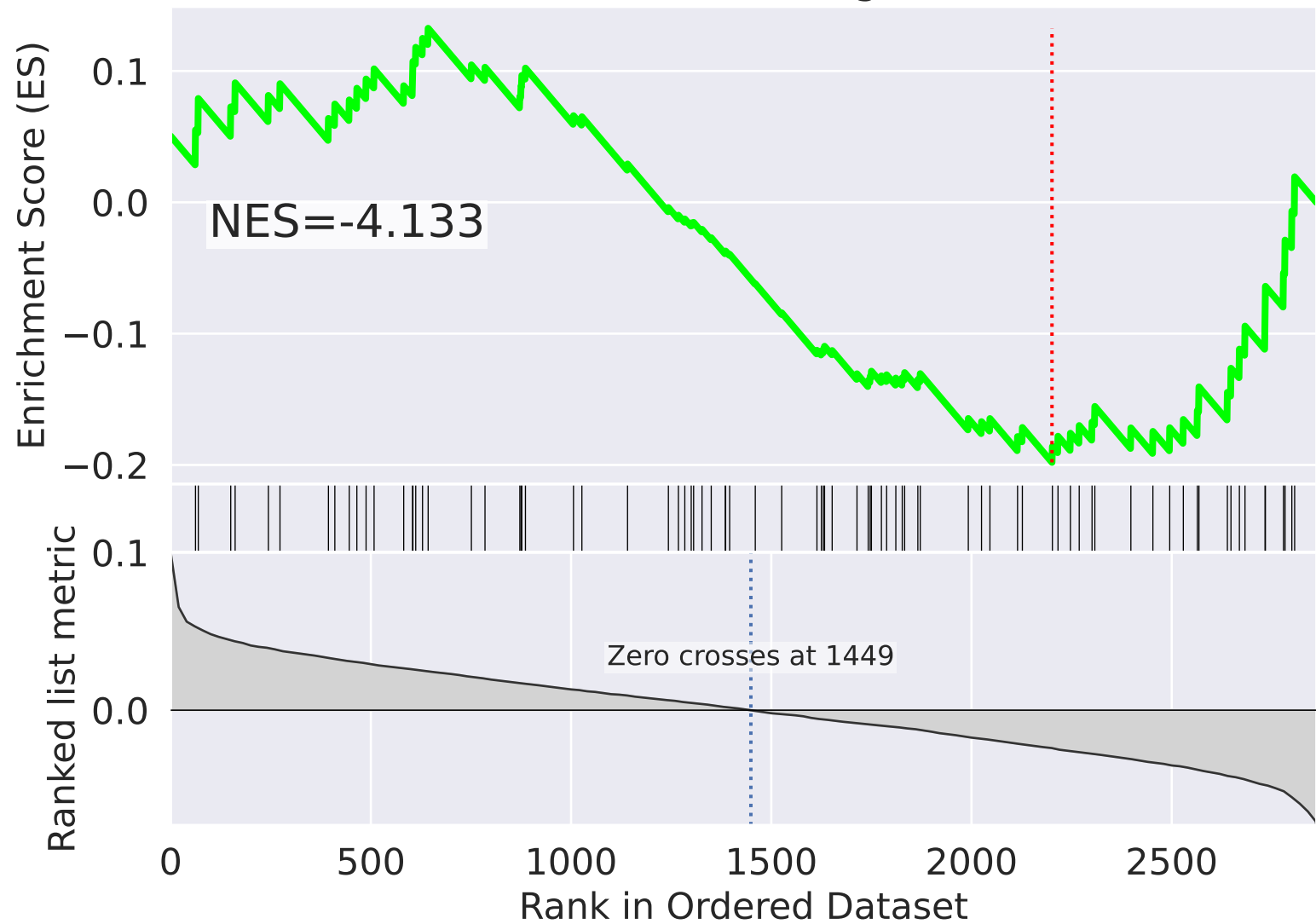
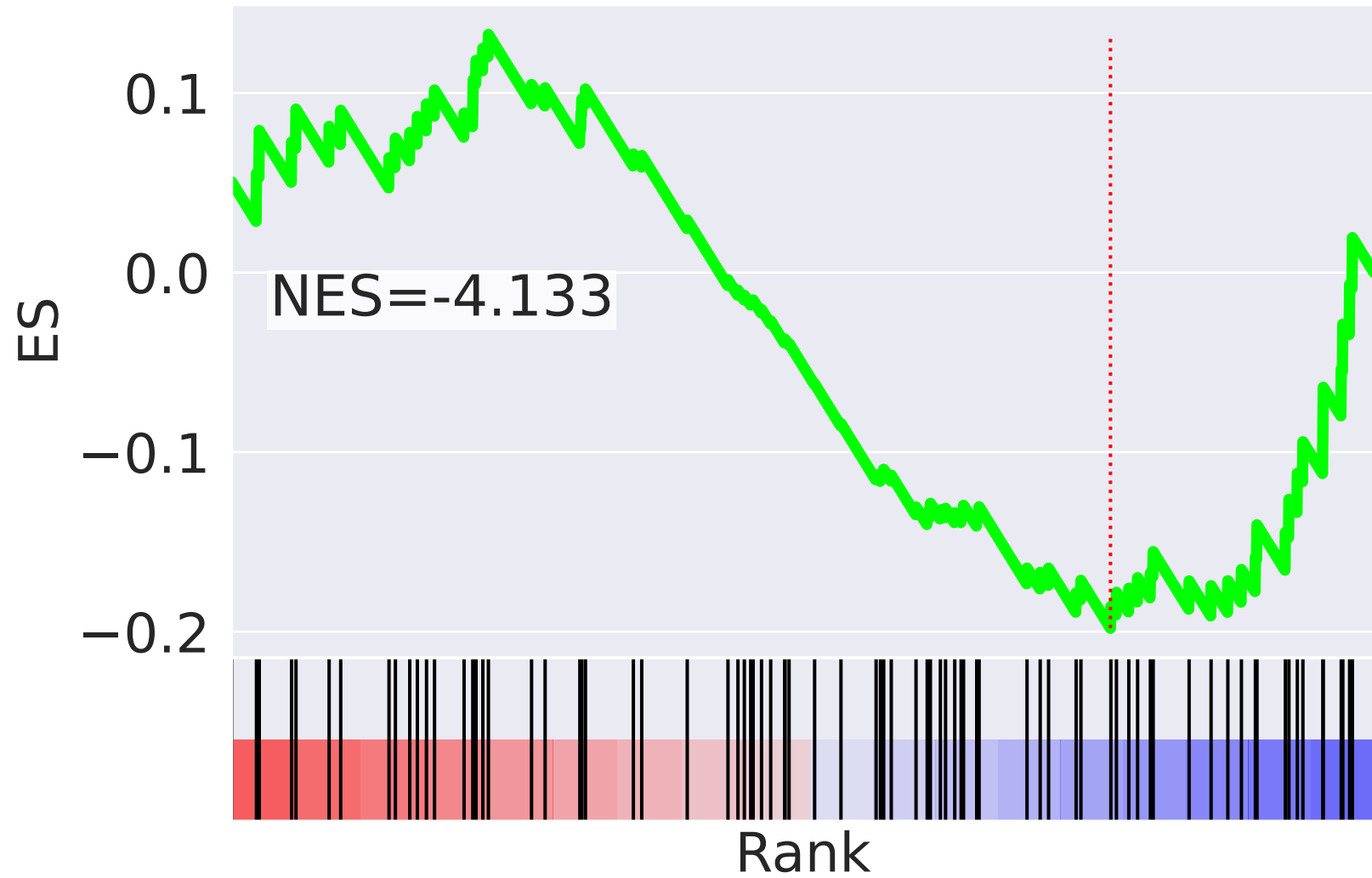


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=1$

mitochondrial translational elongation (GO:0070125)



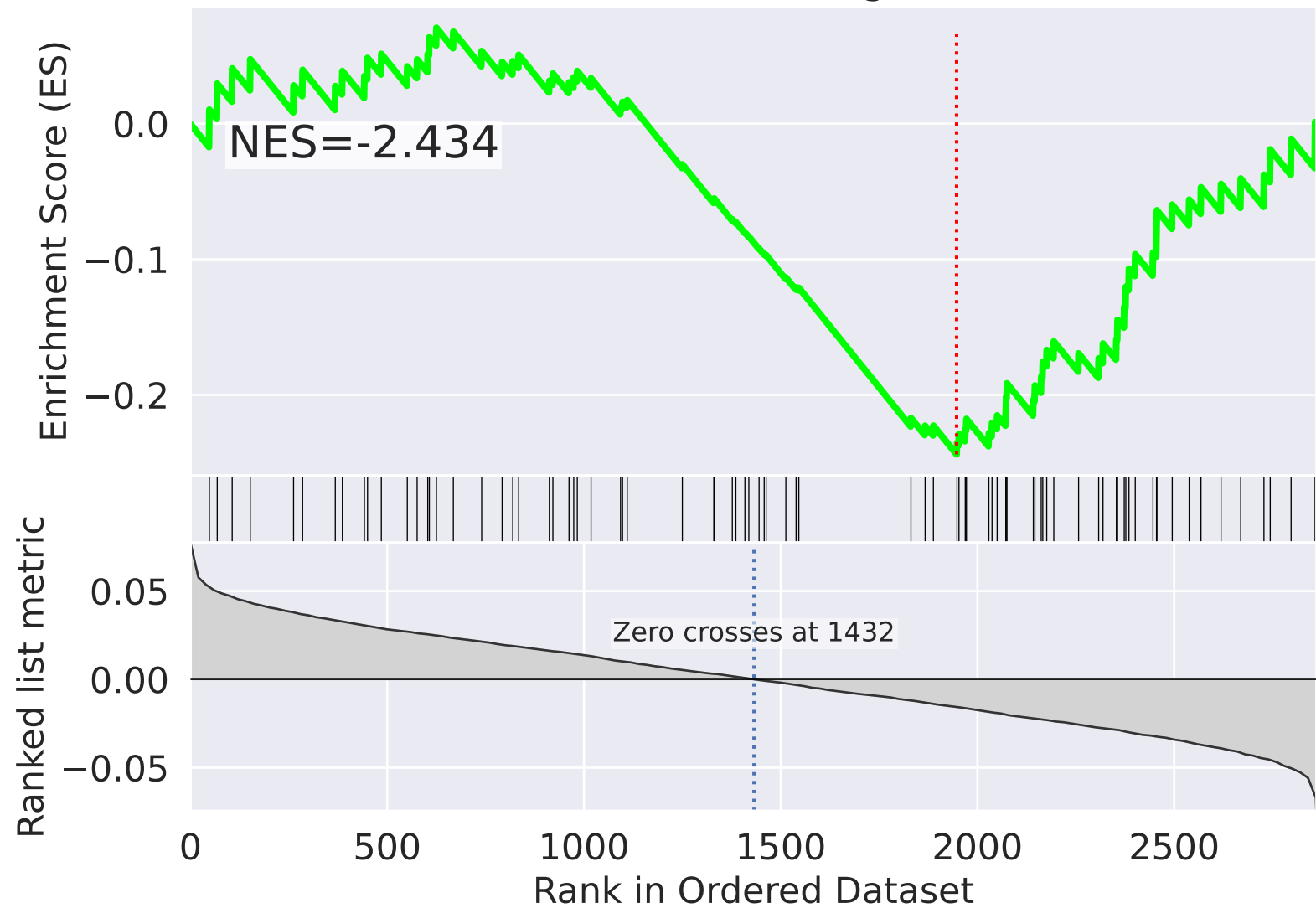
mitochondrial translational elongation (GO:0070125)



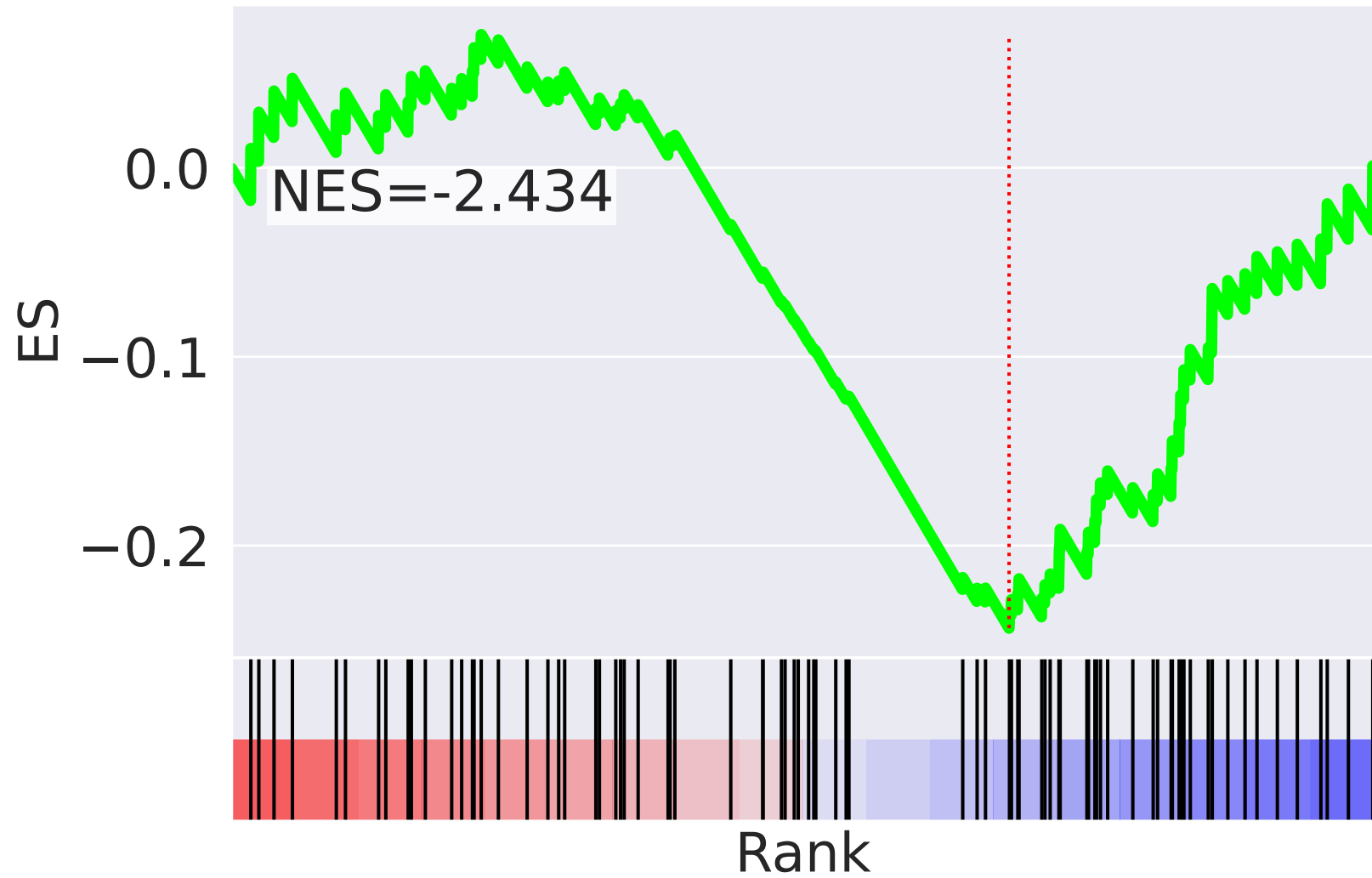
NES		SET
-4.483		mitochondrial respiratory chain complex I assembly (GO:0032981)
-4.336		mitochondrial translational termination (GO:0070126)
-4.133		mitochondrial translational elongation (GO:0070125)
3.809		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-3.793		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.796		extracellular matrix organization (GO:0030198)
-2.678		mitochondrial translation (GO:0032543)
2.635		RNA splicing, via transesterification reactions (GO:0000375)
2.564		establishment of protein localization to plasma membrane (GO:0090002)
2.532		meiotic cell cycle (GO:0051321)
2.489		integrin-mediated signaling pathway (GO:0007229)
2.486		protein localization to chromatin (GO:0071168)
2.422		humoral immune response (GO:0006959)
2.418		cortical actin cytoskeleton organization (GO:0030866)
2.320		cell surface receptor signaling pathway (GO:0007166)


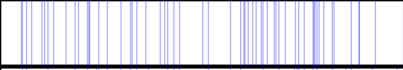
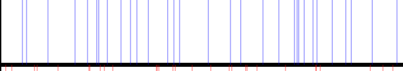
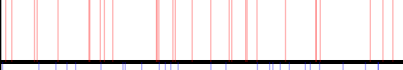
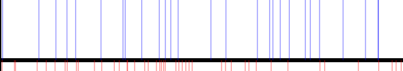
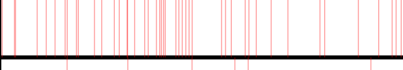
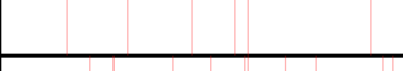

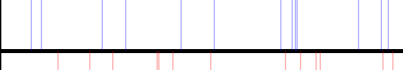
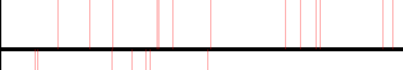
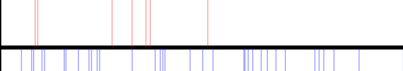



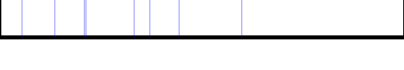
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=2$

mitochondrial translational elongation (GO:0070125)



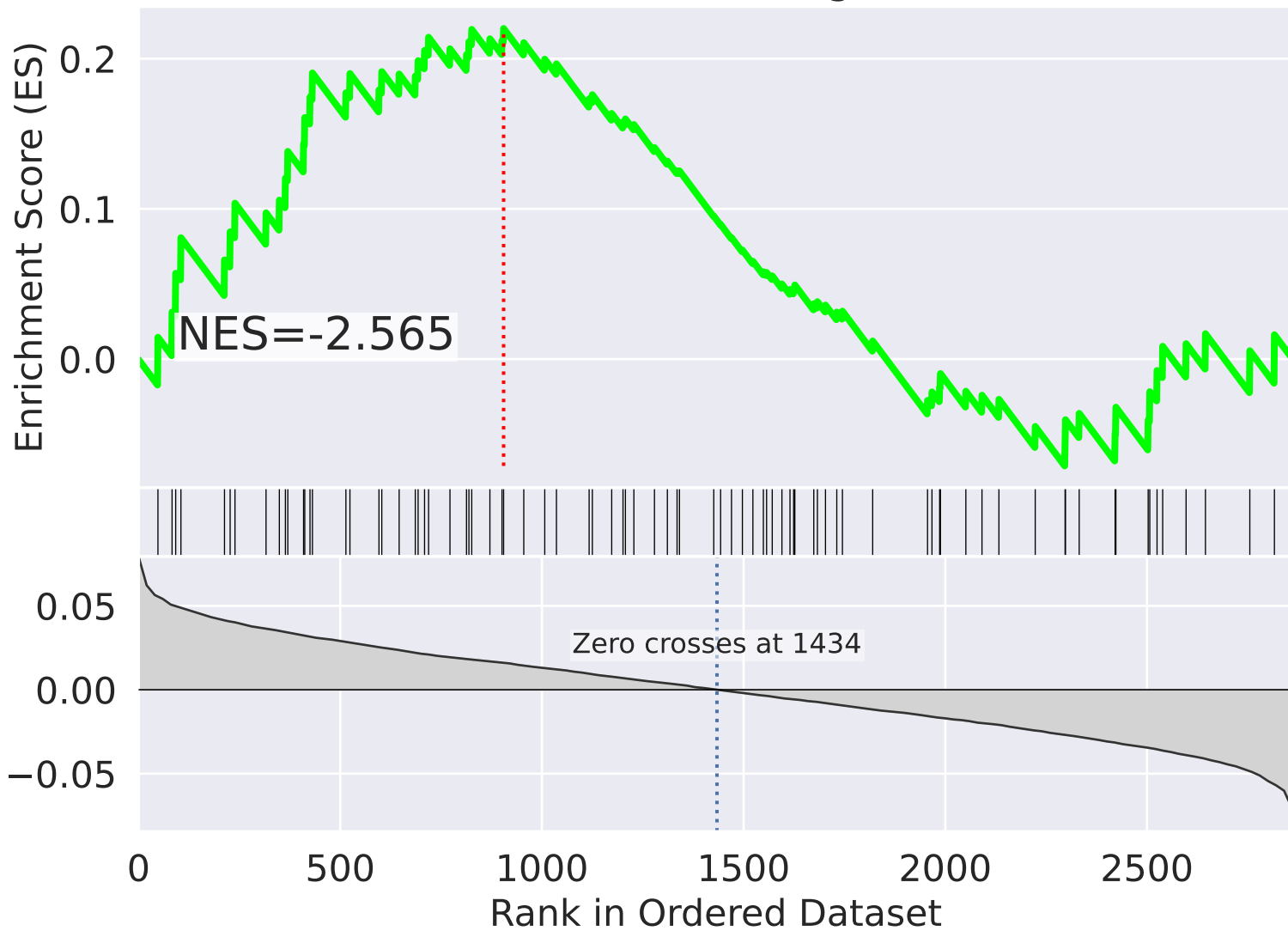
mitochondrial translational elongation (GO:0070125)



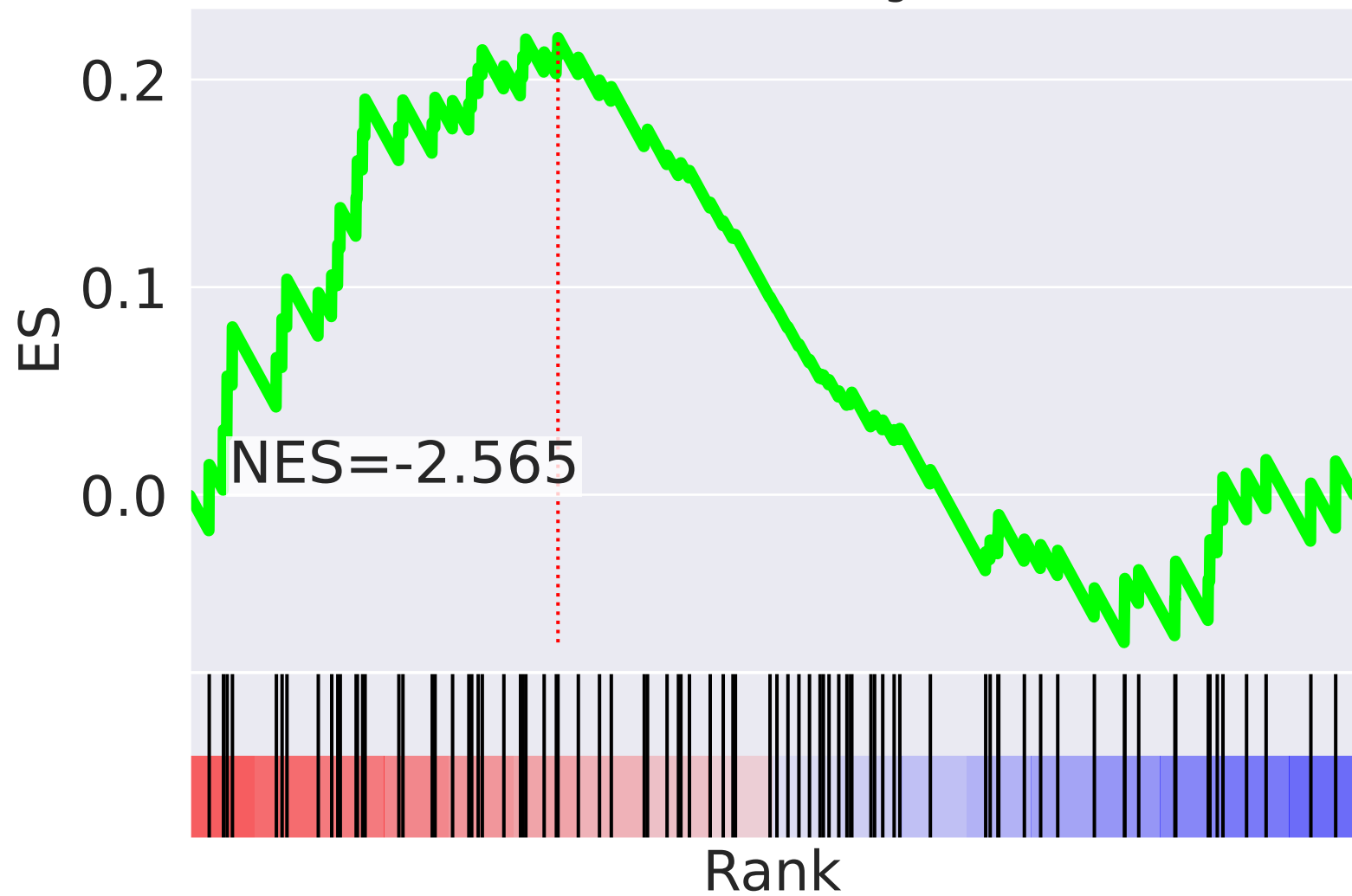
NES		SET
-3.476		mitochondrial respiratory chain complex I assembly (GO:0032981)
-3.380		mRNA export from nucleus (GO:0006406)
-3.203		mRNA 3'-end processing (GO:0031124)
3.071		mitotic metaphase plate congression (GO:0007080)
-2.978		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.941		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
2.785		positive regulation of protein export from nucleus (GO:0046827)
2.780		regulation of mitotic spindle assembly (GO:1901673)
-2.779		cellular response to lipopolysaccharide (GO:0071222)
2.776		cell separation after cytokinesis (GO:0000920)
2.775		positive regulation of substrate adhesion-dependent cell spreading (GO:1900026)
-2.760		regulation of gene silencing by miRNA (GO:0060964)
-2.658		cholesterol biosynthetic process (GO:0006695)
2.645		regulation of DNA replication (GO:0006275)
-2.625		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)

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)



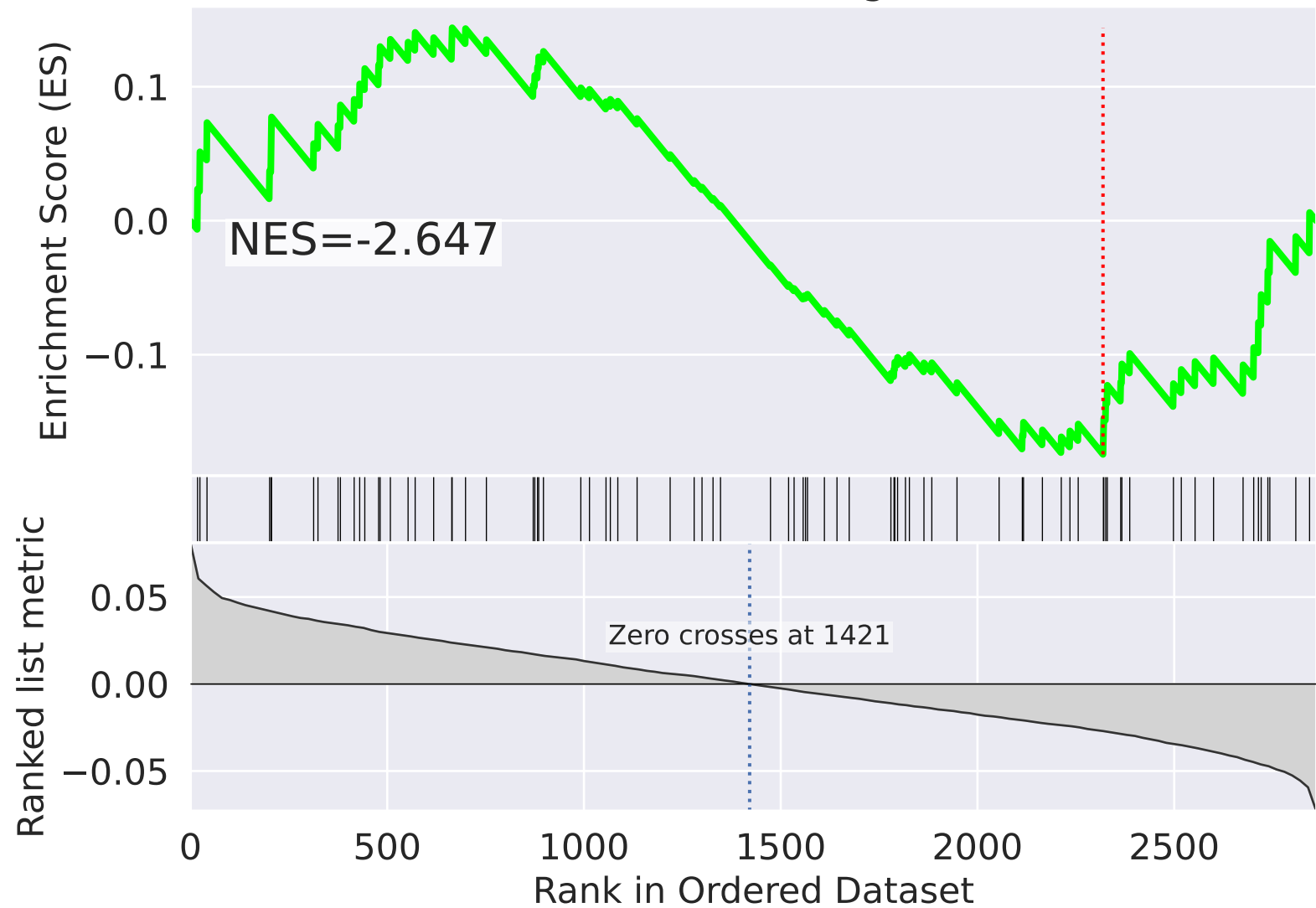
mitochondrial translational elongation (GO:0070125)



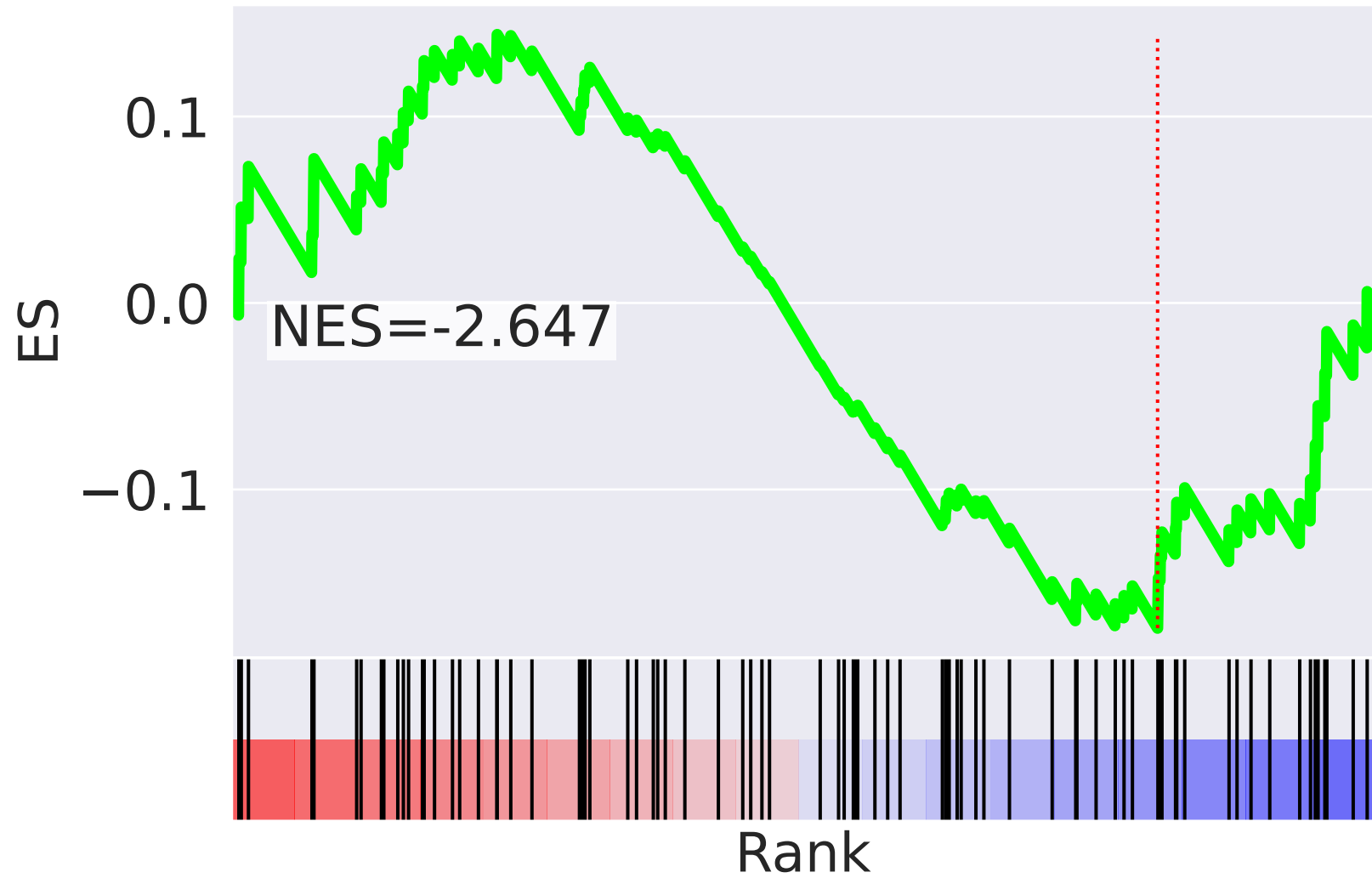
NES		SET
3.410		positive regulation of canonical Wnt signaling pathway (GO:0090263)
3.334		protein polyubiquitination (GO:0000209)
3.029		regulation of cellular amino acid metabolic process (GO:0006521)
2.966		spindle assembly (GO:0051225)
2.910		response to virus (GO:0009615)
2.894		tumor necrosis factor-mediated signaling pathway (GO:0033209)
2.882		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
2.720		positive regulation of cell proliferation (GO:0008284)
2.677		protein K48-linked ubiquitination (GO:0070936)
2.606		MAPK cascade (GO:0000165)
2.602		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
-2.583		positive regulation of osteoblast differentiation (GO:0045669)
2.580		negative regulation of canonical Wnt signaling pathway (GO:0090090)
-2.565		mitochondrial translational elongation (GO:0070125)
2.547		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)

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)





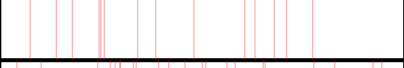

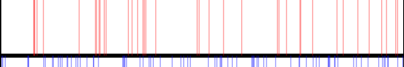
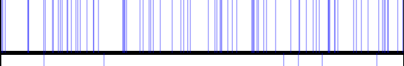


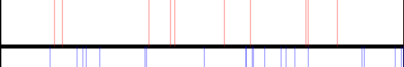
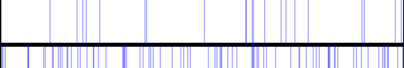
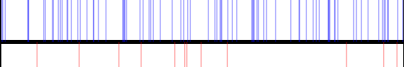
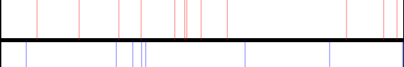
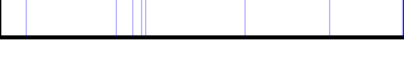


mitochondrial translational elongation (GO:0070125)



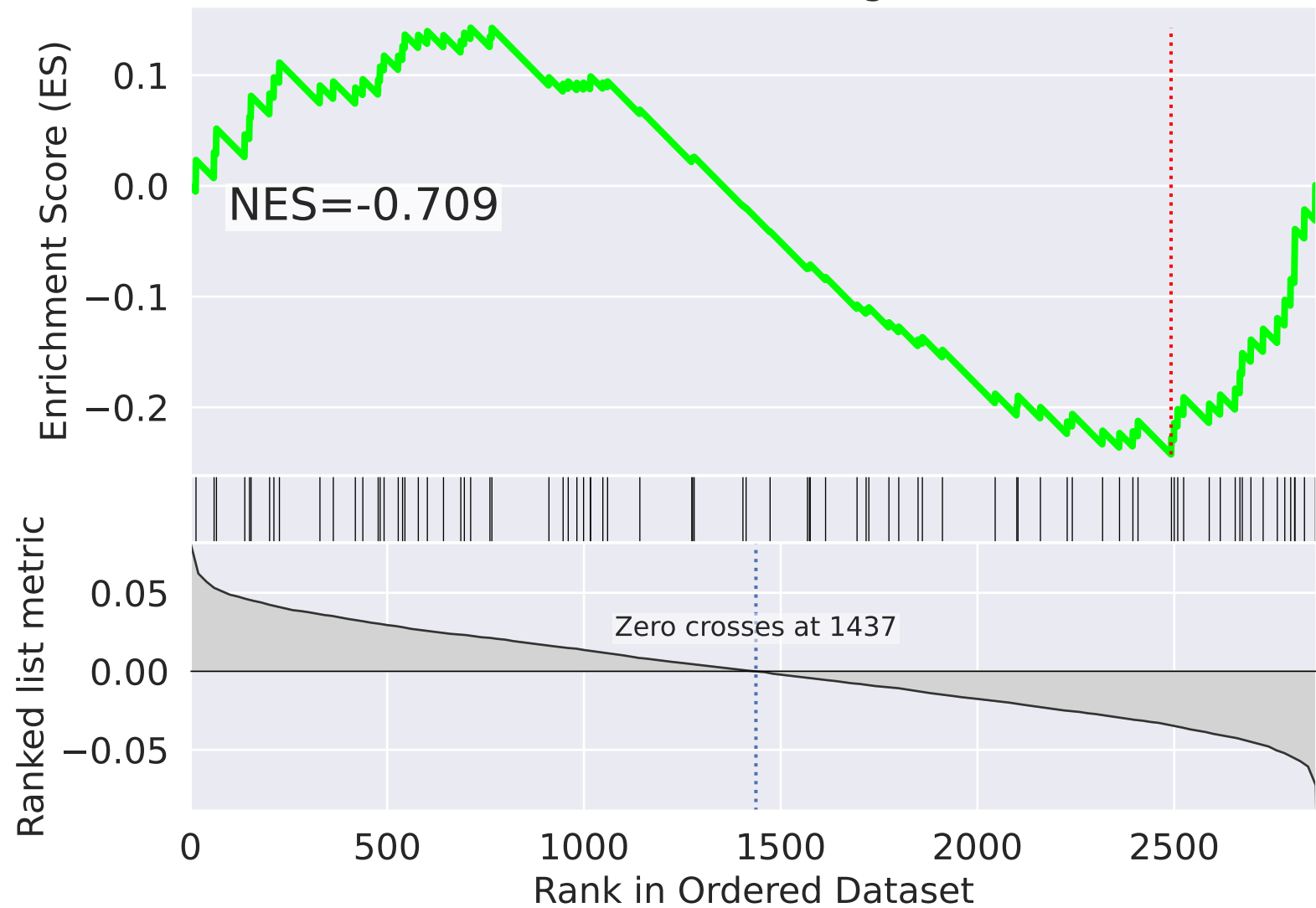
NES

SET

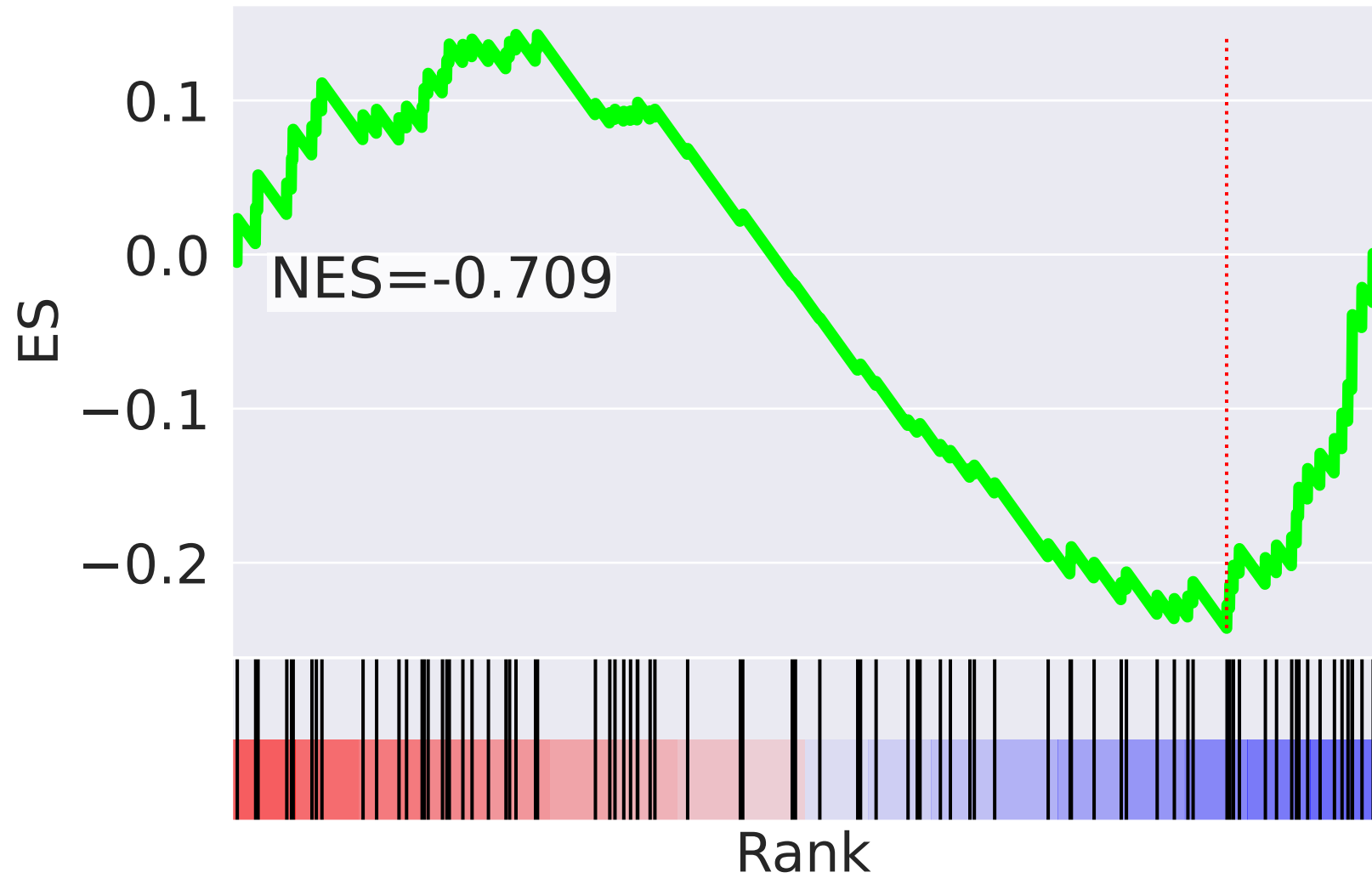
3.318		multivesicular body assembly (GO:0036258)
3.314		double-strand break repair (GO:0006302)
-3.088		endosome organization (GO:0007032)
-3.074		regulation of mitotic nuclear division (GO:0007088)
2.881		nucleus organization (GO:0006997)
2.871		movement of cell or subcellular component (GO:0006928)
2.831		macroautophagy (GO:0016236)
-2.821		mitochondrial translational termination (GO:0070126)
-2.817		insulin-like growth factor receptor signaling pathway (GO:0048009)
2.797		mRNA 3'-splice site recognition (GO:0000389)
2.763		protein K63-linked ubiquitination (GO:0070534)
-2.743		RNA processing (GO:0006396)
-2.647		mitochondrial translational elongation (GO:0070125)
2.636		regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)
-2.565		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)

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

mitochondrial translational elongation (GO:0070125)



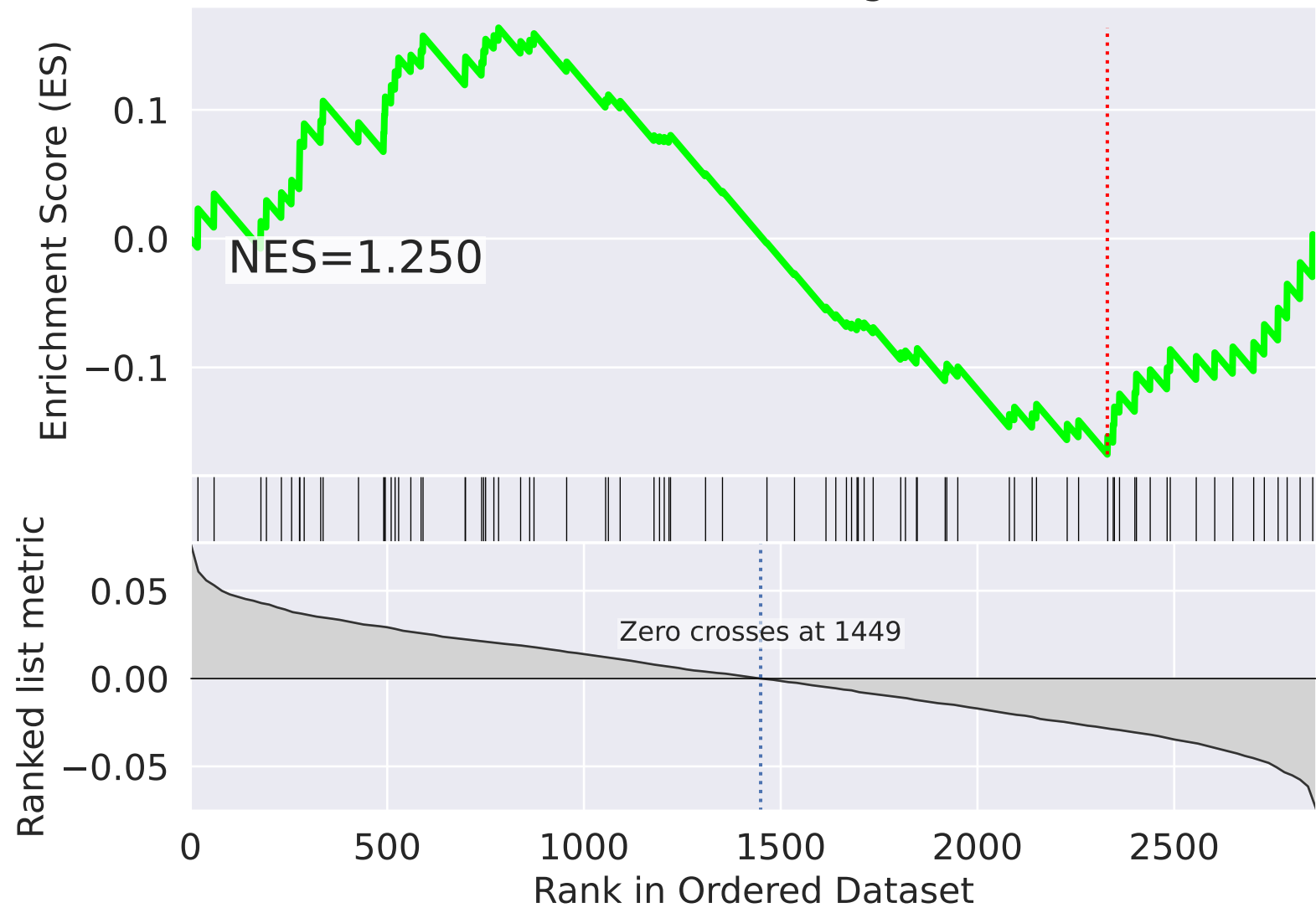
mitochondrial translational elongation (GO:0070125)



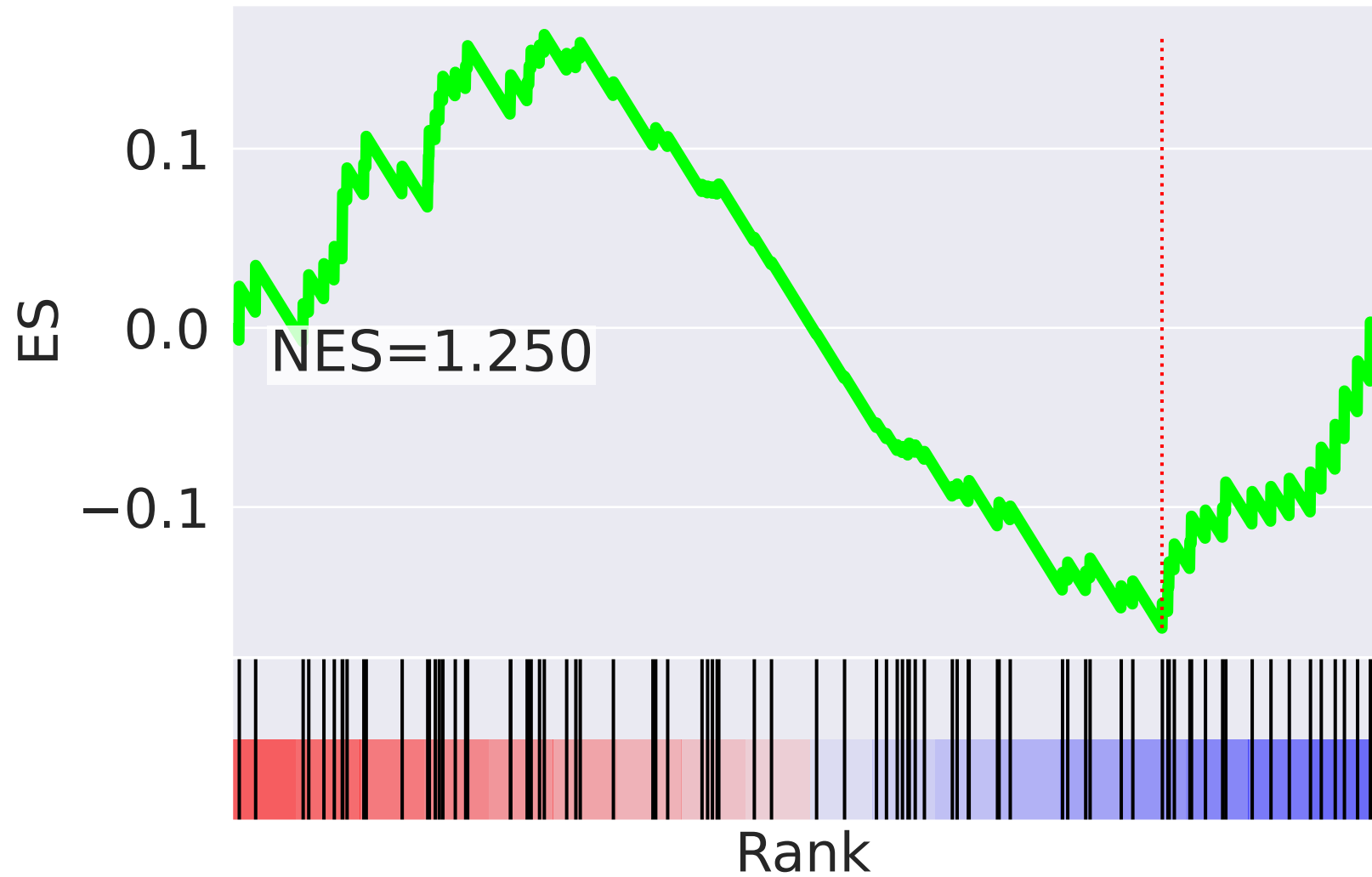
NES		SET
2.838		interferon-gamma-mediated signaling pathway (GO:0060333)
2.633		peptidyl-serine phosphorylation (GO:0018105)
-2.458		mismatch repair (GO:0006298)
-2.409		negative regulation of telomere maintenance via telomerase (GO:0032211)
-2.328		positive regulation of epithelial cell migration (GO:0010634)
-2.301		protein localization to kinetochore (GO:0034501)
-2.237		nuclear-transcribed mRNA catabolic process (GO:0000956)
-2.235		fatty-acyl-CoA biosynthetic process (GO:0046949)
2.225		mitotic sister chromatid segregation (GO:0000070)
-2.215		positive regulation of telomere maintenance via telomerase (GO:0032212)
-2.162		mRNA cleavage (GO:0006379)
-2.151		protein K63-linked deubiquitination (GO:0070536)
-2.140		histone mRNA catabolic process (GO:0071044)
2.138		positive regulation of JUN kinase activity (GO:0043507)
-2.125		regulation of mitophagy (GO:1903146)

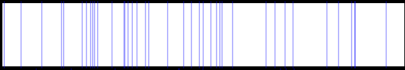

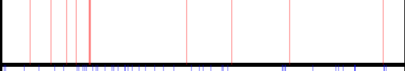
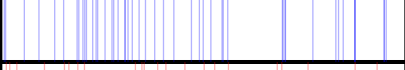
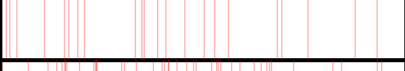
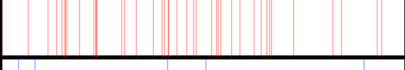
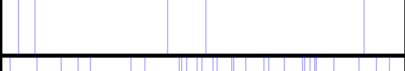
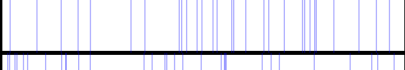
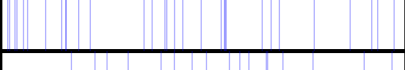




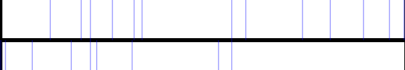

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=6$

mitochondrial translational elongation (GO:0070125)



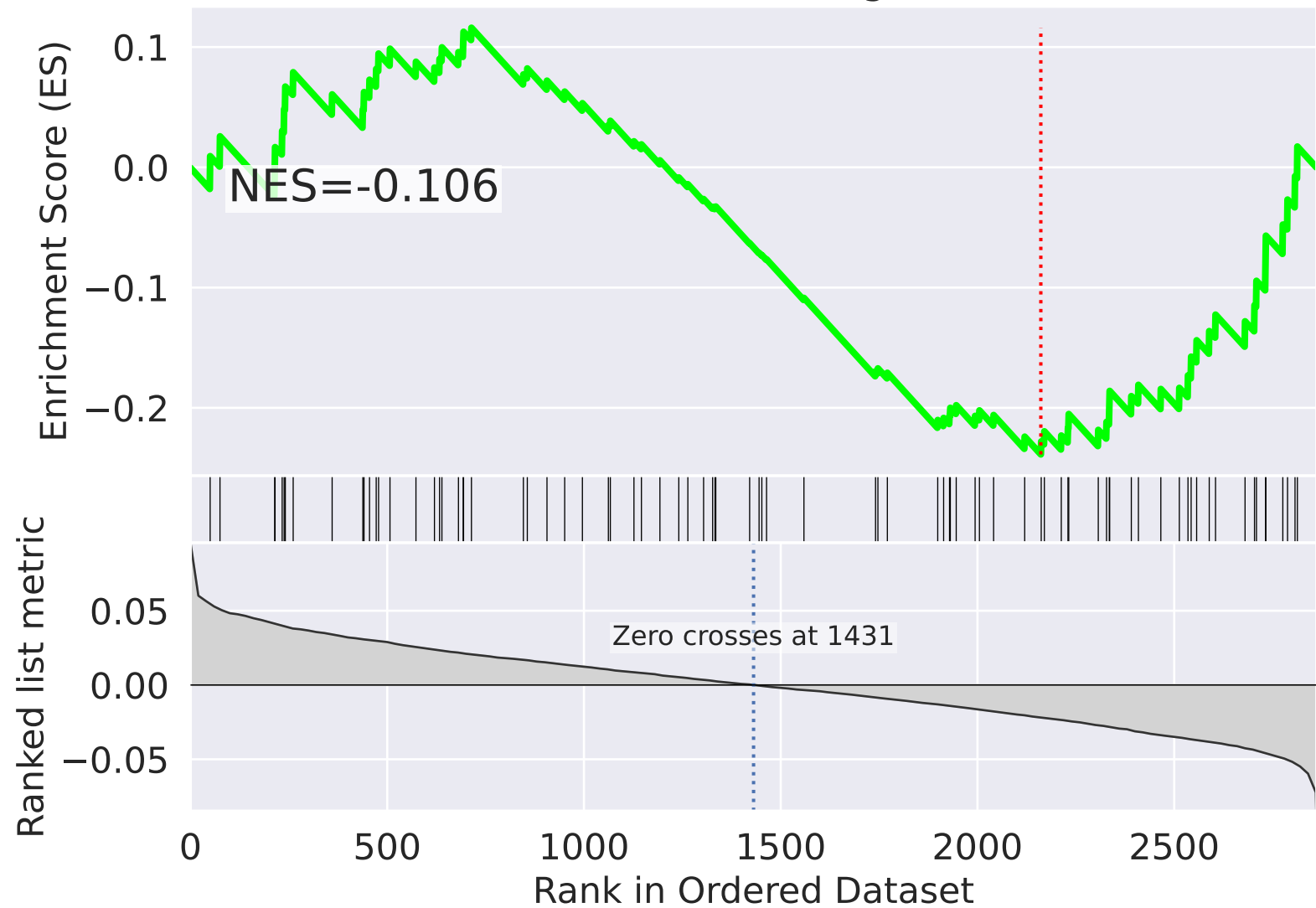
mitochondrial translational elongation (GO:0070125)



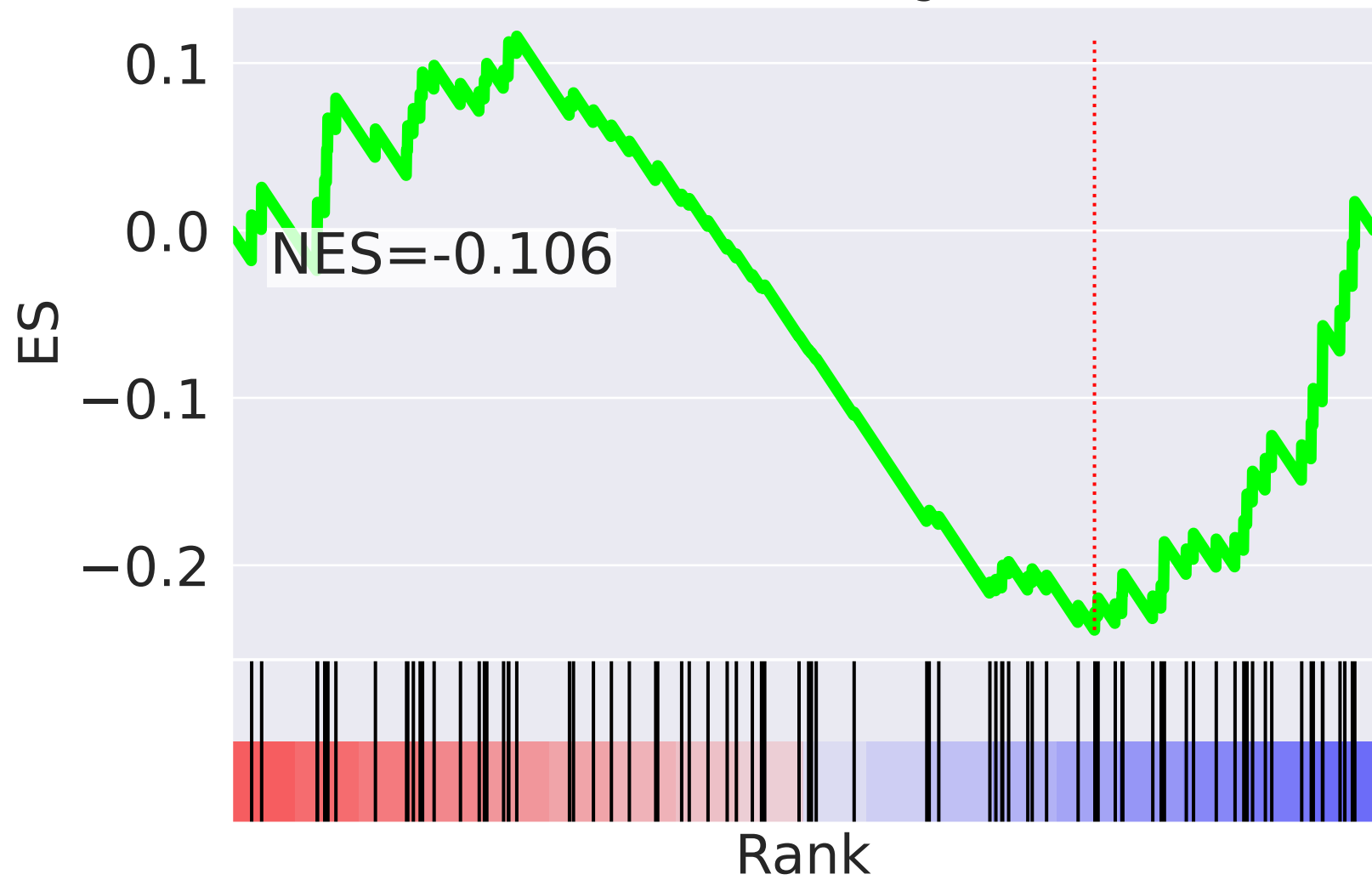
NES		SET
-3.538		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-3.092		cellular response to hydrogen peroxide (GO:0070301)
2.948		global genome nucleotide-excision repair (GO:0070911)
-2.830		ER to Golgi vesicle-mediated transport (GO:0006888)
2.681		positive regulation of cell migration (GO:0030335)
2.678		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.669		regulation of phosphoprotein phosphatase activity (GO:0043666)
-2.657		interstrand cross-link repair (GO:0036297)
-2.566		mitotic nuclear envelope disassembly (GO:0007077)
-2.519		maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462)
2.462		nucleosome disassembly (GO:0006337)
-2.427		intra-Golgi vesicle-mediated transport (GO:0006891)
-2.340		regulation of endocytosis (GO:0030100)
-2.318		error-prone translesion synthesis (GO:0042276)
-2.291		negative regulation of type I interferon production (GO:0032480)


