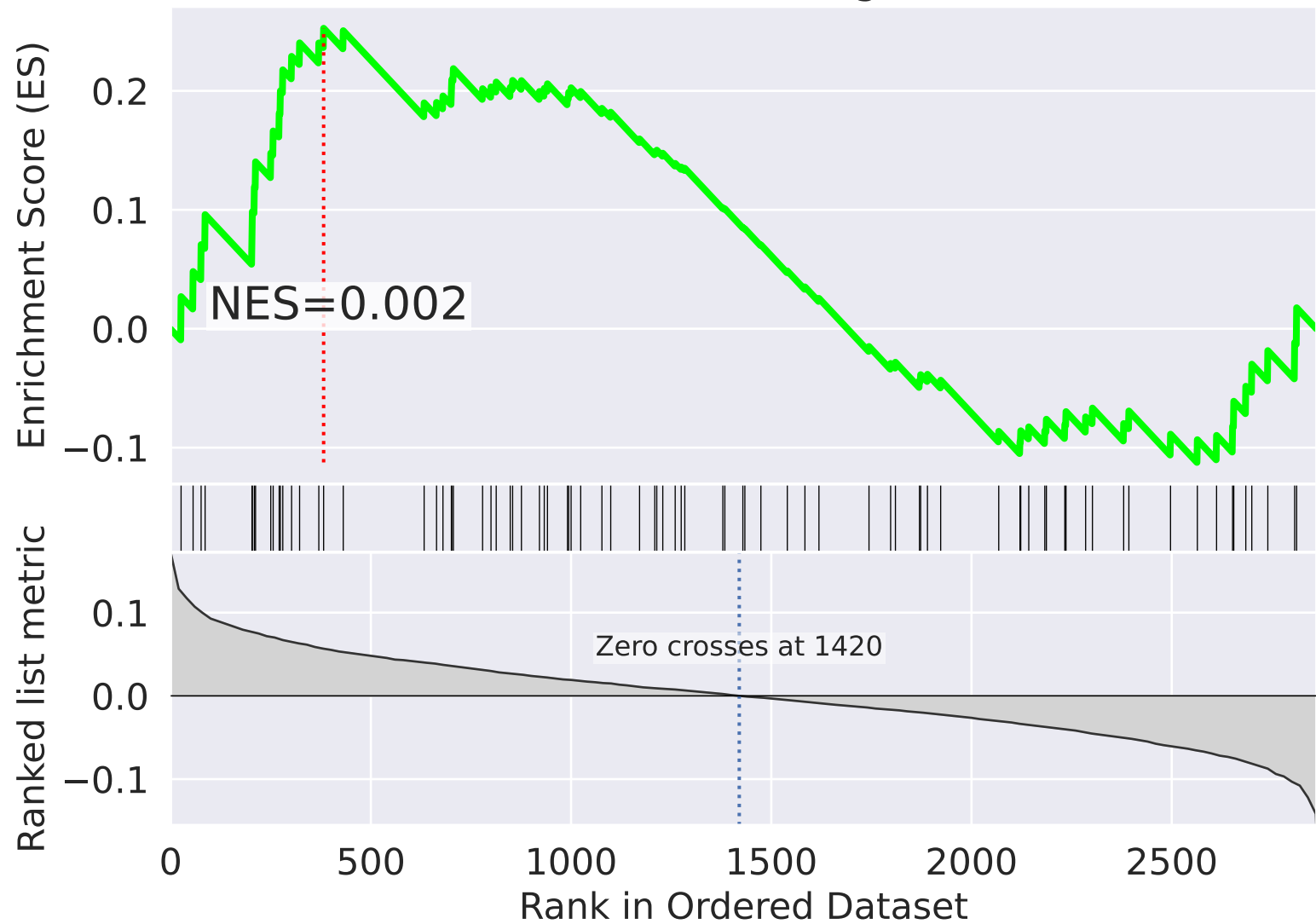
NES

SET

-4.611		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.318		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.971		protein K11-linked ubiquitination (GO:0070979)
-2.828		negative regulation of cell proliferation (GO:0008285)
-2.775		platelet aggregation (GO:0070527)
-2.743		cell-matrix adhesion (GO:0007160)
2.705		protein tetramerization (GO:0051262)
2.686		type I interferon signaling pathway (GO:0060337)
-2.634		mitochondrial respiratory chain complex III assembly (GO:0034551)
-2.568		centriole replication (GO:0007099)
2.551		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.542		transcription initiation from RNA polymerase II promoter (GO:0006367)
2.513		interferon-gamma-mediated signaling pathway (GO:0060333)
2.505		histone H2A acetylation (GO:0043968)
2.445		cholesterol biosynthetic process (GO:0006695)

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

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

ES

0.2

0.1

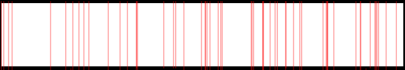
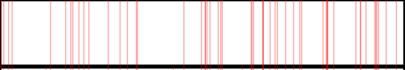
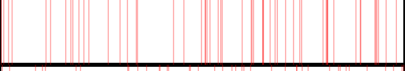
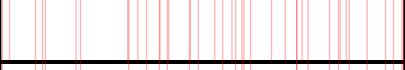
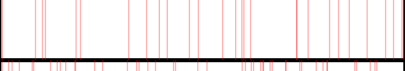
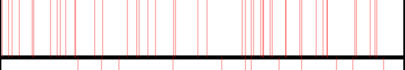
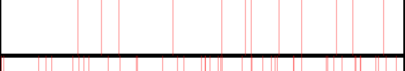
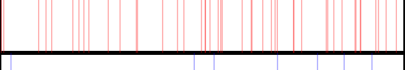
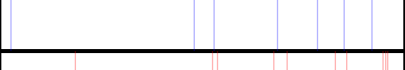

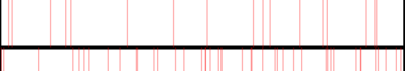
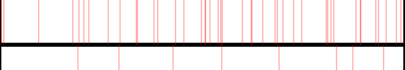

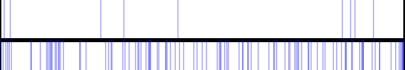
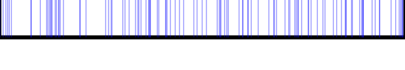
0.0

-0.1

NES=0.002

Rank

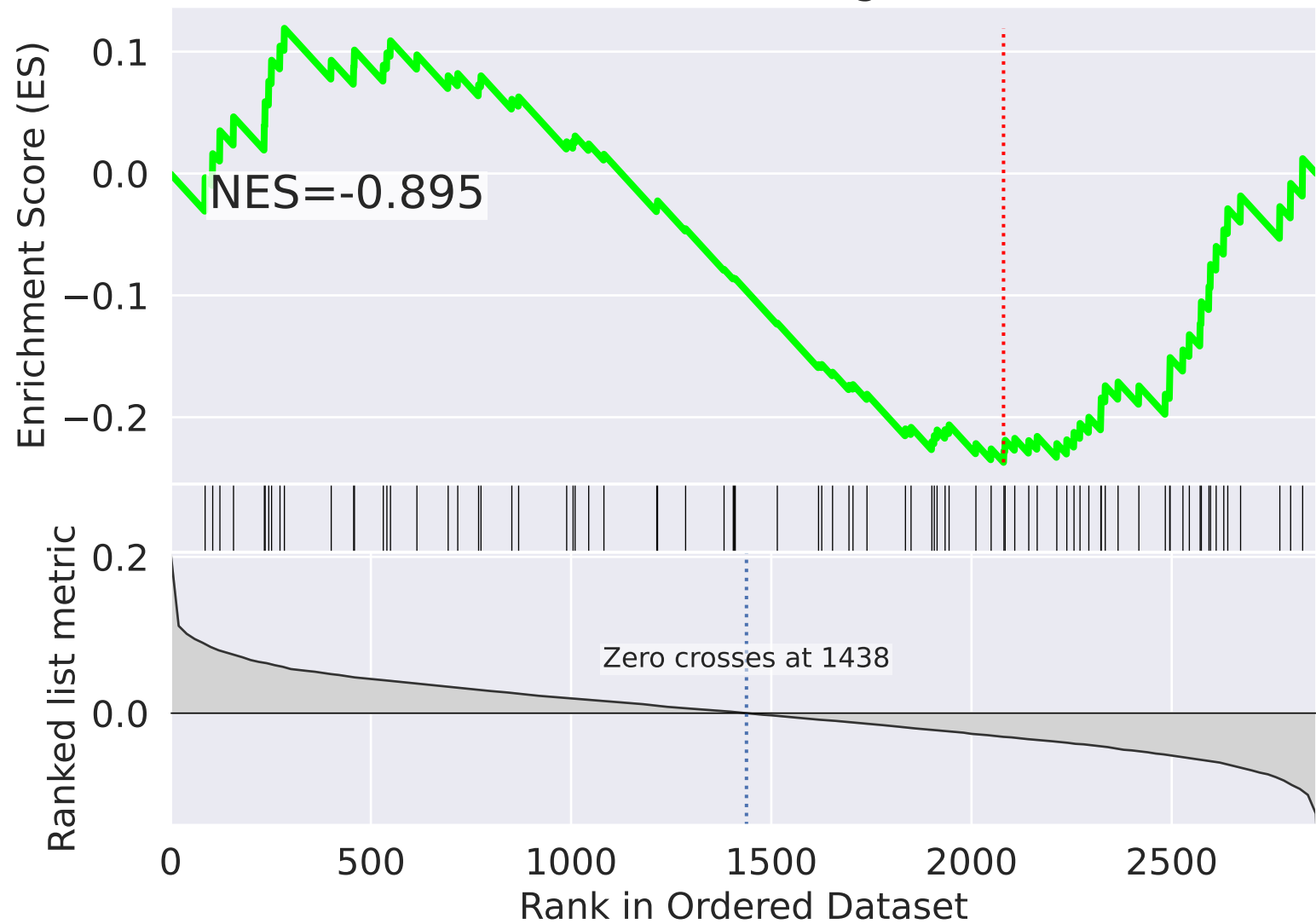


NES		SET
4.685		anaphase-promoting complex-dependent catabolic process (GO:0031145)
4.211		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
3.974		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
3.713		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.634		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.153		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
3.050		nucleotide-excision repair, DNA damage recognition (GO:0000715)
2.945		NIK/NF-kappaB signaling (GO:0038061)
-2.902		positive regulation of osteoblast differentiation (GO:0045669)
2.882		nucleosome disassembly (GO:0006337)
2.854		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
2.821		positive regulation of canonical Wnt signaling pathway (GO:0090263)
2.800		protein deneddylation (GO:0000338)
-2.777		DNA-templated transcription, initiation (GO:0006352)
-2.745		rRNA processing (GO:0006364)

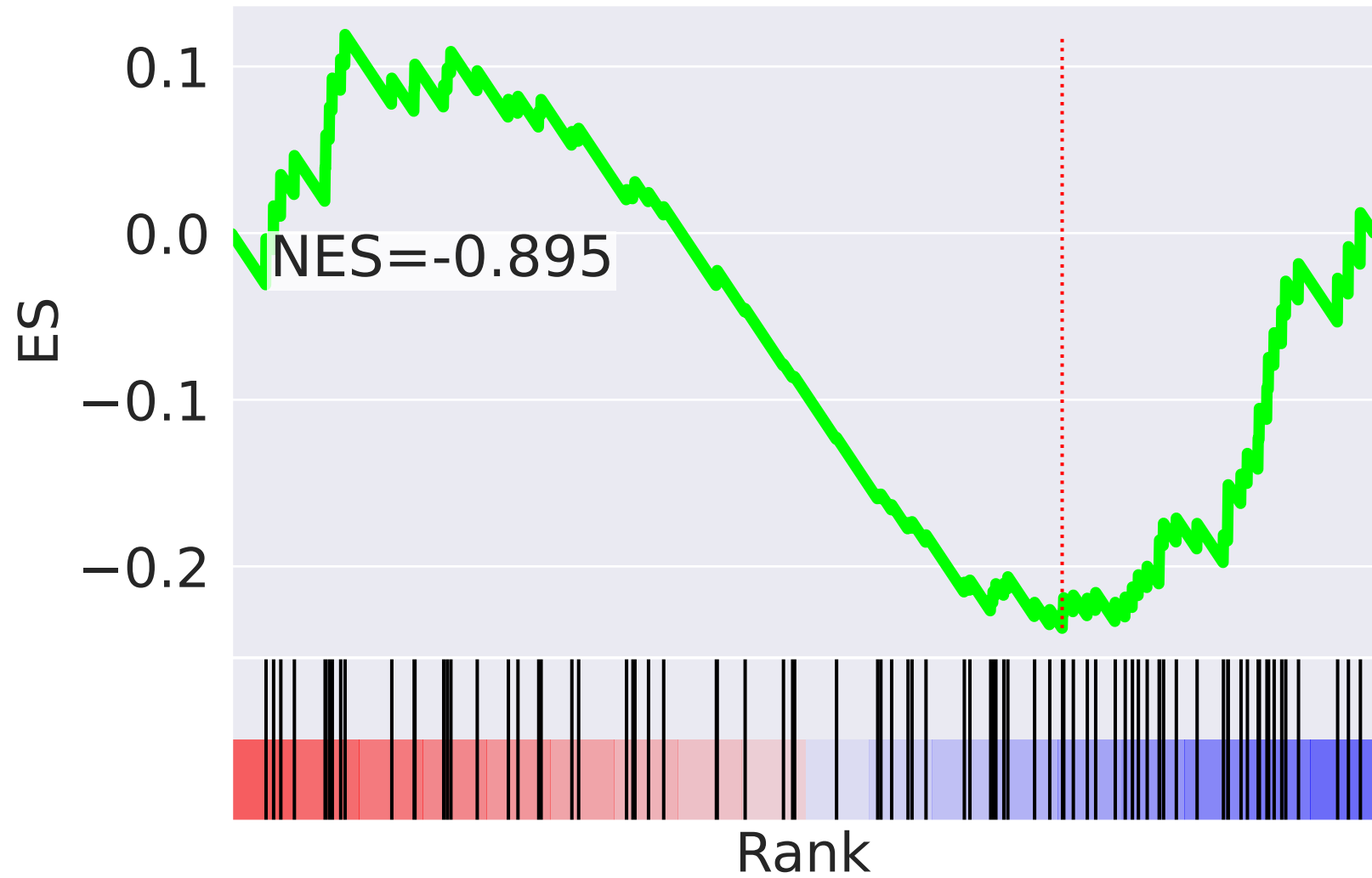


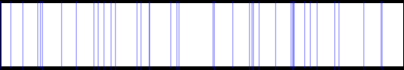
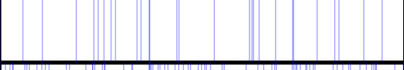
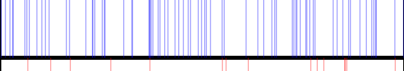
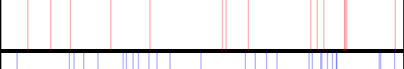
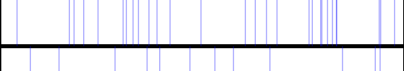

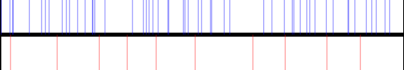
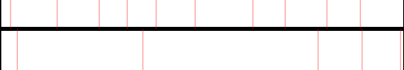
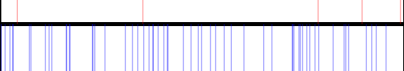
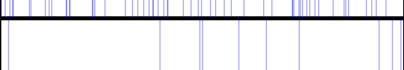


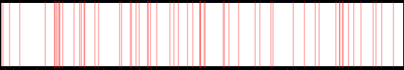


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=11$

# mitochondrial translational elongation (GO:0070125)



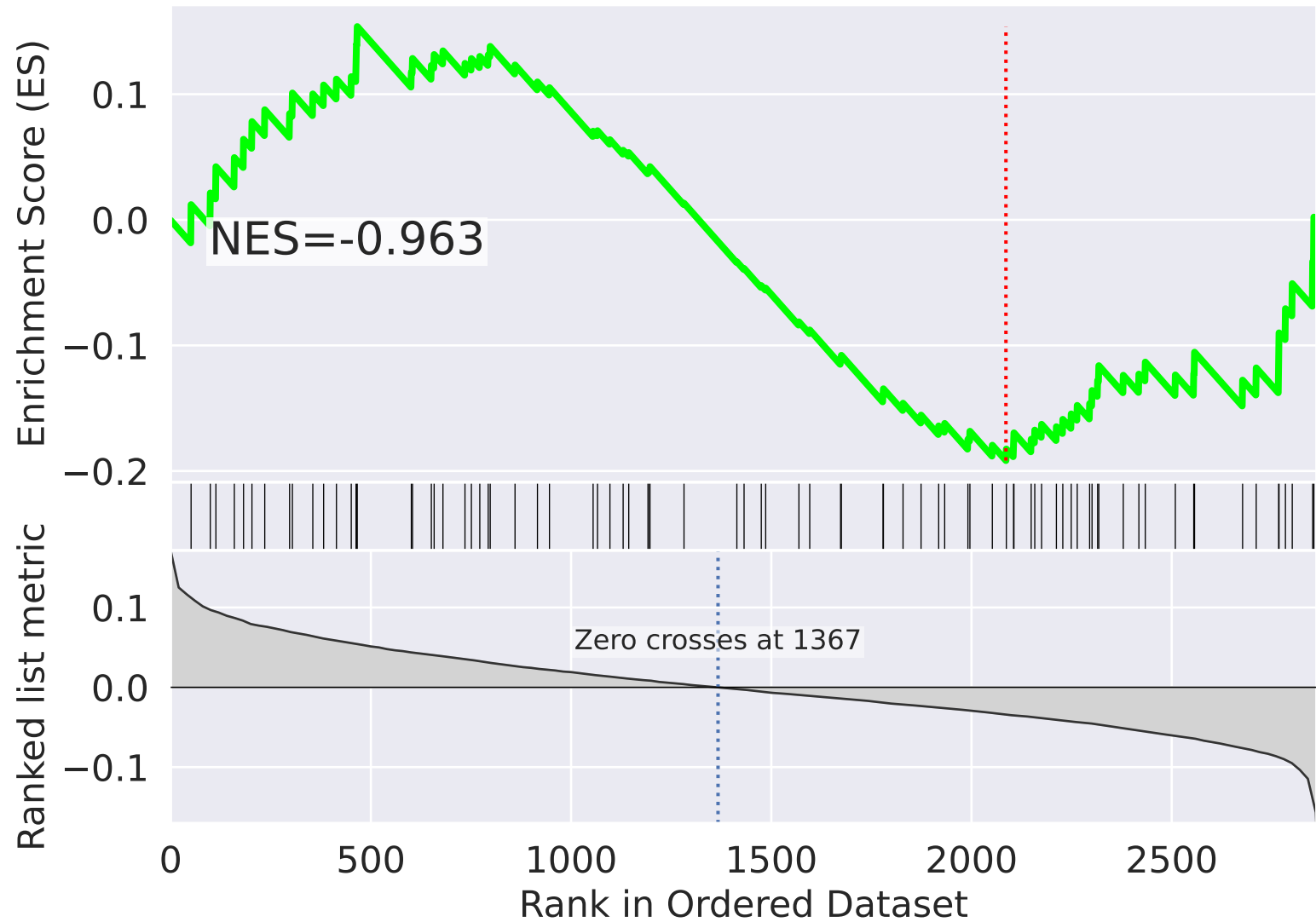
mitochondrial translational elongation (GO:0070125)



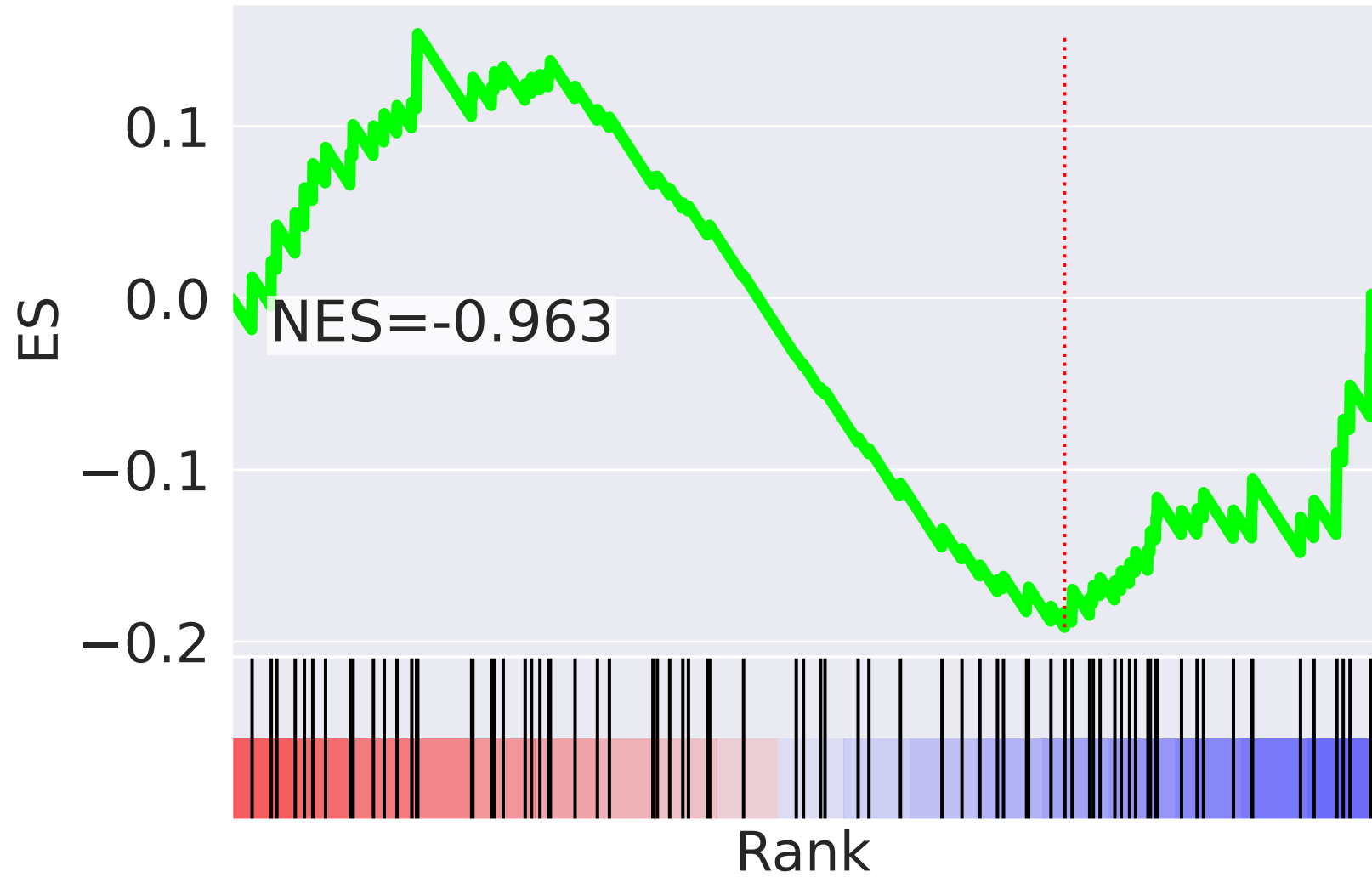
NES		SET
-3.596		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.587		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.429		MAPK cascade (GO:0000165)
3.342		ATP-dependent chromatin remodeling (GO:0043044)
-3.221		chromosome segregation (GO:0007059)
-3.147		spliceosomal complex assembly (GO:0000245)
-3.065		negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.941		heme biosynthetic process (GO:0006783)
2.933		positive regulation of ATPase activity (GO:0032781)
-2.878		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-2.849		cell-matrix adhesion (GO:0007160)
-2.839		mitotic metaphase plate congression (GO:0007080)
-2.829		viral life cycle (GO:0019058)
2.793		transcription elongation from RNA polymerase II promoter (GO:0006368)
2.708		positive regulation of neuron differentiation (GO:0045666)

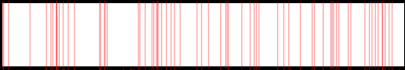
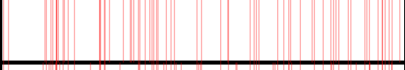
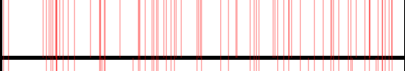
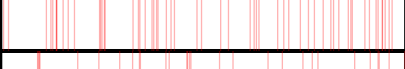
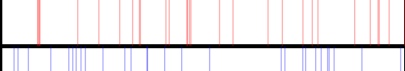

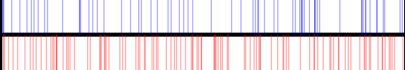
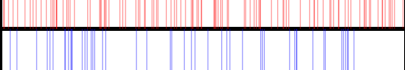
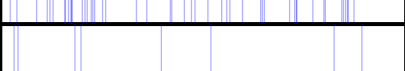

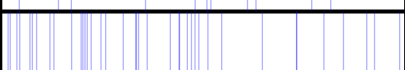




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=12$

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

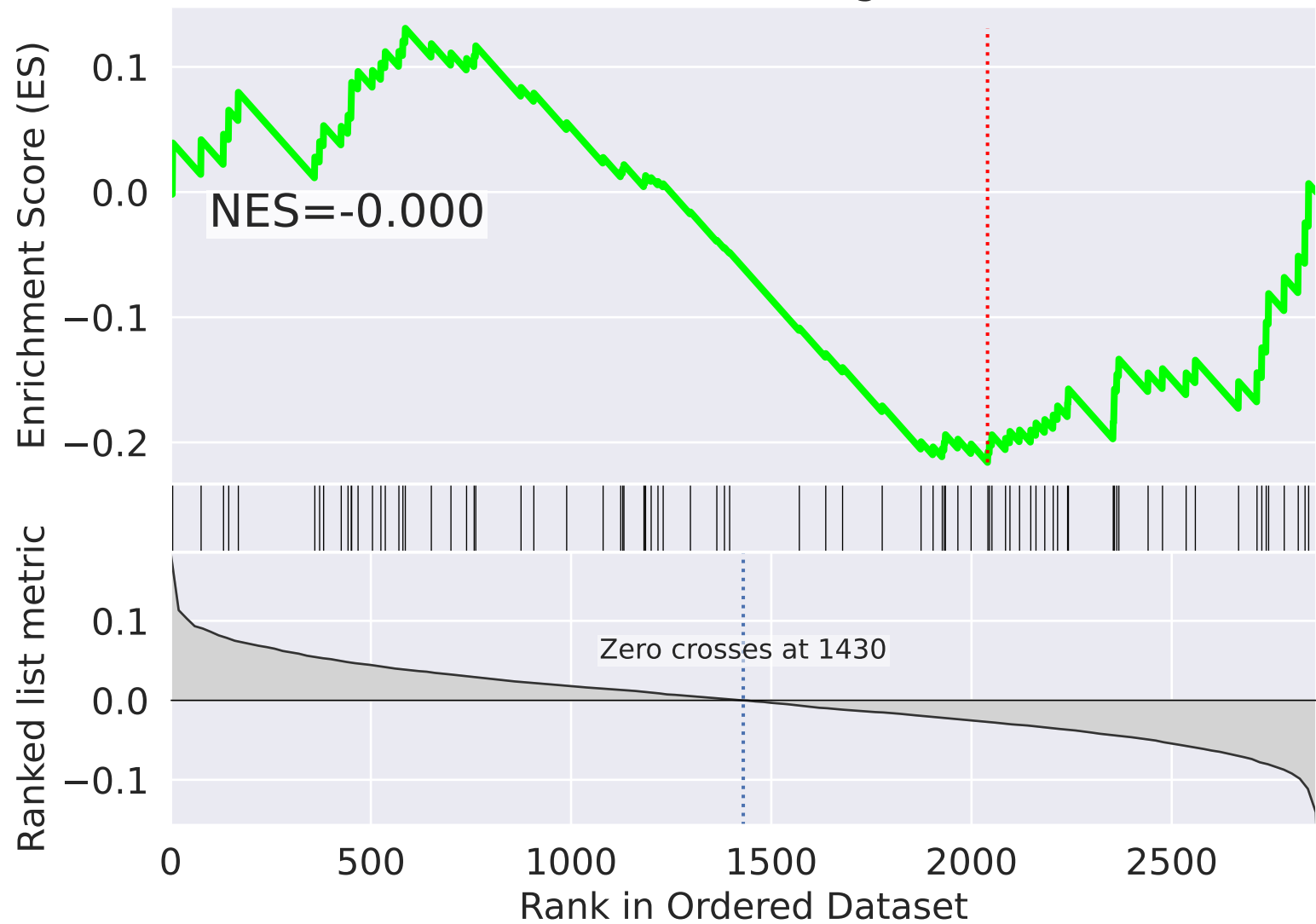


NES		SET
5.094		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
4.836		translational initiation (GO:0006413)
4.157		viral transcription (GO:0019083)
4.020		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
3.660		interstrand cross-link repair (GO:0036297)
-3.562		phosphatidylinositol-mediated signaling (GO:0048015)
-3.534		transcription initiation from RNA polymerase II promoter (GO:0006367)
3.485		rRNA processing (GO:0006364)
-2.959		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.894		phosphorylation (GO:0016310)
-2.852		regulation of defense response to virus by virus (GO:0050690)
-2.823		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.795		negative regulation of TOR signaling (GO:0032007)
-2.773		protein autophosphorylation (GO:0046777)
2.722		negative regulation of cell growth (GO:0030308)

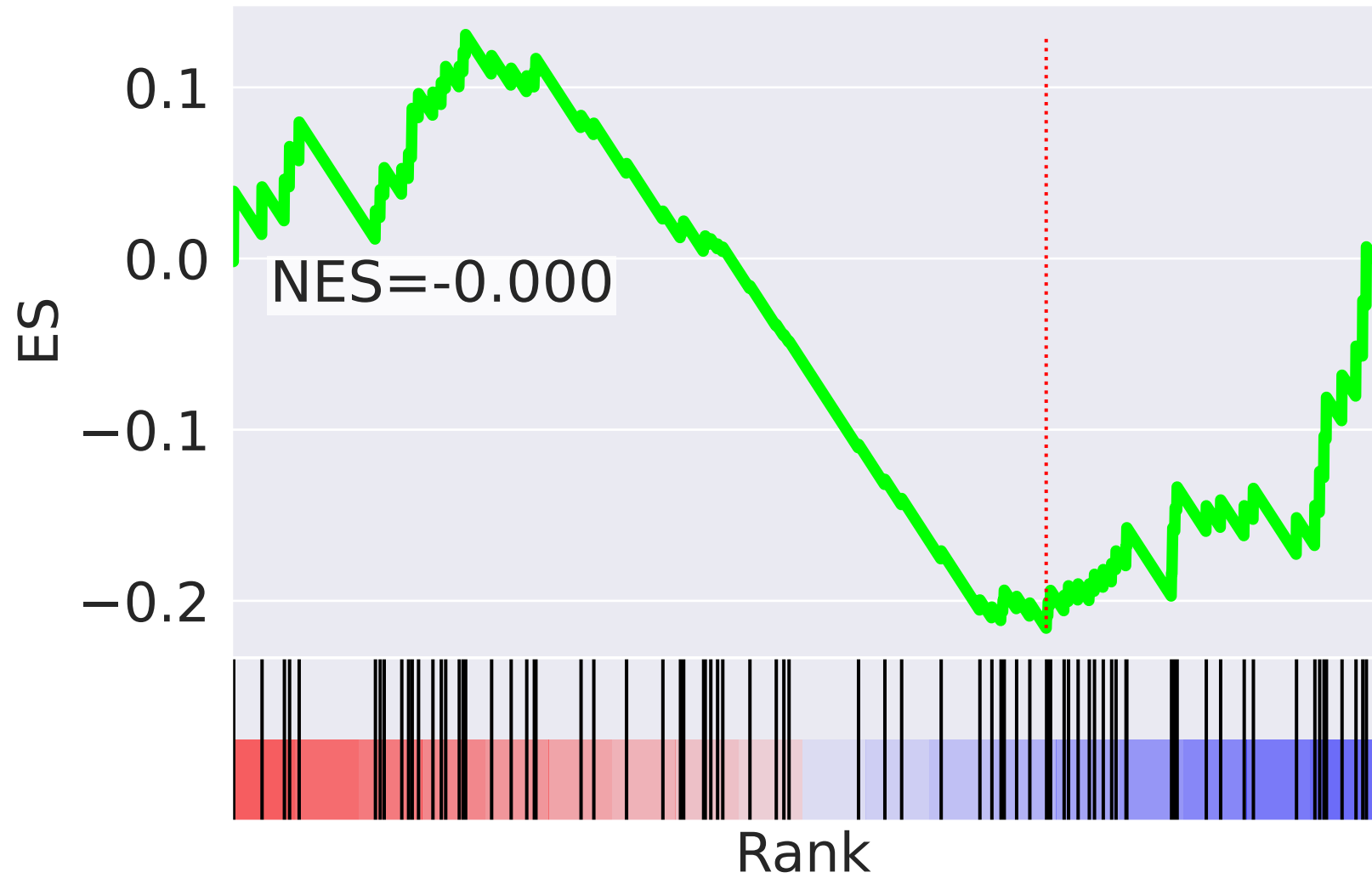


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=13$

# mitochondrial translational elongation (GO:0070125)



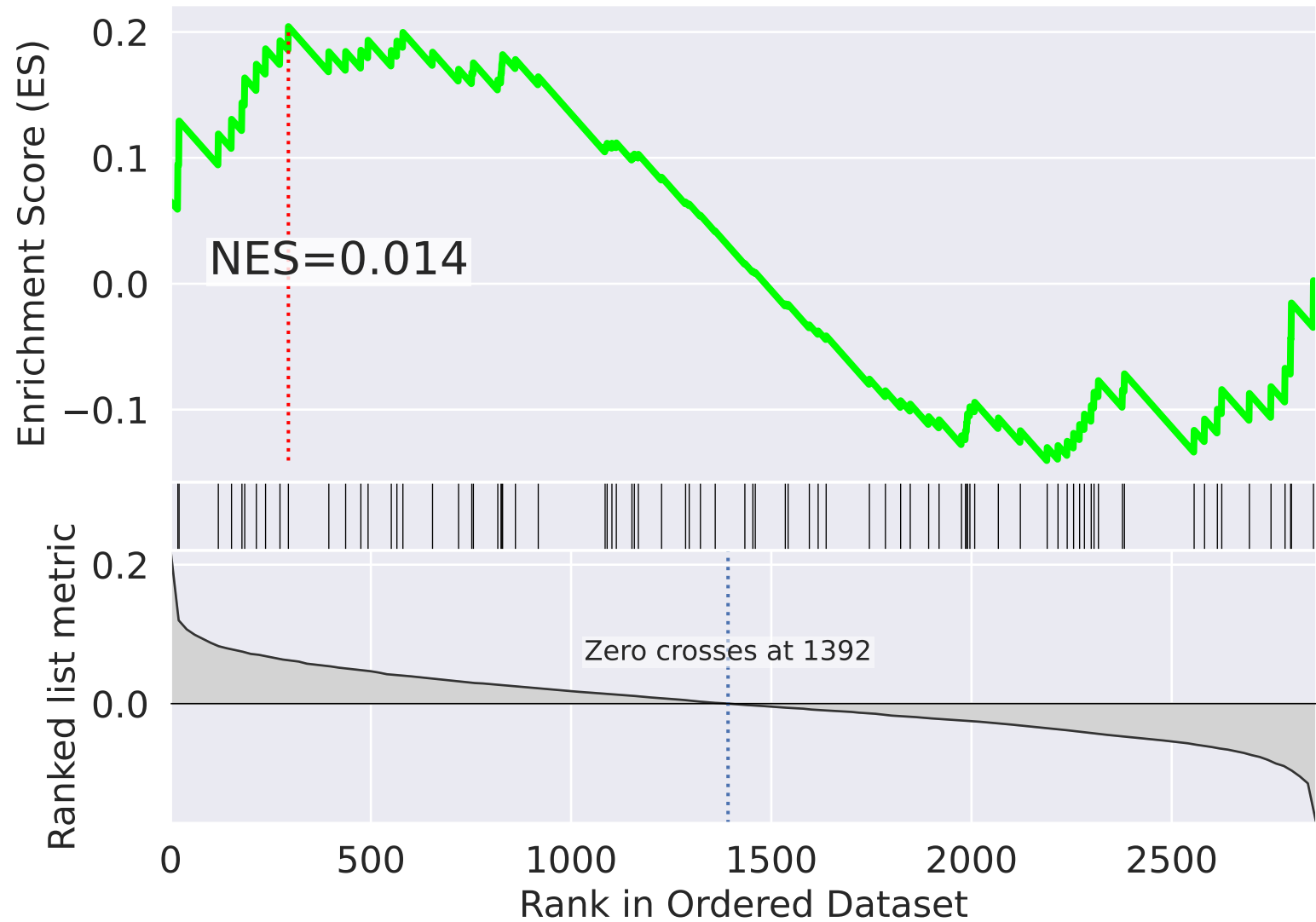
# mitochondrial translational elongation (GO:0070125)



NES	SET
4.945	Fc-epsilon receptor signaling pathway (GO:0038095)
4.635	T cell receptor signaling pathway (GO:0050852)
4.580	regulation of cellular amino acid metabolic process (GO:0006521)
4.394	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
4.387	stimulatory C-type lectin receptor signaling pathway (GO:0002223)
4.371	positive regulation of canonical Wnt signaling pathway (GO:0090263)
4.364	protein polyubiquitination (GO:0000209)
4.312	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
4.274	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
4.104	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
4.058	tumor necrosis factor-mediated signaling pathway (GO:0033209)
3.930	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
3.809	anaphase-promoting complex-dependent catabolic process (GO:0031145)
3.655	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
3.639	regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)

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

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

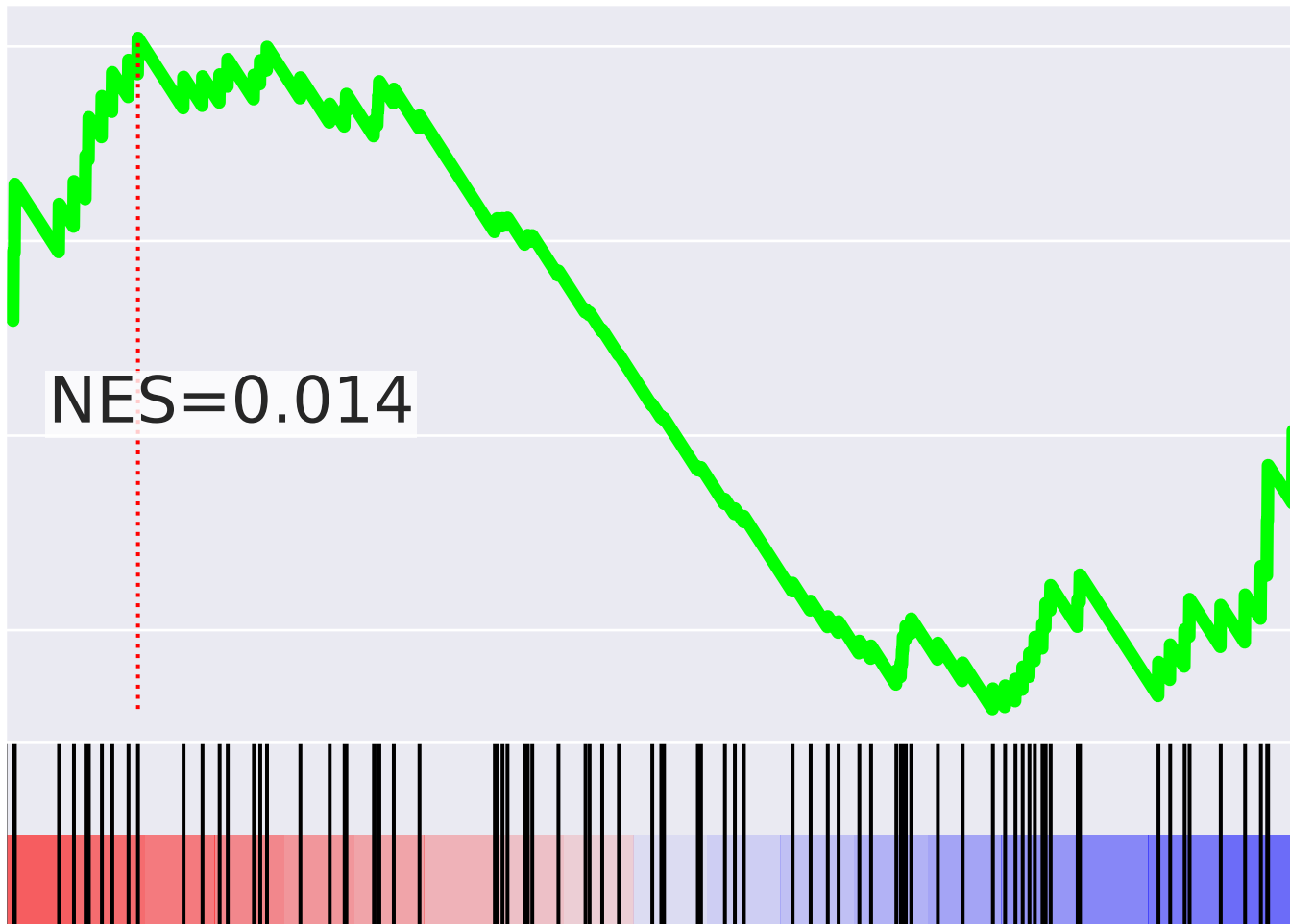
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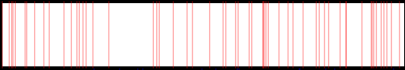

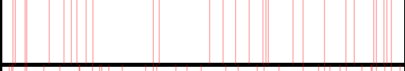
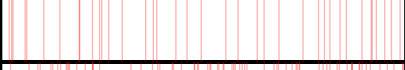
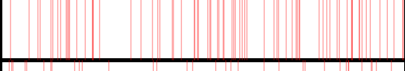
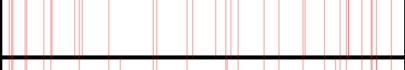


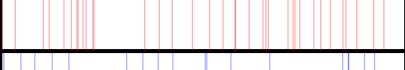

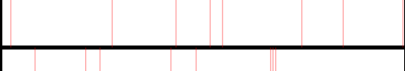

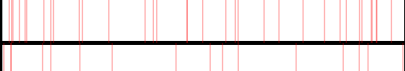
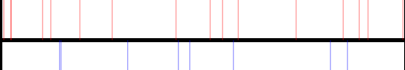

0.0

-0.1

NES=0.014

Rank

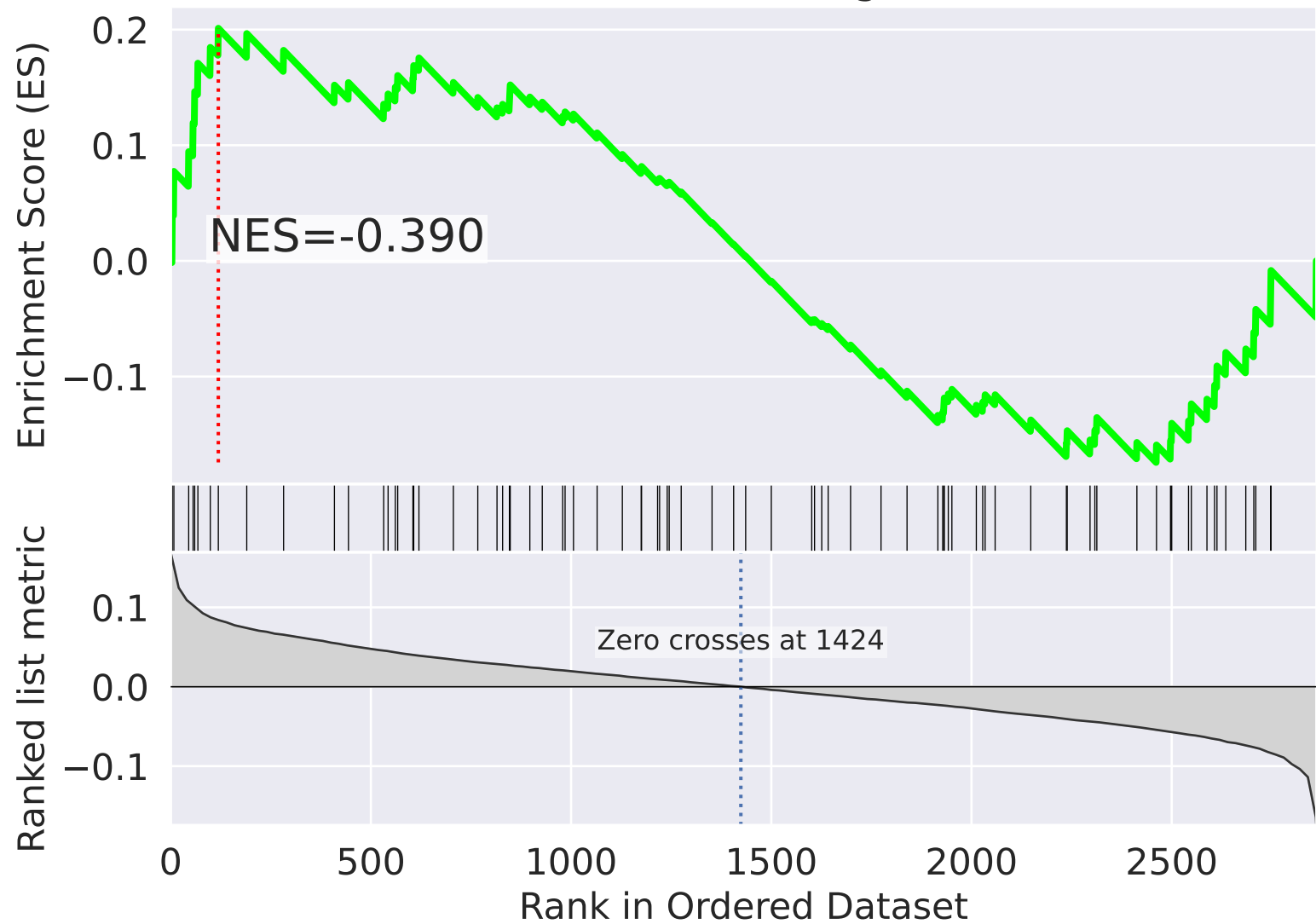


NES		SET
3.997		mRNA export from nucleus (GO:0006406)
-3.560		transcription from RNA polymerase III promoter (GO:0006383)
3.456		RNA export from nucleus (GO:0006405)
3.248		protein sumoylation (GO:0016925)
3.016		protein ubiquitination (GO:0016567)
2.973		regulation of gene silencing by miRNA (GO:0060964)
2.969		viral process (GO:0016032)
2.955		tricarboxylic acid cycle (GO:0006099)
2.952		termination of RNA polymerase II transcription (GO:0006369)
-2.905		termination of RNA polymerase I transcription (GO:0006363)
2.863		intracellular steroid hormone receptor signaling pathway (GO:0030518)
2.827		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.808		intracellular transport of virus (GO:0075733)
2.778		androgen receptor signaling pathway (GO:0030521)
-2.749		muscle contraction (GO:0006936)

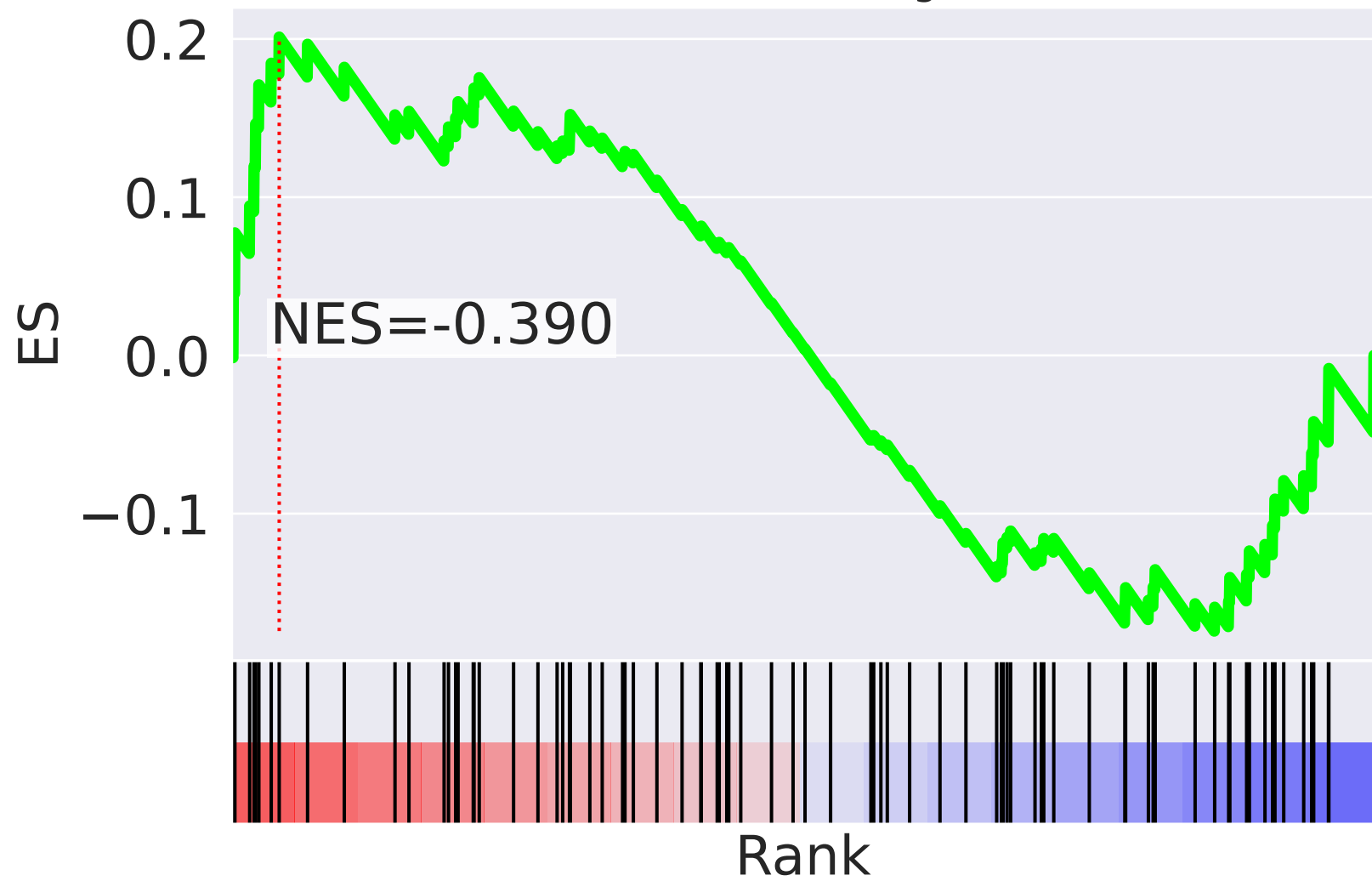


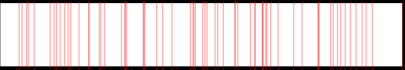
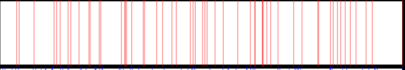
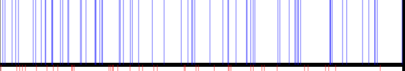
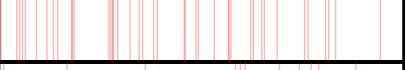

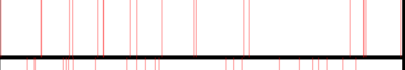
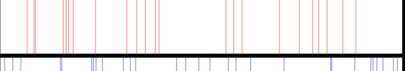
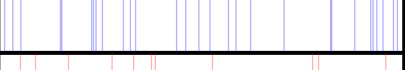
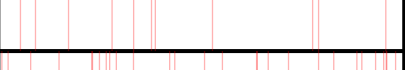
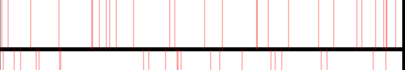
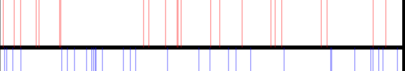
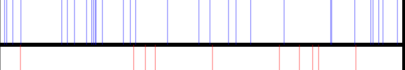