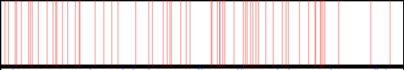


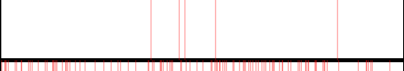
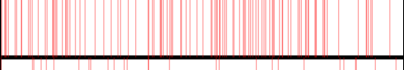


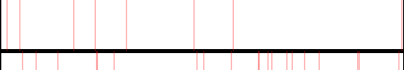

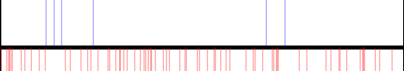
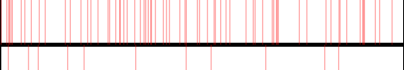
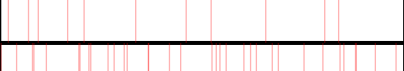
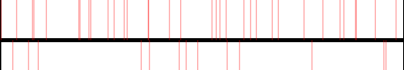

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=7$

mitochondrial translational elongation (GO:0070125)



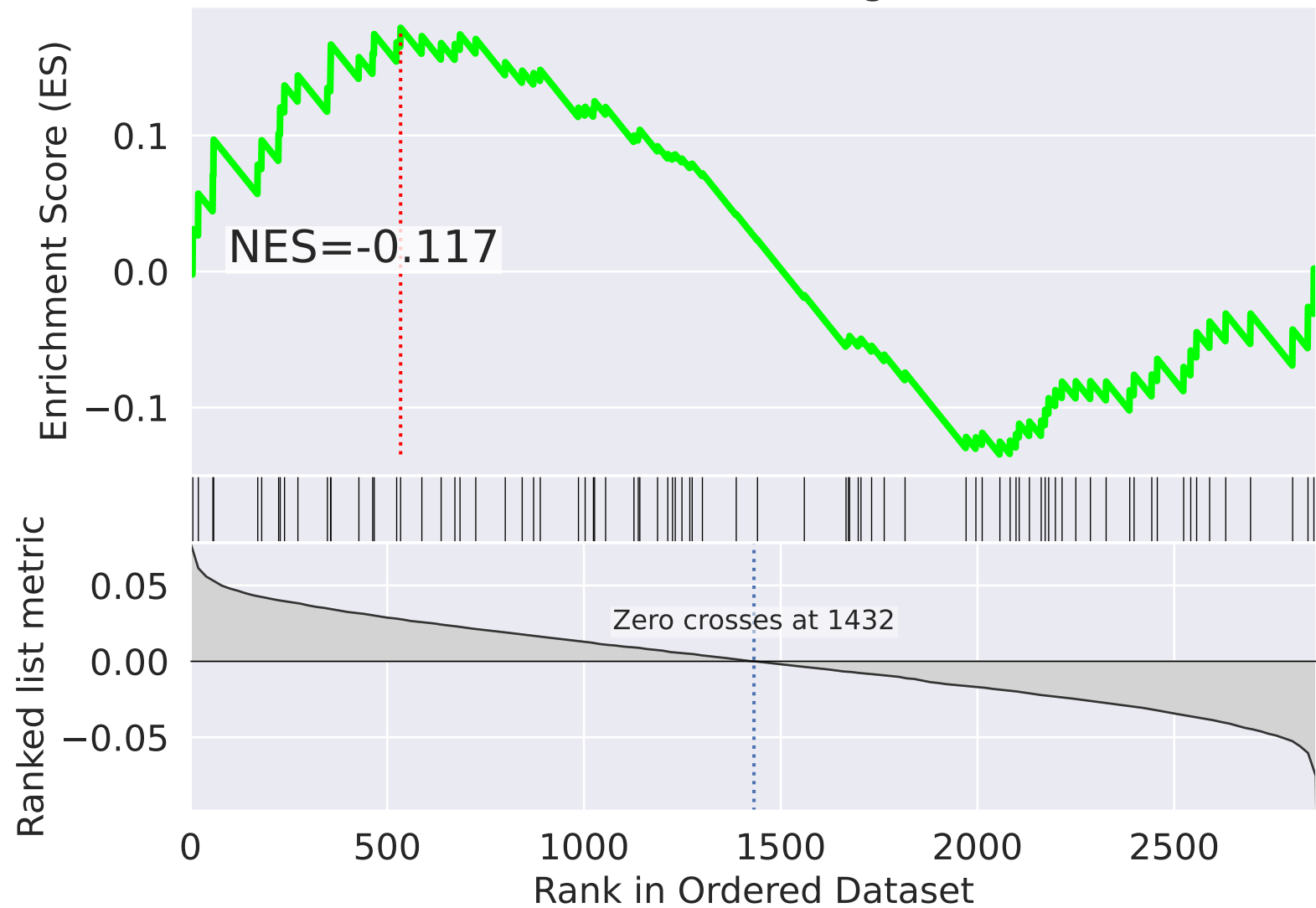
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.821		transcription from RNA polymerase III promoter (GO:0006383)
2.734		transcription elongation from RNA polymerase II promoter (GO:0006368)
-2.658		regulation of cell shape (GO:0008360)
-2.624		negative regulation of translation (GO:0017148)
2.621		regulation of telomere maintenance (GO:0032204)
2.593		transcription from RNA polymerase II promoter (GO:0006366)
2.575		tRNA export from nucleus (GO:0006409)
2.550		negative regulation of myeloid cell differentiation (GO:0045638)
2.531		cellular nitrogen compound metabolic process (GO:0034641)
2.521		regulation of cholesterol biosynthetic process (GO:0045540)
-2.505		ventricular septum morphogenesis (GO:0060412)
2.503		sister chromatid cohesion (GO:0007062)
2.488		positive regulation of transcription elongation from RNA polymerase II promoter (GO:0032968)
2.480		regulation of gene silencing by miRNA (GO:0060964)
2.466		cellular response to lipopolysaccharide (GO:0071222)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

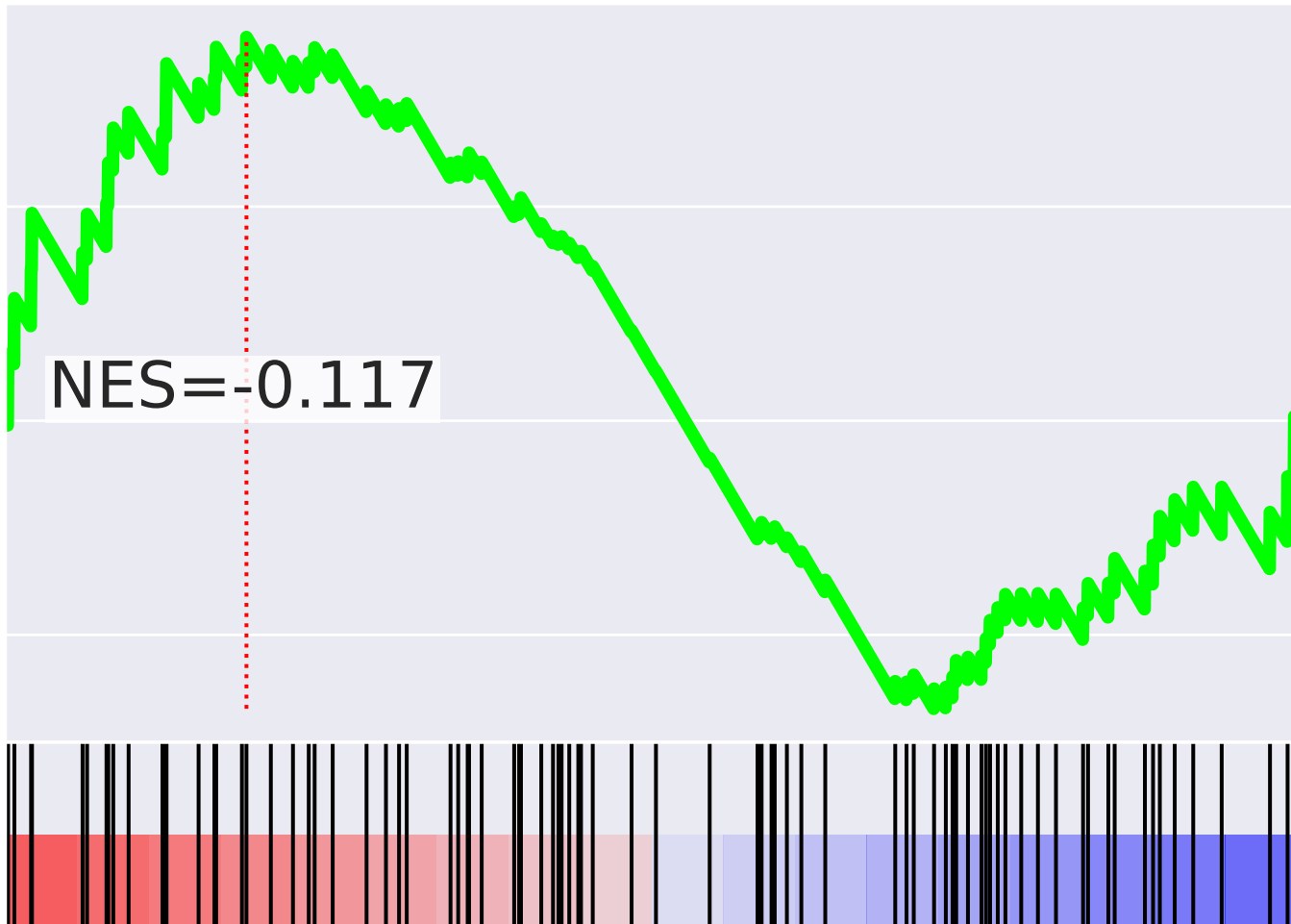
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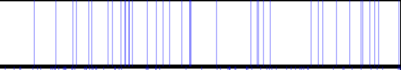
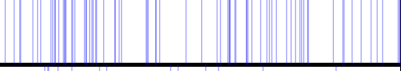
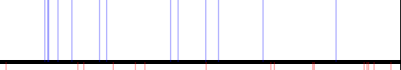
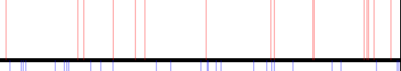
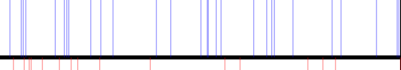

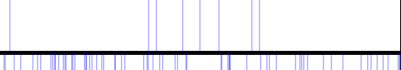
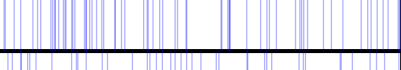
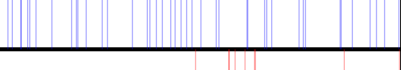
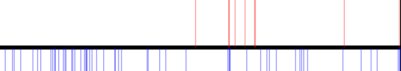
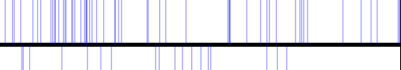
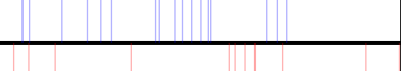
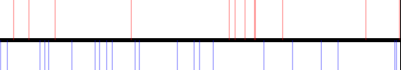

0.0

-0.1

NES=-0.117

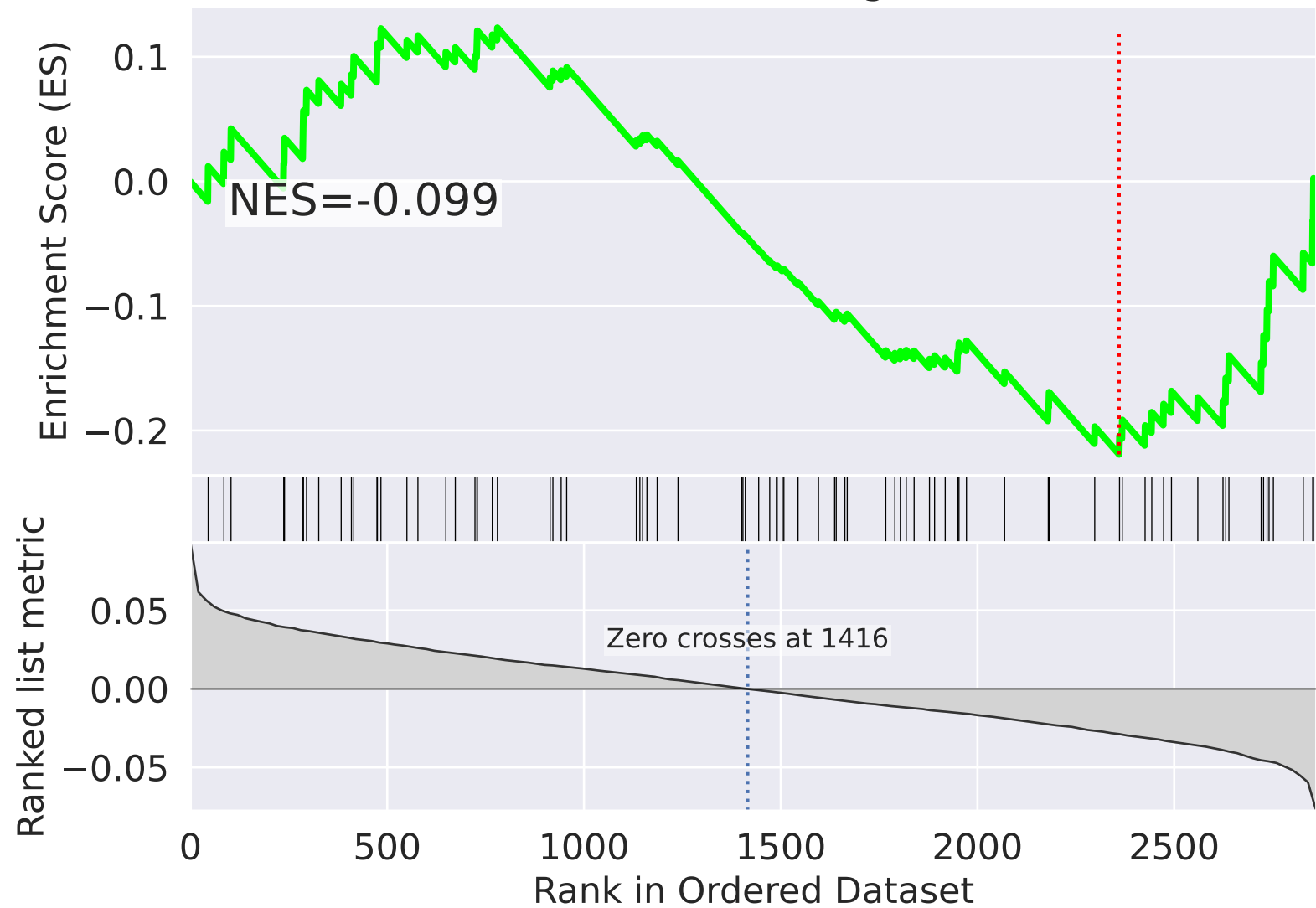
Rank



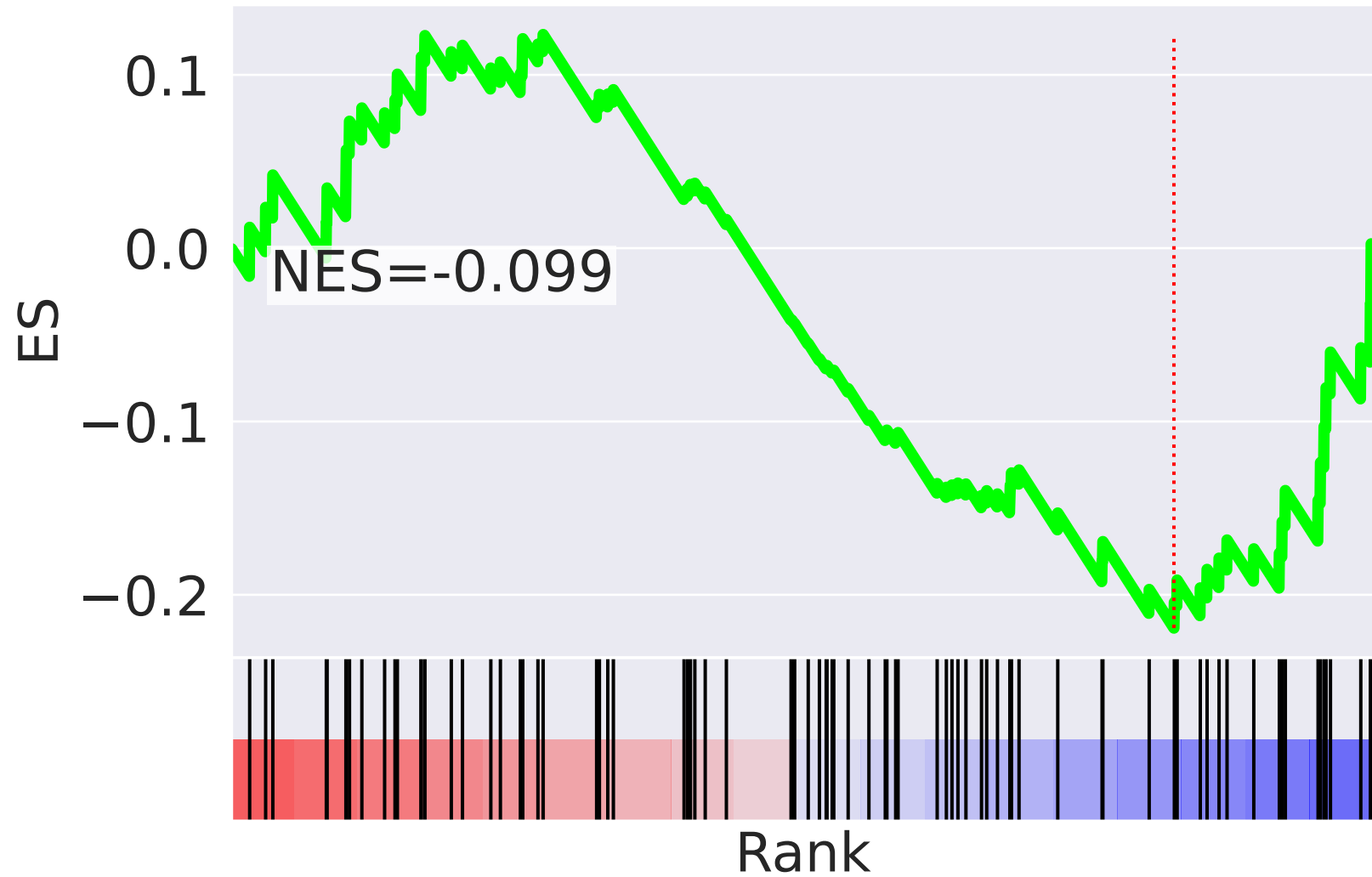
NES		SET
3.158		negative regulation of protein kinase B signaling (GO:0051898)
-3.071		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-3.060		viral transcription (GO:0019083)
-3.053		protein N-linked glycosylation via asparagine (GO:0018279)
2.969		androgen receptor signaling pathway (GO:0030521)
-2.917		chromosome segregation (GO:0007059)
2.911		generation of precursor metabolites and energy (GO:0006091)
-2.853		spindle organization (GO:0007051)
-2.841		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.741		mitotic cell cycle (GO:0000278)
2.693		TRIF-dependent toll-like receptor signaling pathway (GO:0035666)
-2.612		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.589		CENP-A containing nucleosome assembly (GO:0034080)
2.530		regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)
-2.496		ubiquitin-dependent ERAD pathway (GO:0030433)

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

mitochondrial translational elongation (GO:0070125)



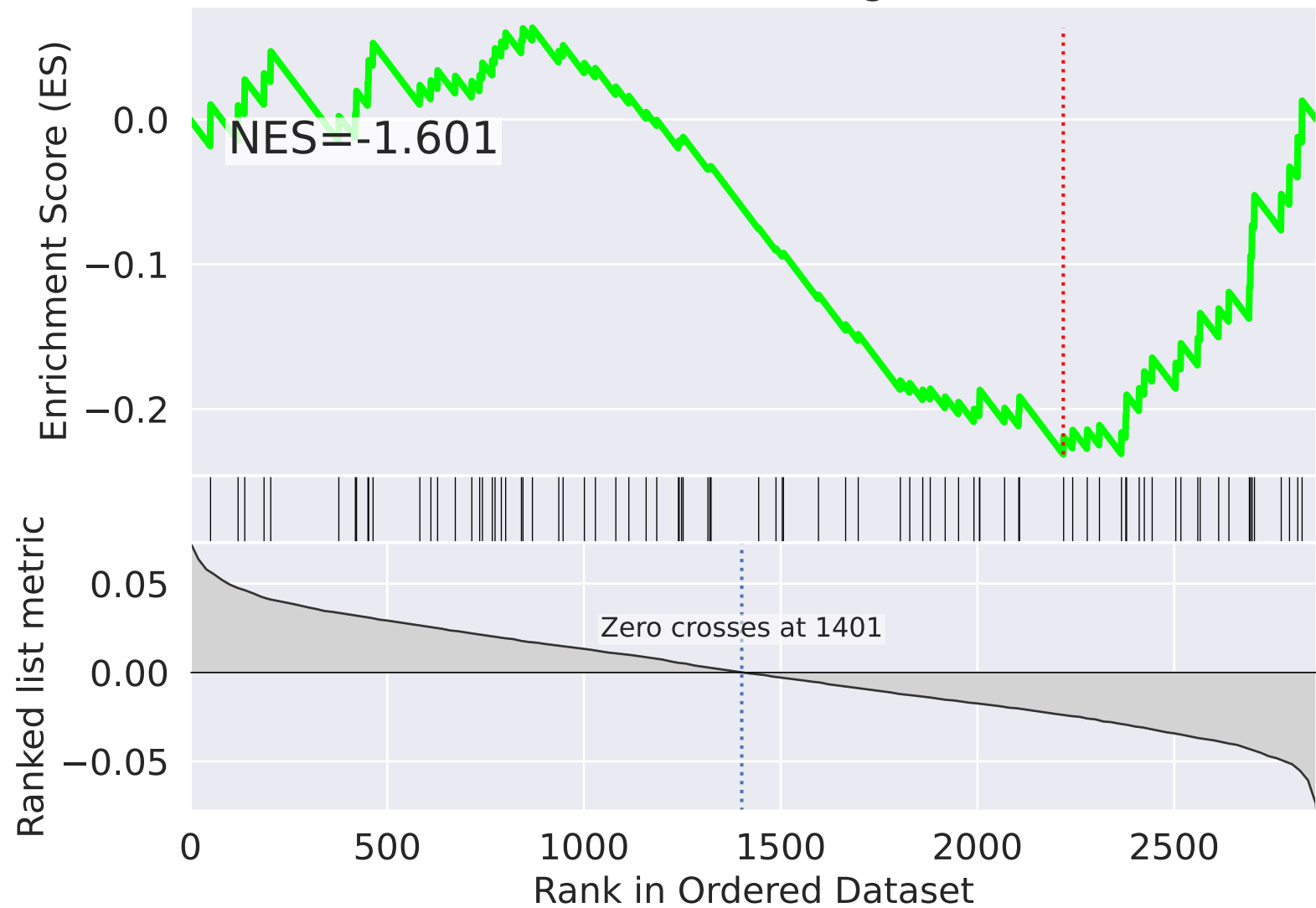
mitochondrial translational elongation (GO:0070125)



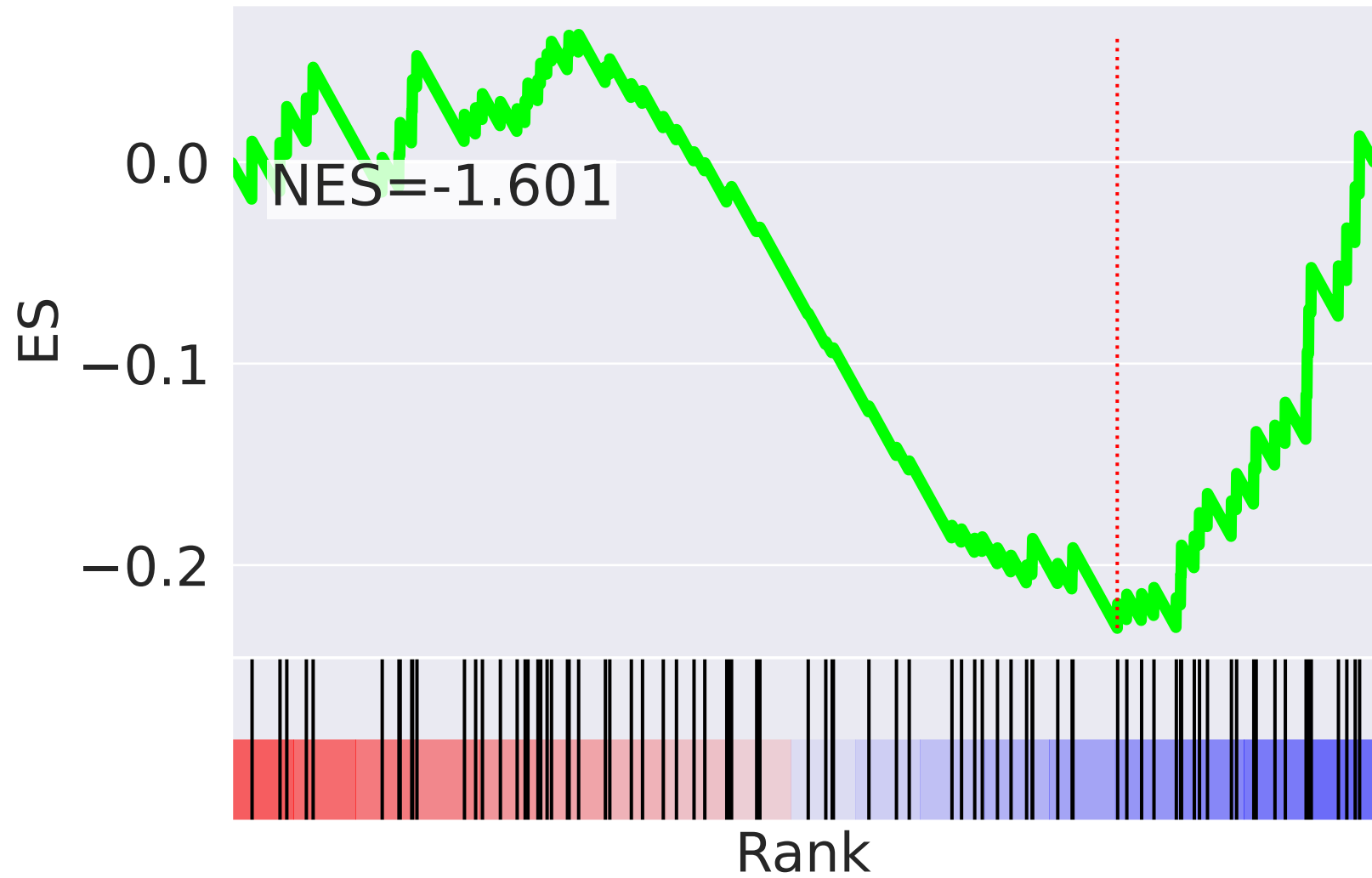
NES		SET
-2.956		positive regulation of ERK1 and ERK2 cascade (GO:0070374)
-2.906		mRNA methylation (GO:0080009)
-2.884		exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay (GO:0043928)
2.880		cellular response to transforming growth factor beta stimulus (GO:0071560)
2.866		humoral immune response (GO:0006959)
2.603		positive regulation of translation (GO:0045727)
2.578		generation of precursor metabolites and energy (GO:0006091)
2.571		positive regulation of muscle cell differentiation (GO:0051149)
2.558		regulation of transcription, DNA-templated (GO:0006355)
-2.515		endoplasmic reticulum organization (GO:0007029)
-2.434		axonogenesis (GO:0007409)
2.431		cytoplasmic translation (GO:0002181)
2.423		apoptotic process (GO:0006915)
-2.419		regulation of microtubule-based process (GO:0032886)
2.388		negative regulation of transforming growth factor beta receptor signaling pathway (GO:0030512)


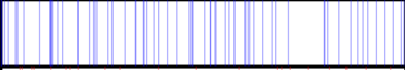
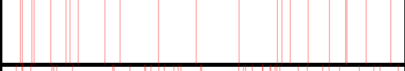
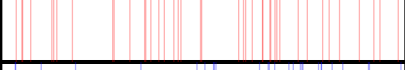
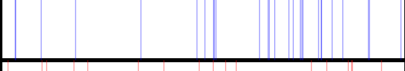

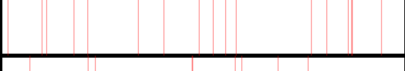

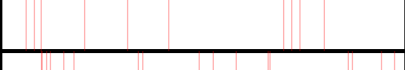
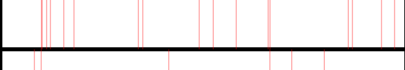
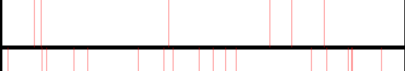

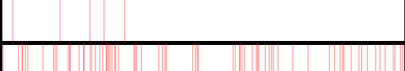
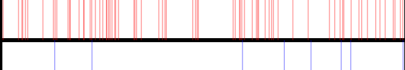
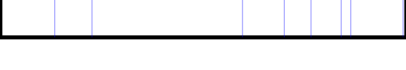
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=10$

mitochondrial translational elongation (GO:0070125)



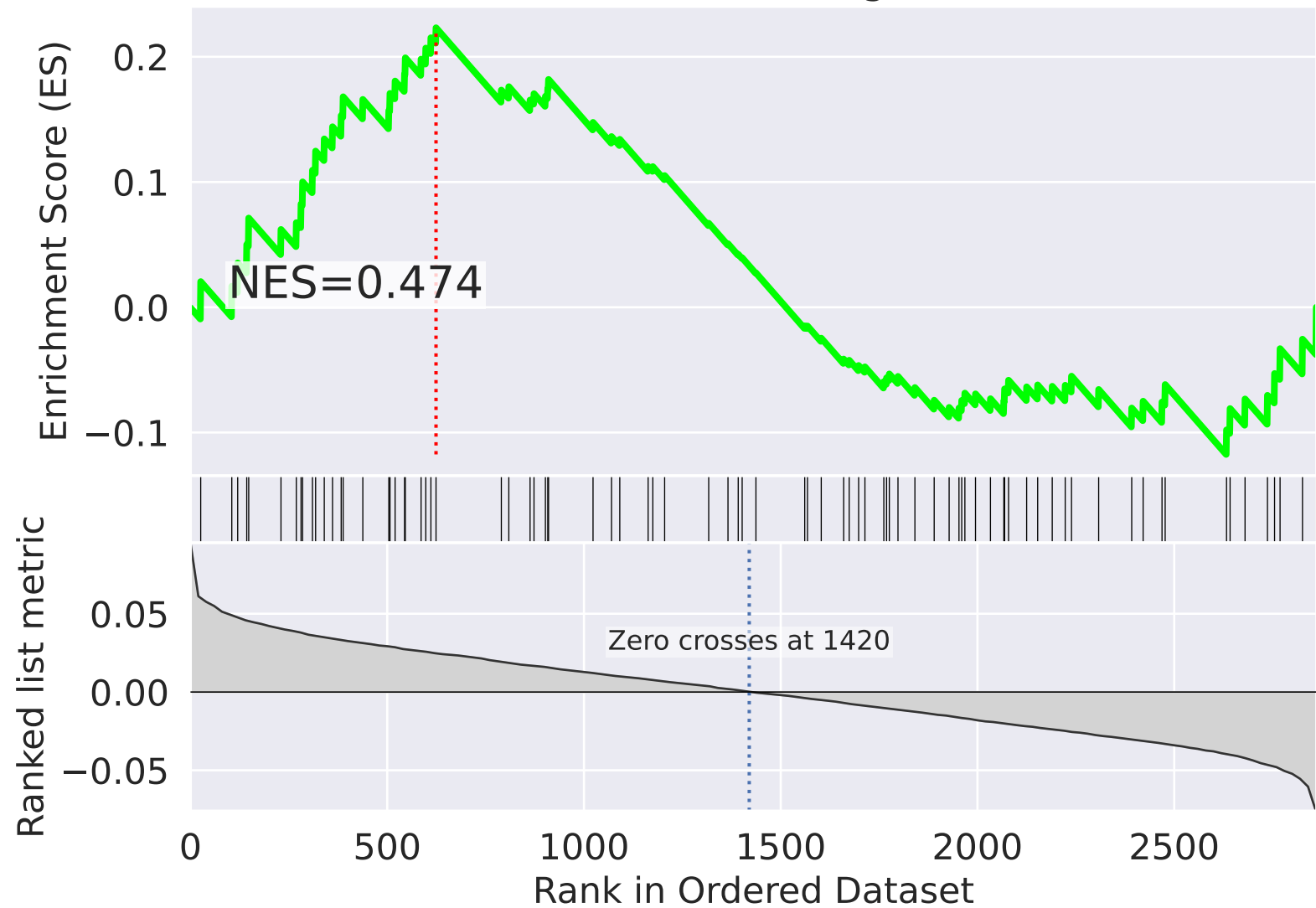
mitochondrial translational elongation (GO:0070125)



NES		SET
-3.027		positive regulation of protein serine/threonine kinase activity (GO:0071902)
-2.991		protein phosphorylation (GO:0006468)
2.961		protein homooligomerization (GO:0051260)
2.834		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
-2.779		ephrin receptor signaling pathway (GO:0048013)
2.686		transcription elongation from RNA polymerase I promoter (GO:0006362)
2.686		transcription initiation from RNA polymerase I promoter (GO:0006361)
2.640		protein destabilization (GO:0031648)
2.628		cell-matrix adhesion (GO:0007160)
2.622		positive regulation of gene expression, epigenetic (GO:0045815)
2.599		substrate adhesion-dependent cell spreading (GO:0034446)
2.545		termination of RNA polymerase I transcription (GO:0006363)
2.525		GPI anchor biosynthetic process (GO:0006506)
2.517		protein ubiquitination (GO:0016567)
-2.503		purine ribonucleoside monophosphate biosynthetic process (GO:0009168)

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

mitochondrial translational elongation (GO:0070125)



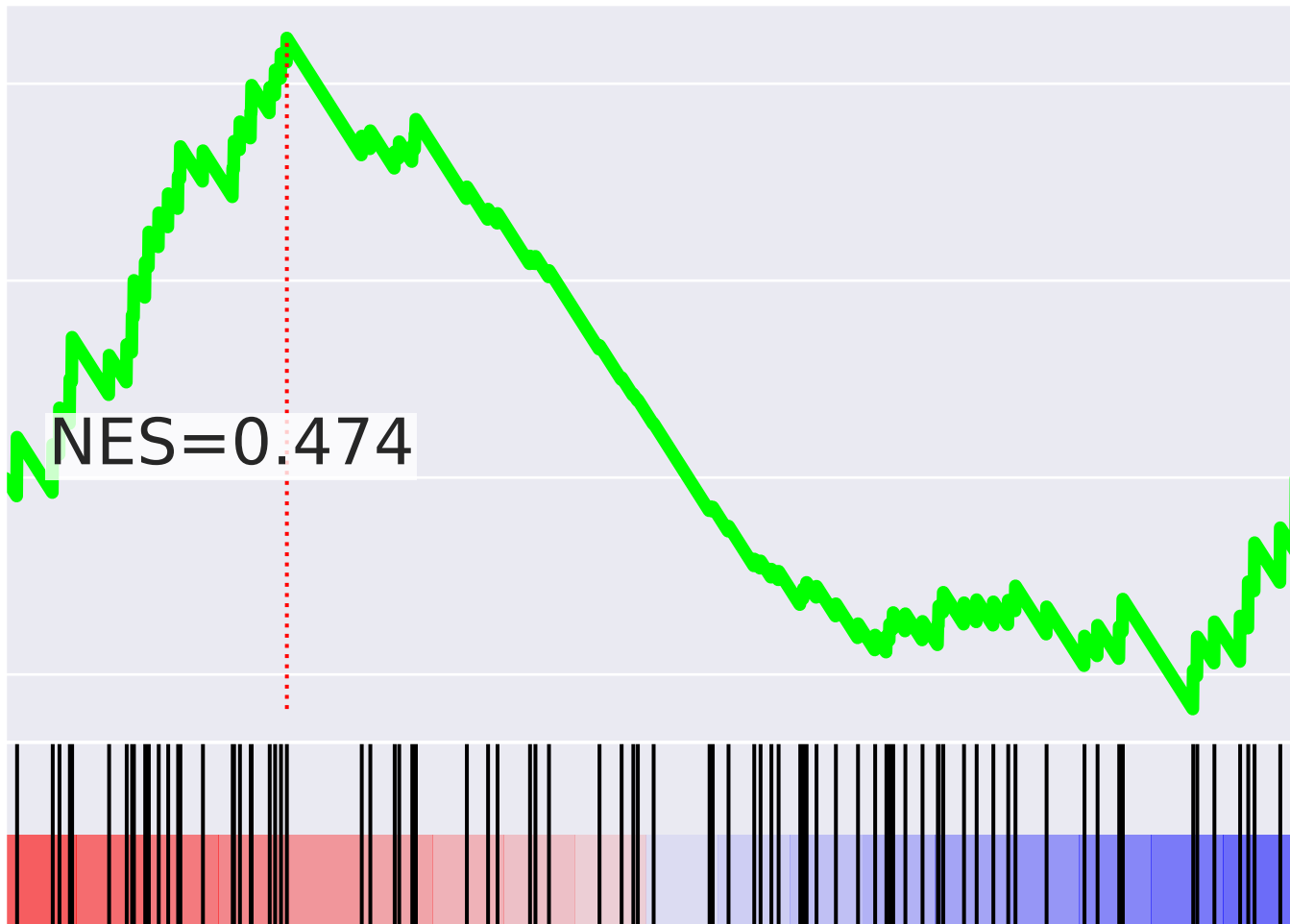
mitochondrial translational elongation (GO:0070125)


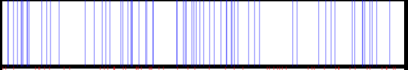
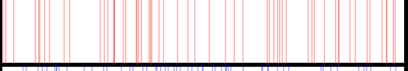
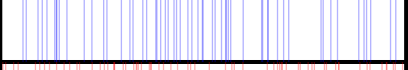
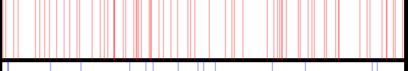
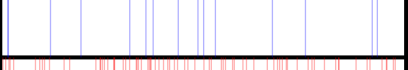
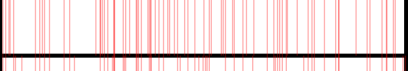
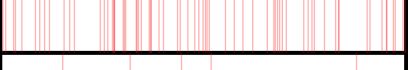
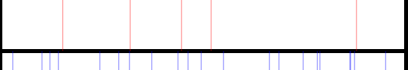




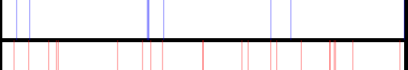

ES

0.2
0.1
0.0
-0.1

NES=0.474

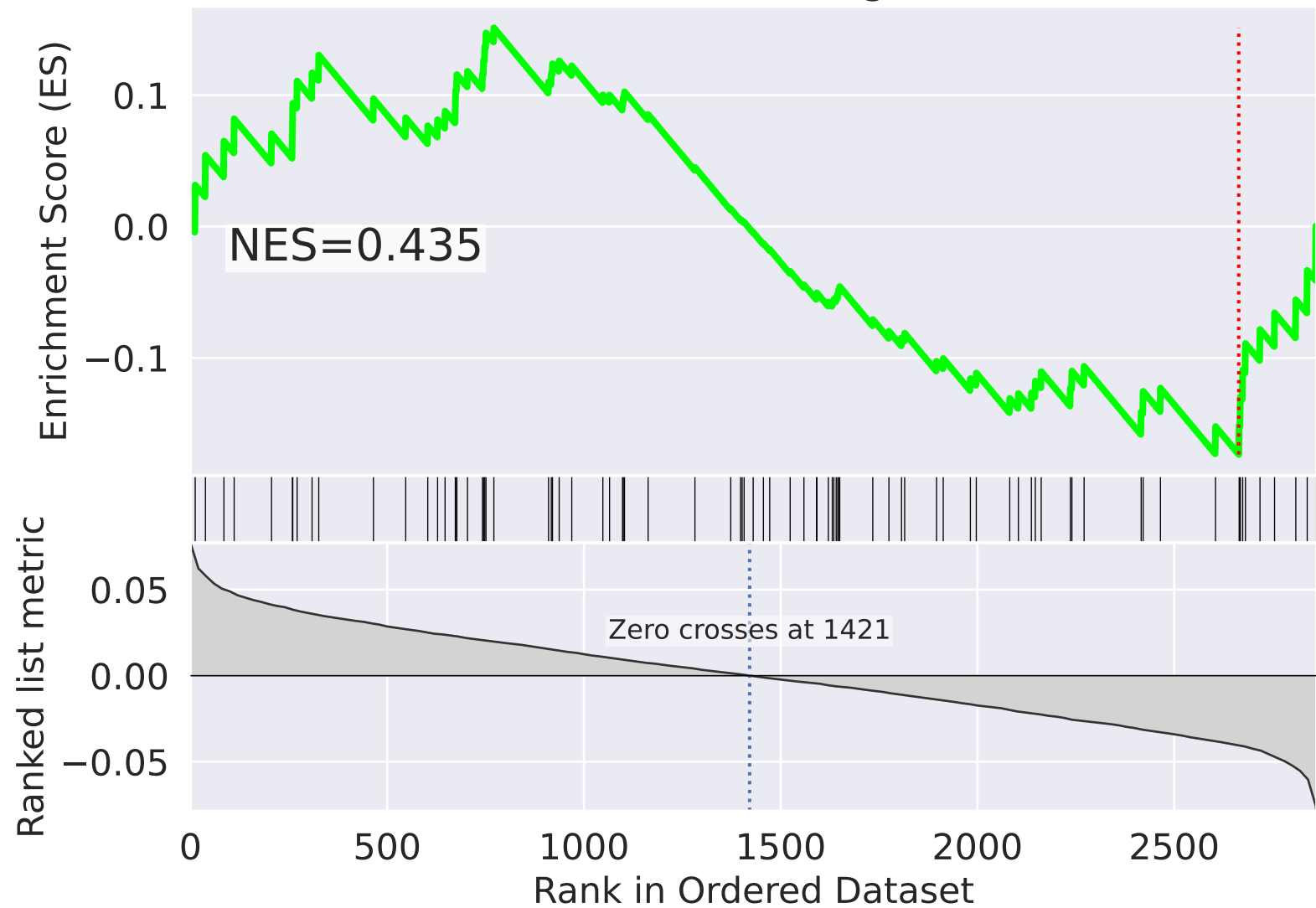
Rank



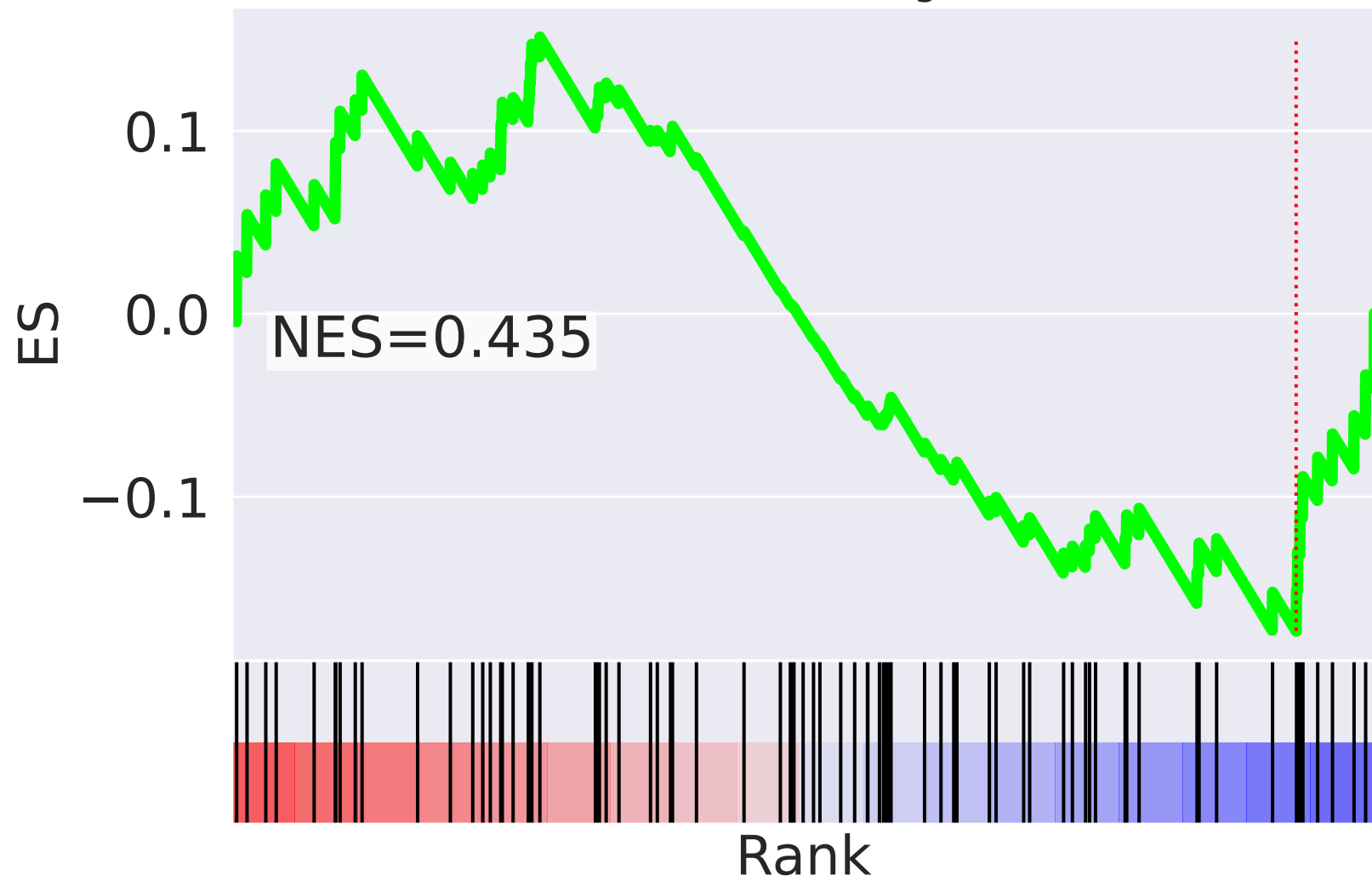
NES		SET
-3.628		spliceosomal snRNP assembly (GO:0000387)
-2.915		DNA replication (GO:0006260)
2.862		SRP-dependent cotranslational protein targeting to membrane (GO:0006614)
-2.839		G2/M transition of mitotic cell cycle (GO:0000086)
2.805		translational initiation (GO:0006413)
-2.714		cellular response to ionizing radiation (GO:0071479)
2.706		viral transcription (GO:0019083)
2.702		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
2.659		regulation of phosphoprotein phosphatase activity (GO:0043666)
-2.630		IRE1-mediated unfolded protein response (GO:0036498)
-2.629		cell separation after cytokinesis (GO:0000920)
-2.615		regulation of cytokinesis (GO:0032465)
2.592		positive regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
-2.557		nuclear import (GO:0051170)
2.554		blood coagulation (GO:0007596)

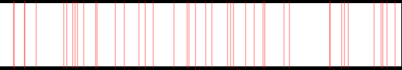





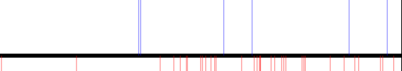
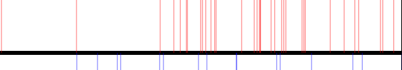
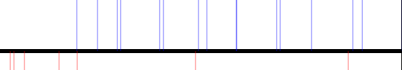
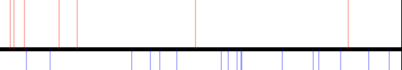


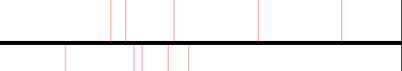
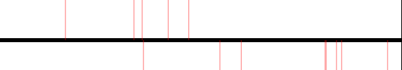
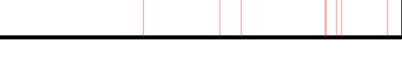
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=12$

mitochondrial translational elongation (GO:0070125)



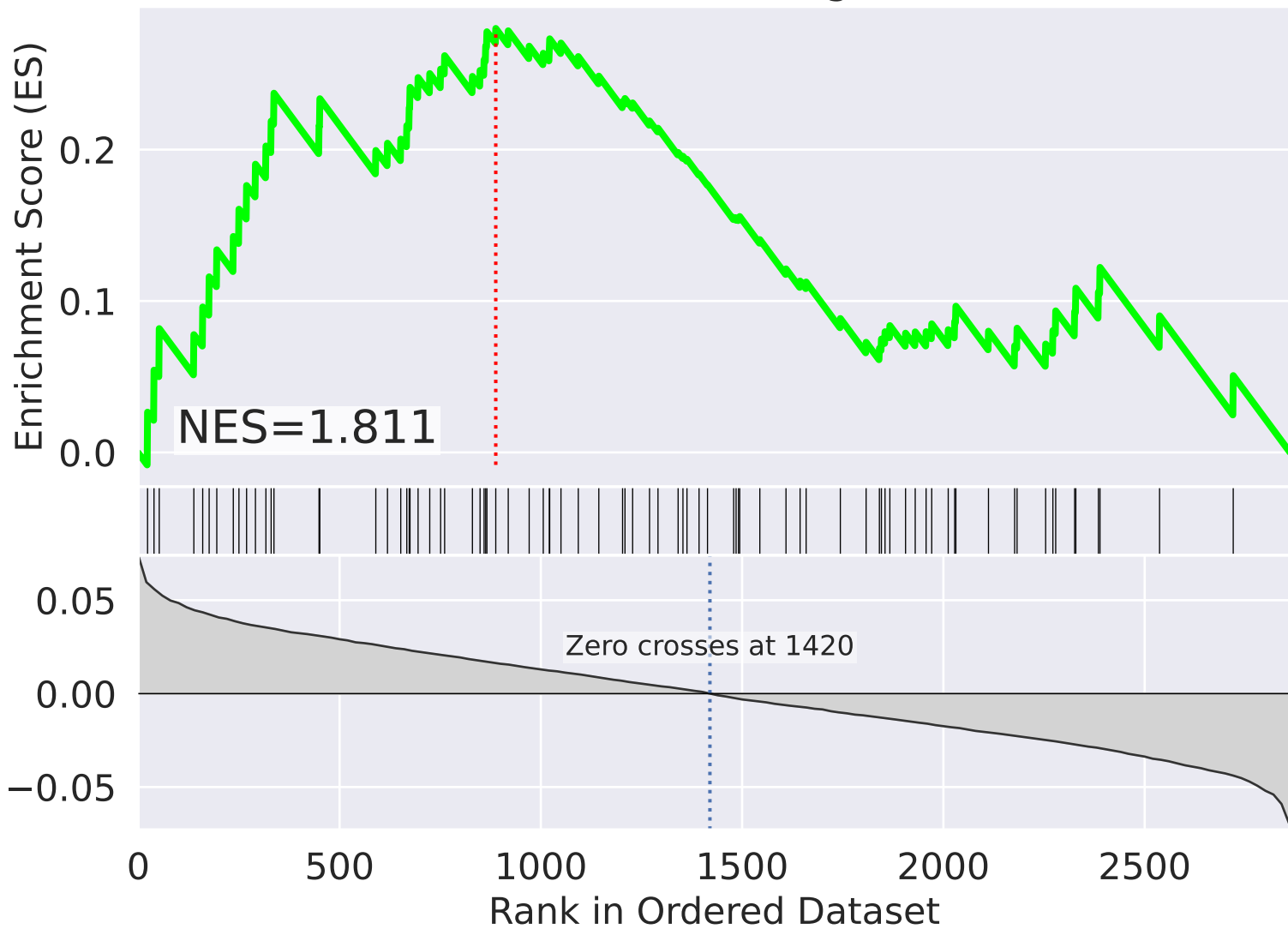
mitochondrial translational elongation (GO:0070125)



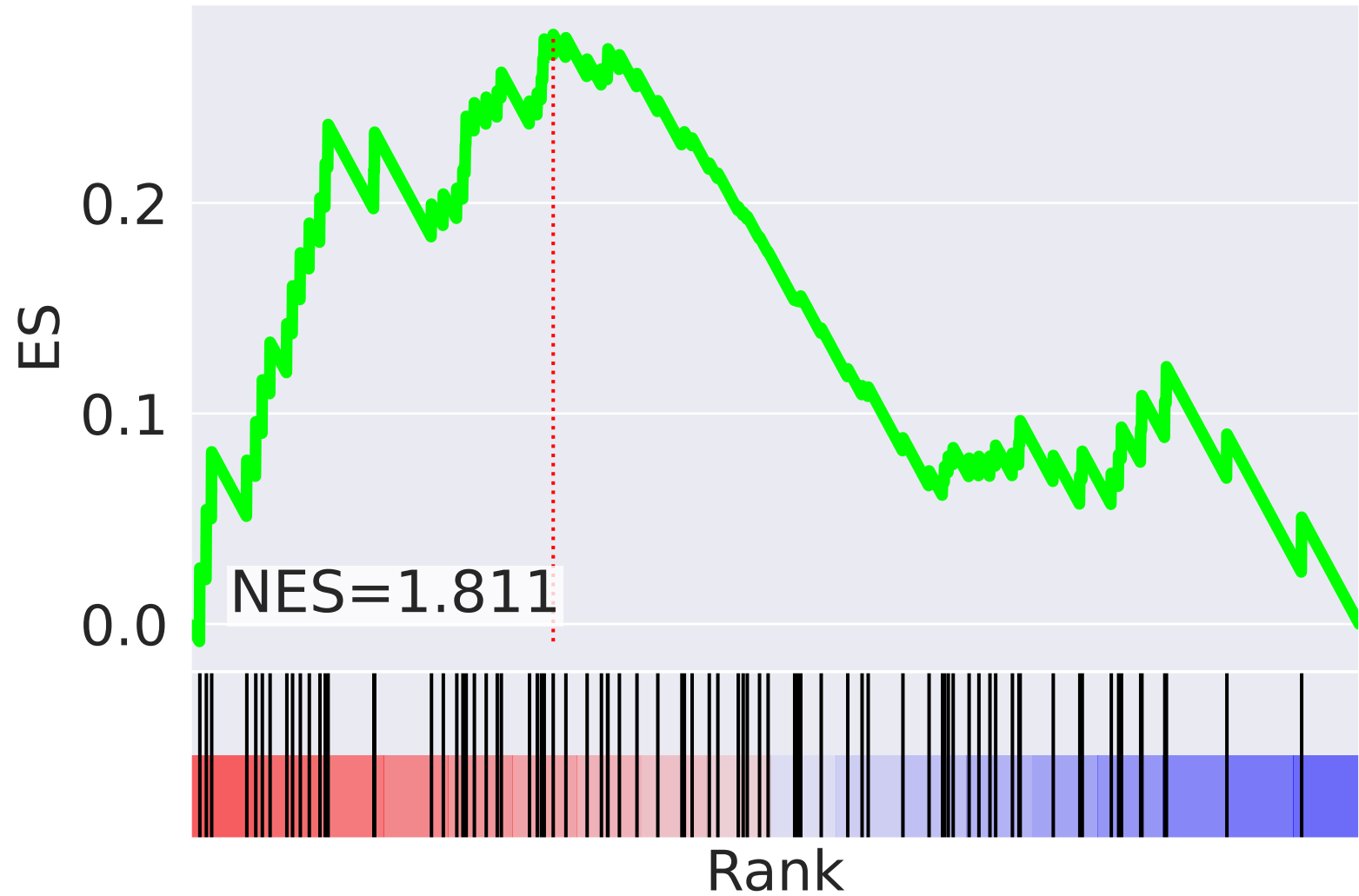
NES		SET
2.785		positive regulation of gene expression (GO:0010628)
2.741		positive regulation of glucose import (GO:0046326)
-2.672		positive regulation of mitotic metaphase/anaphase transition (GO:0045842)
2.653		heart looping (GO:0001947)
2.646		cellular response to drug (GO:0035690)
-2.609		nucleotide-excision repair, DNA gap filling (GO:0006297)
-2.607		nuclear envelope organization (GO:0006998)
2.599		regulation of macroautophagy (GO:0016241)
-2.500		mitotic spindle organization (GO:0007052)
2.495		ERK1 and ERK2 cascade (GO:0070371)
-2.494		DNA replication initiation (GO:0006270)
-2.388		centriole replication (GO:0007099)
2.326		positive regulation of bone mineralization (GO:0030501)
2.322		negative regulation of translational initiation (GO:0045947)
2.318		positive regulation of neuron differentiation (GO:0045666)





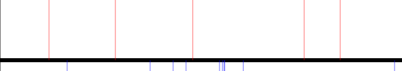
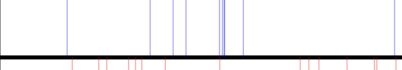

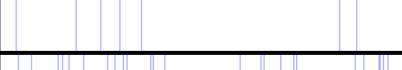

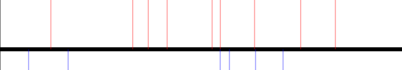
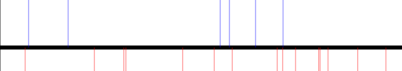


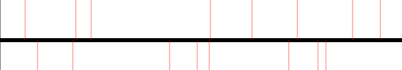

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=13$

mitochondrial translational elongation (GO:0070125)



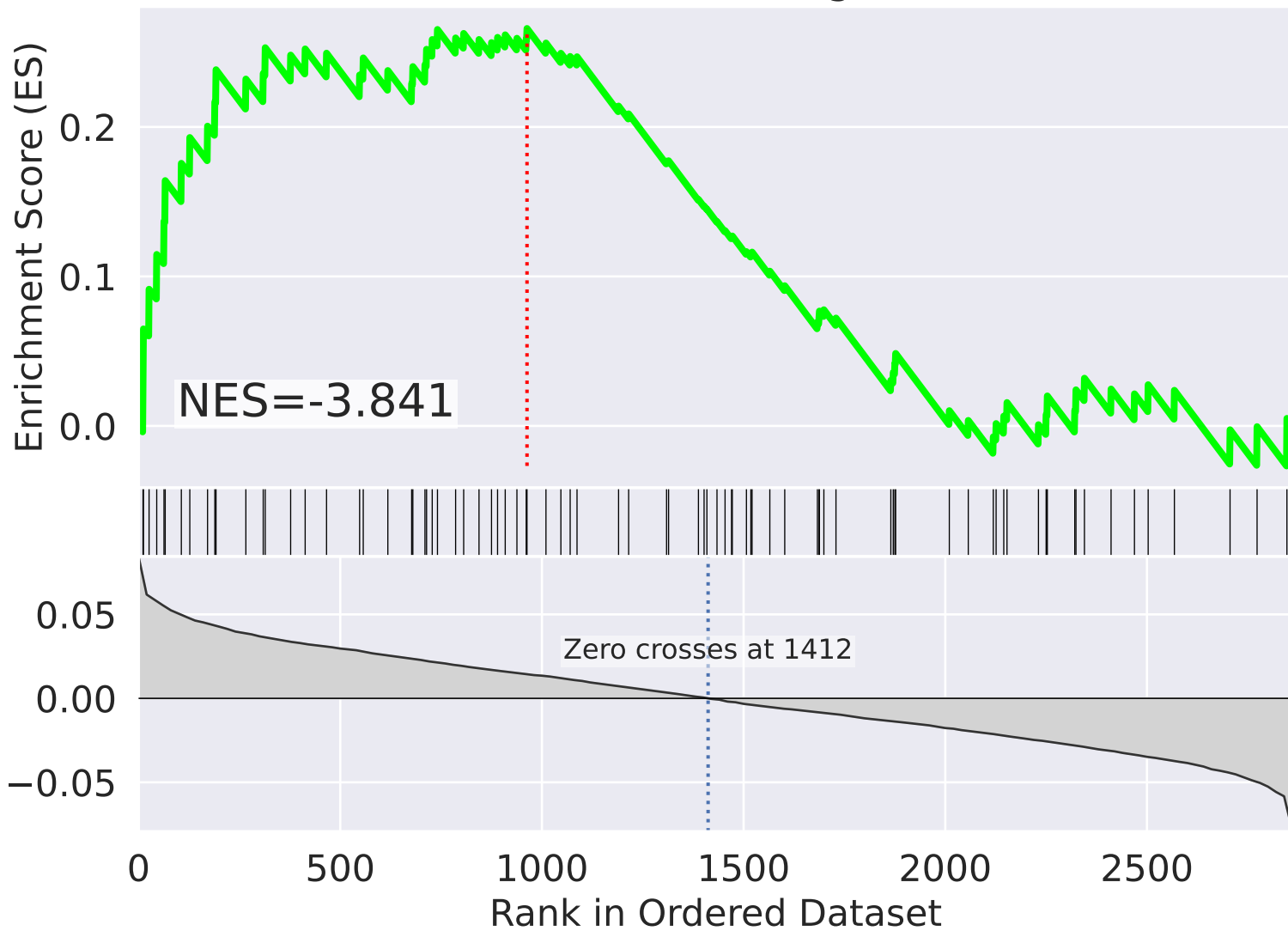
mitochondrial translational elongation (GO:0070125)