The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=15$

# mitochondrial translational elongation (GO:0070125)



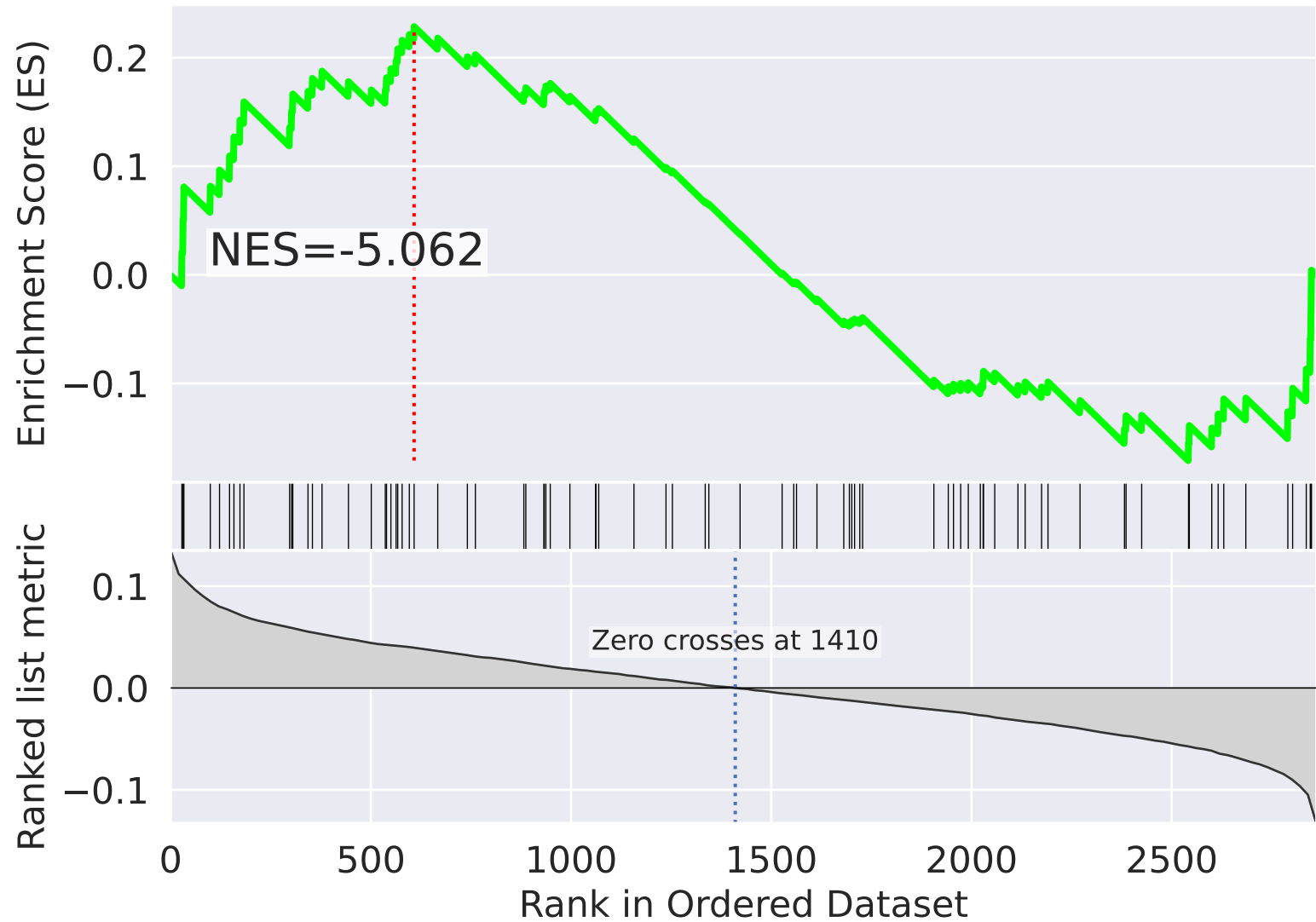
mitochondrial translational elongation (GO:0070125)



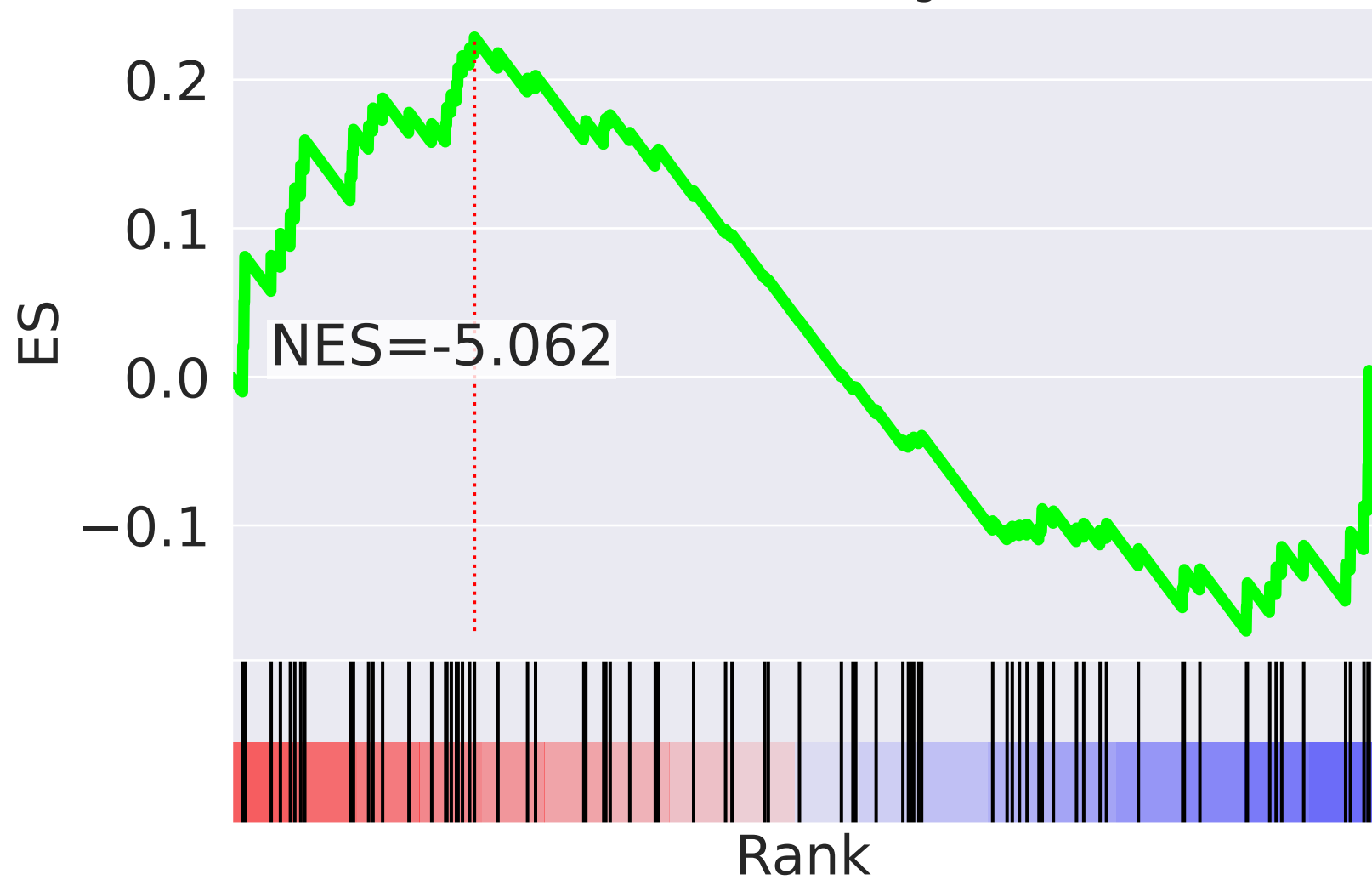
NES		SET
3.850		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.156		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-3.045		sister chromatid cohesion (GO:0007062)
3.033		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.981		JNK cascade (GO:0007254)
2.943		multivesicular body assembly (GO:0036258)
2.862		positive regulation of NF-kappaB transcription factor activity (GO:0051092)
-2.841		viral process (GO:0016032)
2.833		regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)
2.766		interstrand cross-link repair (GO:0036297)
2.719		negative regulation of gene expression (GO:0010629)
-2.684		mitotic nuclear envelope disassembly (GO:0007077)
2.679		nucleotide-binding oligomerization domain containing signaling pathway (GO:0070423)
2.667		positive regulation of cell differentiation (GO:0045597)
2.664		positive regulation of GTPase activity (GO:0043547)

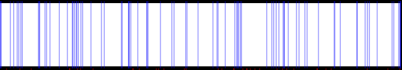
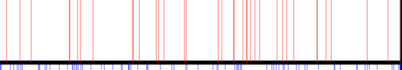
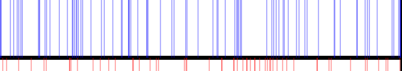
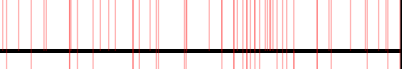



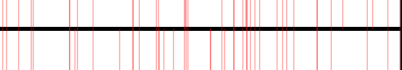
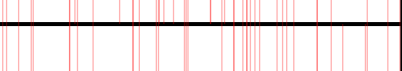

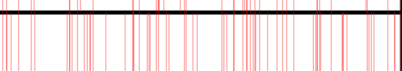
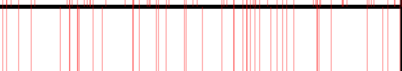

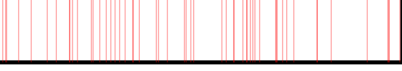

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=16$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

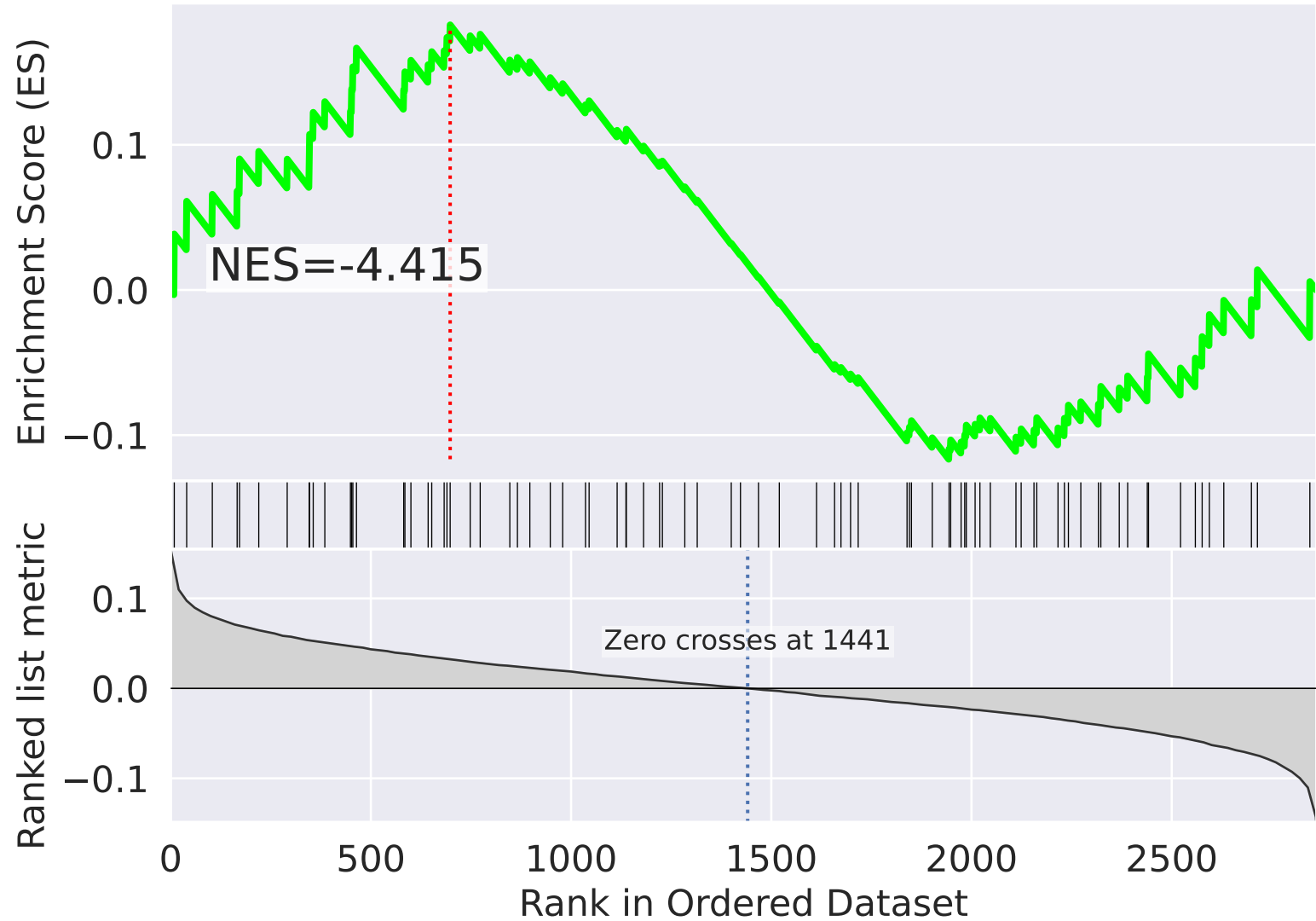


NES		SET
-5.062		mitochondrial translational elongation (GO:0070125)
5.025		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
-4.971		mitochondrial translational termination (GO:0070126)
4.936		anaphase-promoting complex-dependent catabolic process (GO:0031145)
4.928		regulation of cellular amino acid metabolic process (GO:0006521)
4.926		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
4.889		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
4.858		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
4.839		NIK/NF-kappaB signaling (GO:0038061)
4.798		negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
4.699		tumor necrosis factor-mediated signaling pathway (GO:0033209)
4.653		MAPK cascade (GO:0000165)
4.608		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
4.504		positive regulation of canonical Wnt signaling pathway (GO:0090263)
4.455		regulation of mRNA stability (GO:0043488)

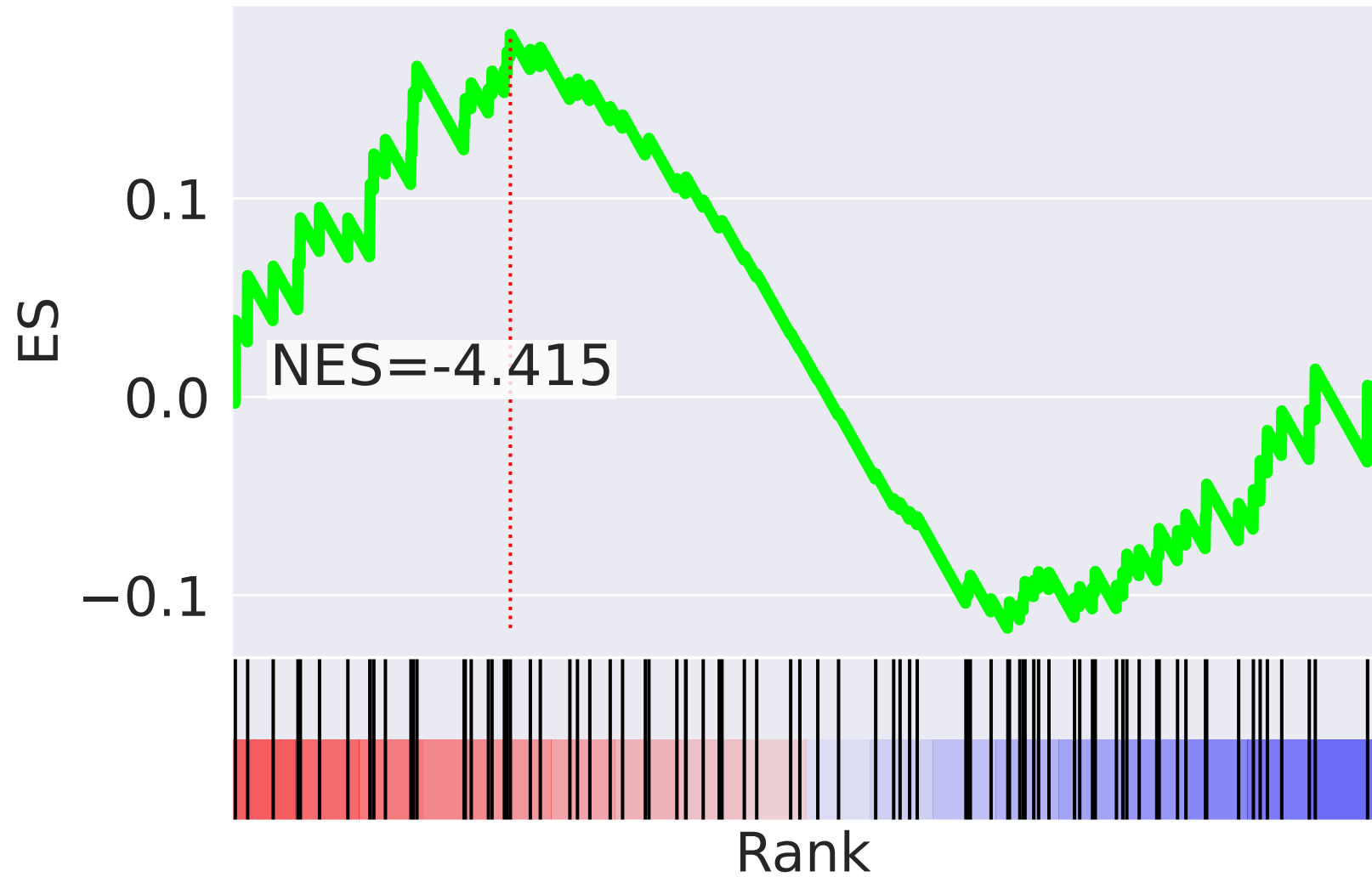


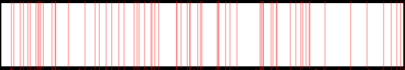
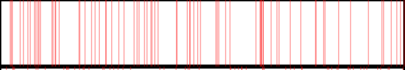
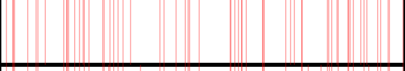
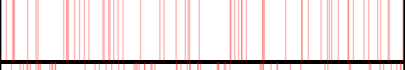
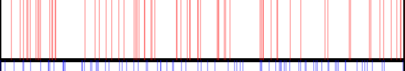
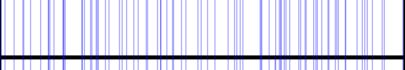
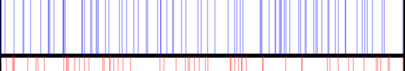
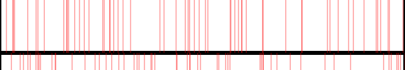
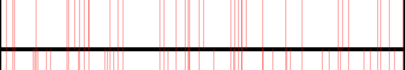
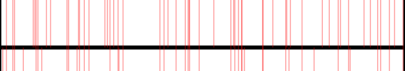

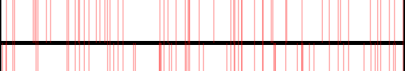
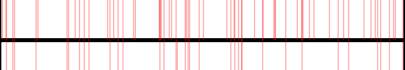
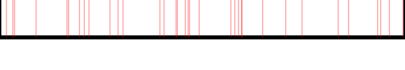
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=17$

# mitochondrial translational elongation (GO:0070125)



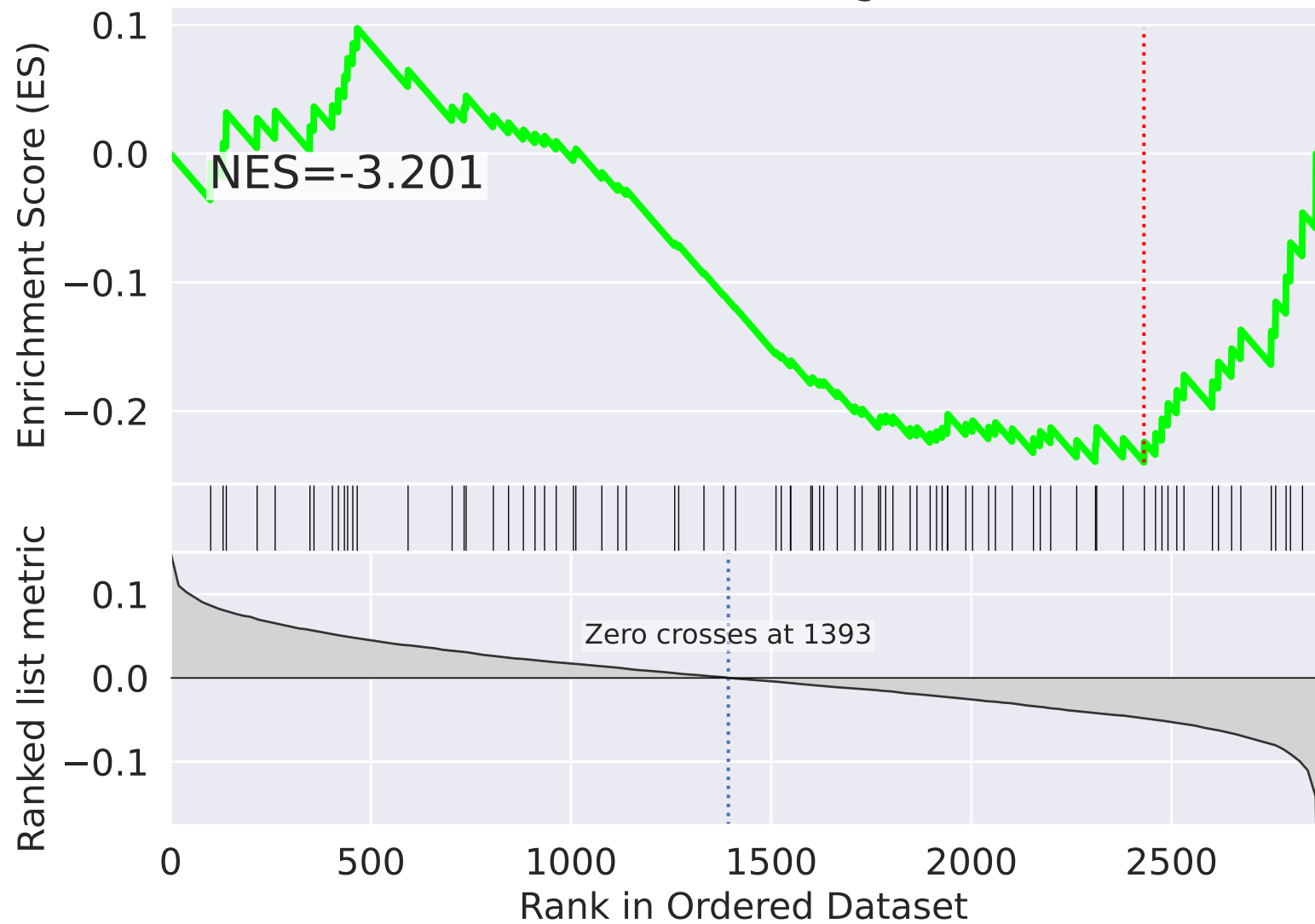
mitochondrial translational elongation (GO:0070125)



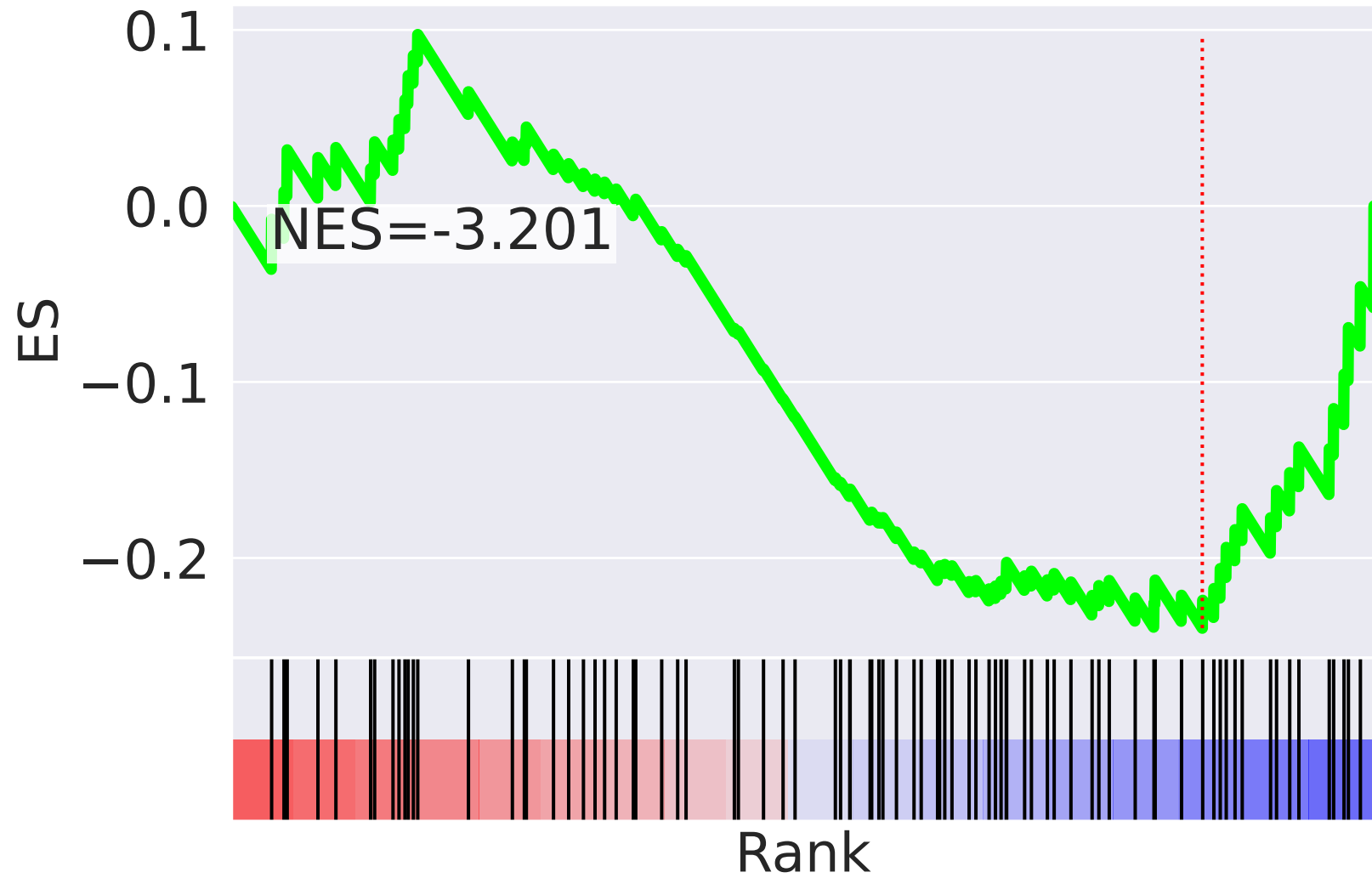
NES		SET
5.257		translational initiation (GO:0006413)
4.668		viral transcription (GO:0019083)
4.623		Fc-epsilon receptor signaling pathway (GO:0038095)
4.586		T cell receptor signaling pathway (GO:0050852)
4.501		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-4.429		mitochondrial translational termination (GO:0070126)
-4.415		mitochondrial translational elongation (GO:0070125)
4.360		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
4.109		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
4.026		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
3.921		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
3.851		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
3.850		anaphase-promoting complex-dependent catabolic process (GO:0031145)
3.768		protein polyubiquitination (GO:0000209)
3.742		regulation of cellular amino acid metabolic process (GO:0006521)

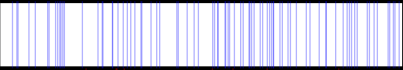

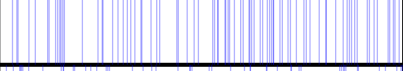
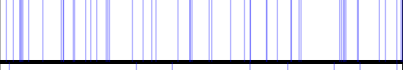


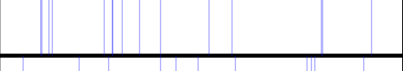




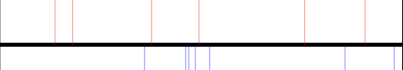
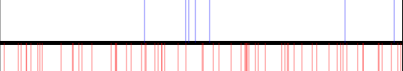
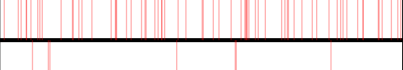

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=18$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

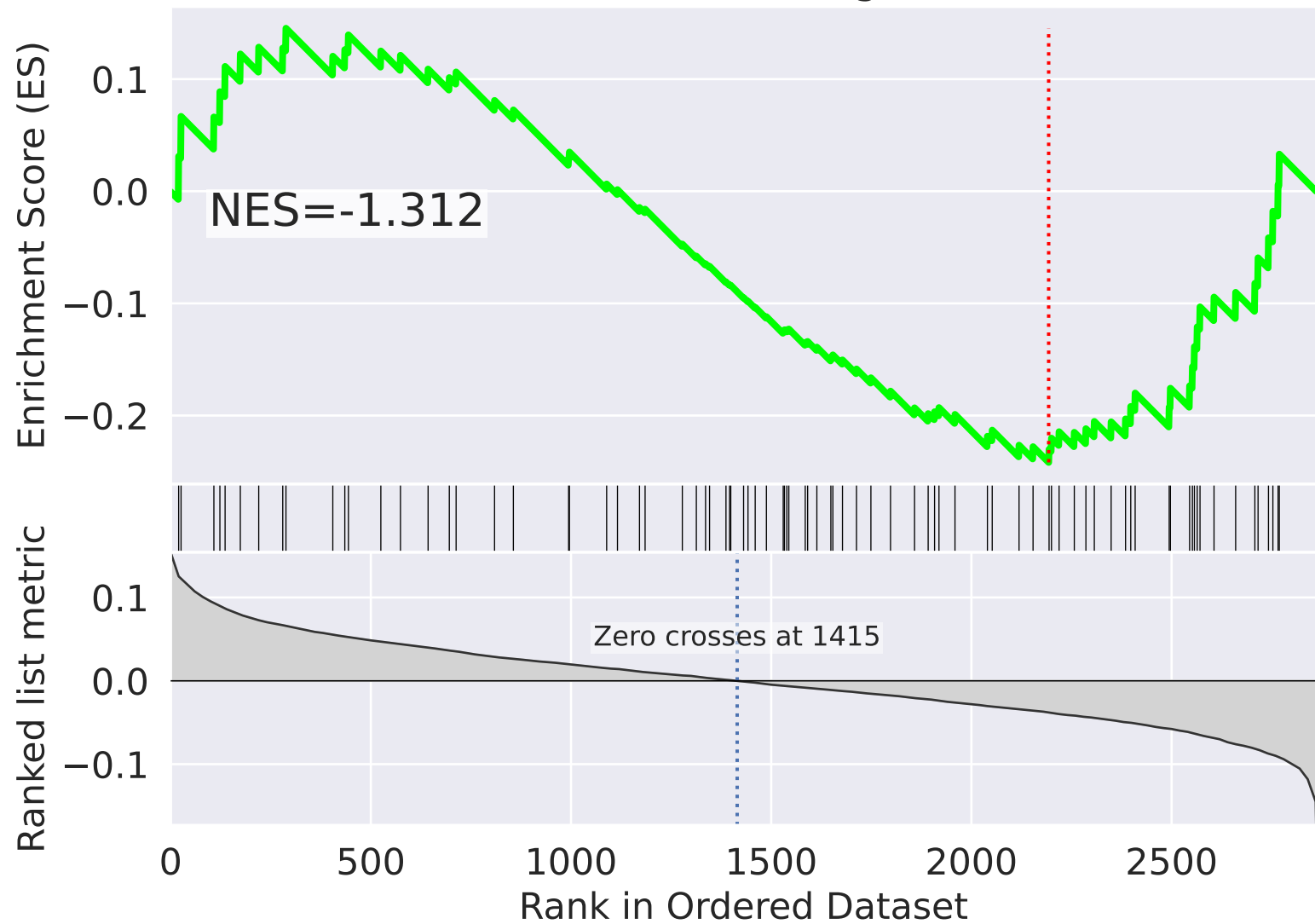


NES		SET
-3.357		mitochondrial translational termination (GO:0070126)
3.290		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
-3.201		mitochondrial translational elongation (GO:0070125)
-2.950		G1/S transition of mitotic cell cycle (GO:0000082)
-2.893		glycosaminoglycan biosynthetic process (GO:0006024)
-2.838		positive regulation of telomerase RNA localization to Cajal body (GO:1904874)
-2.823		replication fork processing (GO:0031297)
-2.791		negative regulation of protein binding (GO:0032091)
-2.784		nucleotide-excision repair, DNA gap filling (GO:0006297)
-2.761		IRE1-mediated unfolded protein response (GO:0036498)
2.726		endocytosis (GO:0006897)
2.699		nucleocytoplasmic transport (GO:0006913)
-2.643		peptidyl-tyrosine phosphorylation (GO:0018108)
2.641		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.594		receptor internalization (GO:0031623)

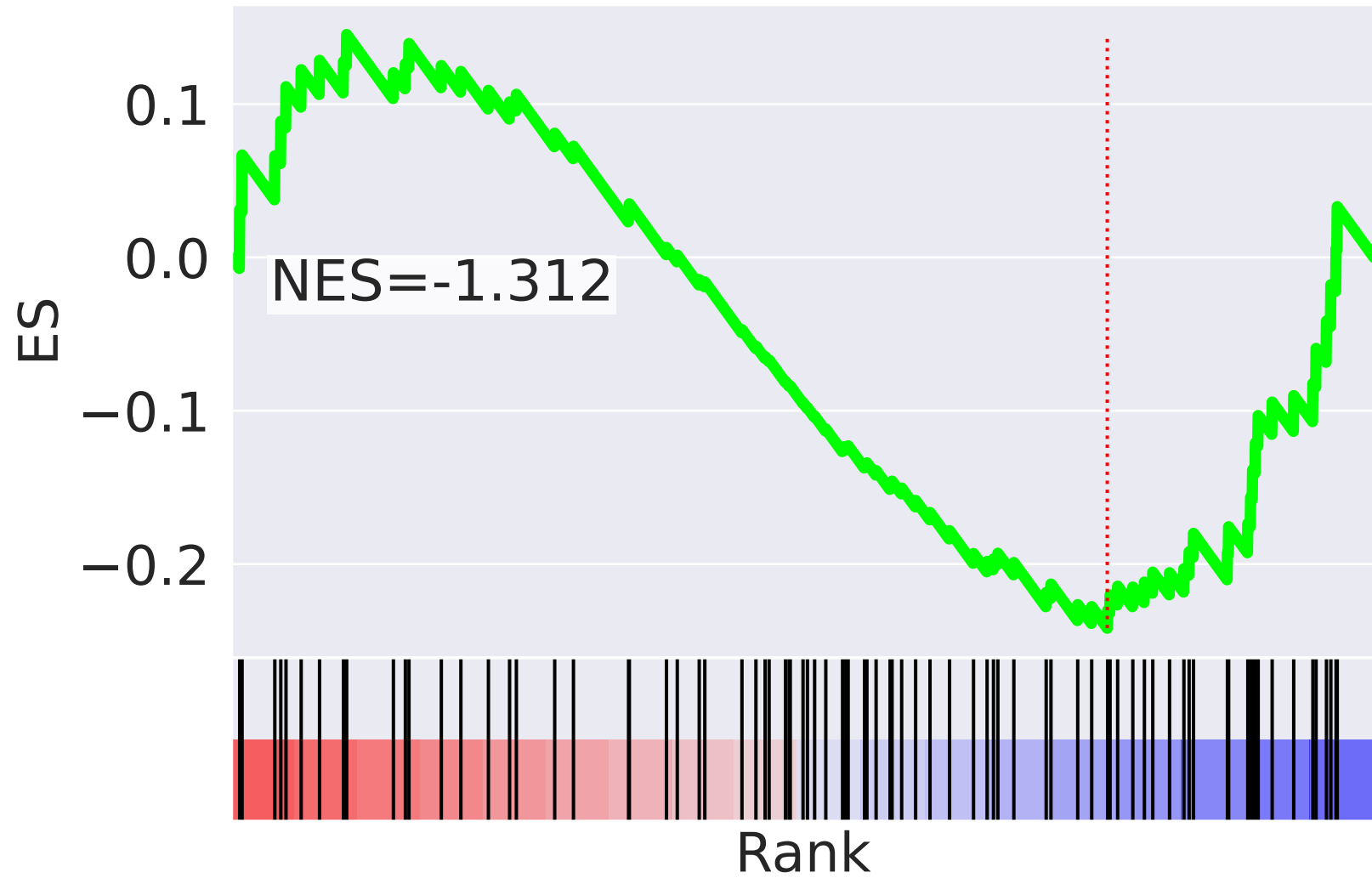


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=19$

# mitochondrial translational elongation (GO:0070125)



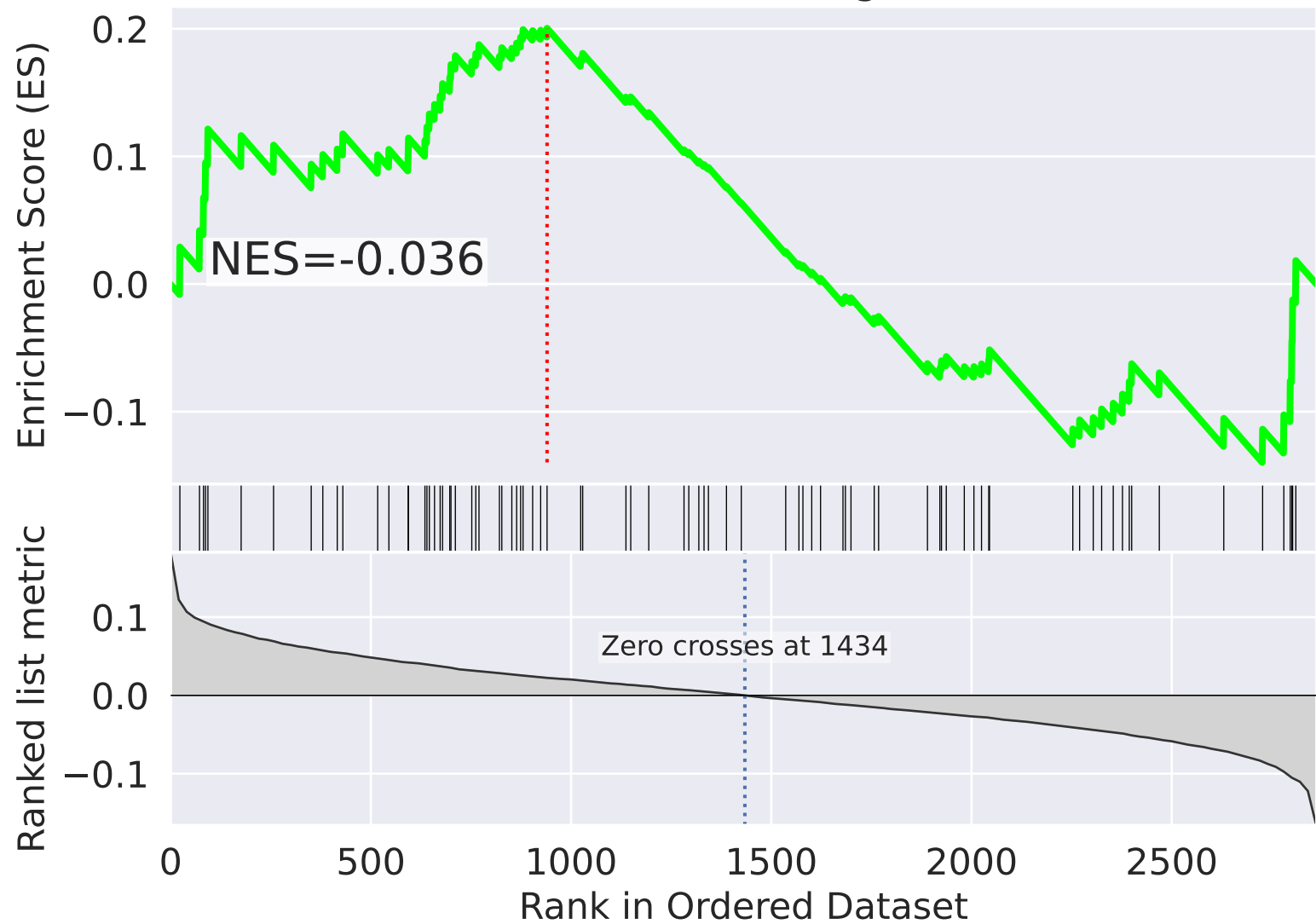
mitochondrial translational elongation (GO:0070125)



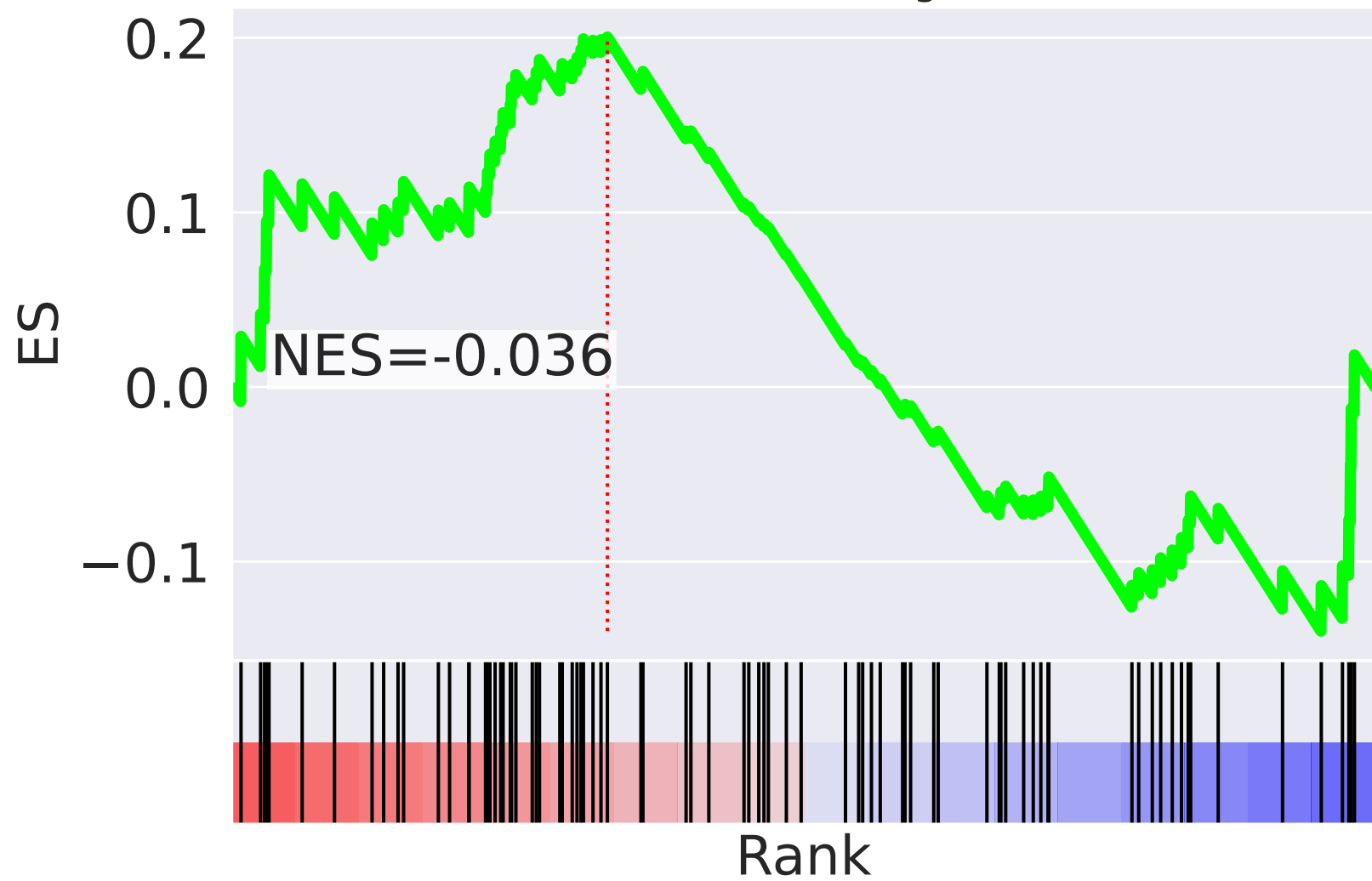
NES		SET
-3.155		RNA splicing (GO:0008380)
3.030		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
2.898		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.878		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.724		beta-catenin-TCF complex assembly (GO:1904837)
-2.651		centriole replication (GO:0007099)
2.648		cilium assembly (GO:0060271)
-2.615		spliceosomal complex assembly (GO:0000245)
2.615		translational initiation (GO:0006413)
-2.596		central nervous system development (GO:0007417)
-2.520		positive regulation of transcription initiation from RNA polymerase II promoter (GO:0060261)
-2.497		protein localization to kinetochore (GO:0034501)
-2.473		cytoplasmic microtubule organization (GO:0031122)
-2.471		iron-sulfur cluster assembly (GO:0016226)
2.463		viral transcription (GO:0019083)

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

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

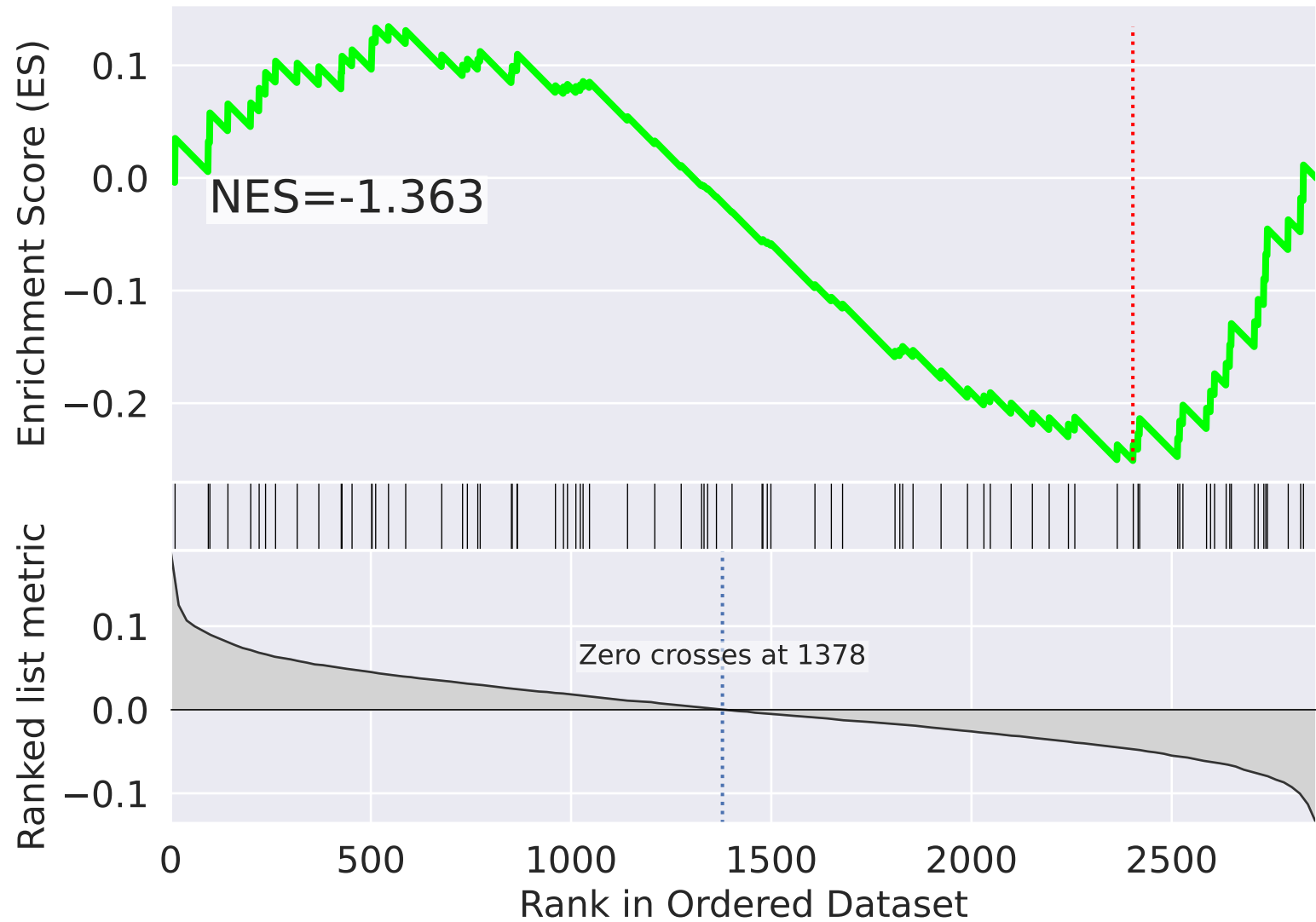


NES	SET
5.044	stimulatory C-type lectin receptor signaling pathway (GO:0002223)
4.536	Fc-epsilon receptor signaling pathway (GO:0038095)
4.519	T cell receptor signaling pathway (GO:0050852)
4.259	NIK/NF-kappaB signaling (GO:0038061)
4.216	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
4.172	tumor necrosis factor-mediated signaling pathway (GO:0033209)
4.144	regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
4.125	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
4.037	regulation of cellular amino acid metabolic process (GO:0006521)
3.918	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
3.868	negative regulation of canonical Wnt signaling pathway (GO:0090090)
3.787	positive regulation of NF-kappaB transcription factor activity (GO:0051092)
3.772	transmembrane transport (GO:0055085)
3.698	positive regulation of canonical Wnt signaling pathway (GO:0090263)
3.642	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)

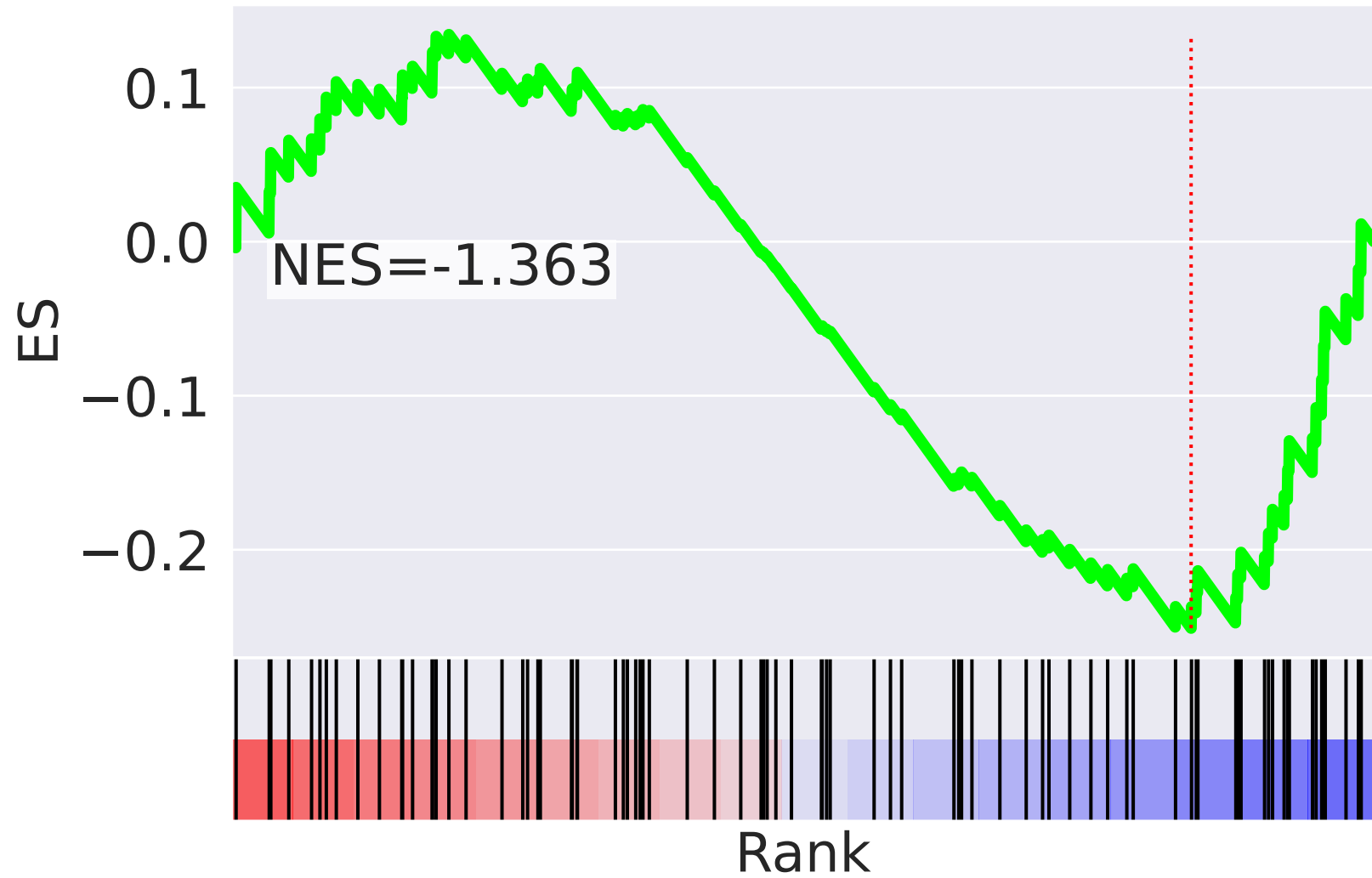


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=21$

# mitochondrial translational elongation (GO:0070125)



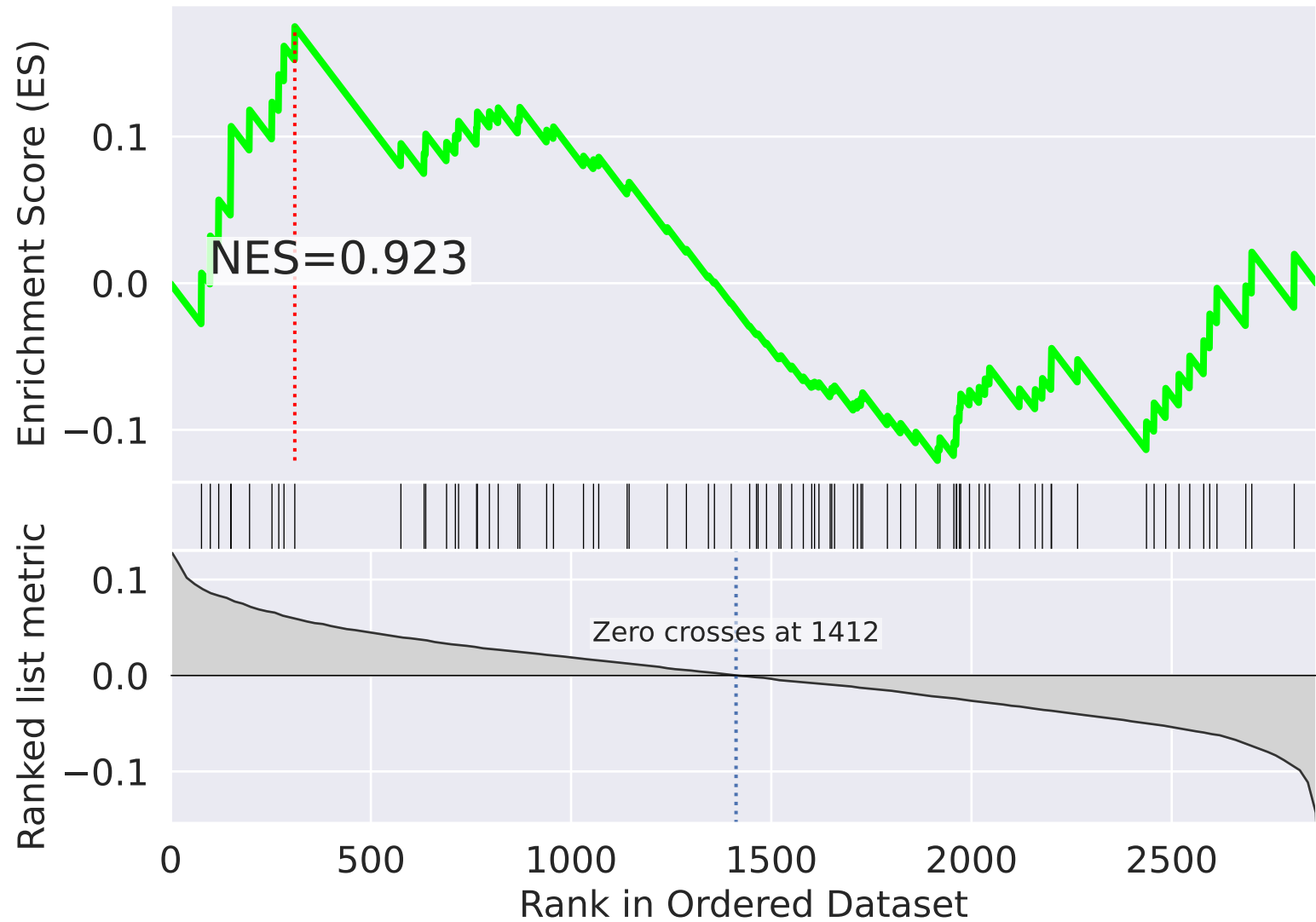
mitochondrial translational elongation (GO:0070125)



NES		SET
-3.277		regulation of cell proliferation (GO:0042127)
3.090		negative regulation of TOR signaling (GO:0032007)
3.080		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-2.930		nucleotide-excision repair, DNA damage recognition (GO:0000715)
-2.874		protein deneddylation (GO:0000338)
-2.864		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.863		tricarboxylic acid cycle (GO:0006099)
2.840		membrane organization (GO:0061024)
2.825		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.676		intracellular protein transport (GO:0006886)
2.647		nucleobase-containing compound metabolic process (GO:0006139)
-2.617		positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)
2.595		positive regulation of DNA-templated transcription, elongation (GO:0032786)
2.495		cellular response to lipopolysaccharide (GO:0071222)
2.493		transferrin transport (GO:0033572)

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

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

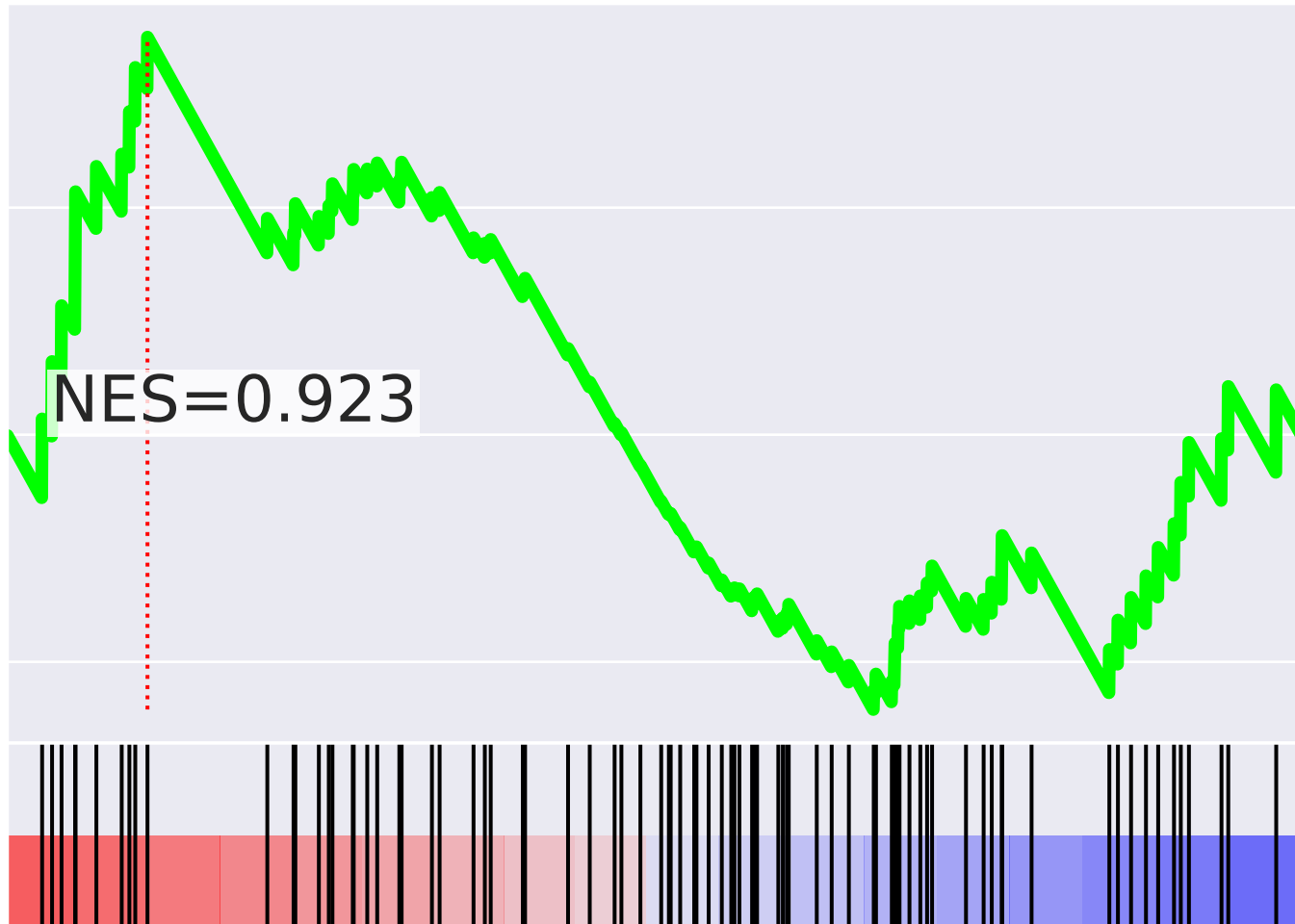
ES

NES=0.923

-0.1

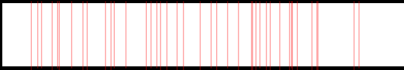
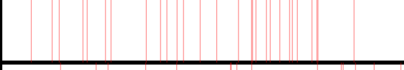
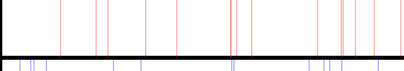
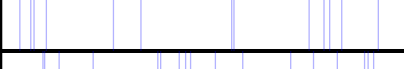

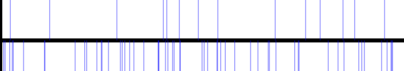
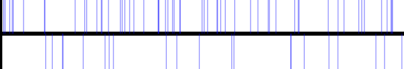
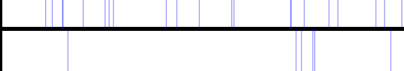


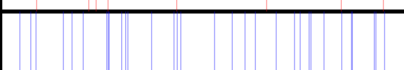
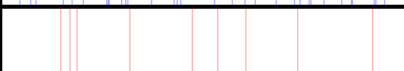



0.1

Rank



NES

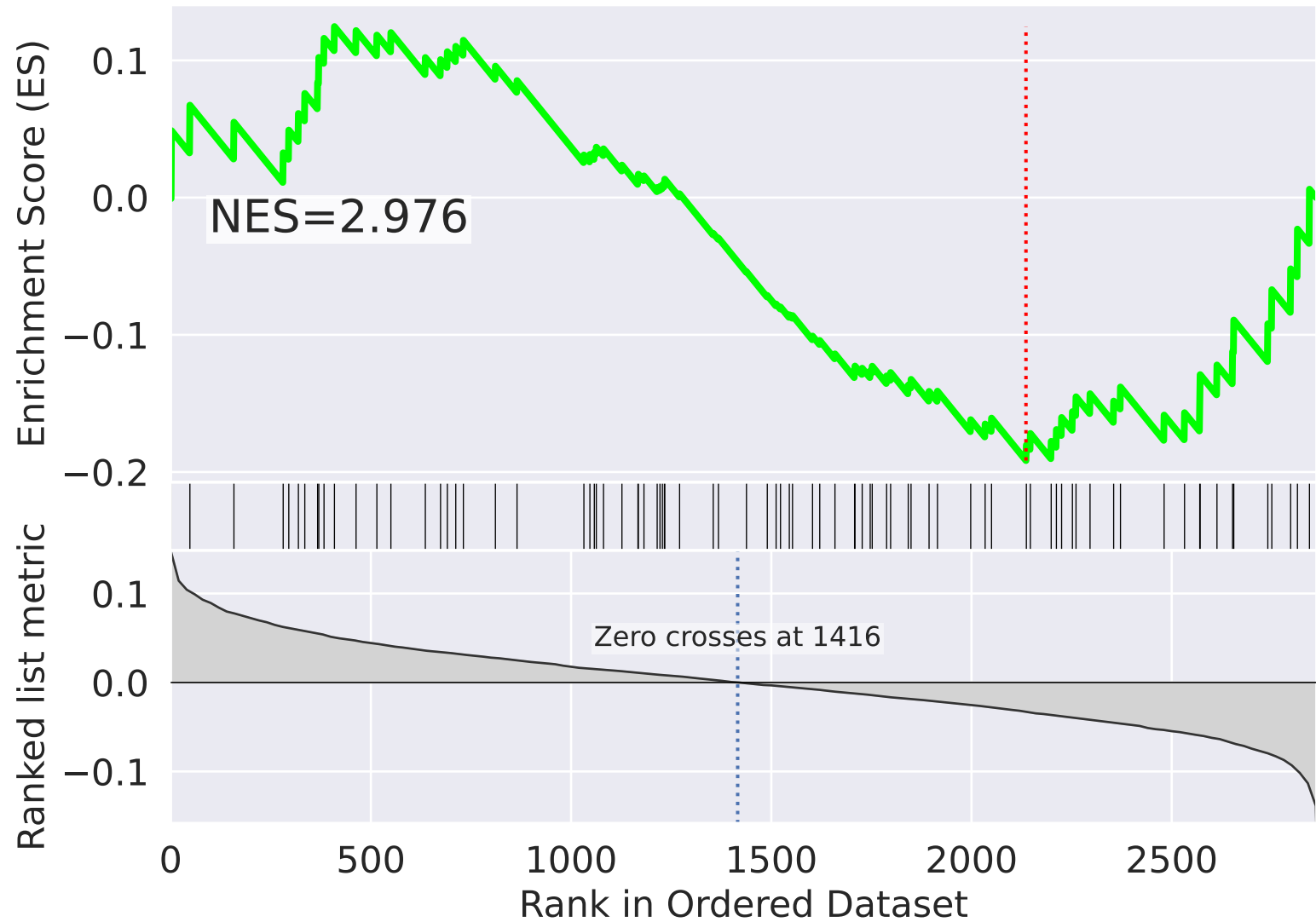
SET

5.524		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.642		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.209		tricarboxylic acid cycle (GO:0006099)
-2.856		transcription from RNA polymerase III promoter (GO:0006383)
-2.759		regulation of small GTPase mediated signal transduction (GO:0051056)
-2.745		regulation of mitophagy (GO:1903146)
-2.703		G2/M transition of mitotic cell cycle (GO:0000086)
-2.692		positive regulation of type I interferon production (GO:0032481)
-2.631		adherens junction organization (GO:0034332)
2.597		respiratory chain complex IV assembly (GO:0008535)
2.516		cellular nitrogen compound metabolic process (GO:0034641)
-2.475		transcription, DNA-templated (GO:0006351)
2.456		spermatogenesis (GO:0007283)
-2.451		hemopoiesis (GO:0030097)
-2.448		microtubule bundle formation (GO:0001578)

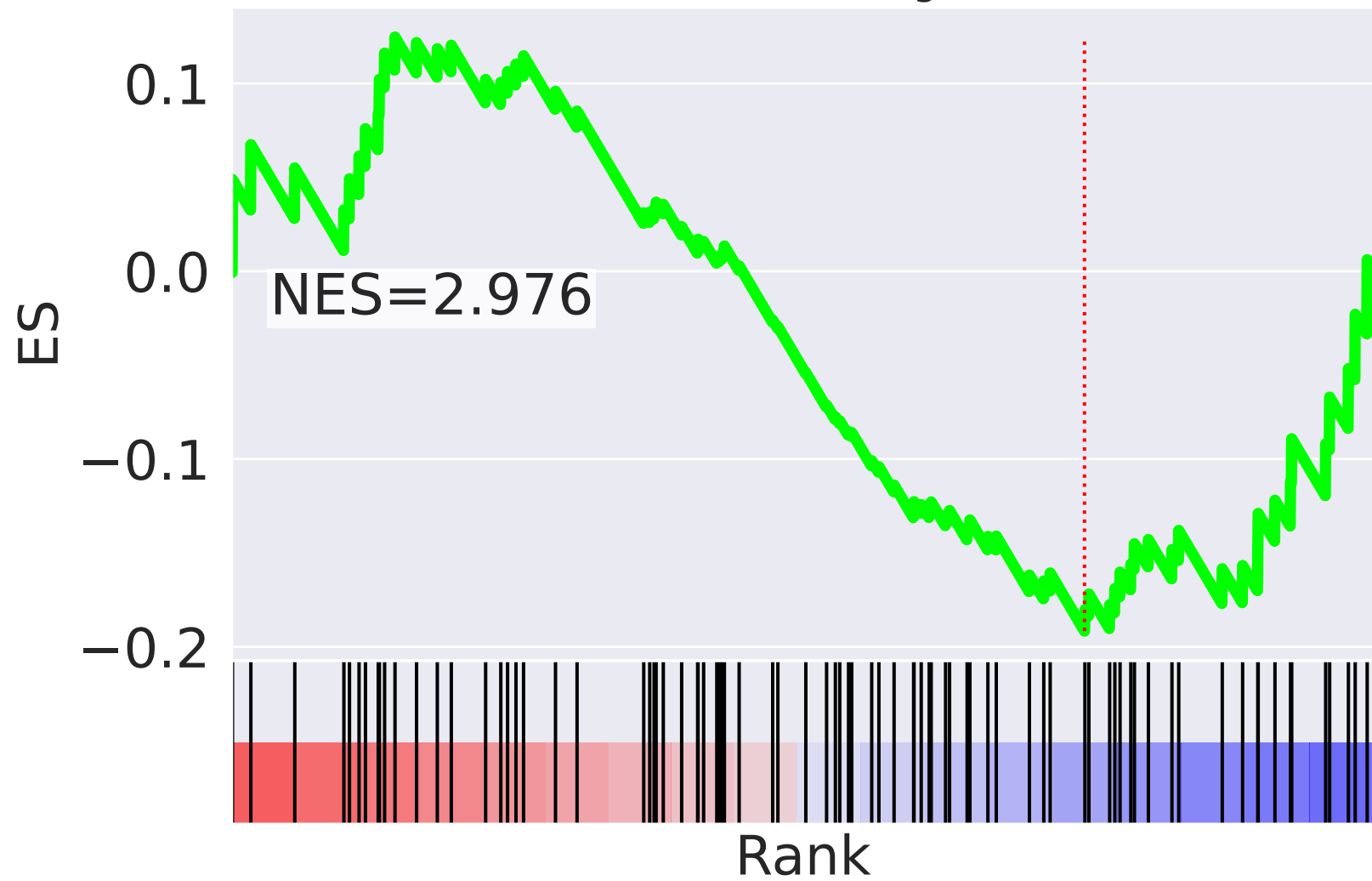


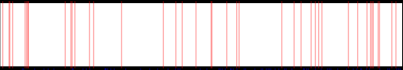
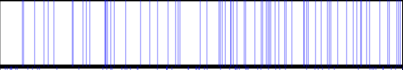
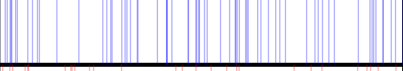
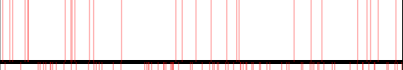
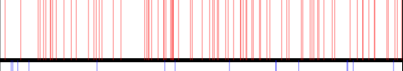
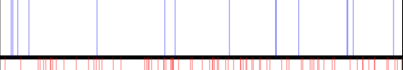
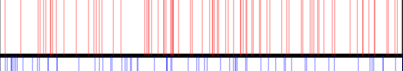
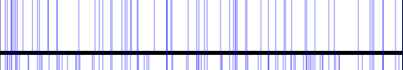
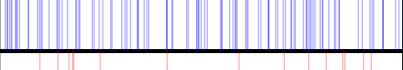
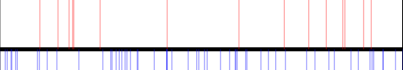
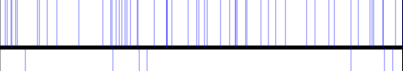




The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=23$

# mitochondrial translational elongation (GO:0070125)



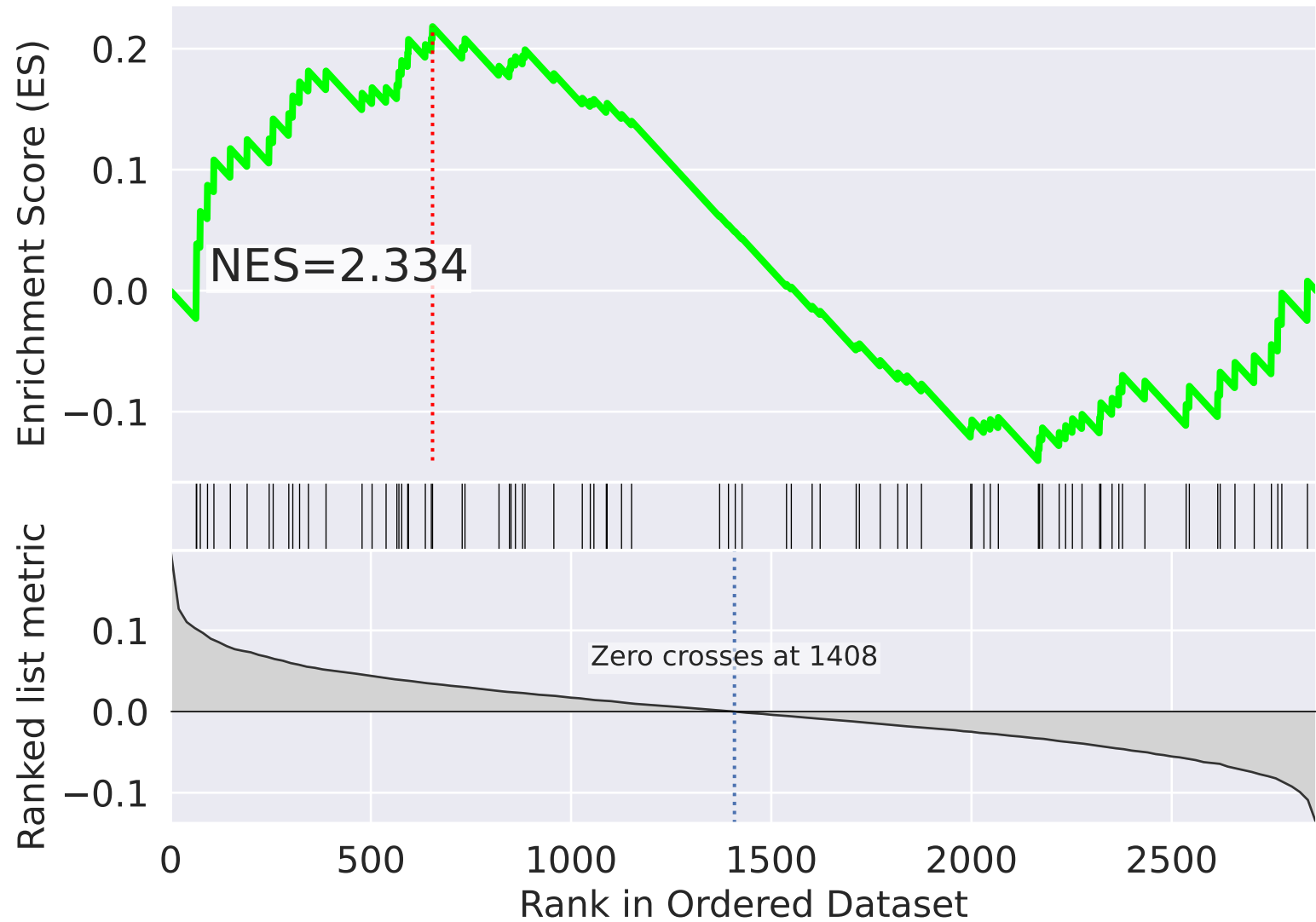
mitochondrial translational elongation (GO:0070125)



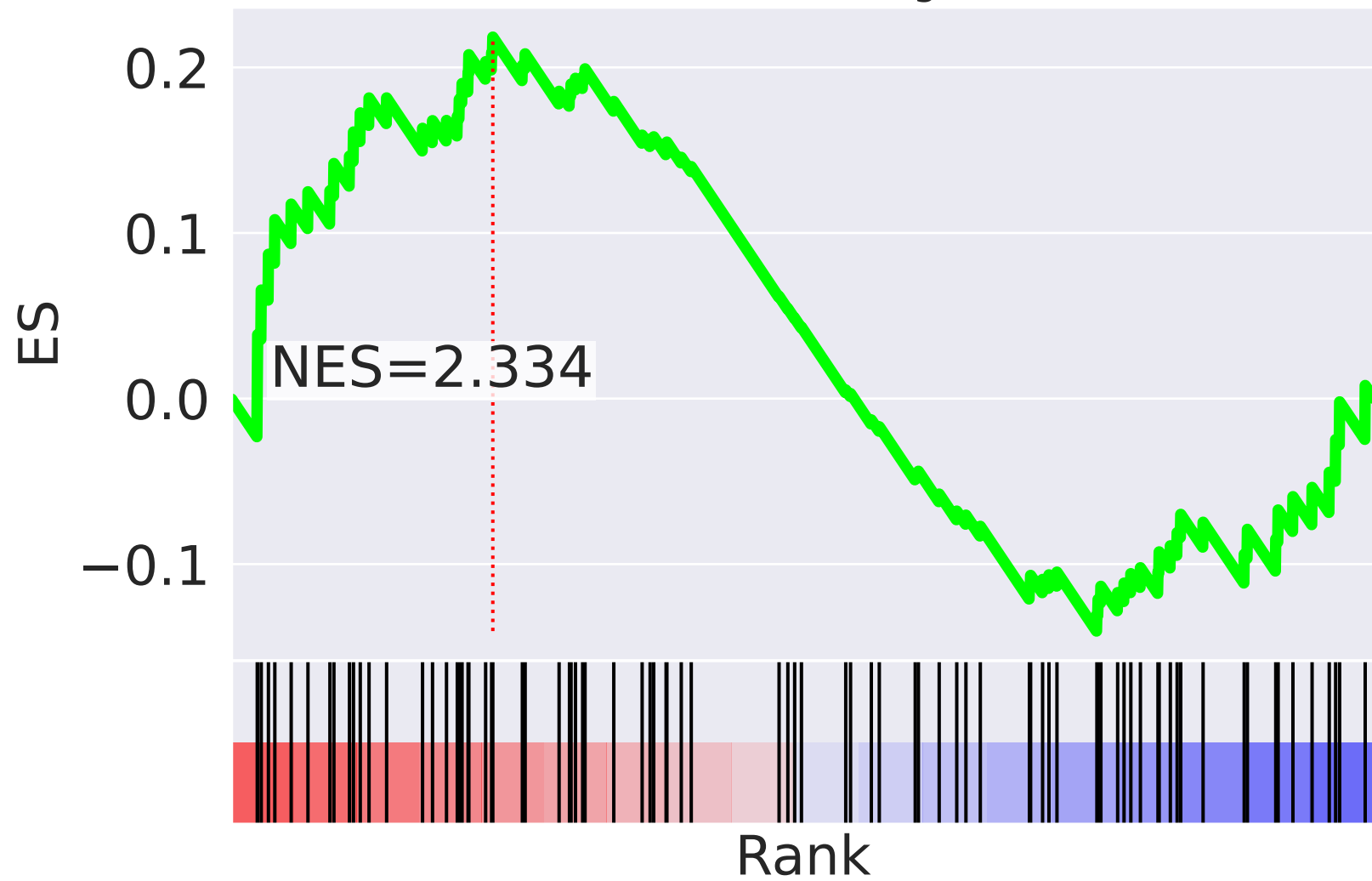
NES		SET
3.876		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.319		positive regulation of cell proliferation (GO:0008284)
-3.016		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.984		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.976		mitochondrial translational elongation (GO:0070125)
-2.958		positive regulation of protein catabolic process (GO:0045732)
2.867		mitochondrial translational termination (GO:0070126)
-2.850		translational initiation (GO:0006413)
-2.812		rRNA processing (GO:0006364)
2.793		tricarboxylic acid cycle (GO:0006099)
-2.751		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.634		protein targeting to membrane (GO:0006612)
-2.542		negative regulation of protein binding (GO:0032091)
-2.521		positive regulation of GTPase activity (GO:0043547)
-2.500		establishment of endothelial intestinal barrier (GO:0090557)



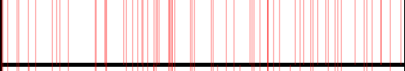
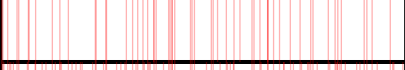
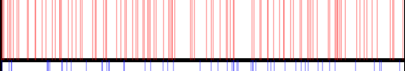
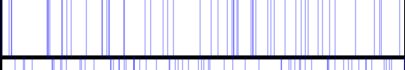
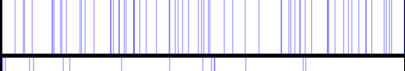
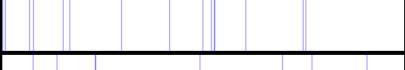

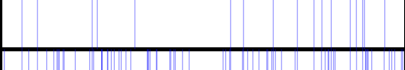
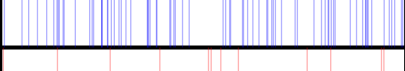


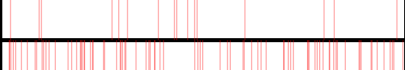
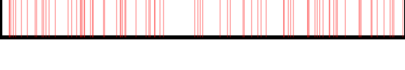
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=24$

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

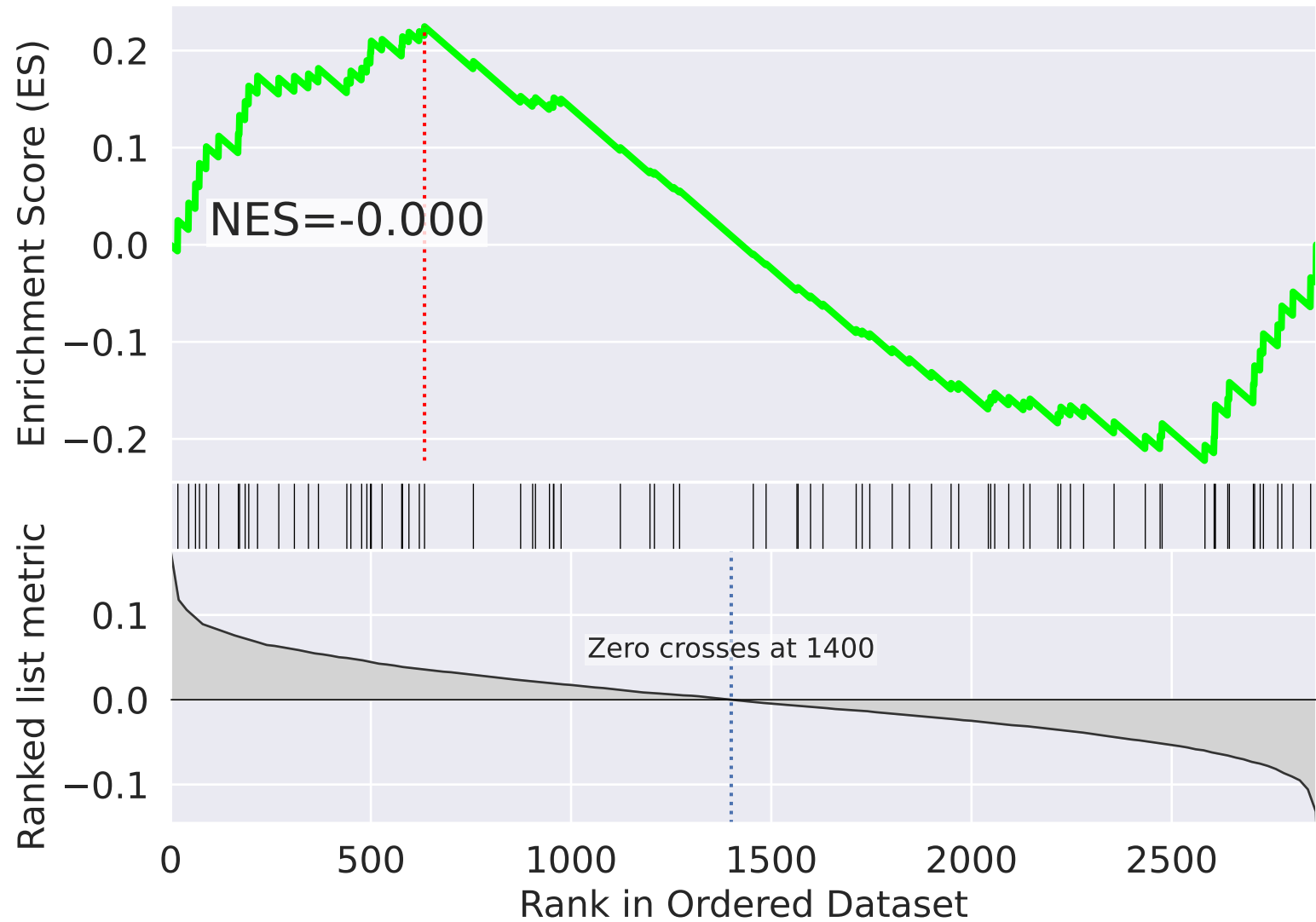


NES		SET
3.827		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.230		regulation of mitotic spindle assembly (GO:1901673)
3.127		translational initiation (GO:0006413)
3.099		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
3.060		translation (GO:0006412)
-3.041		membrane organization (GO:0061024)
-2.861		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.852		cellular response to amino acid starvation (GO:0034198)
-2.829		regulation of cytokinesis (GO:0032465)
-2.801		DNA damage checkpoint (GO:0000077)
-2.771		regulation of signal transduction by p53 class mediator (GO:1901796)
2.750		cellular response to epidermal growth factor stimulus (GO:0071364)
2.730		regulation of cell motility (GO:2000145)
2.656		generation of precursor metabolites and energy (GO:0006091)
2.627		mitochondrial translational termination (GO:0070126)



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

# mitochondrial translational elongation (GO:0070125)



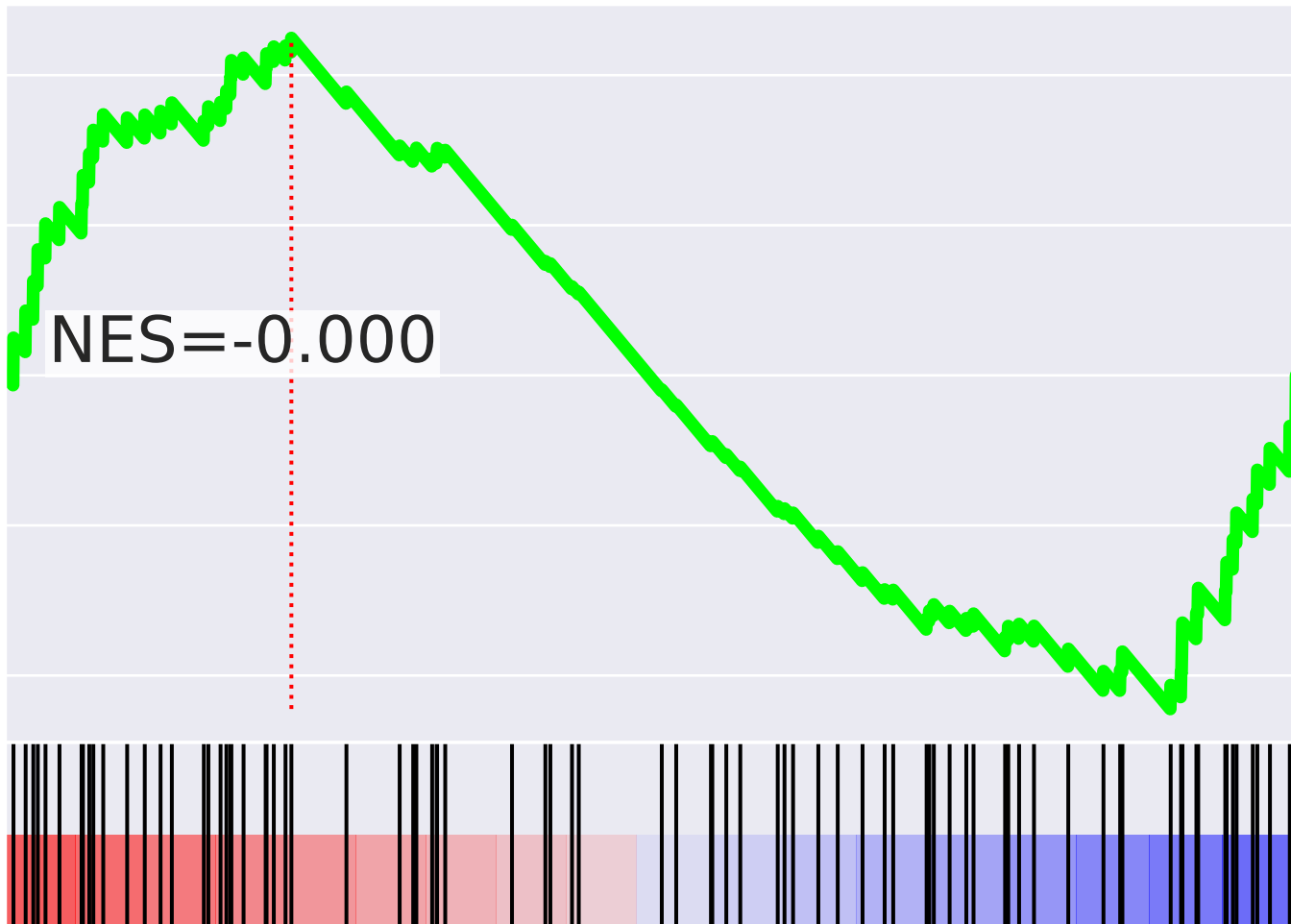
mitochondrial translational elongation (GO:0070125)



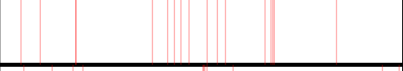
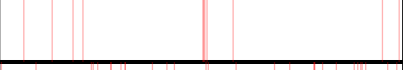
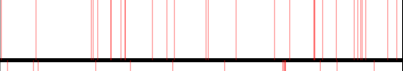
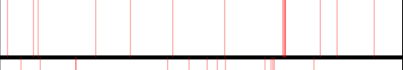
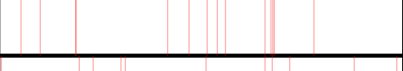
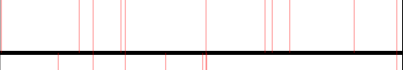
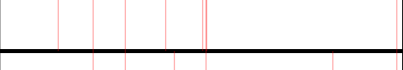
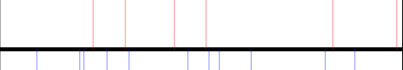


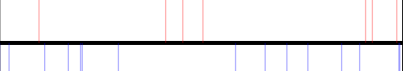


ES

0.2  
0.1  
0.0  
-0.1  
-0.2

NES=-0.000

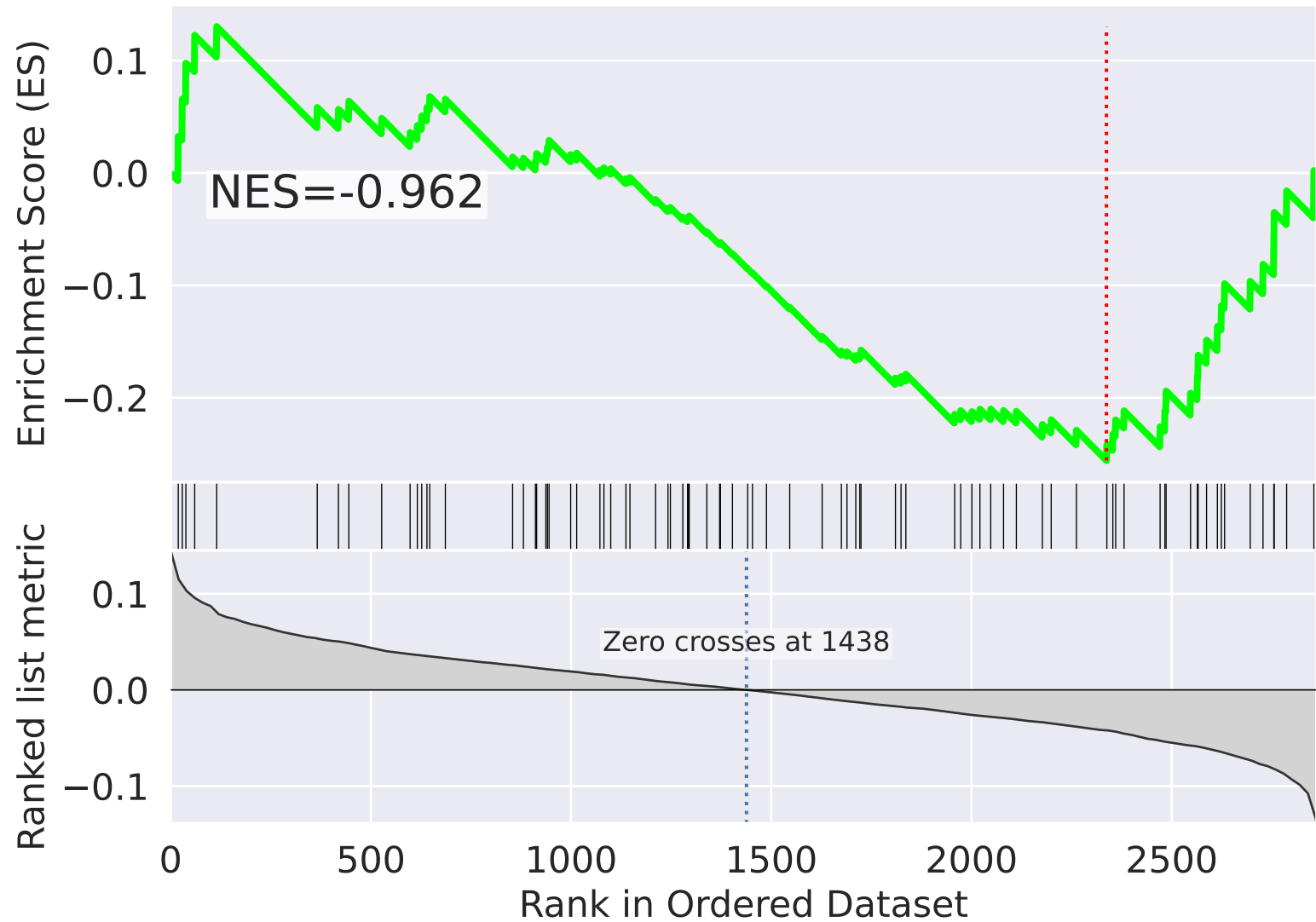
Rank



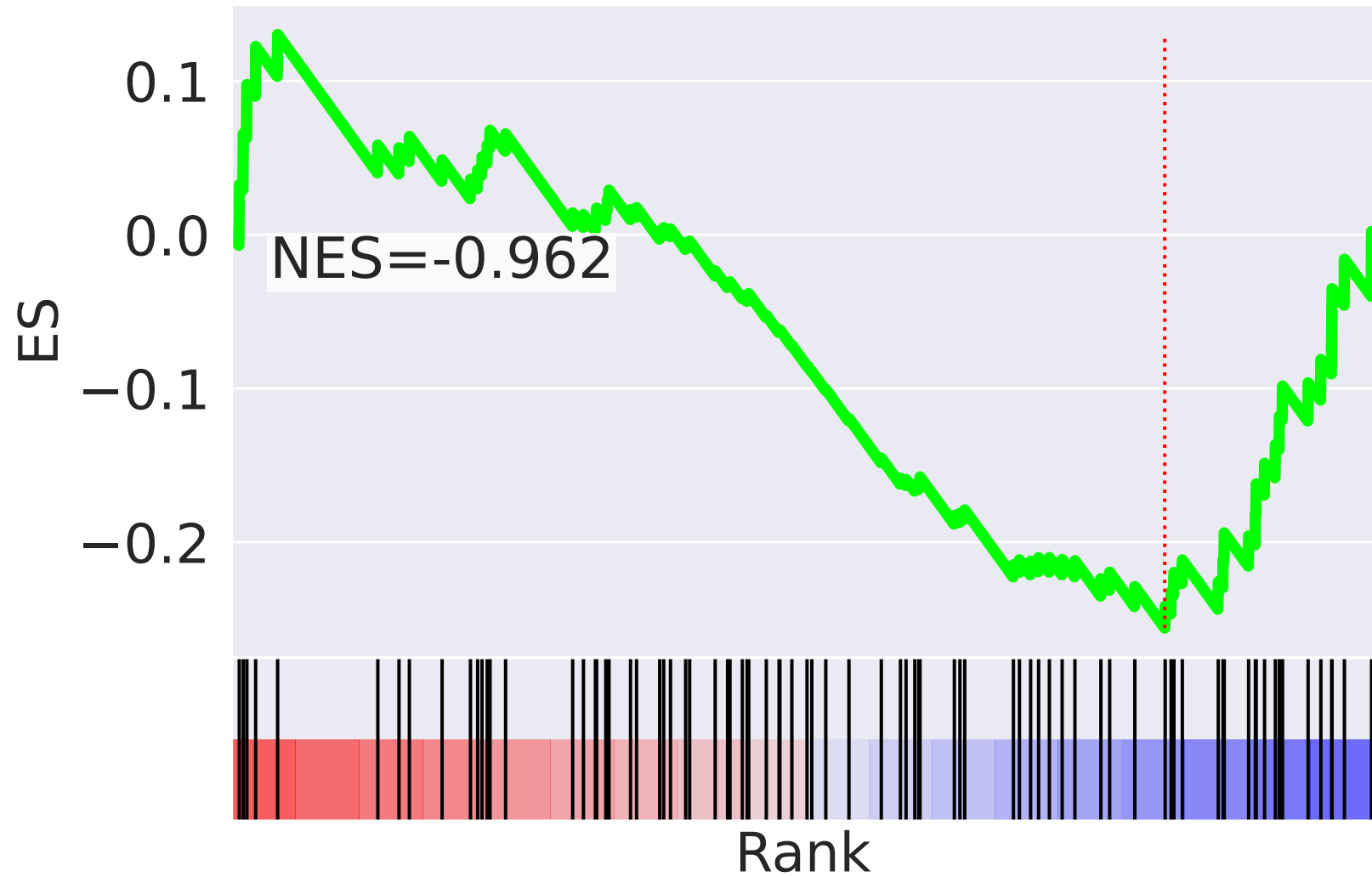
NES		SET
3.819		nervous system development (GO:0007399)
3.328		retrograde transport, endosome to Golgi (GO:0042147)
3.084		transferrin transport (GO:0033572)
2.993		negative regulation of TOR signaling (GO:0032007)
2.980		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.946		tricarboxylic acid cycle (GO:0006099)
2.933		phagosome acidification (GO:0090383)
2.929		regulation of defense response to virus by virus (GO:0050690)
2.781		clathrin-dependent endocytosis (GO:0072583)
2.760		low-density lipoprotein particle receptor catabolic process (GO:0032802)
-2.754		negative regulation of protein ubiquitination (GO:0031397)
-2.748		positive regulation of protein kinase activity (GO:0045860)
2.663		regulation of endocytosis (GO:0030100)
-2.642		spliceosomal snRNP assembly (GO:0000387)
2.617		low-density lipoprotein particle clearance (GO:0034383)



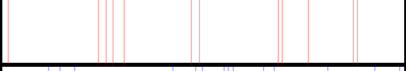
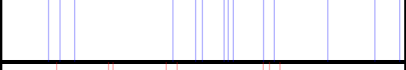

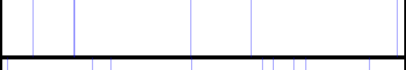


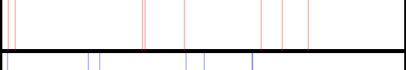
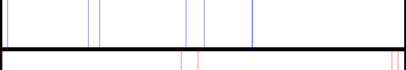



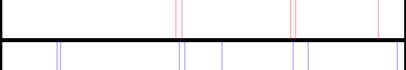

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=26$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

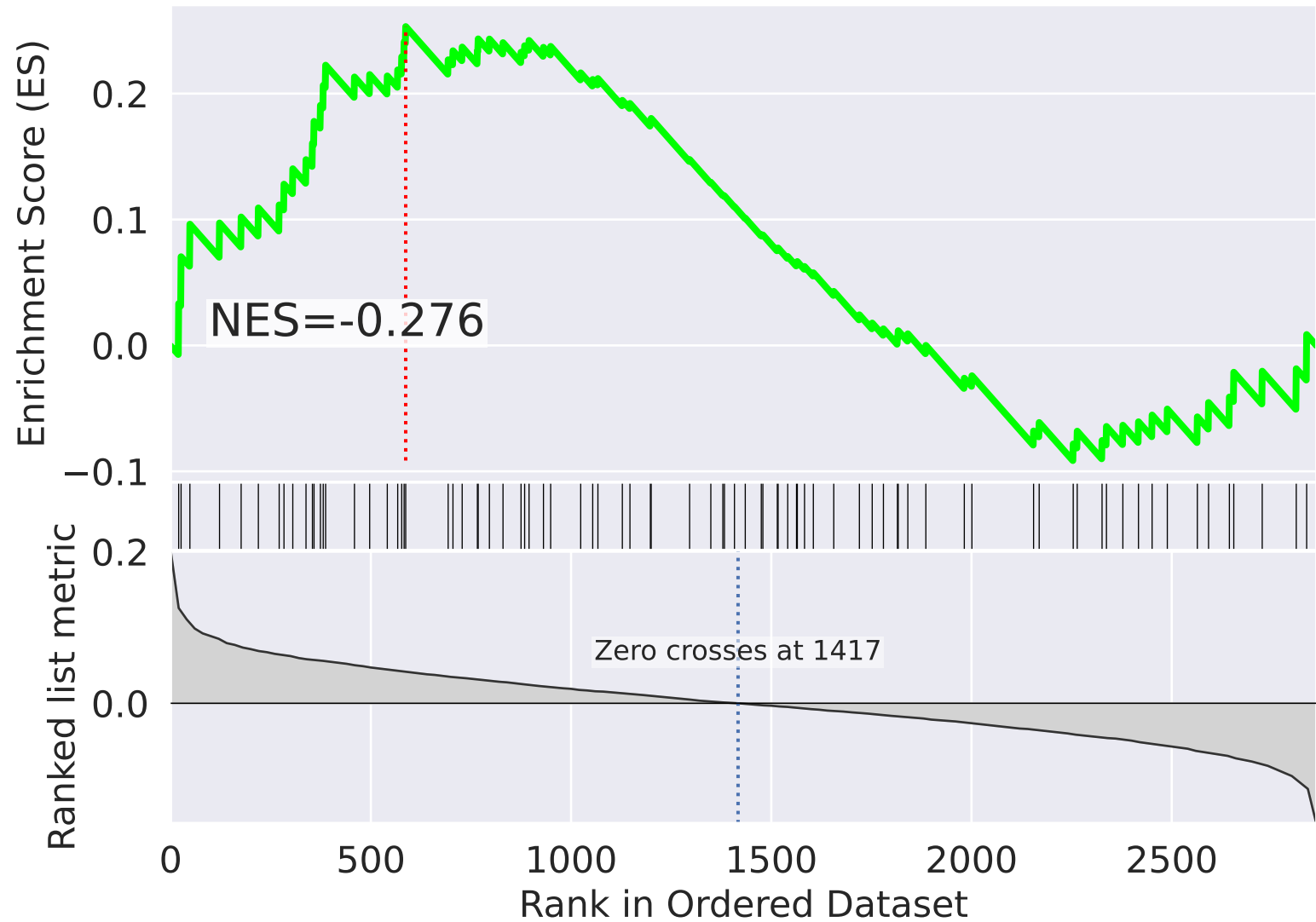


NES		SET
-2.802		protein ubiquitination (GO:0016567)
2.783		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.760		regulation of gene expression (GO:0010468)
-2.688		T cell costimulation (GO:0031295)
2.551		xenobiotic metabolic process (GO:0006805)
-2.458		stress fiber assembly (GO:0043149)
-2.453		protein destabilization (GO:0031648)
2.447		mRNA processing (GO:0006397)
2.406		positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)
-2.387		histone monoubiquitination (GO:0010390)
2.373		regulation of focal adhesion assembly (GO:0051893)
-2.370		maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463)
2.338		positive regulation of cell cycle (GO:0045787)
2.334		protein transport (GO:0015031)
-2.322		intrinsic apoptotic signaling pathway (GO:0097193)

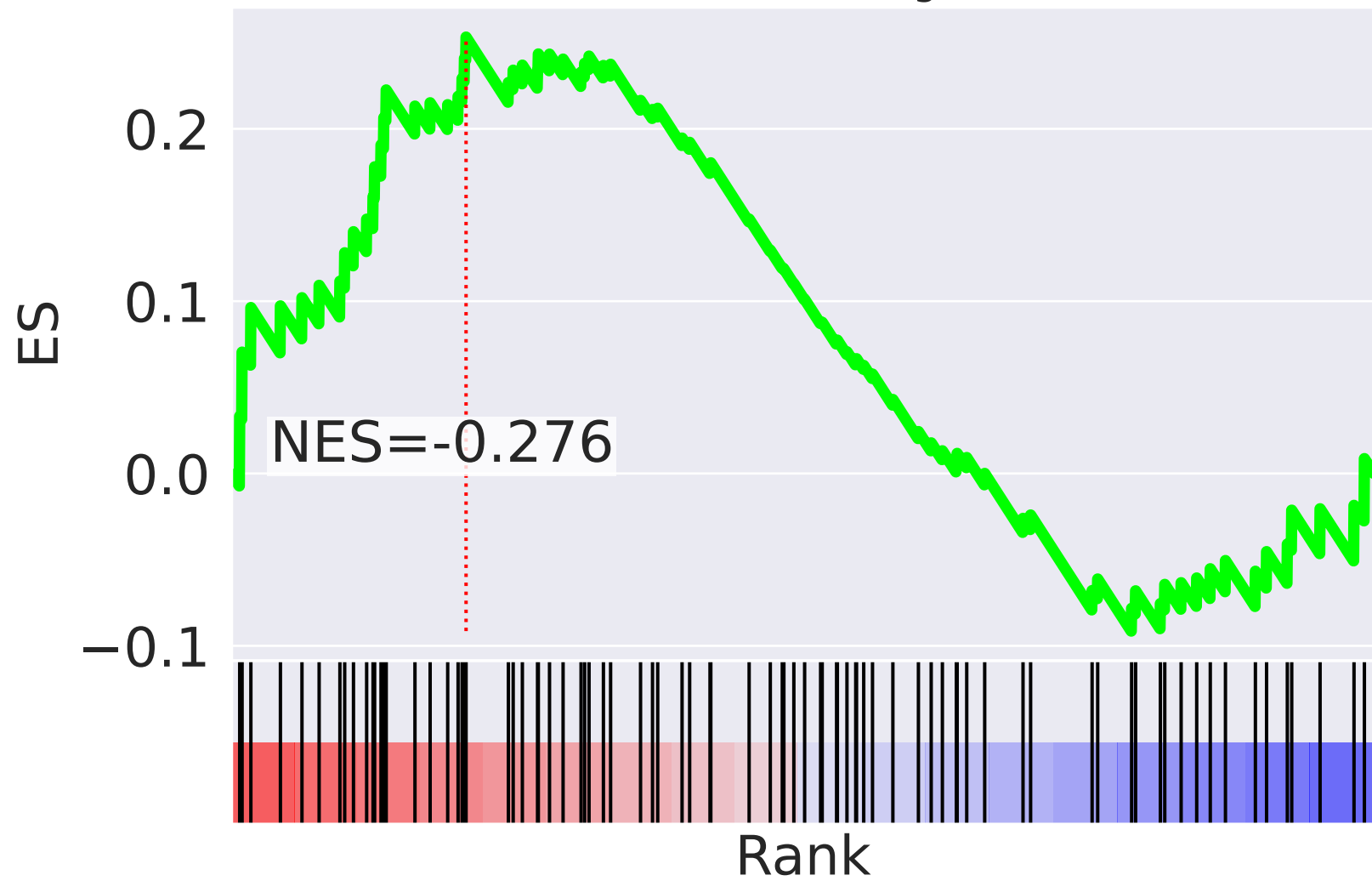


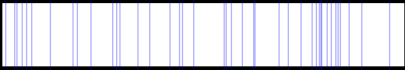
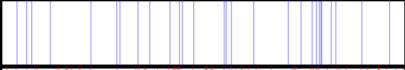
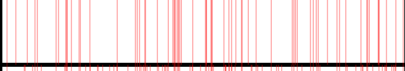
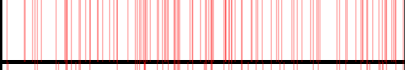
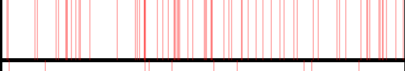
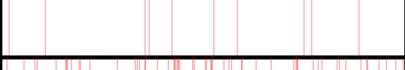
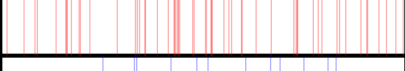
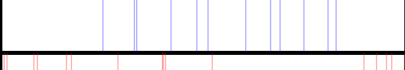
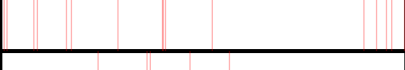
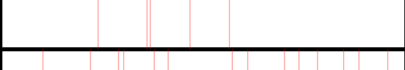