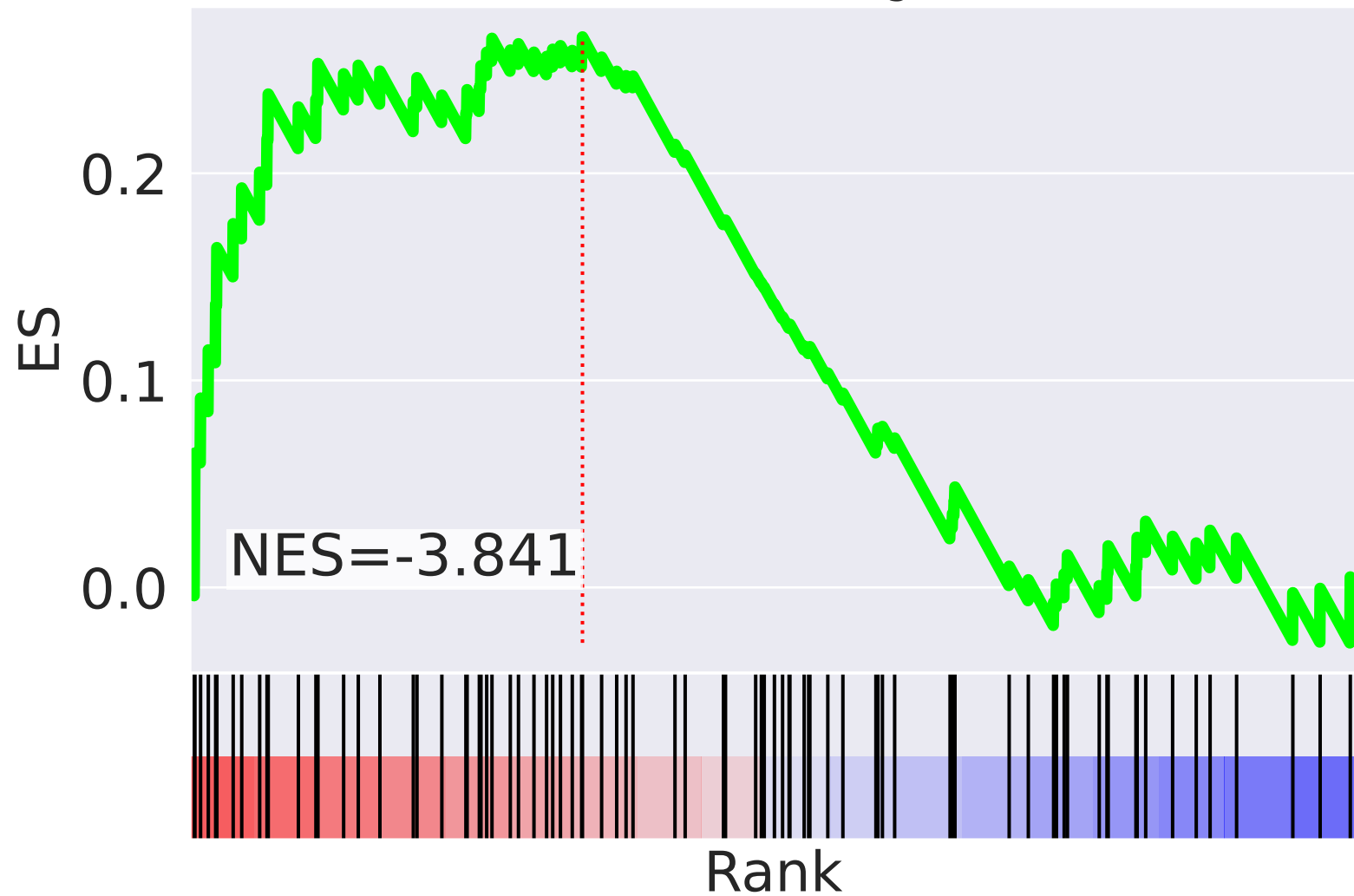
NES		SET
3.007		respiratory chain complex IV assembly (GO:0008535)
2.787		telomere maintenance (GO:0000723)
-2.737		substantia nigra development (GO:0021762)
2.663		mitotic sister chromatid cohesion (GO:0007064)
2.650		positive regulation of Notch signaling pathway (GO:0045747)
-2.578		sensory perception of sound (GO:0007605)
2.554		regulation of transcription involved in G1/S transition of mitotic cell cycle (GO:0000083)
-2.545		negative regulation of gene expression, epigenetic (GO:0045814)
-2.541		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.539		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.509		meiotic cell cycle (GO:0051321)
2.484		positive regulation of protein ubiquitination (GO:0031398)
-2.431		apical junction assembly (GO:0043297)
2.396		DNA double-strand break processing (GO:0000729)
2.376		regulation of protein localization (GO:0032880)

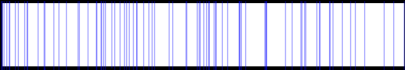
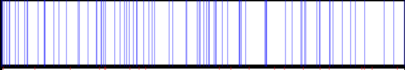
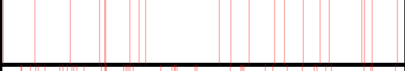
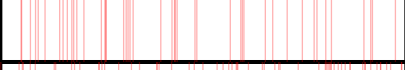
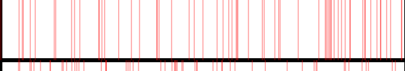
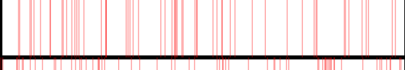
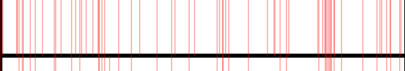
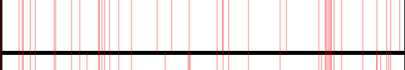
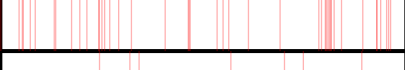
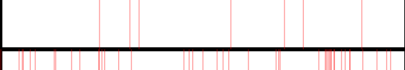
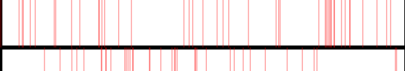
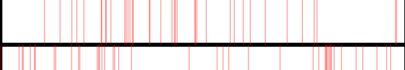
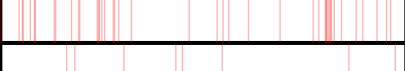
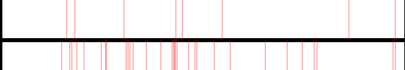
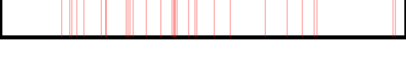
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=14$

mitochondrial translational elongation (GO:0070125)



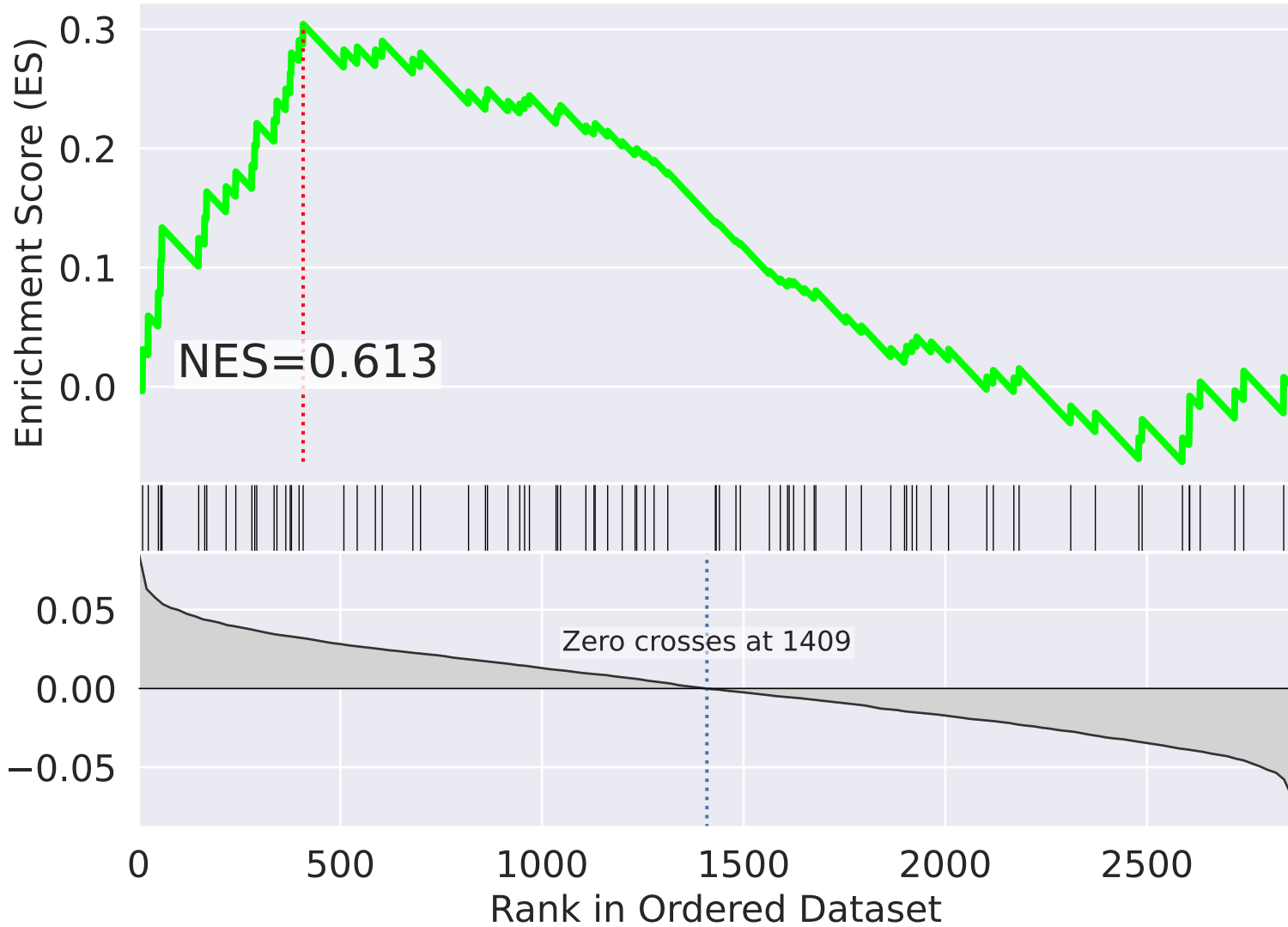
mitochondrial translational elongation (GO:0070125)



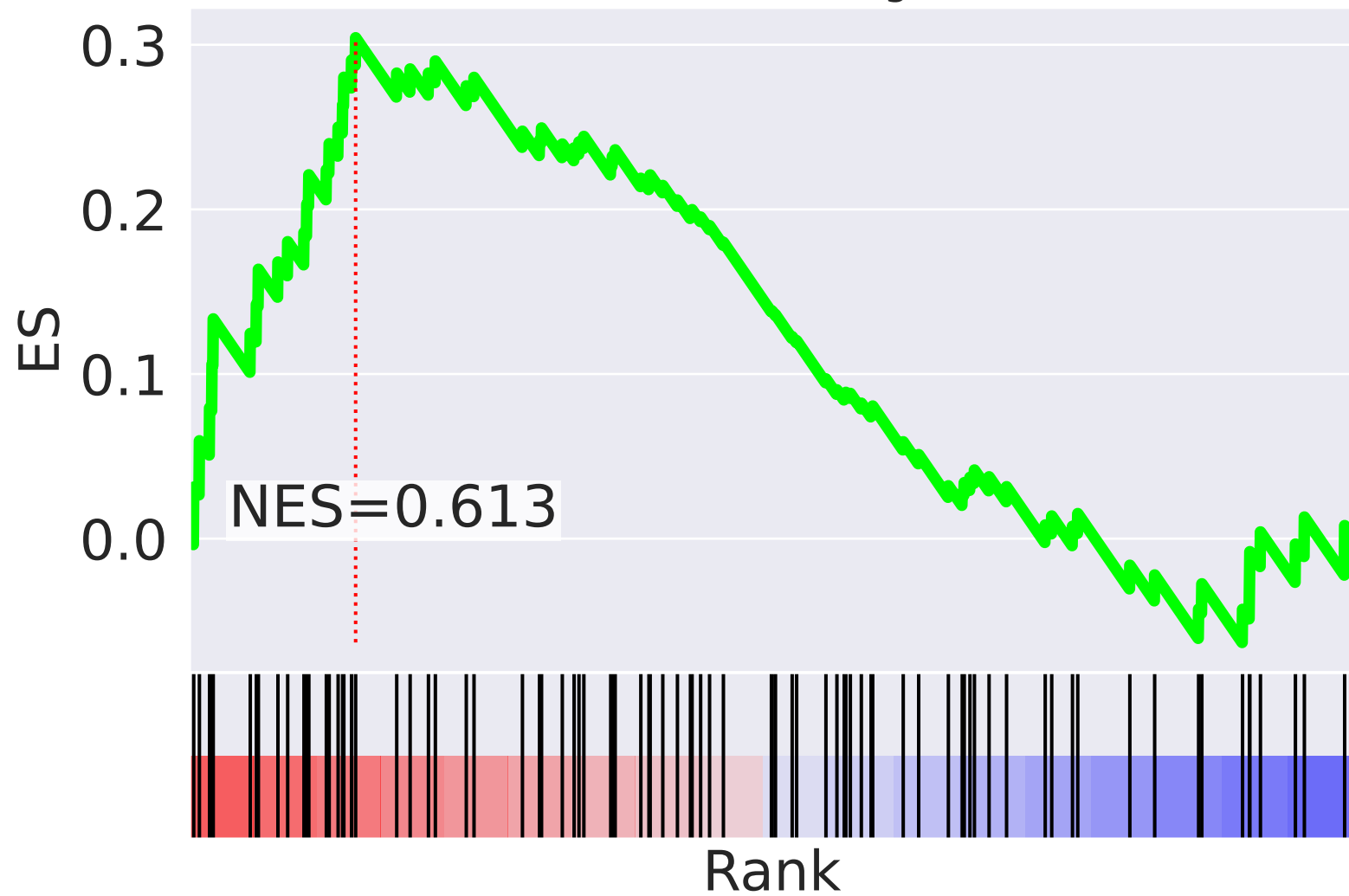
NES		SET
-3.841		mitochondrial translational elongation (GO:0070125)
-3.641		mitochondrial translational termination (GO:0070126)
3.258		ion transmembrane transport (GO:0034220)
3.240		regulation of cellular response to heat (GO:1900034)
3.195		Fc-epsilon receptor signaling pathway (GO:0038095)
3.180		mRNA export from nucleus (GO:0006406)
3.109		protein polyubiquitination (GO:0000209)
2.979		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
2.960		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
2.948		proton transport (GO:0015992)
2.932		tumor necrosis factor-mediated signaling pathway (GO:0033209)
2.923		protein sumoylation (GO:0016925)
2.902		transmembrane transport (GO:0055085)
2.872		positive regulation of DNA-templated transcription, elongation (GO:0032786)
2.806		mitotic nuclear envelope disassembly (GO:0007077)

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

mitochondrial translational elongation (GO:0070125)


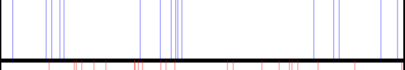
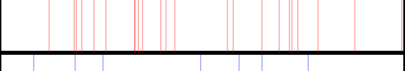

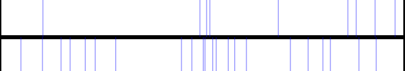
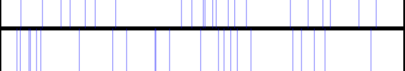

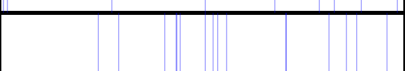
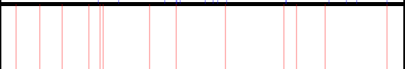


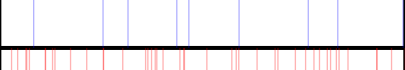
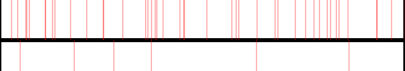
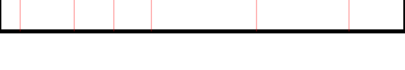



mitochondrial translational elongation (GO:0070125)



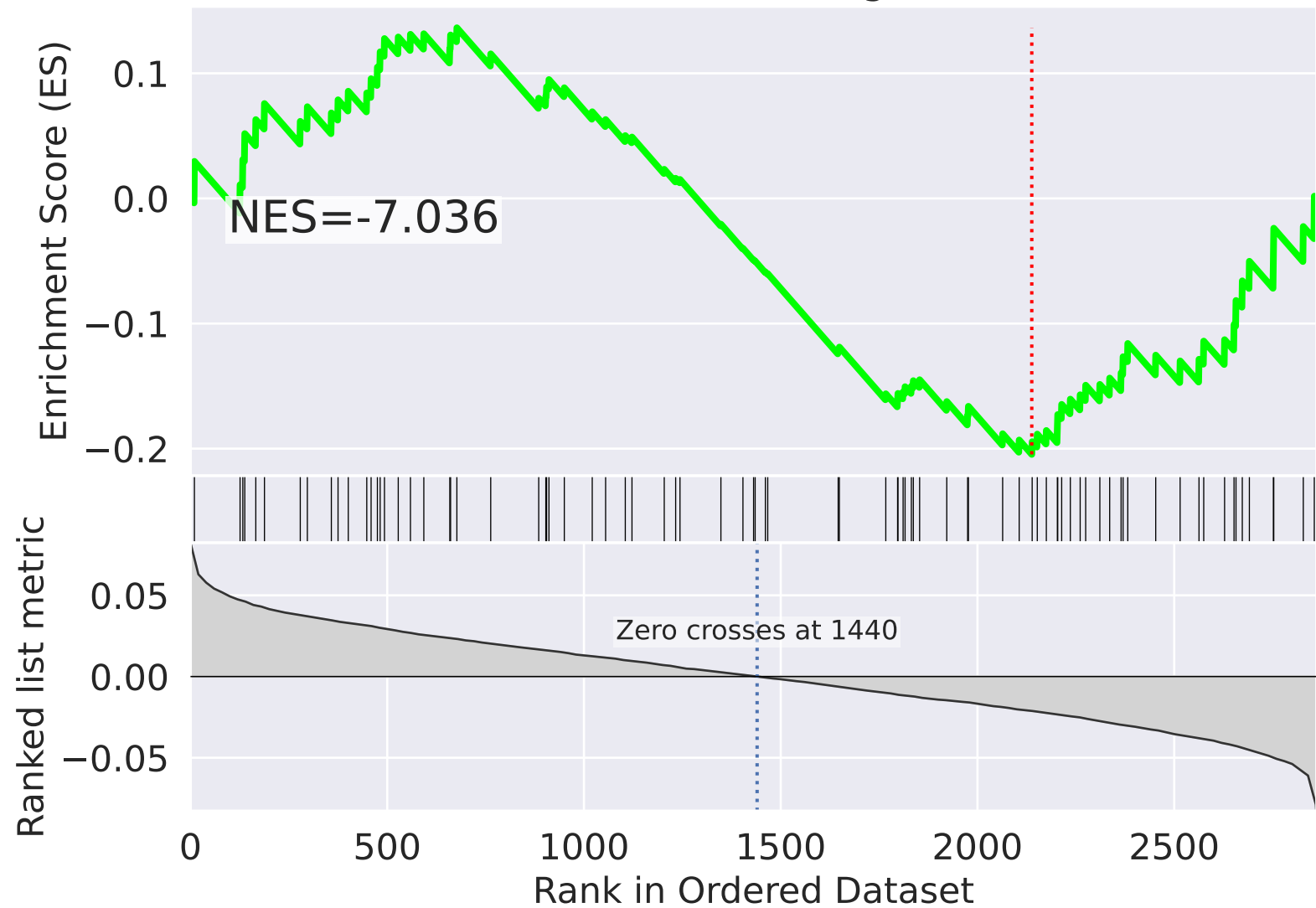
NES

SET

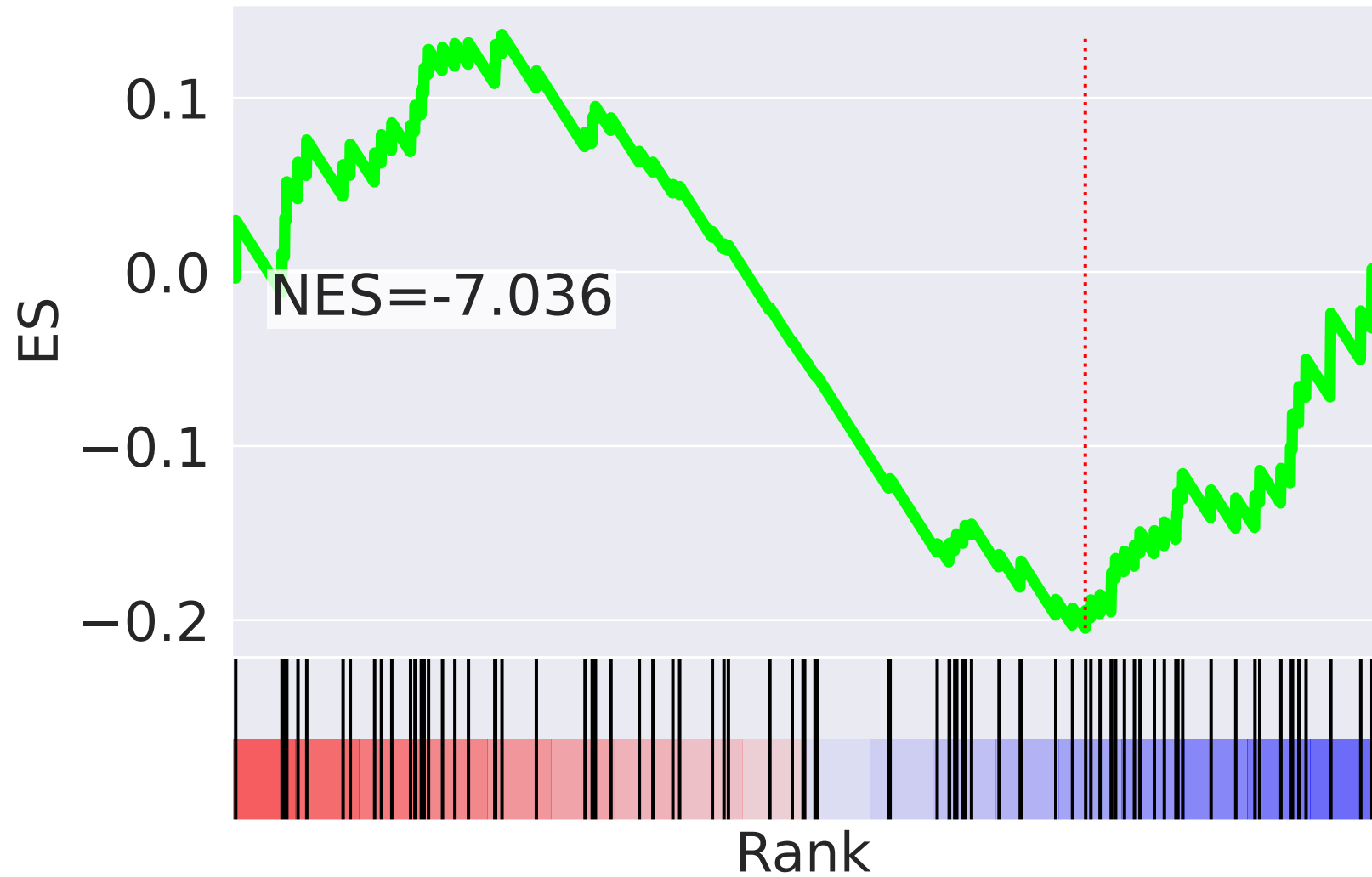
-2.841		protein complex assembly (GO:0006461)
-2.721		generation of precursor metabolites and energy (GO:0006091)
2.710		protein import into nucleus (GO:0006606)
-2.609		base-excision repair (GO:0006284)
-2.577		negative regulation of phosphatase activity (GO:0010923)
-2.506		Golgi organization (GO:0007030)
-2.436		Ras protein signal transduction (GO:0007265)
-2.433		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
-2.390		cellular response to oxidative stress (GO:0034599)
2.386		nucleobase-containing small molecule interconversion (GO:0015949)
-2.366		execution phase of apoptosis (GO:0097194)
-2.353		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
-2.326		mismatch repair (GO:0006298)
2.247		transmembrane transport (GO:0055085)
2.246		nucleocytoplasmic transport (GO:0006913)

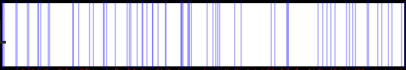
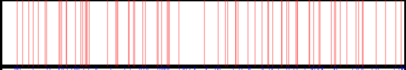
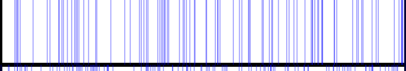
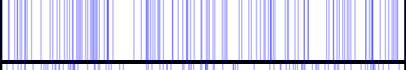
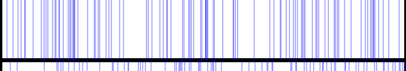
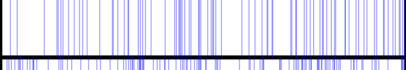
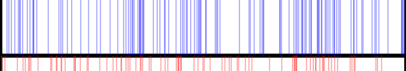
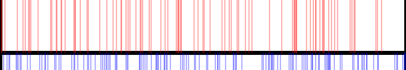
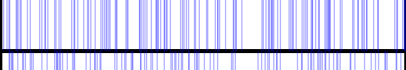
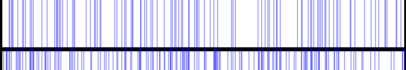
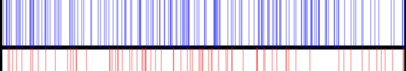
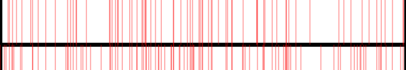
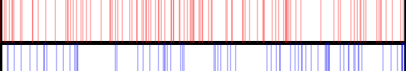
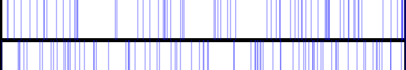
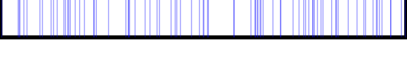
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=16$

mitochondrial translational elongation (GO:0070125)



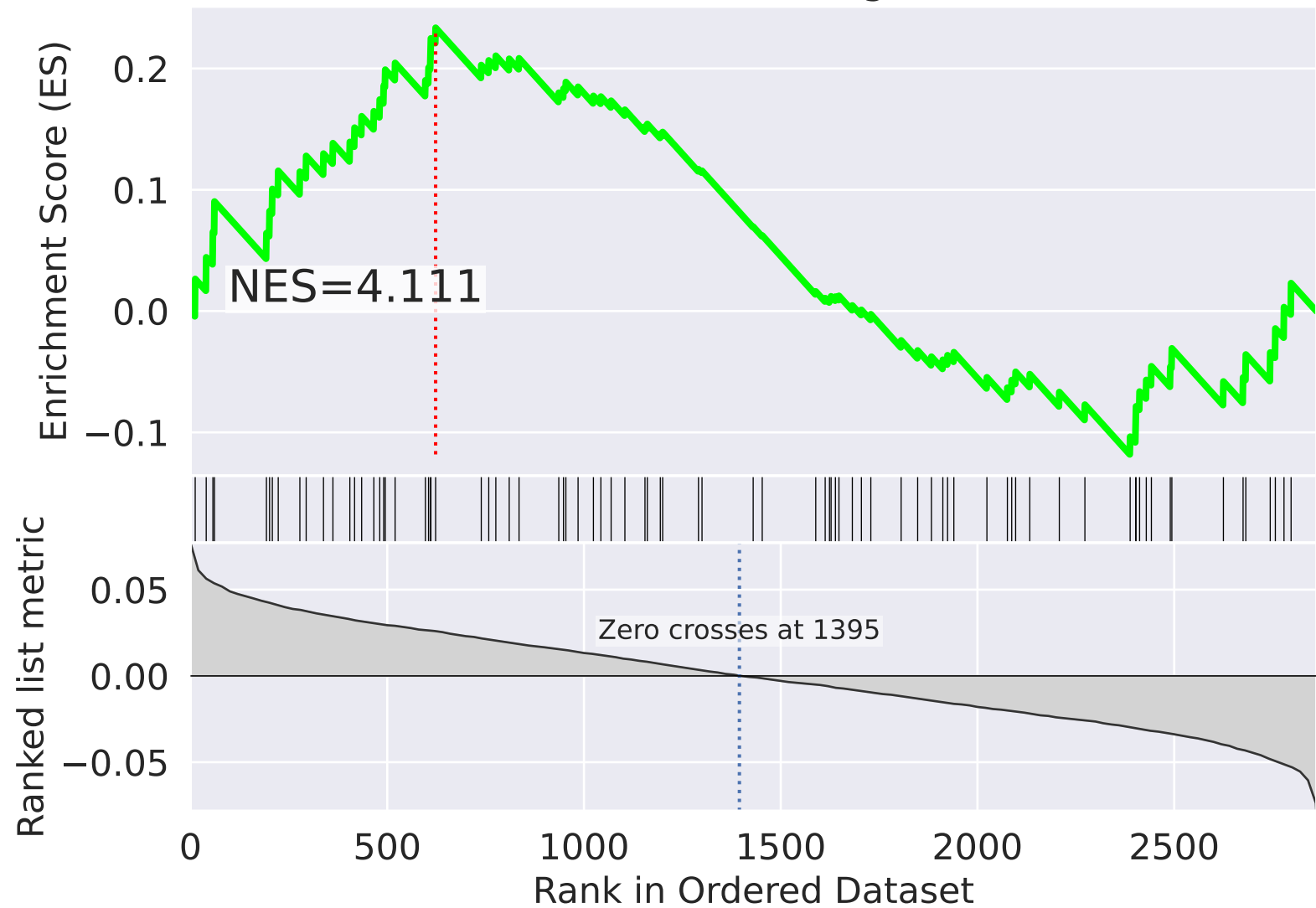
mitochondrial translational elongation (GO:0070125)



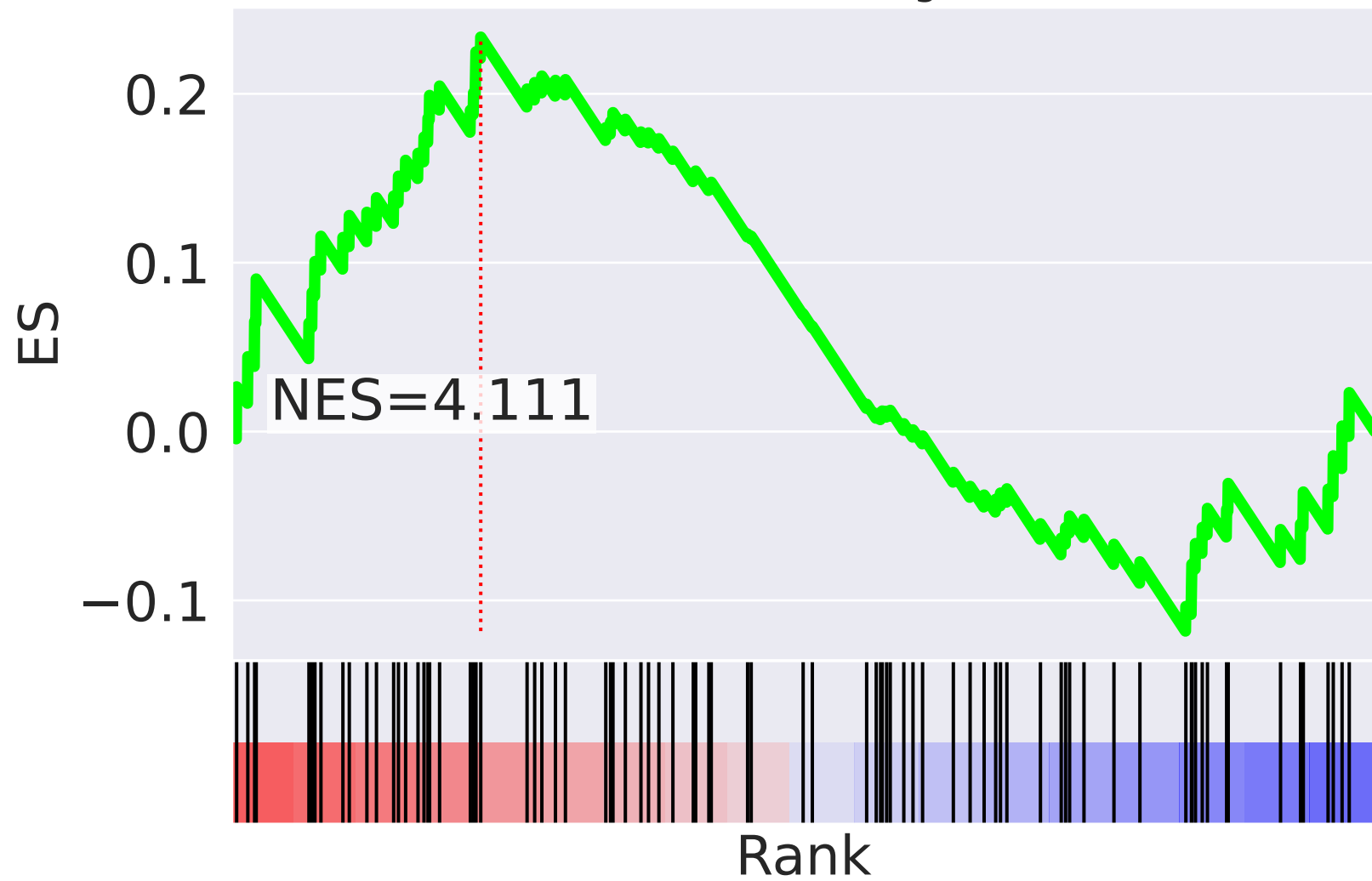
NES		SET
-12.441		protein phosphorylation (GO:0006468)
inf		protein ubiquitination (GO:0016567)
-9.336		negative regulation of transcription, DNA-templated (GO:0045892)
-9.127		mRNA splicing, via spliceosome (GO:0000398)
-8.819		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-8.648		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-8.605		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
inf		neutrophil degranulation (GO:0043312)
-8.263		positive regulation of transcription, DNA-templated (GO:0045893)
-8.142		transcription from RNA polymerase II promoter (GO:0006366)
-8.009		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
7.992		viral transcription (GO:0019083)
7.855		rRNA processing (GO:0006364)
-7.794		regulation of transcription, DNA-templated (GO:0006355)
-7.175		mitochondrial translational termination (GO:0070126)


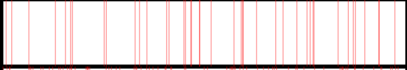
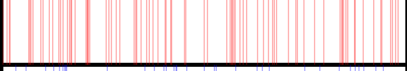
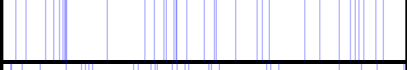
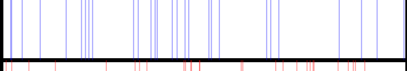
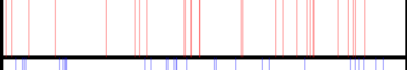
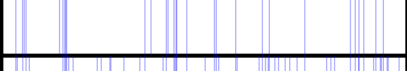
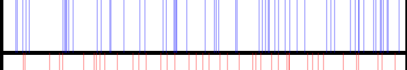
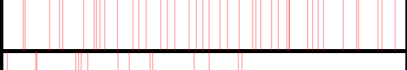
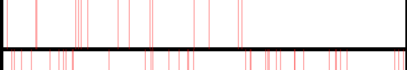
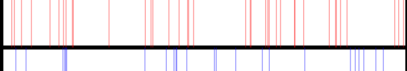
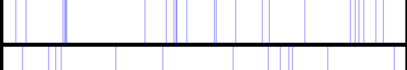
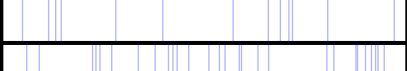
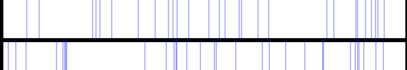
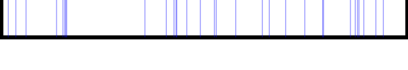
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=17$

mitochondrial translational elongation (GO:0070125)



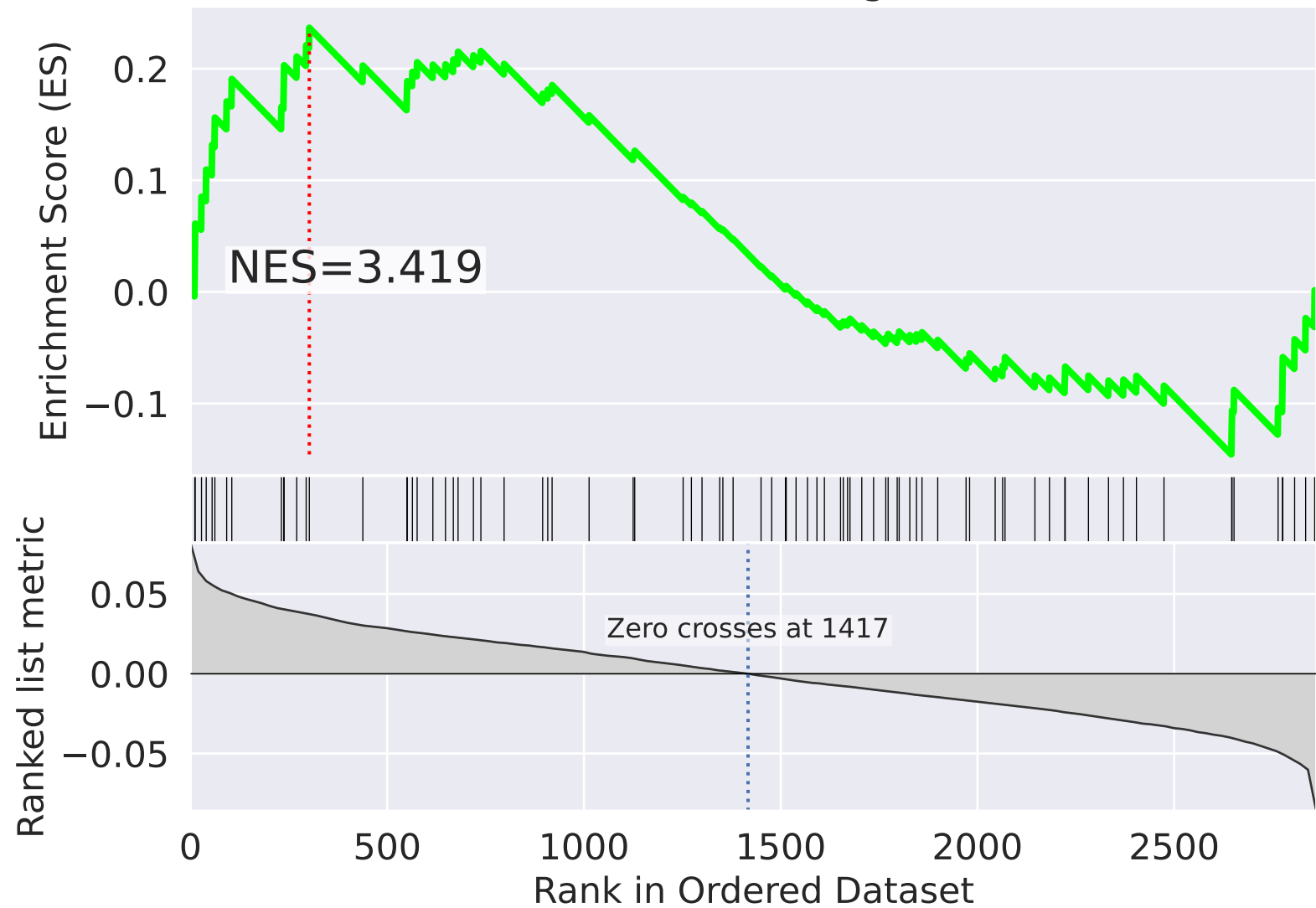
mitochondrial translational elongation (GO:0070125)



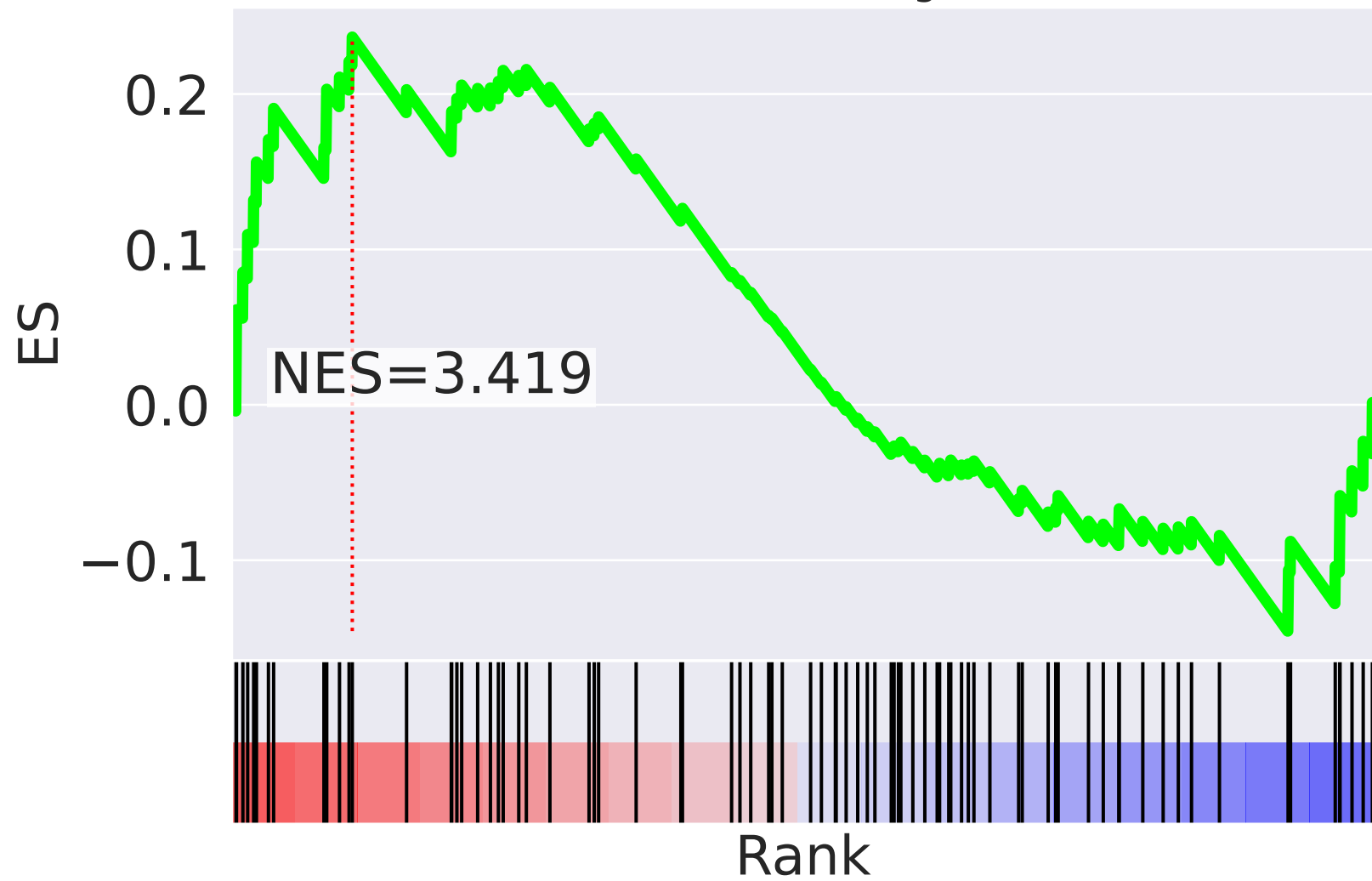
NES		SET
4.111		mitochondrial translational elongation (GO:0070125)
4.015		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.980		mitochondrial translational termination (GO:0070126)
-3.424		regulation of gene silencing by miRNA (GO:0060964)
-3.298		phosphatidylinositol-mediated signaling (GO:0048015)
3.140		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-3.082		viral process (GO:0016032)
-3.056		mRNA export from nucleus (GO:0006406)
2.967		mitotic cell cycle (GO:0000278)
2.933		telomere maintenance (GO:0000723)
2.869		protein complex assembly (GO:0006461)
-2.823		regulation of glucose transport (GO:0010827)
-2.786		cellular response to lipopolysaccharide (GO:0071222)
-2.745		protein autophosphorylation (GO:0046777)
-2.739		mitotic nuclear envelope disassembly (GO:0007077)

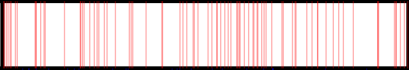
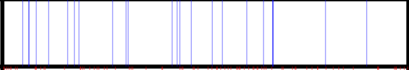
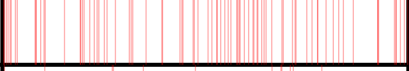

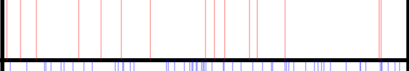
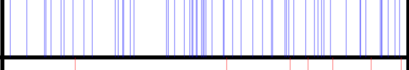
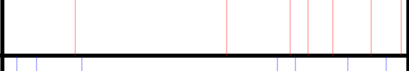
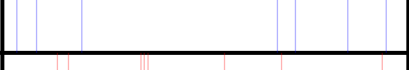




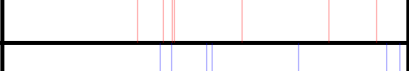


The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=18$

mitochondrial translational elongation (GO:0070125)



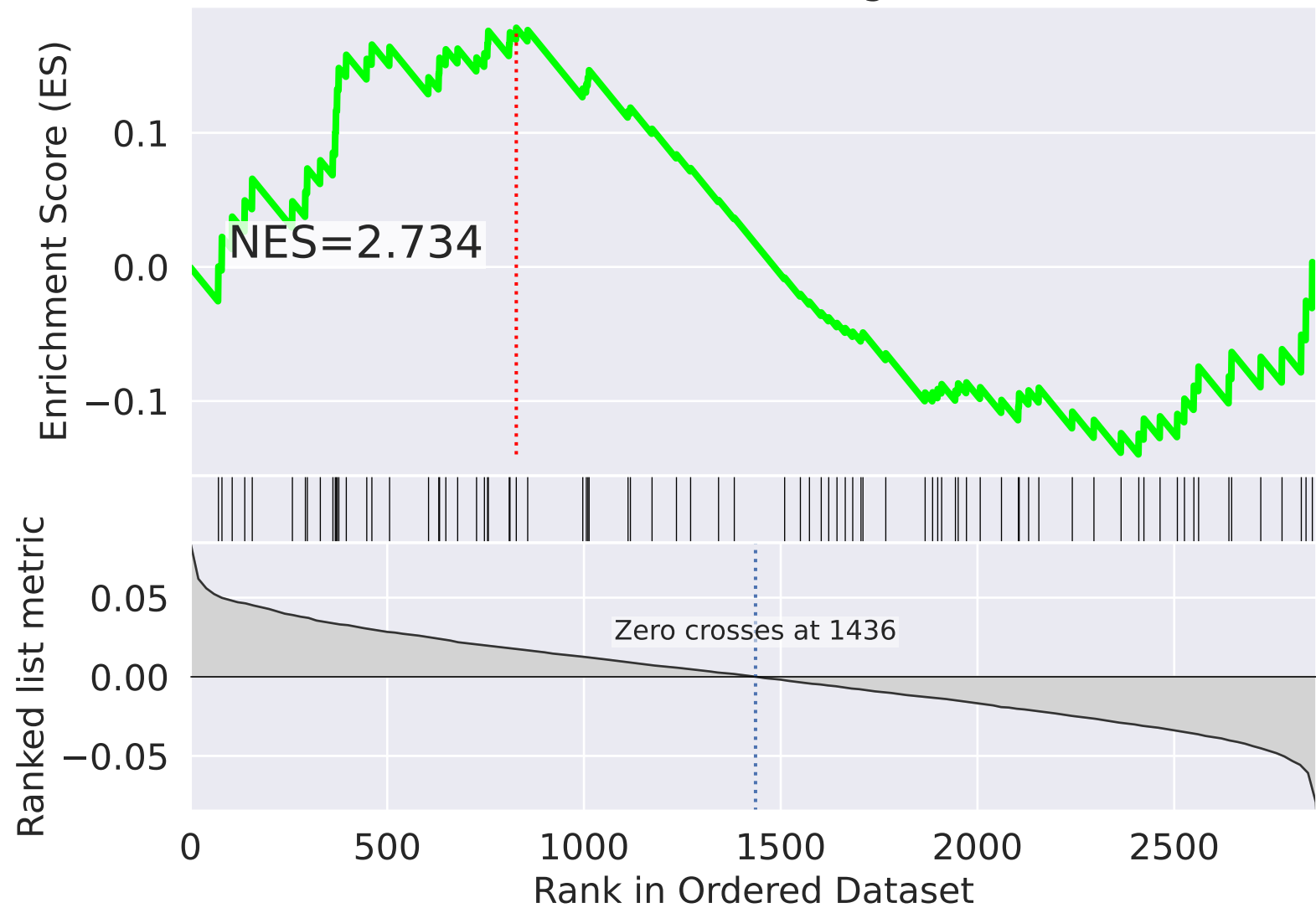
mitochondrial translational elongation (GO:0070125)



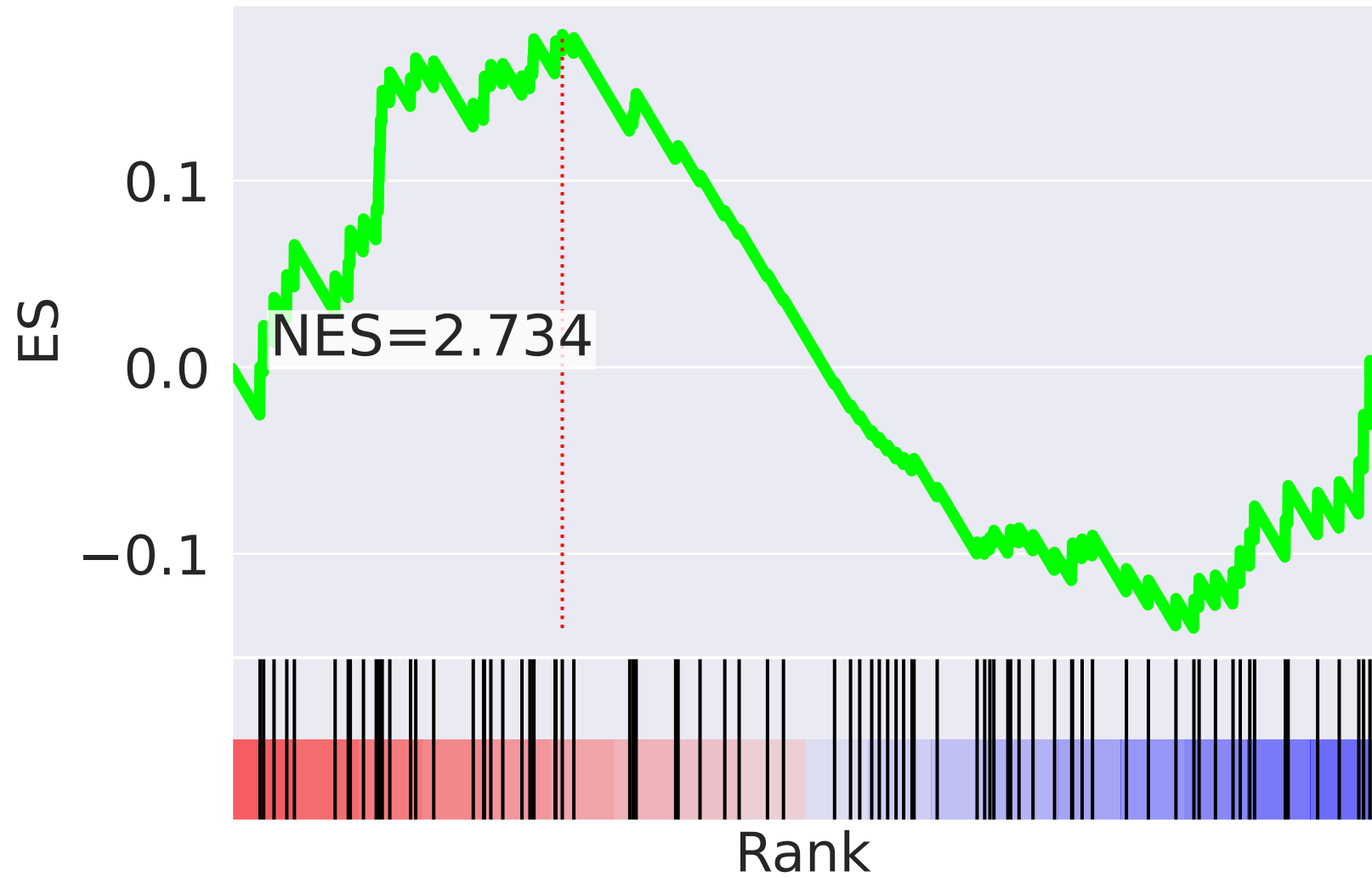
NES		SET
3.419		mitochondrial translational elongation (GO:0070125)
-3.274		COPII vesicle coating (GO:0048208)
3.105		mitochondrial translational termination (GO:0070126)
2.818		stress-activated MAPK cascade (GO:0051403)
2.796		positive regulation of protein ubiquitination (GO:0031398)
-2.777		mRNA export from nucleus (GO:0006406)
2.718		regulation of endocytosis (GO:0030100)
-2.617		metaphase plate congression (GO:0051310)
2.612		protein glycosylation (GO:0006486)
2.513		regulation of cell growth (GO:0001558)
2.499		cell differentiation (GO:0030154)
2.495		global genome nucleotide-excision repair (GO:0070911)
2.493		protein import into peroxisome matrix (GO:0016558)
-2.451		positive regulation of osteoblast differentiation (GO:0045669)
-2.424		beta-catenin-TCF complex assembly (GO:1904837)

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)


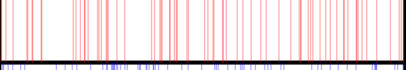
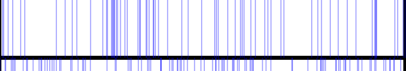
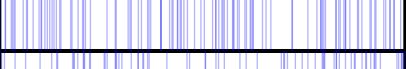
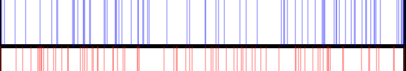
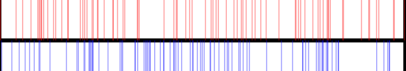
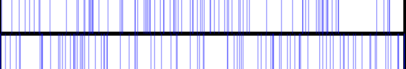
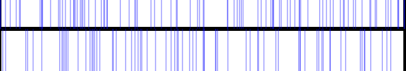
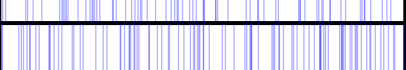
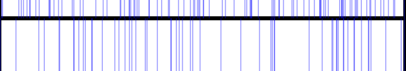
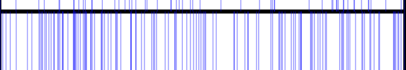
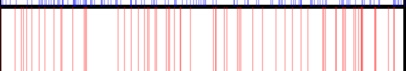

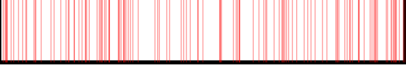



mitochondrial translational elongation (GO:0070125)



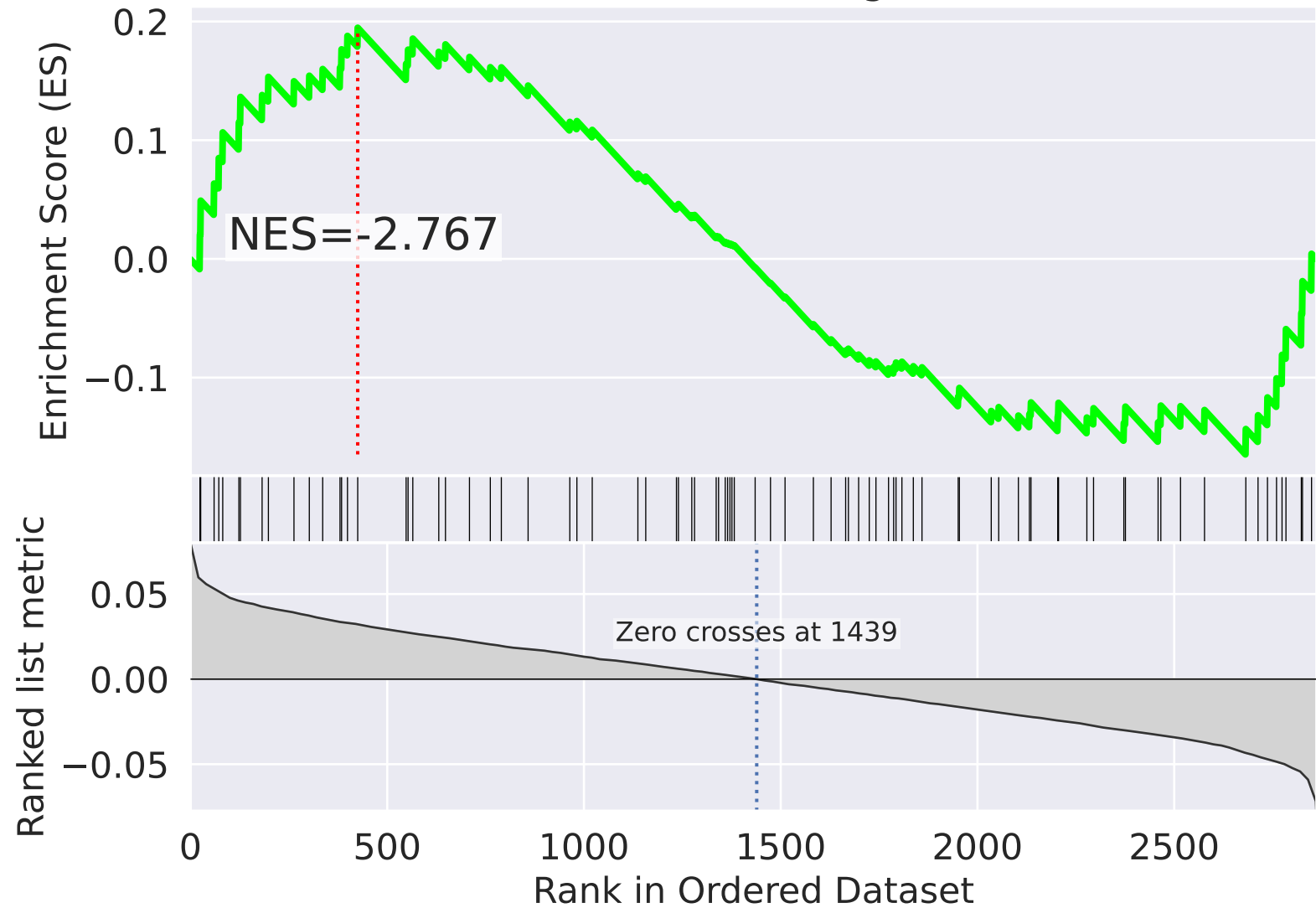
NES

SET

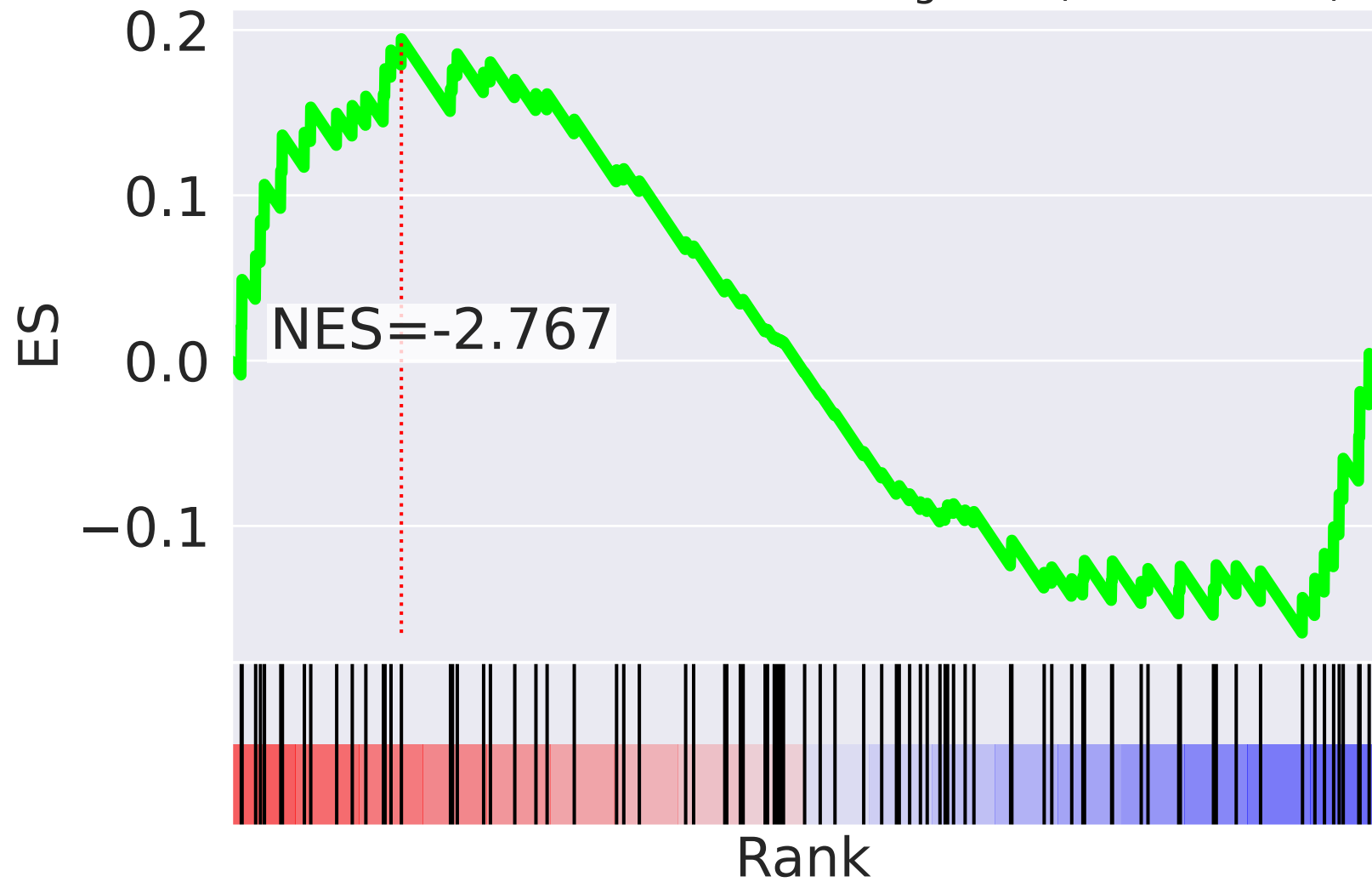
5.610		MAPK cascade (GO:0000165)
5.515		positive regulation of cell proliferation (GO:0008284)
-5.363		sister chromatid cohesion (GO:0007062)
-5.239		transcription from RNA polymerase II promoter (GO:0006366)
-4.645		regulation of signal transduction by p53 class mediator (GO:1901796)
4.425		negative regulation of apoptotic process (GO:0043066)
-4.344		neutrophil degranulation (GO:0043312)
-4.285		negative regulation of transcription, DNA-templated (GO:0045892)
-3.969		protein ubiquitination (GO:0016567)
-3.922		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-3.727		negative regulation of cell proliferation (GO:0008285)
-3.705		positive regulation of transcription, DNA-templated (GO:0045893)
3.699		transcription initiation from RNA polymerase II promoter (GO:0006367)
3.583		protein polyubiquitination (GO:0000209)
3.430		mRNA splicing, via spliceosome (GO:0000398)