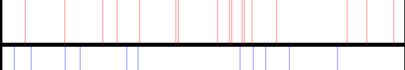
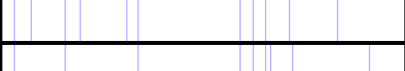
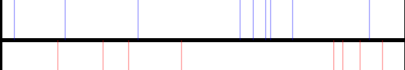
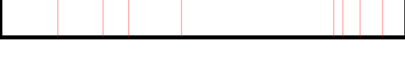
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=27$

# mitochondrial translational elongation (GO:0070125)



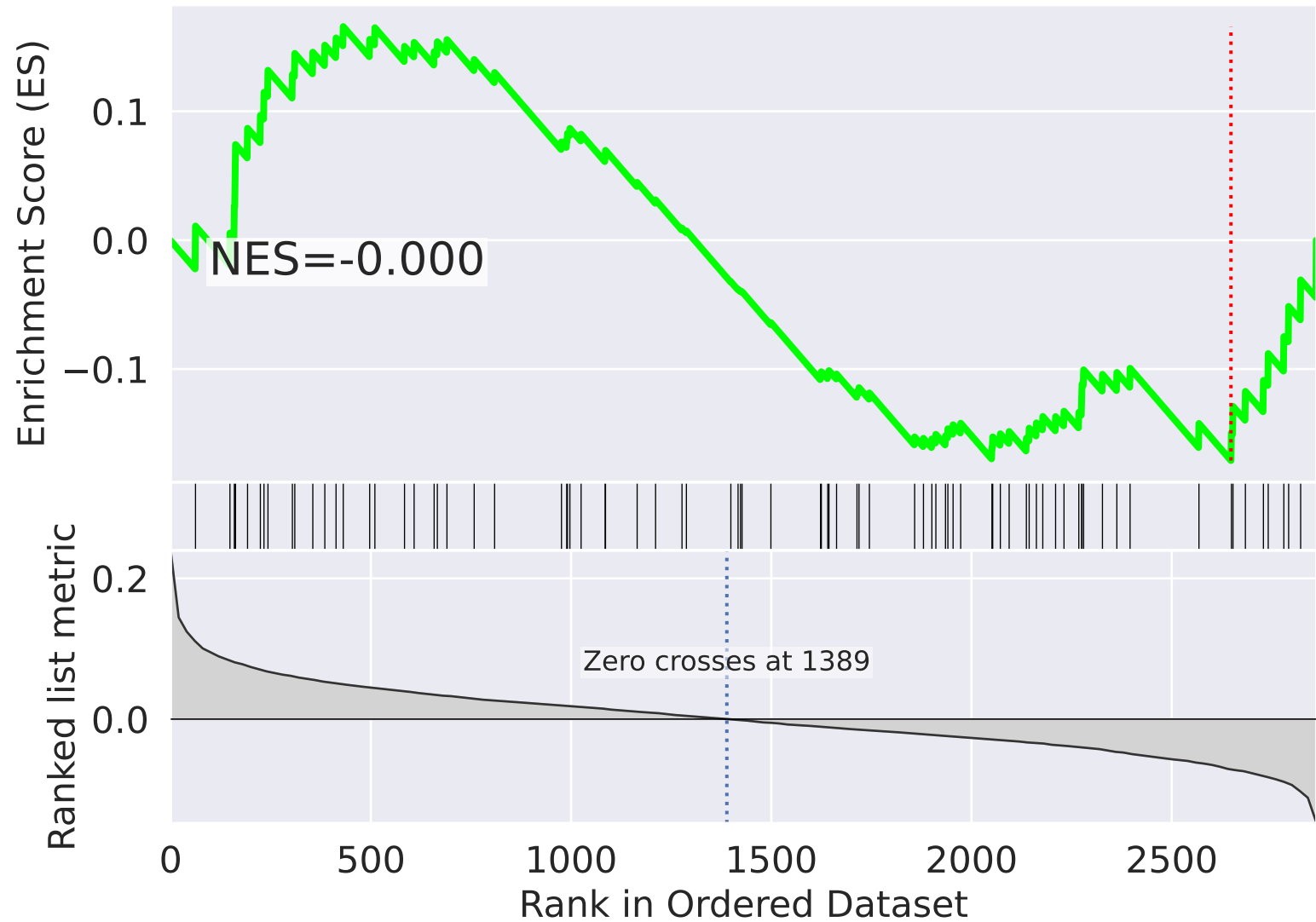
mitochondrial translational elongation (GO:0070125)



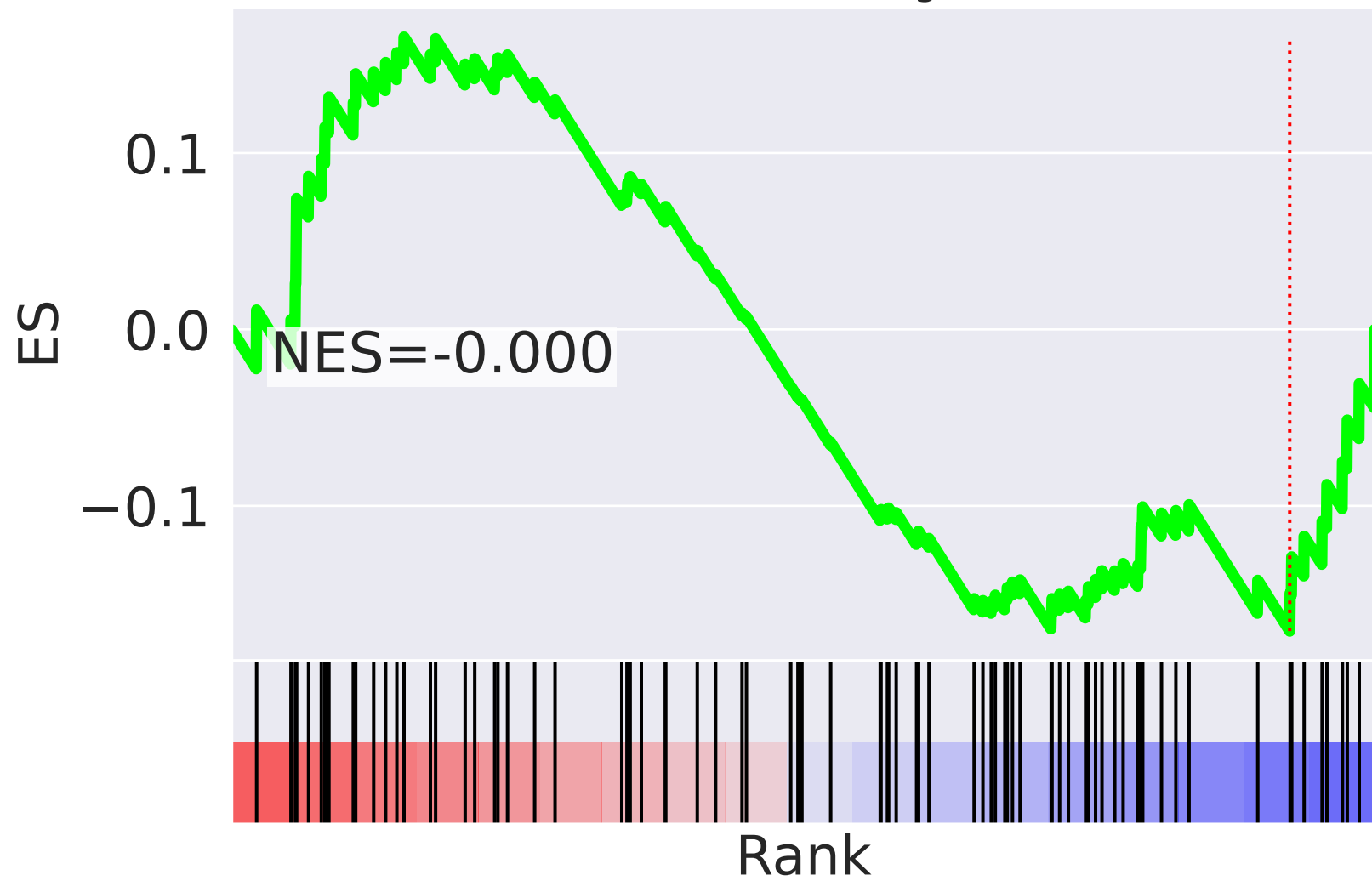
NES		SET
-4.978		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.579		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
4.352		translational initiation (GO:0006413)
4.297		rRNA processing (GO:0006364)
3.927		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.473		negative regulation of protein kinase B signaling (GO:0051898)
3.299		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.913		protein targeting to mitochondrion (GO:0006626)
2.844		ribosomal large subunit biogenesis (GO:0042273)
2.782		positive regulation of rRNA processing (GO:2000234)
2.725		regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0000079)
2.670		maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462)
-2.664		autophagosome assembly (GO:0000045)
-2.546		mitophagy (GO:0000422)
2.520		telomere maintenance via telomerase (GO:0007004)




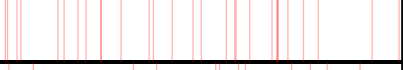
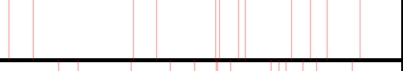

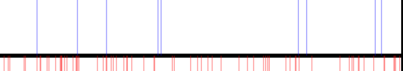
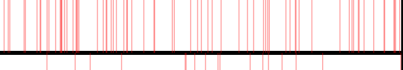
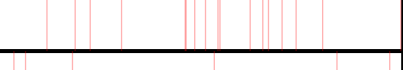
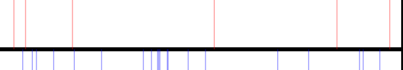


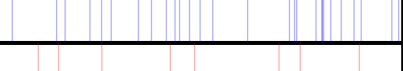

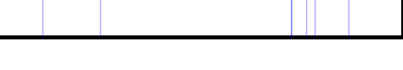
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=28$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

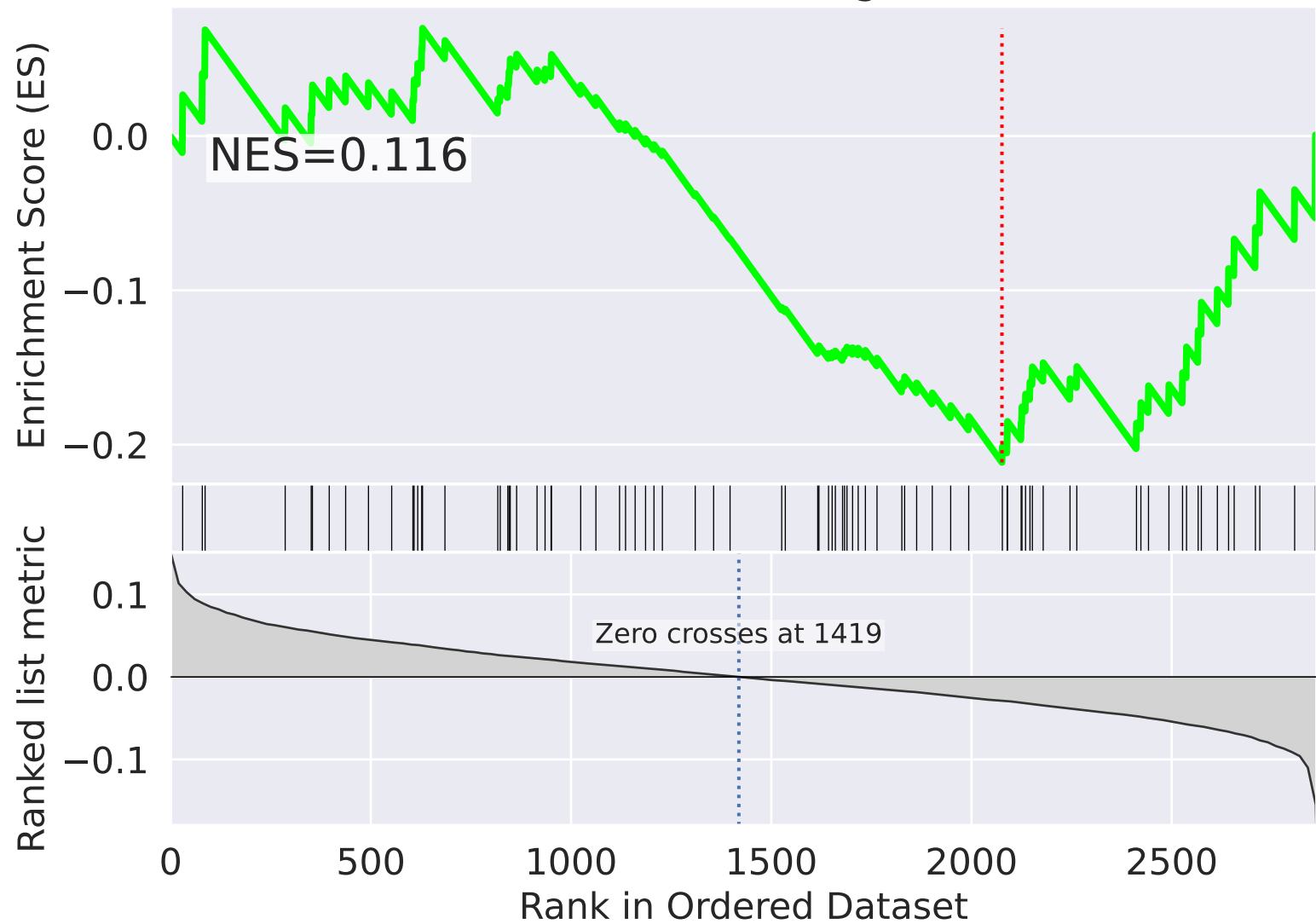


NES		SET
-3.039		epidermal growth factor receptor signaling pathway (GO:0007173)
-3.031		centrosome duplication (GO:0051298)
3.000		ion transmembrane transport (GO:0034220)
2.920		interstrand cross-link repair (GO:0036297)
2.843		retrograde protein transport, ER to cytosol (GO:0030970)
2.836		tricarboxylic acid cycle (GO:0006099)
-2.820		cell-matrix adhesion (GO:0007160)
2.756		protein phosphorylation (GO:0006468)
2.727		transferrin transport (GO:0033572)
2.719		humoral immune response (GO:0006959)
-2.713		microtubule-based movement (GO:0007018)
-2.712		protein deneddylation (GO:0000338)
-2.653		chromosome segregation (GO:0007059)
2.638		cellular nitrogen compound metabolic process (GO:0034641)
-2.618		positive regulation of substrate adhesion-dependent cell spreading (GO:1900026)

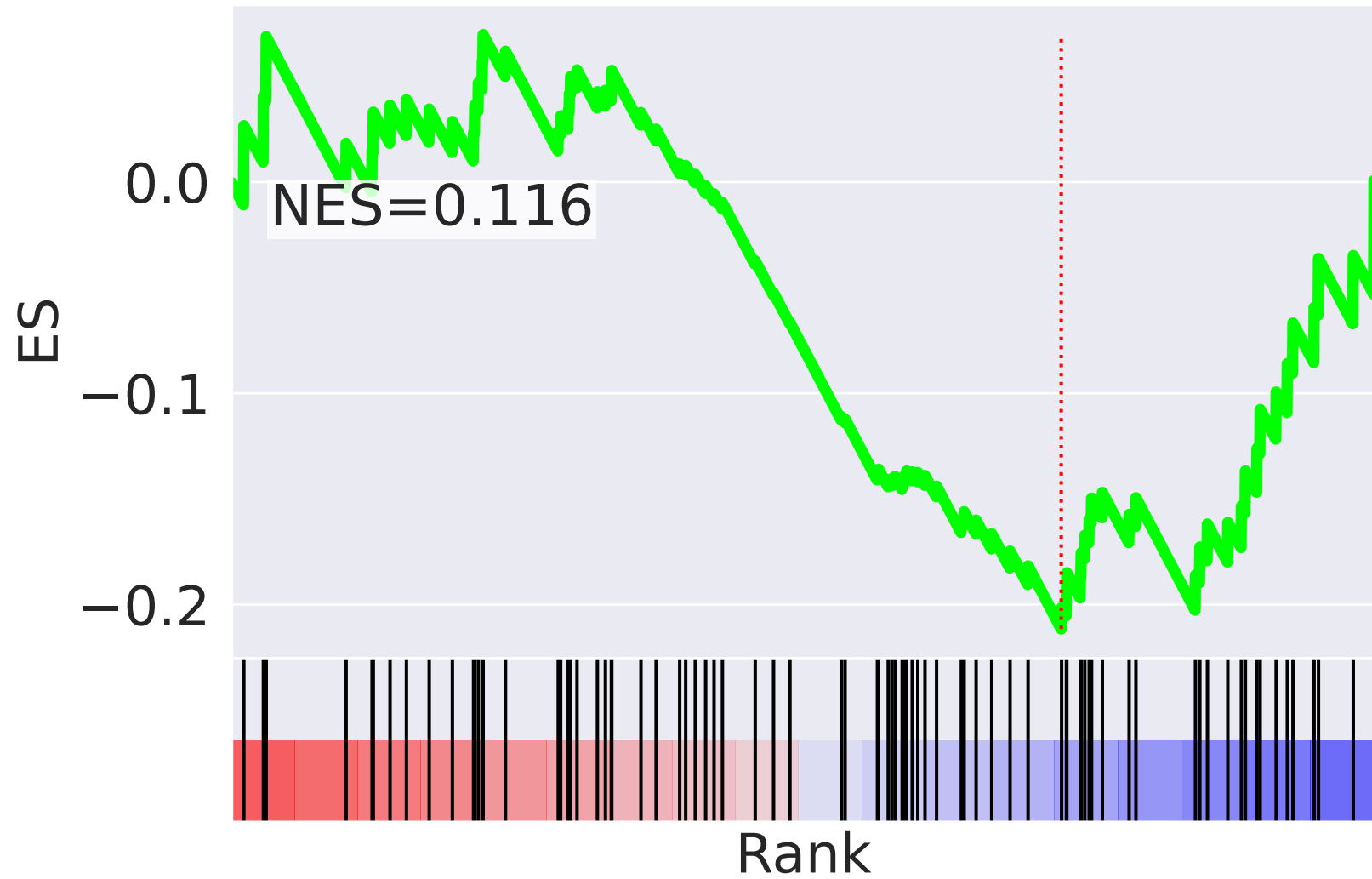


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=29$

# mitochondrial translational elongation (GO:0070125)

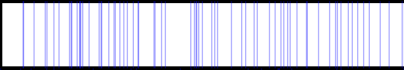




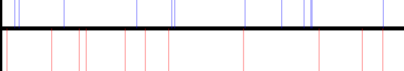
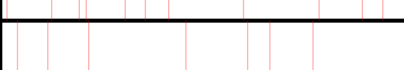
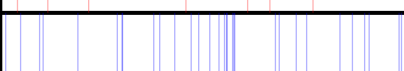
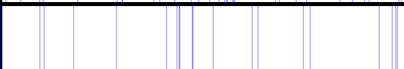

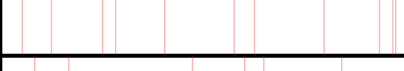

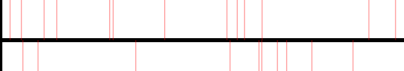
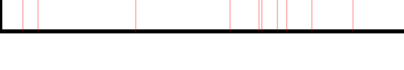



mitochondrial translational elongation (GO:0070125)



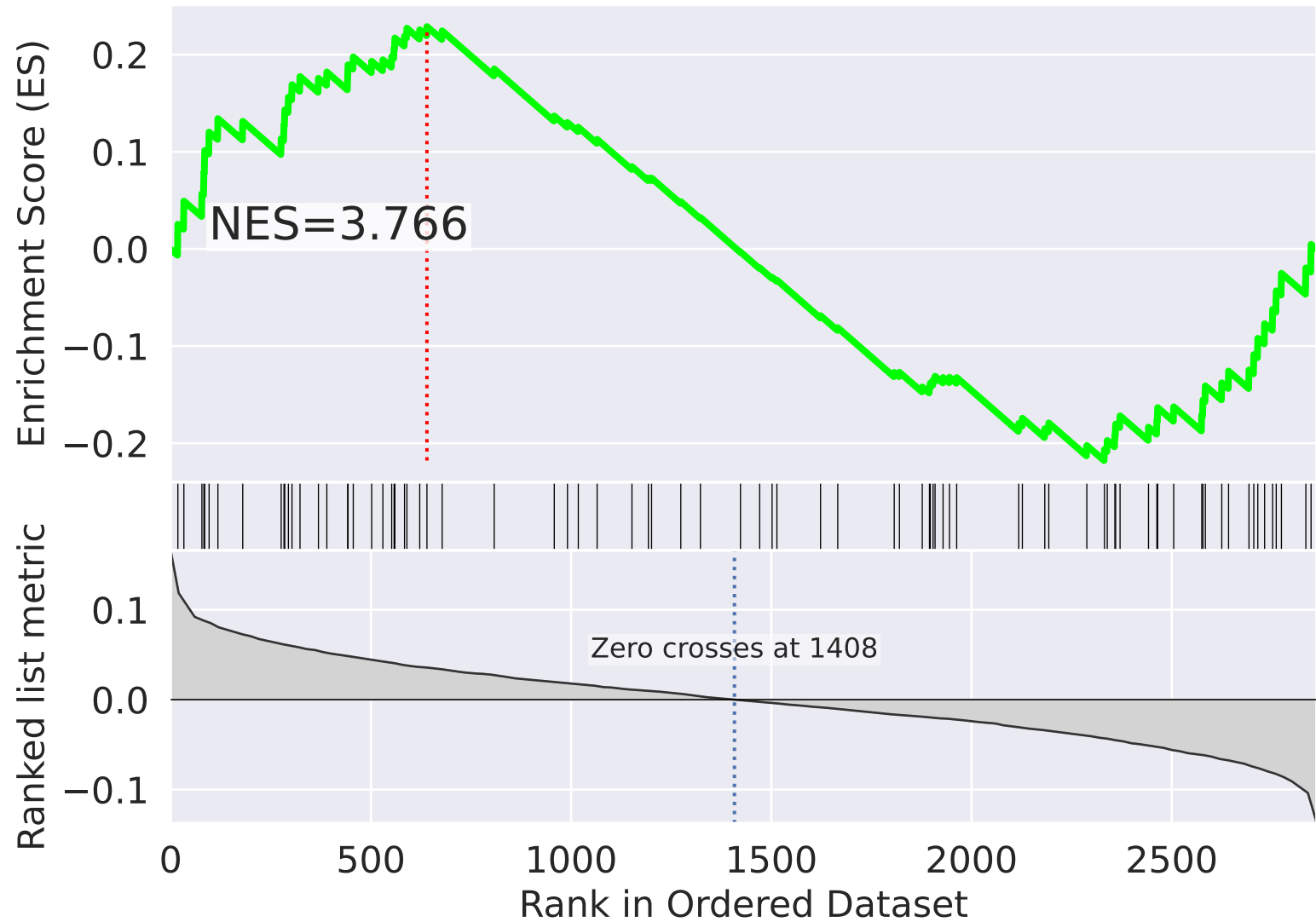
NES

SET

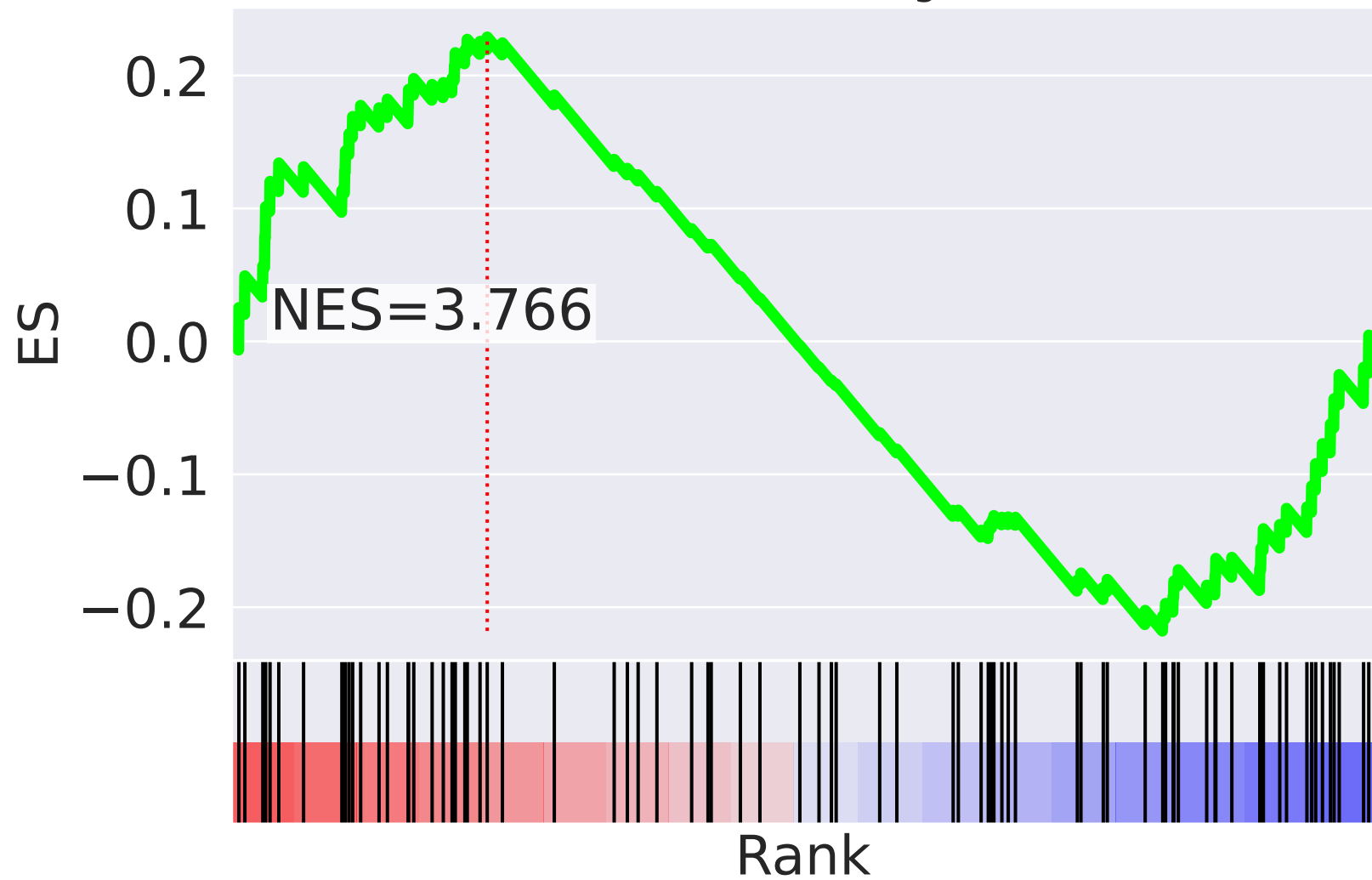
-3.439		sister chromatid cohesion (GO:0007062)
-3.297		strand displacement (GO:0000732)
-3.195		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.950		DNA replication (GO:0006260)
-2.901		DNA synthesis involved in DNA repair (GO:0000731)
-2.803		beta-catenin-TCF complex assembly (GO:1904837)
2.753		positive regulation of protein serine/threonine kinase activity (GO:0071902)
2.722		maturation of SSU-rRNA (GO:0030490)
-2.668		regulation of apoptotic process (GO:0042981)
-2.649		phosphatidylinositol biosynthetic process (GO:0006661)
-2.536		histone mRNA catabolic process (GO:0071044)
2.308		endocytosis (GO:0006897)
2.304		endocytic recycling (GO:0032456)
2.300		heart development (GO:0007507)
2.281		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  $z=30$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

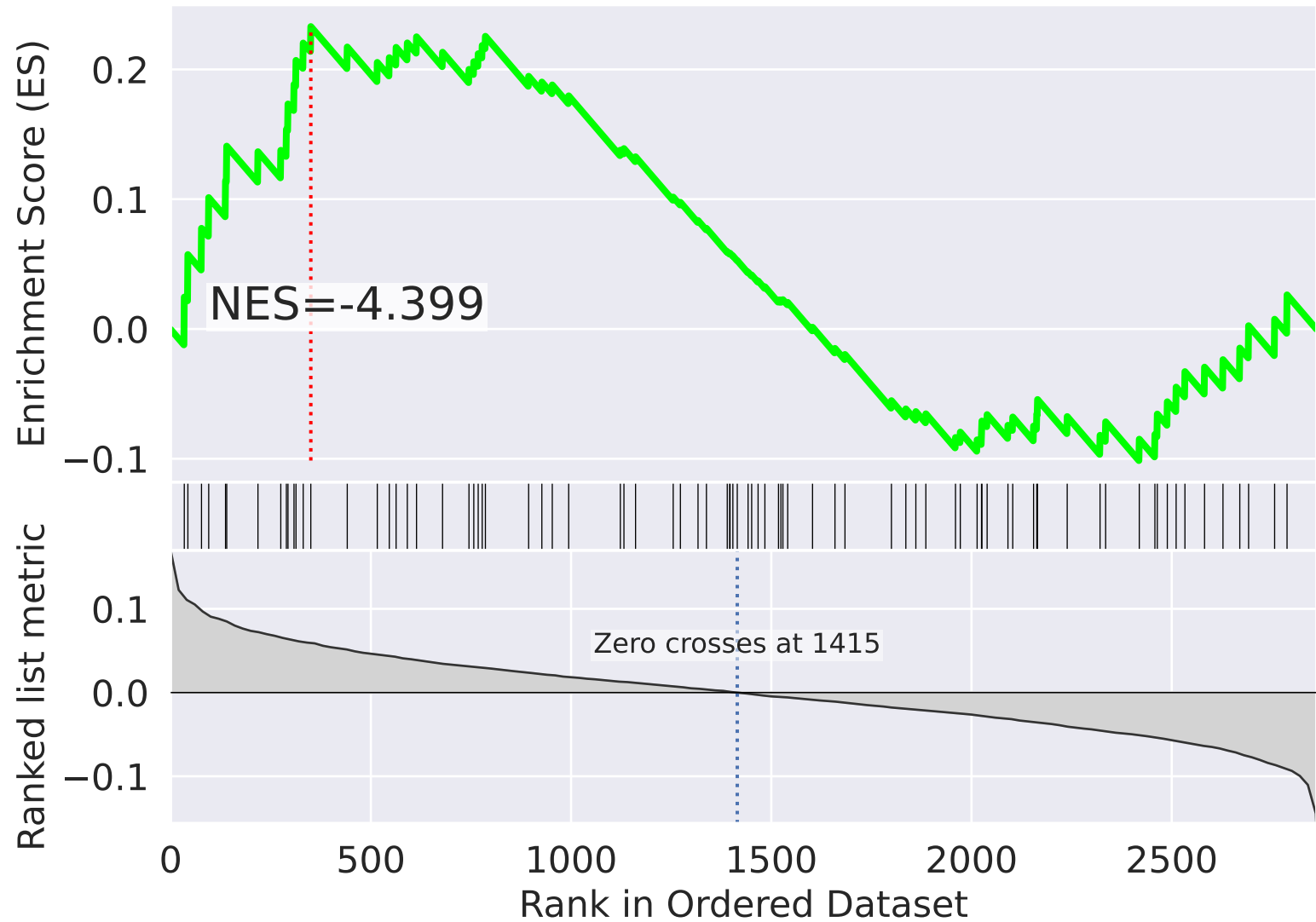


NES		SET
5.182		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.283		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.814		mitochondrial translational termination (GO:0070126)
3.766		mitochondrial translational elongation (GO:0070125)
-3.344		G2/M transition of mitotic cell cycle (GO:0000086)
-3.276		chromosome segregation (GO:0007059)
-3.063		response to endoplasmic reticulum stress (GO:0034976)
-2.824		spliceosomal snRNP assembly (GO:0000387)
2.817		mitochondrial translation (GO:0032543)
-2.743		ventricular septum morphogenesis (GO:0060412)
-2.730		positive regulation of translation (GO:0045727)
-2.643		tRNA 5'-leader removal (GO:0001682)
-2.610		snRNA processing (GO:0016180)
-2.481		protein import into peroxisome matrix (GO:0016558)
-2.455		positive regulation of osteoblast differentiation (GO:0045669)



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)

ES

0.2

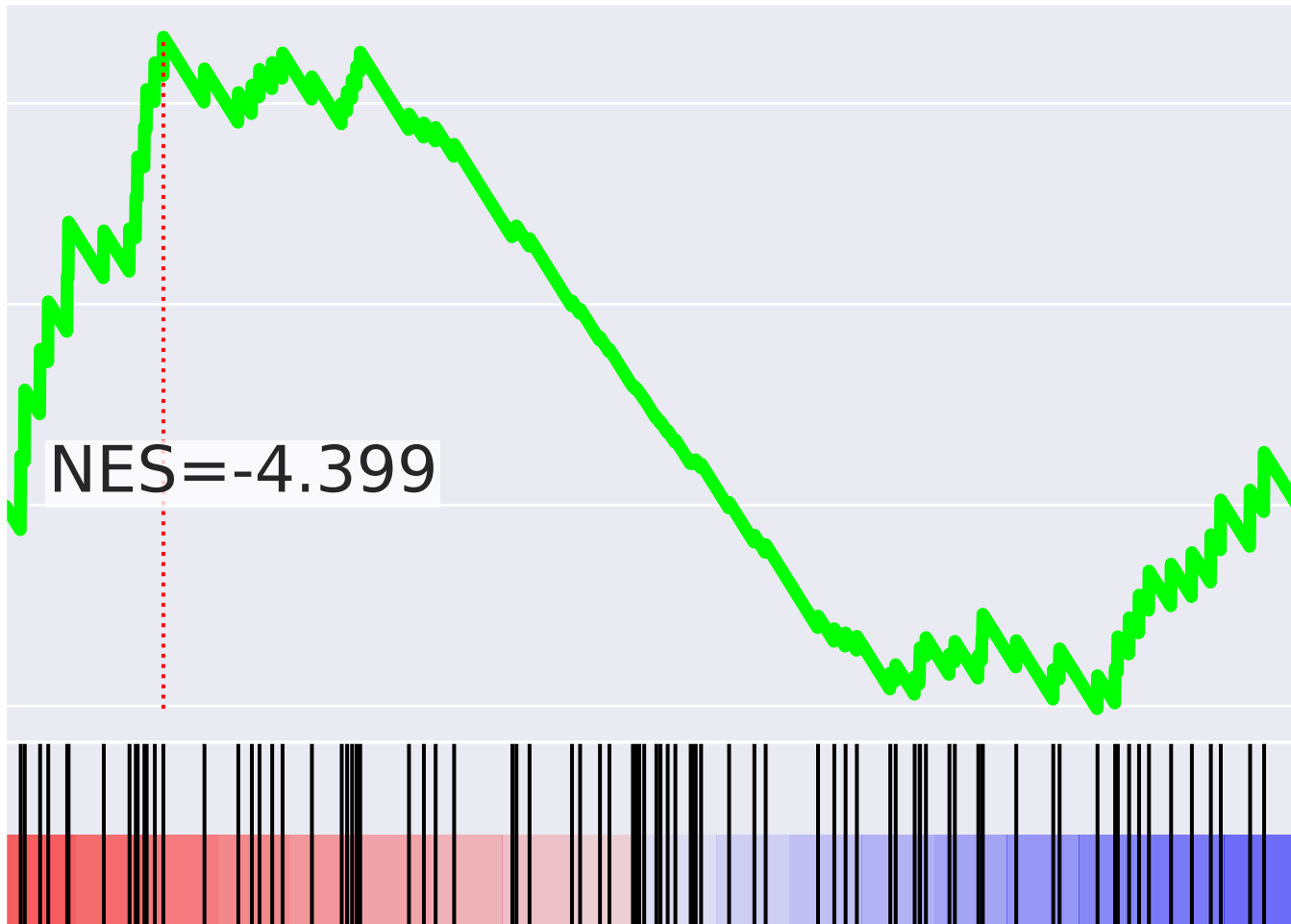
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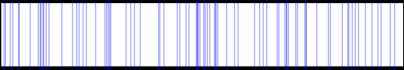
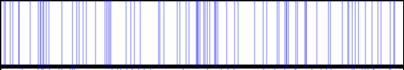

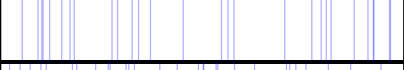
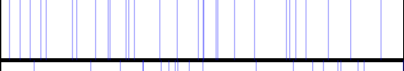
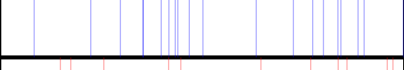


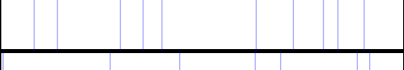

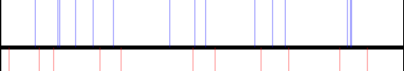

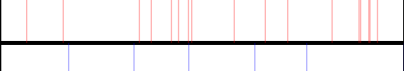
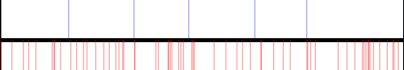
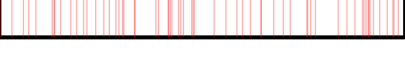
0.0

-0.1

NES=-4.399

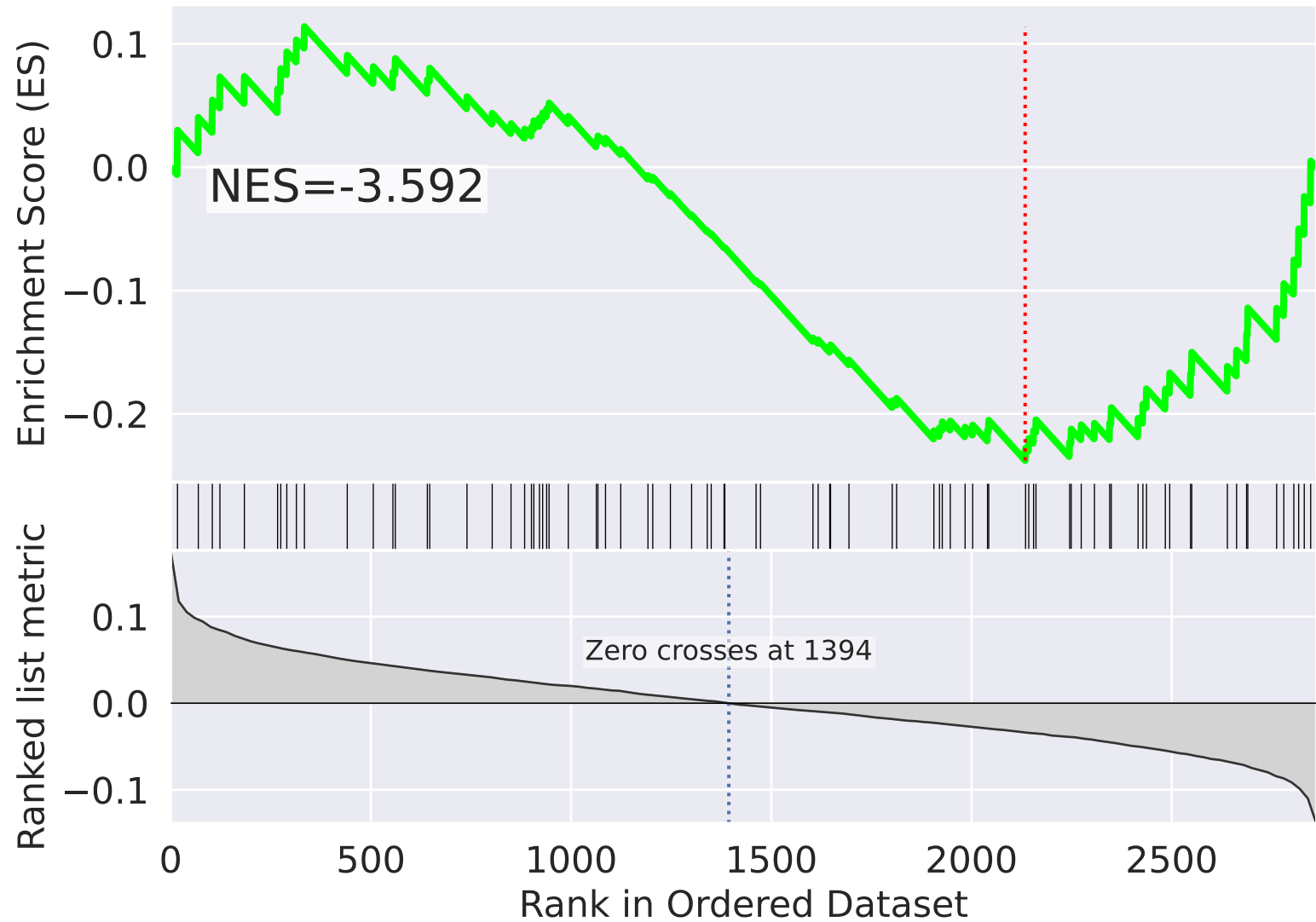
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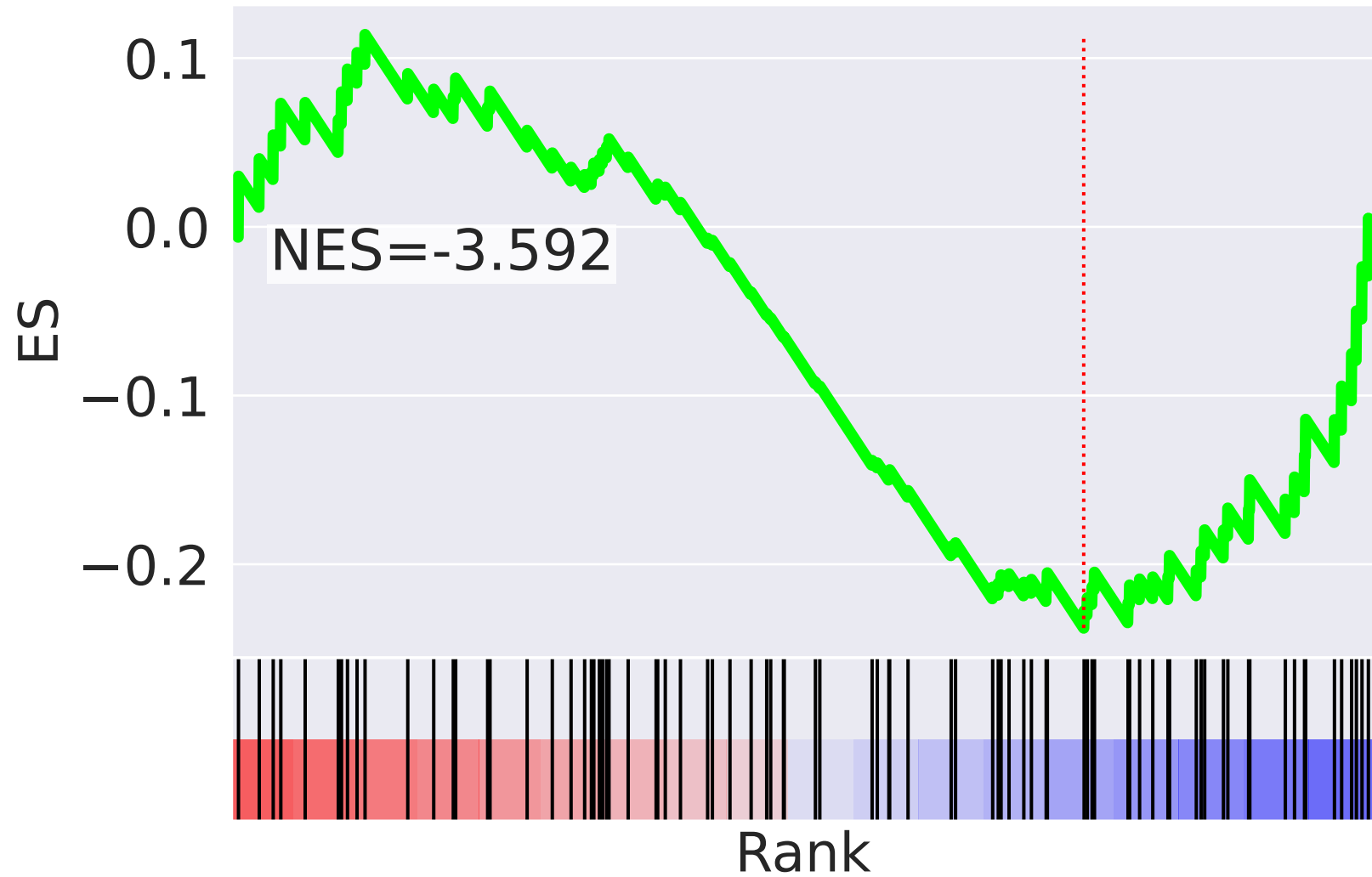
NES		SET
-4.399		mitochondrial translational elongation (GO:0070125)
-4.341		mitochondrial translational termination (GO:0070126)
-4.061		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.049		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.641		mitochondrial translation (GO:0032543)
-2.628		regulation of cholesterol biosynthetic process (GO:0045540)
2.602		positive regulation of transcription elongation from RNA polymerase II promoter (GO:0032968)
2.554		mitotic cytokinesis (GO:0000281)
-2.540		cholesterol biosynthetic process (GO:0006695)
-2.471		nucleobase-containing compound metabolic process (GO:0006139)
-2.453		positive regulation of protein catabolic process (GO:0045732)
2.387		regulation of circadian rhythm (GO:0042752)
2.384		positive regulation of gene expression, epigenetic (GO:0045815)
-2.379		exocytosis (GO:0006887)
2.357		transcription elongation from RNA polymerase II promoter (GO:0006368)

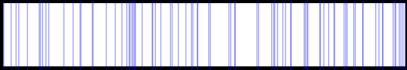
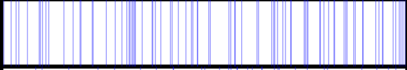
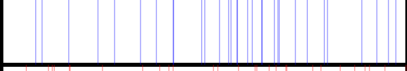
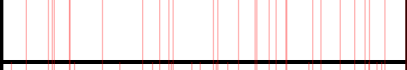
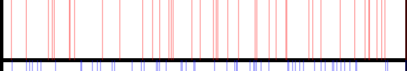
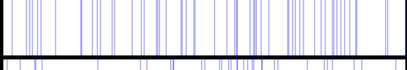
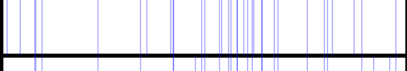
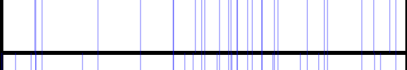
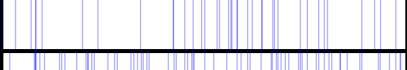
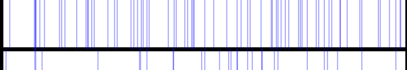
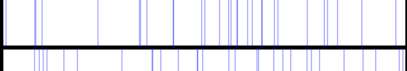

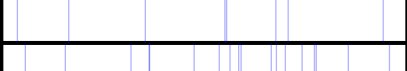

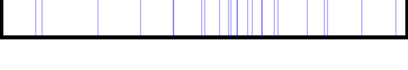
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=32$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

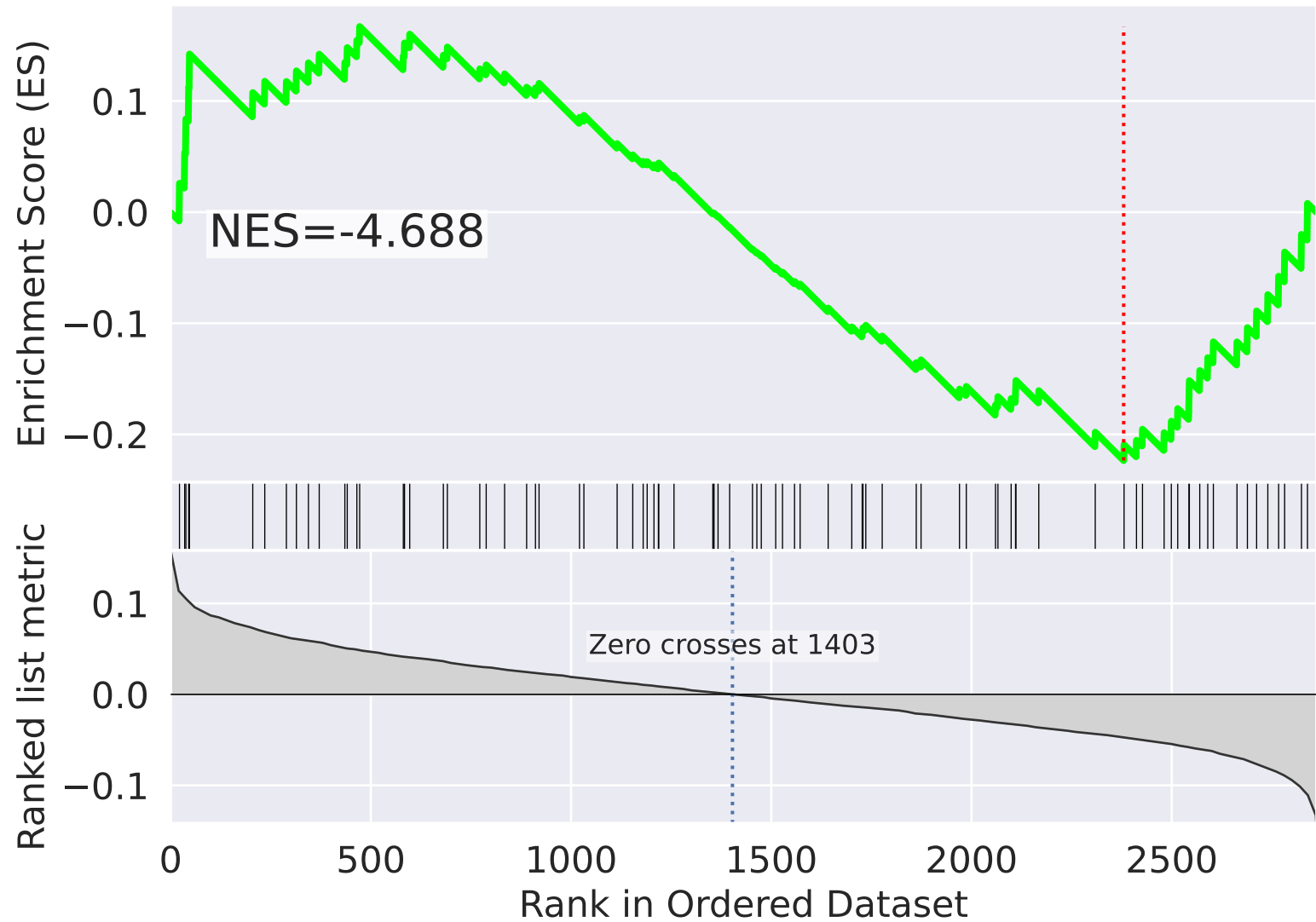


NES		SET
-3.611		mitochondrial translational termination (GO:0070126)
-3.592		mitochondrial translational elongation (GO:0070125)
-3.357		mitotic nuclear envelope disassembly (GO:0007077)
2.888		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.857		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.762		G2/M transition of mitotic cell cycle (GO:0000086)
-2.677		intracellular transport of virus (GO:0075733)
-2.673		tRNA export from nucleus (GO:0006409)
-2.649		protein sumoylation (GO:0016925)
-2.638		sister chromatid cohesion (GO:0007062)
-2.599		viral process (GO:0016032)
-2.565		mitochondrial translation (GO:0032543)
-2.563		regulation of cell migration (GO:0030334)
-2.547		CENP-A containing nucleosome assembly (GO:0034080)
-2.538		regulation of glucose transport (GO:0010827)

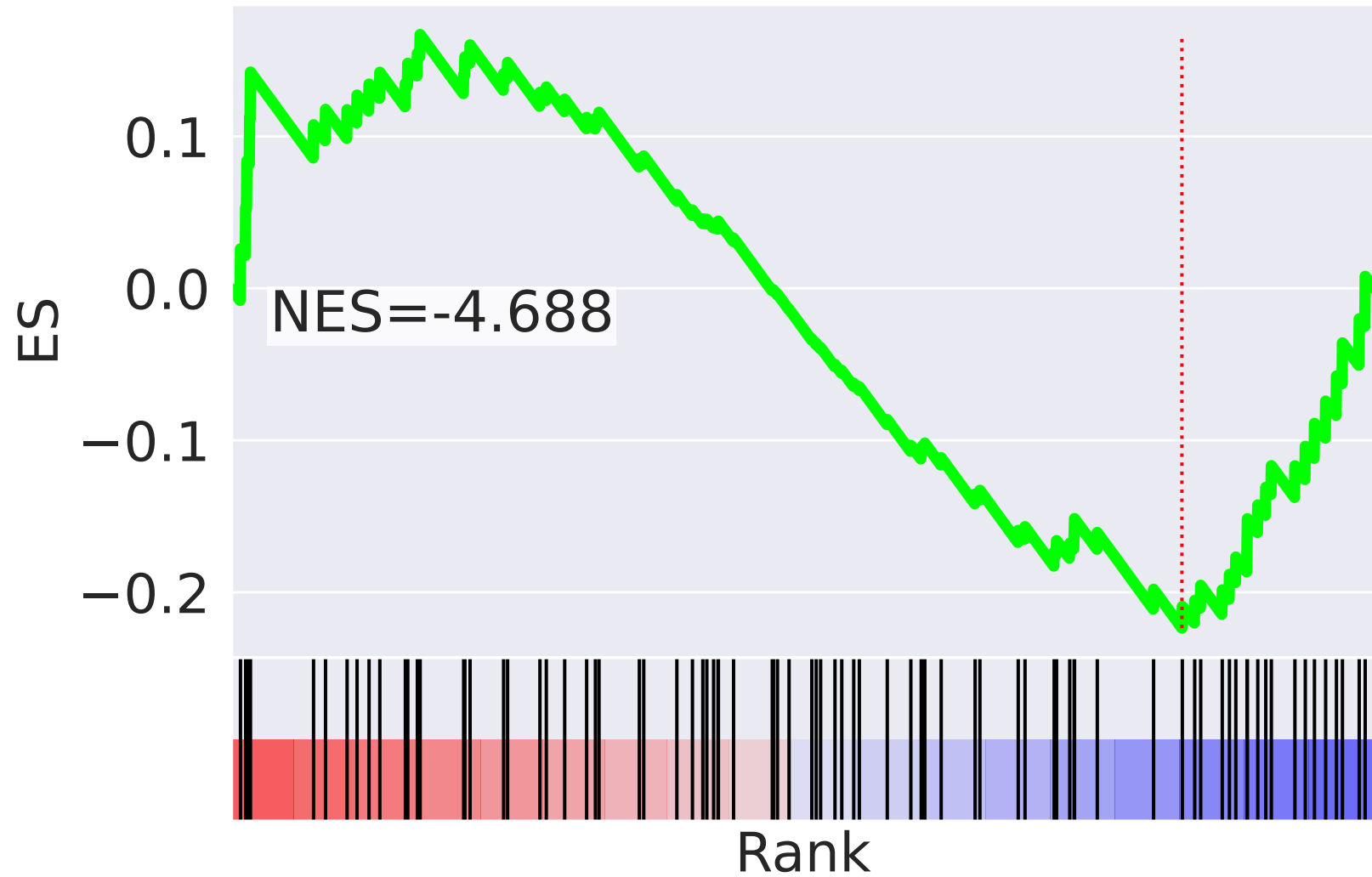


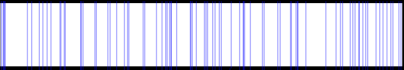
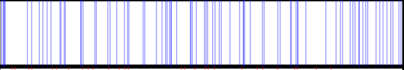
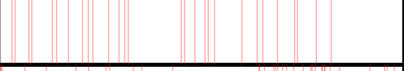

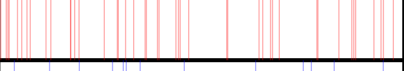

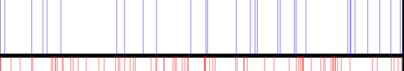

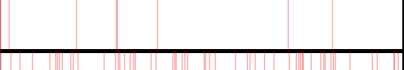
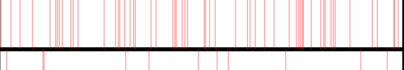

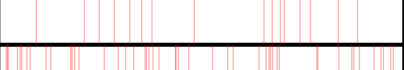
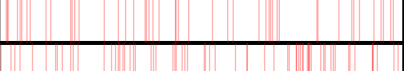
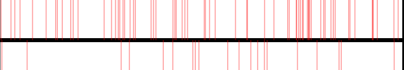
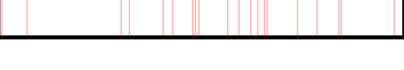
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=33$

# mitochondrial translational elongation (GO:0070125)



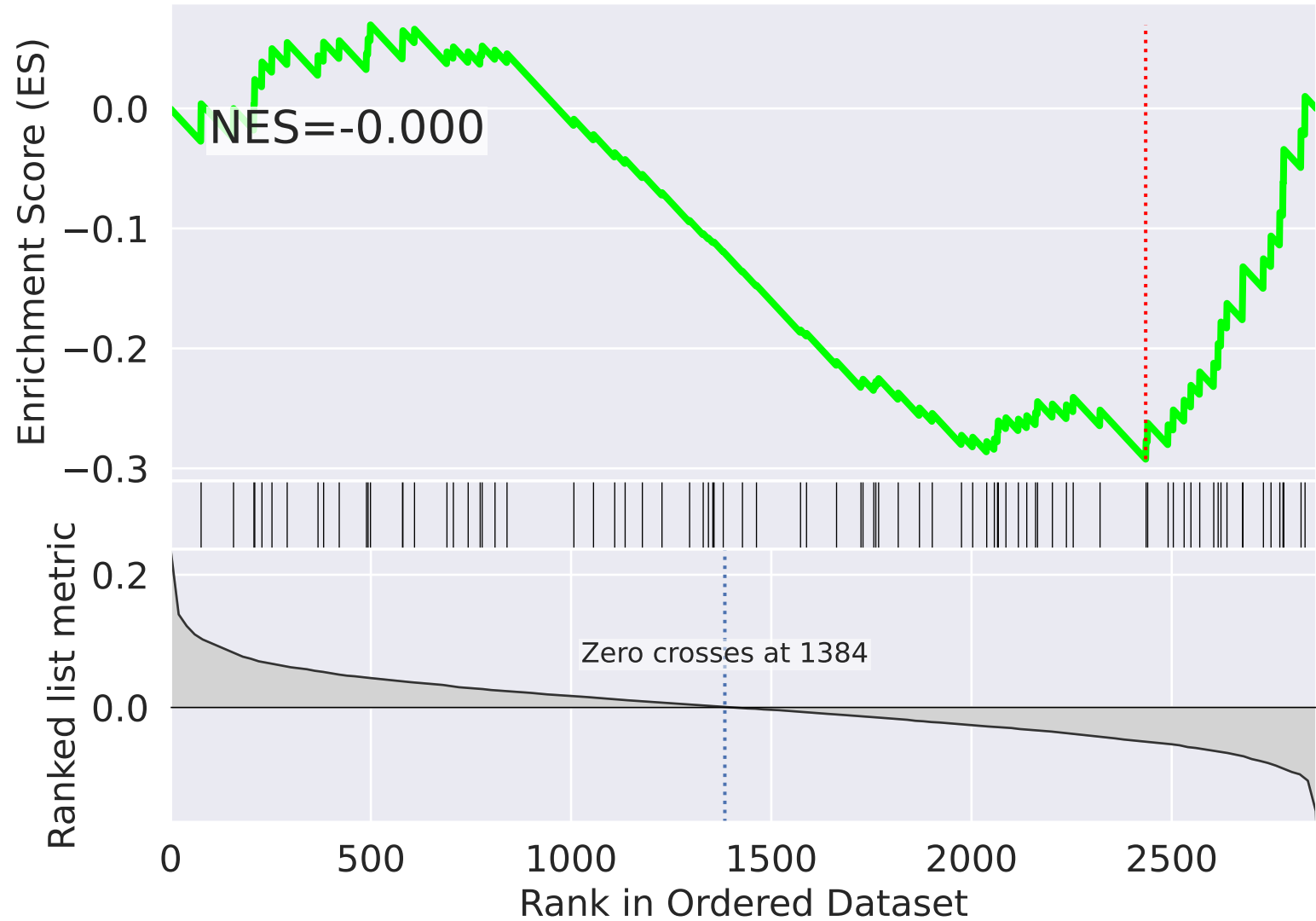
mitochondrial translational elongation (GO:0070125)



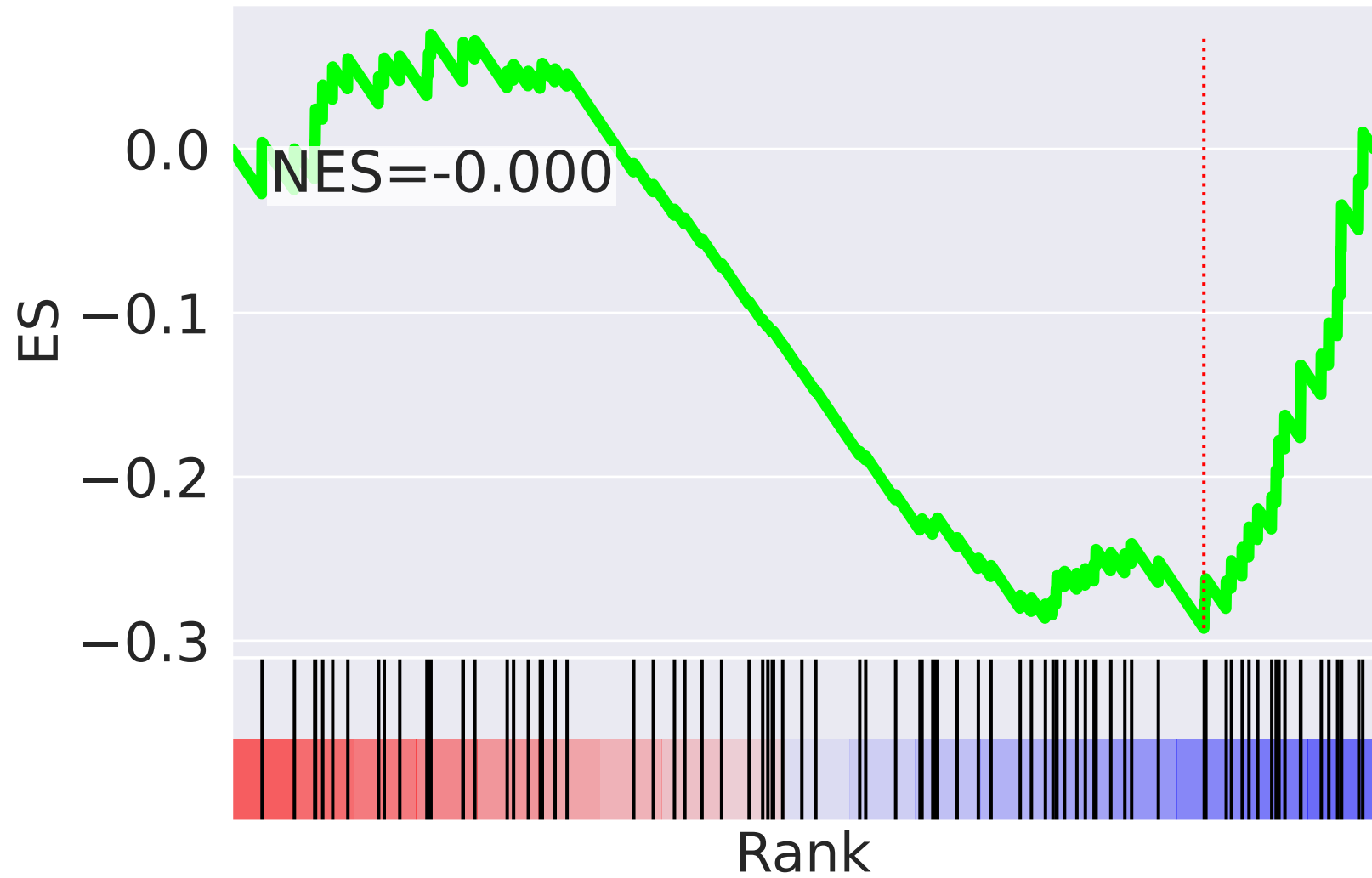
NES		SET
-4.688		mitochondrial translational elongation (GO:0070125)
-4.516		mitochondrial translational termination (GO:0070126)
3.260		phosphatidylinositol-mediated signaling (GO:0048015)
3.189		chromatin remodeling (GO:0006338)
3.110		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-2.958		transcription from RNA polymerase III promoter (GO:0006383)
-2.915		mitochondrial translation (GO:0032543)
2.885		viral transcription (GO:0019083)
2.851		clathrin-dependent endocytosis (GO:0072583)
2.823		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
2.810		positive regulation of transcription elongation from RNA polymerase II promoter (GO:0032968)
2.736		regulation of mitotic cell cycle (GO:0007346)
2.734		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
2.719		translational initiation (GO:0006413)
2.687		regulation of protein stability (GO:0031647)

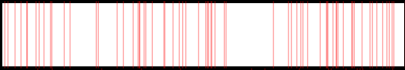
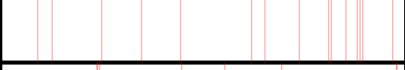

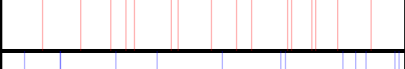

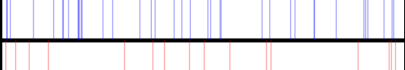


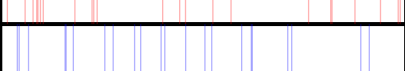



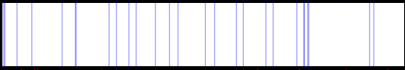


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=34$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

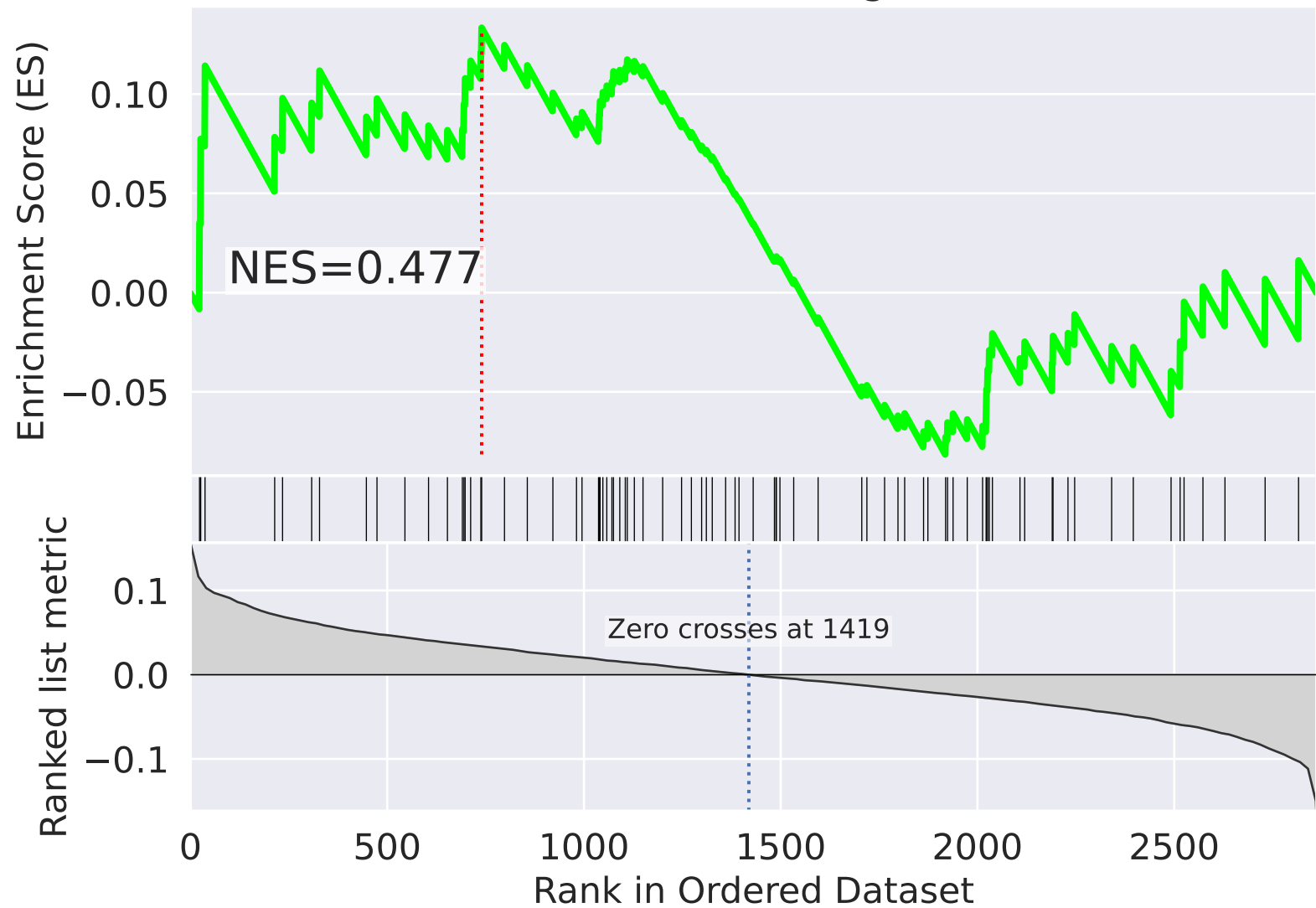


NES		SET
3.134		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.106		tricarboxylic acid cycle (GO:0006099)
3.064		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)
2.943		nervous system development (GO:0007399)
-2.943		transcription from RNA polymerase III promoter (GO:0006383)
-2.825		macroautophagy (GO:0016236)
2.770		cellular response to oxidative stress (GO:0034599)
2.741		humoral immune response (GO:0006959)
2.679		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.677		RNA metabolic process (GO:0016070)
-2.645		protein N-linked glycosylation (GO:0006487)
-2.609		autophagosome assembly (GO:0000045)
-2.597		dolichol-linked oligosaccharide biosynthetic process (GO:0006488)
-2.552		chromosome segregation (GO:0007059)
2.538		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  $z=35$

# mitochondrial translational elongation (GO:0070125)



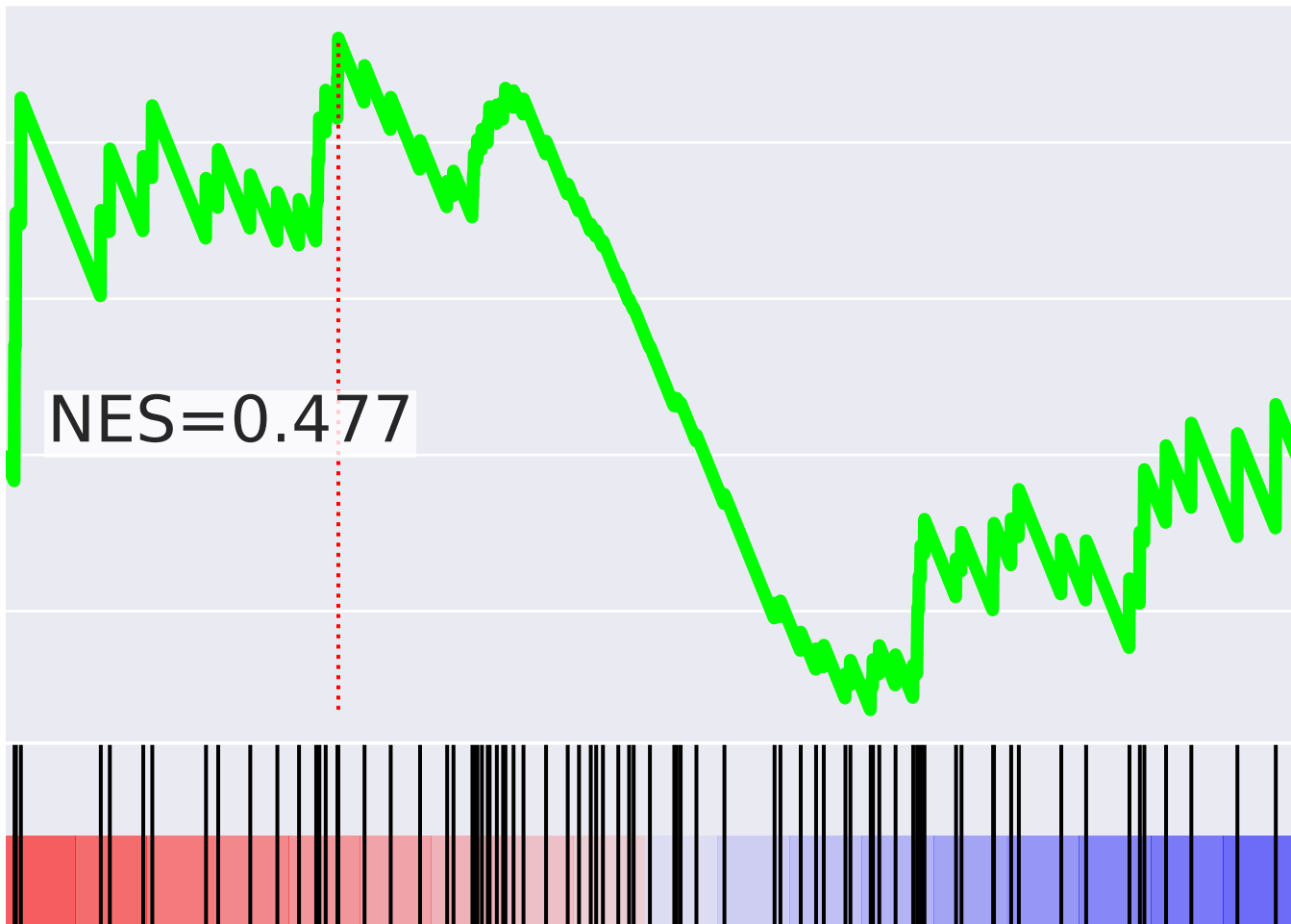
# mitochondrial translational elongation (GO:0070125)



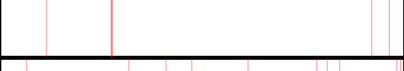
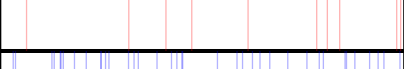


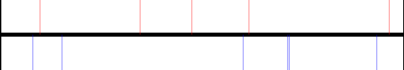

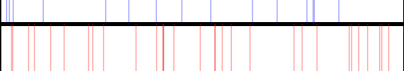
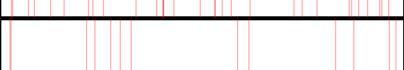


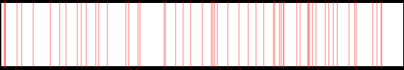
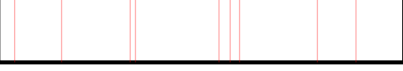

ES

0.10  
0.05  
0.00  
-0.05

NES=0.477

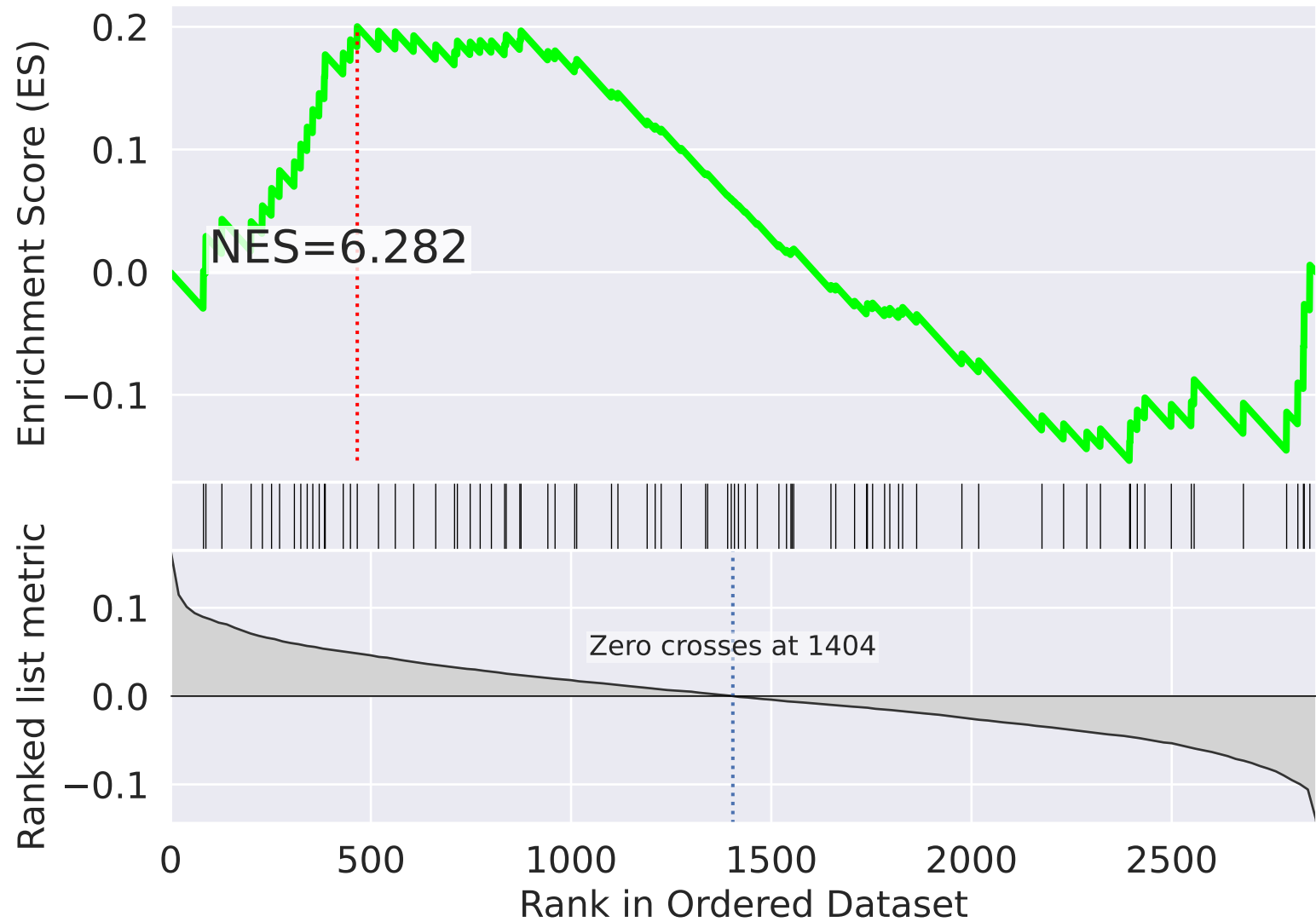
Rank



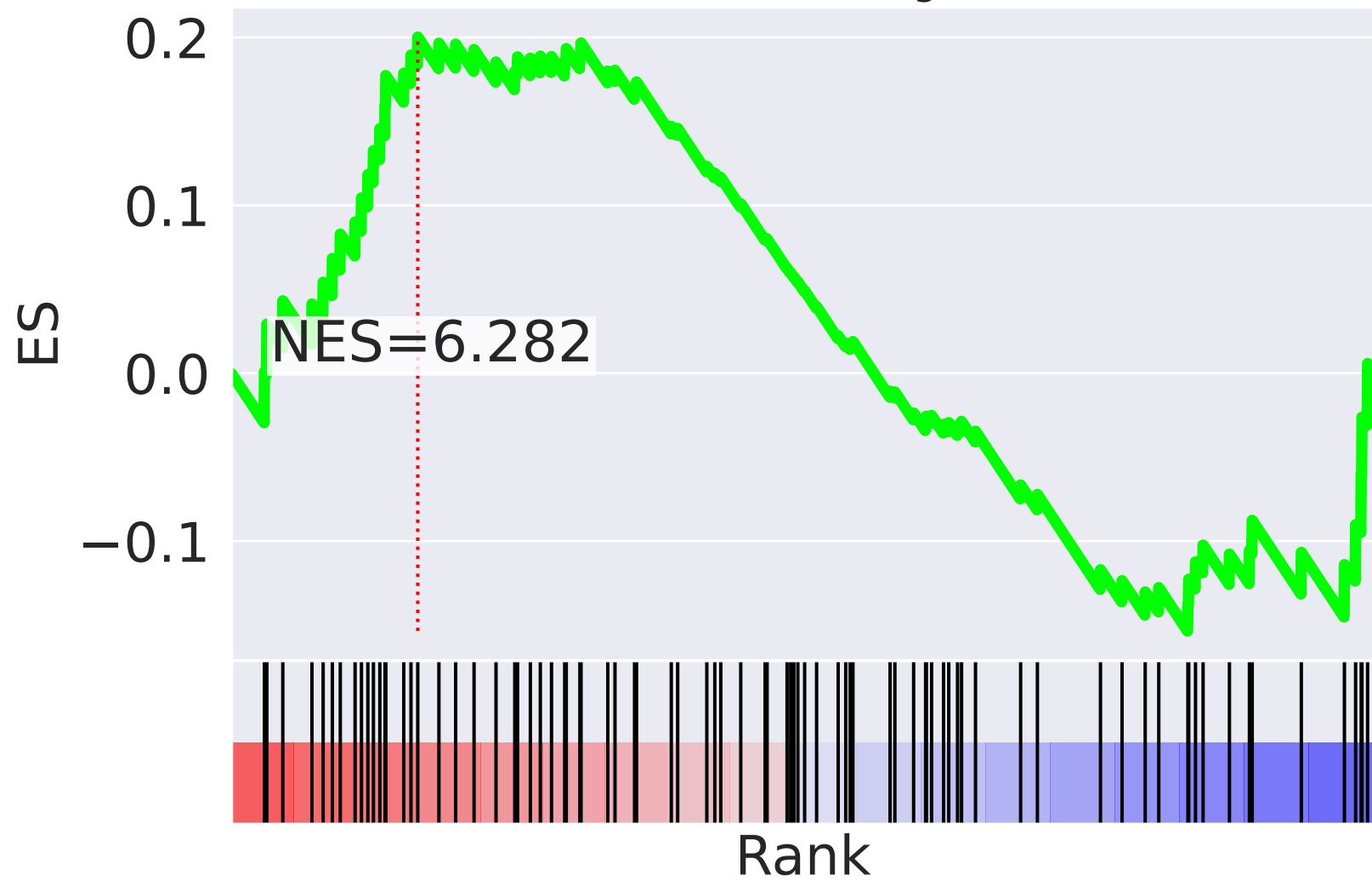
NES		SET
-3.246		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
2.913		regulation of cell motility (GO:2000145)
2.753		anoikis (GO:0043276)
2.725		bicellular tight junction assembly (GO:0070830)
-2.699		macroautophagy (GO:0016236)
-2.482		protein dephosphorylation (GO:0006470)
2.374		neural tube closure (GO:0001843)
-2.351		nuclear mRNA surveillance (GO:0071028)
-2.331		positive regulation of protein catabolic process (GO:0045732)
2.315		mRNA 3'-end processing (GO:0031124)
2.305		heart development (GO:0007507)
2.240		amino acid transport (GO:0006865)
2.219		viral mRNA export from host cell nucleus (GO:0046784)
2.217		anaphase-promoting complex-dependent catabolic process (GO:0031145)
2.163		erythrocyte differentiation (GO:0030218)

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)

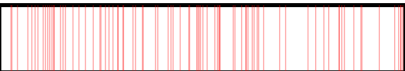
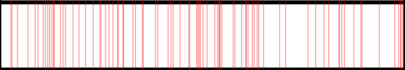

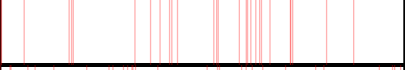
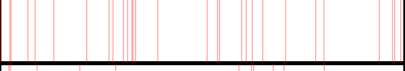

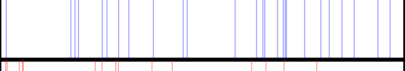


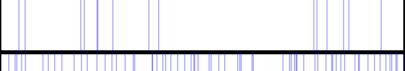
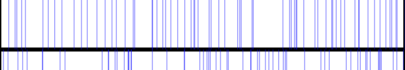
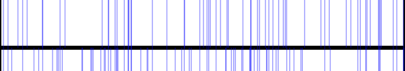
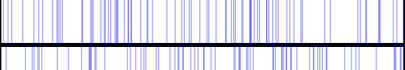

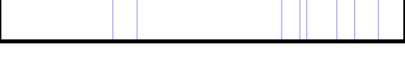


mitochondrial translational elongation (GO:0070125)



NES

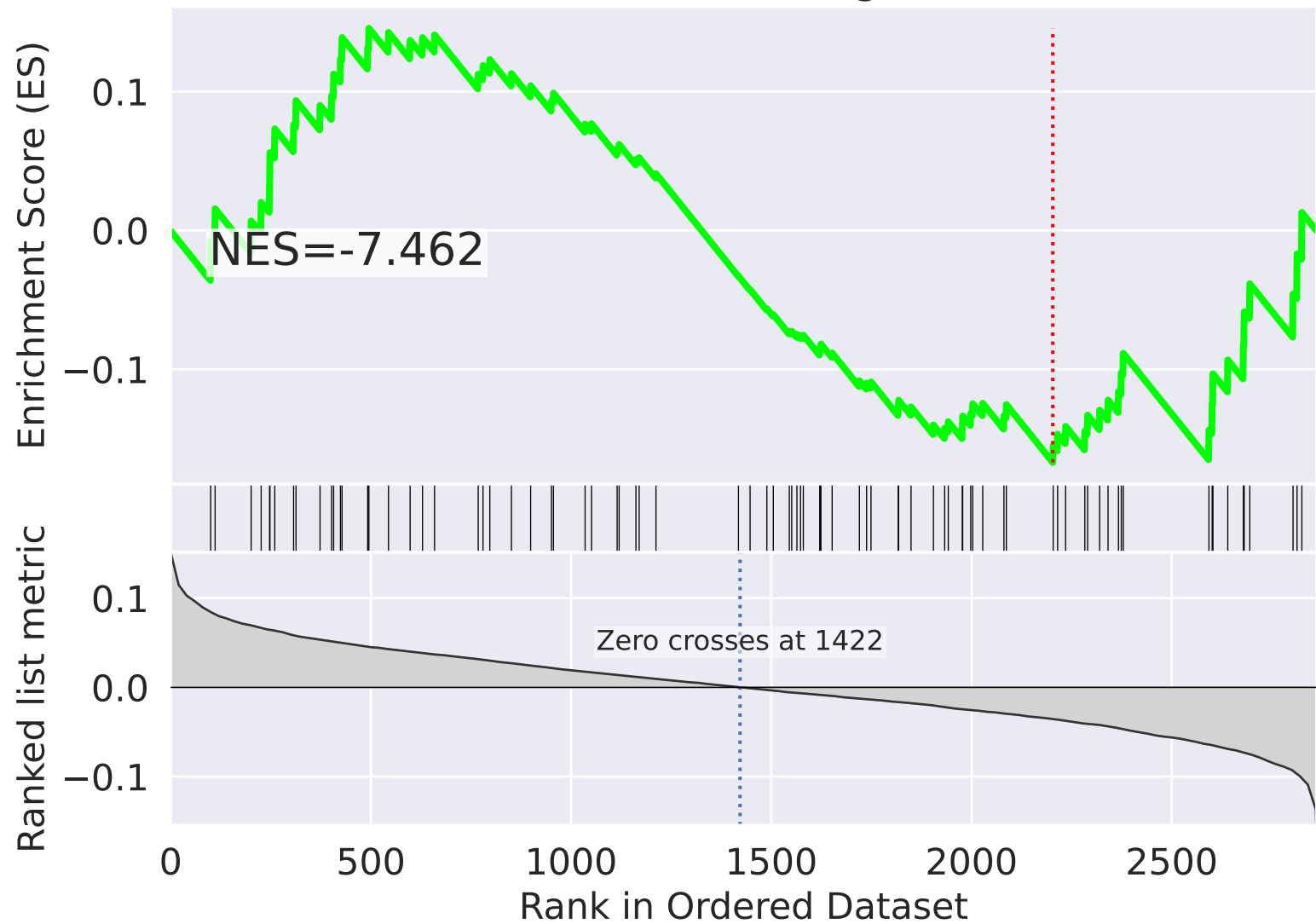
SET

6.282		mitochondrial translational elongation (GO:0070125)
6.260		mitochondrial translational termination (GO:0070126)
4.988		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.023		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.297		mitochondrial translation (GO:0032543)
3.265		aerobic respiration (GO:0009060)
-3.252		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
3.228		tricarboxylic acid cycle (GO:0006099)
-2.949		response to endoplasmic reticulum stress (GO:0034976)
-2.923		positive regulation of protein catabolic process (GO:0045732)
-2.879		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.842		Fc-epsilon receptor signaling pathway (GO:0038095)
-2.836		post-translational protein modification (GO:0043687)
-2.812		regulation of signal transduction by p53 class mediator (GO:1901796)
-2.780		activation of protein kinase activity (GO:0032147)

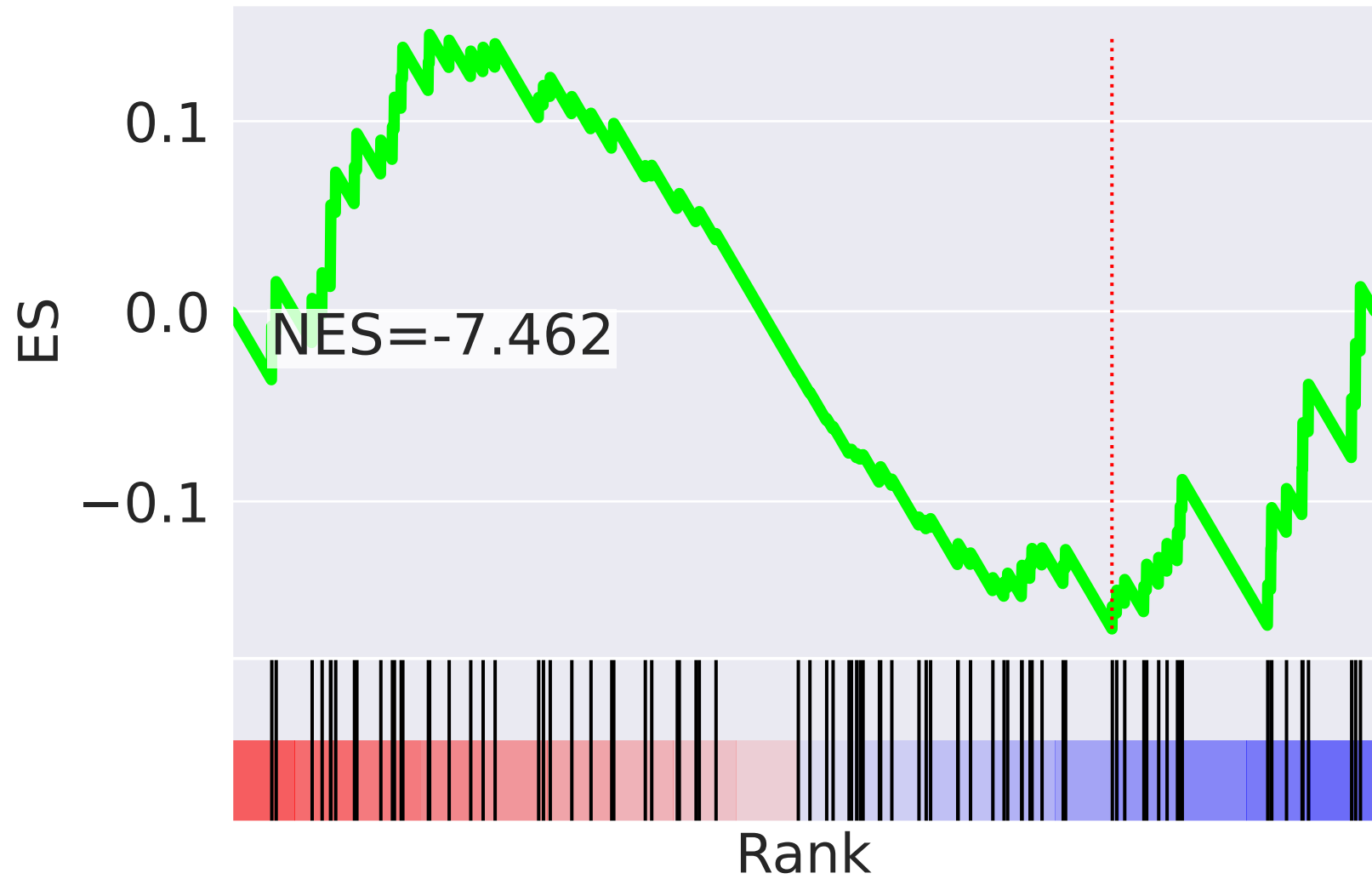


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=37$

# mitochondrial translational elongation (GO:0070125)

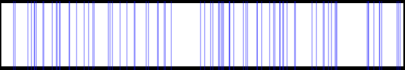
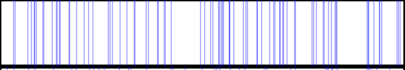
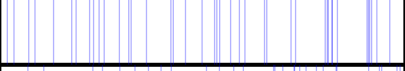
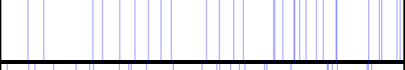
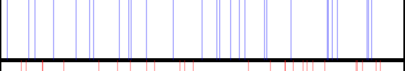
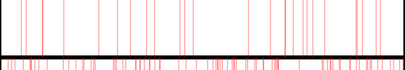
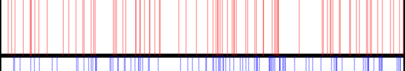
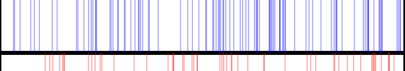
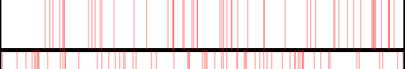
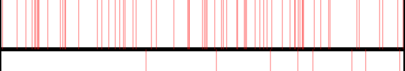
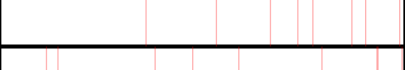

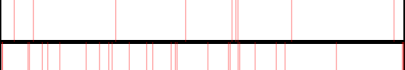
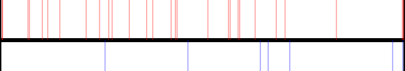
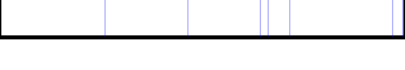


# mitochondrial translational elongation (GO:0070125)



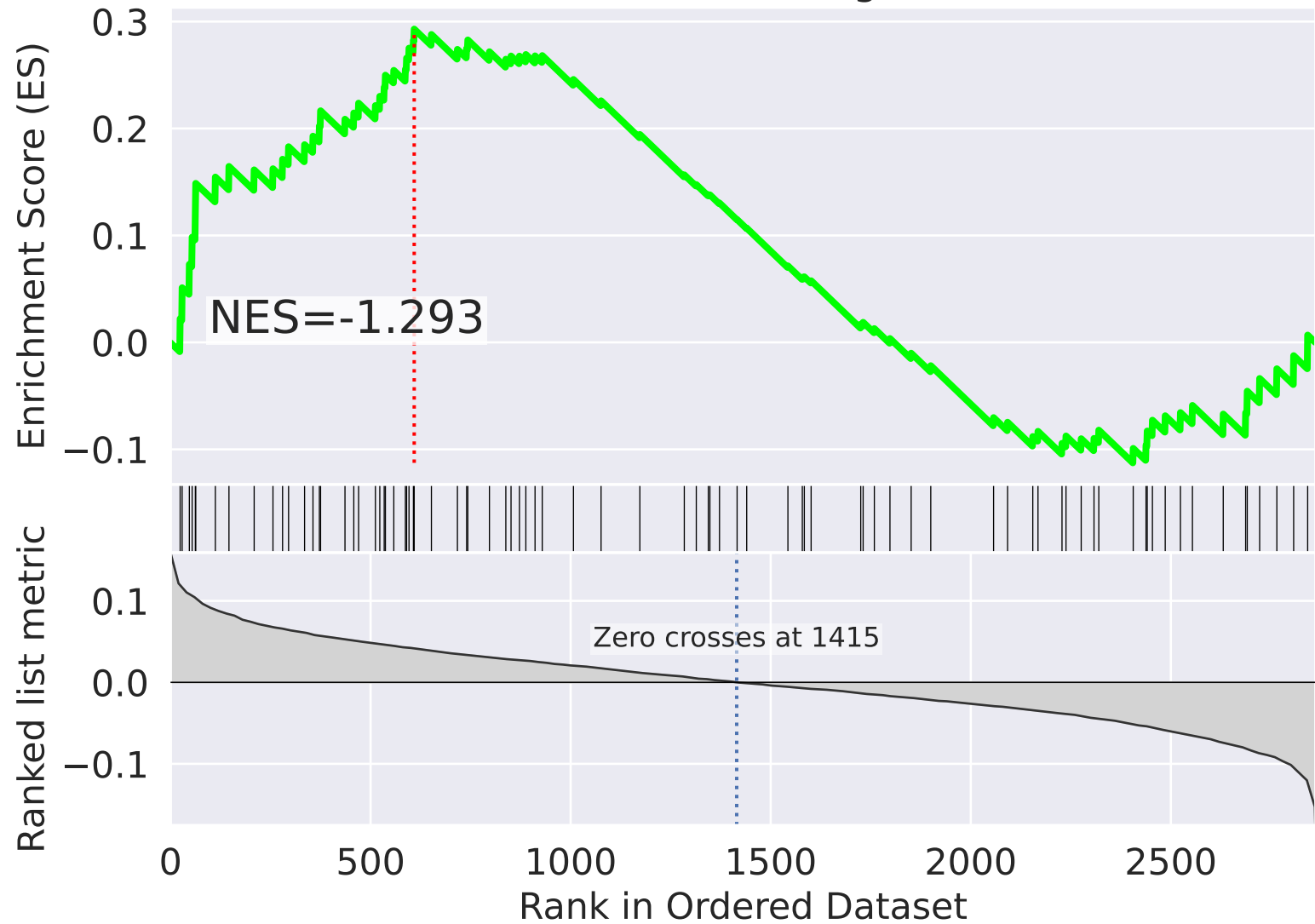
NES

SET

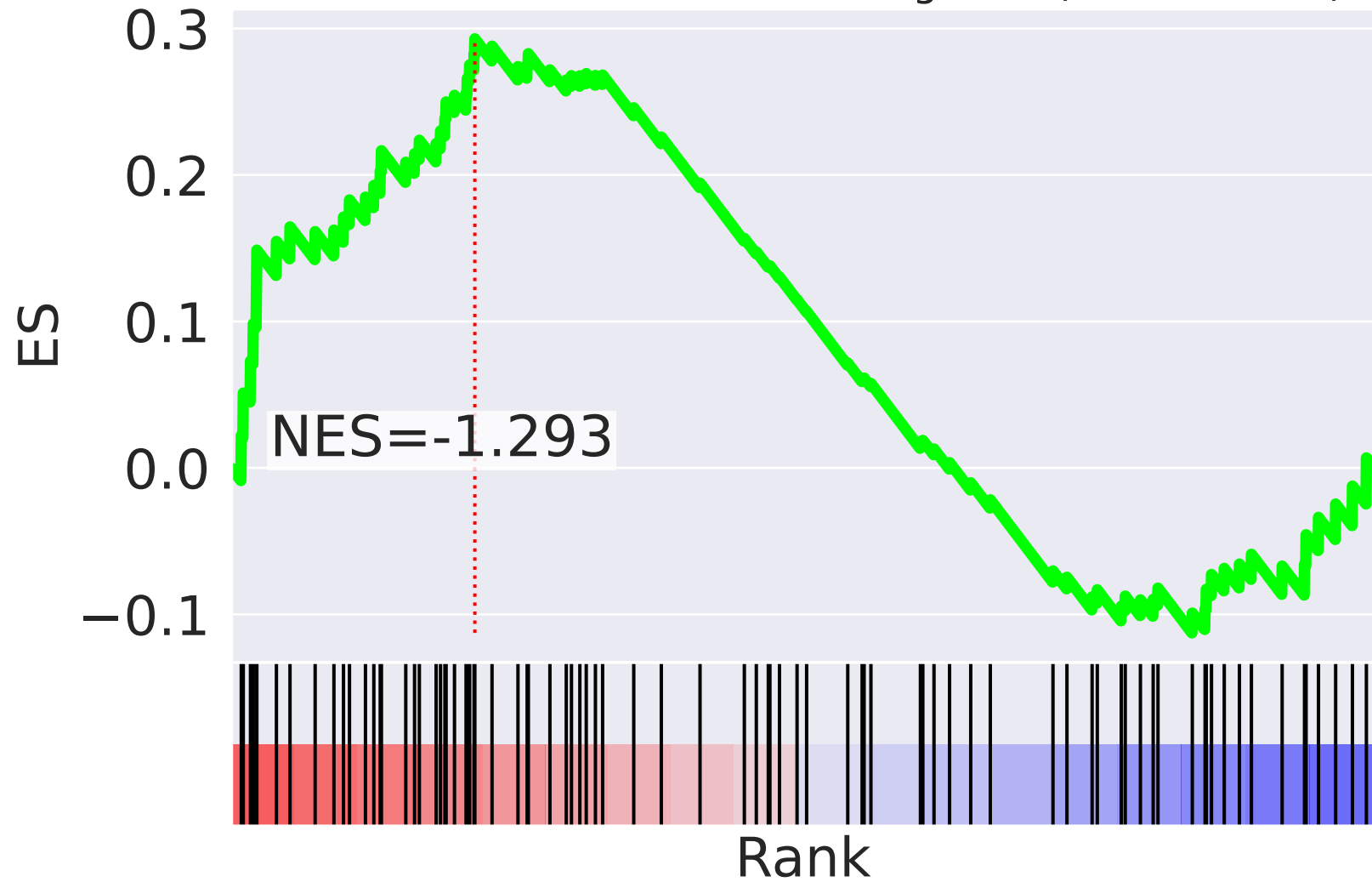
-7.469		mitochondrial translational termination (GO:0070126)
-7.462		mitochondrial translational elongation (GO:0070125)
-4.990		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.535		mitochondrial translation (GO:0032543)
-4.021		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.625		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
3.606		post-translational protein modification (GO:0043687)
-3.470		translation (GO:0006412)
3.333		membrane organization (GO:0061024)
2.916		DNA replication (GO:0006260)
2.865		positive regulation of neuron differentiation (GO:0045666)
2.825		ESCRT III complex disassembly (GO:1904903)
2.750		hippo signaling (GO:0035329)
2.679		interstrand cross-link repair (GO:0036297)
-2.663		BMP signaling pathway (GO:0030509)