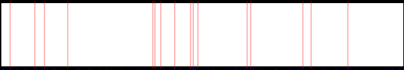
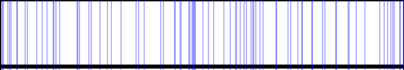
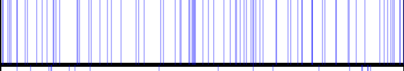




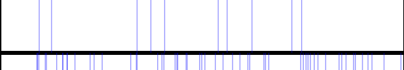
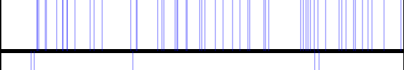
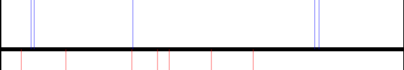



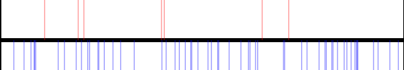

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=20$

mitochondrial translational elongation (GO:0070125)



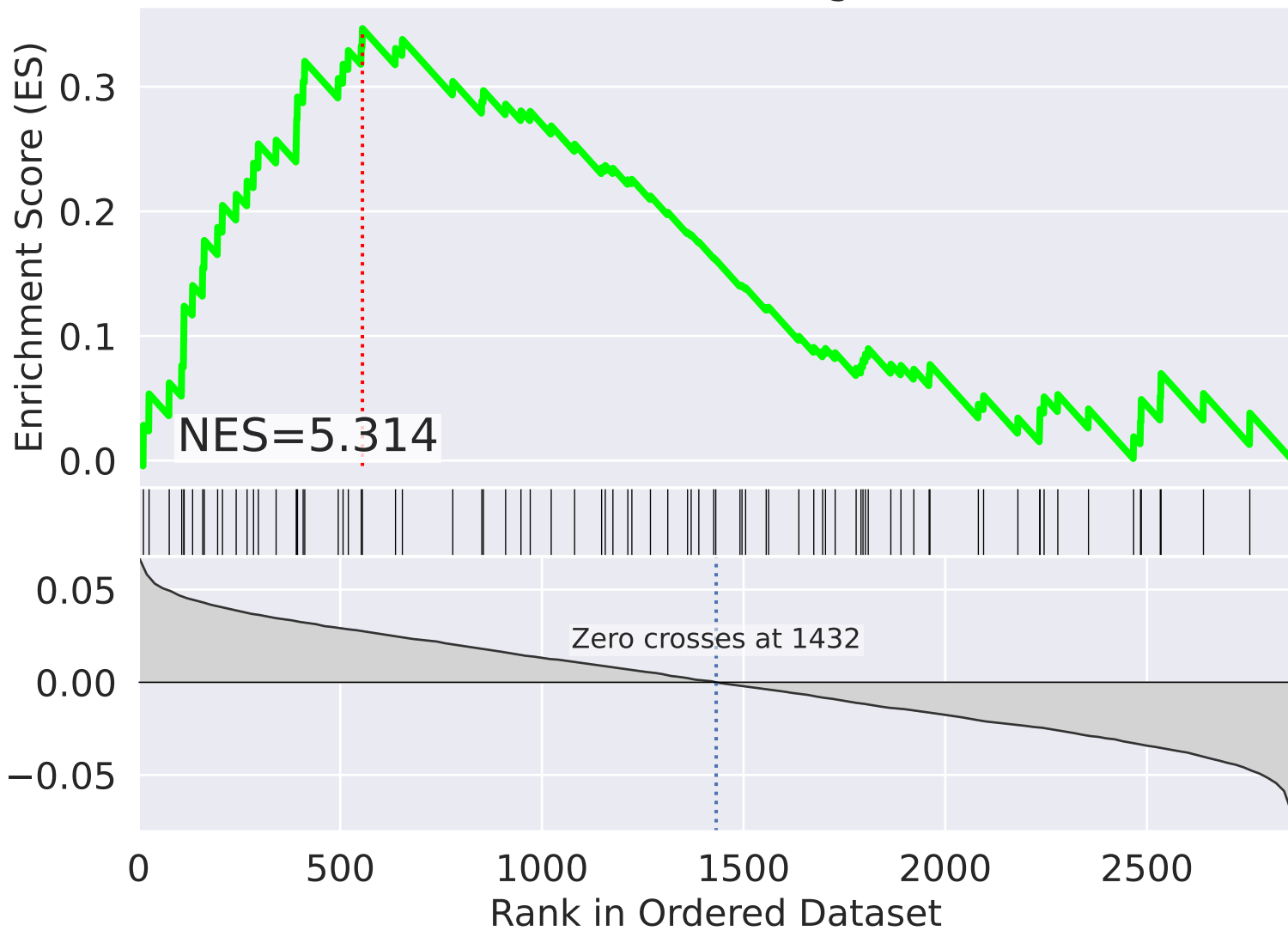
mitochondrial translational elongation (GO:0070125)



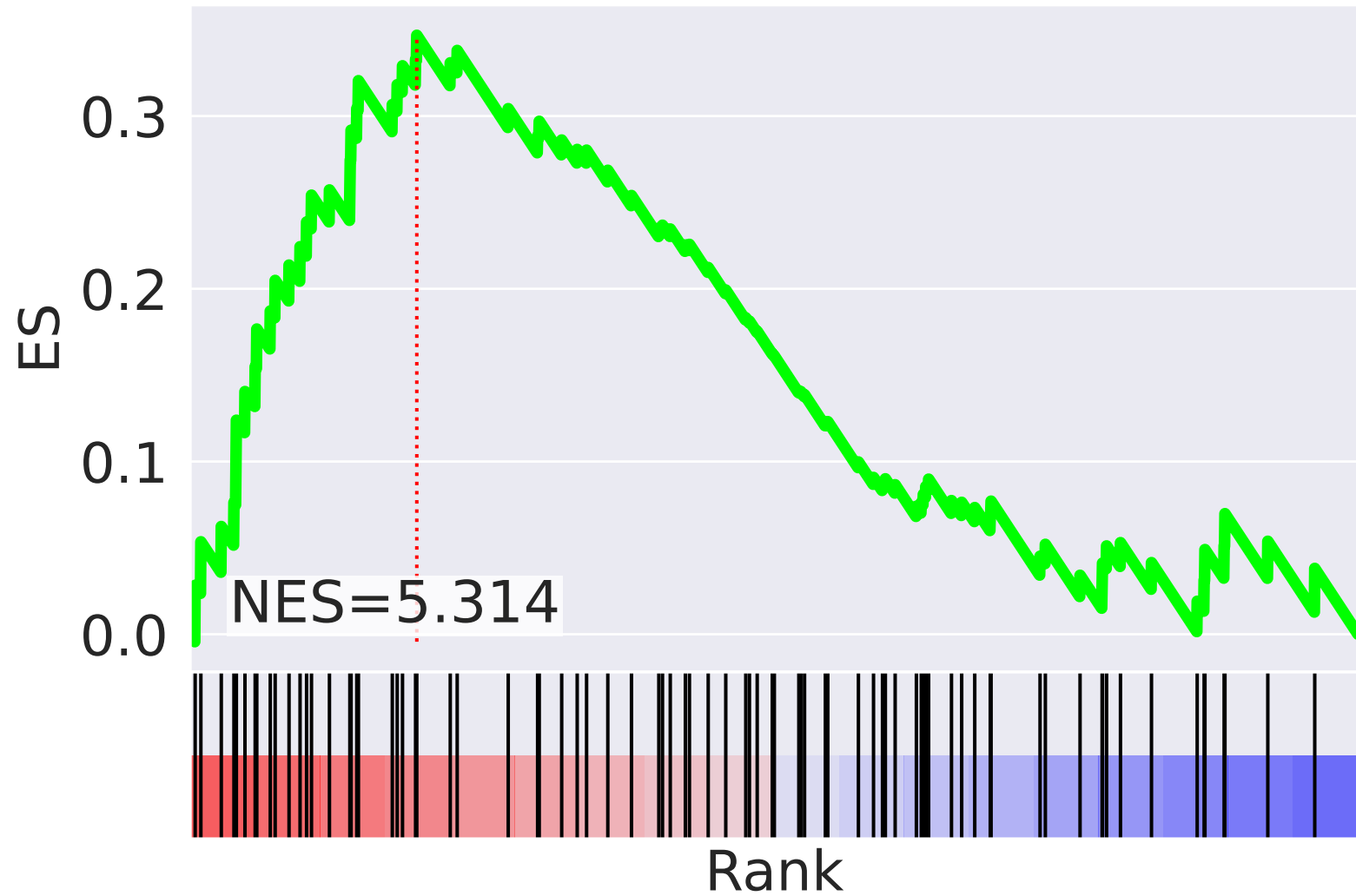
NES		SET
2.837		cellular response to oxidative stress (GO:0034599)
-2.767		mitochondrial translational elongation (GO:0070125)
-2.741		mitochondrial translational termination (GO:0070126)
-2.731		positive regulation of GTPase activity (GO:0043547)
-2.593		cellular response to mechanical stimulus (GO:0071260)
-2.469		nucleosome assembly (GO:0006334)
-2.419		protein import into mitochondrial matrix (GO:0030150)
-2.406		bicellular tight junction assembly (GO:0070830)
-2.385		membrane organization (GO:0061024)
-2.384		negative regulation of telomerase activity (GO:0051974)
2.384		negative regulation of gene expression, epigenetic (GO:0045814)
-2.285		mitotic G2 DNA damage checkpoint (GO:0007095)
-2.259		cellular senescence (GO:0090398)
2.243		mitochondrial transport (GO:0006839)
-2.165		negative regulation of cell proliferation (GO:0008285)


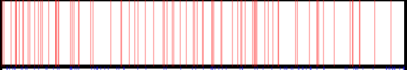
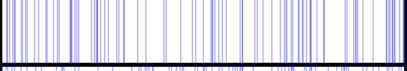
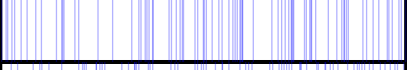
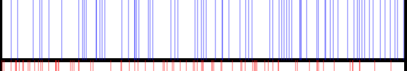
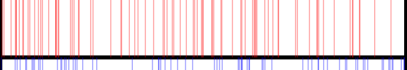
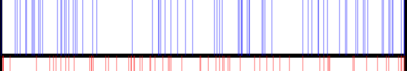
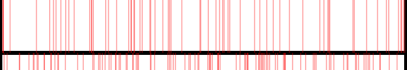
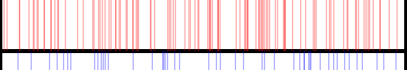
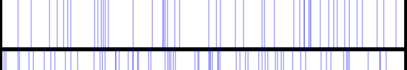
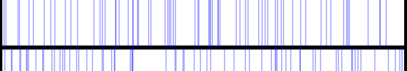
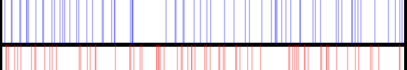
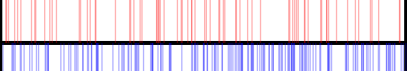
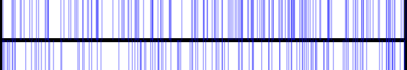

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=21$

mitochondrial translational elongation (GO:0070125)



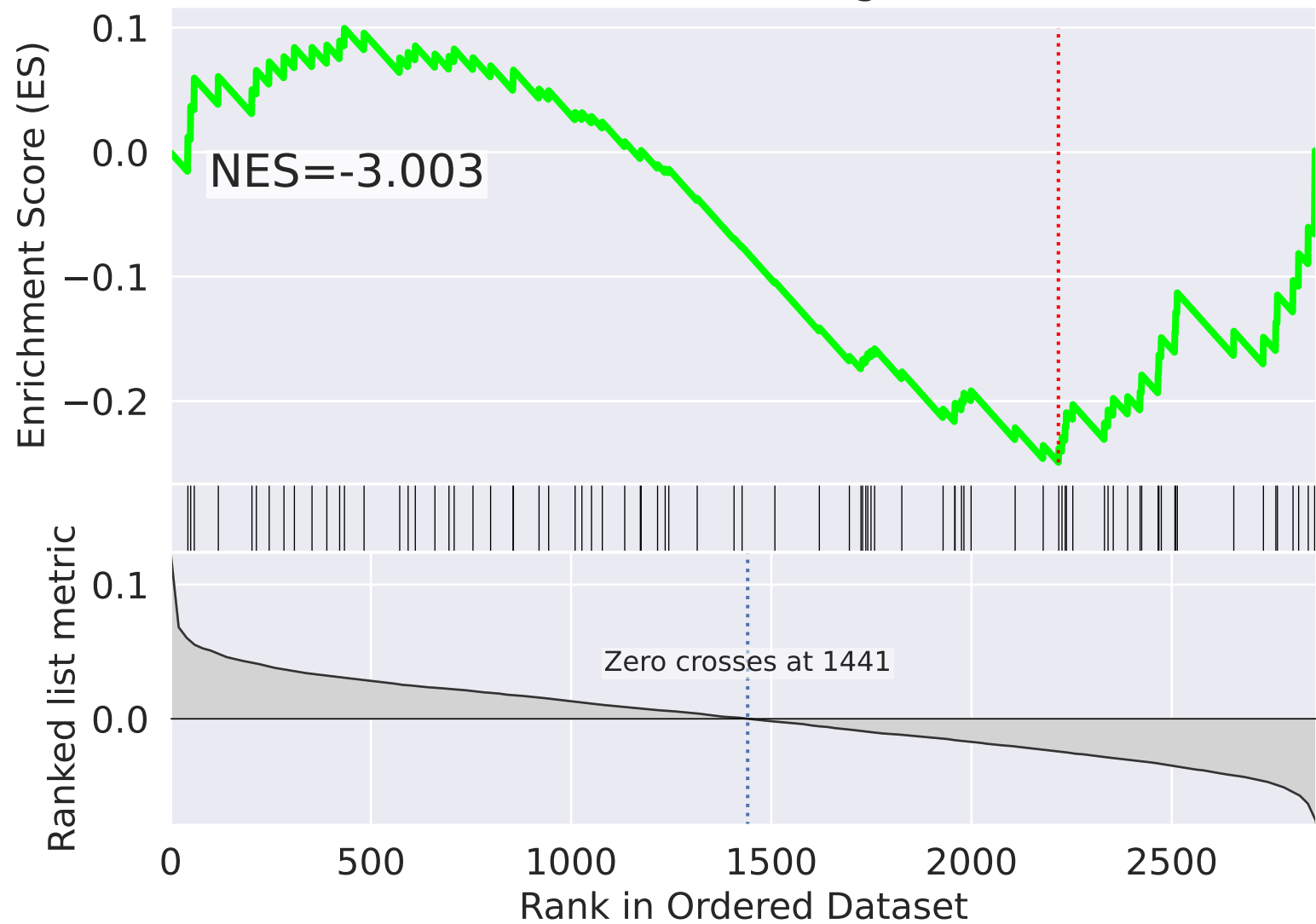
mitochondrial translational elongation (GO:0070125)



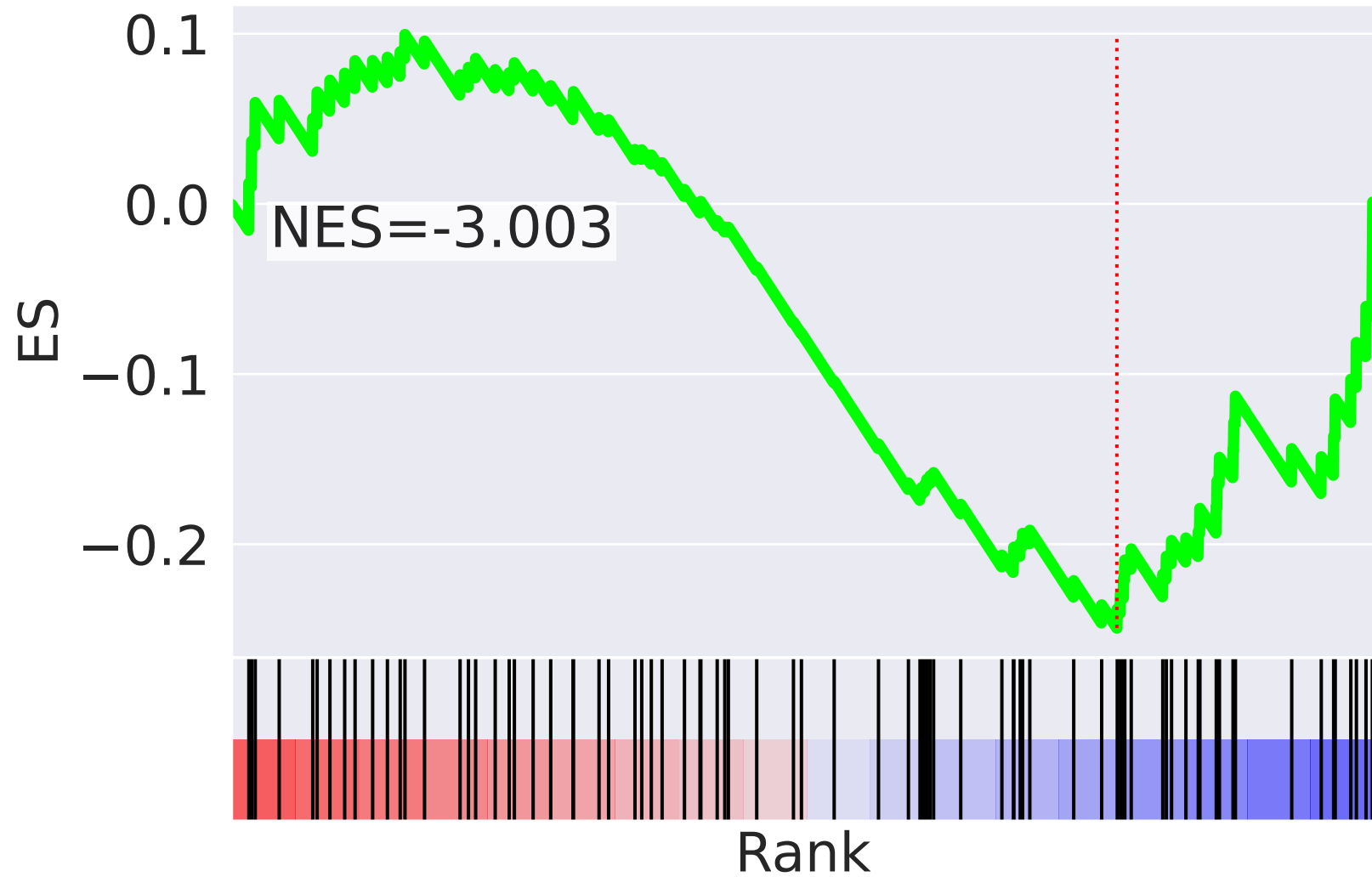
NES		SET
-5.842		mRNA splicing, via spliceosome (GO:0000398)
5.314		mitochondrial translational elongation (GO:0070125)
-5.277		negative regulation of transcription, DNA-templated (GO:0045892)
-5.248		negative regulation of apoptotic process (GO:0043066)
-5.151		protein ubiquitination (GO:0016567)
5.032		mitochondrial translational termination (GO:0070126)
-4.943		regulation of transcription, DNA-templated (GO:0006355)
4.735		transcription initiation from RNA polymerase II promoter (GO:0006367)
4.048		rRNA processing (GO:0006364)
-3.727		RNA splicing (GO:0008380)
-3.717		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-3.630		sister chromatid cohesion (GO:0007062)
3.600		MAPK cascade (GO:0000165)
-3.316		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
-3.280		positive regulation of transcription, DNA-templated (GO:0045893)

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

mitochondrial translational elongation (GO:0070125)


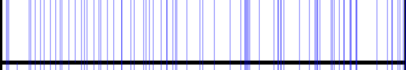
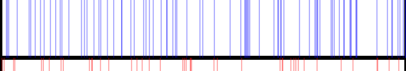
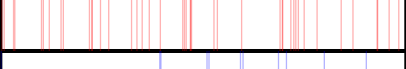


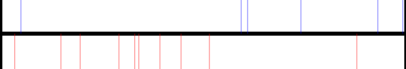
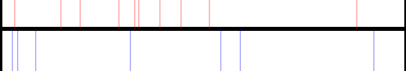









mitochondrial translational elongation (GO:0070125)



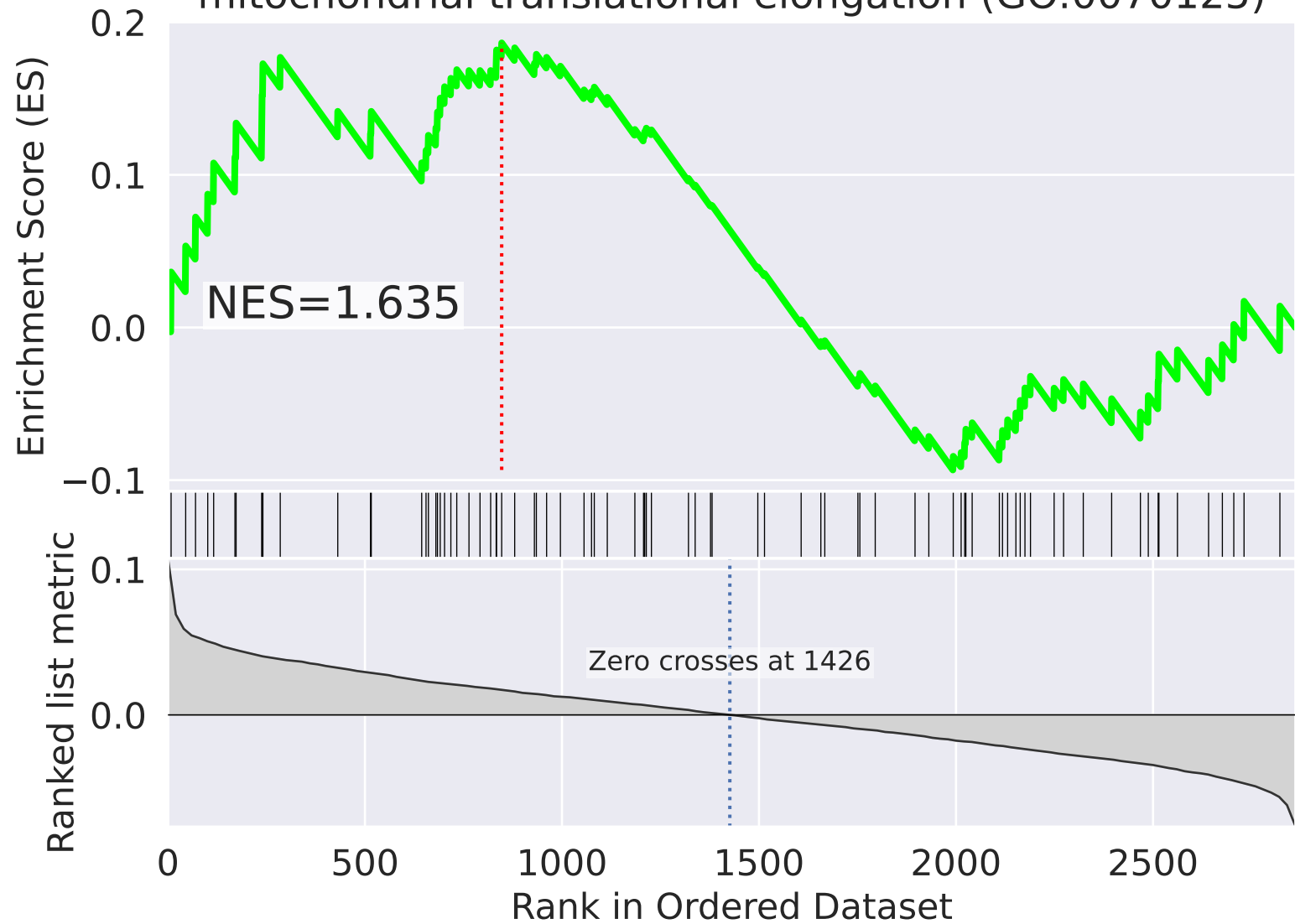
NES

SET

3.128		transcription elongation from RNA polymerase II promoter (GO:0006368)
-3.096		mitochondrial translational termination (GO:0070126)
-3.003		mitochondrial translational elongation (GO:0070125)
2.900		transmembrane transport (GO:0055085)
-2.888		protein K63-linked ubiquitination (GO:0070534)
-2.766		attachment of spindle microtubules to kinetochore (GO:0008608)
-2.653		anoikis (GO:0043276)
2.608		bicellular tight junction assembly (GO:0070830)
-2.605		metaphase plate congression (GO:0051310)
-2.586		t-circle formation (GO:0090656)
-2.580		sister chromatid cohesion (GO:0007062)
-2.564		I-kappaB kinase/NF-kappaB signaling (GO:0007249)
2.552		cellular response to lipopolysaccharide (GO:0071222)
2.531		negative regulation of mRNA polyadenylation (GO:1900364)
-2.519		pentose-phosphate shunt (GO:0006098)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

0.2
0.1
0.0
-0.1

NES=1.635

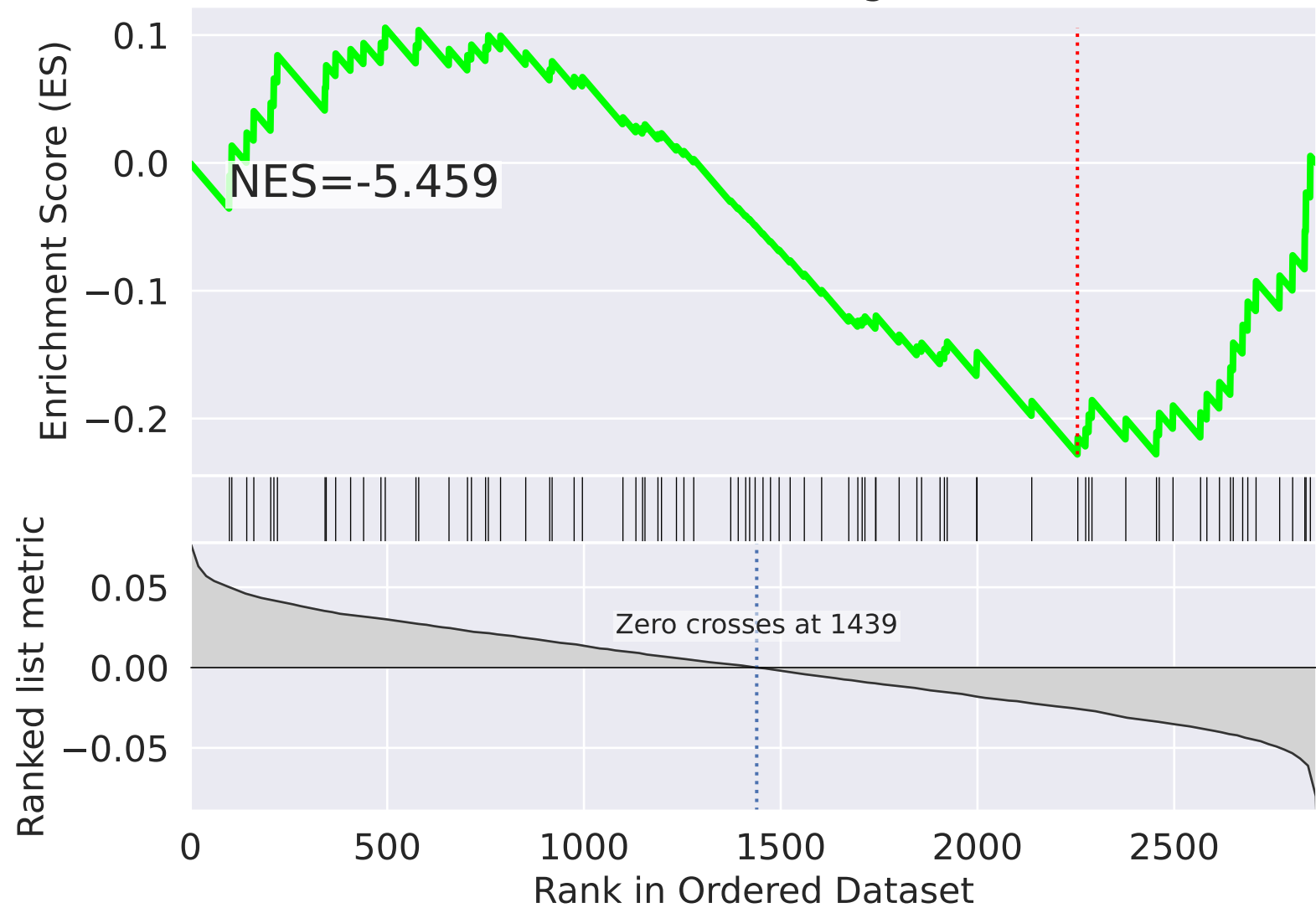
Rank



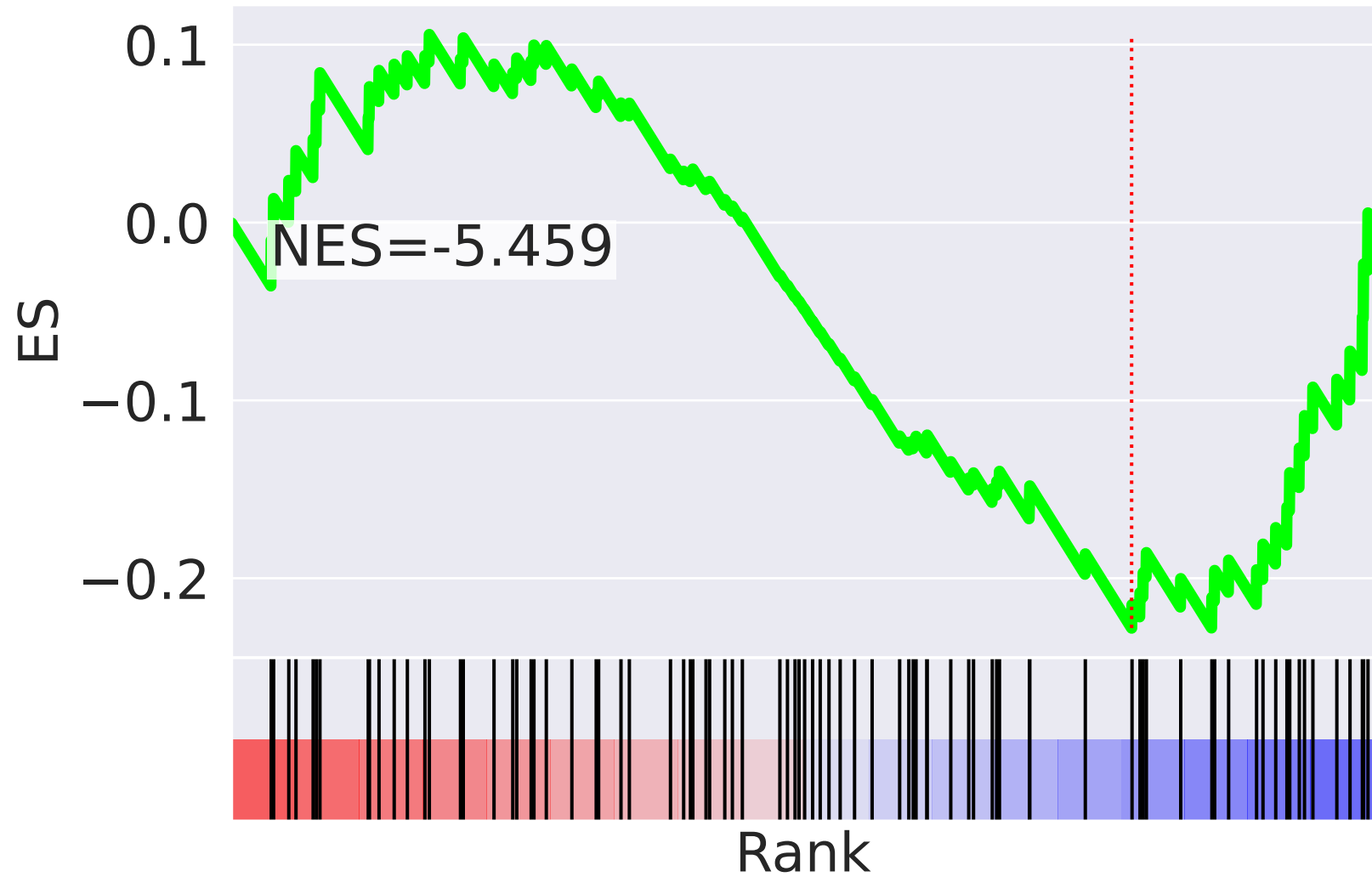
NES		SET
2.776		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
-2.724		cytokine-mediated signaling pathway (GO:0019221)
-2.592		positive regulation of epithelial cell migration (GO:0010634)
2.511		B cell receptor signaling pathway (GO:0050853)
2.489		positive regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032436)
-2.448		cytoplasmic microtubule organization (GO:0031122)
-2.421		response to interleukin-1 (GO:0070555)
2.399		cellular calcium ion homeostasis (GO:0006874)
2.382		multicellular organism development (GO:0007275)
-2.369		spindle organization (GO:0007051)
-2.351		regulation of GTPase activity (GO:0043087)
-2.325		negative regulation of extrinsic apoptotic signaling pathway (GO:2001237)
2.316		ion transmembrane transport (GO:0034220)
2.267		humoral immune response (GO:0006959)
2.262		negative regulation of protein kinase B signaling (GO:0051898)

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)

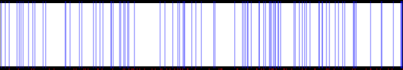
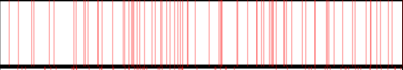
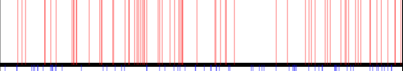
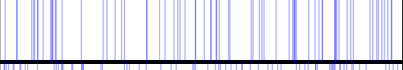
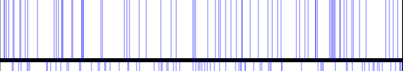
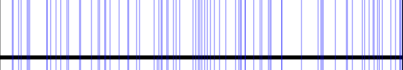
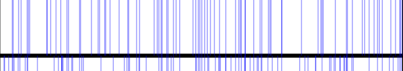
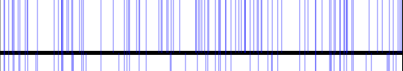
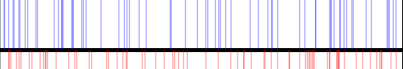
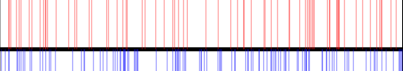
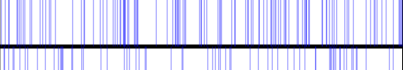
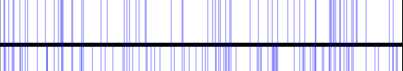
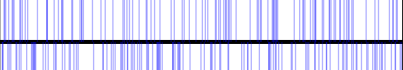
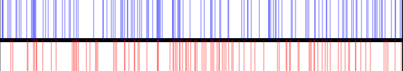



mitochondrial translational elongation (GO:0070125)



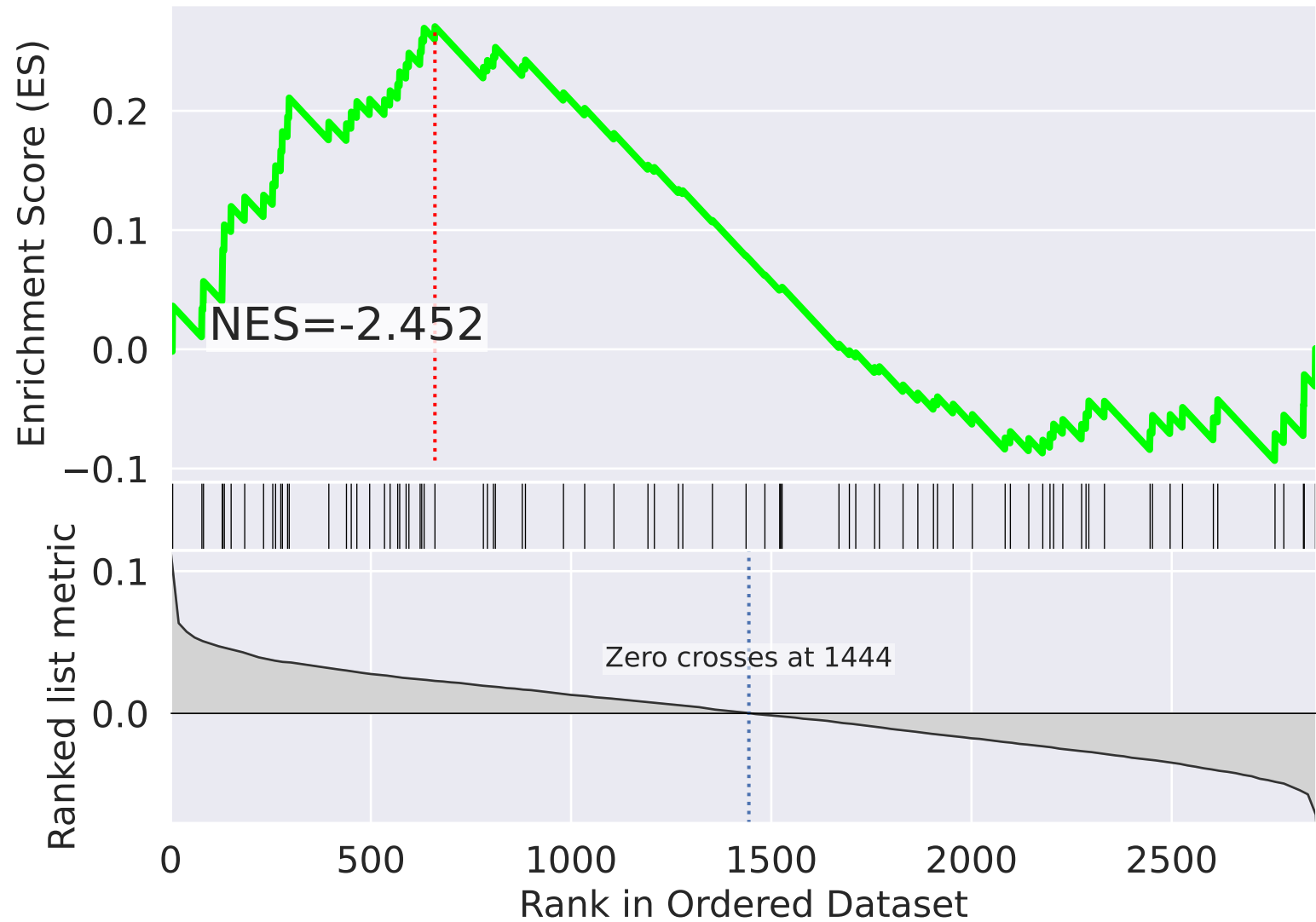
NES

SET

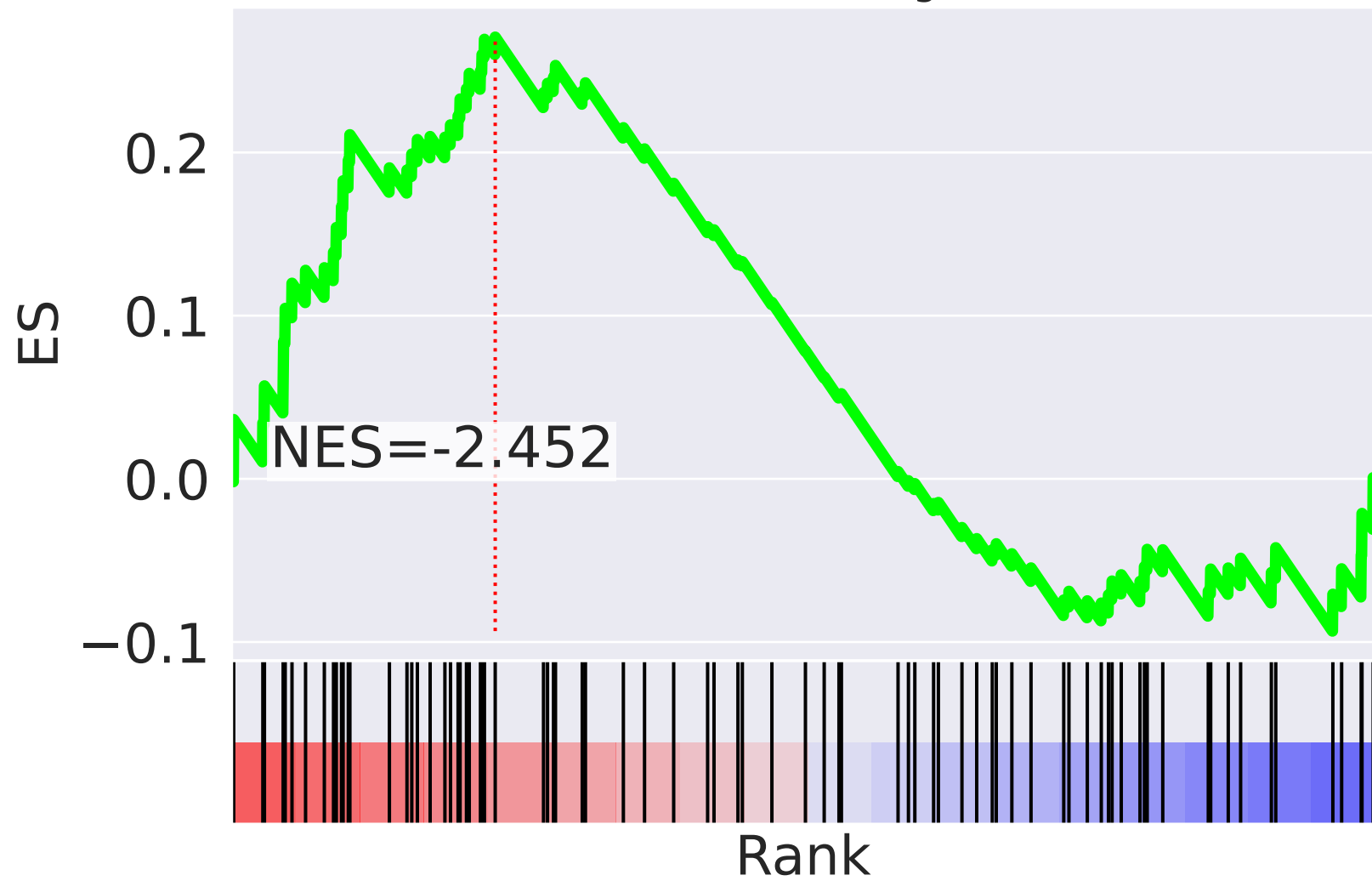
-6.468		negative regulation of transcription, DNA-templated (GO:0045892)
6.202		regulation of signal transduction by p53 class mediator (GO:1901796)
6.200		protein phosphorylation (GO:0006468)
-5.853		regulation of transcription, DNA-templated (GO:0006355)
-5.517		viral transcription (GO:0019083)
-5.459		mitochondrial translational elongation (GO:0070125)
-5.416		mitochondrial translational termination (GO:0070126)
-4.769		translation (GO:0006412)
-4.596		translational initiation (GO:0006413)
4.502		positive regulation of cell proliferation (GO:0008284)
-3.884		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
-3.870		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-3.619		rRNA processing (GO:0006364)
-3.422		positive regulation of transcription, DNA-templated (GO:0045893)
3.390		signal transduction (GO:0007165)

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

mitochondrial translational elongation (GO:0070125)





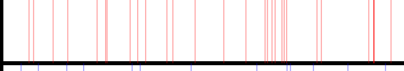
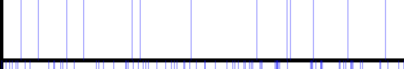
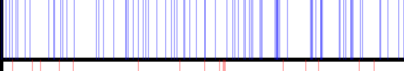
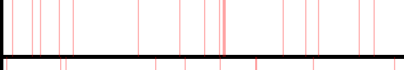

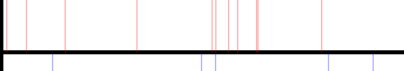
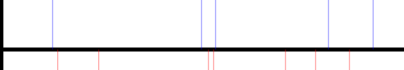
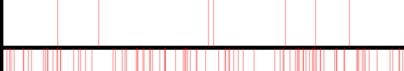
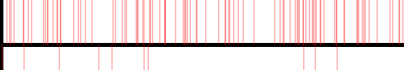




mitochondrial translational elongation (GO:0070125)



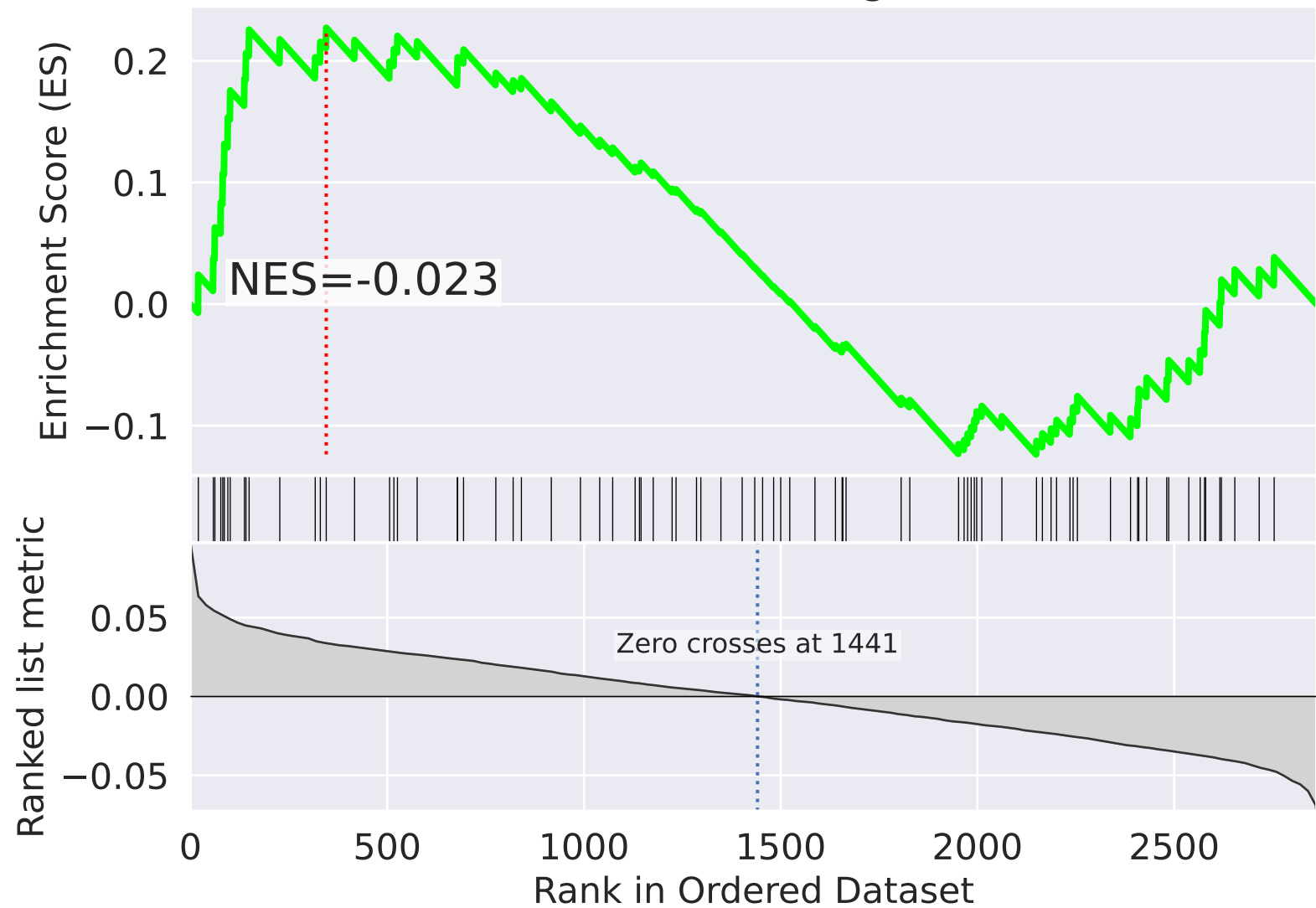
NES

SET

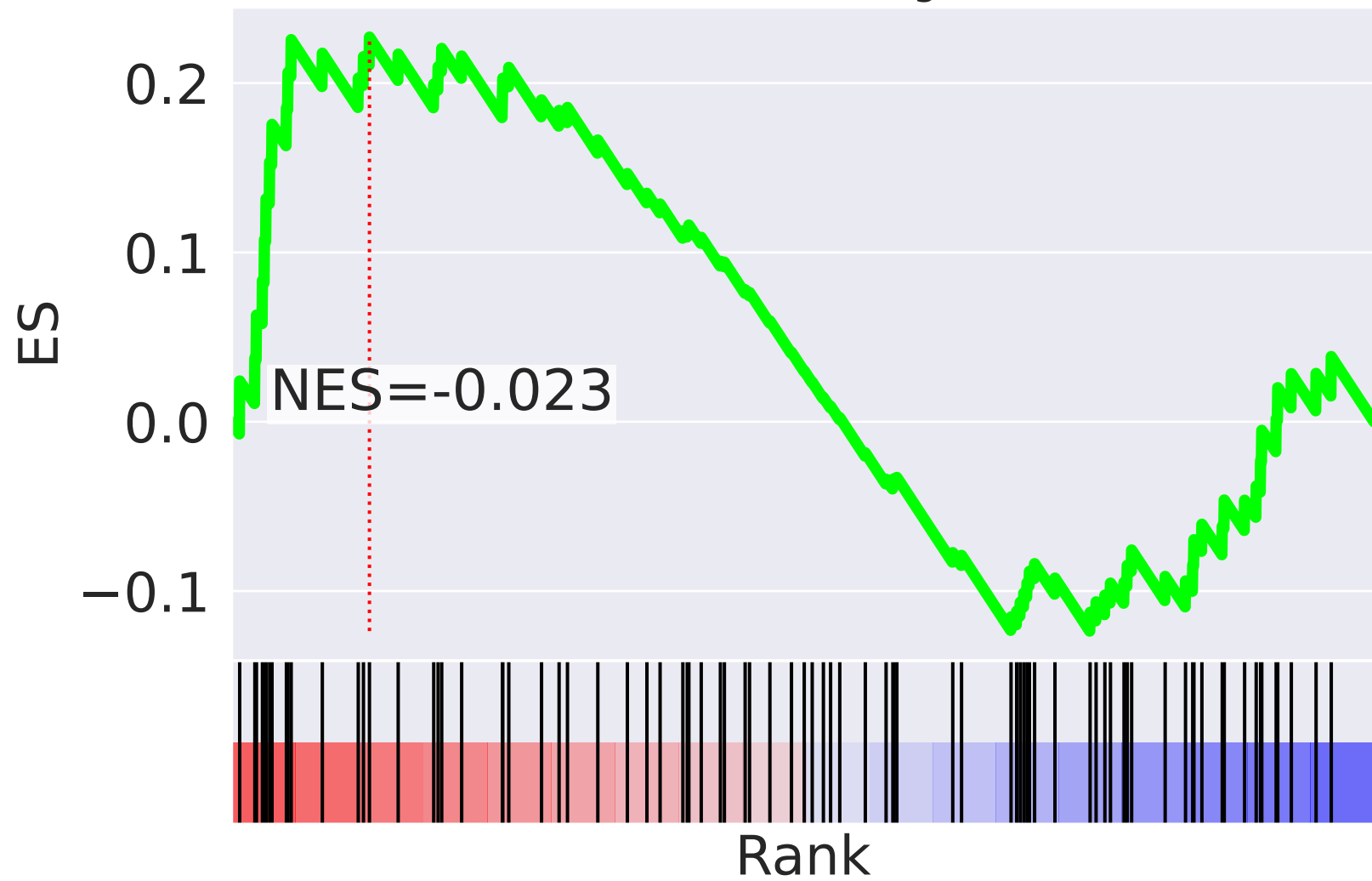
3.153		humoral immune response (GO:0006959)
2.934		regulation of autophagy (GO:0010506)
2.922		positive regulation of TOR signaling (GO:0032008)
2.884		interferon-gamma-mediated signaling pathway (GO:0060333)
2.835		RNA export from nucleus (GO:0006405)
-2.763		G-protein coupled receptor signaling pathway (GO:0007186)
-2.731		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
2.722		response to virus (GO:0009615)
2.681		negative regulation of protein kinase B signaling (GO:0051898)
2.661		negative regulation of cell migration (GO:0030336)
-2.632		fatty-acyl-CoA biosynthetic process (GO:0046949)
2.566		ossification (GO:0001503)
2.542		negative regulation of transcription, DNA-templated (GO:0045892)
2.533		negative regulation of neuron apoptotic process (GO:0043524)
-2.531		mitotic DNA replication checkpoint (GO:0033314)

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)



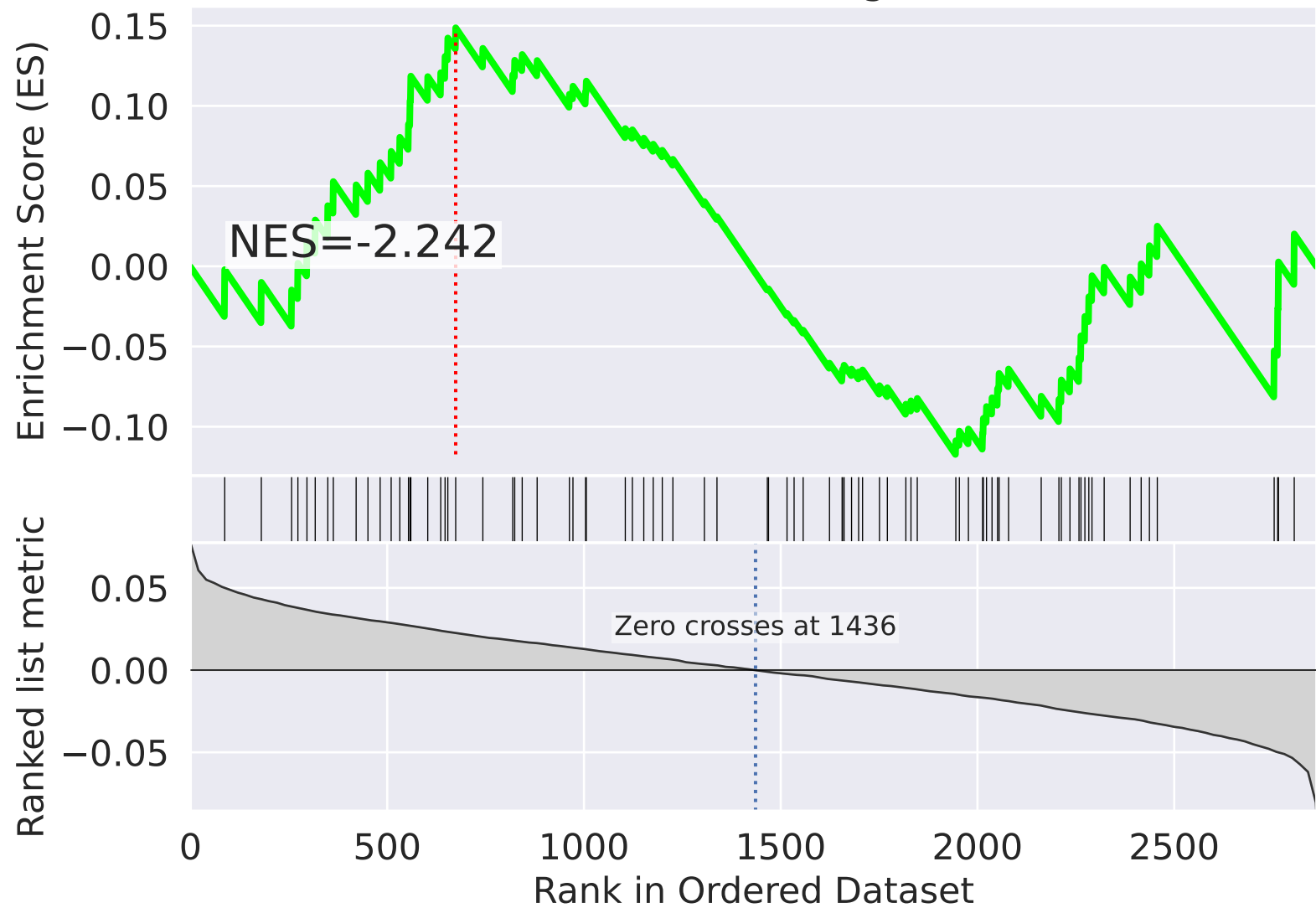
mitochondrial translational elongation (GO:0070125)



NES		SET
-2.796		activation of MAPKK activity (GO:0000186)
-2.406		bicellular tight junction assembly (GO:0070830)
-2.395		Arp2/3 complex-mediated actin nucleation (GO:0034314)
-2.363		mitotic G1 DNA damage checkpoint (GO:0031571)
2.360		glucose homeostasis (GO:0042593)
2.333		animal organ morphogenesis (GO:0009887)
-2.329		protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0042787)
-2.324		protein K69-linked ufmylation (GO:1990592)
2.303		positive regulation of protein serine/threonine kinase activity (GO:0071902)
2.300		nervous system development (GO:0007399)
2.282		low-density lipoprotein particle receptor catabolic process (GO:0032802)
-2.271		positive regulation of stress fiber assembly (GO:0051496)
-2.269		negative regulation of JAK-STAT cascade (GO:0046426)
-2.246		intrinsic apoptotic signaling pathway (GO:0097193)
-2.244		cell cycle checkpoint (GO:0000075)

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)