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

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

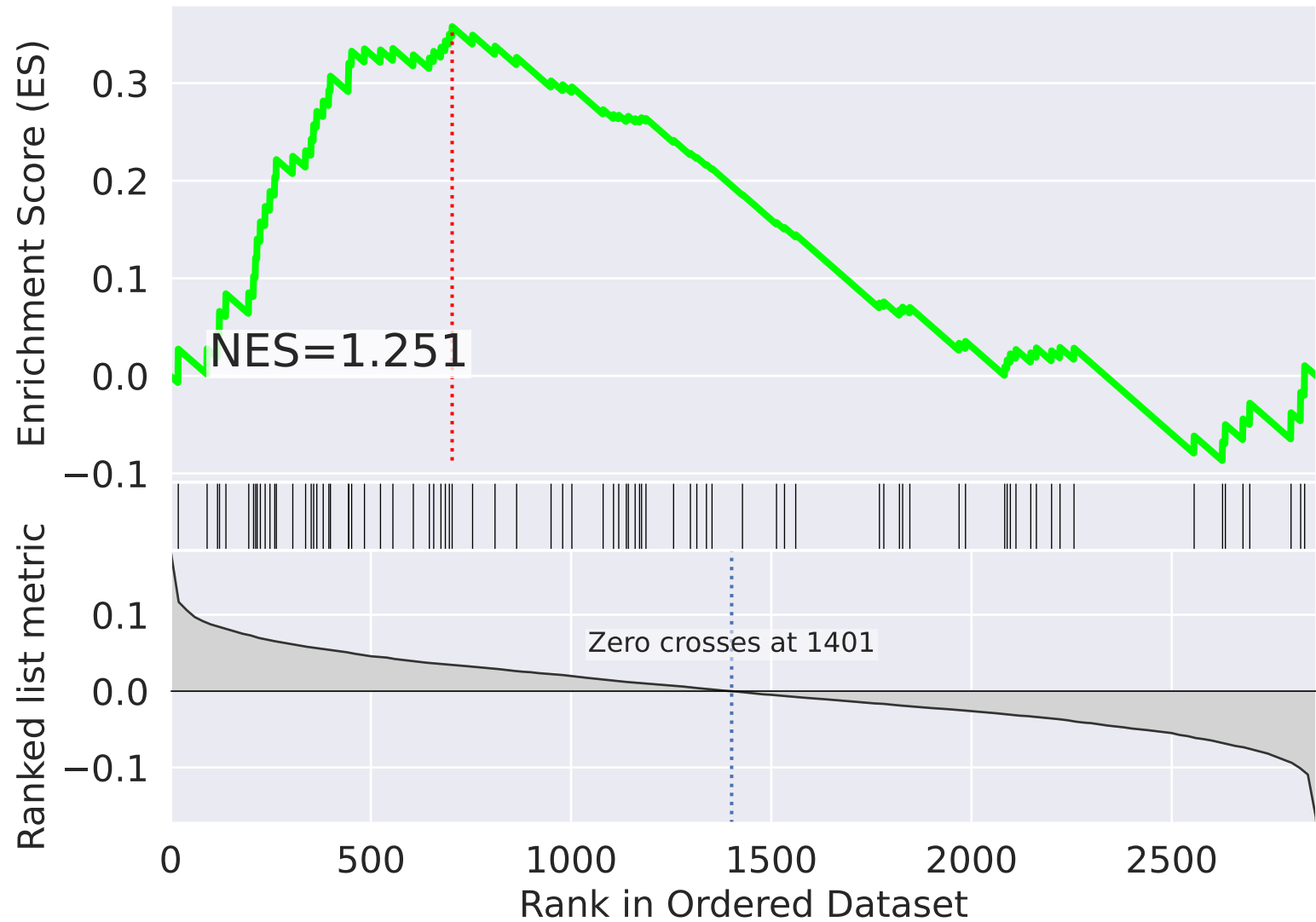


NES	SET
3.995	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
3.934	T cell receptor signaling pathway (GO:0050852)
3.906	MAPK cascade (GO:0000165)
3.892	stimulatory C-type lectin receptor signaling pathway (GO:0002223)
3.867	NIK/NF-kappaB signaling (GO:0038061)
3.786	Fc-epsilon receptor signaling pathway (GO:0038095)
3.741	tumor necrosis factor-mediated signaling pathway (GO:0033209)
3.741	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
3.673	regulation of cellular amino acid metabolic process (GO:0006521)
3.619	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
3.617	regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
3.528	centrosome cycle (GO:0007098)
3.491	protein polyubiquitination (GO:0000209)
3.450	transmembrane transport (GO:0055085)
3.277	positive regulation of canonical Wnt signaling pathway (GO:0090263)

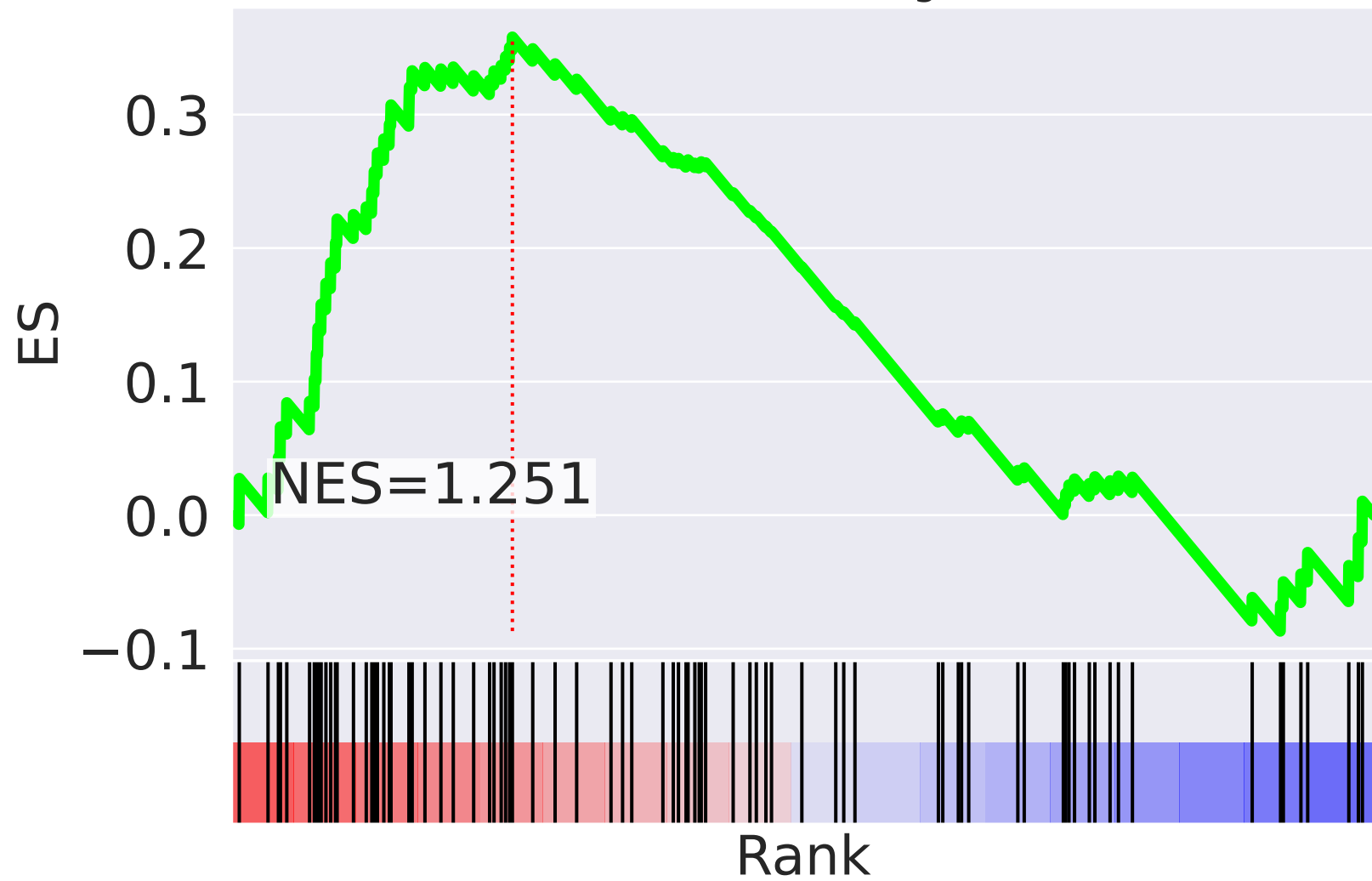




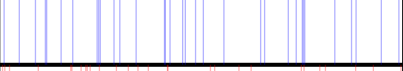
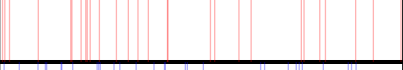
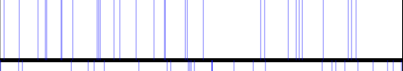
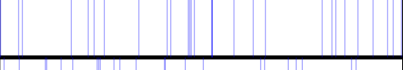

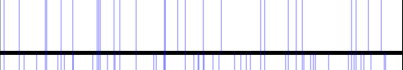
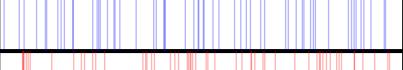
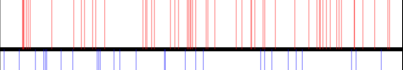
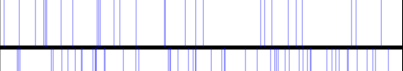
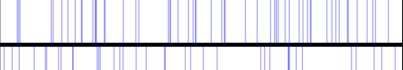
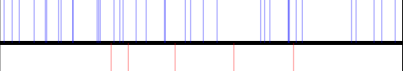


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=39$

# mitochondrial translational elongation (GO:0070125)



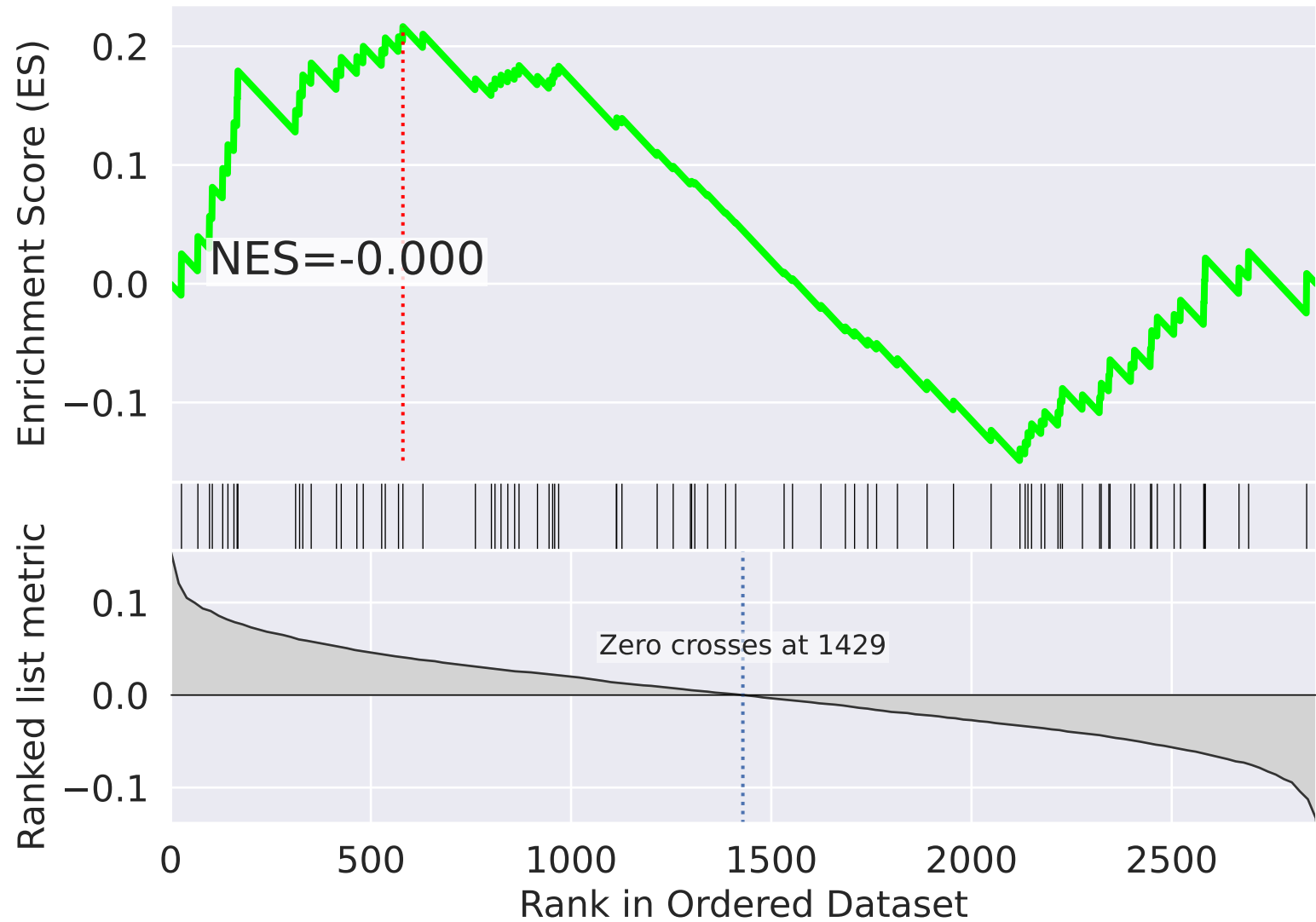
mitochondrial translational elongation (GO:0070125)



NES		SET
4.851		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.859		regulation of cellular response to heat (GO:1900034)
-3.821		intracellular transport of virus (GO:0075733)
3.749		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.682		mitotic nuclear envelope disassembly (GO:0007077)
-3.123		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
-3.110		regulation of glucose transport (GO:0010827)
-3.104		tRNA export from nucleus (GO:0006409)
-3.091		mRNA export from nucleus (GO:0006406)
3.010		negative regulation of cell proliferation (GO:0008285)
-3.006		viral process (GO:0016032)
-2.893		G2/M transition of mitotic cell cycle (GO:0000086)
-2.848		protein sumoylation (GO:0016925)
2.780		negative regulation of intrinsic apoptotic signaling pathway (GO:2001243)
-2.778		nucleotide-excision repair, DNA damage recognition (GO:0000715)

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)



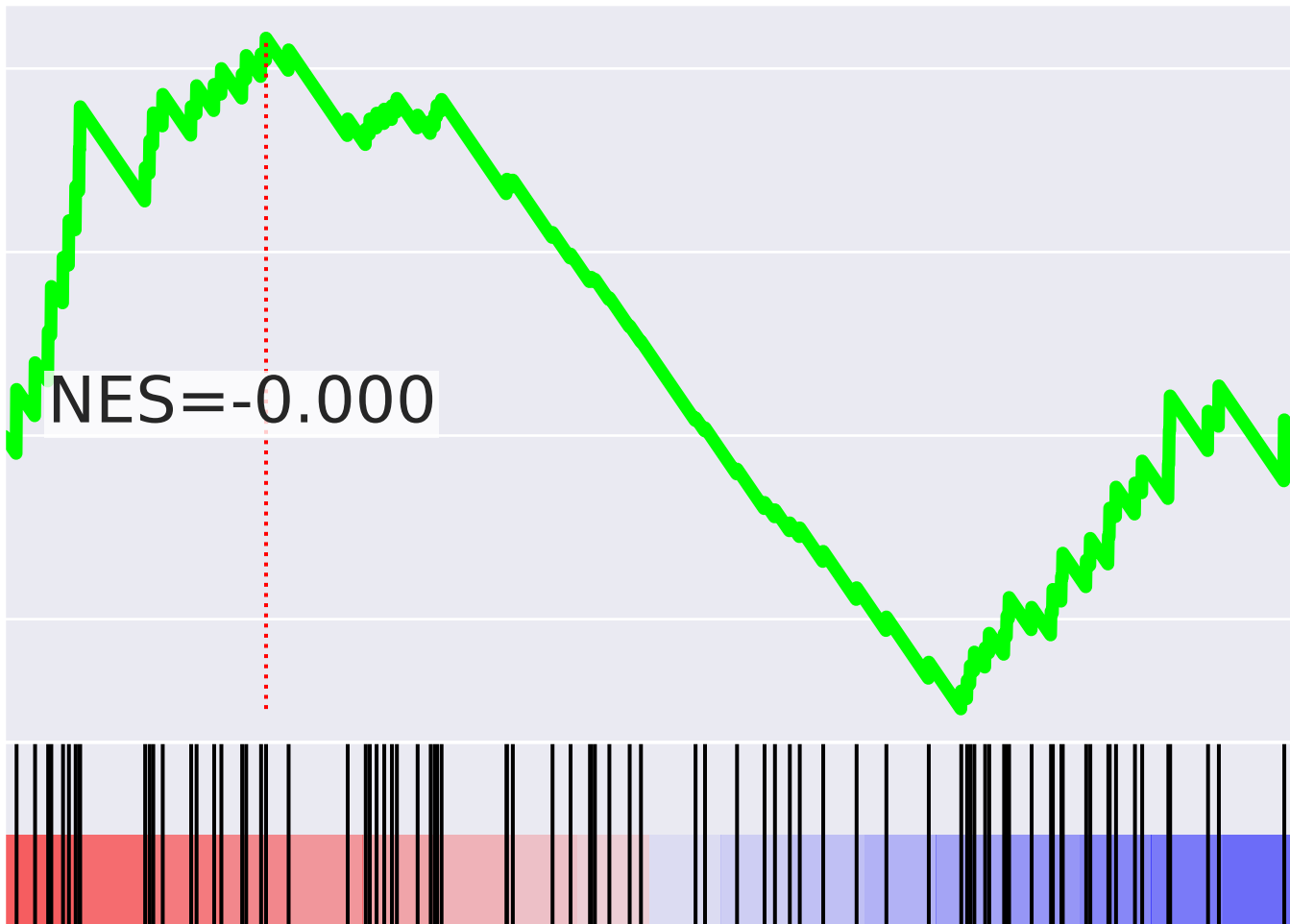
mitochondrial translational elongation (GO:0070125)

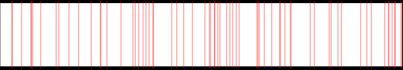

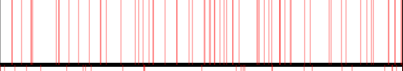
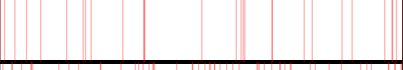
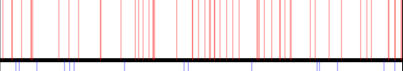
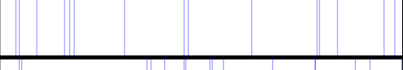
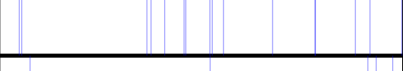








ES

0.2  
0.1  
0.0  
-0.1

NES=-0.000

Rank

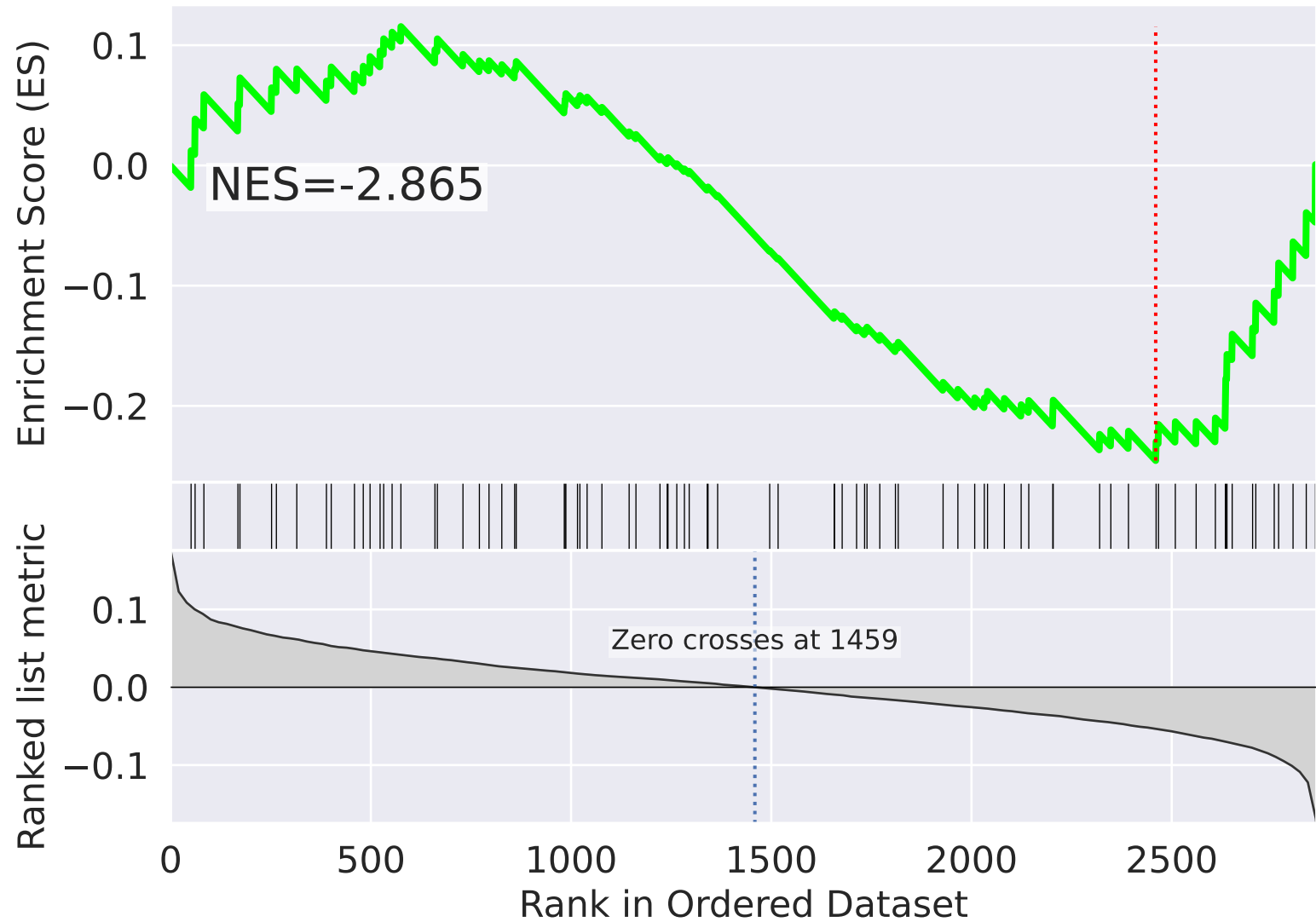


NES		SET
4.015		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-3.020		negative regulation of protein kinase activity (GO:0006469)
3.007		translational initiation (GO:0006413)
2.945		RNA export from nucleus (GO:0006405)
2.834		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.715		nervous system development (GO:0007399)
-2.678		glucose homeostasis (GO:0042593)
-2.637		cell cycle checkpoint (GO:0000075)
-2.631		kidney development (GO:0001822)
-2.613		mitotic DNA replication checkpoint (GO:0033314)
-2.600		negative regulation of phosphatase activity (GO:0010923)
-2.593		membrane fusion (GO:0061025)
-2.573		phosphatidylinositol-mediated signaling (GO:0048015)
-2.463		iron-sulfur cluster assembly (GO:0016226)
-2.460		COPII vesicle coating (GO:0048208)

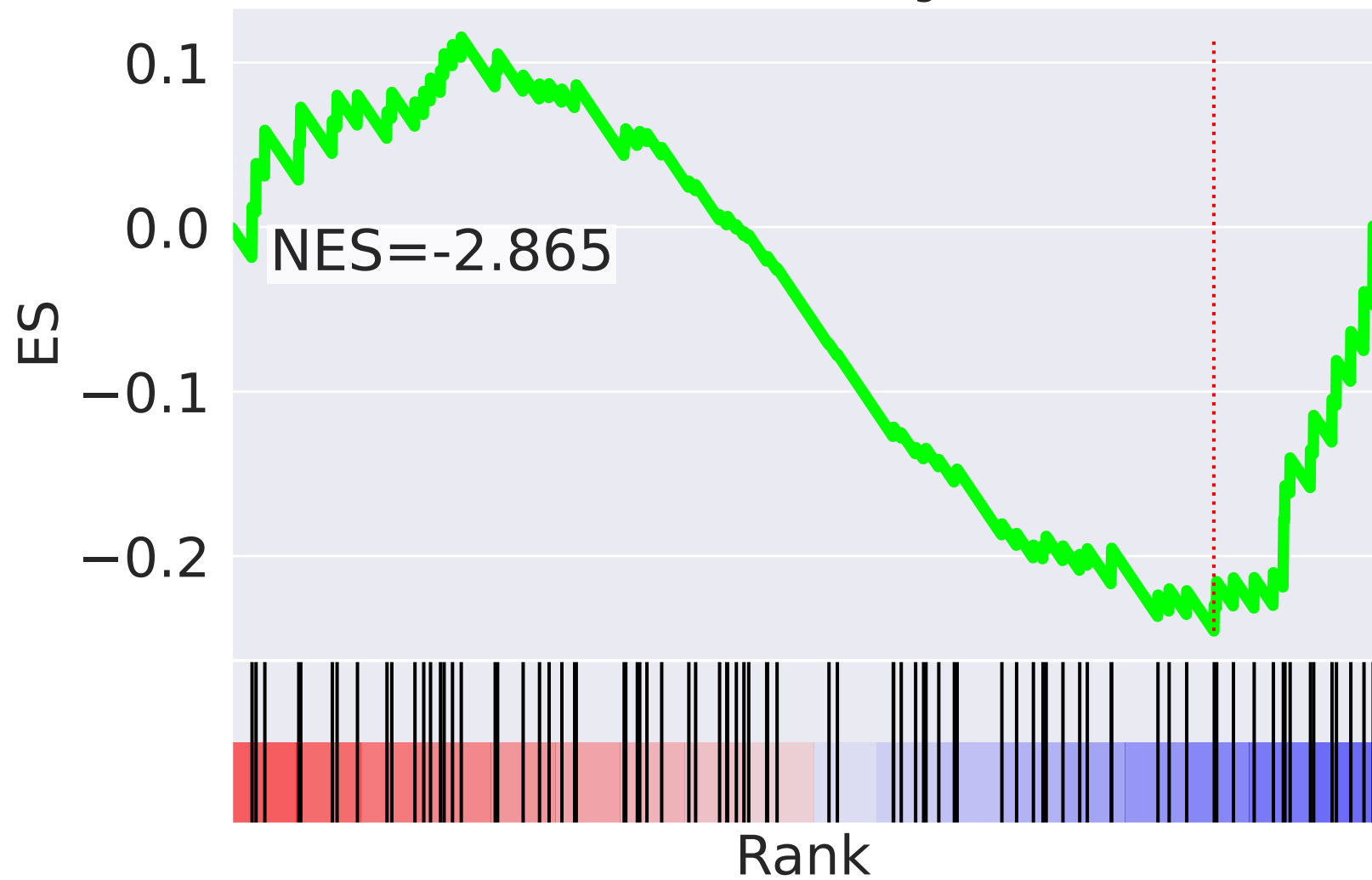


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=41$

# mitochondrial translational elongation (GO:0070125)

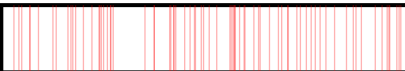

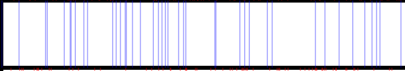
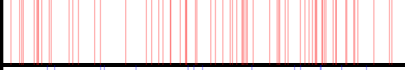
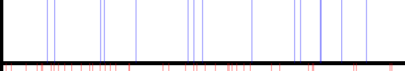
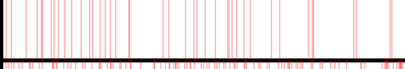
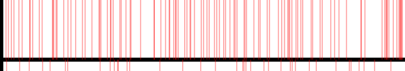
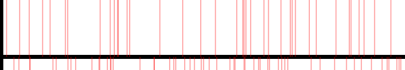
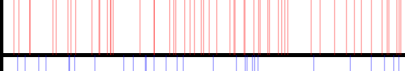
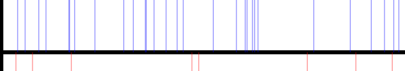
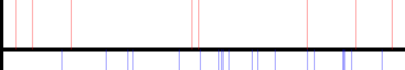
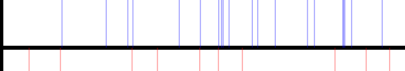

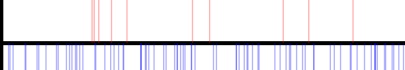
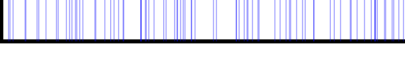


mitochondrial translational elongation (GO:0070125)



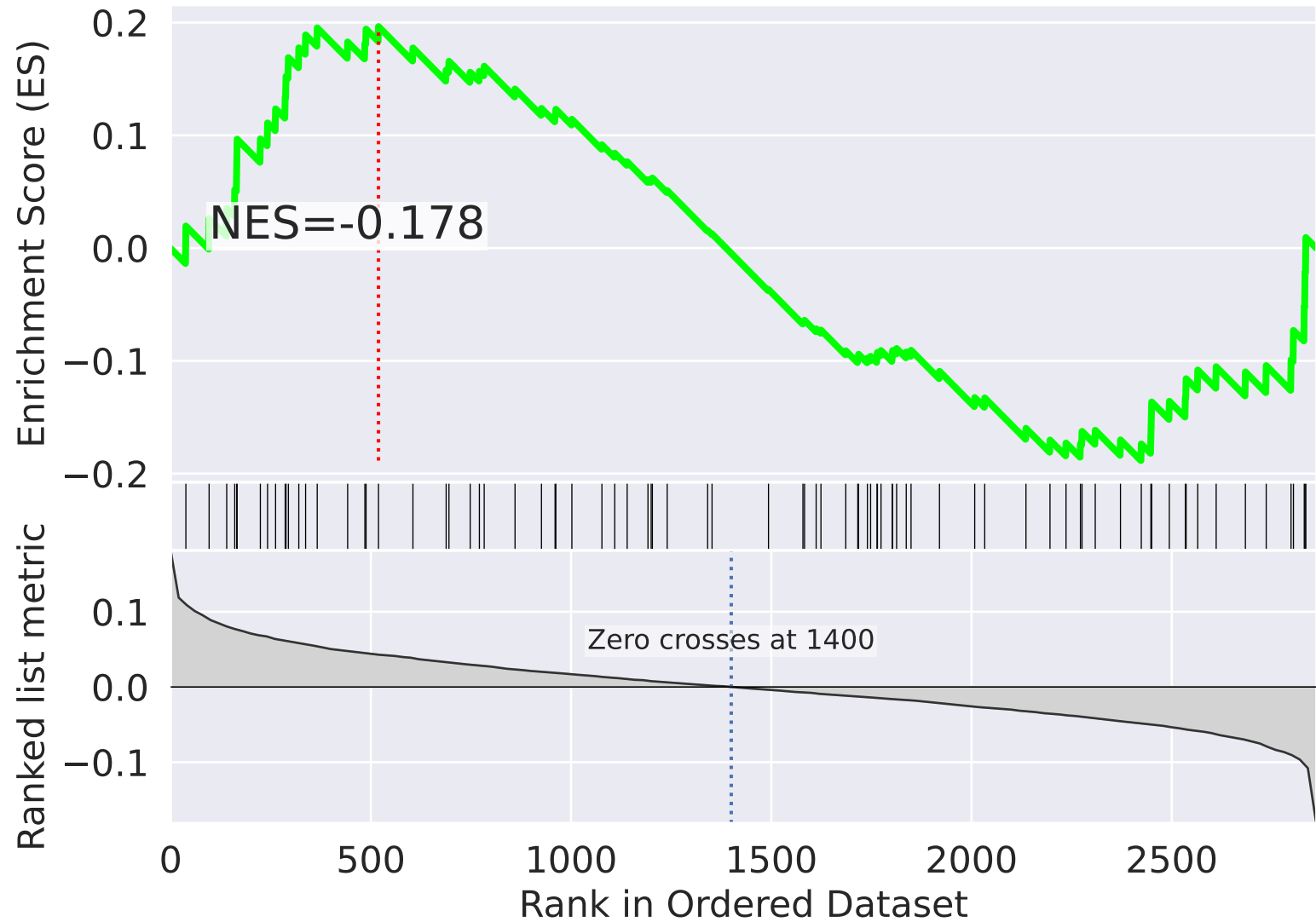
NES

SET

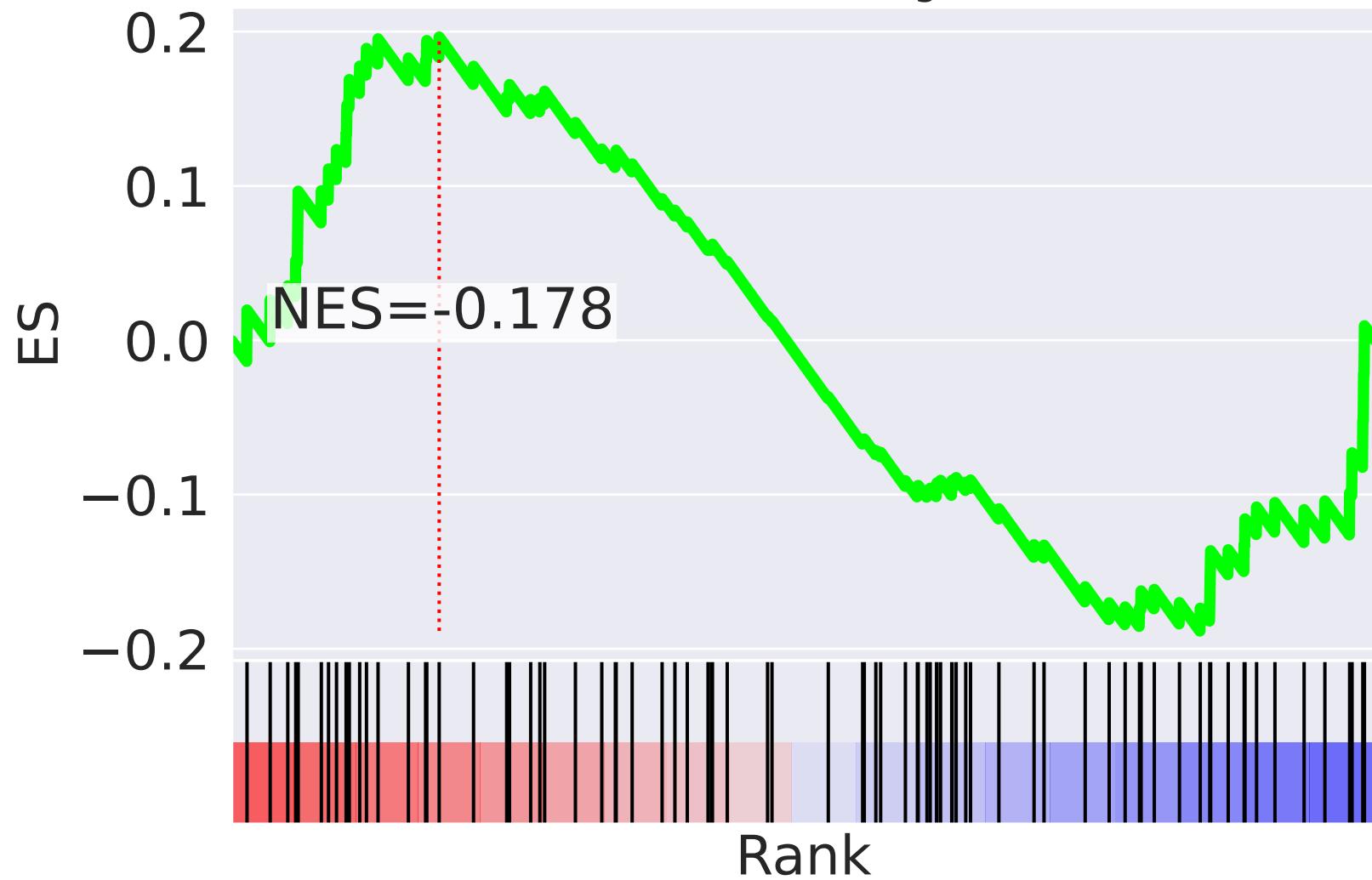
4.202		viral transcription (GO:0019083)
3.937		translational initiation (GO:0006413)
-3.657		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.595		sister chromatid cohesion (GO:0007062)
-3.408		tricarboxylic acid cycle (GO:0006099)
3.288		mitotic cell cycle (GO:0000278)
3.223		rRNA processing (GO:0006364)
3.184		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
3.164		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-3.094		mitochondrial translation (GO:0032543)
3.080		dolichol-linked oligosaccharide biosynthetic process (GO:0006488)
-3.045		regulation of cholesterol biosynthetic process (GO:0045540)
2.996		cytoplasmic microtubule organization (GO:0031122)
2.867		nucleosome disassembly (GO:0006337)
-2.865		mitochondrial translational elongation (GO:0070125)

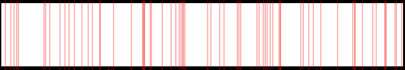
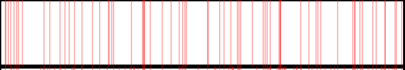
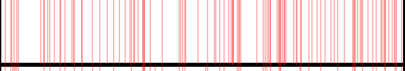
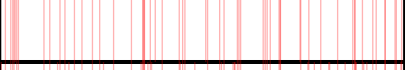
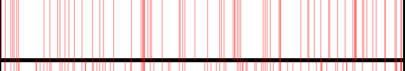
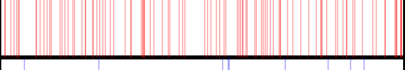
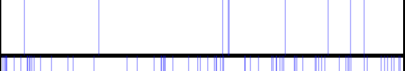
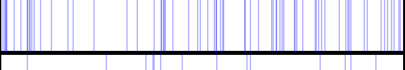
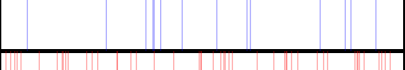
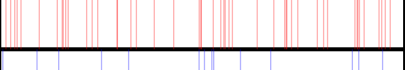
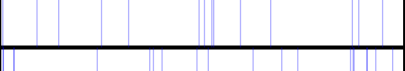
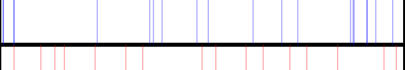
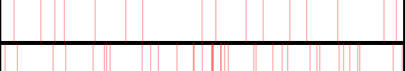
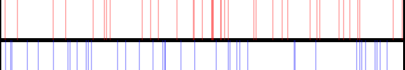
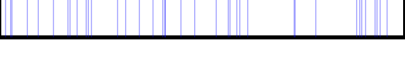
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=42$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

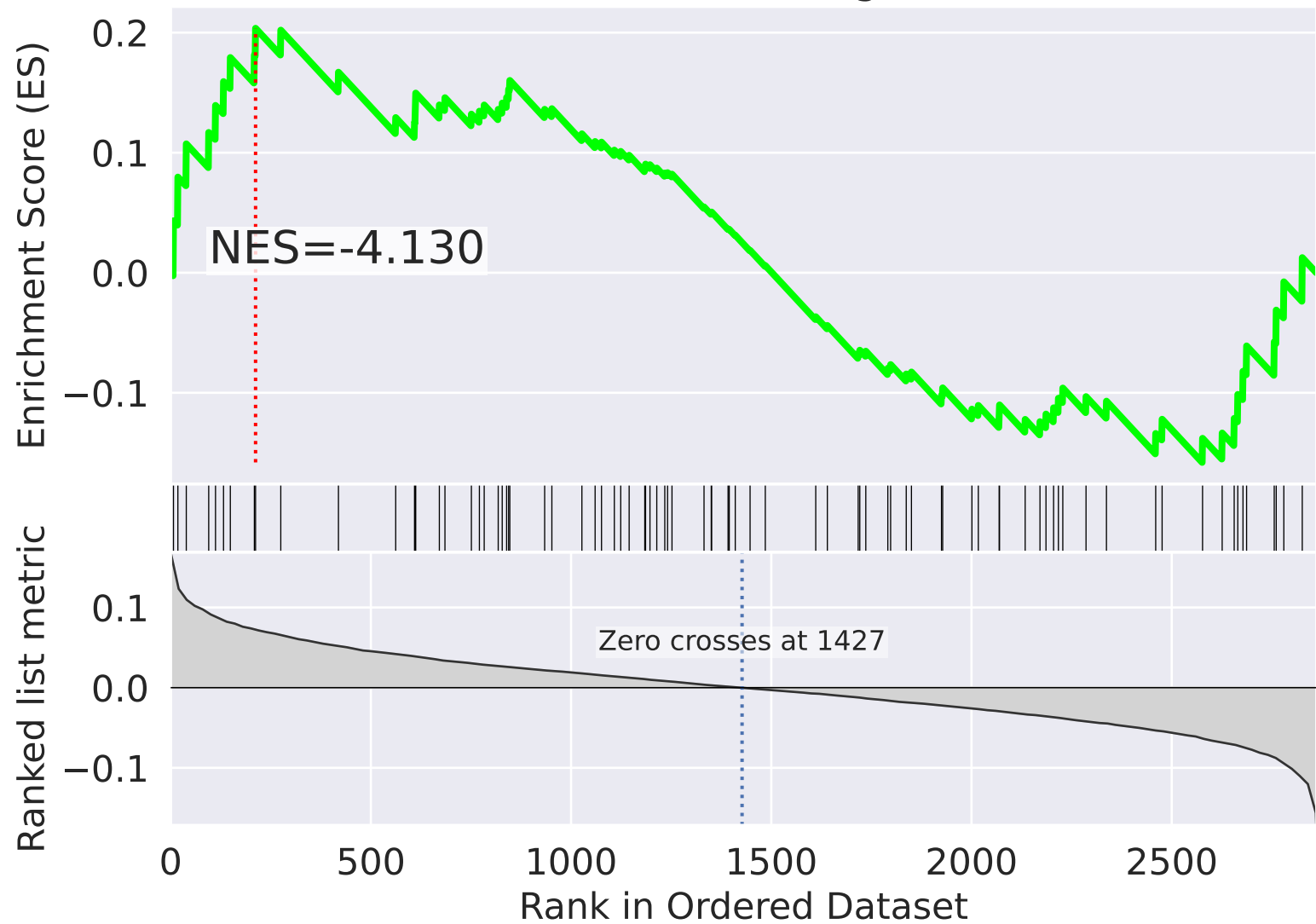


NES		SET
4.373		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
4.339		translational initiation (GO:0006413)
4.221		rRNA processing (GO:0006364)
4.071		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
3.799		viral transcription (GO:0019083)
3.491		translation (GO:0006412)
-2.986		intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (GO:0042771)
-2.927		protein phosphorylation (GO:0006468)
-2.862		T cell costimulation (GO:0031295)
2.772		regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
-2.746		intra-Golgi vesicle-mediated transport (GO:0006891)
-2.722		regulation of protein stability (GO:0031647)
2.721		ribosomal large subunit biogenesis (GO:0042273)
2.696		protein complex assembly (GO:0006461)
-2.686		cell cycle arrest (GO:0007050)



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

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2

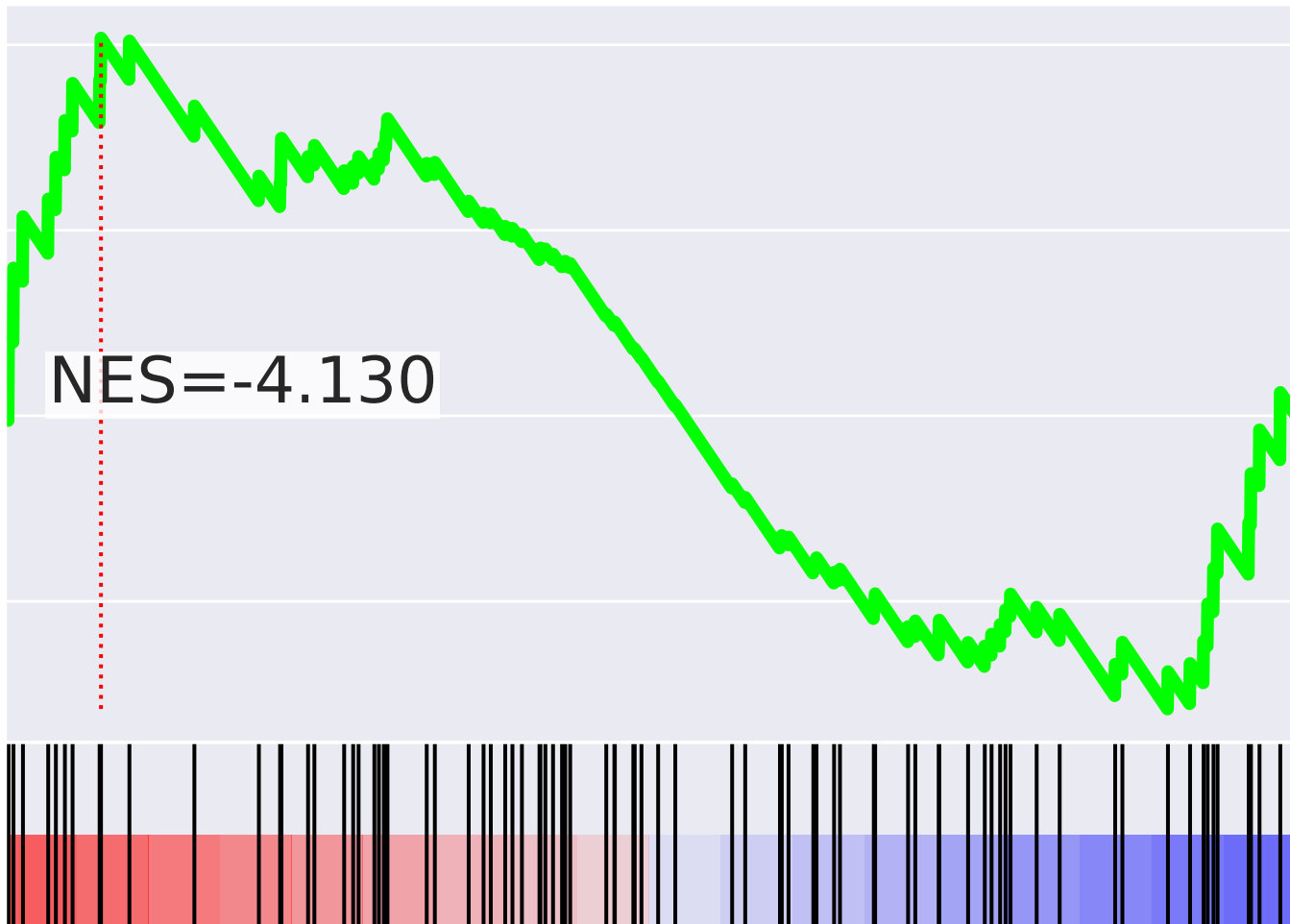
0.1

0.0

-0.1


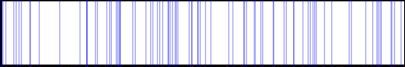
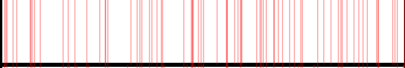
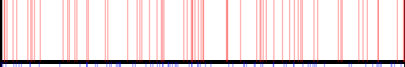
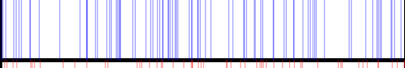
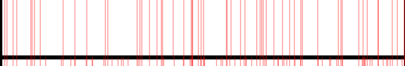
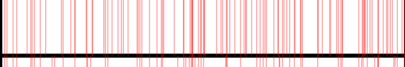
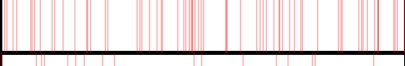

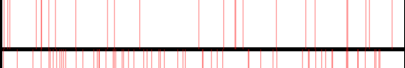
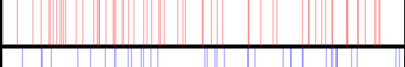
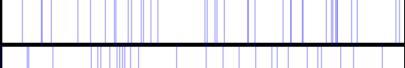
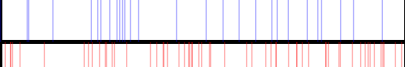
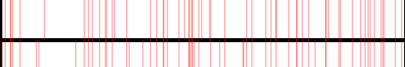
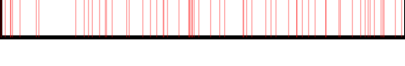
NES=-4.130

Rank



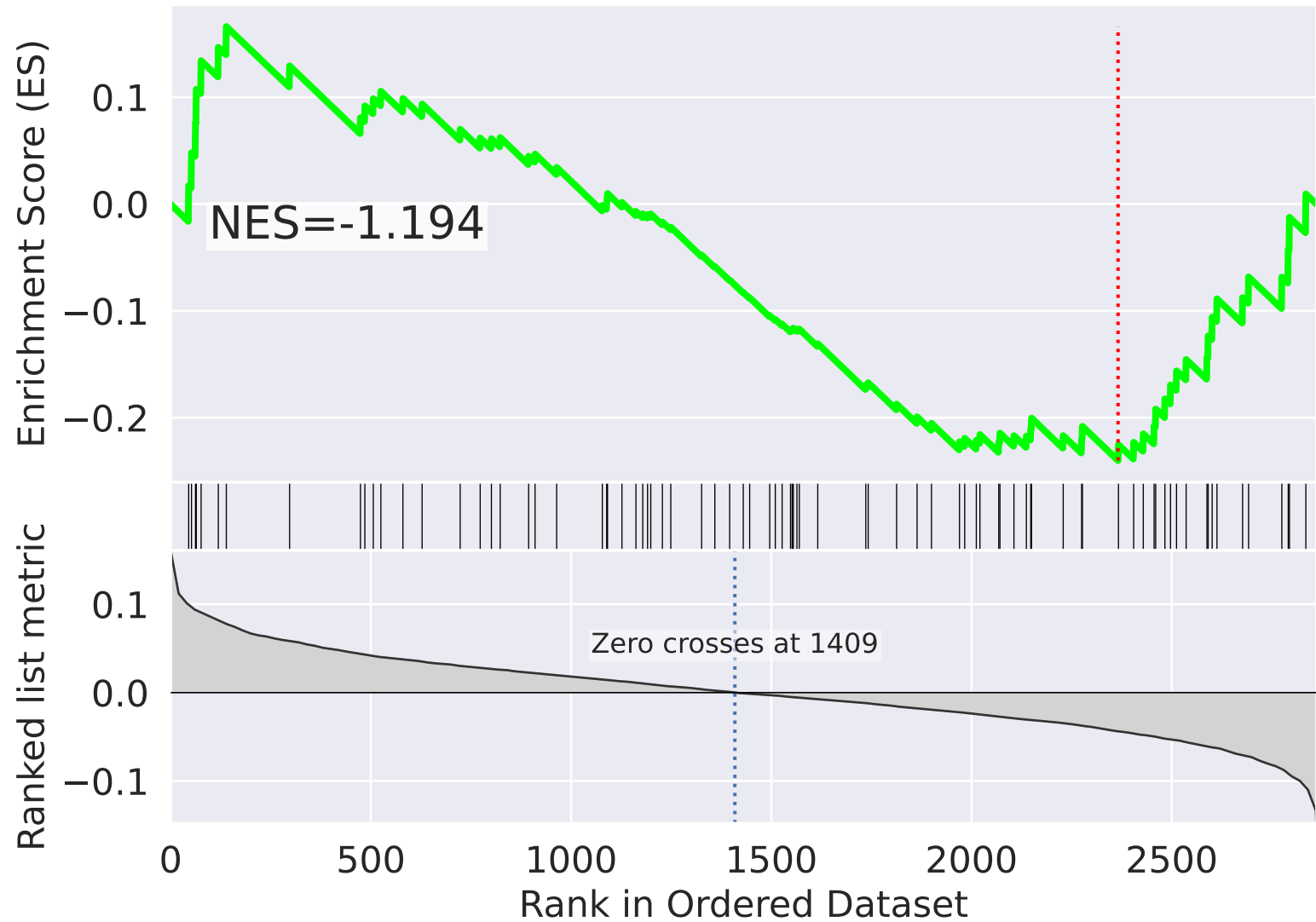
NES

SET

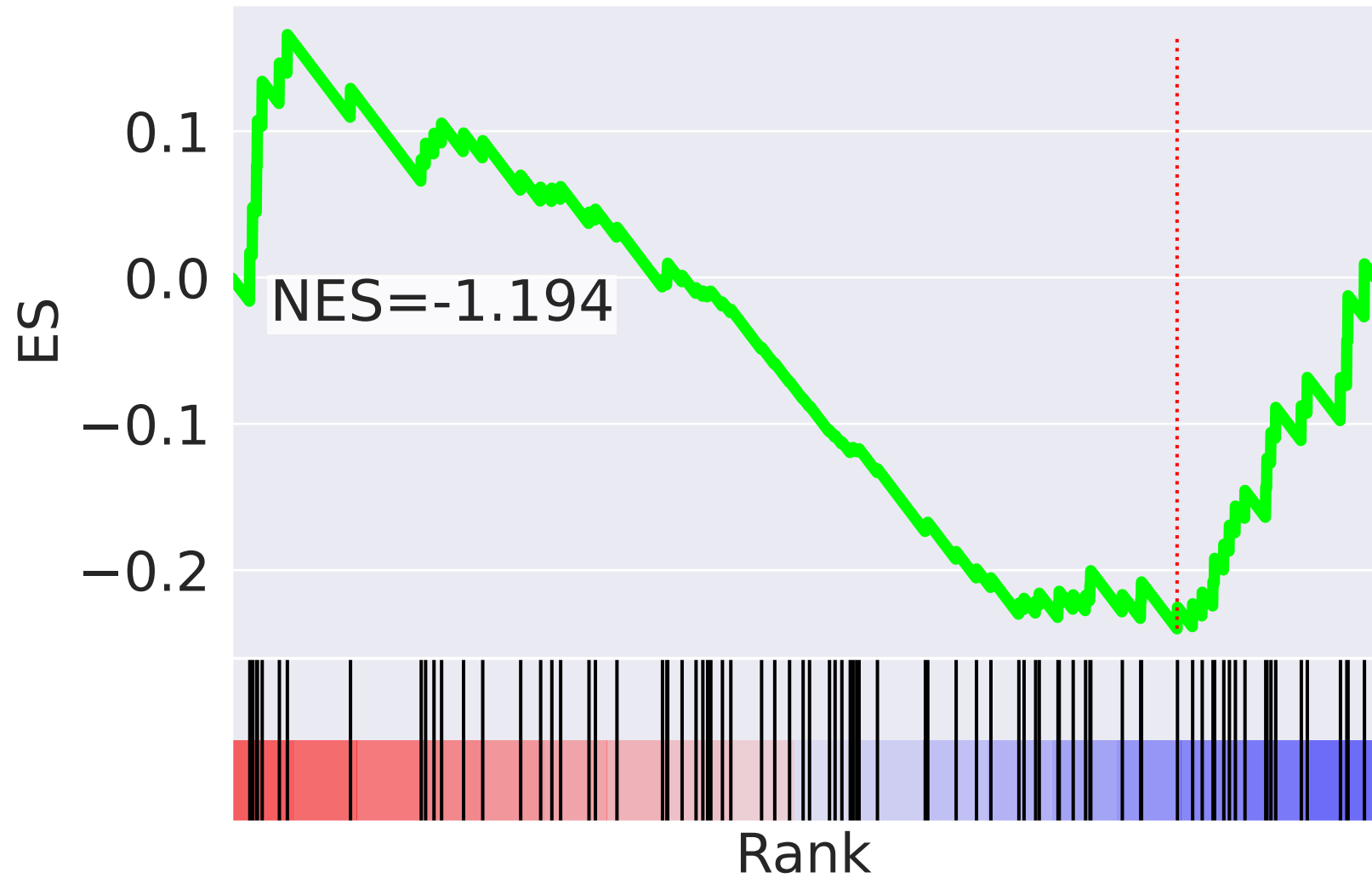
-4.257		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.130		mitochondrial translational elongation (GO:0070125)
4.062		viral transcription (GO:0019083)
3.988		translational initiation (GO:0006413)
-3.829		mitochondrial translational termination (GO:0070126)
3.808		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
3.681		rRNA processing (GO:0006364)
3.589		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.566		platelet activation (GO:0030168)
3.506		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
3.375		transcription elongation from RNA polymerase II promoter (GO:0006368)
-3.326		macroautophagy (GO:0016236)
-3.251		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.225		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
3.139		Fc-epsilon receptor signaling pathway (GO:0038095)