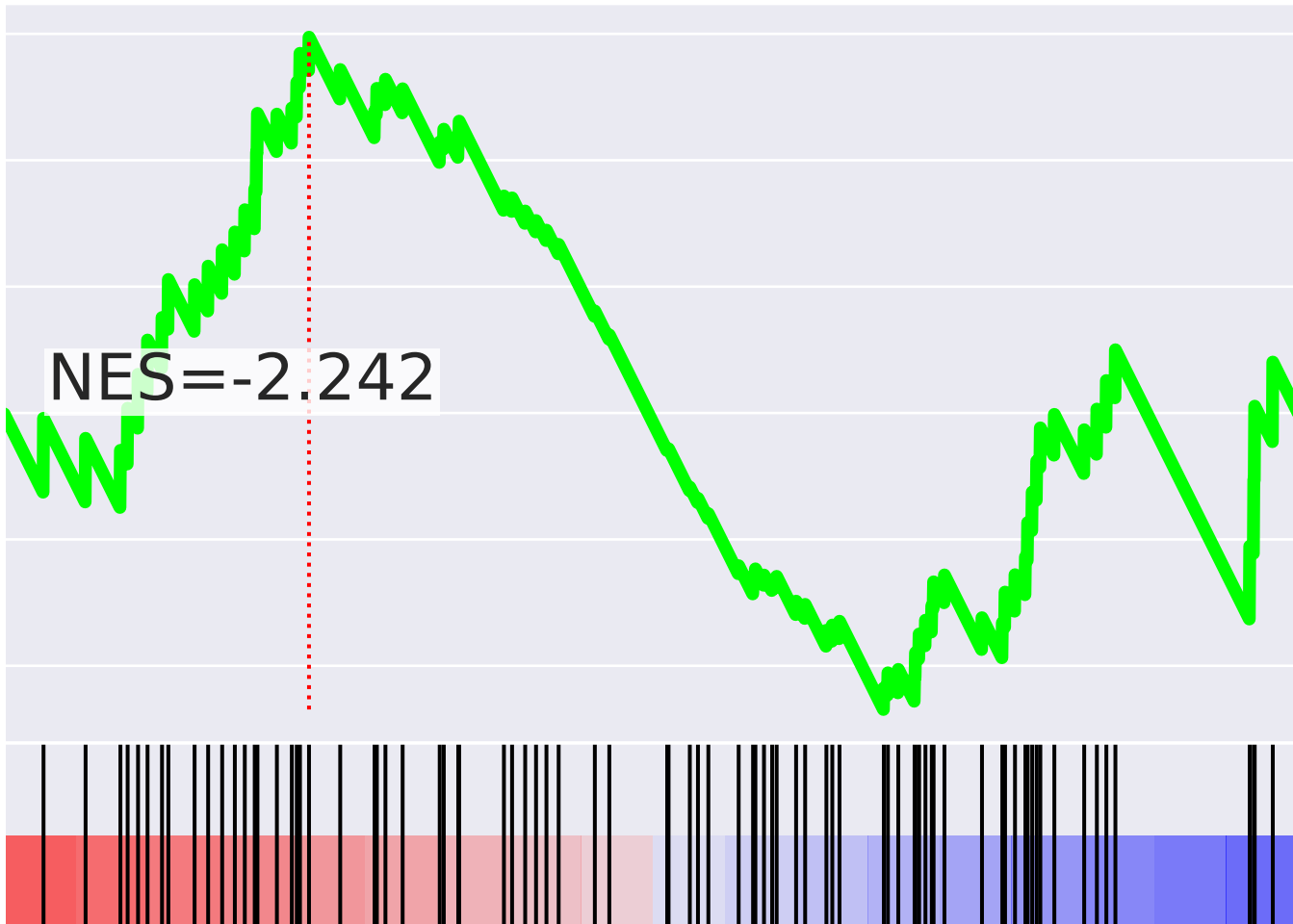
mitochondrial translational elongation (GO:0070125)

ES

0.15
0.10
0.05
0.00
-0.05
-0.10

NES=-2.242

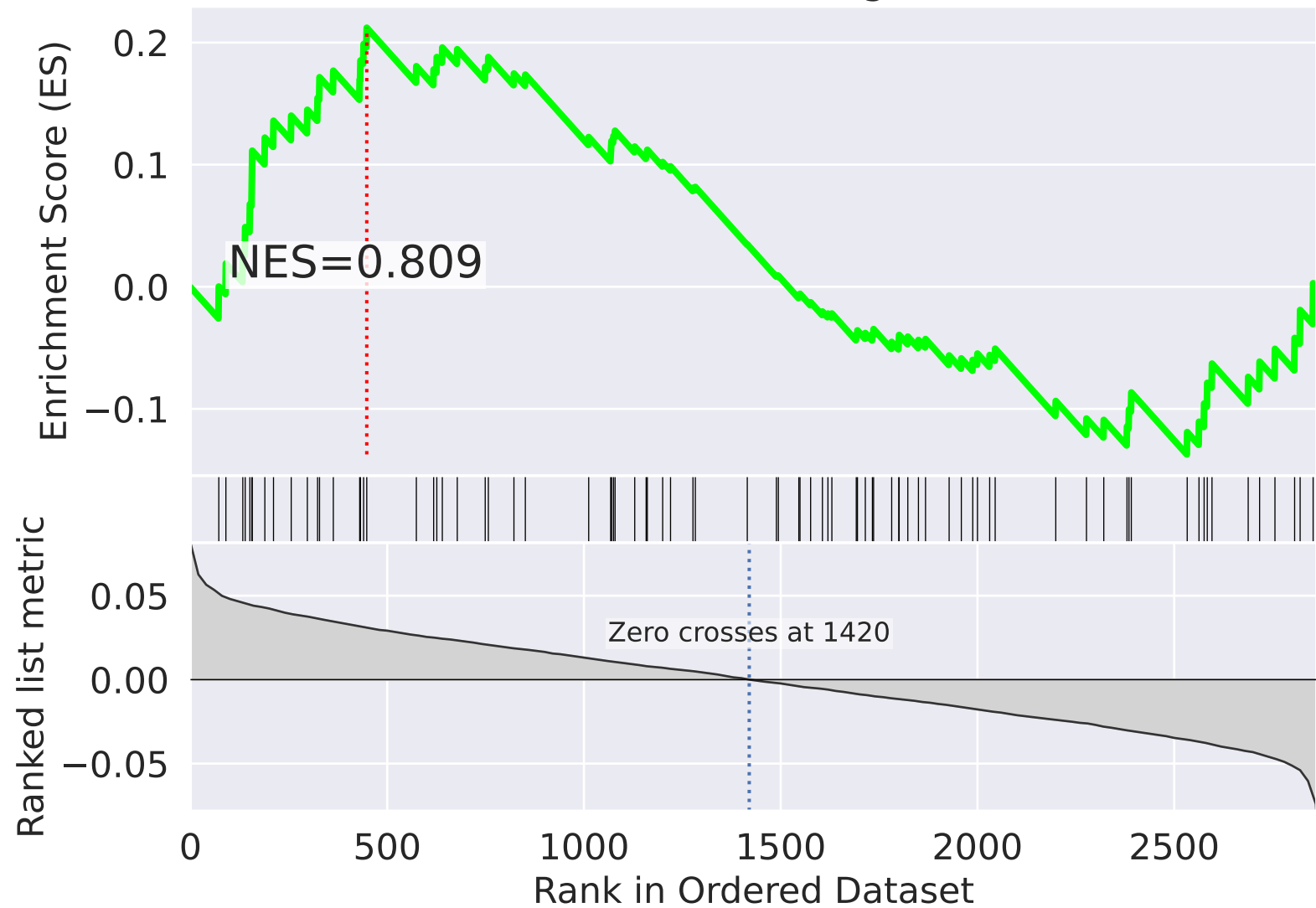
Rank



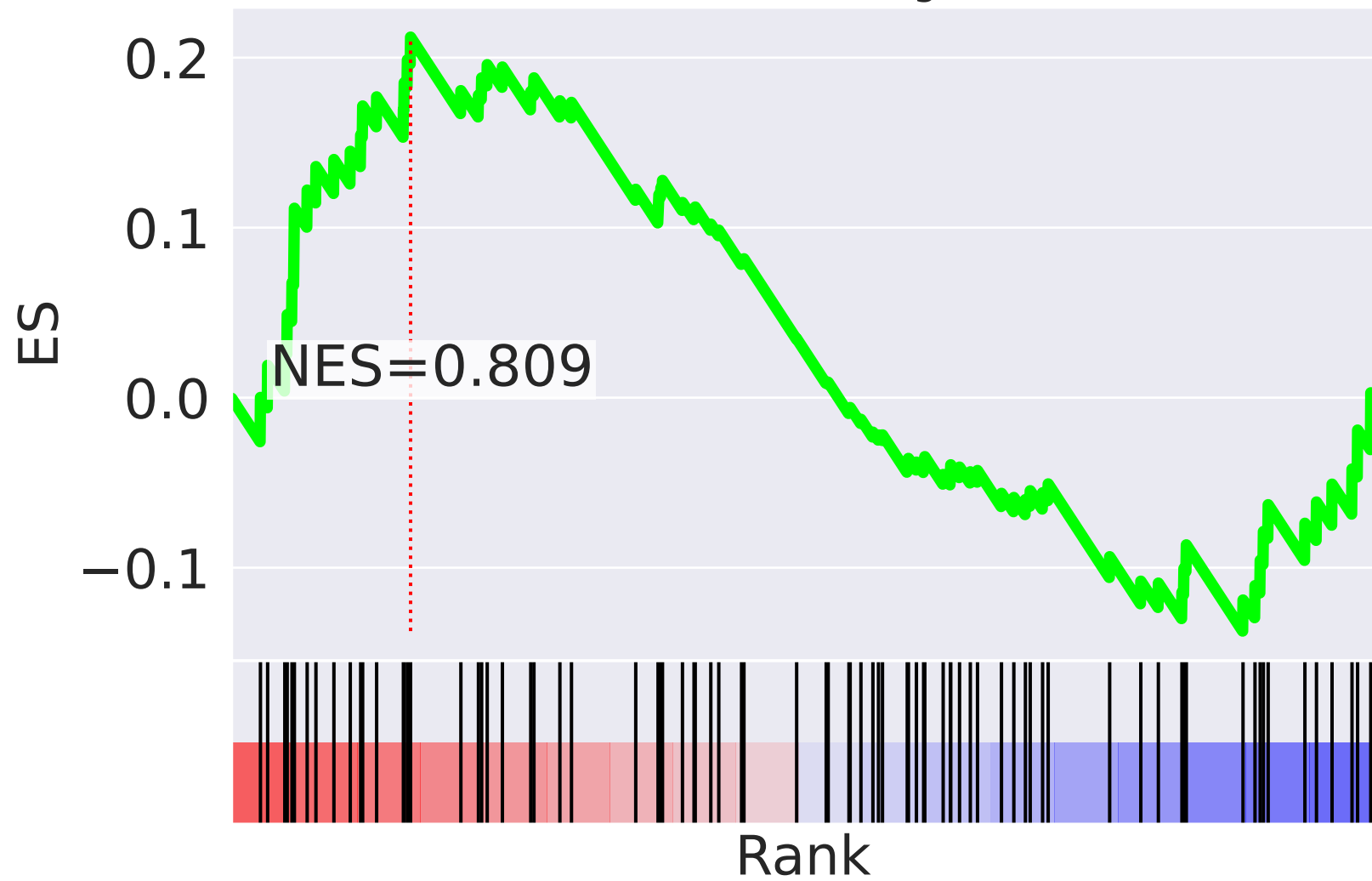
NES		SET
3.455		interstrand cross-link repair (GO:0036297)
-2.888		mRNA 3'-end processing (GO:0031124)
2.870		global genome nucleotide-excision repair (GO:0070911)
2.806		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.725		cellular response to UV (GO:0034644)
2.719		regulation of DNA replication (GO:0006275)
2.617		nucleotide-excision repair (GO:0006289)
-2.593		termination of RNA polymerase II transcription (GO:0006369)
-2.488		negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (GO:1902176)
-2.416		cell cycle arrest (GO:0007050)
-2.394		cellular response to amino acid stimulus (GO:0071230)
2.365		nucleotide-excision repair, preincision complex assembly (GO:0006294)
-2.339		regulation of protein localization (GO:0032880)
2.314		negative regulation of anoikis (GO:2000811)
-2.304		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 $z=28$

mitochondrial translational elongation (GO:0070125)



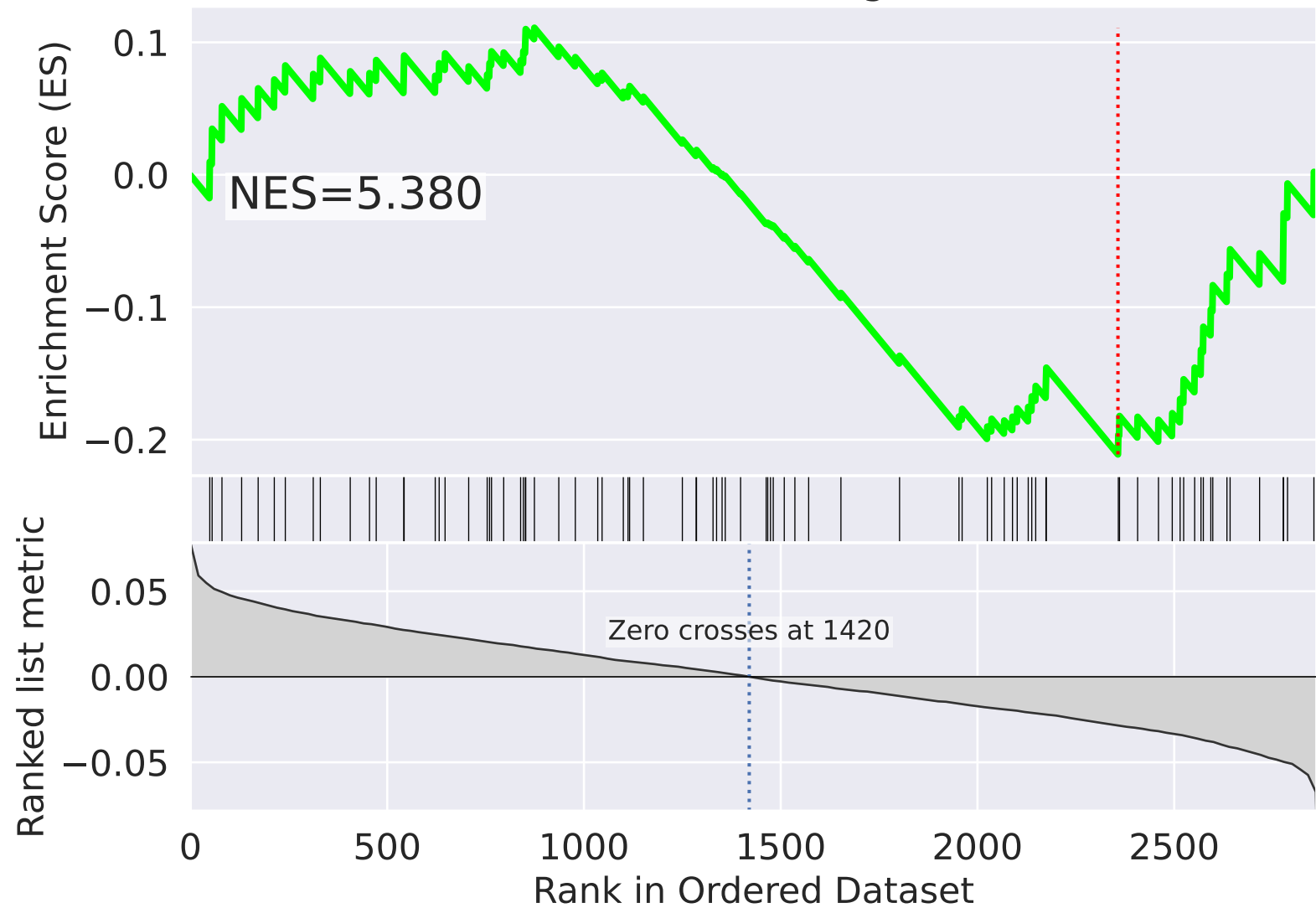
mitochondrial translational elongation (GO:0070125)



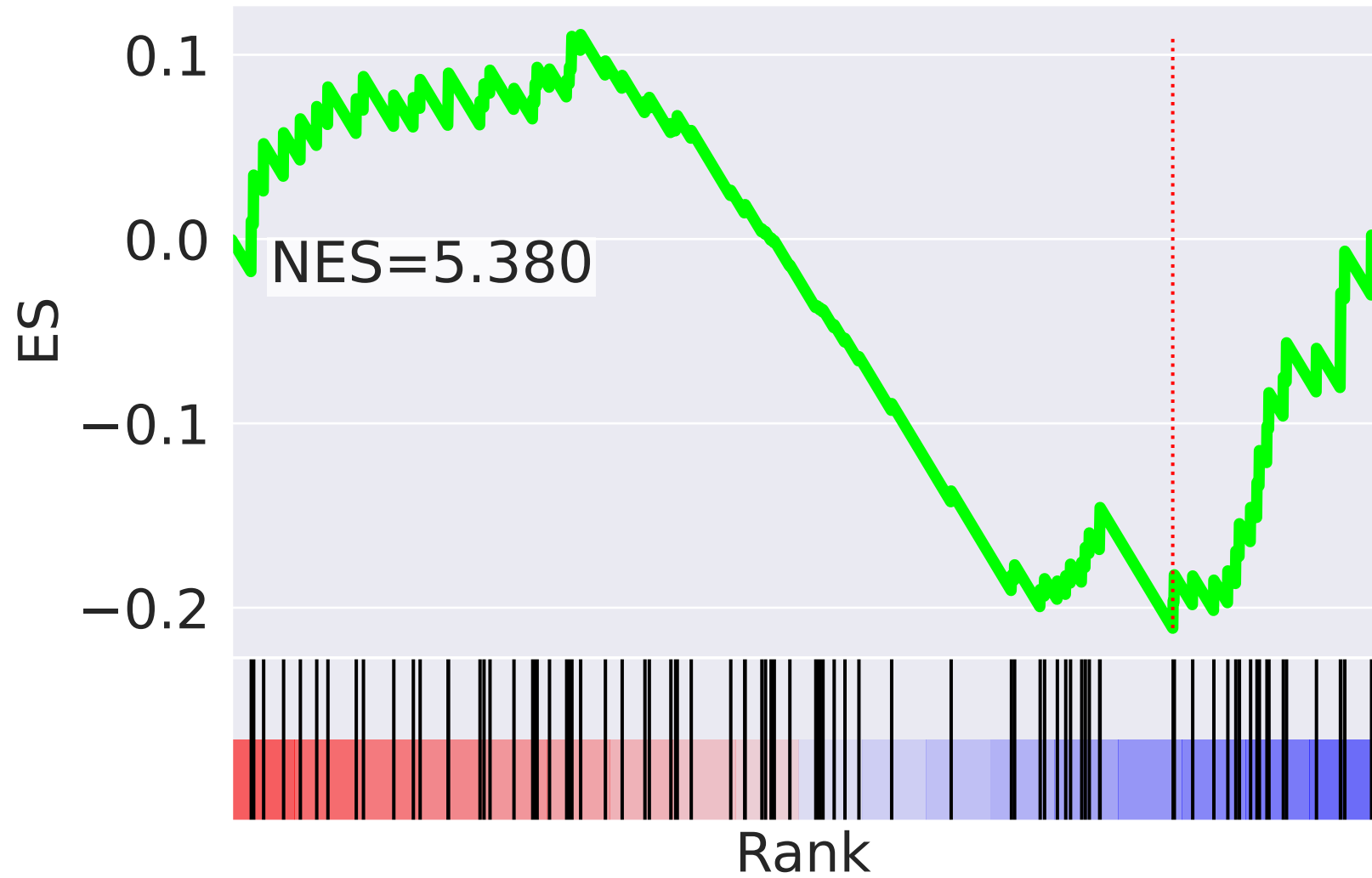
NES		SET
3.393		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
3.155		tumor necrosis factor-mediated signaling pathway (GO:0033209)
2.986		I-kappaB kinase/NF-kappaB signaling (GO:0007249)
-2.930		glucose homeostasis (GO:0042593)
-2.856		beta-catenin-TCF complex assembly (GO:1904837)
2.838		regulation of mRNA stability (GO:0043488)
2.836		positive regulation of protein targeting to mitochondrion (GO:1903955)
2.797		regulation of gene expression (GO:0010468)
-2.780		transcription-coupled nucleotide-excision repair (GO:0006283)
2.663		activation of NF-kappaB-inducing kinase activity (GO:0007250)
2.655		negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
2.635		regulation of focal adhesion assembly (GO:0051893)
2.573		positive regulation of canonical Wnt signaling pathway (GO:0090263)
2.568		regulation of cellular amino acid metabolic process (GO:0006521)
2.477		regulation of cell motility (GO:2000145)

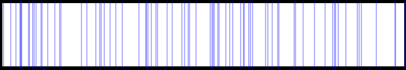
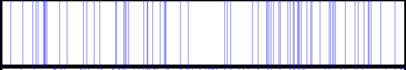
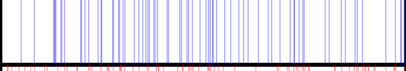
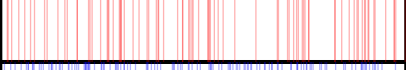
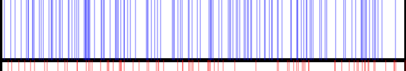
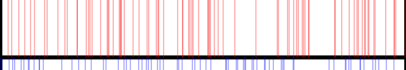
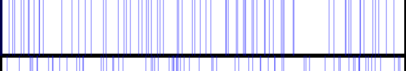
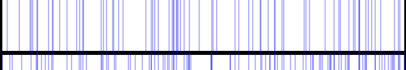
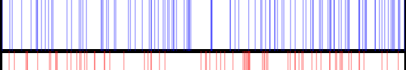
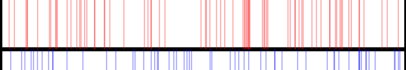
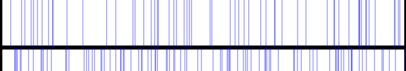
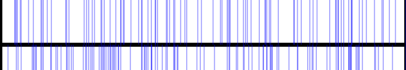
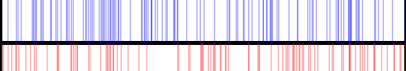
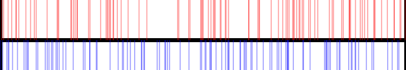
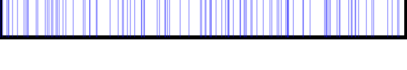
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=29$

mitochondrial translational elongation (GO:0070125)



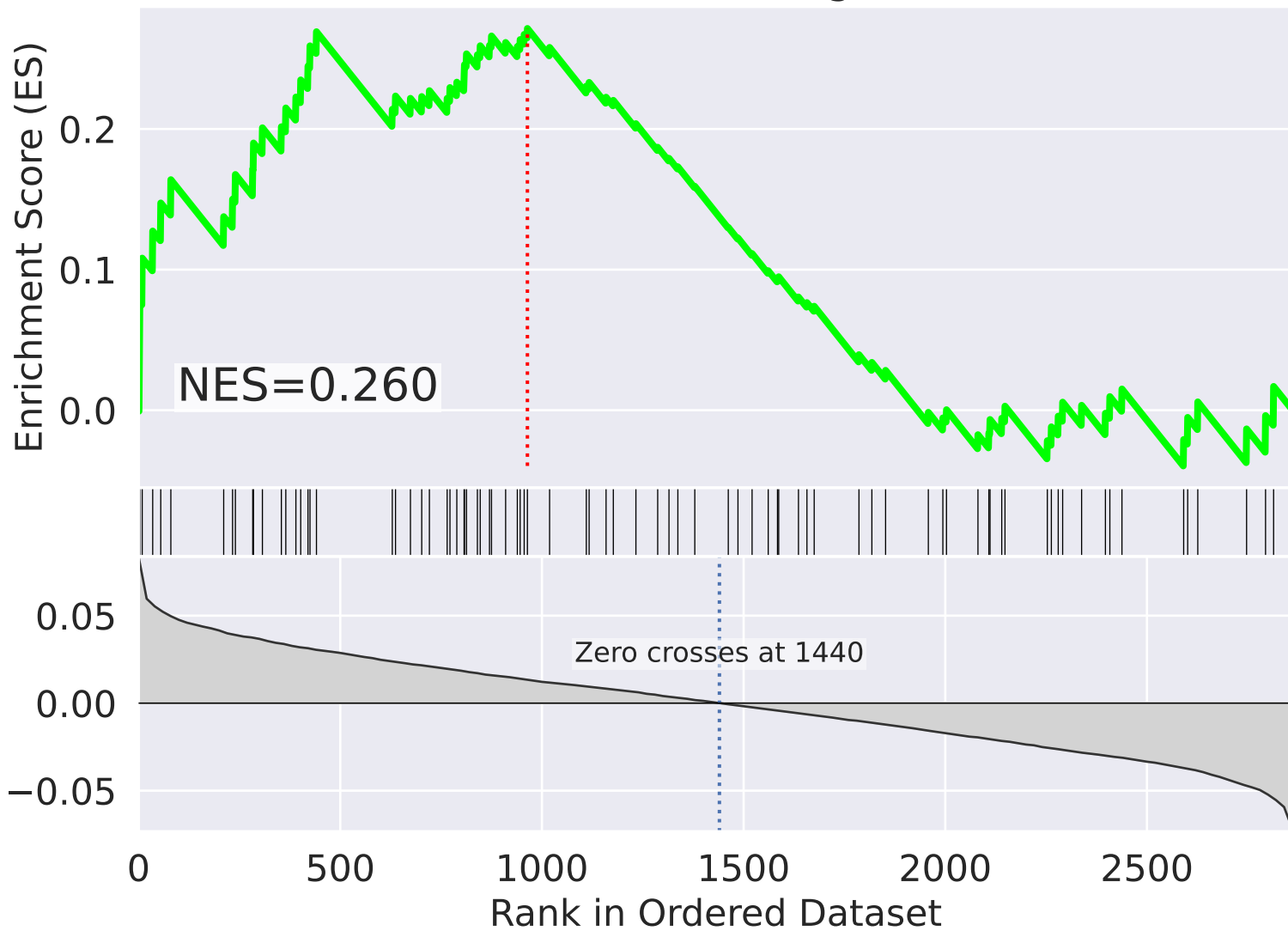
mitochondrial translational elongation (GO:0070125)



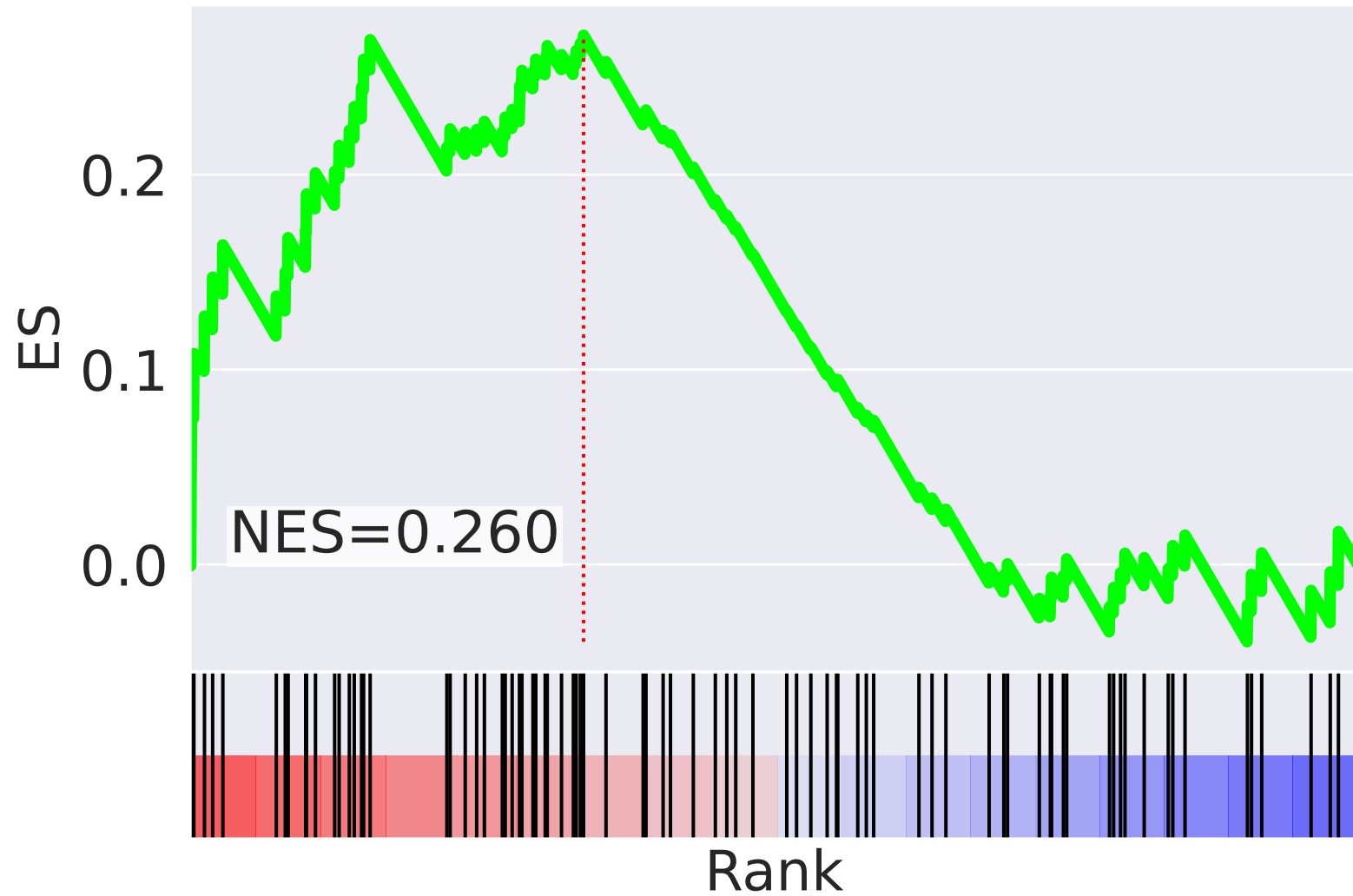
NES		SET
-6.000		negative regulation of apoptotic process (GO:0043066)
-5.984		protein phosphorylation (GO:0006468)
-5.485		positive regulation of cell proliferation (GO:0008284)
5.380		mitochondrial translational elongation (GO:0070125)
-5.296		positive regulation of transcription, DNA-templated (GO:0045893)
5.006		mitochondrial translational termination (GO:0070126)
-4.631		regulation of transcription, DNA-templated (GO:0006355)
-4.531		MAPK cascade (GO:0000165)
-4.494		protein deubiquitination (GO:0016579)
4.480		regulation of signal transduction by p53 class mediator (GO:1901796)
-4.306		T cell receptor signaling pathway (GO:0050852)
-4.259		negative regulation of transcription, DNA-templated (GO:0045892)
-4.207		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
4.175		translation (GO:0006412)
-4.155		transcription from RNA polymerase II promoter (GO:0006366)

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)



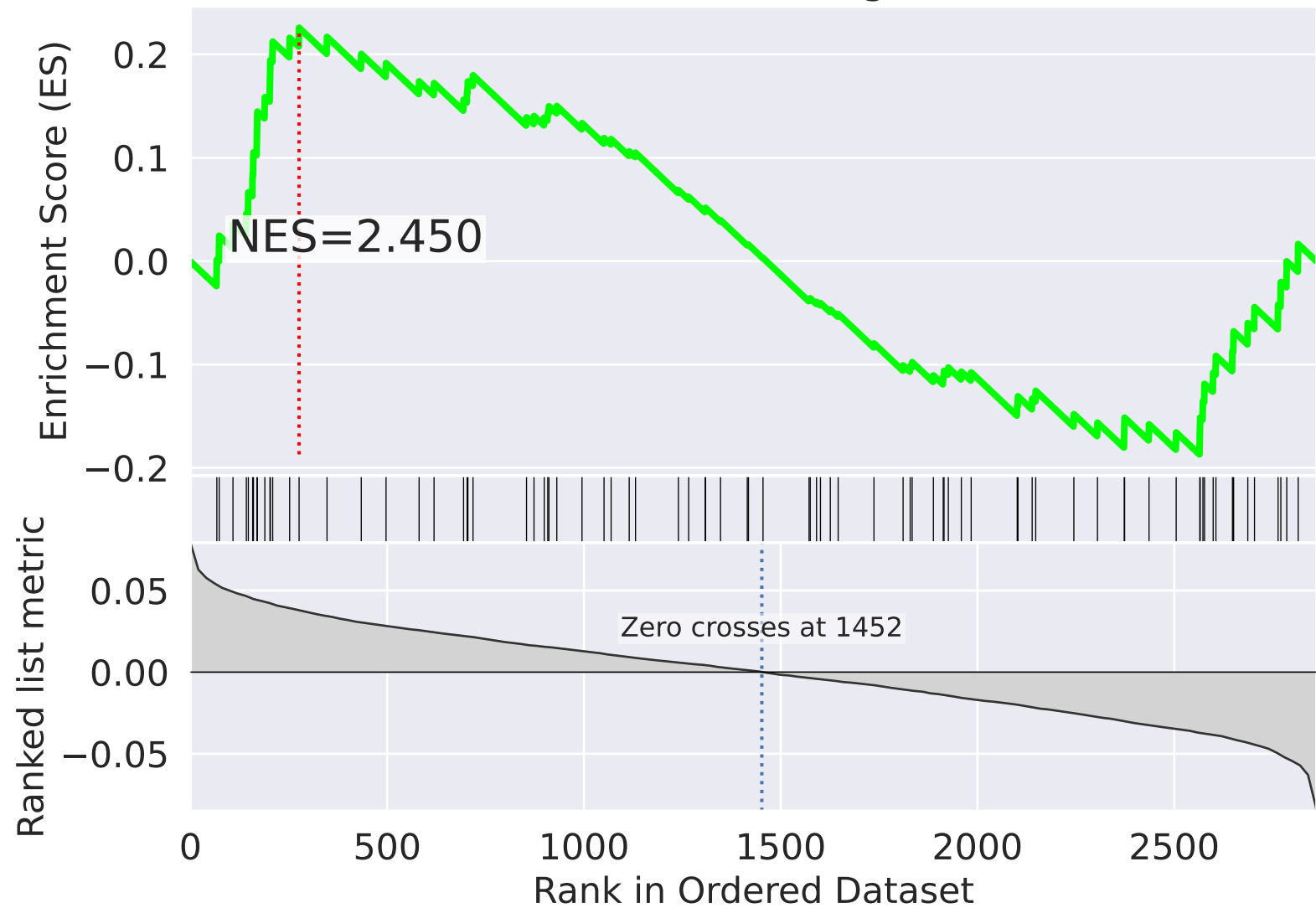
mitochondrial translational elongation (GO:0070125)



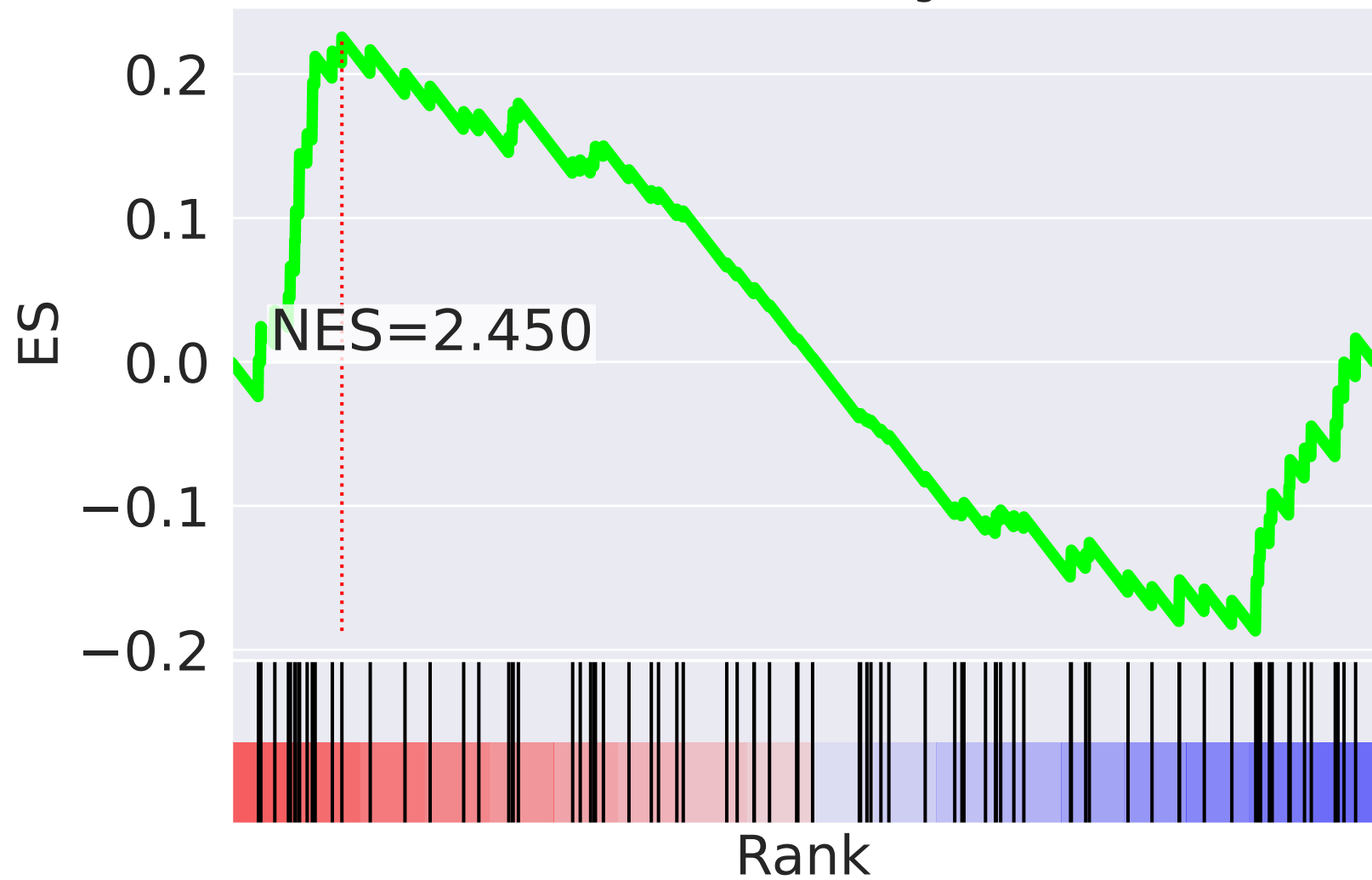
NES		SET
-3.012		mRNA transcription from RNA polymerase II promoter (GO:0042789)
2.845		termination of RNA polymerase II transcription (GO:0006369)
-2.746		histone H3 acetylation (GO:0043966)
-2.731		positive regulation of erythrocyte differentiation (GO:0045648)
2.642		mRNA 3'-end processing (GO:0031124)
2.626		cytokinesis (GO:0000910)
2.553		reciprocal meiotic recombination (GO:0007131)
-2.544		JNK cascade (GO:0007254)
2.543		positive regulation of ERK1 and ERK2 cascade (GO:0070374)
2.531		vascular endothelial growth factor receptor signaling pathway (GO:0048010)
2.531		positive regulation of mRNA 3'-end processing (GO:0031442)
2.498		regulation of protein localization (GO:0032880)
2.468		cellular response to indole-3-methanol (GO:0071681)
-2.459		mitochondrial respiratory chain complex III assembly (GO:0034551)
2.448		mitochondrial respiratory chain complex I assembly (GO:0032981)



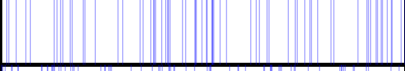
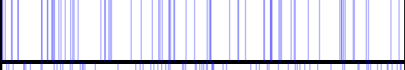
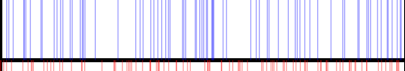
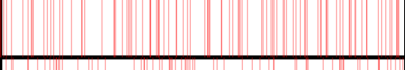
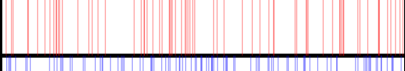
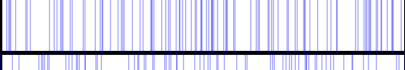
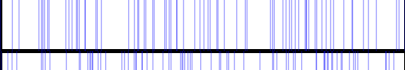
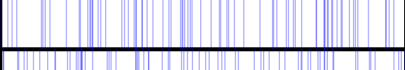
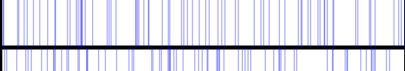
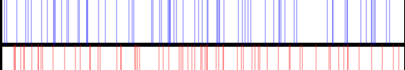
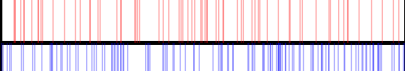
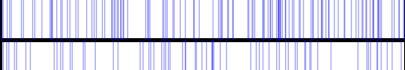
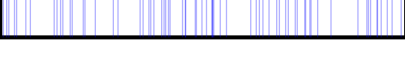
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=31$

mitochondrial translational elongation (GO:0070125)



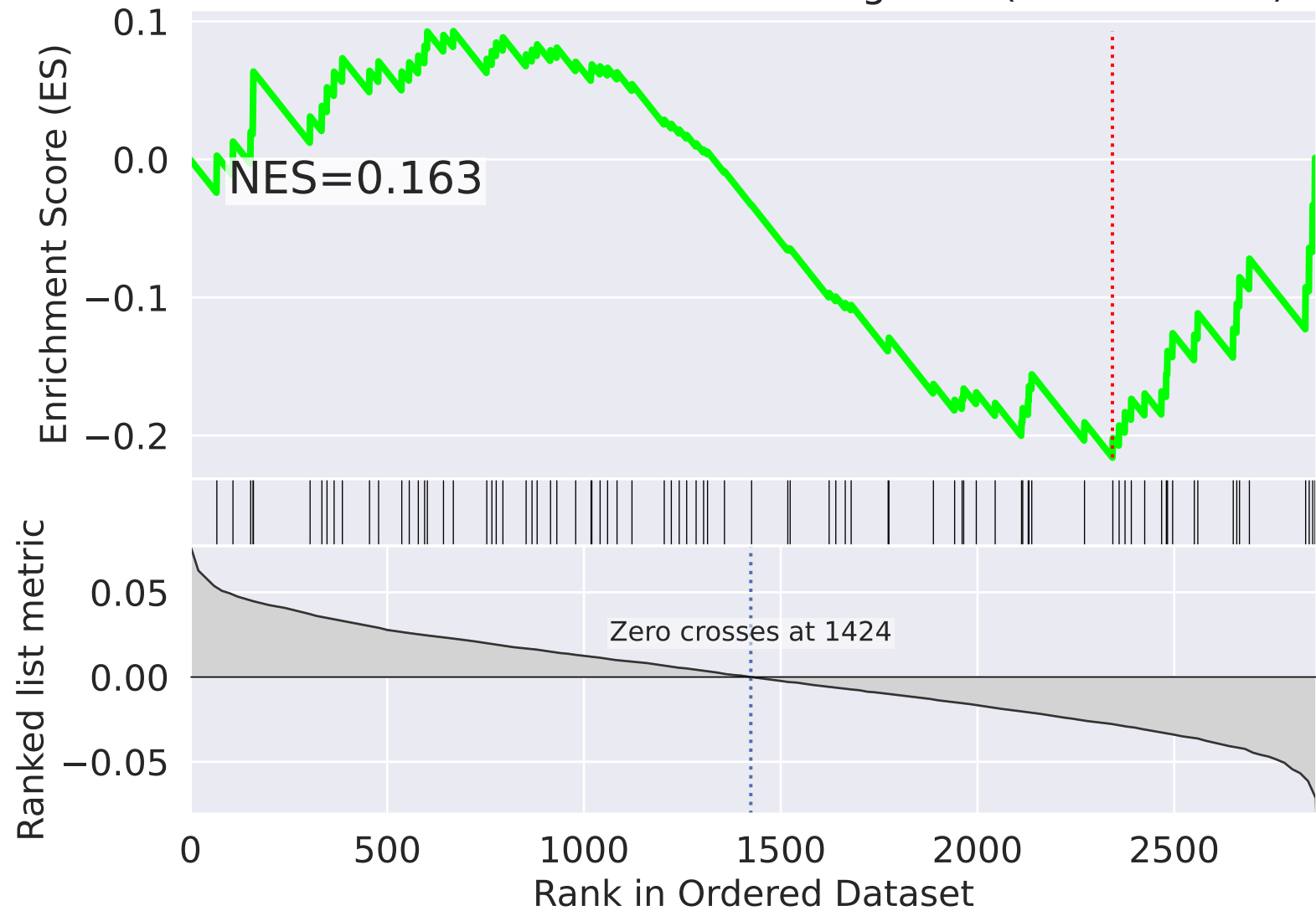
mitochondrial translational elongation (GO:0070125)



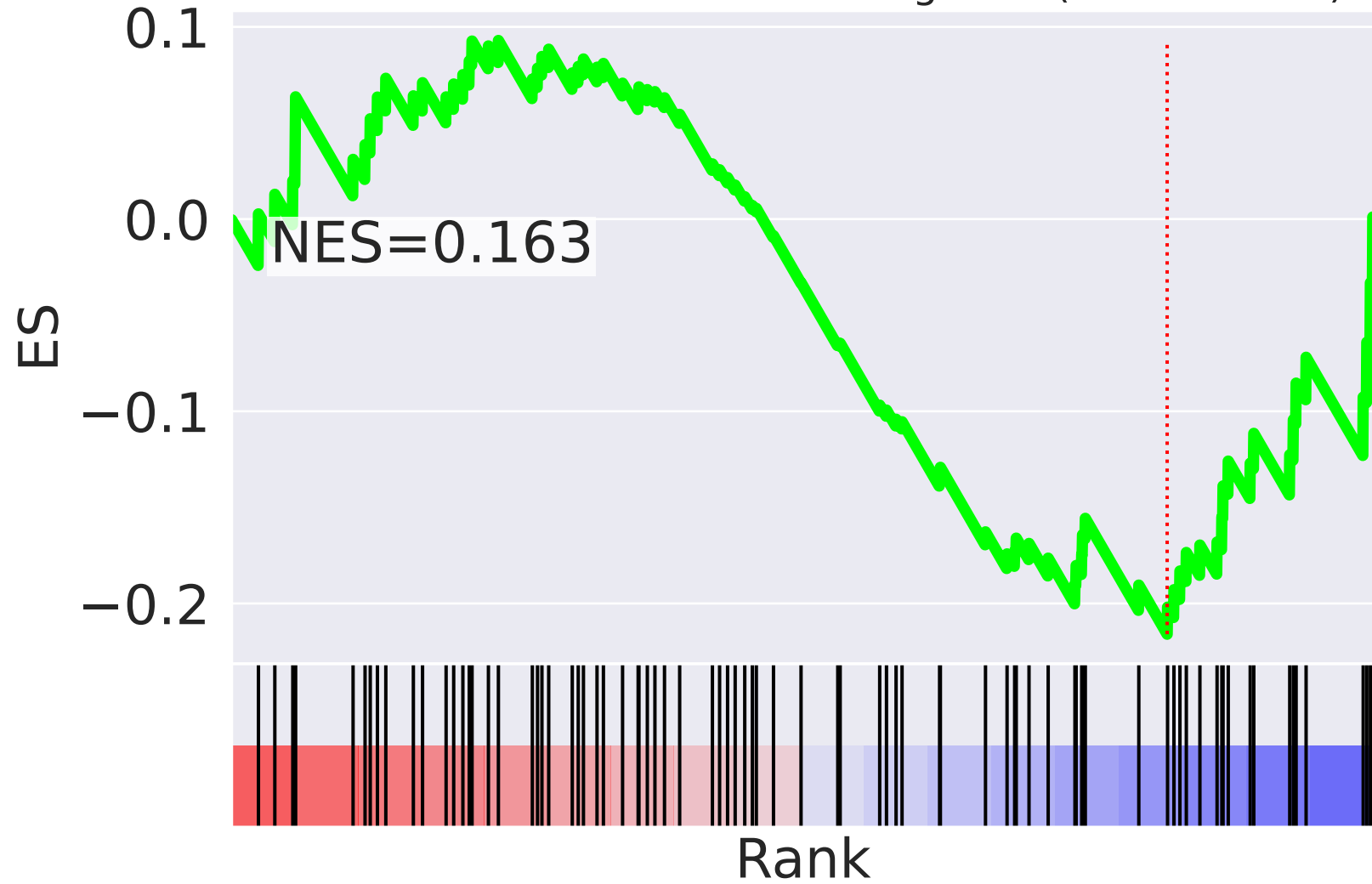
NES		SET
-5.999		rRNA processing (GO:0006364)
-4.776		signal transduction (GO:0007165)
-4.722		translational initiation (GO:0006413)
-4.711		MAPK cascade (GO:0000165)
-4.110		viral transcription (GO:0019083)
4.036		regulation of transcription from RNA polymerase II promoter (GO:0006357)
4.008		protein phosphorylation (GO:0006468)
-3.913		translation (GO:0006412)
-3.907		protein ubiquitination (GO:0016567)
-3.783		regulation of signal transduction by p53 class mediator (GO:1901796)
-3.549		regulation of transcription, DNA-templated (GO:0006355)
-3.392		positive regulation of cell proliferation (GO:0008284)
3.384		sister chromatid cohesion (GO:0007062)
-3.167		mRNA splicing, via spliceosome (GO:0000398)
-3.104		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)

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

mitochondrial translational elongation (GO:0070125)






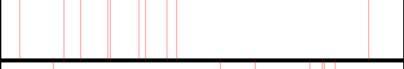
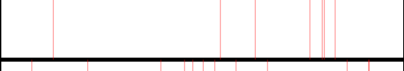
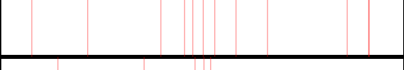
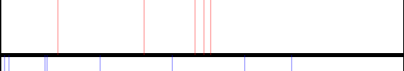

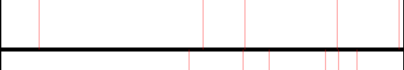

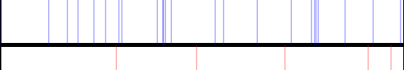
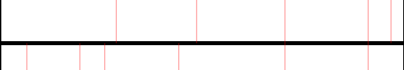
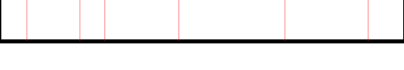


mitochondrial translational elongation (GO:0070125)



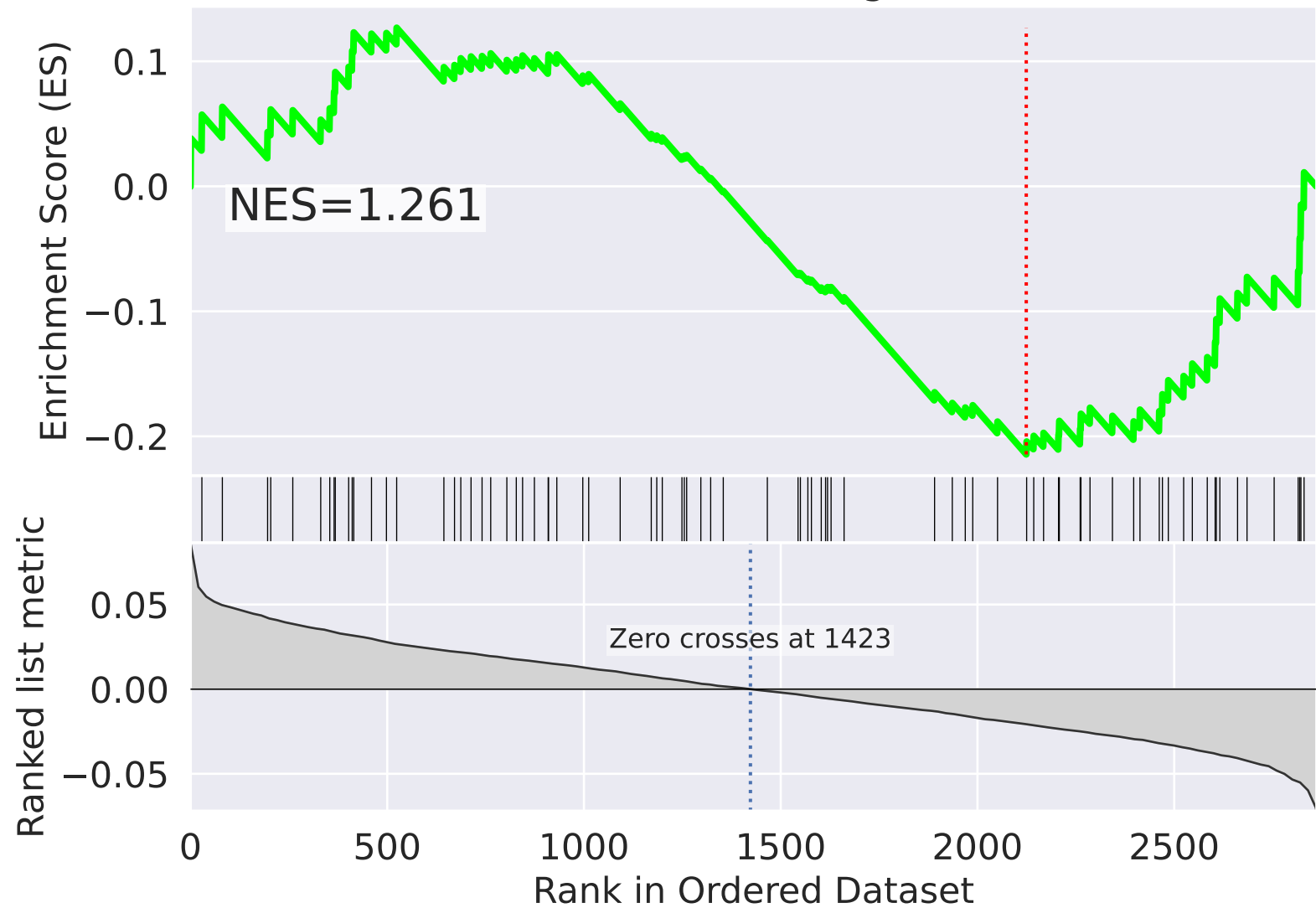
NES

SET

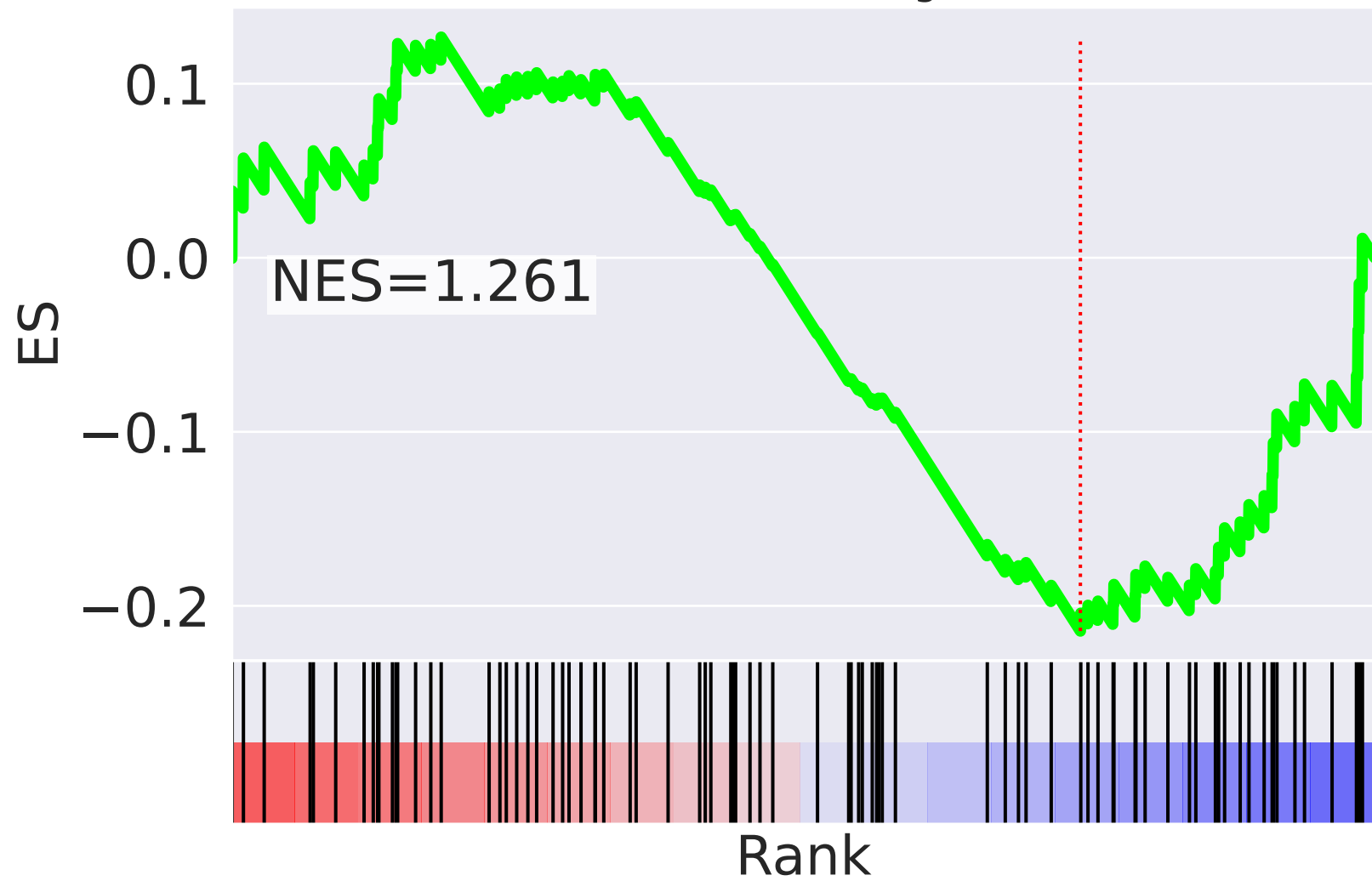
-2.606		protein targeting to mitochondrion (GO:0006626)
-2.587		protein targeting to membrane (GO:0006612)
2.569		positive regulation of angiogenesis (GO:0045766)
2.441		regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)
-2.359		mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)
2.322		protein homotetramerization (GO:0051289)
2.300		telomere capping (GO:0016233)
2.292		tRNA modification (GO:0006400)
2.253		dolichyl diphosphate biosynthetic process (GO:0006489)
-2.246		cellular respiration (GO:0045333)
2.227		cellular response to indole-3-methanol (GO:0071681)
2.216		protein targeting to ER (GO:0045047)
-2.177		COPII vesicle coating (GO:0048208)
2.169		cellular response to estradiol stimulus (GO:0071392)
2.138		positive regulation of myoblast differentiation (GO:0045663)

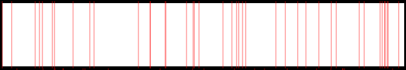

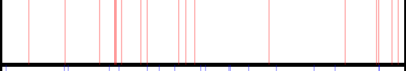
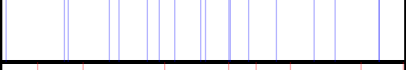


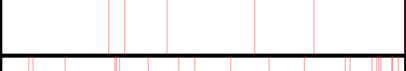
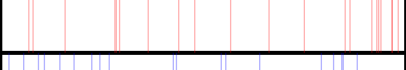

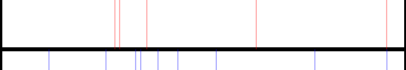


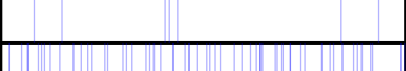
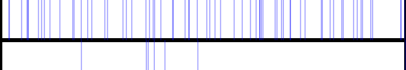
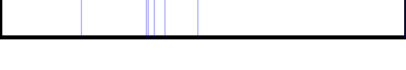
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=33$

mitochondrial translational elongation (GO:0070125)



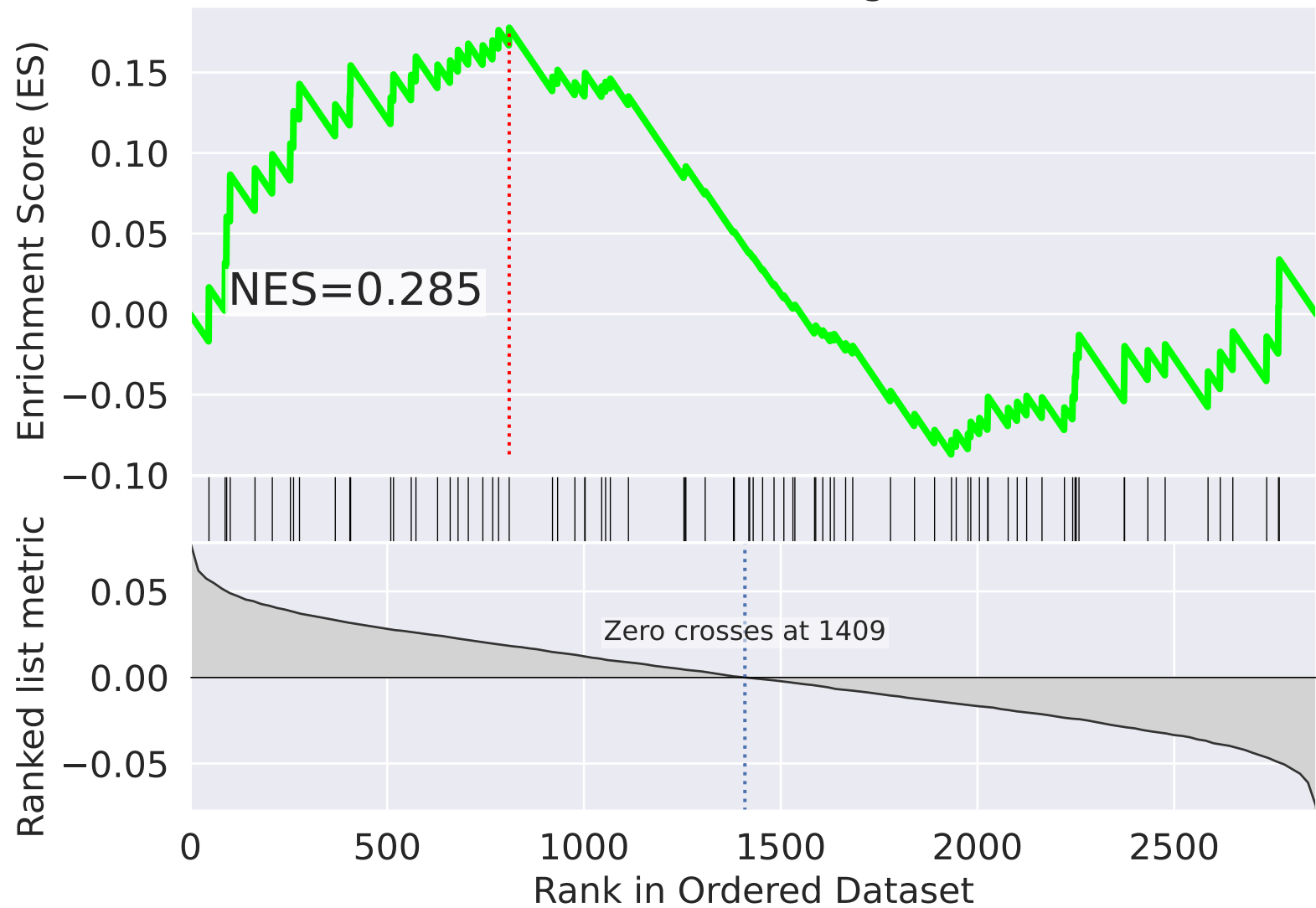
mitochondrial translational elongation (GO:0070125)



NES		SET
2.974		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.934		osteoblast differentiation (GO:0001649)
2.848		epidermal growth factor receptor signaling pathway (GO:0007173)
-2.746		CENP-A containing nucleosome assembly (GO:0034080)
2.699		negative regulation of DNA replication (GO:0008156)
2.691		peptidyl-tyrosine autophosphorylation (GO:0038083)
2.672		skeletal muscle tissue development (GO:0007519)
2.656		axon guidance (GO:0007411)
-2.580		strand displacement (GO:0000732)
2.567		regulation of cytoskeleton organization (GO:0051493)
-2.471		endoplasmic reticulum unfolded protein response (GO:0030968)
-2.423		positive regulation of protein export from nucleus (GO:0046827)
-2.415		negative regulation of insulin receptor signaling pathway (GO:0046627)
-2.396		DNA replication (GO:0006260)
-2.370		positive regulation of autophagy (GO:0010508)

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

mitochondrial translational elongation (GO:0070125)



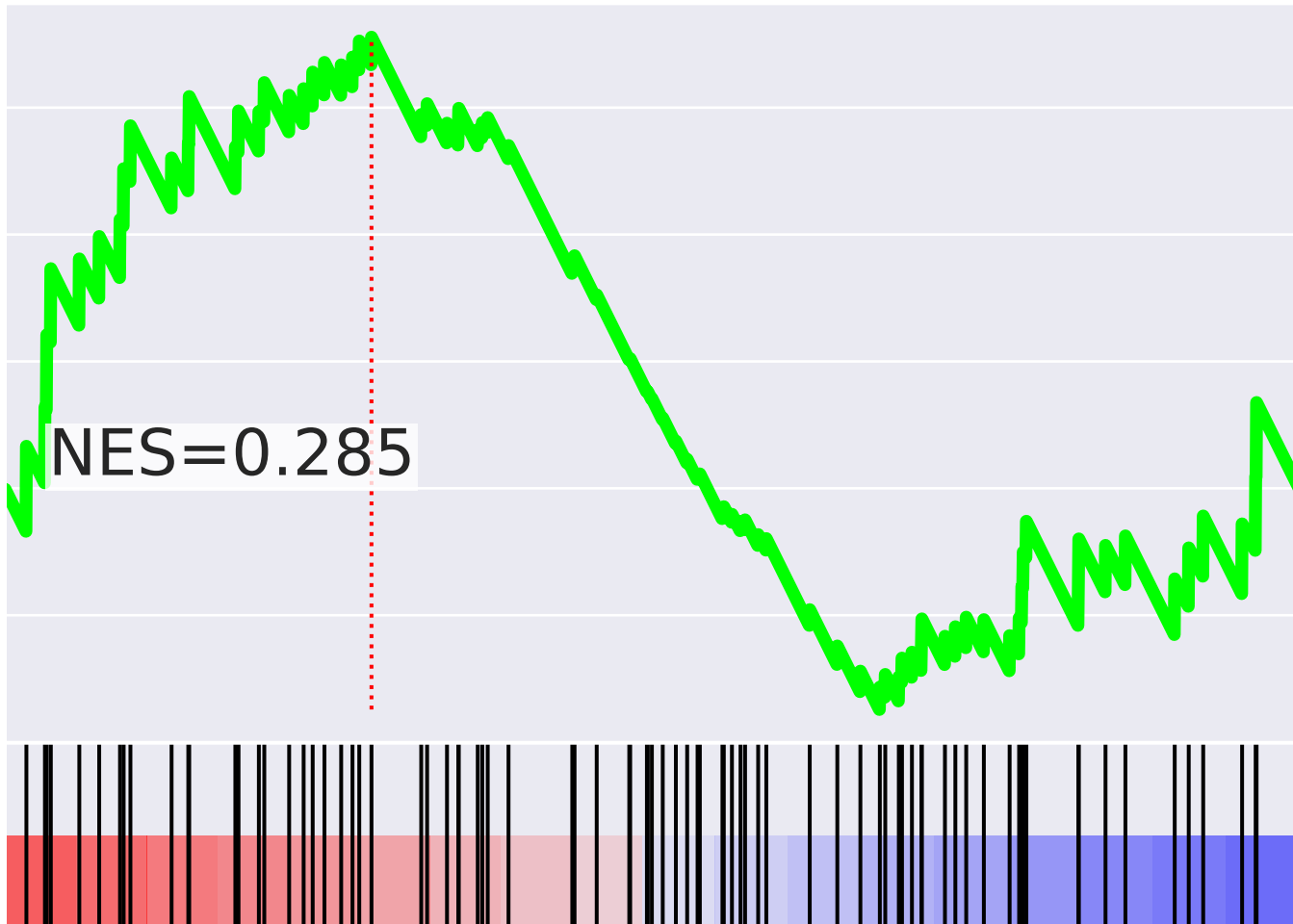
mitochondrial translational elongation (GO:0070125)

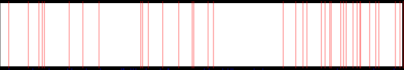
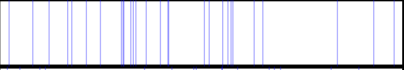
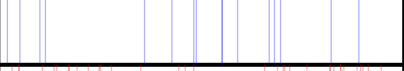
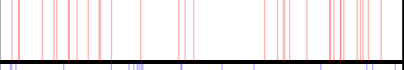
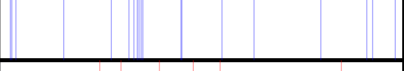

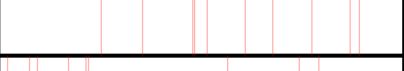



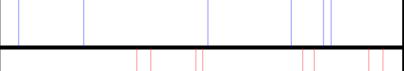

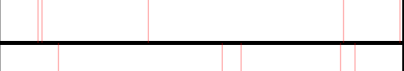


ES

0.15
0.10
0.05
0.00
-0.05
-0.10

NES=0.285

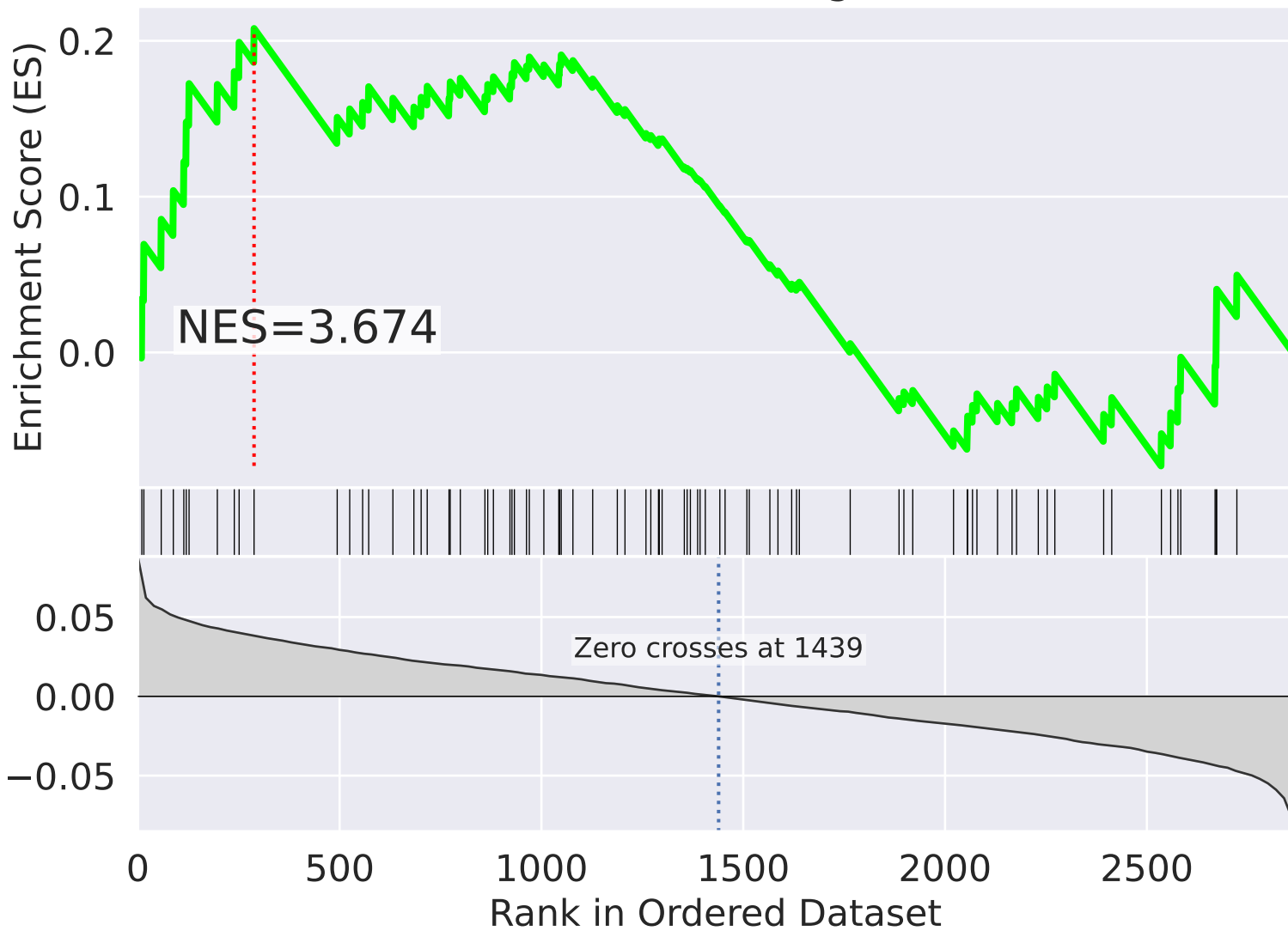
Rank



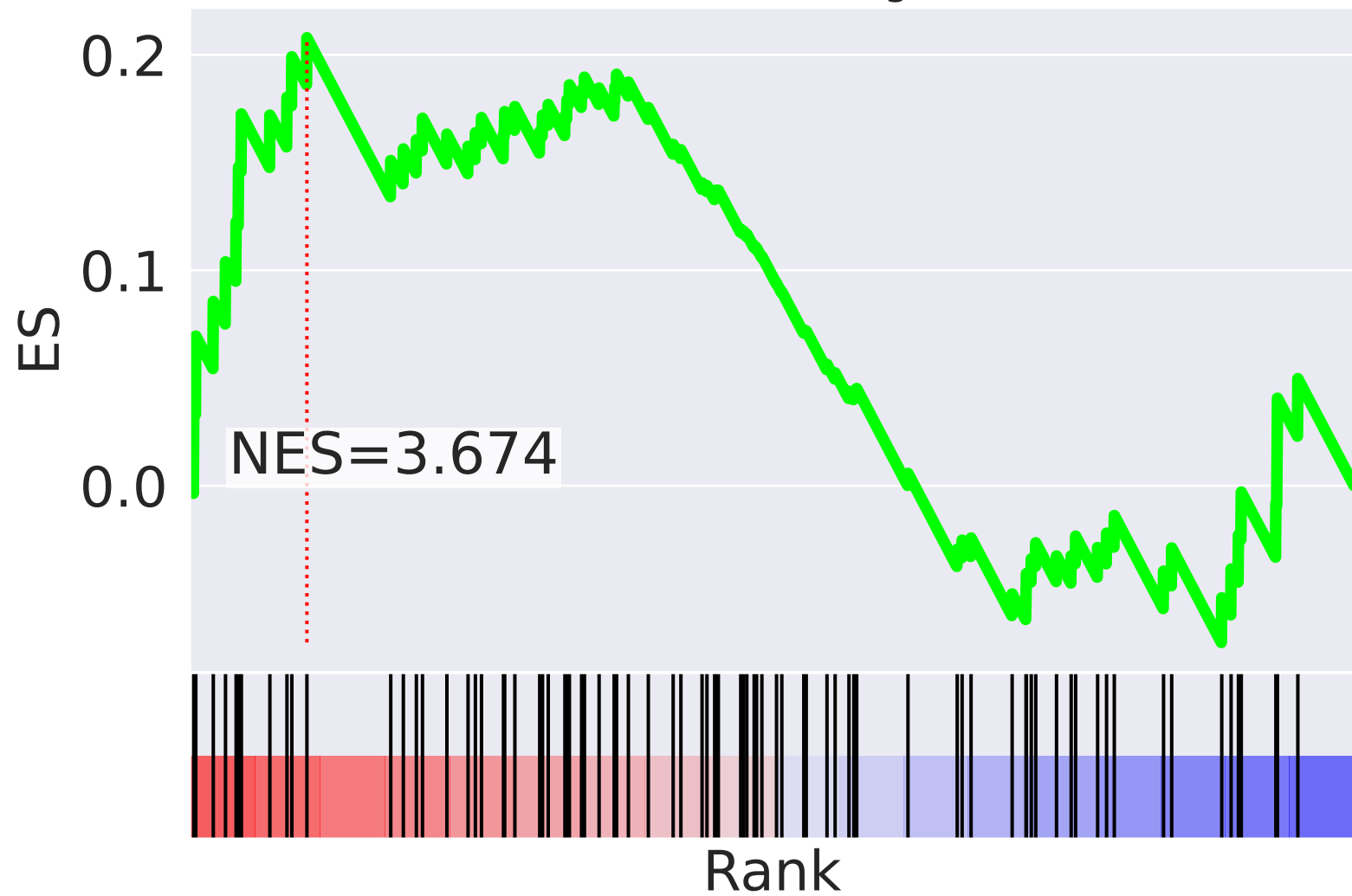
NES		SET
3.086		cell cycle arrest (GO:0007050)
-2.865		chromosome segregation (GO:0007059)
-2.828		positive regulation of cell growth (GO:0030307)
2.778		regulation of macroautophagy (GO:0016241)
-2.604		positive regulation of GTPase activity (GO:0043547)
2.584		protein import into mitochondrial matrix (GO:0030150)
2.564		protein homotetramerization (GO:0051289)
2.480		mitophagy (GO:0000422)
2.451		positive regulation of endothelial cell migration (GO:0010595)
-2.436		kinetochore assembly (GO:0051382)
-2.428		positive regulation of pathway-restricted SMAD protein phosphorylation (GO:0010862)
2.417		protein processing (GO:0016485)
2.413		positive regulation of fibroblast proliferation (GO:0048146)
2.396		positive regulation of Wnt signaling pathway (GO:0030177)
-2.393		somatic stem cell population maintenance (GO:0035019)


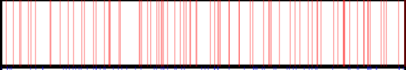
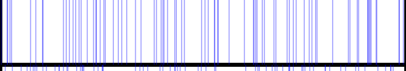
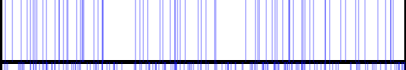
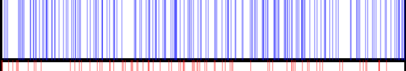
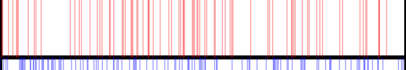
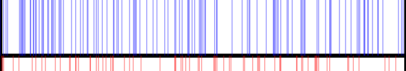
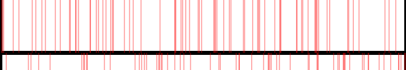
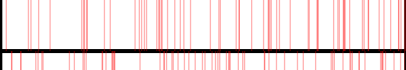
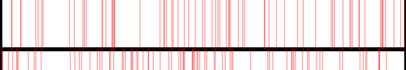
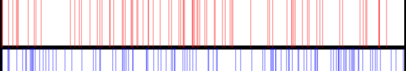
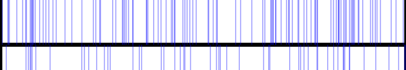
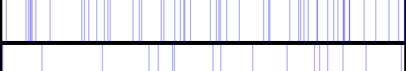
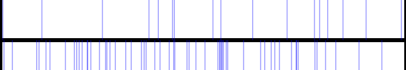
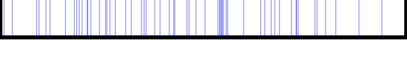
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=35$

mitochondrial translational elongation (GO:0070125)



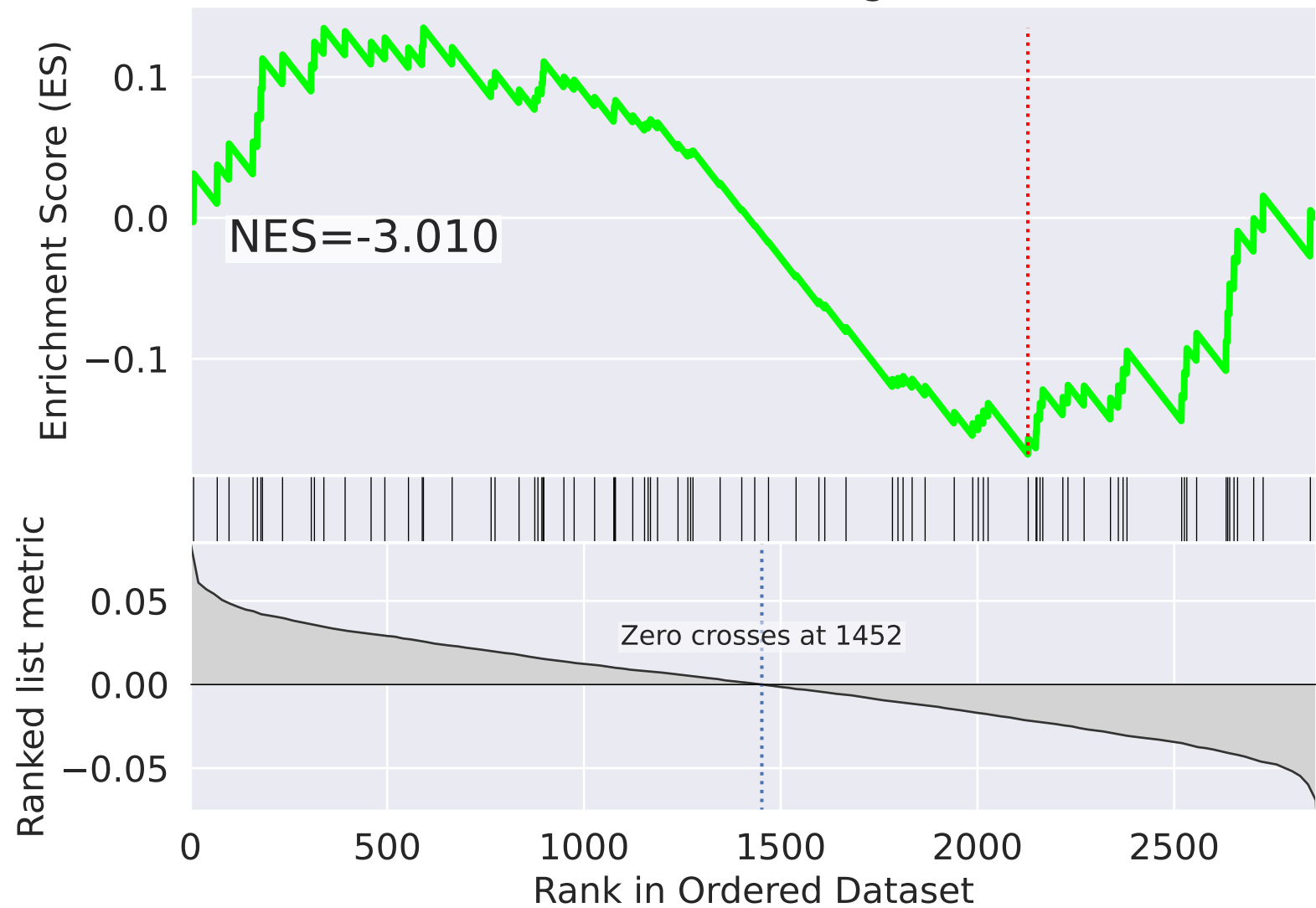
mitochondrial translational elongation (GO:0070125)



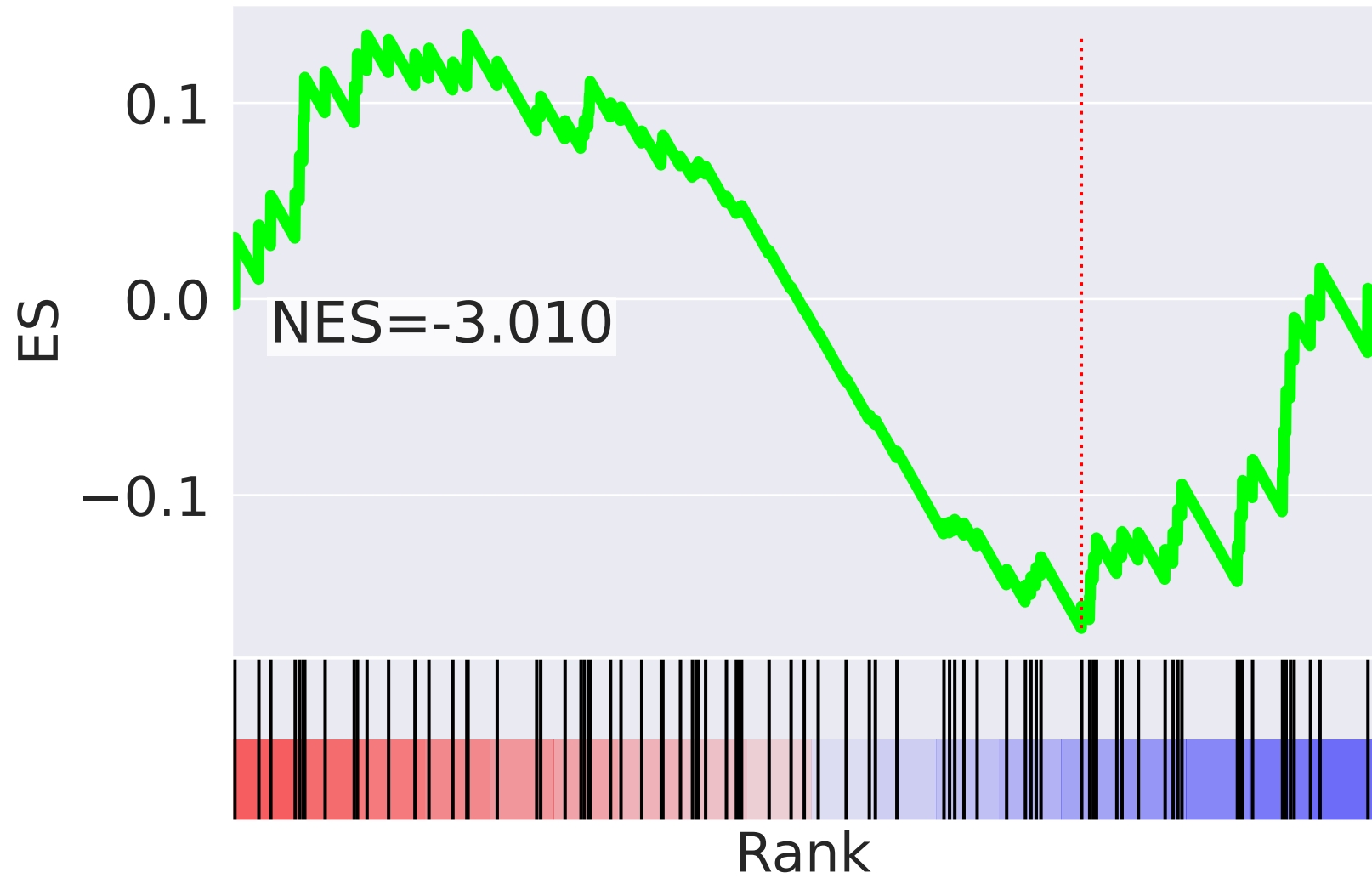
NES		SET
-5.834		neutrophil degranulation (GO:0043312)
5.248		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-5.208		negative regulation of apoptotic process (GO:0043066)
-4.736		regulation of transcription, DNA-templated (GO:0006355)
-4.196		positive regulation of transcription from RNA polymerase II promoter (GO:0045944)
3.674		mitochondrial translational elongation (GO:0070125)
-3.552		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
3.461		regulation of signal transduction by p53 class mediator (GO:1901796)
3.295		protein polyubiquitination (GO:0000209)
3.241		protein phosphorylation (GO:0006468)
3.125		mitochondrial translational termination (GO:0070126)
-3.121		rRNA processing (GO:0006364)
-3.001		regulation of mRNA stability (GO:0043488)
-3.000		positive regulation of telomerase activity (GO:0051973)
-2.992		G2/M transition of mitotic cell cycle (GO:0000086)

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

mitochondrial translational elongation (GO:0070125)



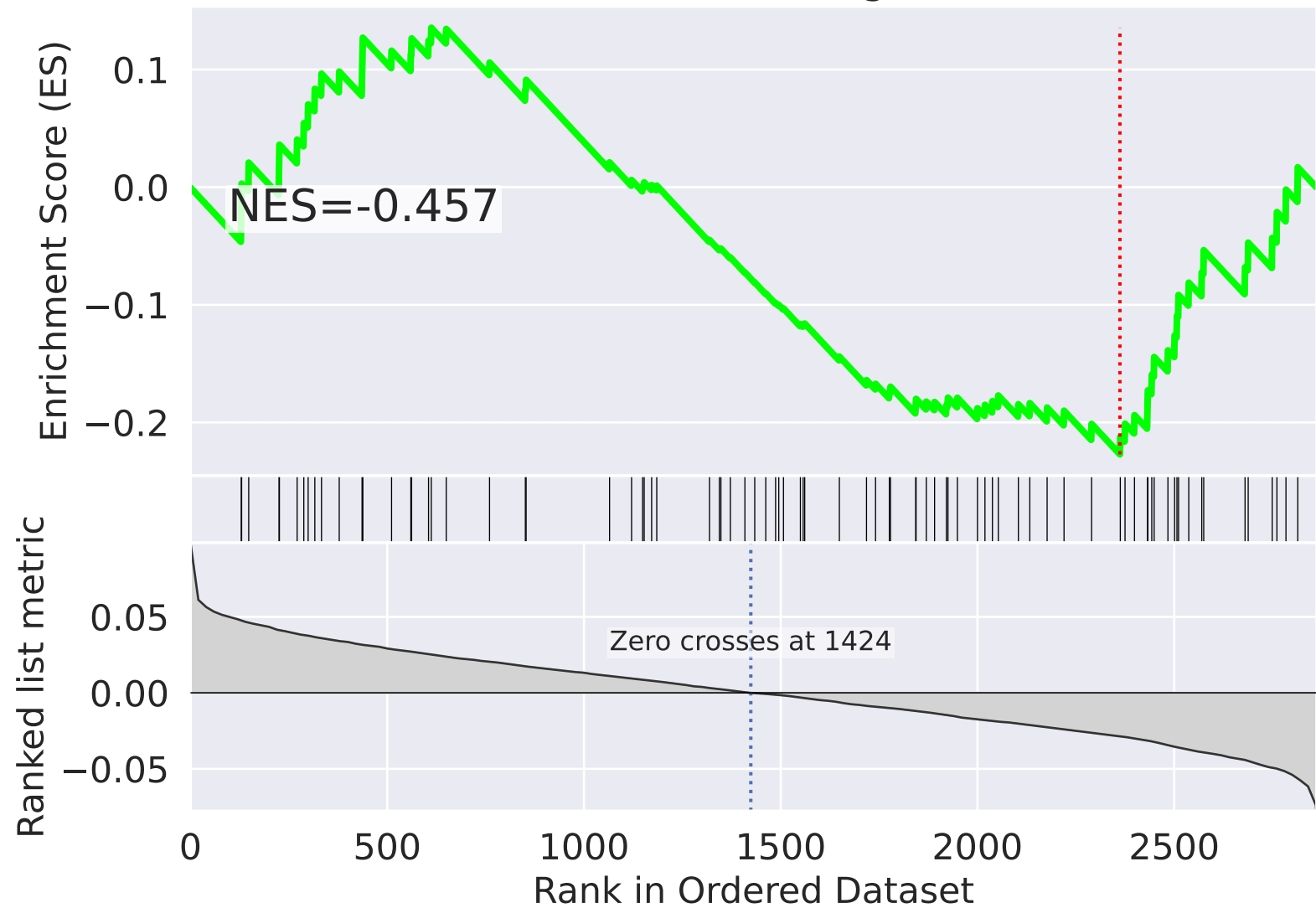
mitochondrial translational elongation (GO:0070125)



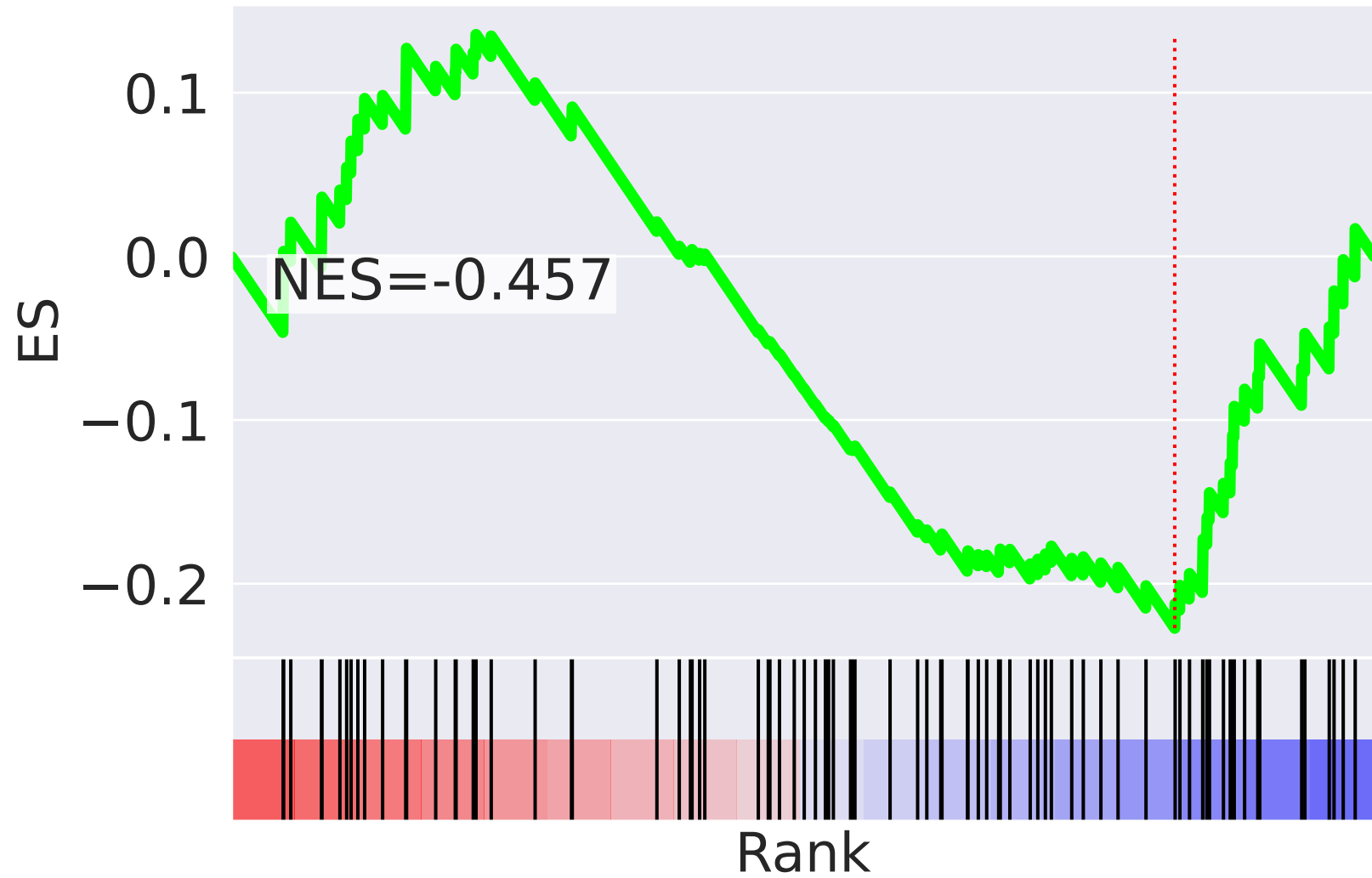
NES		SET
3.245		intracellular transport of virus (GO:0075733)
3.189		regulation of gene silencing by miRNA (GO:0060964)
3.018		viral life cycle (GO:0019058)
-3.010		mitochondrial translational elongation (GO:0070125)
2.962		endosomal transport (GO:0016197)
-2.917		mitochondrial translational termination (GO:0070126)
2.862		negative regulation of protein ubiquitination (GO:0031397)
2.857		protein import into nucleus (GO:0006606)
-2.855		mitochondrial translation (GO:0032543)
2.800		inflammatory response (GO:0006954)
-2.683		ephrin receptor signaling pathway (GO:0048013)
-2.657		canonical Wnt signaling pathway (GO:0060070)
2.585		positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)
-2.508		positive regulation of cell differentiation (GO:0045597)
2.455		mitotic nuclear envelope disassembly (GO:0007077)

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

mitochondrial translational elongation (GO:0070125)



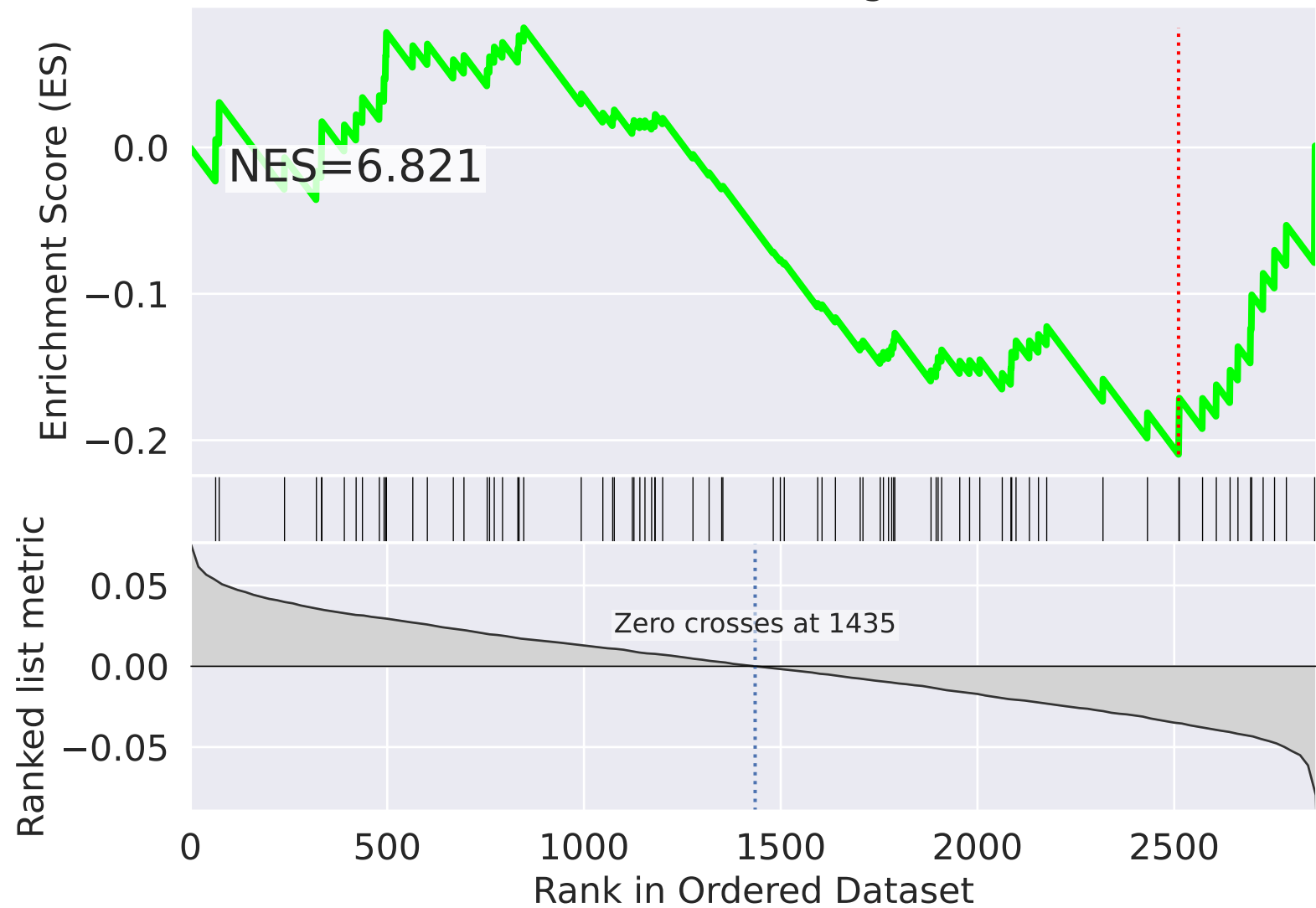
mitochondrial translational elongation (GO:0070125)



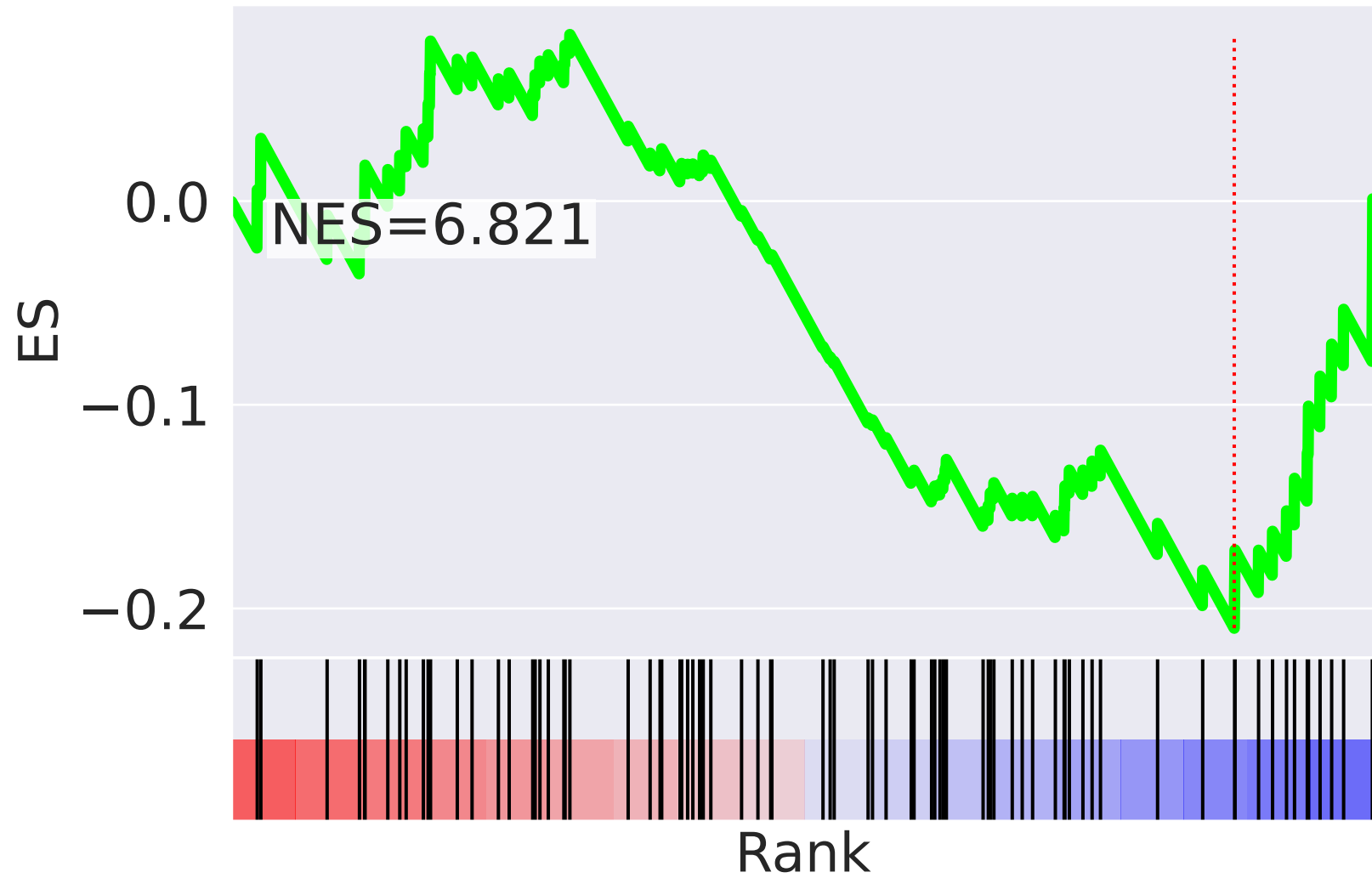
NES		SET
-3.770		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.307		humoral immune response (GO:0006959)
-2.929		JNK cascade (GO:0007254)
-2.892		ER to Golgi vesicle-mediated transport (GO:0006888)
-2.776		global genome nucleotide-excision repair (GO:0070911)
-2.677		outflow tract septum morphogenesis (GO:0003148)
-2.630		nucleotide-excision repair, DNA duplex unwinding (GO:0000717)
2.630		positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900740)
2.607		positive regulation of myoblast differentiation (GO:0045663)
2.587		7-methylguanosine mRNA capping (GO:0006370)
2.573		regulation of transcription from RNA polymerase II promoter (GO:0006357)
2.548		regulation of lipid metabolic process (GO:0019216)
2.492		positive regulation of intrinsic apoptotic signaling pathway (GO:2001244)
2.466		histone H3 acetylation (GO:0043966)
2.447		tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)

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

mitochondrial translational elongation (GO:0070125)

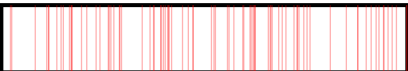


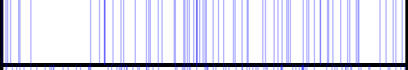

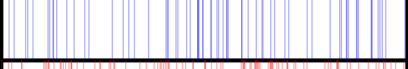
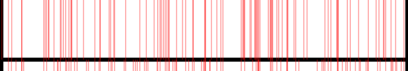
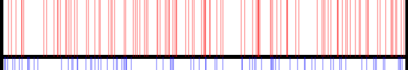
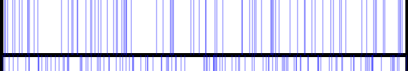
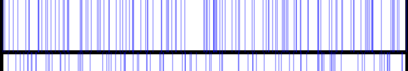
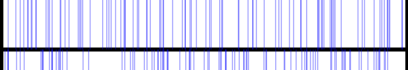
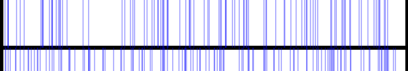

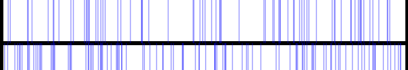
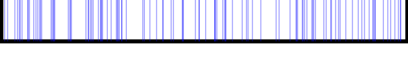


mitochondrial translational elongation (GO:0070125)



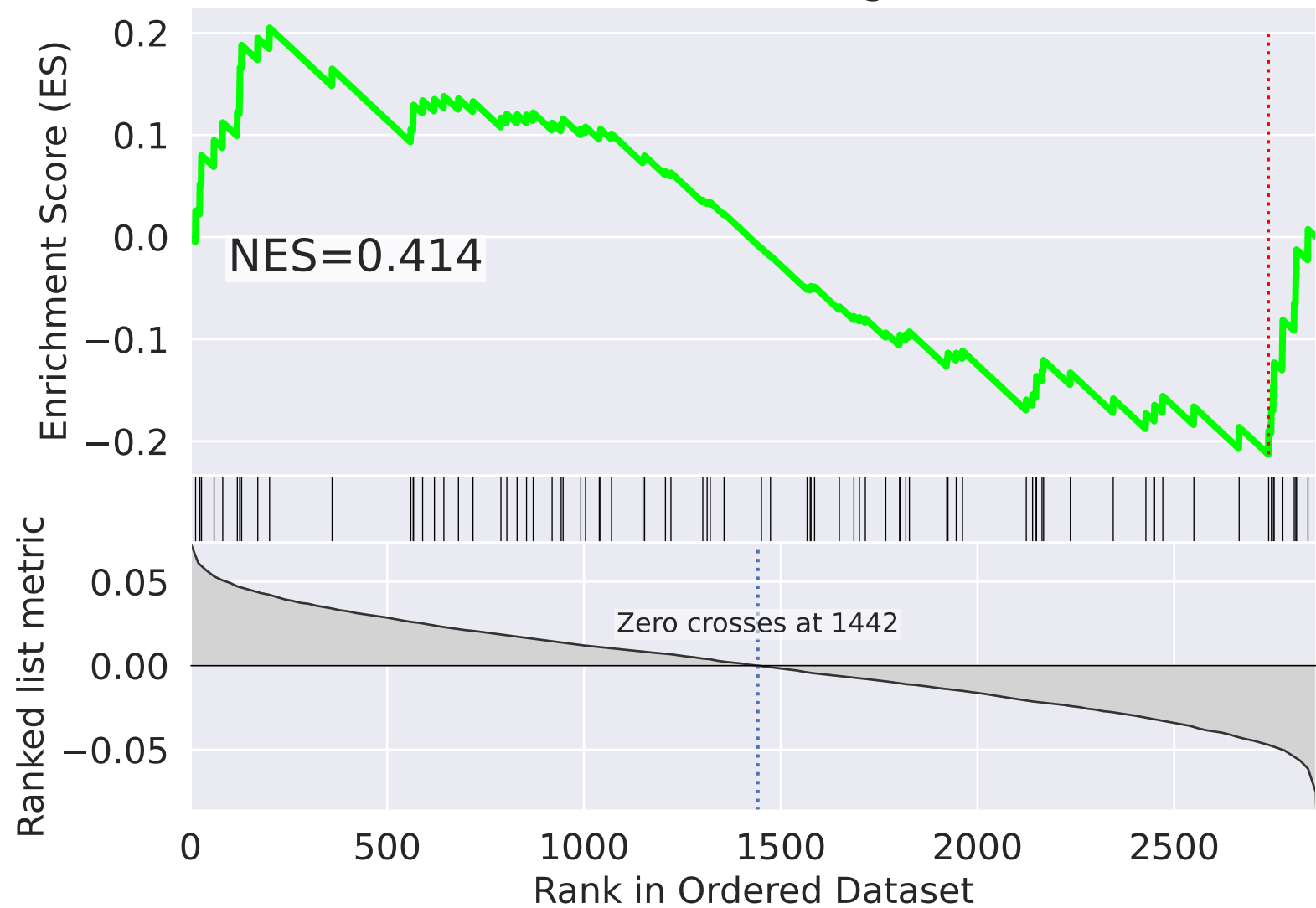
NES

SET

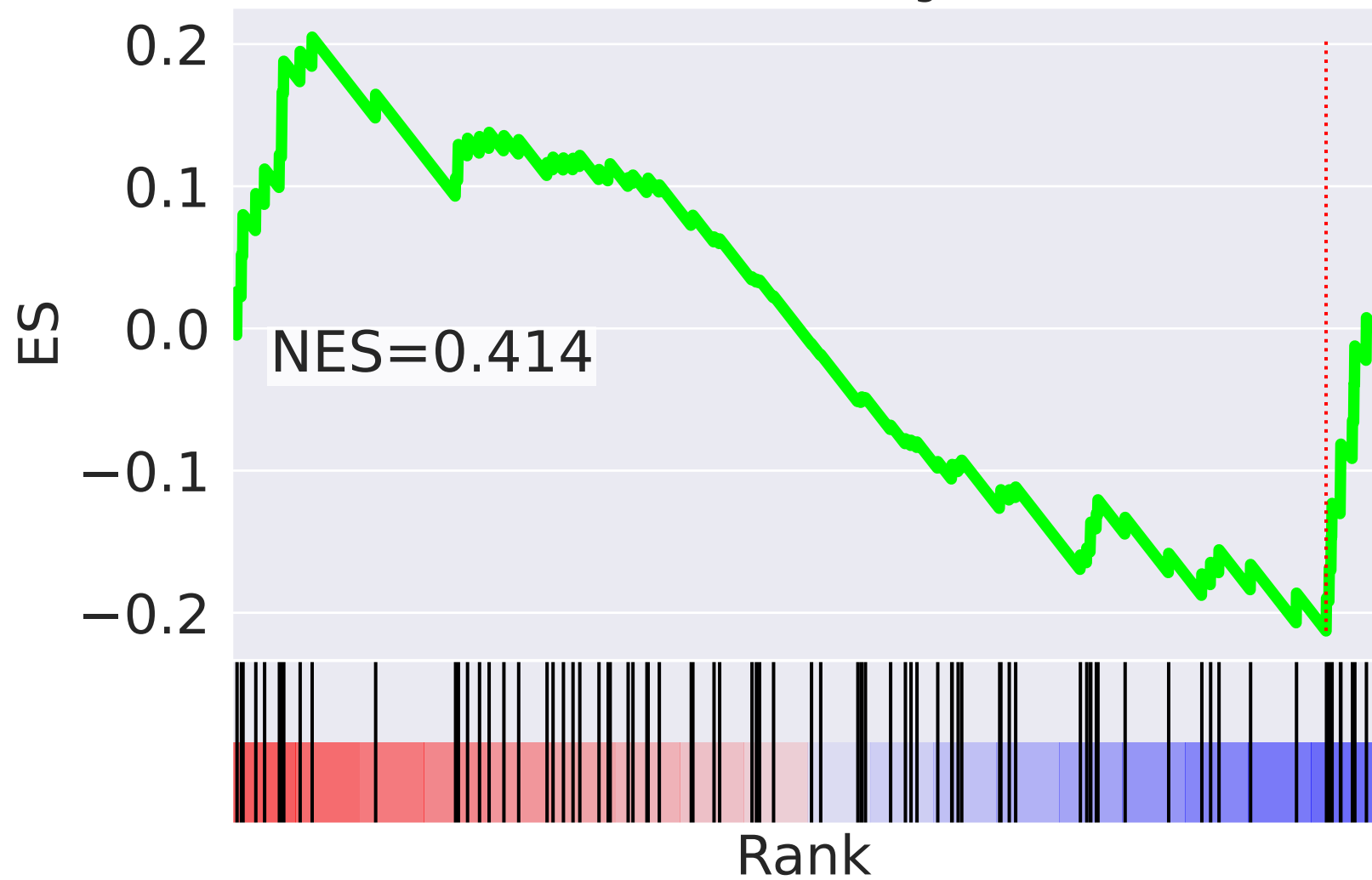
6.821		mitochondrial translational elongation (GO:0070125)
6.641		mitochondrial translational termination (GO:0070126)
-6.520		MAPK cascade (GO:0000165)
-6.051		protein phosphorylation (GO:0006468)
-5.999		signal transduction (GO:0007165)
-5.702		sister chromatid cohesion (GO:0007062)
5.509		translation (GO:0006412)
5.232		rRNA processing (GO:0006364)
-5.148		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-4.830		mRNA splicing, via spliceosome (GO:0000398)
-4.672		negative regulation of transcription, DNA-templated (GO:0045892)
-4.659		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-4.480		positive regulation of transcription, DNA-templated (GO:0045893)
-4.231		regulation of transcription, DNA-templated (GO:0006355)
-4.214		protein deubiquitination (GO:0016579)

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

mitochondrial translational elongation (GO:0070125)



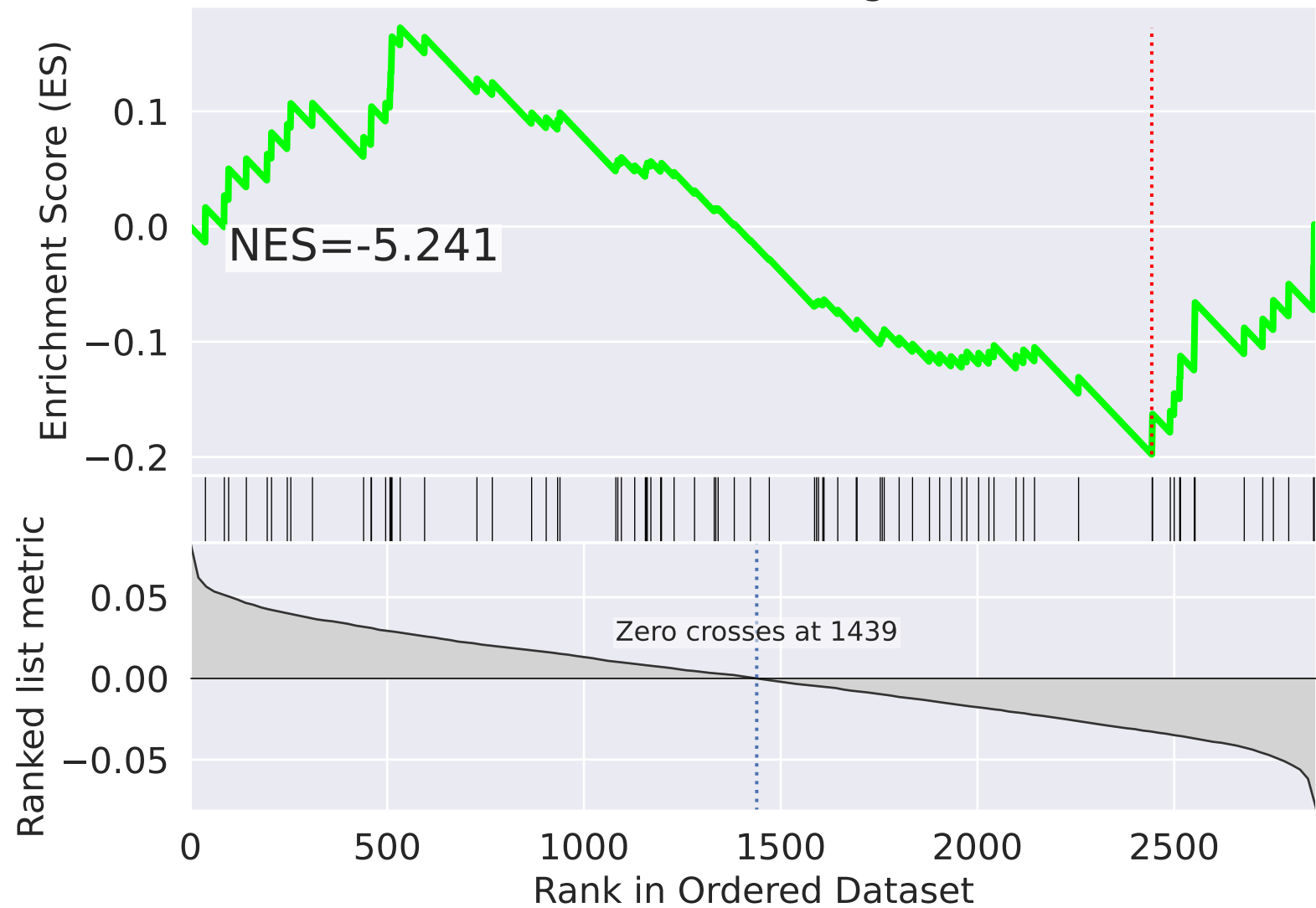
mitochondrial translational elongation (GO:0070125)



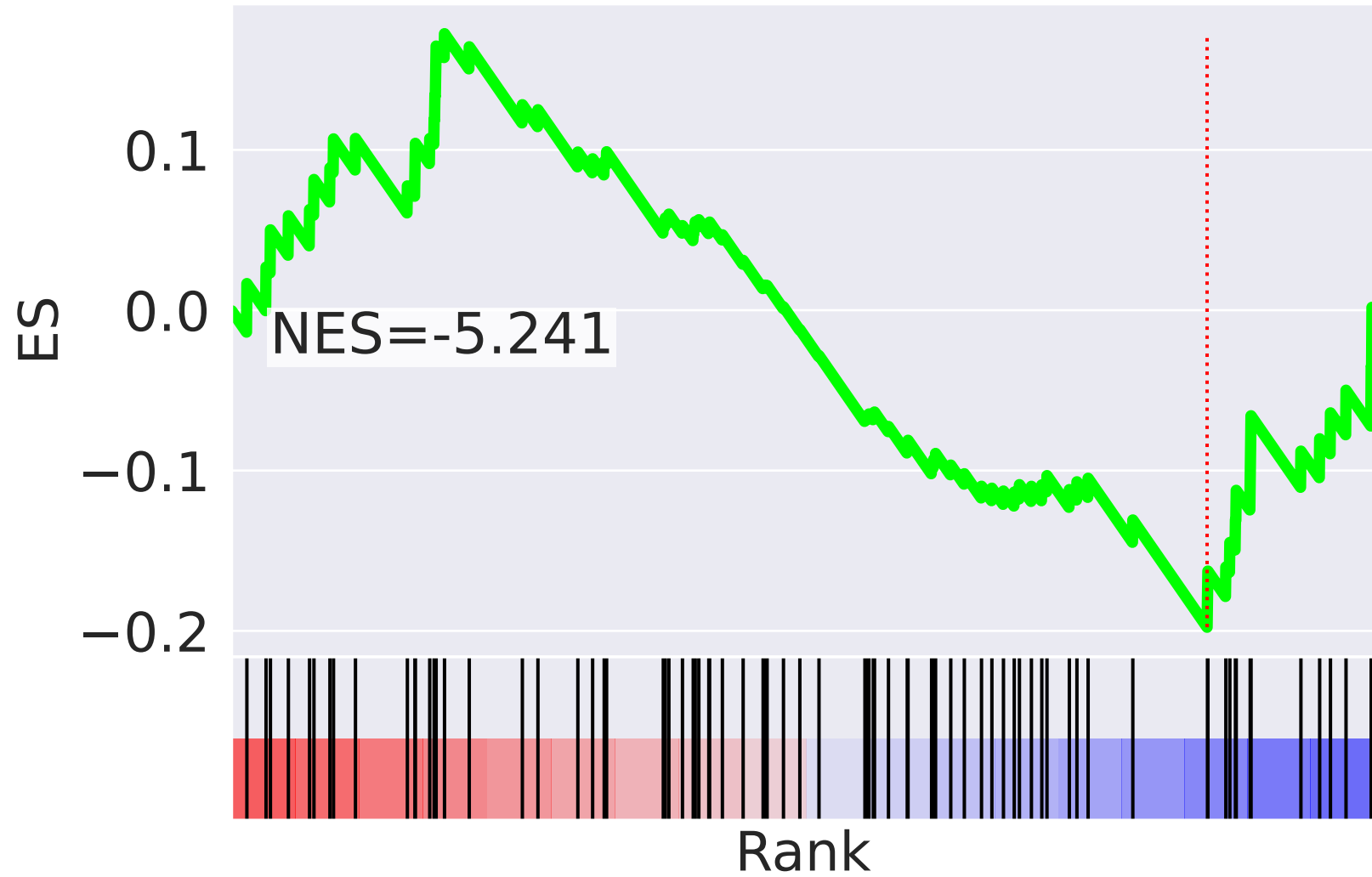
NES	SET
3.069	negative regulation of canonical Wnt signaling pathway (GO:0090090)
2.950	regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)
2.949	post-translational protein modification (GO:0043687)
2.944	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
2.889	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)
-2.870	protein K63-linked ubiquitination (GO:0070534)
2.832	mitotic spindle assembly checkpoint (GO:0007094)
2.794	beta-catenin-TCF complex assembly (GO:1904837)
2.725	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
2.616	MAPK cascade (GO:0000165)
-2.575	peptidyl-tyrosine dephosphorylation (GO:0035335)
2.567	defense response to bacterium (GO:0042742)
-2.547	establishment of protein localization (GO:0045184)
-2.498	negative regulation of signal transduction (GO:0009968)
2.468	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 $z=40$