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

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

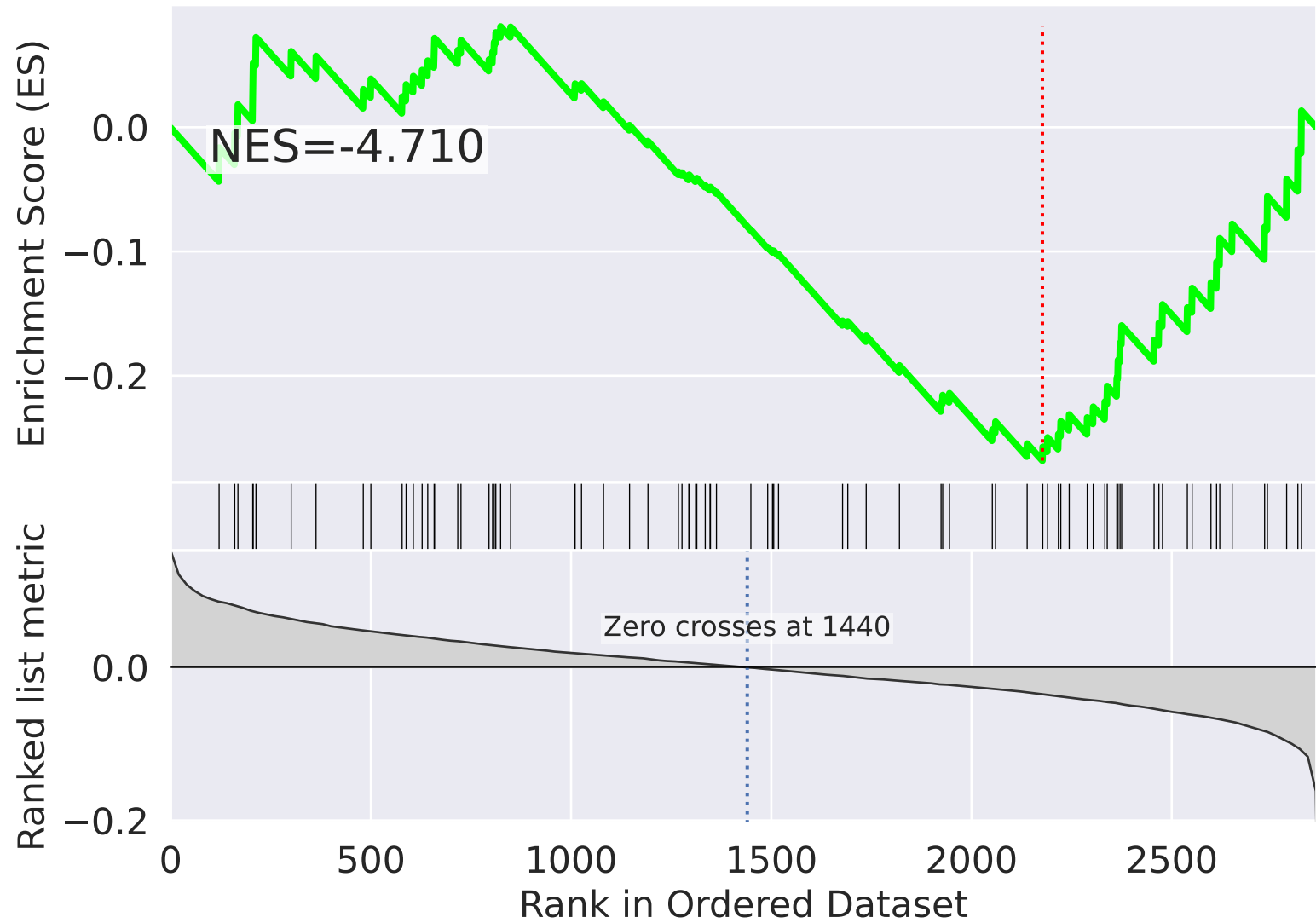


NES	SET
4.619	protein polyubiquitination (GO:0000209)
3.710	intracellular transport of virus (GO:0075733)
3.667	proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
3.525	viral process (GO:0016032)
3.519	anaphase-promoting complex-dependent catabolic process (GO:0031145)
3.400	regulation of gene silencing by miRNA (GO:0060964)
3.397	Fc-epsilon receptor signaling pathway (GO:0038095)
3.356	stimulatory C-type lectin receptor signaling pathway (GO:0002223)
3.320	regulation of glucose transport (GO:0010827)
3.279	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
3.273	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
3.222	mitotic nuclear envelope disassembly (GO:0007077)
3.113	mRNA export from nucleus (GO:0006406)
3.095	transmembrane transport (GO:0055085)
3.043	regulation of cellular amino acid metabolic process (GO:0006521)

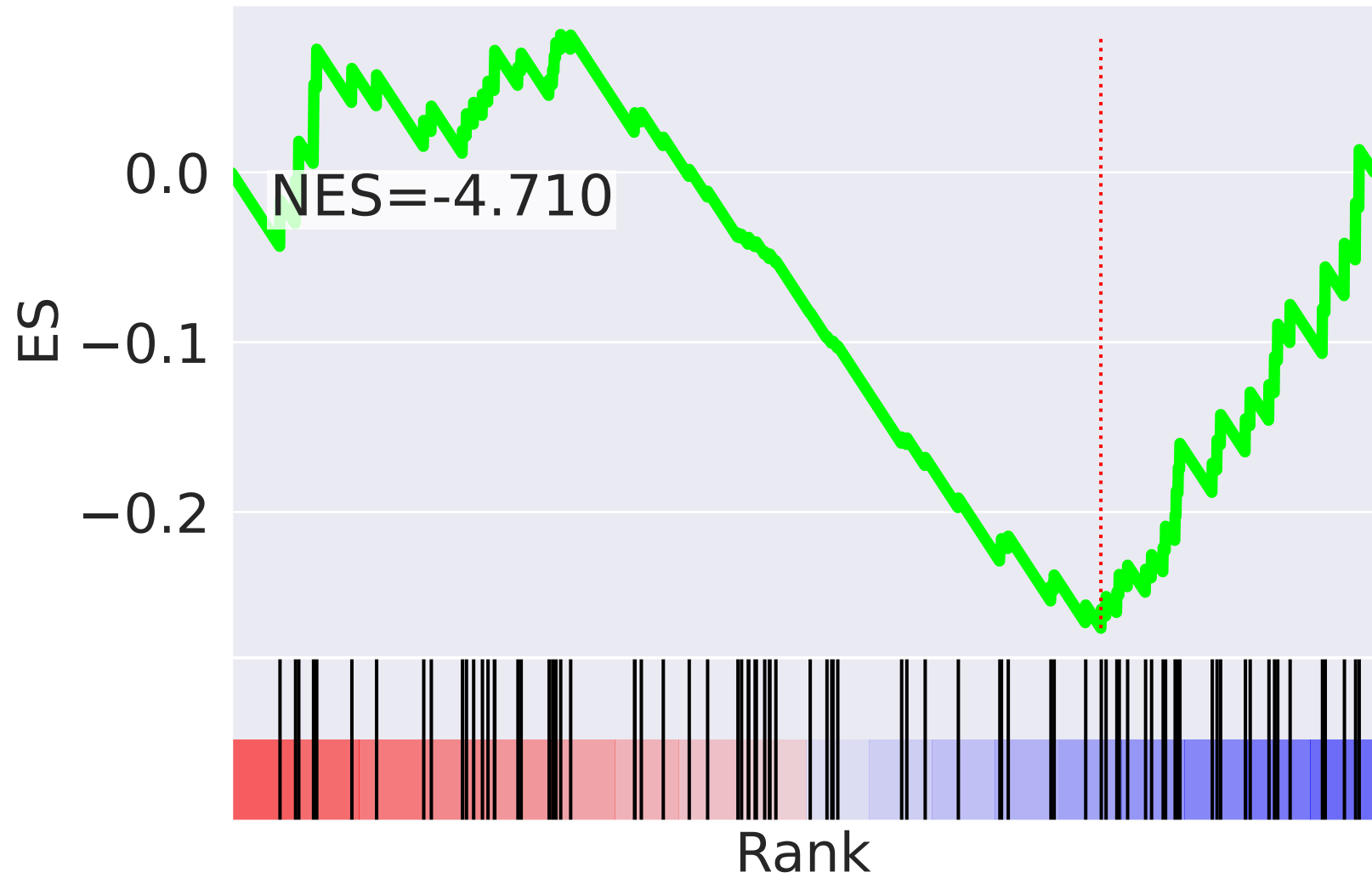



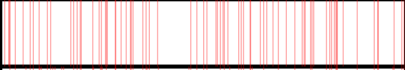
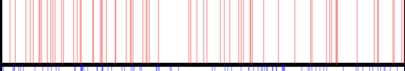
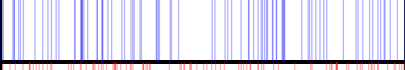
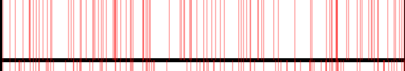
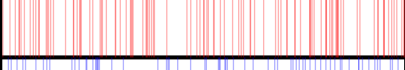
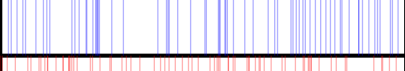
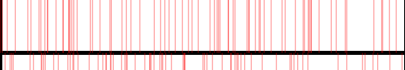
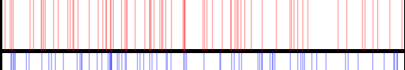
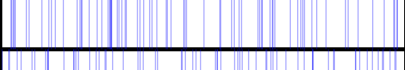
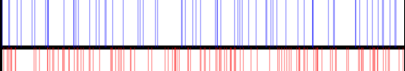
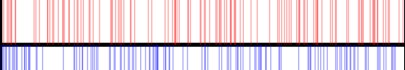
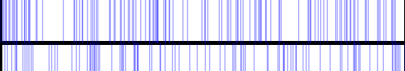
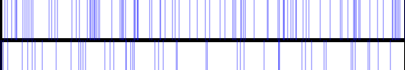

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=45$

# mitochondrial translational elongation (GO:0070125)



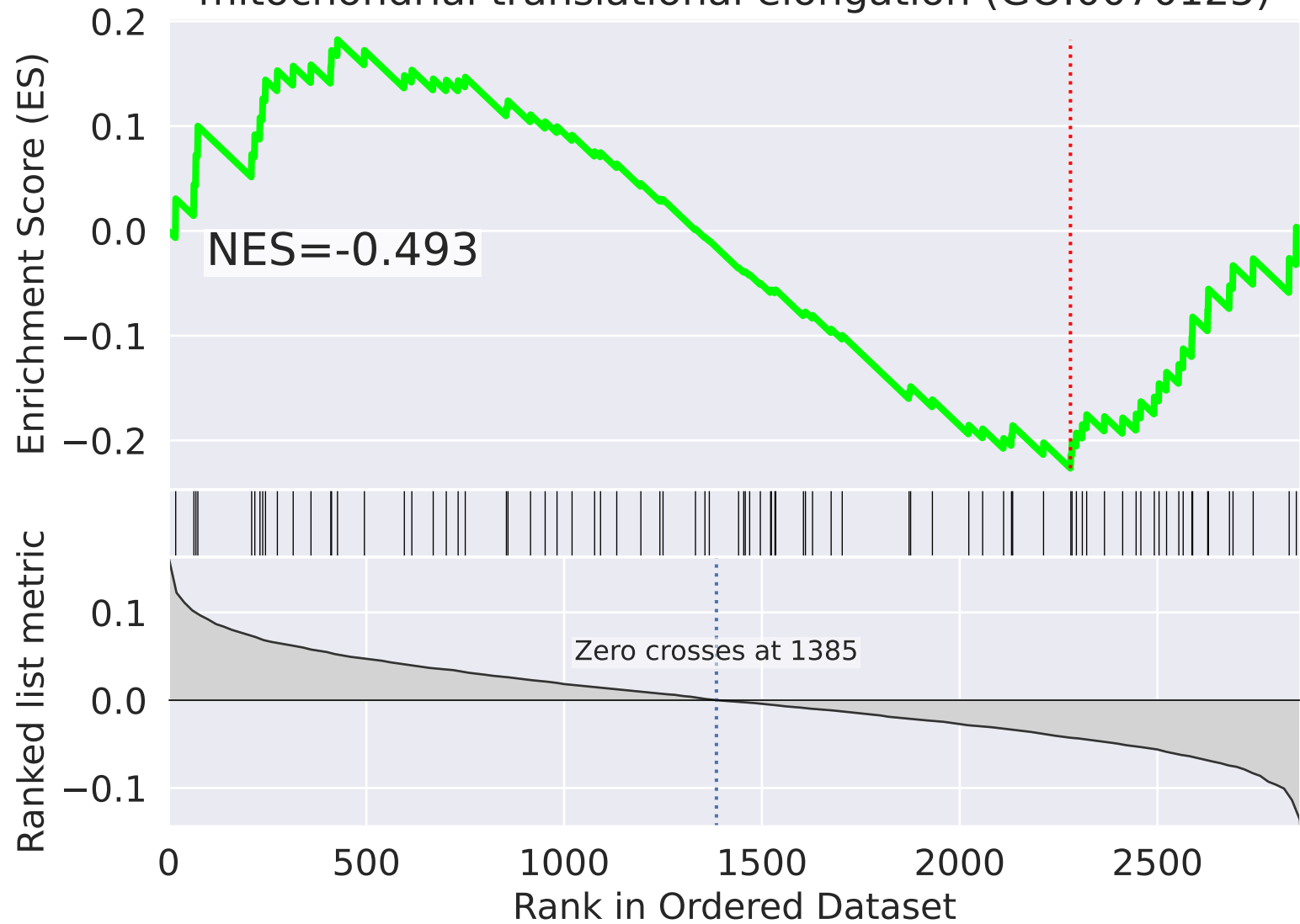
# mitochondrial translational elongation (GO:0070125)



NES		SET
inf		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
inf		viral transcription (GO:0019083)
7.956		translational initiation (GO:0006413)
-7.444		neutrophil degranulation (GO:0043312)
7.232		translation (GO:0006412)
7.066		rRNA processing (GO:0006364)
-7.020		transcription initiation from RNA polymerase II promoter (GO:0006367)
6.712		protein ubiquitination (GO:0016567)
6.319		positive regulation of cell proliferation (GO:0008284)
-6.091		MAPK cascade (GO:0000165)
-5.860		sister chromatid cohesion (GO:0007062)
5.734		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-5.627		mRNA splicing, via spliceosome (GO:0000398)
-5.603		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-5.495		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  $z=46$

# mitochondrial translational elongation (GO:0070125)



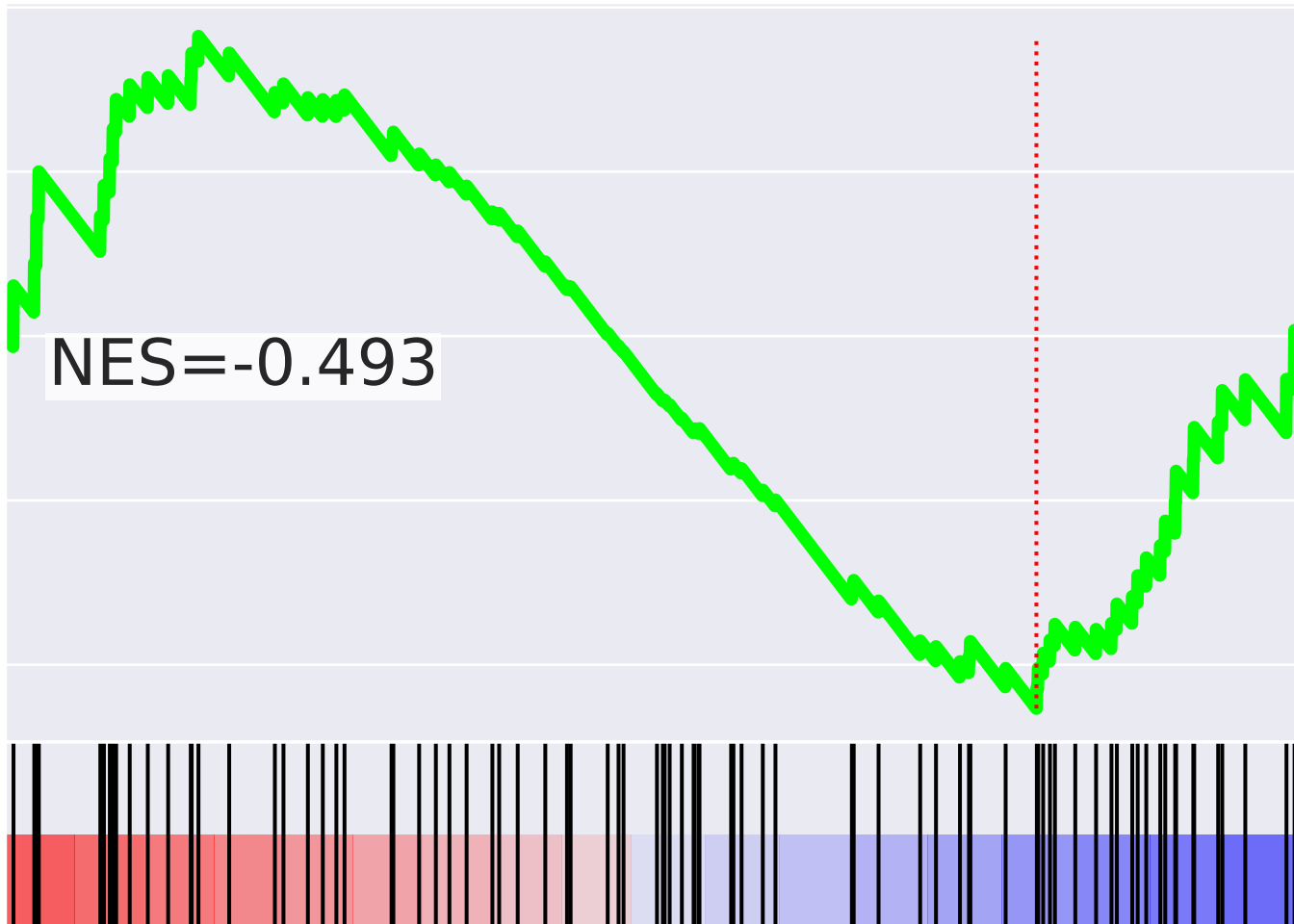
mitochondrial translational elongation (GO:0070125)

ES

0.2  
0.1  
0.0  
-0.1  
-0.2

NES=-0.493

Rank

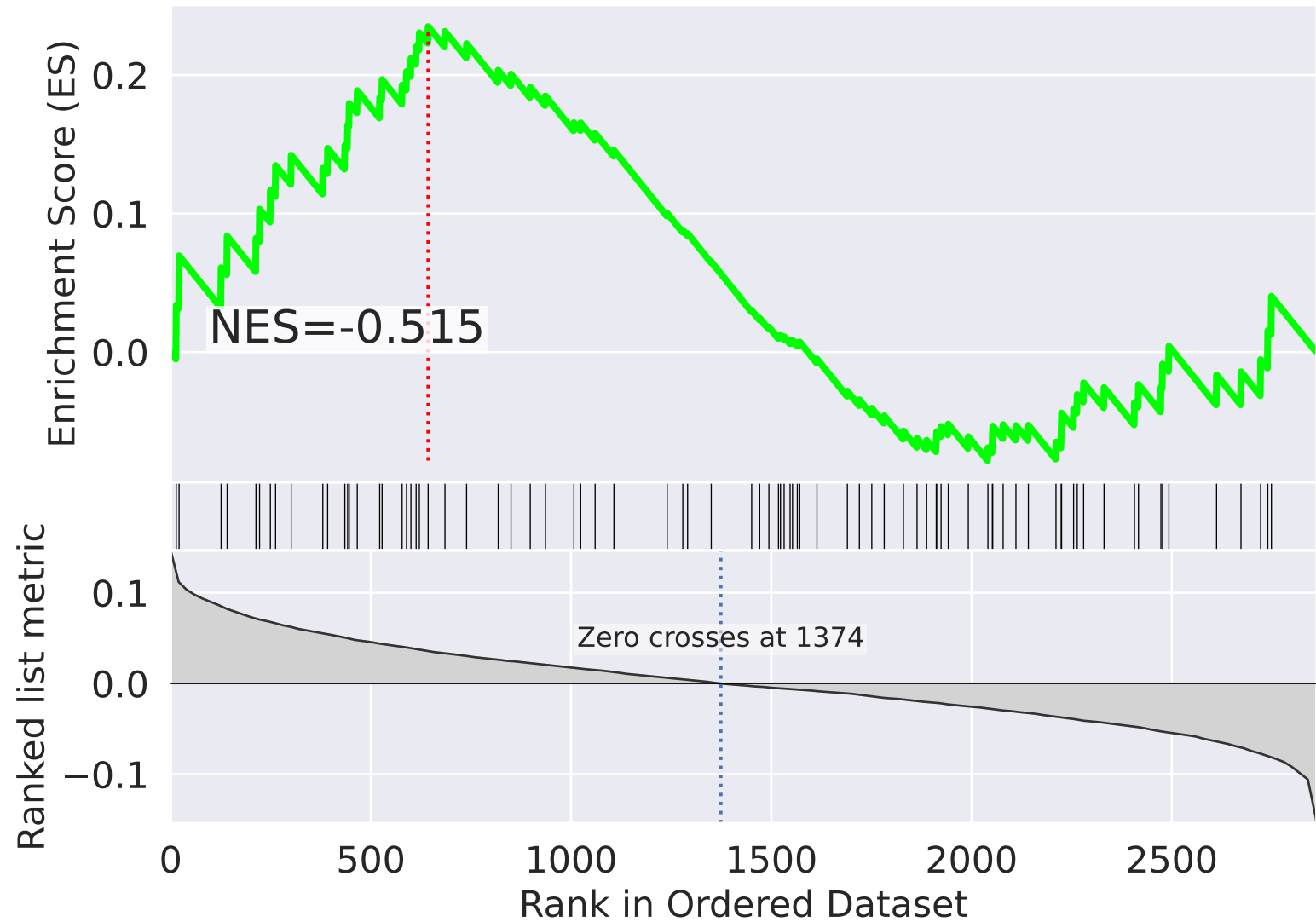


NES		SET
3.054		replication fork processing (GO:0031297)
-2.934		central nervous system development (GO:0007417)
2.931		mitotic cell cycle (GO:0000278)
2.930		interstrand cross-link repair (GO:0036297)
-2.603		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.584		membrane organization (GO:0061024)
2.530		intracellular signal transduction (GO:0035556)
-2.525		ubiquitin-dependent protein catabolic process (GO:0006511)
2.492		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.450		ephrin receptor signaling pathway (GO:0048013)
-2.436		ERBB2 signaling pathway (GO:0038128)
-2.407		exocytosis (GO:0006887)
-2.342		negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
-2.337		positive regulation of protein catabolic process (GO:0045732)
2.321		resolution of meiotic recombination intermediates (GO:0000712)

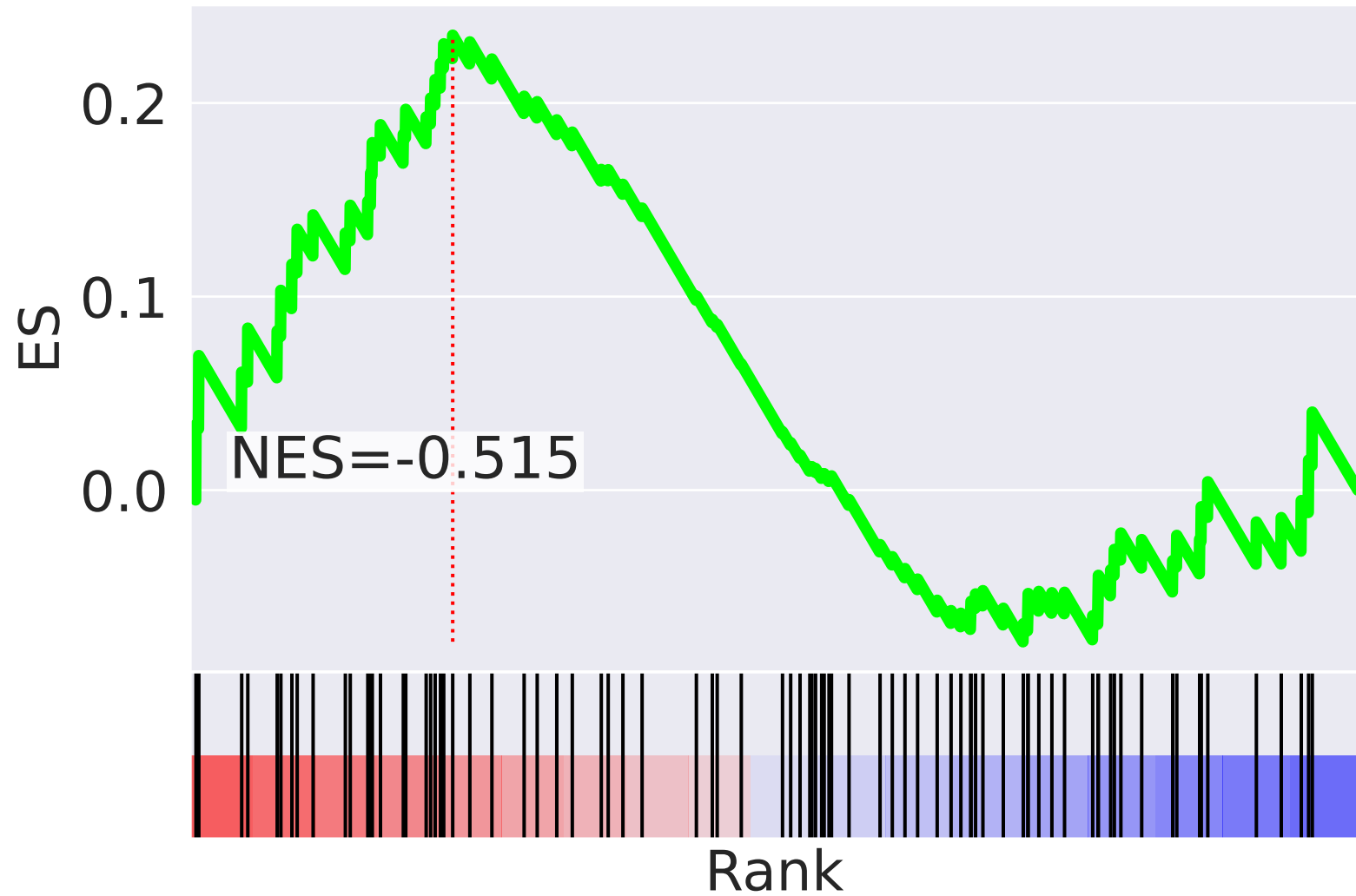


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=47$

# mitochondrial translational elongation (GO:0070125)



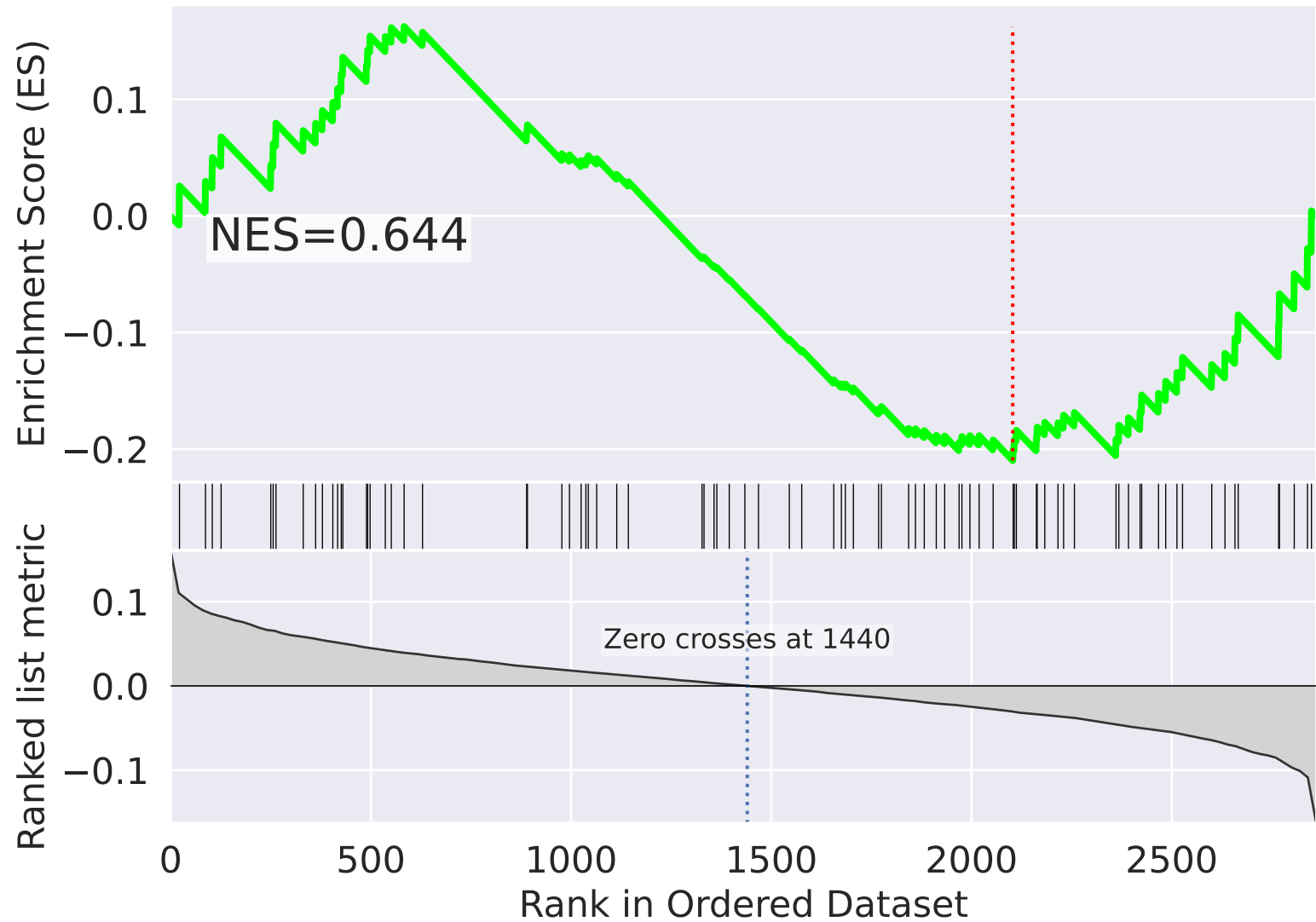
# mitochondrial translational elongation (GO:0070125)



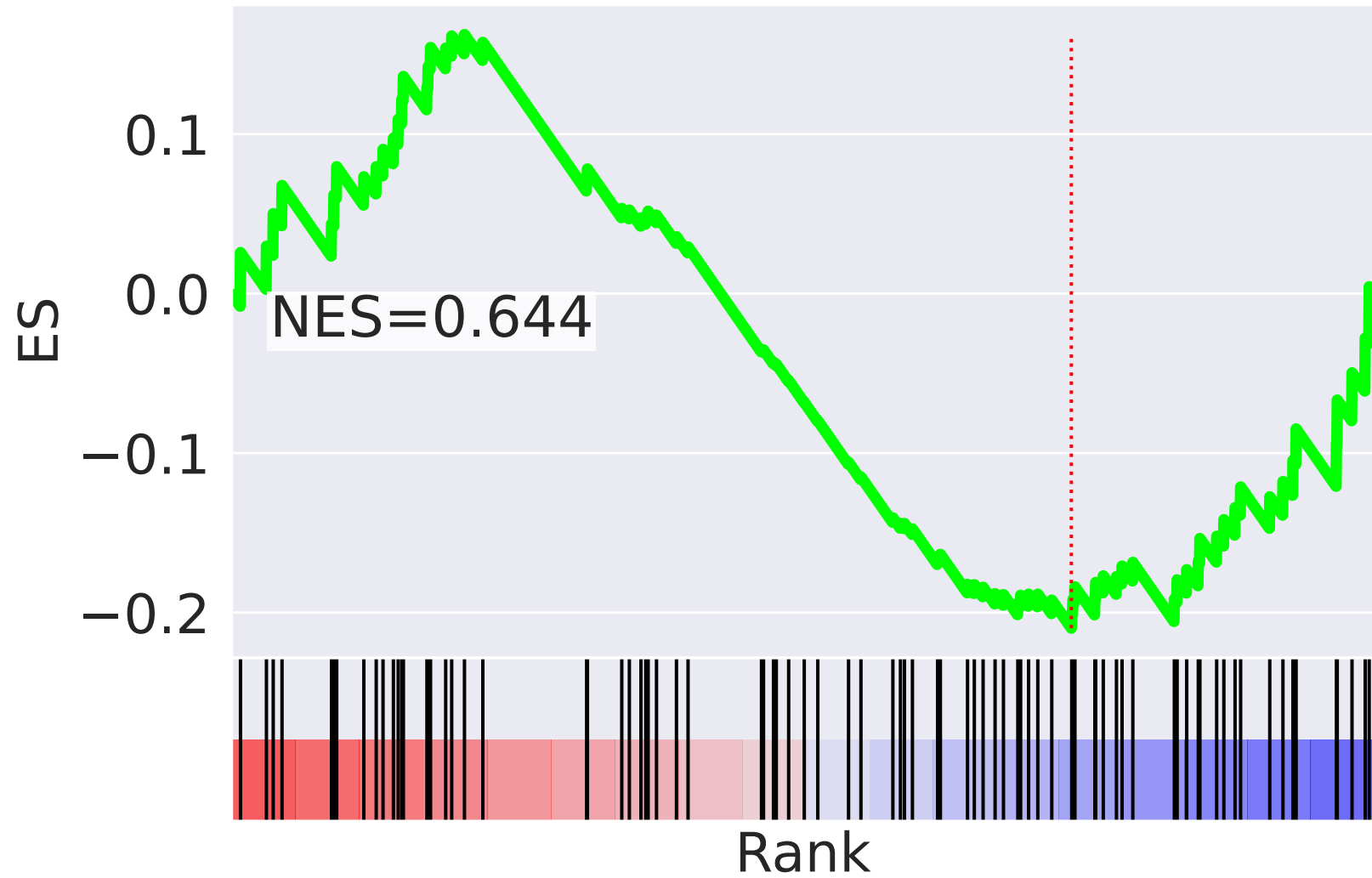
NES		SET
3.402		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.151		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-3.079		ER to Golgi vesicle-mediated transport (GO:0006888)
3.006		regulation of small GTPase mediated signal transduction (GO:0051056)
-2.937		membrane organization (GO:0061024)
-2.936		COPII vesicle coating (GO:0048208)
2.931		translational initiation (GO:0006413)
2.888		generation of precursor metabolites and energy (GO:0006091)
-2.727		integrin-mediated signaling pathway (GO:0007229)
2.541		regulation of circadian rhythm (GO:0042752)
-2.528		positive regulation of viral genome replication (GO:0045070)
-2.509		lysosomal transport (GO:0007041)
-2.482		Golgi organization (GO:0007030)
2.481		regulation of cholesterol biosynthetic process (GO:0045540)
2.454		negative regulation of DNA replication (GO:0008156)


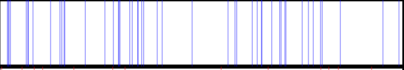


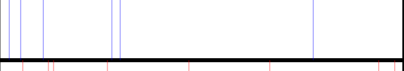

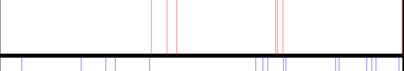
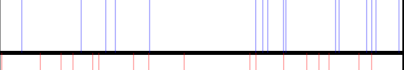
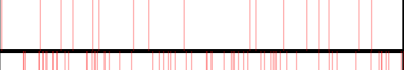
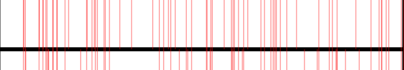
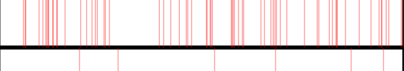
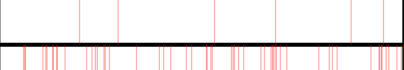
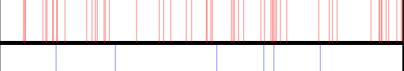
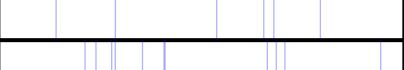
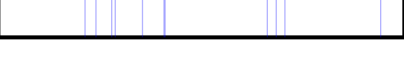
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=48$

# mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

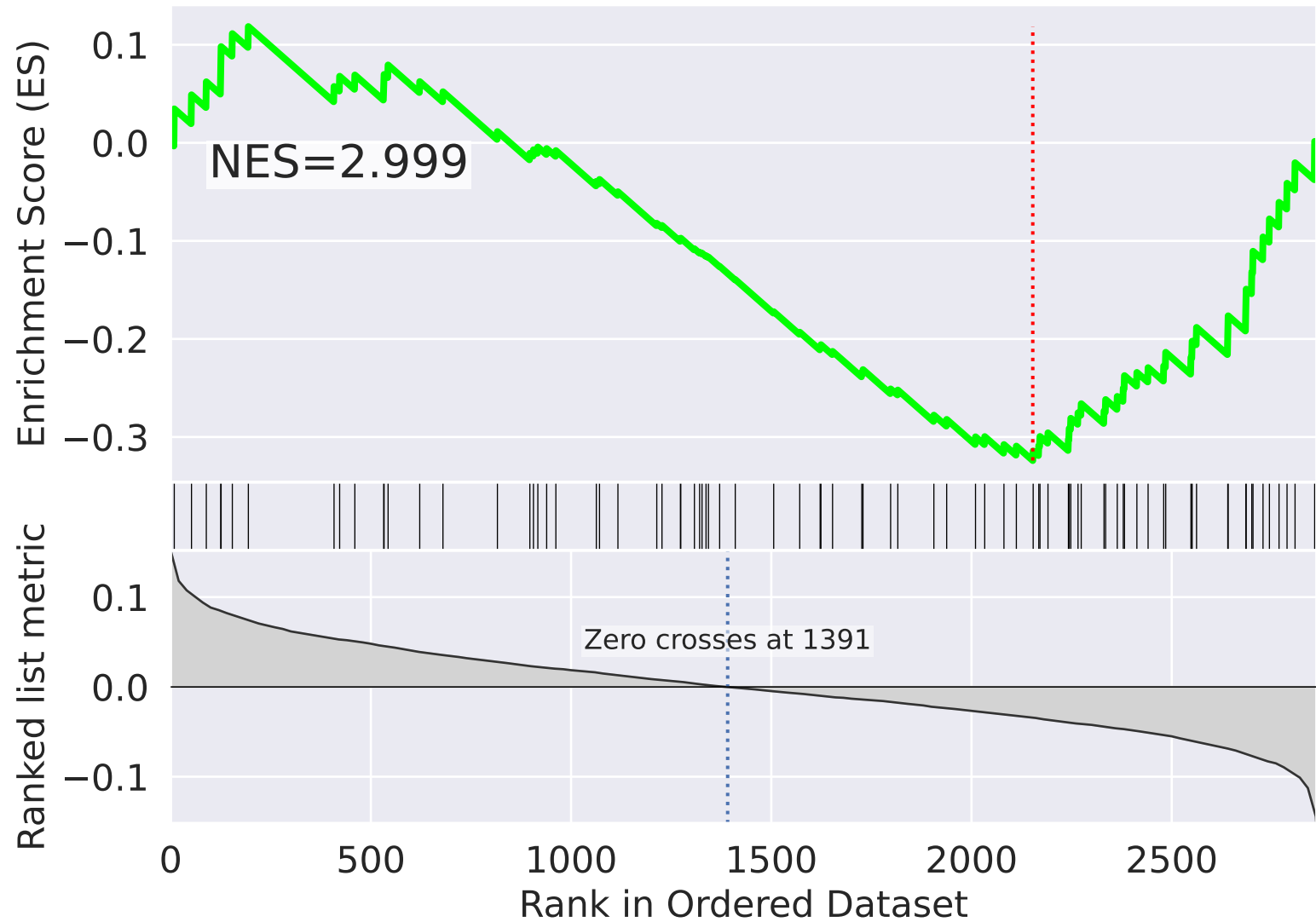


NES		SET
-3.700		membrane organization (GO:0061024)
-3.249		ER to Golgi vesicle-mediated transport (GO:0006888)
3.199		circadian regulation of gene expression (GO:0032922)
-2.935		COPII vesicle coating (GO:0048208)
-2.913		exocytosis (GO:0006887)
2.865		response to unfolded protein (GO:0006986)
2.800		positive regulation of RNA polymerase II transcriptional preinitiation complex assembly (GO:0045899)
-2.618		retrograde transport, endosome to Golgi (GO:0042147)
2.598		positive regulation of gene expression, epigenetic (GO:0045815)
2.589		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.577		translational initiation (GO:0006413)
2.570		protein localization to chromatin (GO:0071168)
2.562		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.495		endosome to lysosome transport (GO:0008333)
-2.486		cilium assembly (GO:0060271)

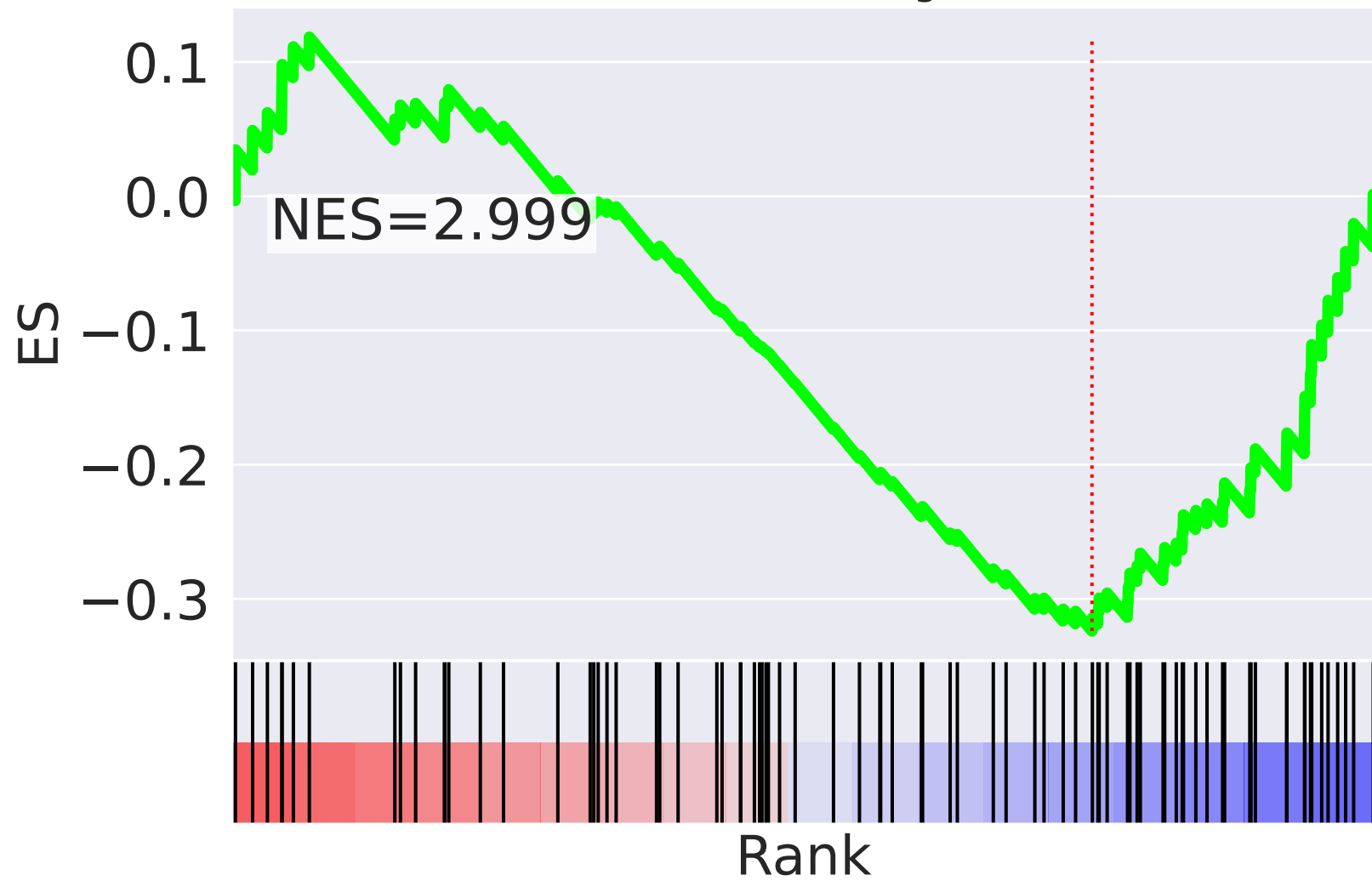




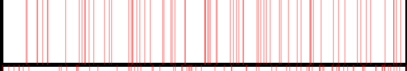
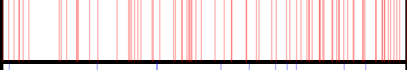
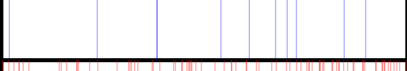
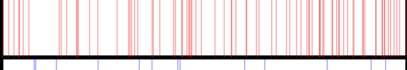
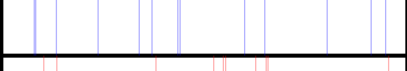
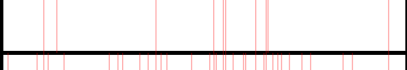
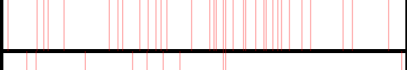
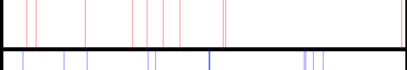

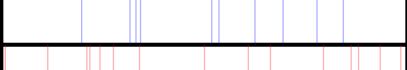

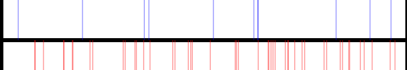
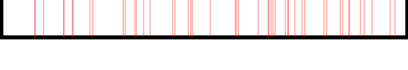
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=49$

# mitochondrial translational elongation (GO:0070125)



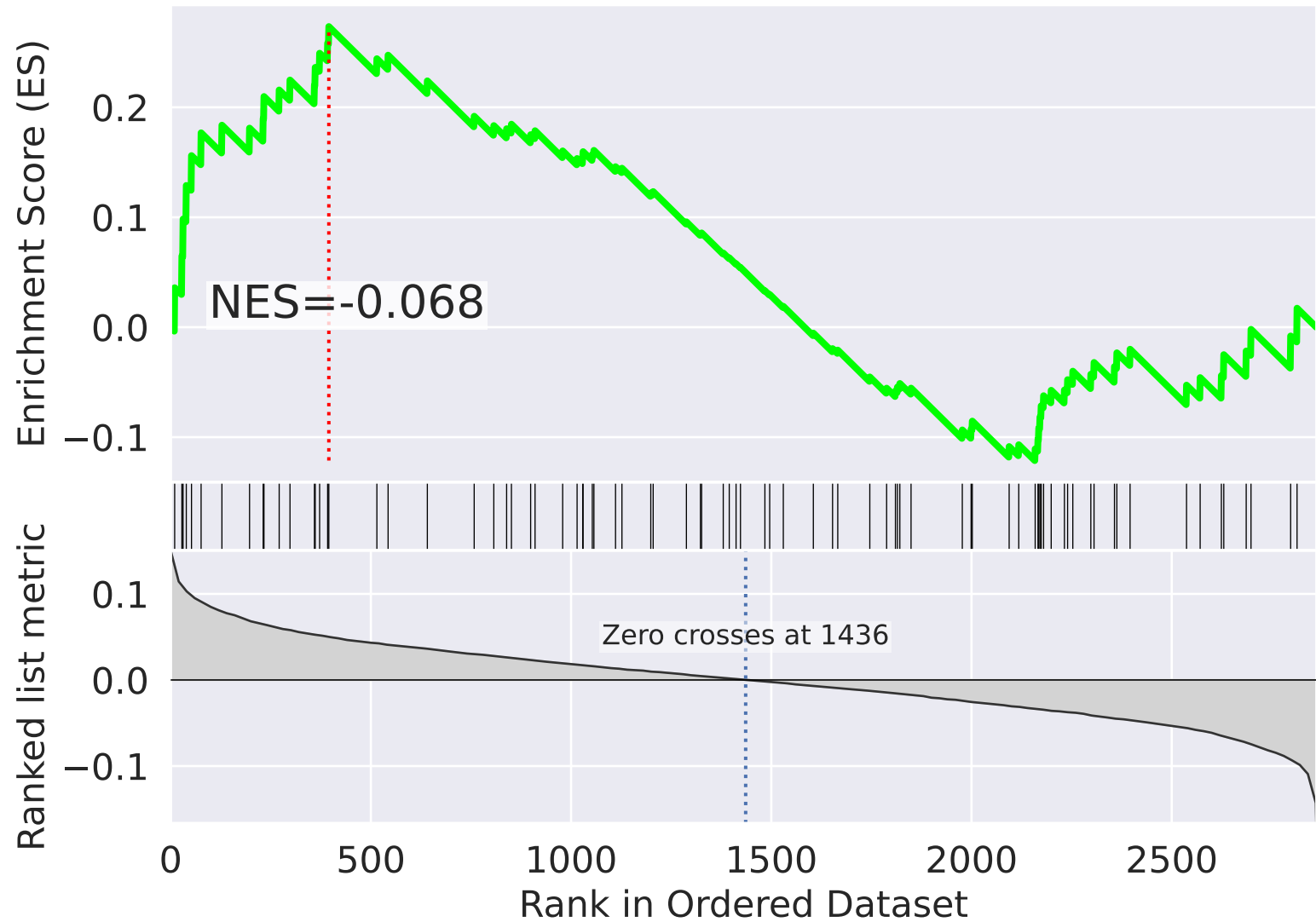
mitochondrial translational elongation (GO:0070125)



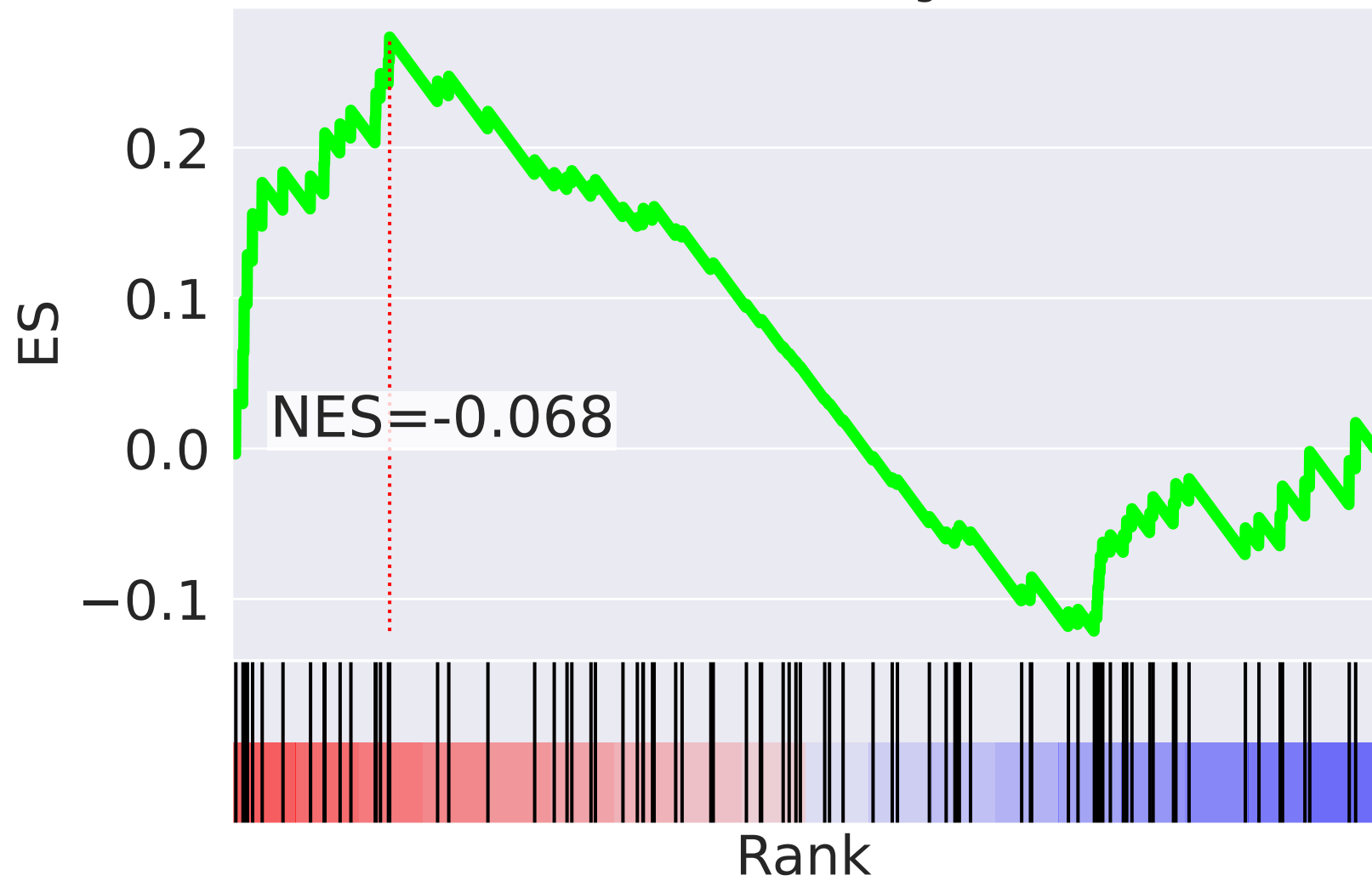
NES		SET
5.187		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.345		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.253		regulation of transcription, DNA-templated (GO:0006355)
3.086		mitochondrial translational termination (GO:0070126)
-3.039		cilium assembly (GO:0060271)
2.999		mitochondrial translational elongation (GO:0070125)
-2.976		transcription from RNA polymerase III promoter (GO:0006383)
2.921		nucleosome disassembly (GO:0006337)
2.882		chromatin remodeling (GO:0006338)
2.826		positive regulation by host of viral transcription (GO:0043923)
-2.730		histone H2A acetylation (GO:0043968)
-2.662		bicellular tight junction assembly (GO:0070830)
2.625		tricarboxylic acid cycle (GO:0006099)
-2.554		cell division (GO:0051301)
2.553		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  $z=50$