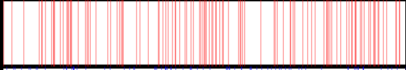
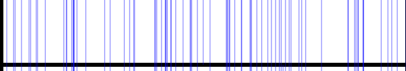
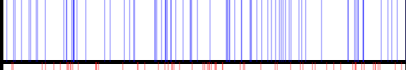
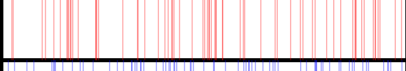
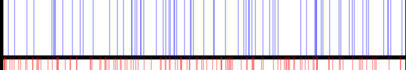
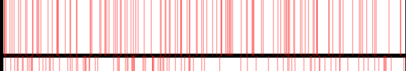
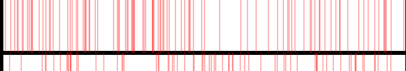
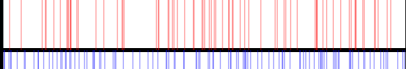
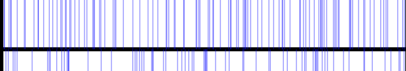
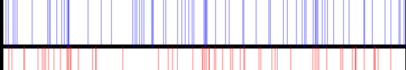
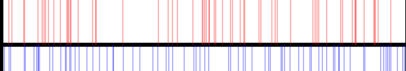
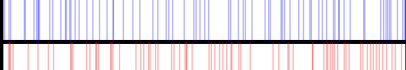
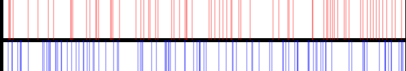
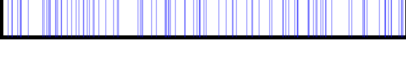
mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

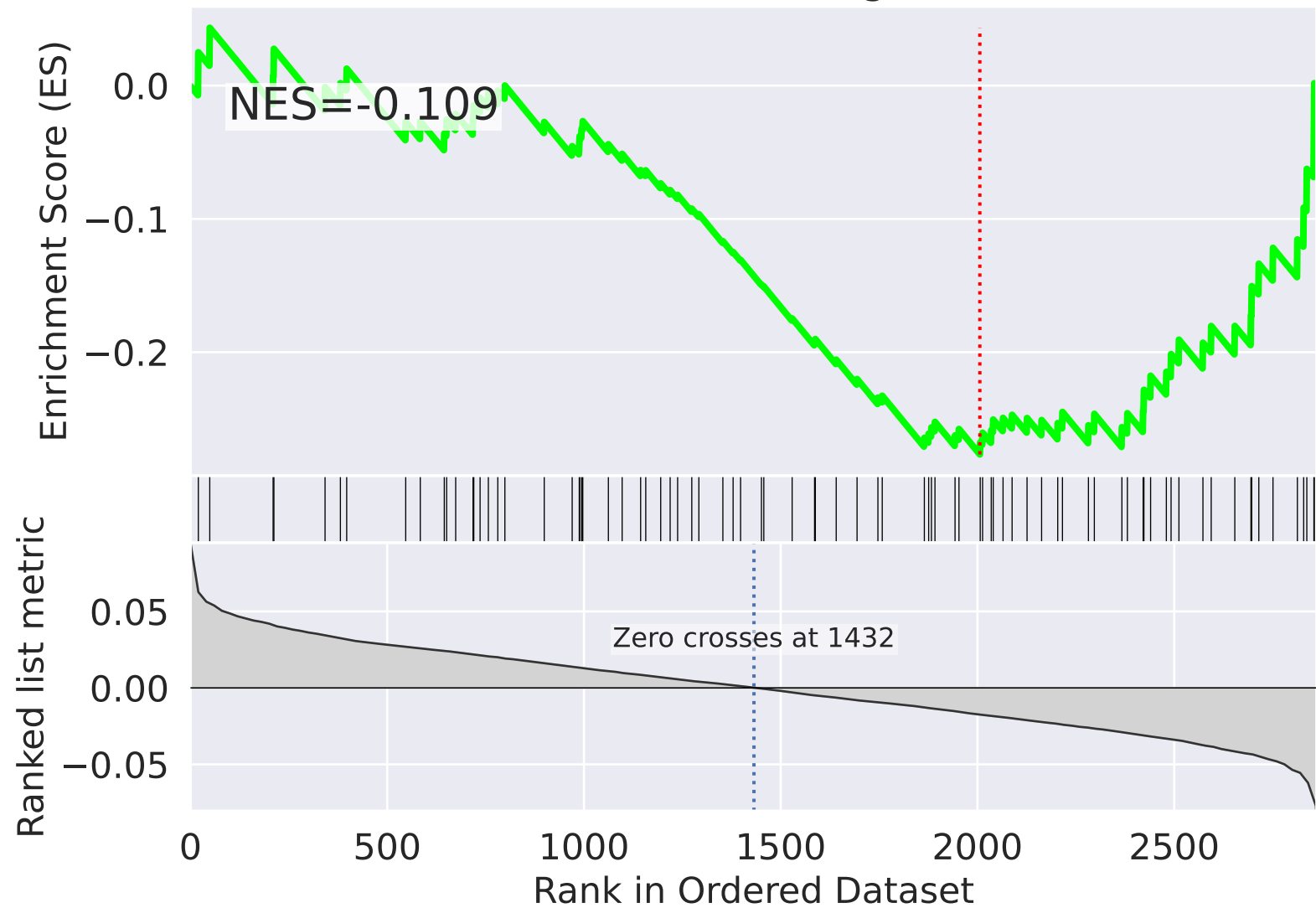


NES SET

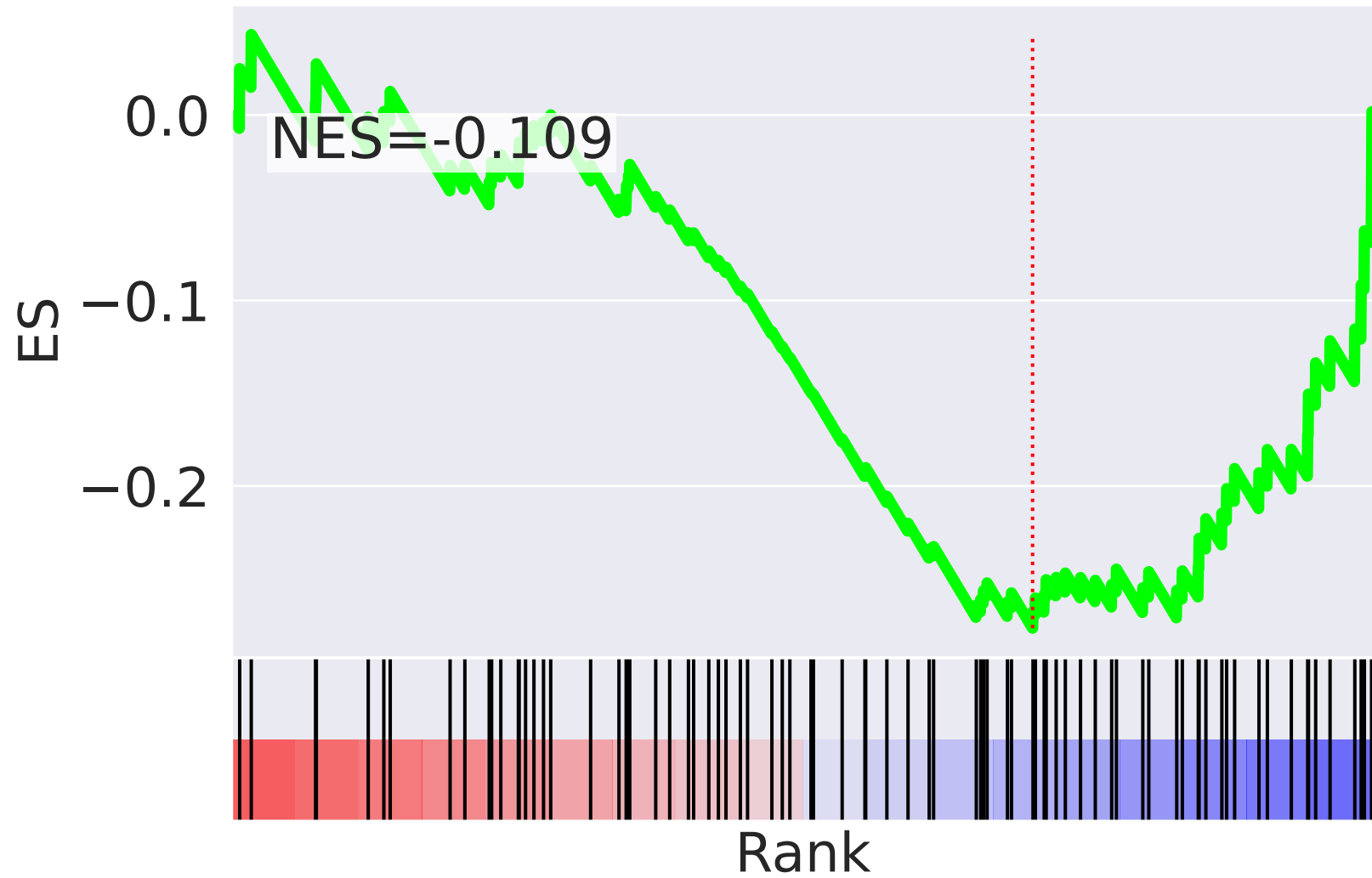
6.087		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
5.377		protein deubiquitination (GO:0016579)
-5.241		mitochondrial translational elongation (GO:0070125)
-5.196		mitochondrial translational termination (GO:0070126)
4.924		protein polyubiquitination (GO:0000209)
-4.352		positive regulation of cell proliferation (GO:0008284)
4.275		mRNA splicing, via spliceosome (GO:0000398)
4.097		regulation of transcription from RNA polymerase II promoter (GO:0006357)
4.032		MAPK cascade (GO:0000165)
-4.013		rRNA processing (GO:0006364)
-3.702		regulation of transcription, DNA-templated (GO:0006355)
3.379		Fc-epsilon receptor signaling pathway (GO:0038095)
-3.368		viral transcription (GO:0019083)
3.339		protein ubiquitination (GO:0016567)
-3.331		signal transduction (GO:0007165)

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

mitochondrial translational elongation (GO:0070125)

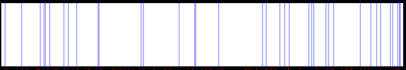
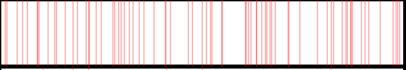




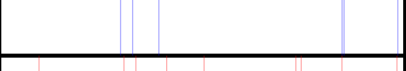
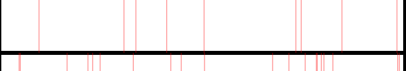


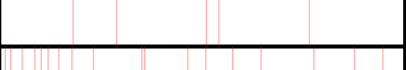






mitochondrial translational elongation (GO:0070125)



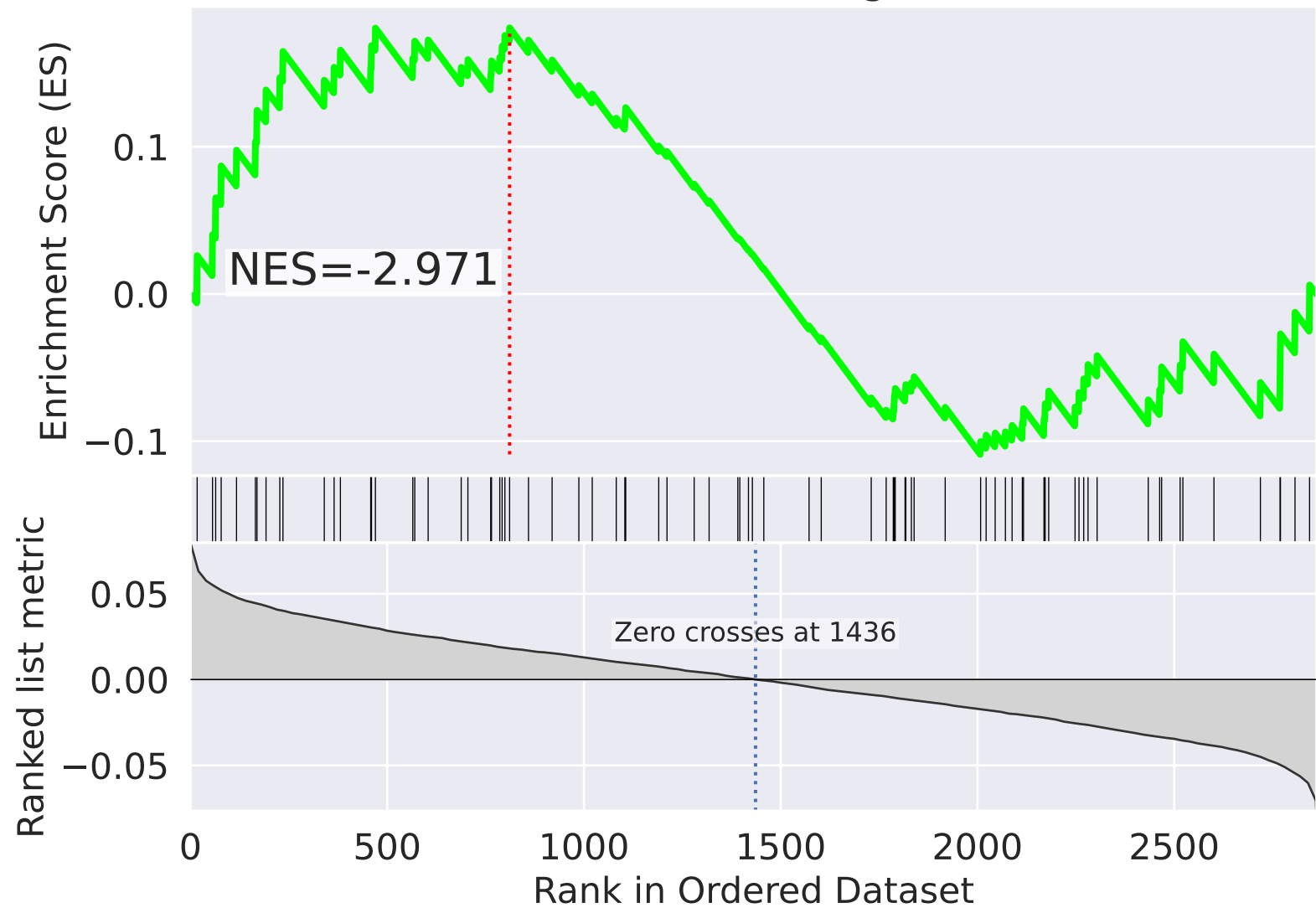
NES

SET

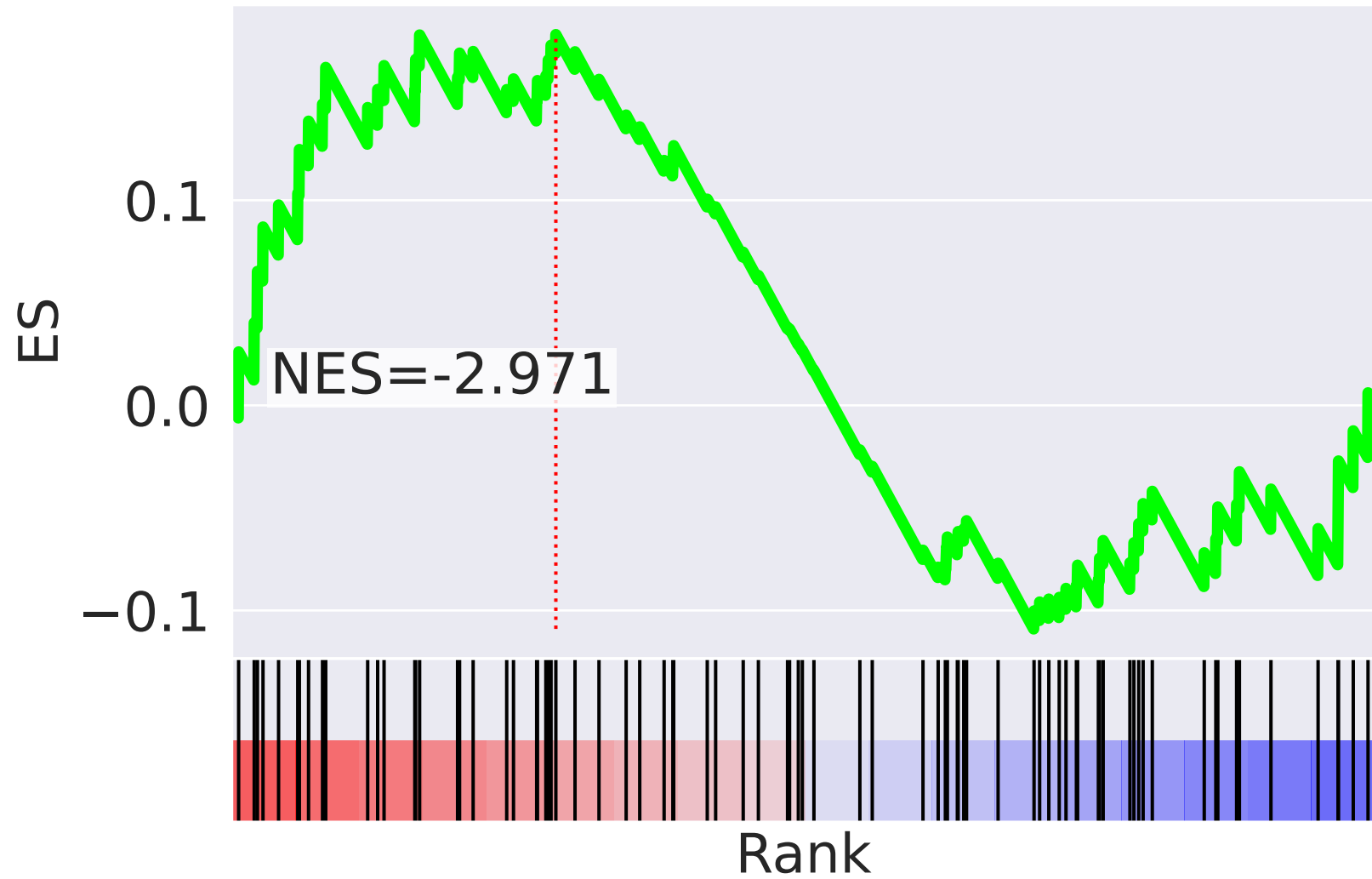
-2.913		ubiquitin-dependent protein catabolic process (GO:0006511)
2.896		regulation of transcription, DNA-templated (GO:0006355)
2.893		humoral immune response (GO:0006959)
-2.711		neuron apoptotic process (GO:0051402)
-2.625		histone H2B ubiquitination (GO:0033523)
-2.542		DNA recombination (GO:0006310)
-2.502		response to UV (GO:0009411)
2.488		response to cytokine (GO:0034097)
2.440		regulation of lipid metabolic process (GO:0019216)
2.417		neural tube closure (GO:0001843)
2.364		neuron differentiation (GO:0030182)
2.344		mitotic spindle assembly (GO:0090307)
2.321		fat cell differentiation (GO:0045444)
-2.311		pentose-phosphate shunt (GO:0006098)
-2.309		mitotic metaphase plate congression (GO:0007080)

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

mitochondrial translational elongation (GO:0070125)



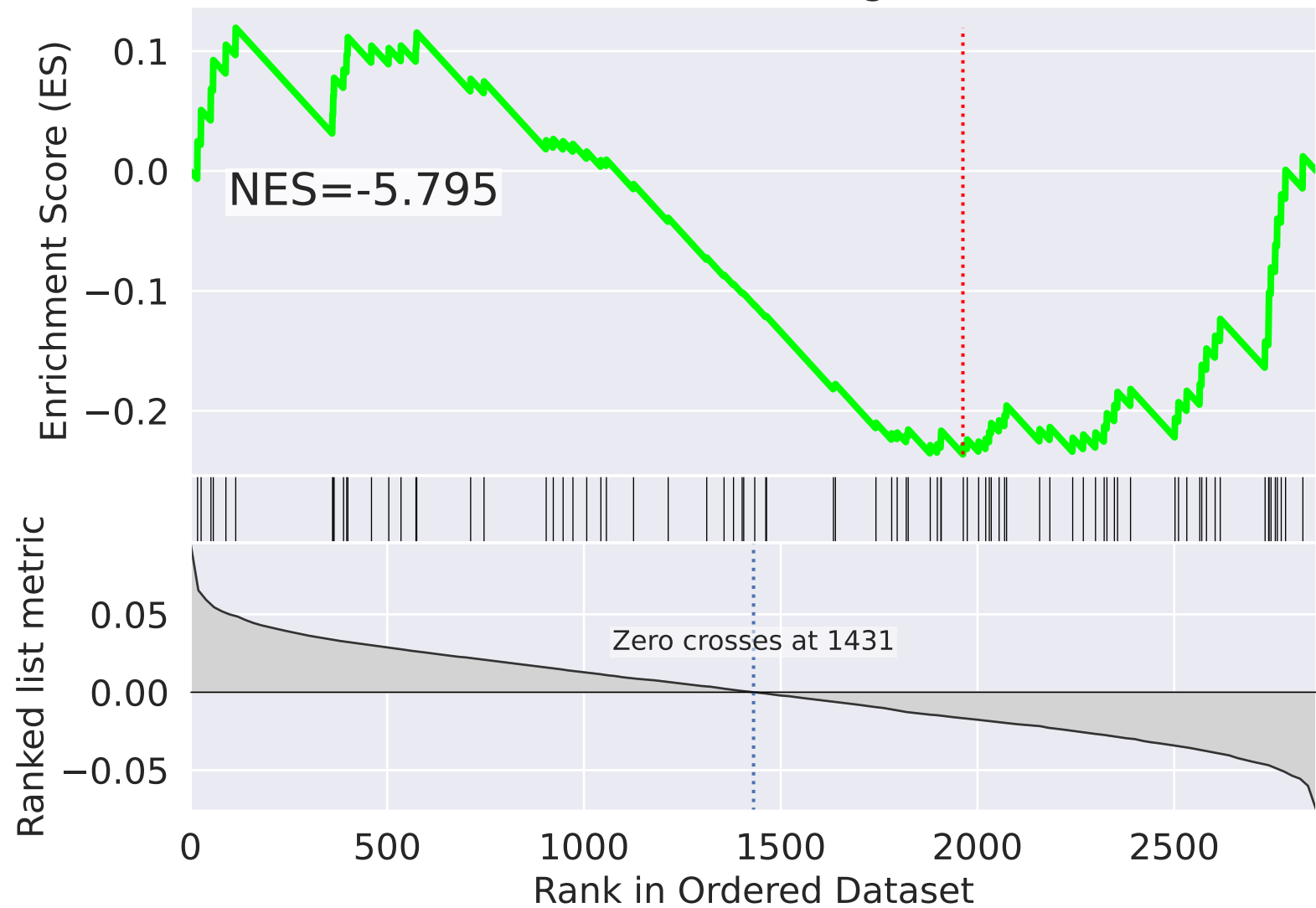
mitochondrial translational elongation (GO:0070125)



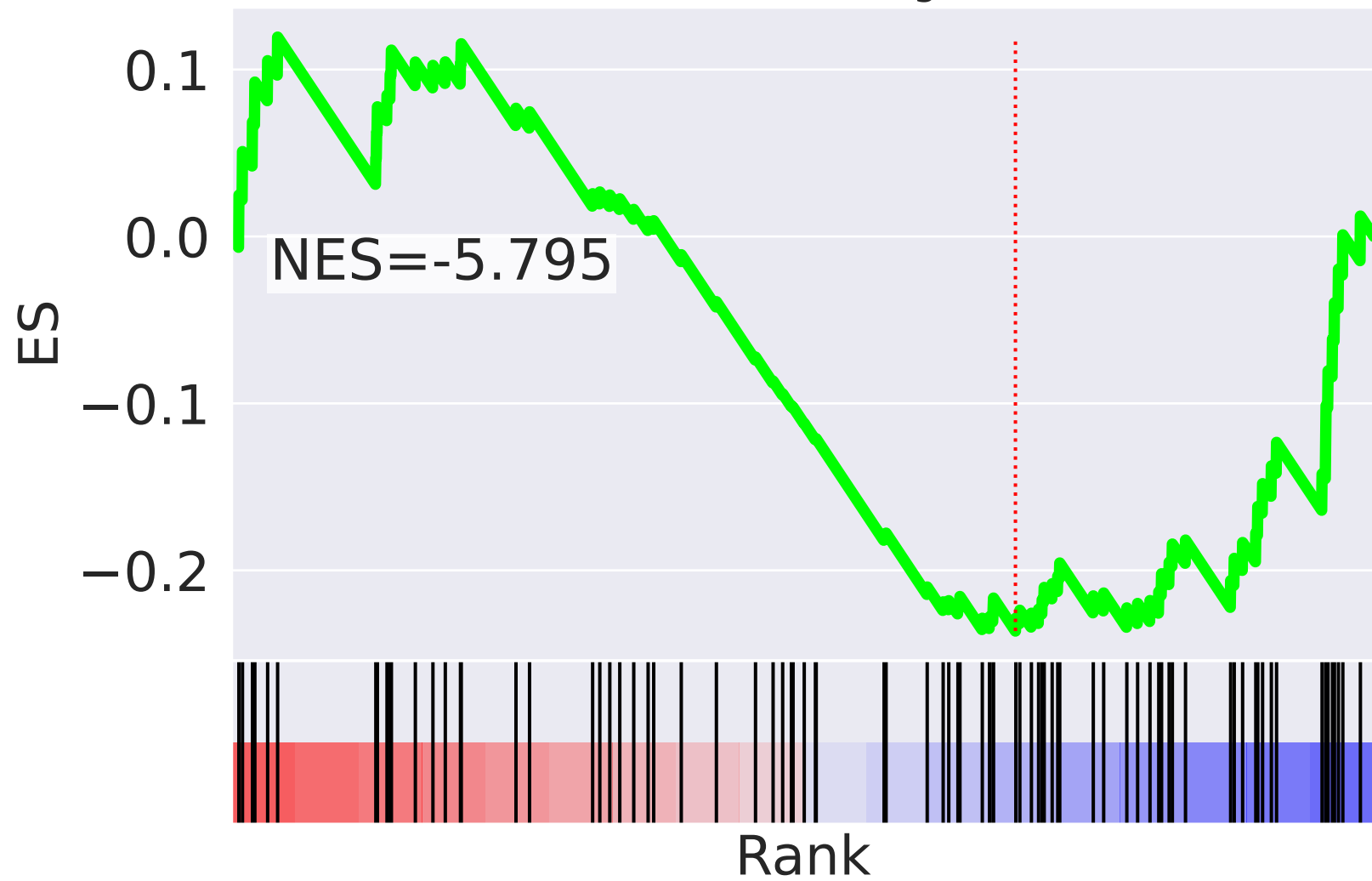
NES		SET
3.325		retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)
-2.971		mitochondrial translational elongation (GO:0070125)
2.890		positive regulation of transforming growth factor beta receptor signaling pathway (GO:0030511)
2.832		MAPK cascade (GO:0000165)
-2.799		mitochondrial translational termination (GO:0070126)
-2.745		phosphorylation (GO:0016310)
2.625		negative regulation of transcription, DNA-templated (GO:0045892)
-2.595		interstrand cross-link repair (GO:0036297)
2.563		response to unfolded protein (GO:0006986)
2.562		intra-Golgi vesicle-mediated transport (GO:0006891)
2.496		RNA processing (GO:0006396)
-2.487		tRNA modification (GO:0006400)
2.468		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.456		nuclear-transcribed mRNA catabolic process (GO:0000956)
2.447		spermatogenesis (GO:0007283)

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

mitochondrial translational elongation (GO:0070125)

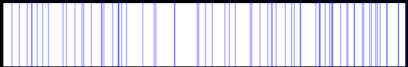
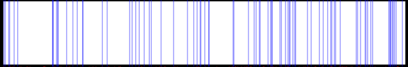
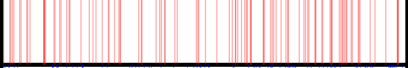
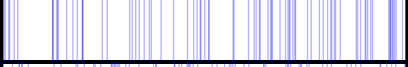
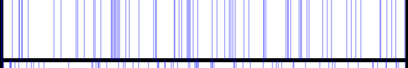
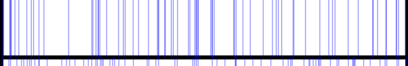
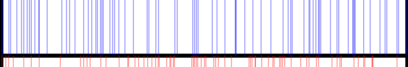
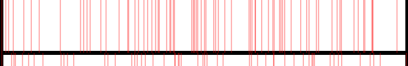
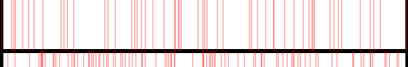
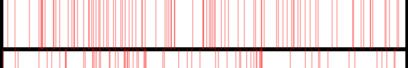
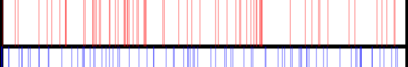
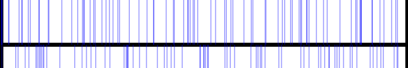
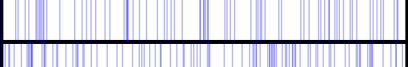
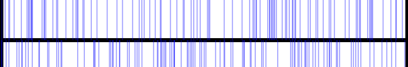



mitochondrial translational elongation (GO:0070125)



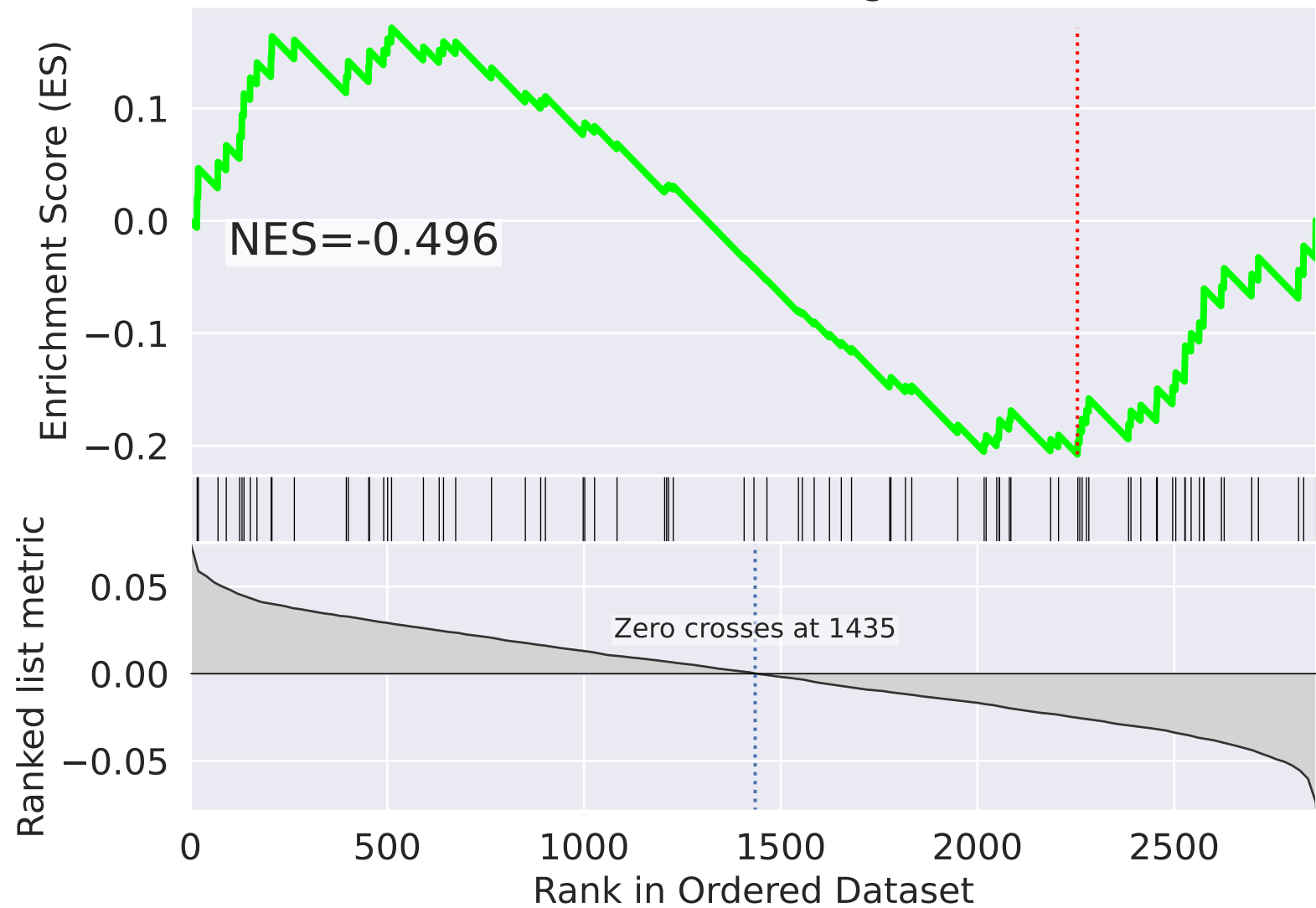
NES

SET

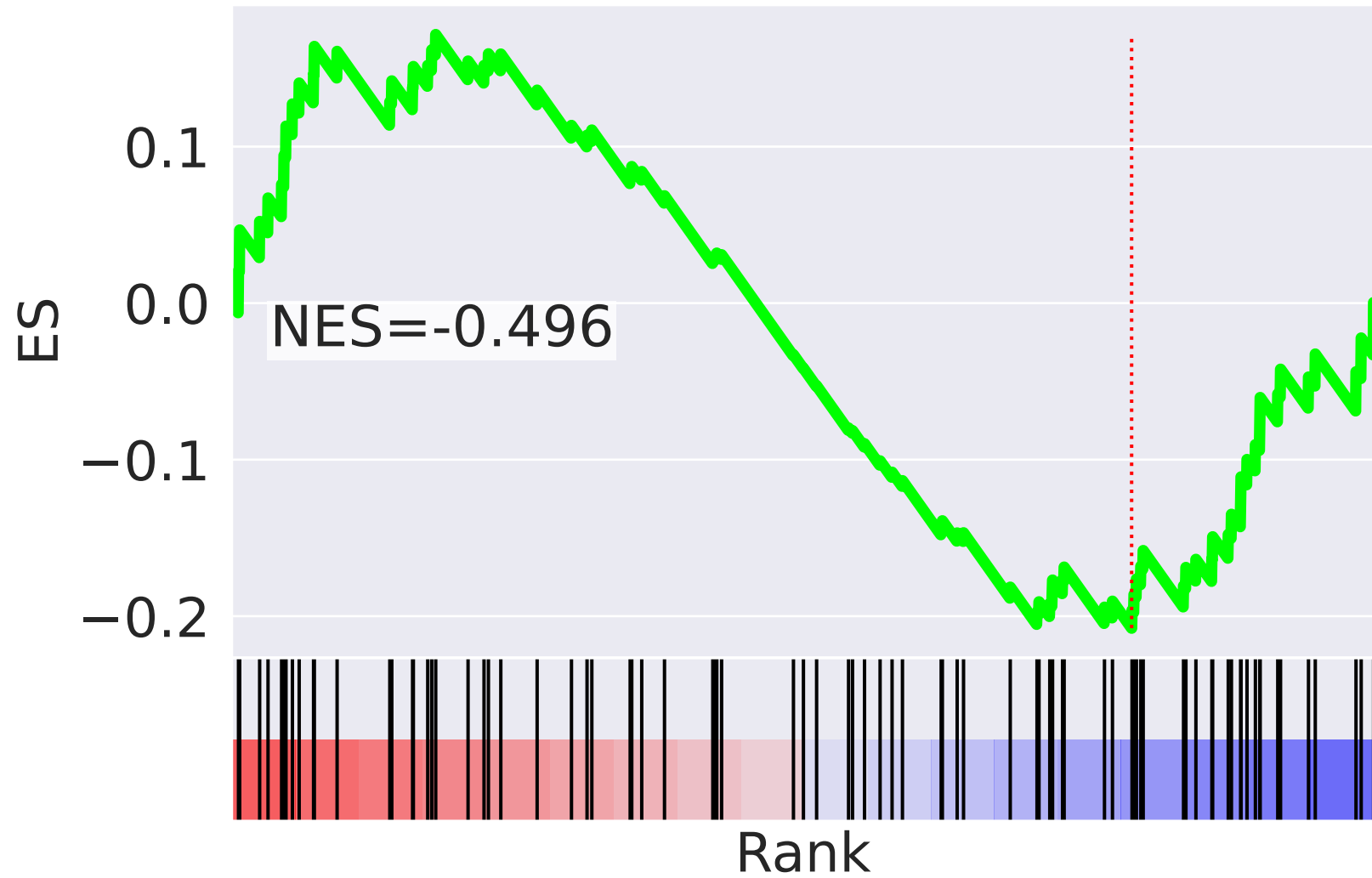
-6.187		positive regulation of cell proliferation (GO:0008284)
-5.795		mitochondrial translational elongation (GO:0070125)
5.676		signal transduction (GO:0007165)
-5.632		mitochondrial translational termination (GO:0070126)
-5.114		MAPK cascade (GO:0000165)
-4.930		regulation of transcription, DNA-templated (GO:0006355)
-4.930		negative regulation of apoptotic process (GO:0043066)
4.408		protein ubiquitination (GO:0016567)
4.380		membrane organization (GO:0061024)
4.071		negative regulation of transcription, DNA-templated (GO:0045892)
4.038		cellular response to DNA damage stimulus (GO:0006974)
-3.865		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-3.756		regulation of signal transduction by p53 class mediator (GO:1901796)
-3.542		translation (GO:0006412)
-3.537		protein deubiquitination (GO:0016579)

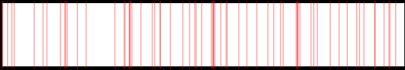

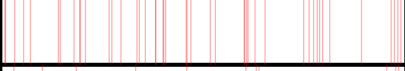


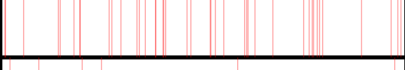

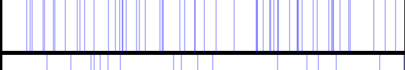


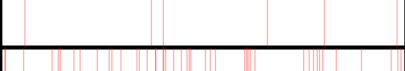
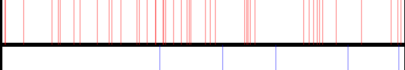
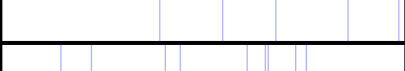
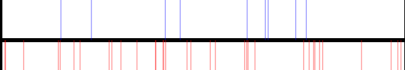
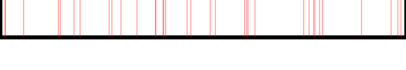
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=44$

mitochondrial translational elongation (GO:0070125)



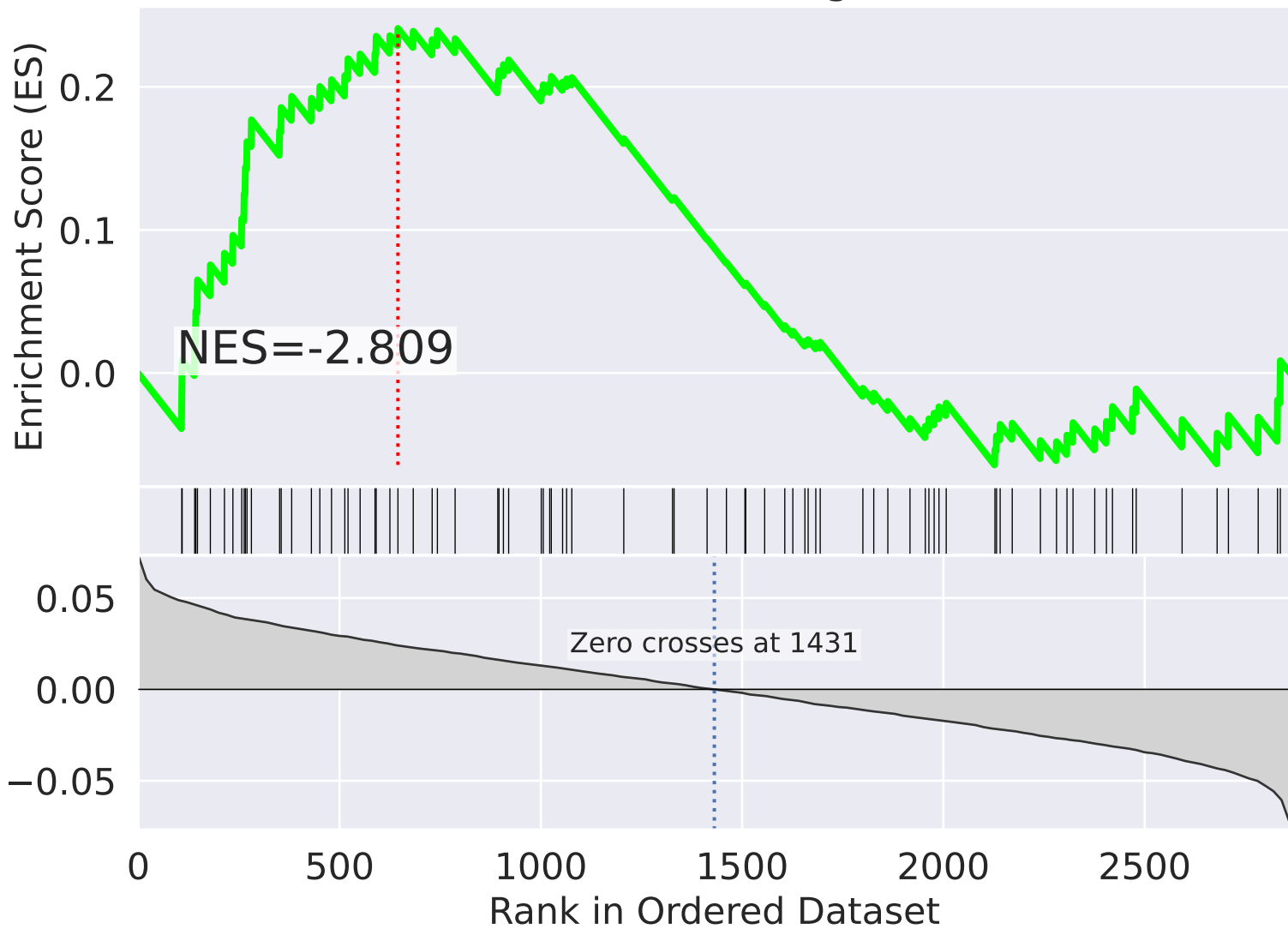
mitochondrial translational elongation (GO:0070125)



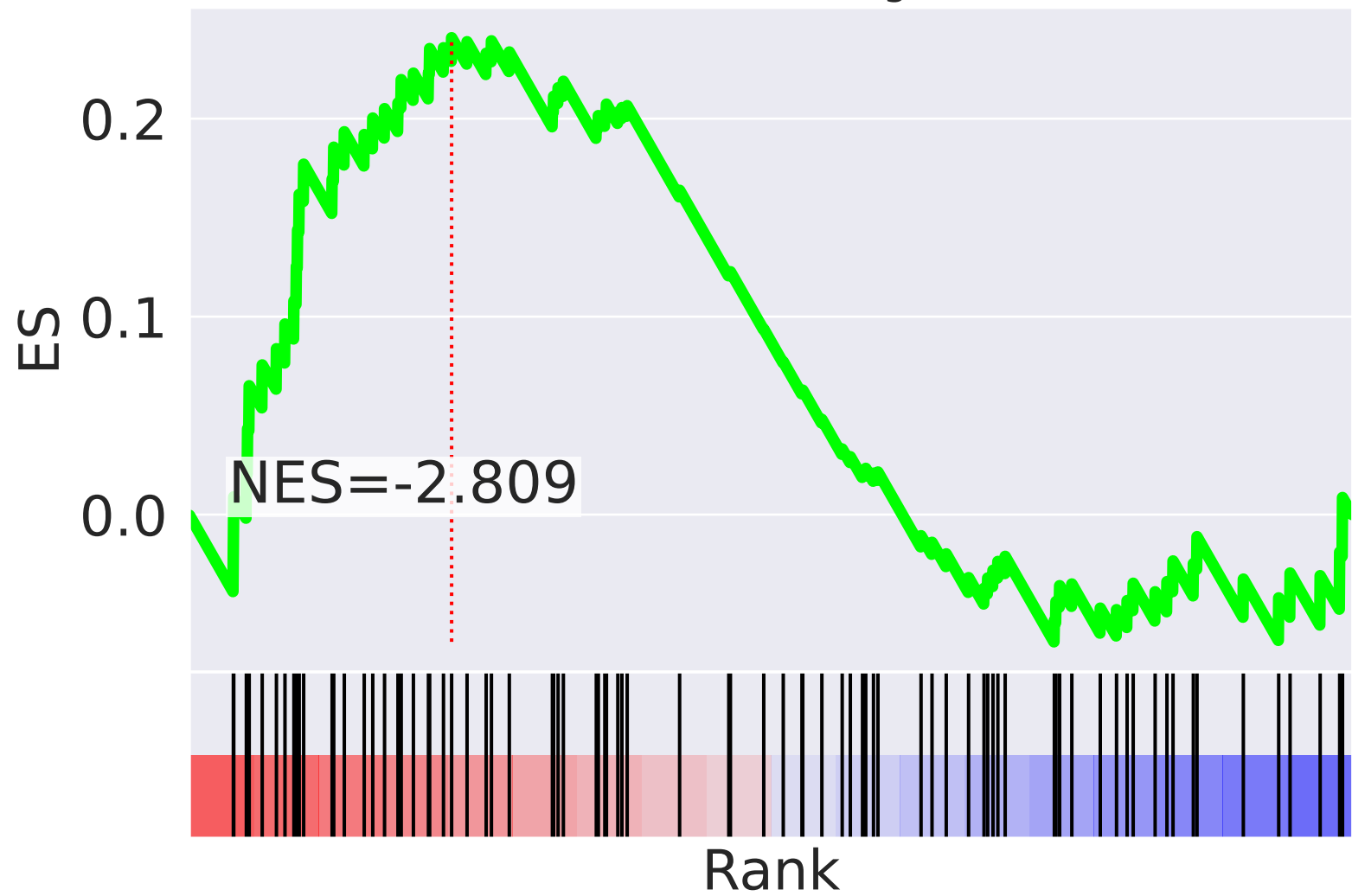
NES		SET
2.826		transcription initiation from RNA polymerase II promoter (GO:0006367)
-2.782		regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
2.650		NIK/NF-kappaB signaling (GO:0038061)
2.638		cytoskeleton organization (GO:0007010)
-2.637		regulation of cardiac conduction (GO:1903779)
2.607		SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)
2.605		skeletal muscle tissue development (GO:0007519)
-2.540		G2/M transition of mitotic cell cycle (GO:0000086)
-2.442		regulation of small GTPase mediated signal transduction (GO:0051056)
-2.388		virion assembly (GO:0019068)
2.362		endosome organization (GO:0007032)
2.360		Wnt signaling pathway, planar cell polarity pathway (GO:0060071)
-2.359		extrinsic apoptotic signaling pathway in absence of ligand (GO:0097192)
-2.352		mitophagy (GO:0000422)
2.346		regulation of cellular amino acid metabolic process (GO:0006521)

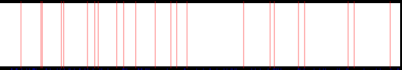
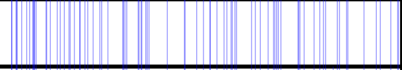
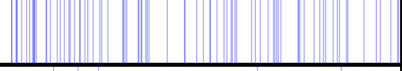
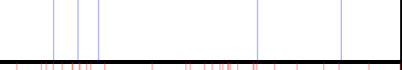
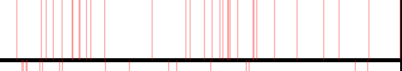
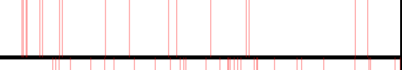
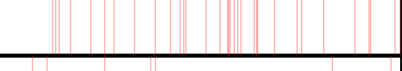
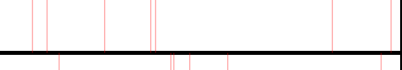
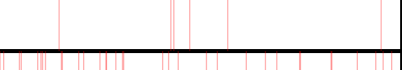
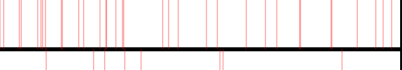


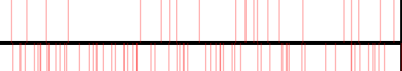
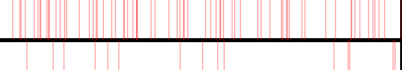
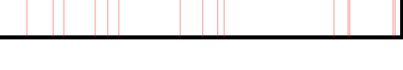
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=45$

mitochondrial translational elongation (GO:0070125)



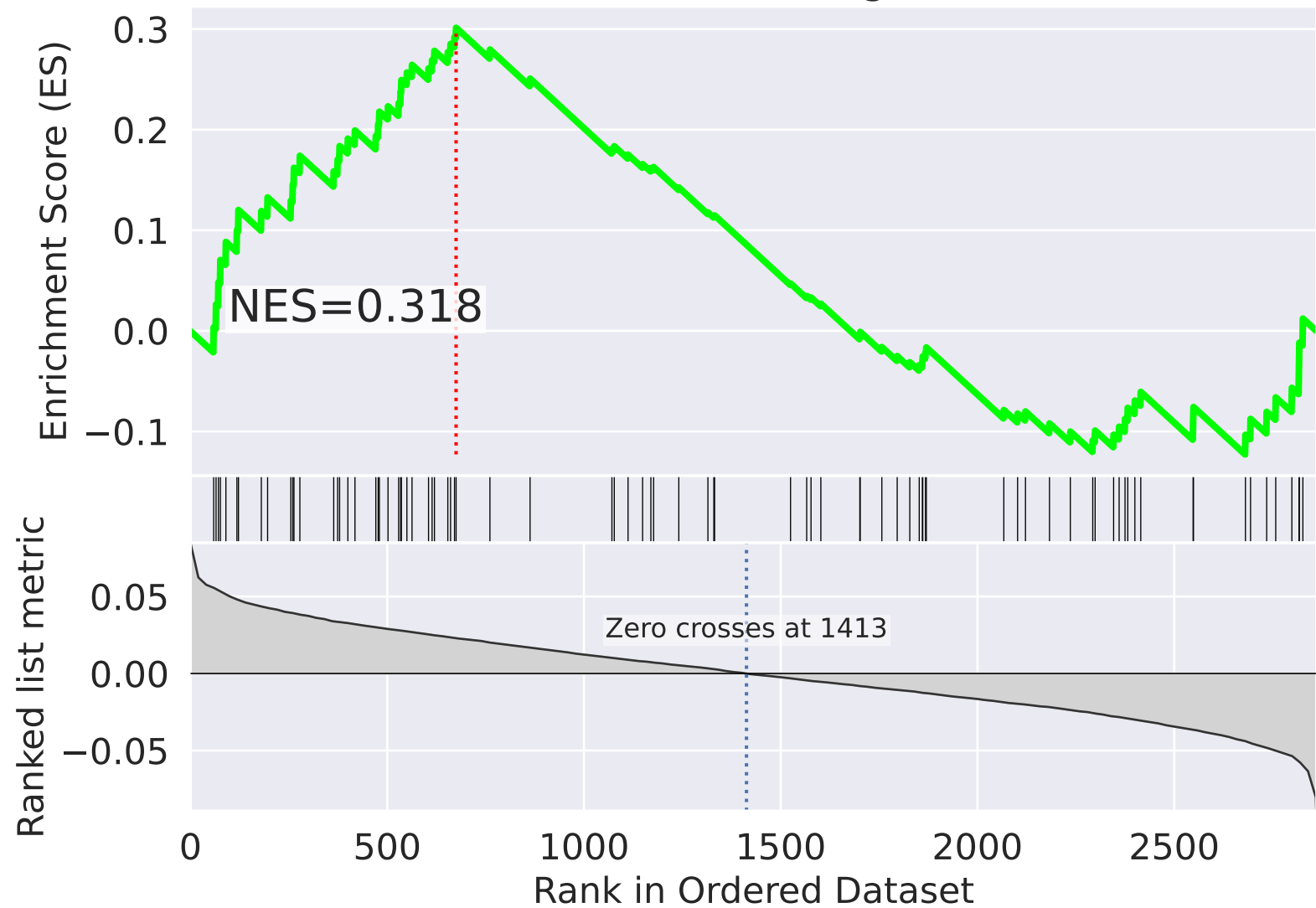
mitochondrial translational elongation (GO:0070125)



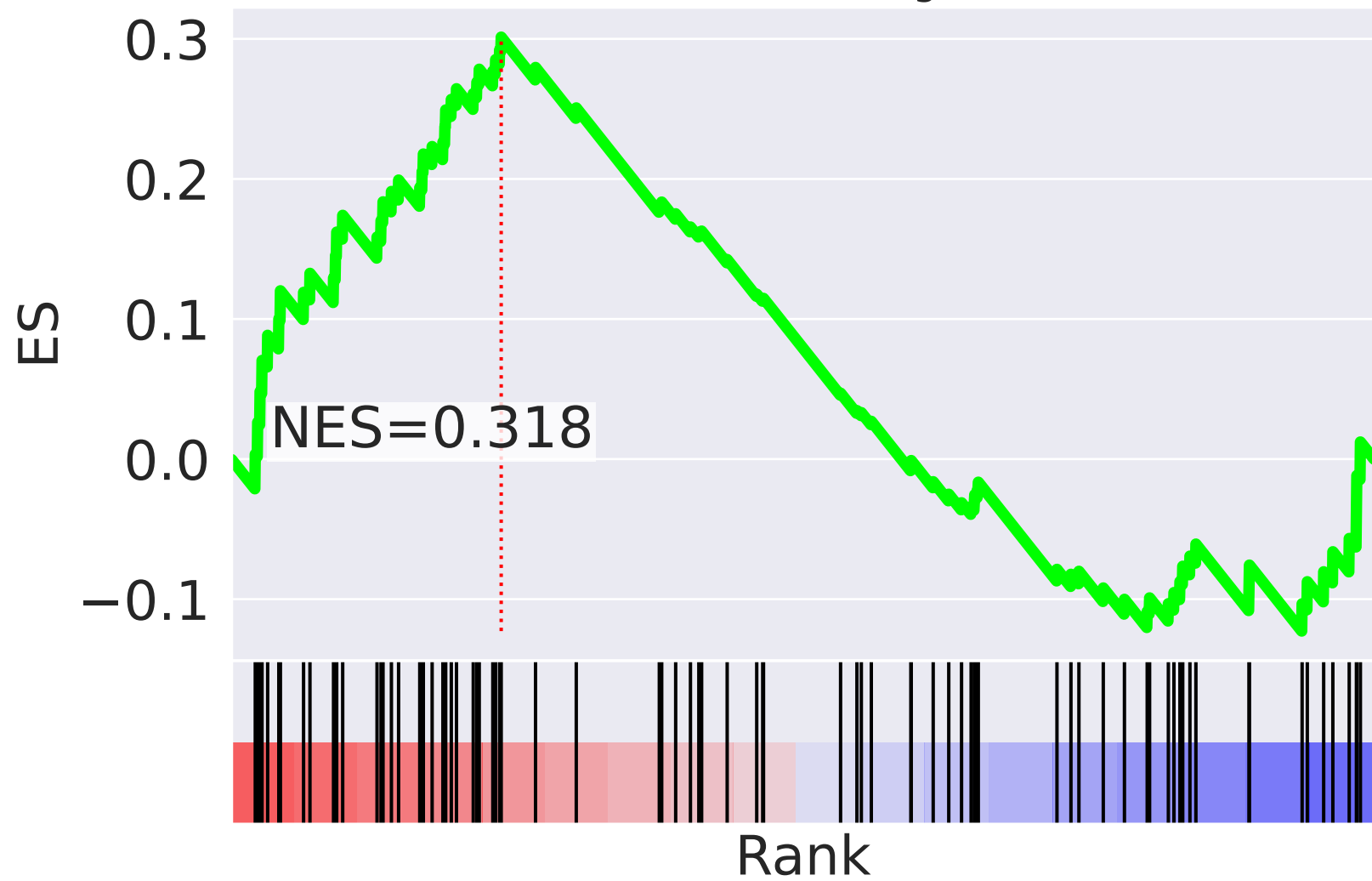
NES		SET
3.045		cellular response to UV (GO:0034644)
-2.921		mitochondrial translational termination (GO:0070126)
-2.809		mitochondrial translational elongation (GO:0070125)
-2.682		regulation of cardiac conduction (GO:1903779)
2.674		intracellular signal transduction (GO:0035556)
2.575		negative regulation of sequence-specific DNA binding transcription factor activity (GO:0043433)
2.551		peptidyl-serine phosphorylation (GO:0018105)
2.539		response to heat (GO:0009408)
2.513		positive regulation of reactive oxygen species metabolic process (GO:2000379)
2.476		chromatin remodeling (GO:0006338)
2.431		regulation of cell migration (GO:0030334)
-2.417		negative regulation of intrinsic apoptotic signaling pathway (GO:2001243)
2.409		blood coagulation (GO:0007596)
2.407		sister chromatid cohesion (GO:0007062)
2.394		response to ionizing radiation (GO:0010212)

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

mitochondrial translational elongation (GO:0070125)



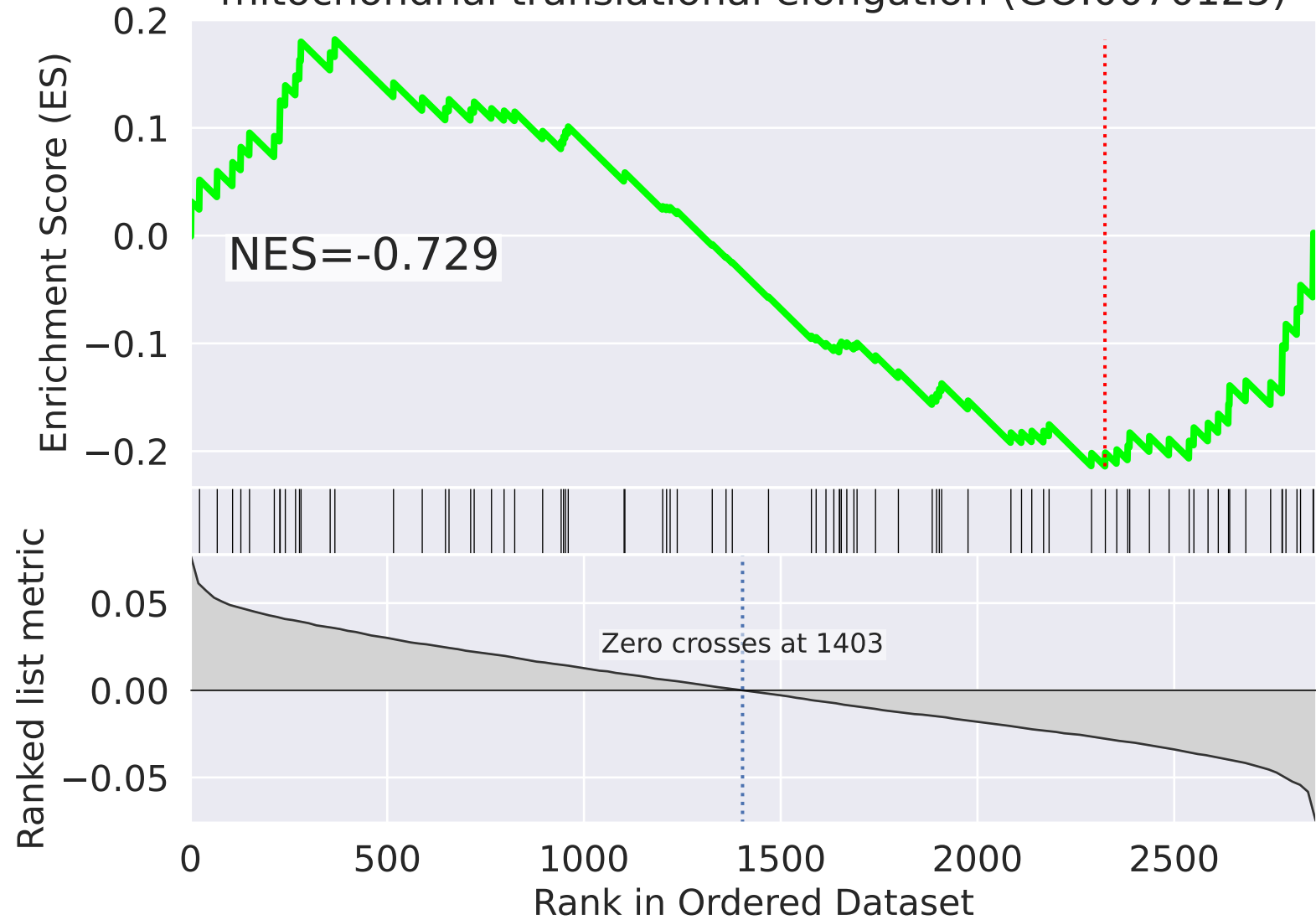
mitochondrial translational elongation (GO:0070125)