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

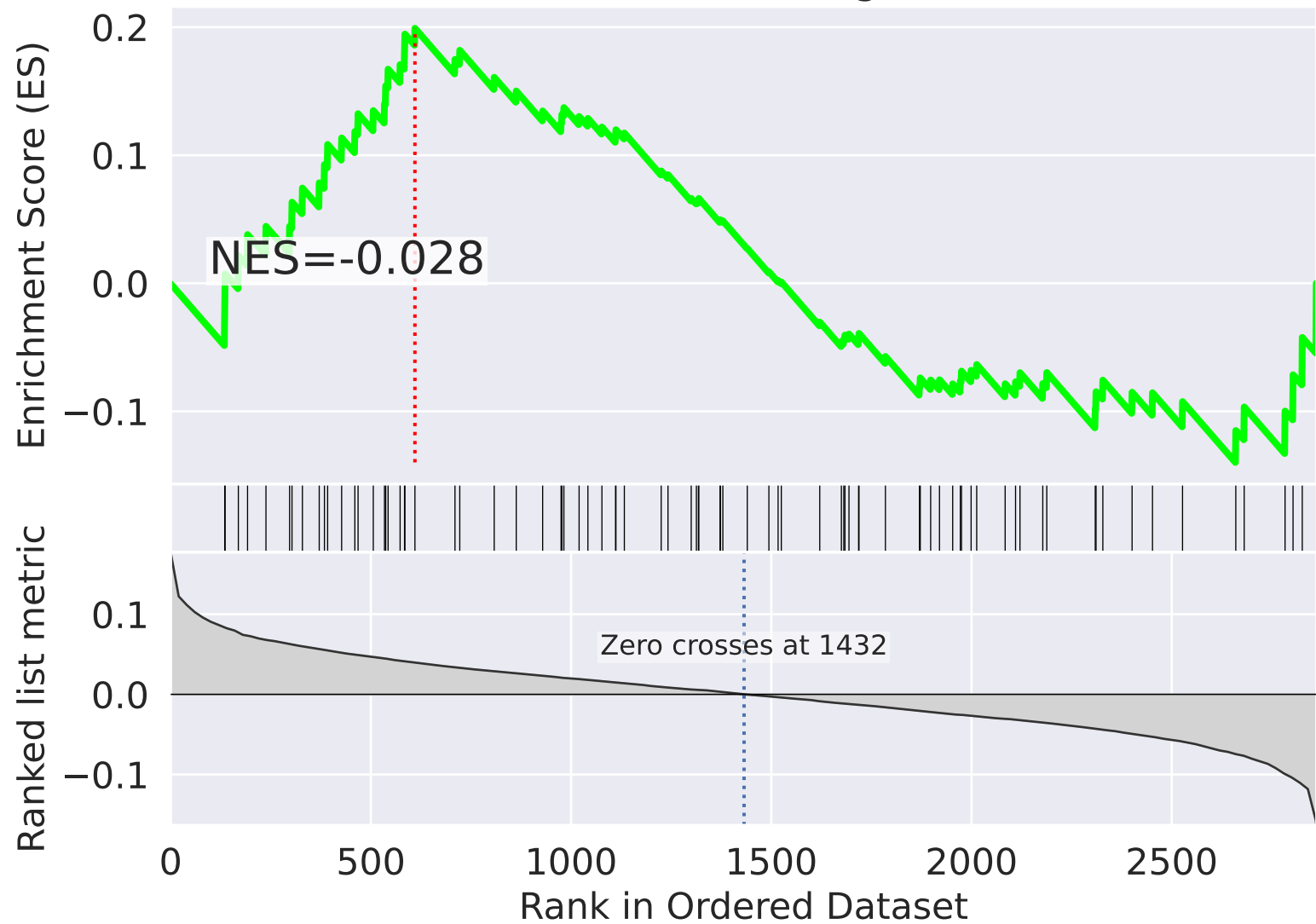


NES	SET
4.359	mRNA export from nucleus (GO:0006406)
4.299	viral process (GO:0016032)
4.193	regulation of cellular response to heat (GO:1900034)
4.177	viral transcription (GO:0019083)
3.939	stimulatory C-type lectin receptor signaling pathway (GO:0002223)
3.929	regulation of glucose transport (GO:0010827)
3.898	protein sumoylation (GO:0016925)
3.839	intracellular transport of virus (GO:0075733)
3.820	tRNA export from nucleus (GO:0006409)
3.818	mitotic nuclear envelope disassembly (GO:0007077)
3.763	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
3.725	regulation of gene silencing by miRNA (GO:0060964)
3.670	positive regulation of canonical Wnt signaling pathway (GO:0090263)
3.552	negative regulation of canonical Wnt signaling pathway (GO:0090090)
3.526	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)

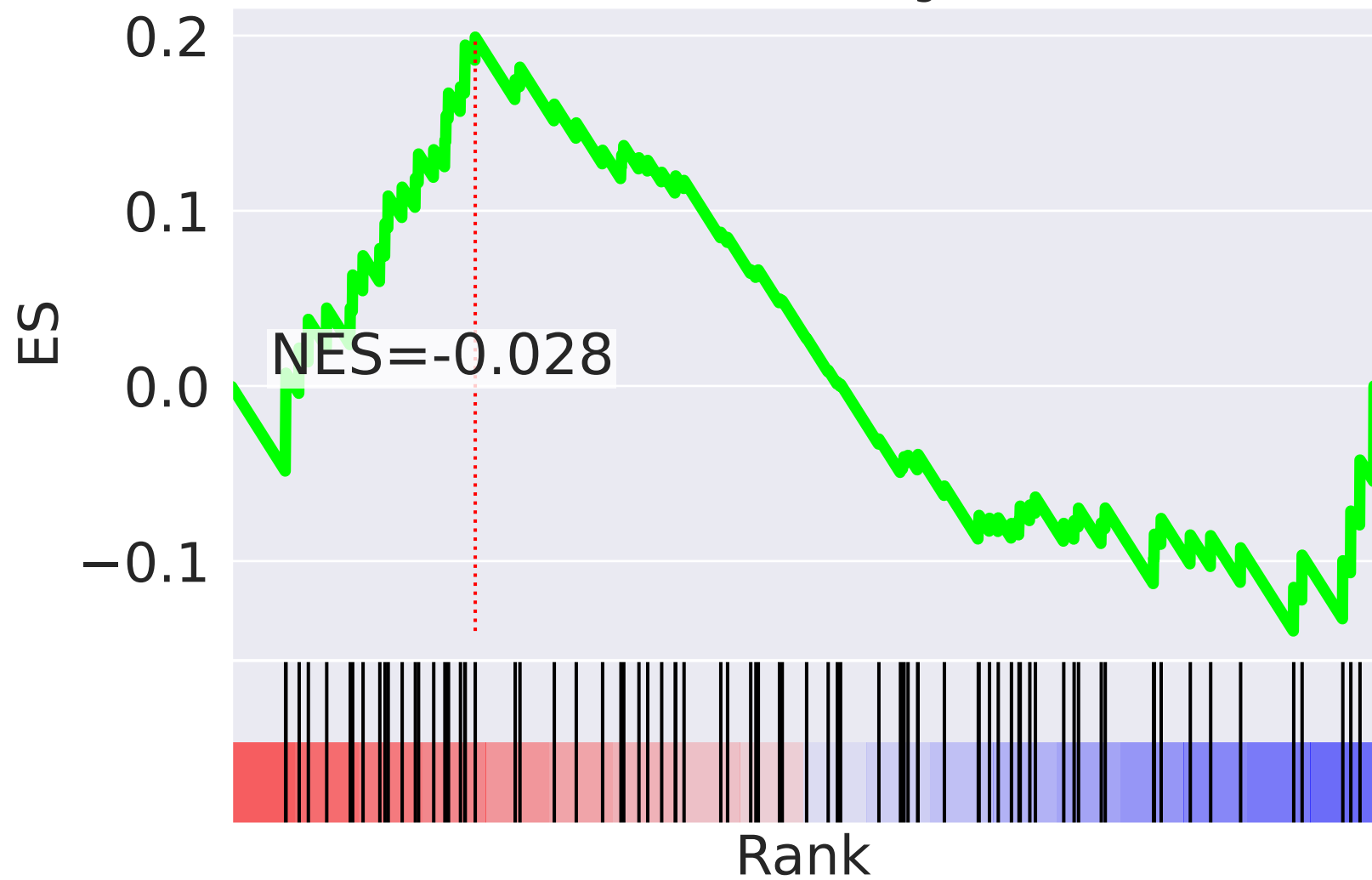


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=51$

# mitochondrial translational elongation (GO:0070125)



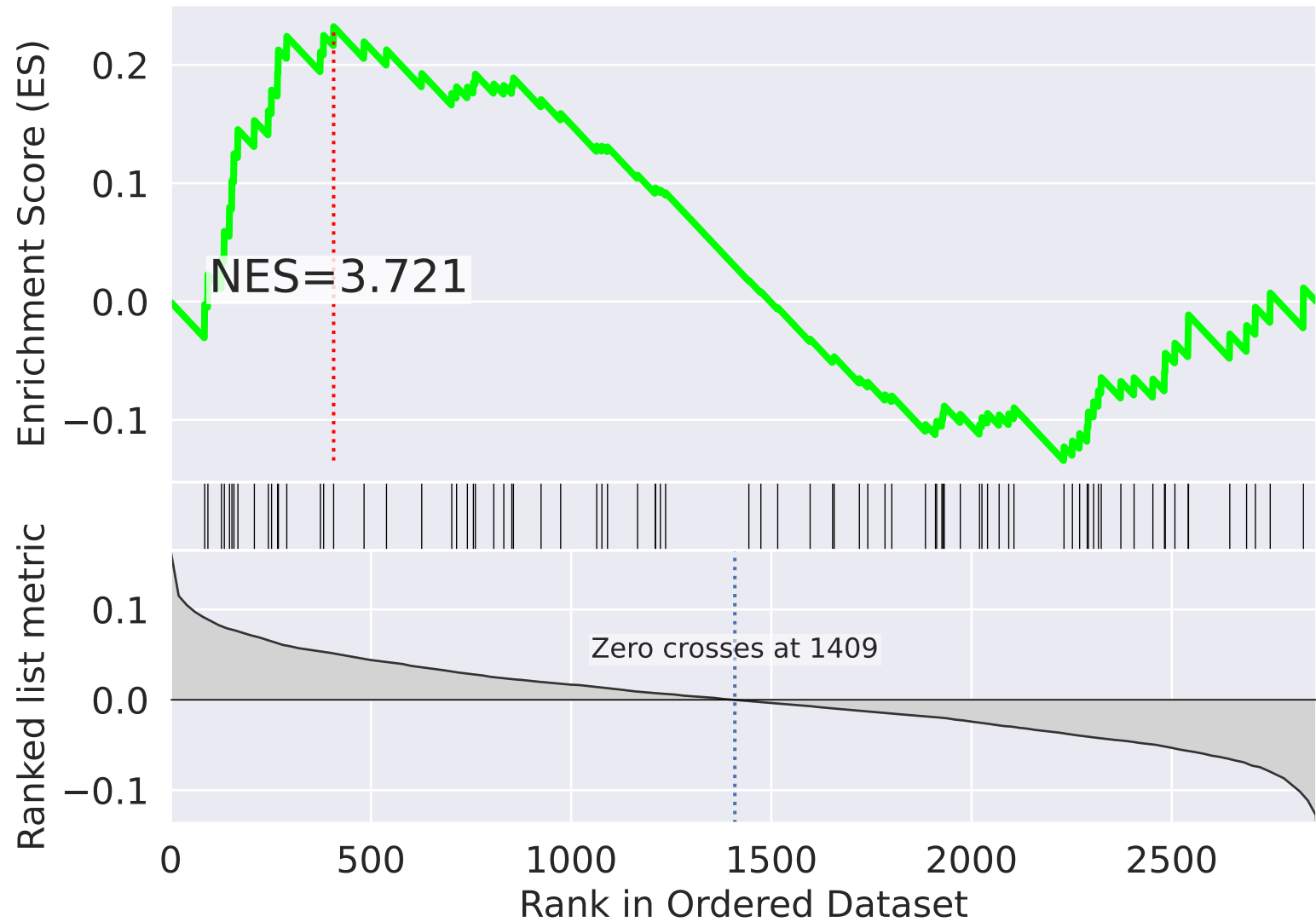
mitochondrial translational elongation (GO:0070125)



NES		SET
3.018		phosphatidylinositol-mediated signaling (GO:0048015)
2.898		mRNA export from nucleus (GO:0006406)
2.884		cellular response to lipopolysaccharide (GO:0071222)
-2.829		cell-matrix adhesion (GO:0007160)
-2.824		proteasome assembly (GO:0043248)
-2.738		cellular response to indole-3-methanol (GO:0071681)
-2.679		substrate adhesion-dependent cell spreading (GO:0034446)
-2.665		transcription from RNA polymerase III promoter (GO:0006383)
2.606		chromatin remodeling (GO:0006338)
-2.601		tRNA modification (GO:0006400)
2.591		osteoblast differentiation (GO:0001649)
2.580		T cell costimulation (GO:0031295)
2.575		negative regulation of TOR signaling (GO:0032007)
-2.562		double-strand break repair via nonhomologous end joining (GO:0006303)
2.541		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  $z=52$

# mitochondrial translational elongation (GO:0070125)



# mitochondrial translational elongation (GO:0070125)

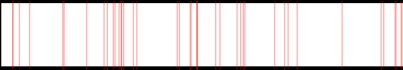
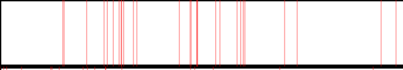
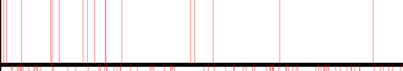
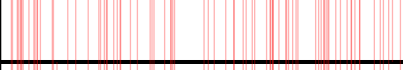
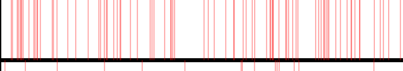
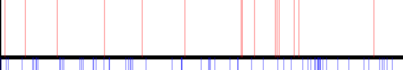
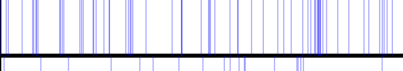

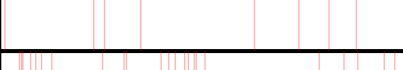
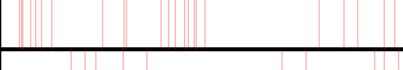





ES

0.2  
0.1  
0.0  
-0.1

NES=3.721

Rank

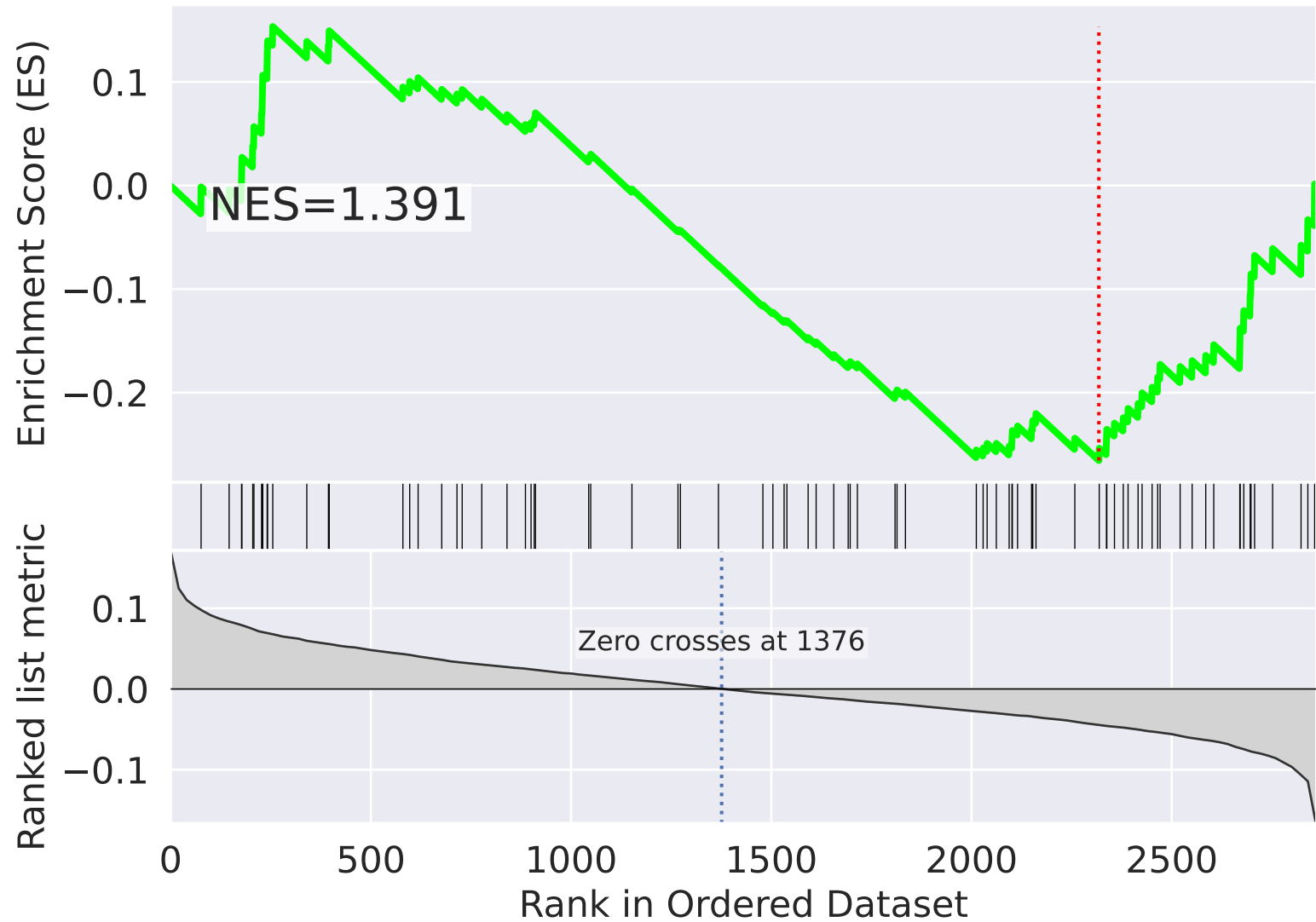


NES		SET
5.417		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.582		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.774		cell differentiation (GO:0030154)
3.741		mitochondrial translational termination (GO:0070126)
3.721		mitochondrial translational elongation (GO:0070125)
3.609		tricarboxylic acid cycle (GO:0006099)
-3.380		transcription initiation from RNA polymerase II promoter (GO:0006367)
-3.148		activation of MAPK activity (GO:0000187)
3.145		cellular nitrogen compound metabolic process (GO:0034641)
3.020		mitochondrion organization (GO:0007005)
2.982		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.820		protein N-linked glycosylation via asparagine (GO:0018279)
2.763		heme biosynthetic process (GO:0006783)
-2.712		peroxisome organization (GO:0007031)
-2.640		dephosphorylation (GO:0016311)

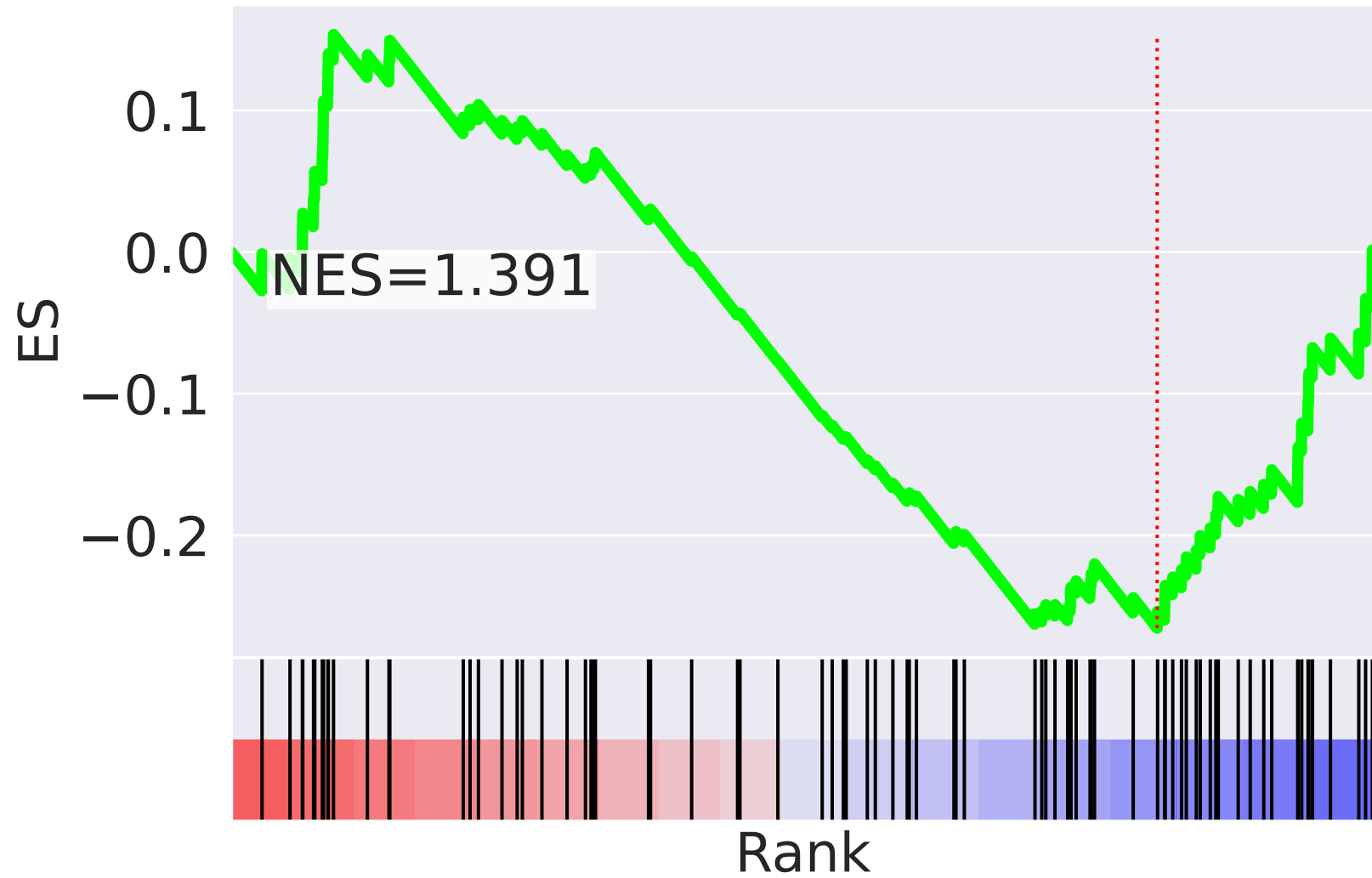


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=53$

# mitochondrial translational elongation (GO:0070125)



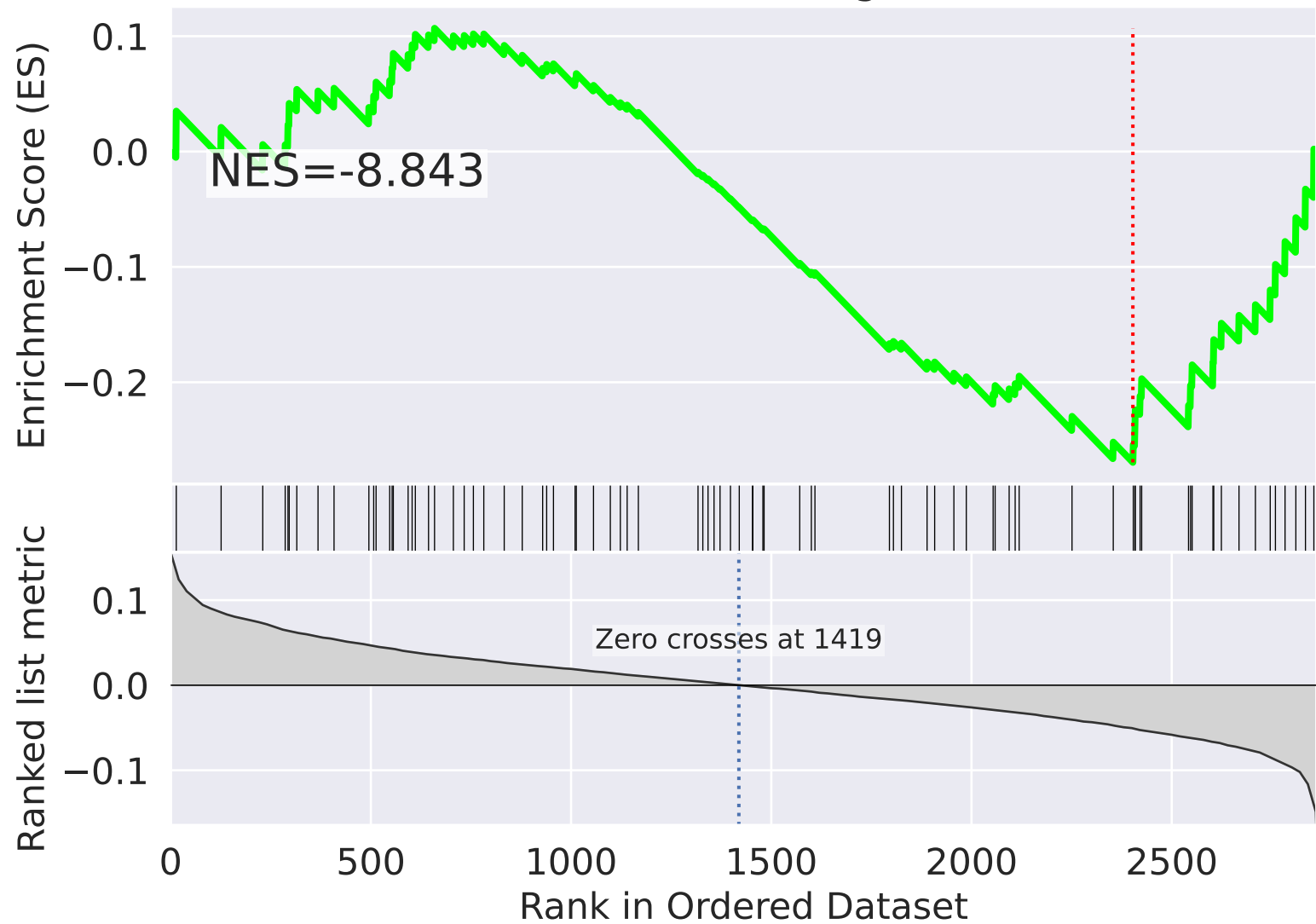
mitochondrial translational elongation (GO:0070125)



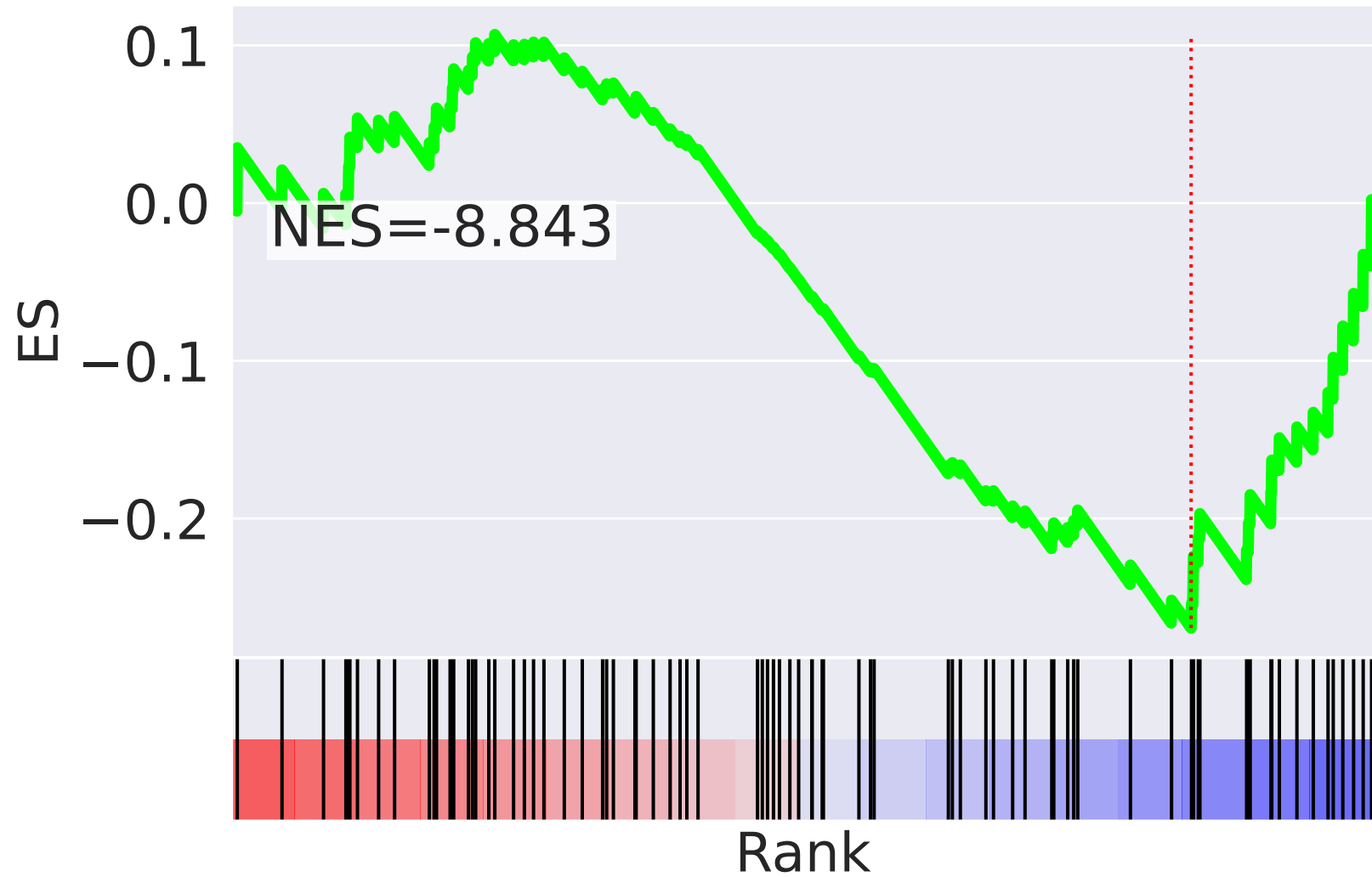
NES		SET
3.786		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.579		membrane organization (GO:0061024)
3.380		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.207		COPII vesicle coating (GO:0048208)
-3.021		histone H3 acetylation (GO:0043966)
-2.996		negative regulation of telomere maintenance via telomerase (GO:0032211)
2.642		negative regulation of DNA damage response, signal transduction by p53 class mediator (GO:0043518)
-2.548		transcription initiation from RNA polymerase II promoter (GO:0006367)
2.533		generation of precursor metabolites and energy (GO:0006091)
-2.521		nuclear mRNA surveillance (GO:0071028)
-2.438		iron-sulfur cluster assembly (GO:0016226)
-2.375		tRNA transcription from RNA polymerase III promoter (GO:0042797)
-2.375		5S class rRNA transcription from RNA polymerase III type 1 promoter (GO:0042791)
-2.368		tRNA modification (GO:0006400)
2.347		isoprenoid biosynthetic process (GO:0008299)

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)

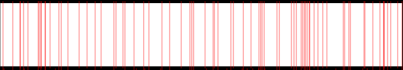
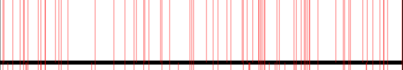
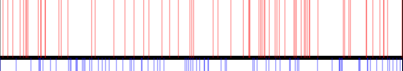

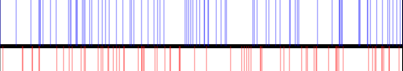
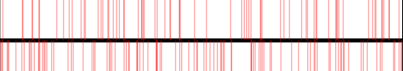
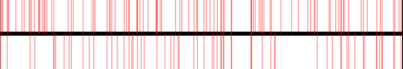
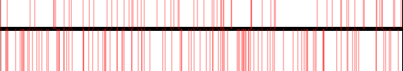
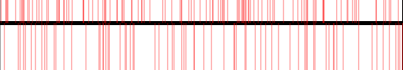
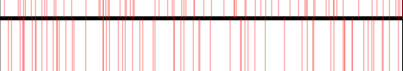
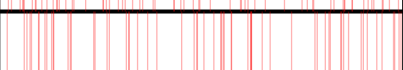
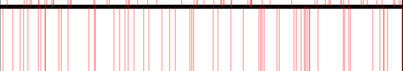

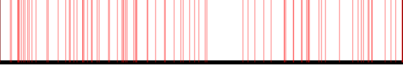



mitochondrial translational elongation (GO:0070125)



# NES

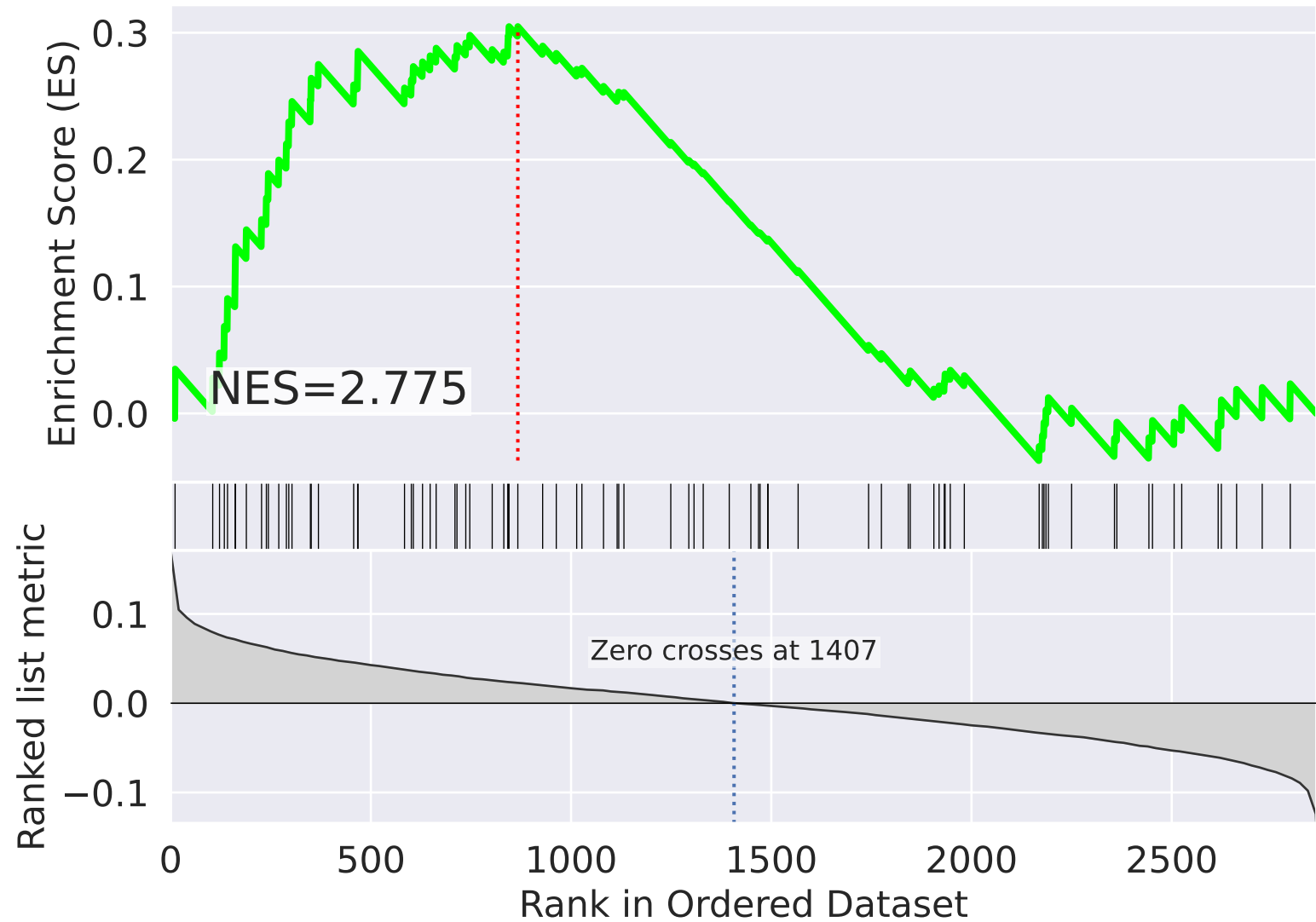
## SET

inf		viral transcription (GO:0019083)
inf		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
inf		translational initiation (GO:0006413)
-8.843		mitochondrial translational elongation (GO:0070125)
-8.602		mitochondrial translational termination (GO:0070126)
7.325		regulation of transcription, DNA-templated (GO:0006355)
7.214		transcription from RNA polymerase II promoter (GO:0006366)
7.148		transcription initiation from RNA polymerase II promoter (GO:0006367)
6.665		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
6.177		protein ubiquitination (GO:0016567)
5.805		protein polyubiquitination (GO:0000209)
5.641		transcription elongation from RNA polymerase II promoter (GO:0006368)
5.556		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
5.382		post-translational protein modification (GO:0043687)
5.300		neutrophil degranulation (GO:0043312)

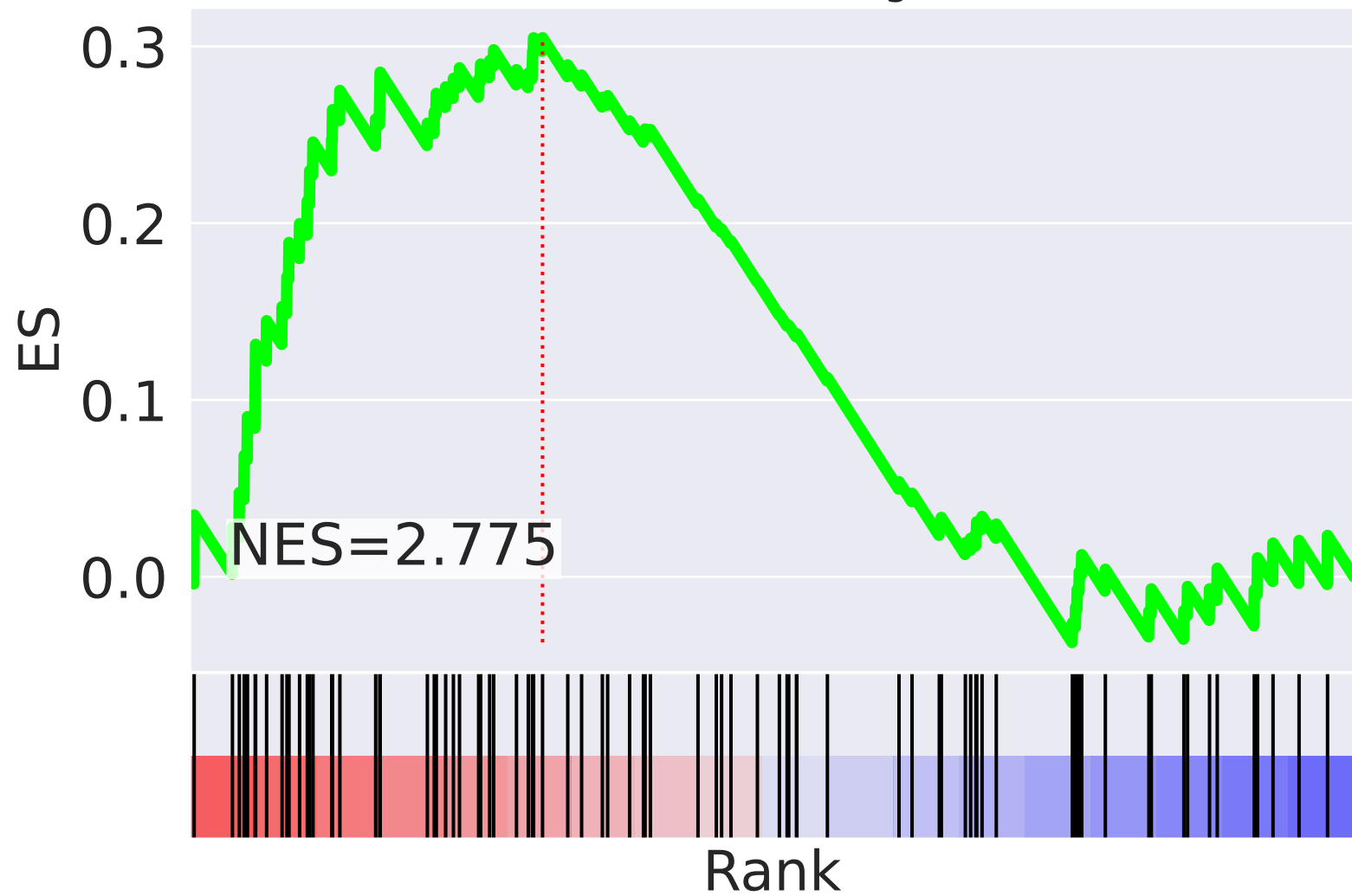



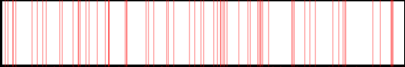

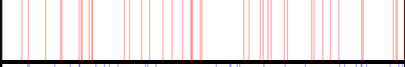
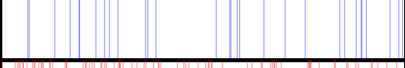
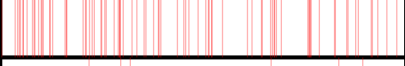
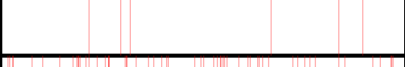
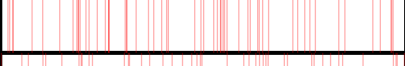
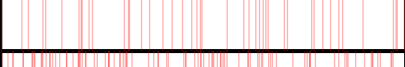
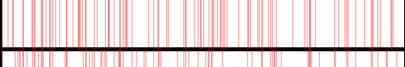
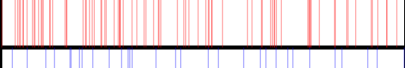



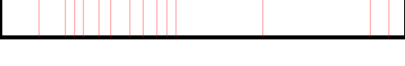
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension  $z=55$

# mitochondrial translational elongation (GO:0070125)



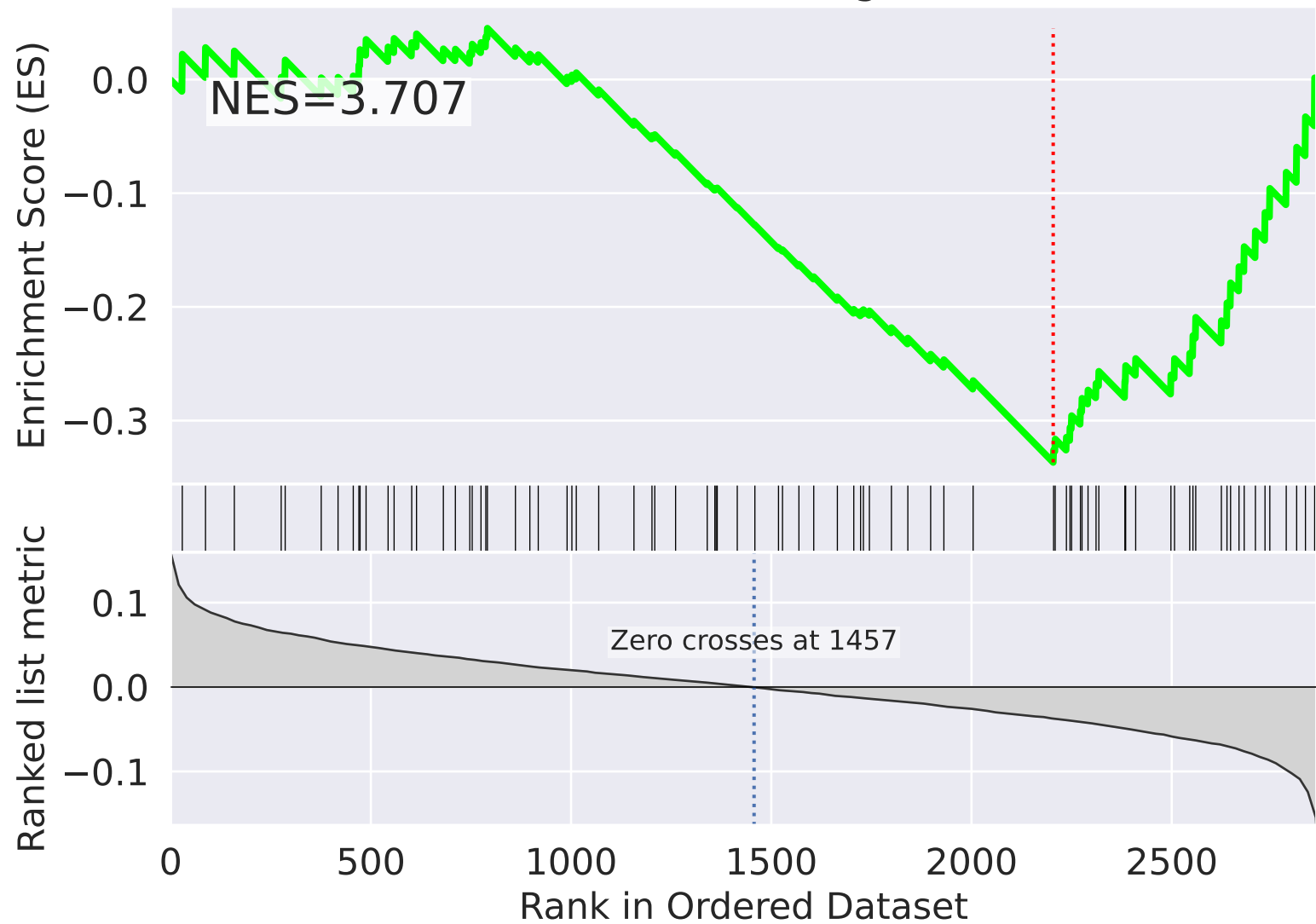
# mitochondrial translational elongation (GO:0070125)



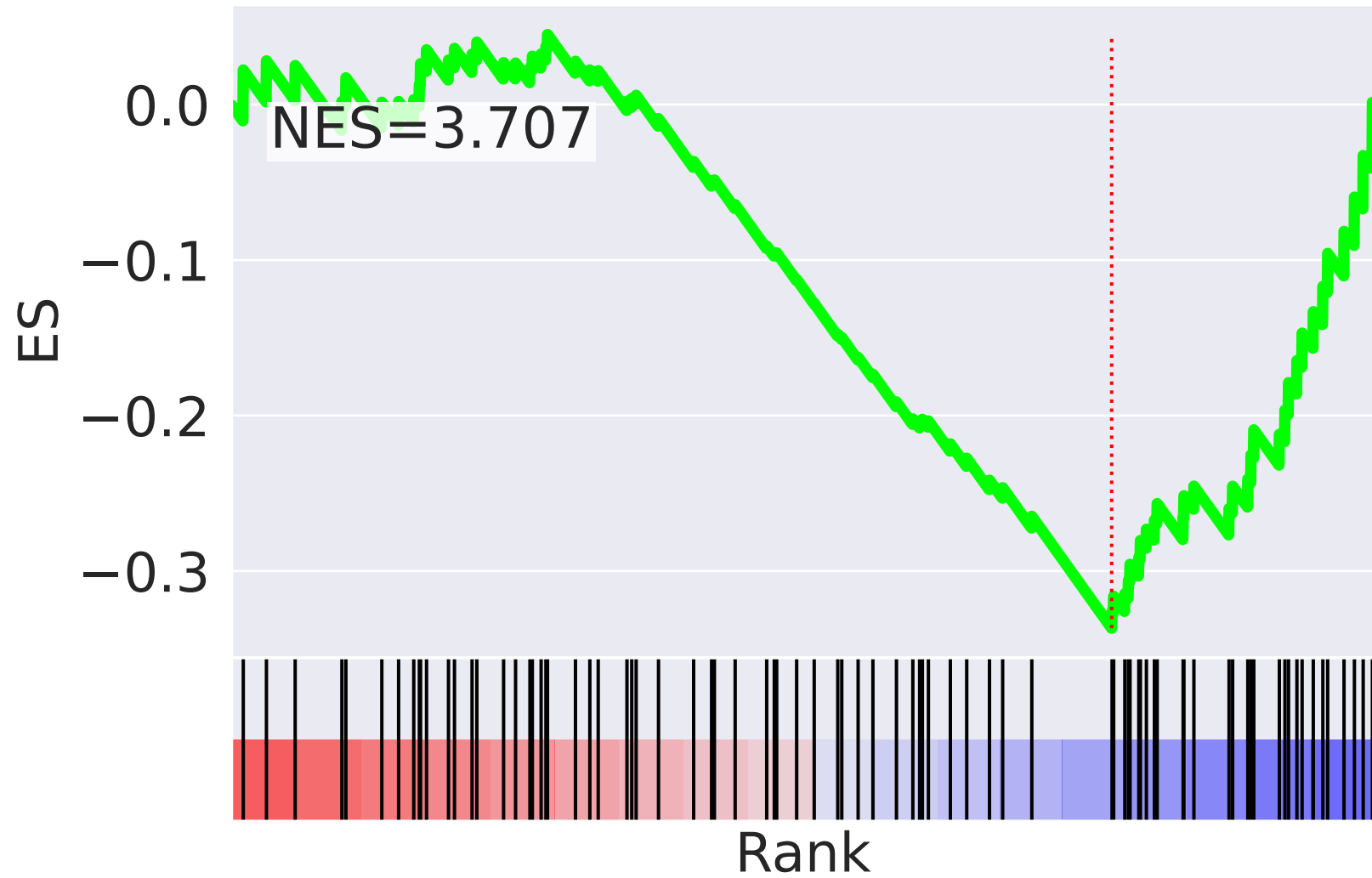
NES		SET
-3.240		microtubule-based movement (GO:0007018)
3.031		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.909		regulation of transcription involved in G1/S transition of mitotic cell cycle (GO:0000083)
2.897		transmembrane transport (GO:0055085)
-2.840		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.775		mitochondrial translational elongation (GO:0070125)
2.768		endoplasmic reticulum mannose trimming (GO:1904380)
2.754		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
2.725		tumor necrosis factor-mediated signaling pathway (GO:0033209)
2.680		translation (GO:0006412)
2.665		mitochondrial translational termination (GO:0070126)
-2.634		regulation of apoptotic process (GO:0042981)
2.572		mitotic chromosome condensation (GO:0007076)
2.540		positive regulation of canonical Wnt signaling pathway (GO:0090263)
2.532		nucleus organization (GO:0006997)

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
4.869		mitochondrial respiratory chain complex I assembly (GO:0032981)
4.120		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
3.707		mitochondrial translational elongation (GO:0070125)
3.678		mitochondrial translational termination (GO:0070126)
3.349		gluconeogenesis (GO:0006094)
-3.310		positive regulation of cell migration (GO:0030335)
-2.928		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.910		regulation of gene silencing by miRNA (GO:0060964)
2.849		mitochondrial translation (GO:0032543)
2.810		protein import into nucleus (GO:0006606)
-2.808		nucleotide-excision repair, DNA incision, 5'-to lesion (GO:0006296)
-2.808		nucleotide-excision repair, DNA incision (GO:0033683)
-2.608		epidermal growth factor receptor signaling pathway (GO:0007173)
2.596		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.588		somatic stem cell population maintenance (GO:0035019)