NES	SET
2.734	positive regulation of GTPase activity (GO:0043547)
-2.600	intracellular estrogen receptor signaling pathway (GO:0030520)
-2.545	regulation of RNA splicing (GO:0043484)
2.418	establishment of endothelial intestinal barrier (GO:0090557)
2.399	ubiquitin-dependent protein catabolic process (GO:0006511)
2.373	regulation of protein localization (GO:0032880)
-2.286	phosphatidylcholine biosynthetic process (GO:0006656)
-2.261	retrograde protein transport, ER to cytosol (GO:0030970)
-2.256	positive regulation of autophagy (GO:0010508)
2.240	regulation of microtubule-based process (GO:0032886)
-2.218	protein methylation (GO:0006479)
2.214	cell-matrix adhesion (GO:0007160)
-2.206	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043154)
-2.202	mRNA processing (GO:0006397)
-2.189	lipid metabolic process (GO:0006629)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)


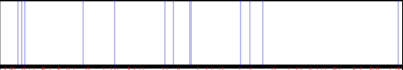
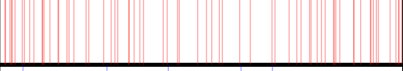
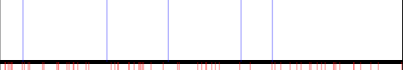
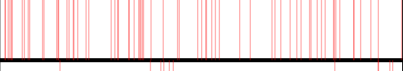
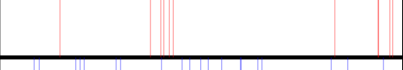
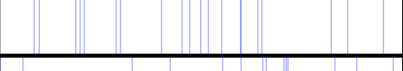

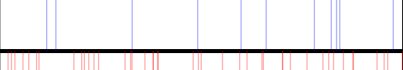
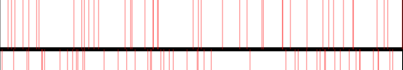
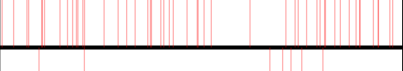

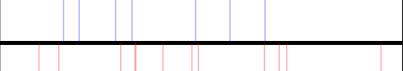
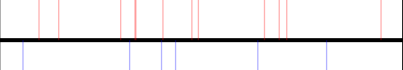
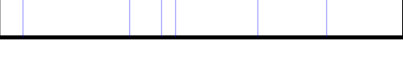
ES

0.2
0.1
0.0
-0.1
-0.2

NES=-0.729

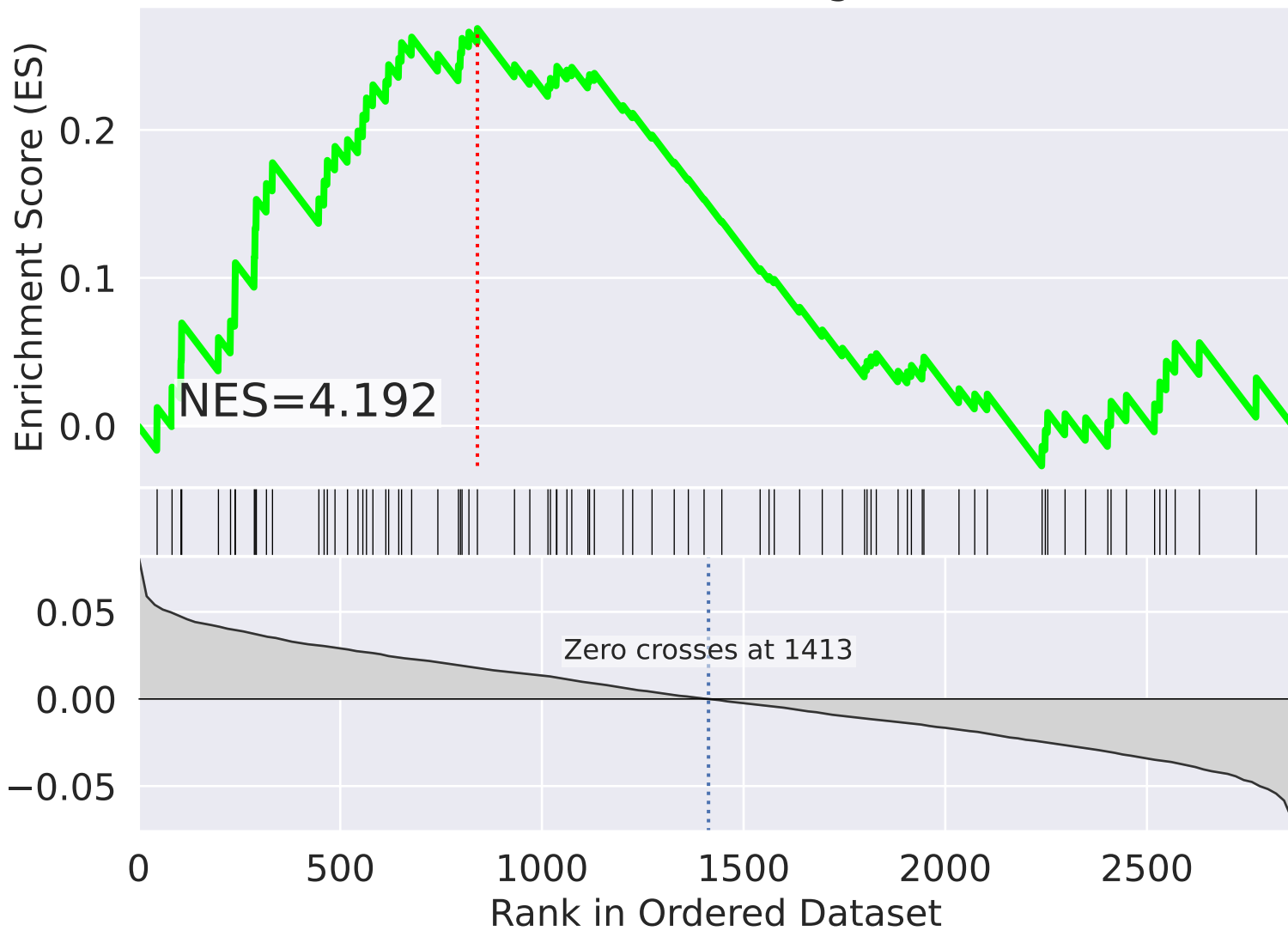
Rank



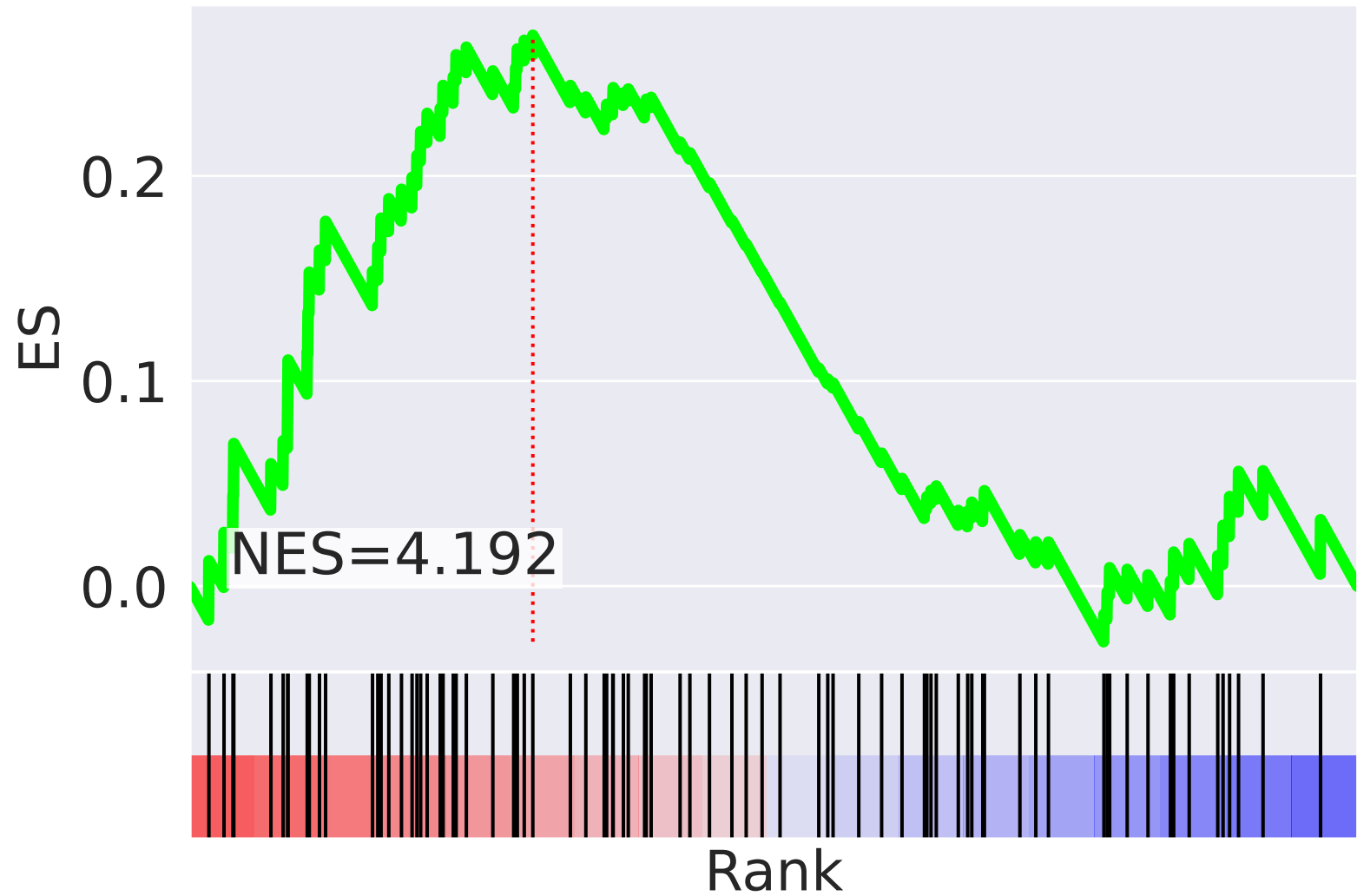
NES		SET
-2.764		cellular response to nerve growth factor stimulus (GO:1990090)
-2.762		DNA recombination (GO:0006310)
2.672		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
-2.632		negative regulation of telomerase activity (GO:0051974)
2.608		translational initiation (GO:0006413)
2.581		snRNA processing (GO:0016180)
-2.540		double-strand break repair via nonhomologous end joining (GO:0006303)
-2.524		nucleotide-excision repair (GO:0006289)
-2.500		global genome nucleotide-excision repair (GO:0070911)
2.494		positive regulation of gene expression (GO:0010628)
2.492		snRNA transcription from RNA polymerase II promoter (GO:0042795)
2.465		positive regulation of erythrocyte differentiation (GO:0045648)
-2.455		positive regulation of osteoblast differentiation (GO:0045669)
2.453		cellular response to epidermal growth factor stimulus (GO:0071364)
-2.435		DNA damage response, signal transduction by p53 class mediator (GO:0030330)

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)

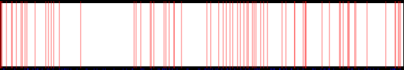
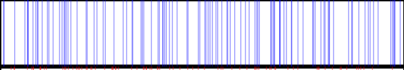
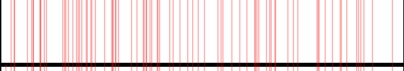
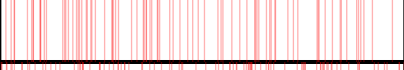
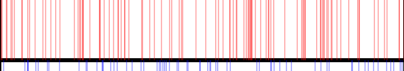
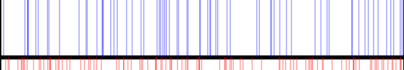
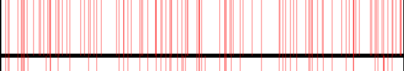
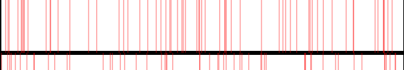
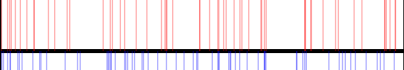
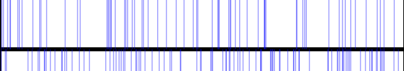
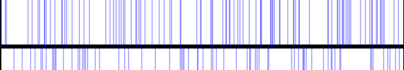
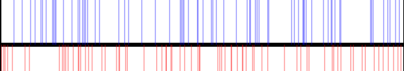
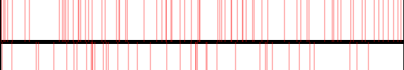
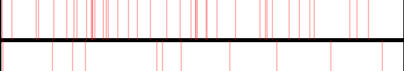
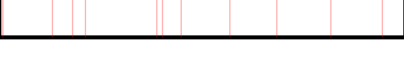


mitochondrial translational elongation (GO:0070125)



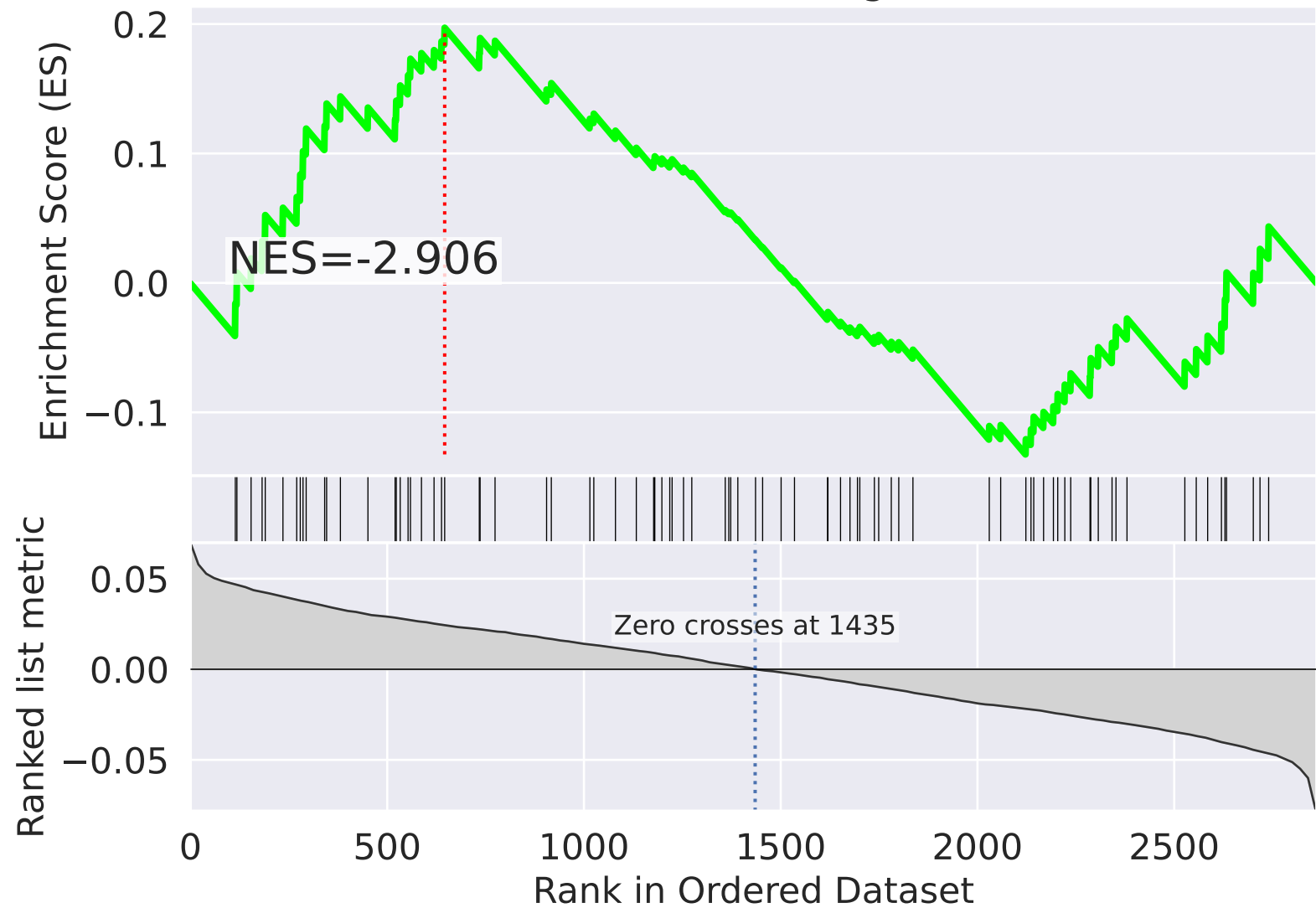
NES

SET

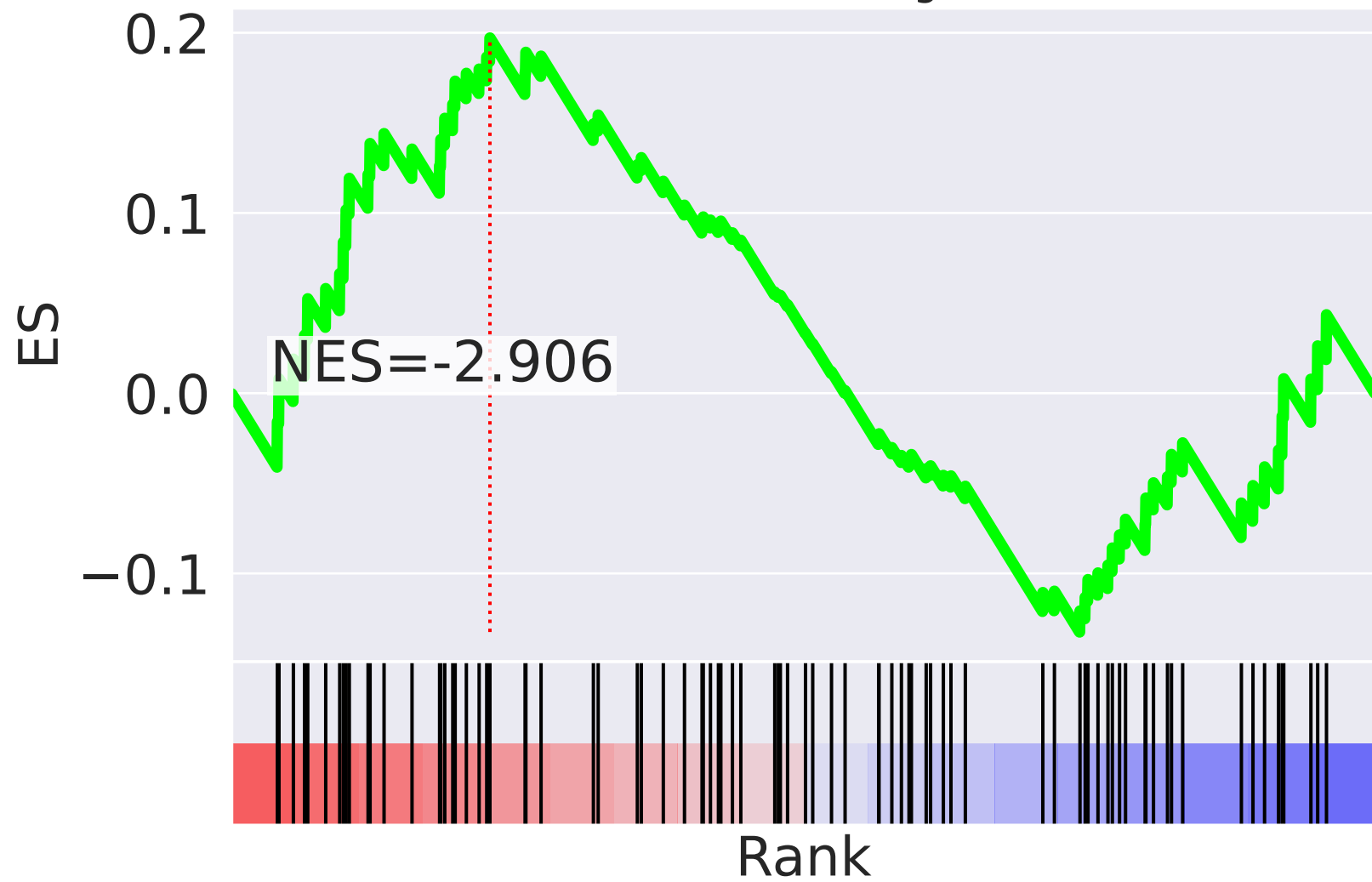
5.652		regulation of transcription, DNA-templated (GO:0006355)
-4.636		rRNA processing (GO:0006364)
4.226		mitochondrial translational termination (GO:0070126)
4.192		mitochondrial translational elongation (GO:0070125)
4.067		signal transduction (GO:0007165)
-3.827		translational initiation (GO:0006413)
3.672		transcription from RNA polymerase II promoter (GO:0006366)
3.620		transcription elongation from RNA polymerase II promoter (GO:0006368)
3.566		positive regulation of apoptotic process (GO:0043065)
-3.496		DNA replication (GO:0006260)
-3.371		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-3.335		protein phosphorylation (GO:0006468)
3.288		protein ubiquitination (GO:0016567)
3.285		mitochondrial respiratory chain complex I assembly (GO:0032981)
3.262		regulation of mitotic spindle assembly (GO:1901673)


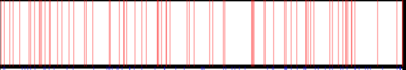
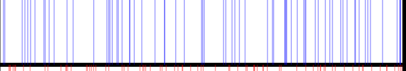
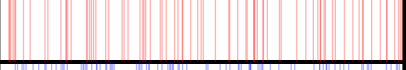
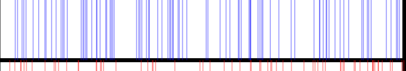
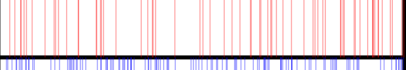
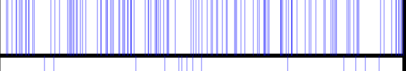
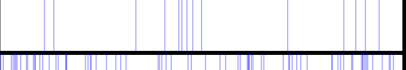
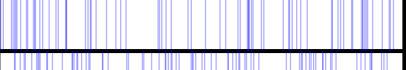
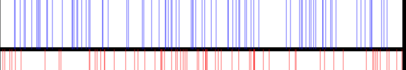
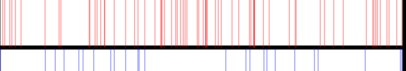
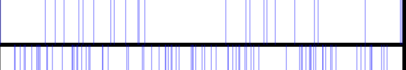
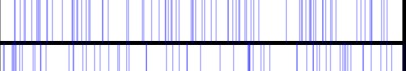

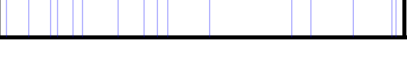
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=49$

mitochondrial translational elongation (GO:0070125)



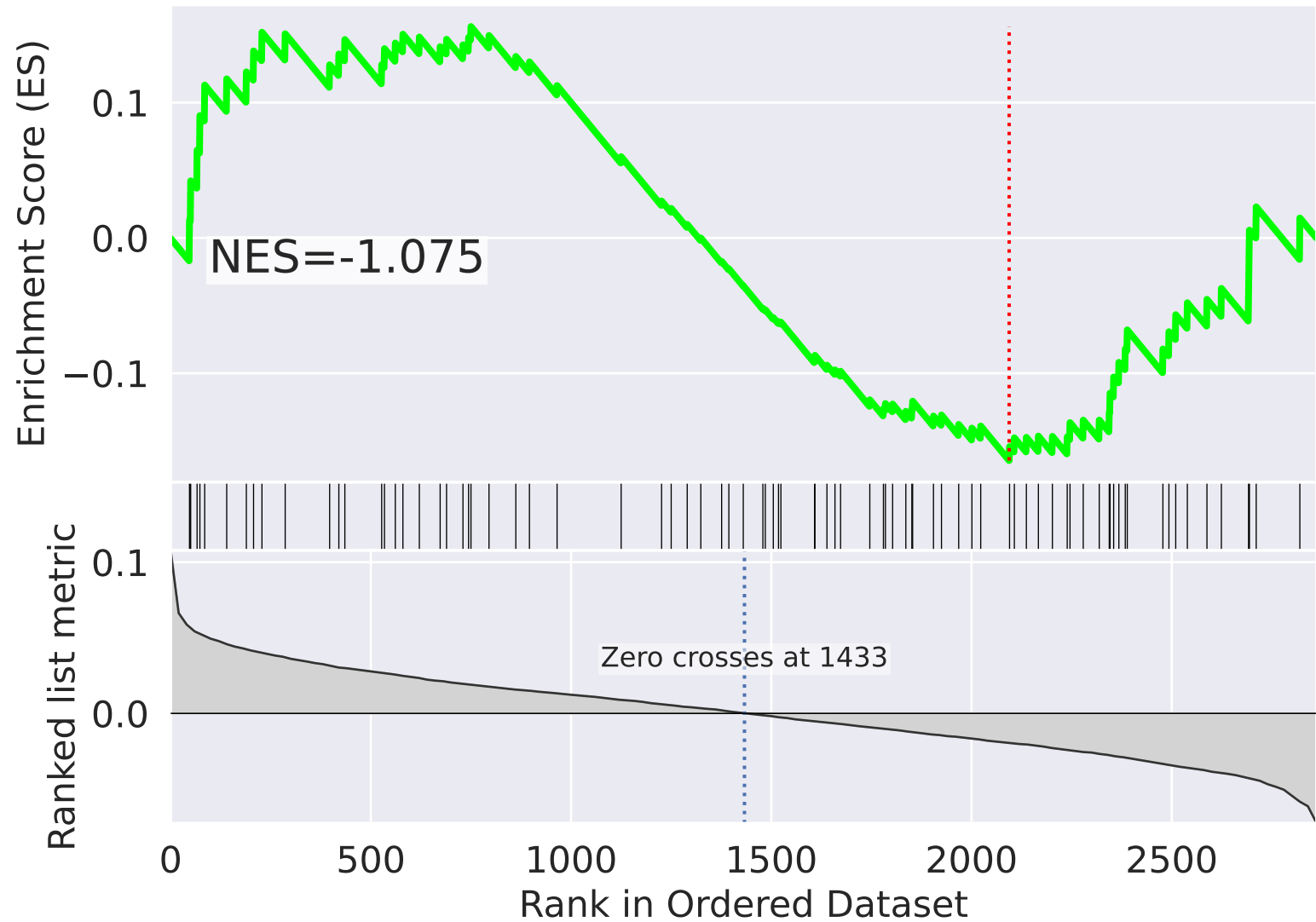
mitochondrial translational elongation (GO:0070125)



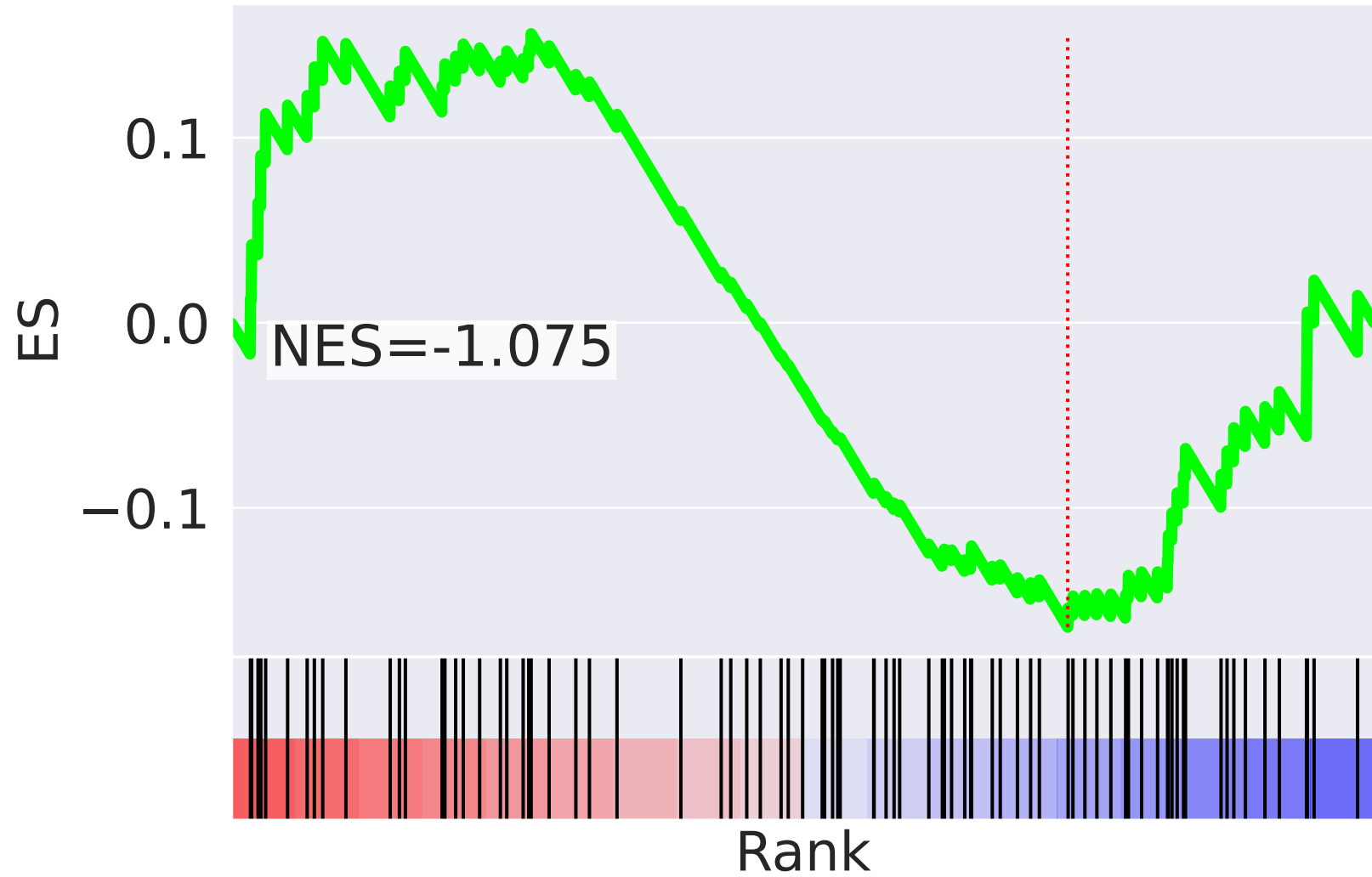
NES		SET
4.210		regulation of signal transduction by p53 class mediator (GO:1901796)
3.991		protein ubiquitination (GO:0016567)
-3.629		cellular response to DNA damage stimulus (GO:0006974)
3.477		negative regulation of apoptotic process (GO:0043066)
-3.453		neutrophil degranulation (GO:0043312)
3.422		sister chromatid cohesion (GO:0007062)
-3.403		mRNA splicing, via spliceosome (GO:0000398)
-3.056		brain development (GO:0007420)
-2.983		viral transcription (GO:0019083)
-2.906		mitochondrial translational elongation (GO:0070125)
2.865		protein phosphorylation (GO:0006468)
-2.859		cell migration (GO:0016477)
-2.823		mitochondrial translational termination (GO:0070126)
-2.678		protein polyubiquitination (GO:0000209)
-2.654		mRNA polyadenylation (GO:0006378)

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

mitochondrial translational elongation (GO:0070125)



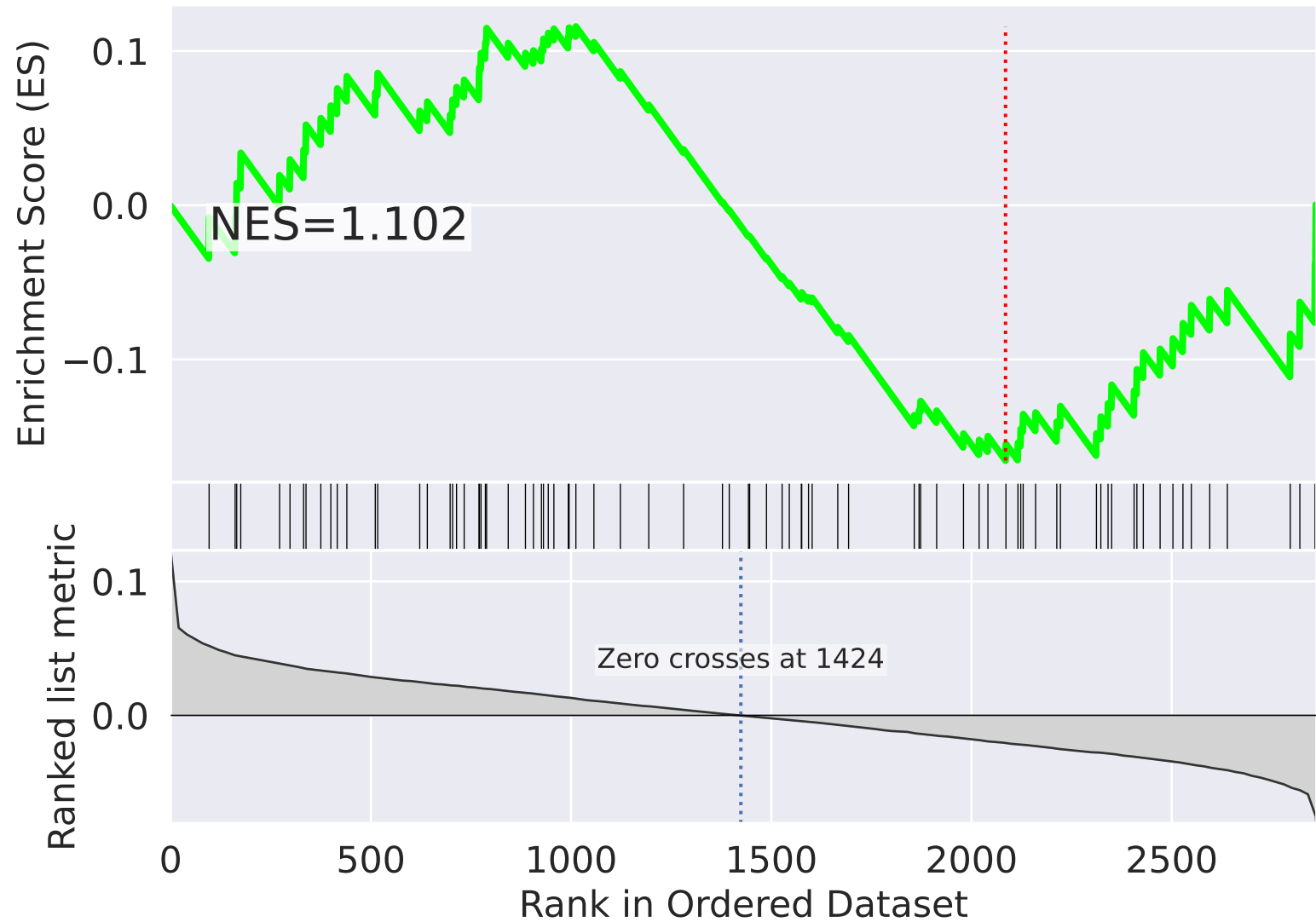
mitochondrial translational elongation (GO:0070125)



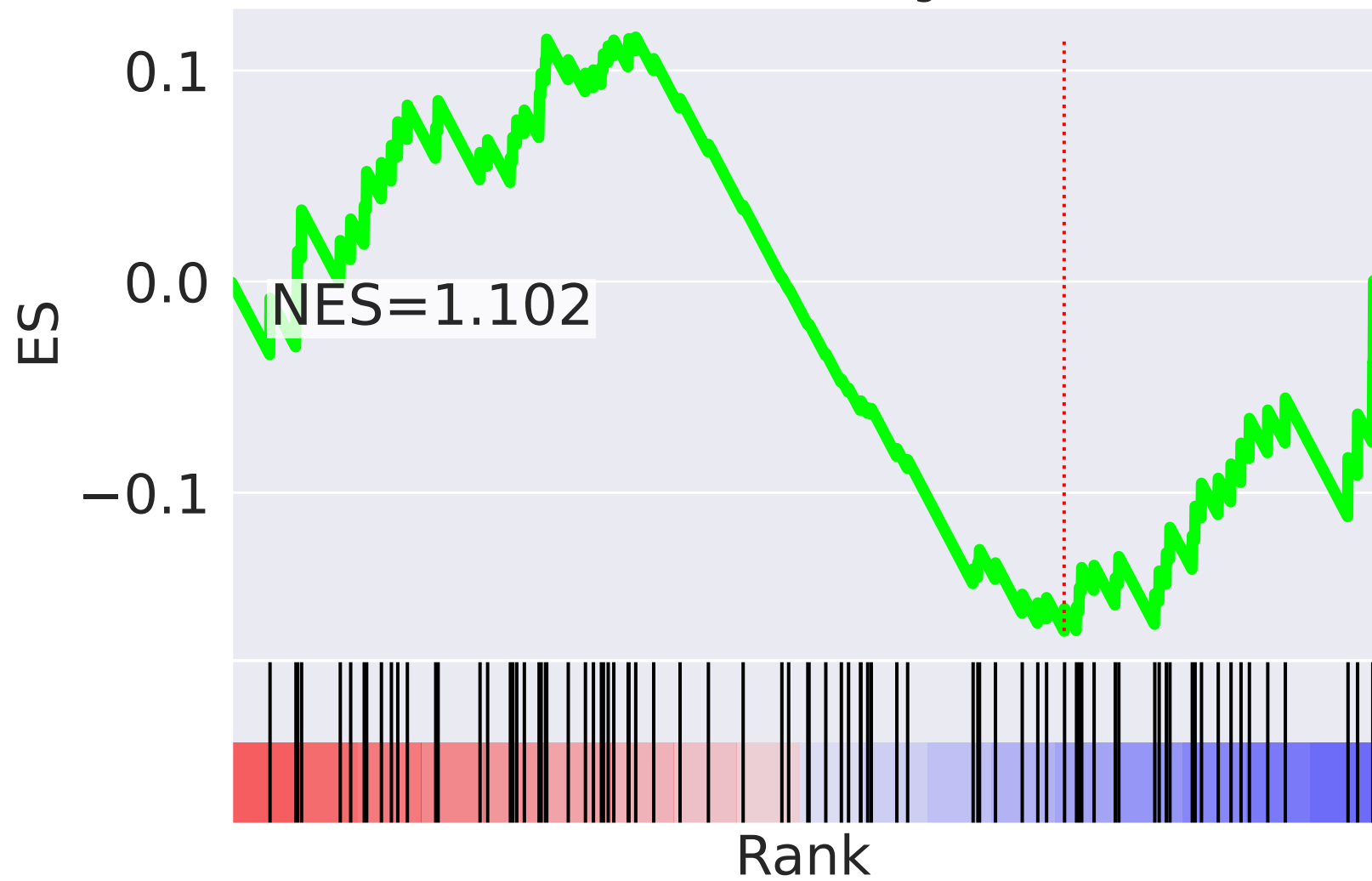
NES		SET
-2.947		positive regulation of substrate adhesion-dependent cell spreading (GO:1900026)
2.895		interferon-gamma-mediated signaling pathway (GO:0060333)
2.743		cellular response to lipopolysaccharide (GO:0071222)
2.734		positive regulation of transforming growth factor beta receptor signaling pathway (GO:0030511)
-2.587		ESCRT III complex disassembly (GO:1904903)
2.570		type I interferon signaling pathway (GO:0060337)
-2.554		DNA replication (GO:0006260)
2.537		humoral immune response (GO:0006959)
-2.522		cell-matrix adhesion (GO:0007160)
-2.505		membrane fusion (GO:0061025)
2.459		regulation of circadian rhythm (GO:0042752)
2.447		positive regulation of histone H3-K4 methylation (GO:0051571)
-2.426		sister chromatid cohesion (GO:0007062)
-2.417		tRNA aminoacylation for protein translation (GO:0006418)
-2.413		nuclear pore complex assembly (GO:0051292)

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)



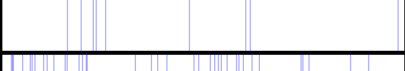
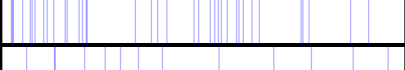

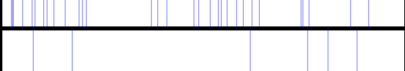
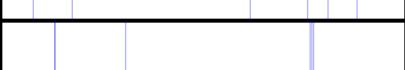



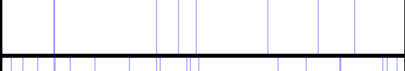
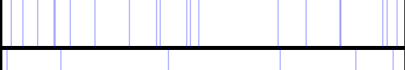
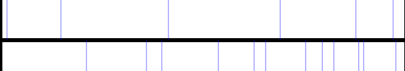
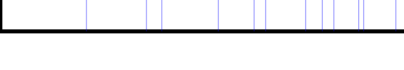



mitochondrial translational elongation (GO:0070125)



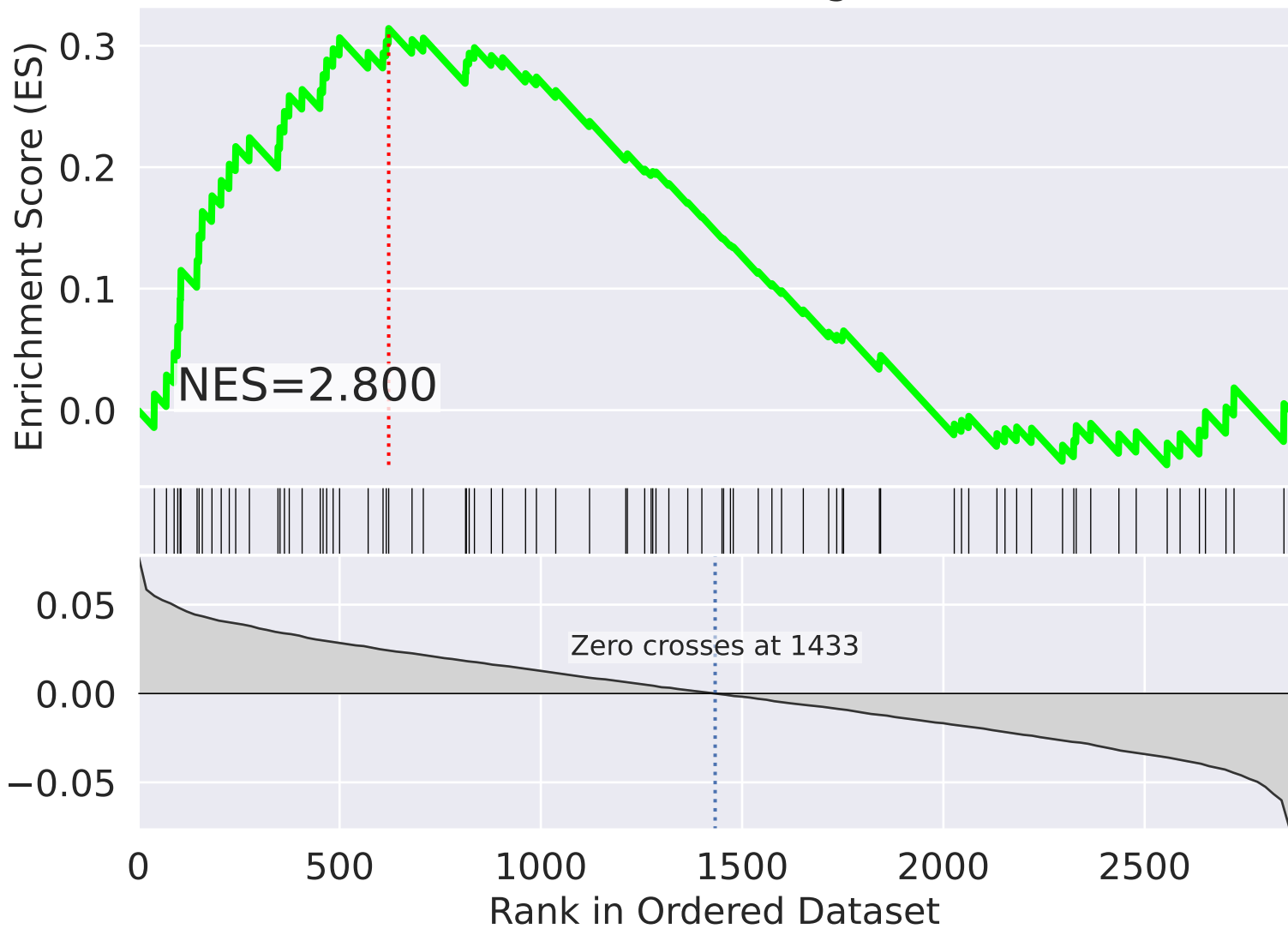
NES

SET

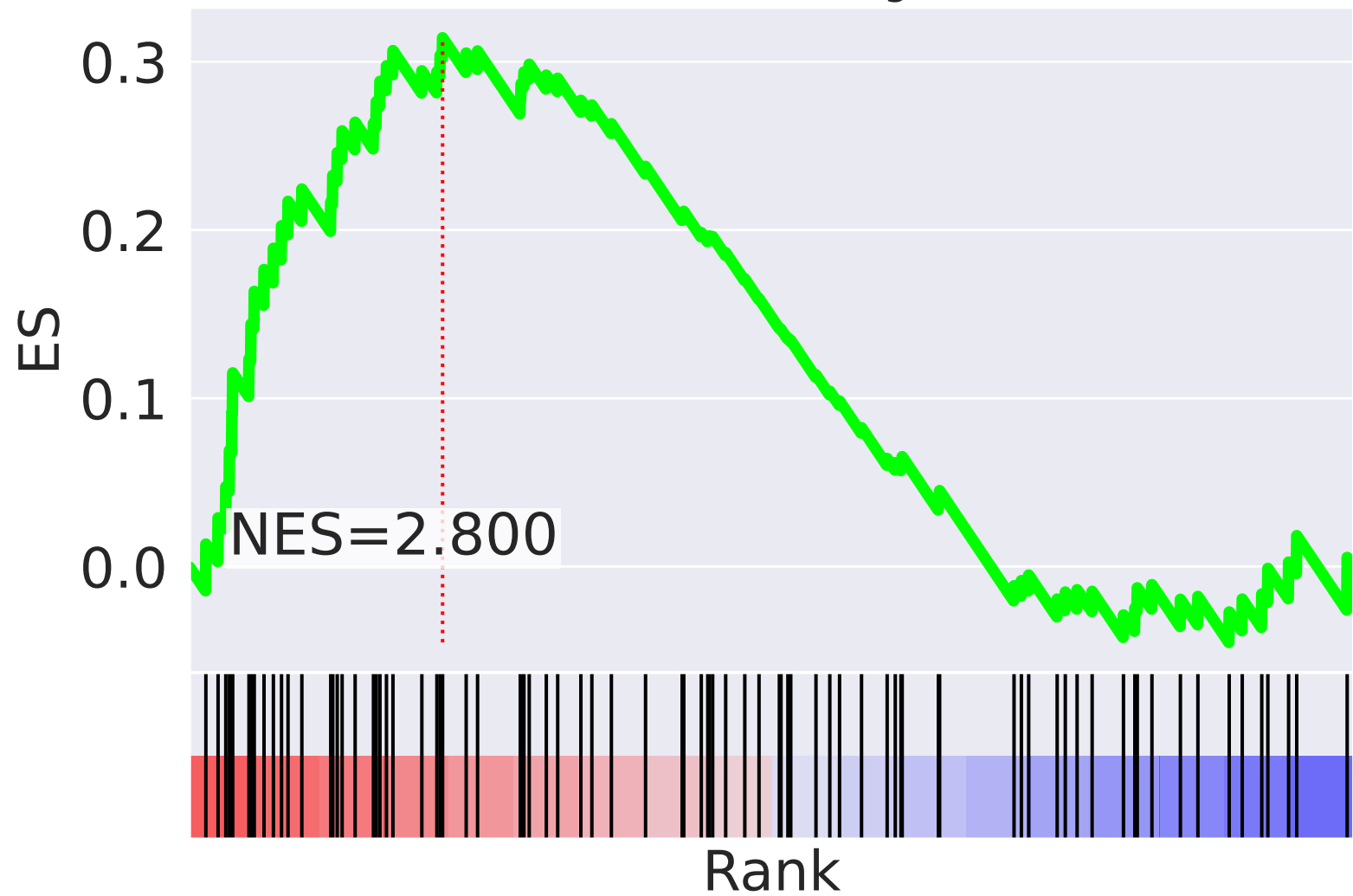
-3.032		positive regulation of epithelial cell migration (GO:0010634)
-2.979		regulation of mitotic cell cycle (GO:0007346)
-2.855		epithelial to mesenchymal transition (GO:0001837)
-2.840		termination of RNA polymerase II transcription (GO:0006369)
-2.836		cellular response to tumor necrosis factor (GO:0071356)
-2.783		mRNA 3'-end processing (GO:0031124)
-2.730		ventricular septum morphogenesis (GO:0060412)
-2.573		dephosphorylation (GO:0016311)
-2.572		negative regulation of peptidyl-serine phosphorylation (GO:0033137)
2.572		humoral immune response (GO:0006959)
-2.561		cortical actin cytoskeleton organization (GO:0030866)
-2.531		regulation of cytokinesis (GO:0032465)
-2.484		phosphatidylinositol biosynthetic process (GO:0006661)
-2.461		response to glucose (GO:0009749)
-2.453		nuclear-transcribed mRNA poly(A) tail shortening (GO:0000289)

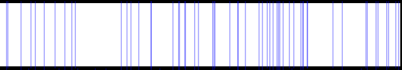
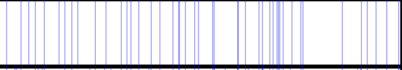
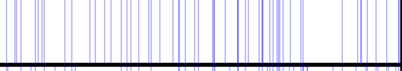
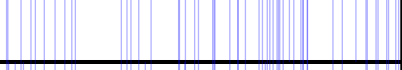
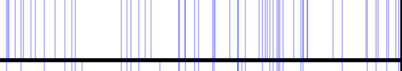
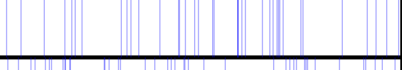
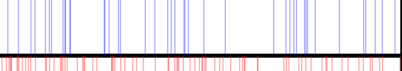
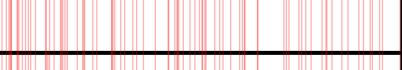
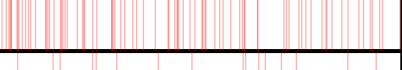
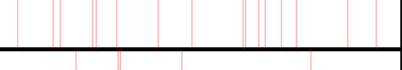
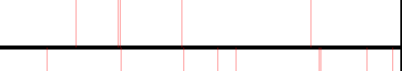
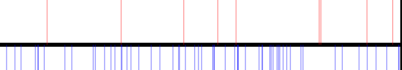
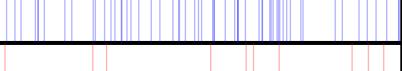
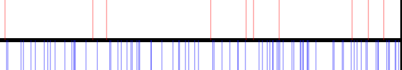
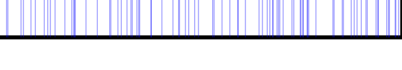
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=52$

mitochondrial translational elongation (GO:0070125)



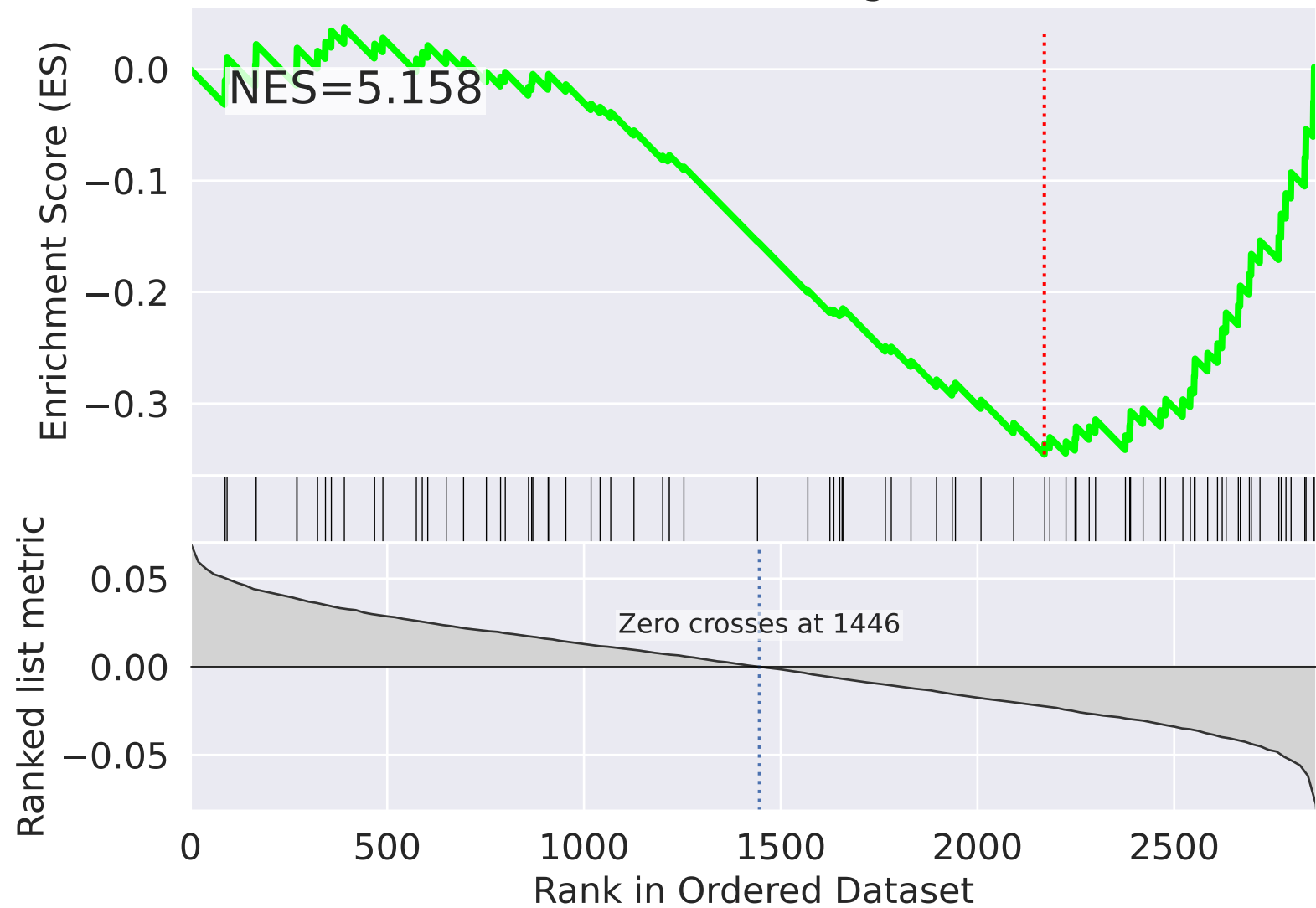
mitochondrial translational elongation (GO:0070125)



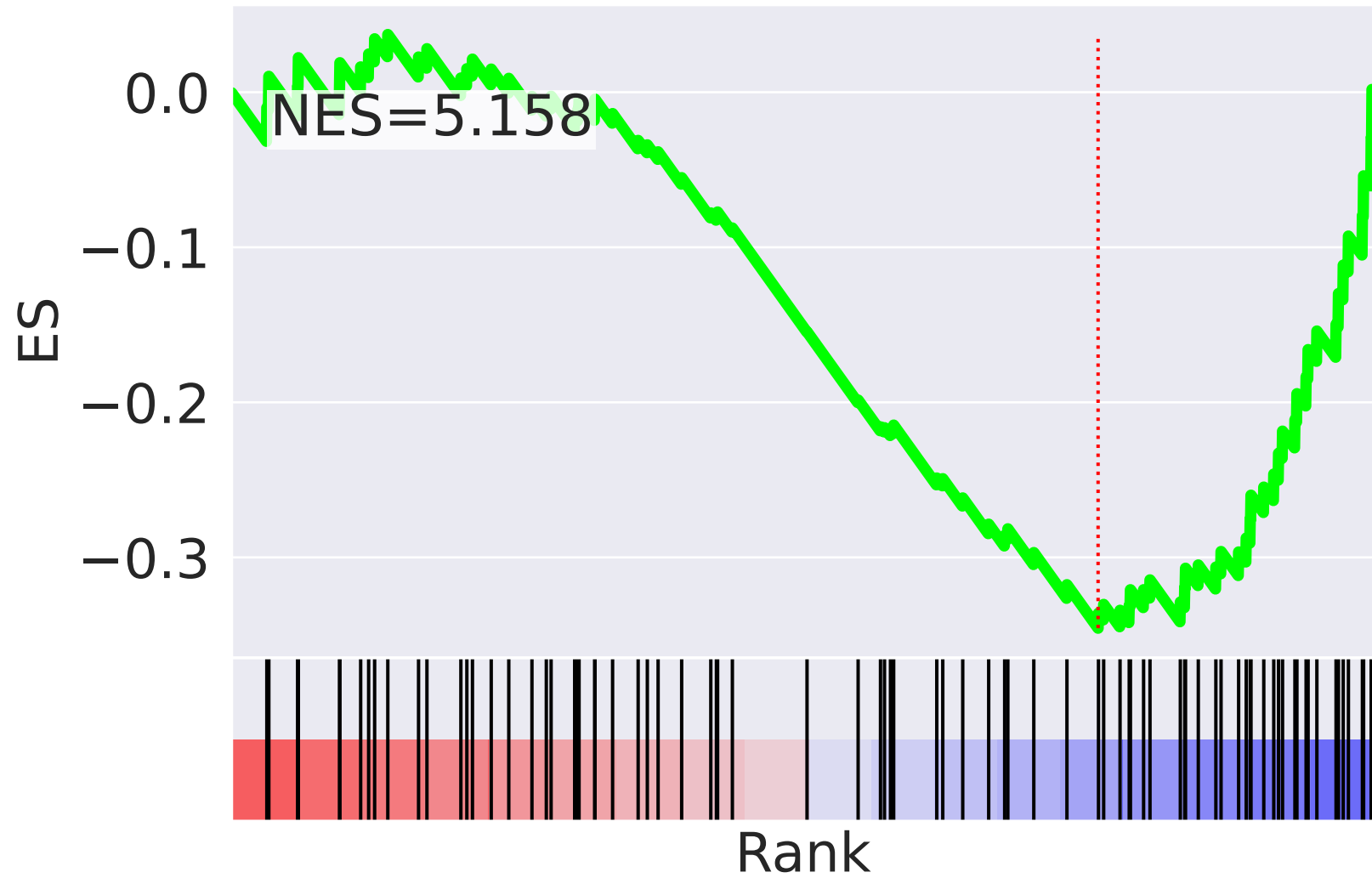
NES		SET
-3.264		positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0051437)
-3.083		NIK/NF-kappaB signaling (GO:0038061)
-2.954		stimulatory C-type lectin receptor signaling pathway (GO:0002223)
-2.948		negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
-2.939		anaphase-promoting complex-dependent catabolic process (GO:0031145)
-2.882		antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)
-2.828		mitotic cell cycle (GO:0000278)
2.825		mitochondrial translational termination (GO:0070126)
2.800		mitochondrial translational elongation (GO:0070125)
2.795		positive regulation of telomerase activity (GO:0051973)
2.787		peptidyl-diphthamide biosynthetic process from peptidyl-histidine (GO:0017183)
2.780		negative regulation of phosphatase activity (GO:0010923)
-2.773		T cell receptor signaling pathway (GO:0050852)
2.713		ribosomal large subunit assembly (GO:0000027)
-2.697		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)

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)

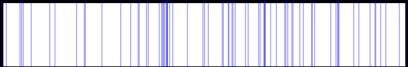
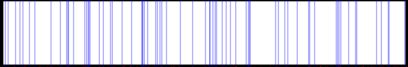
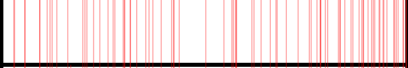
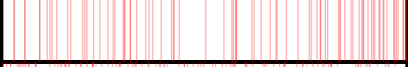
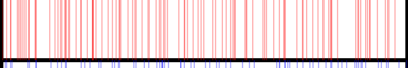
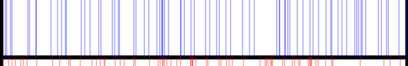
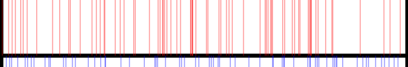
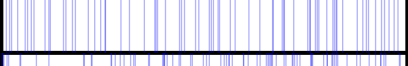
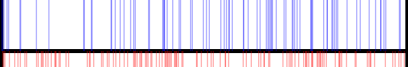
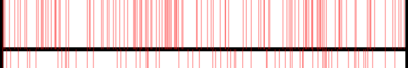
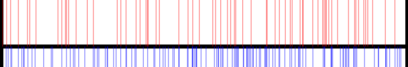
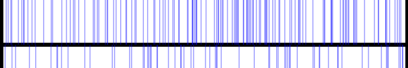
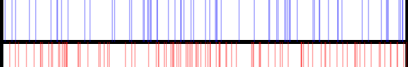
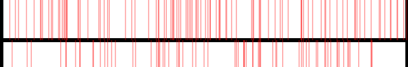
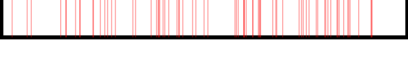


mitochondrial translational elongation (GO:0070125)



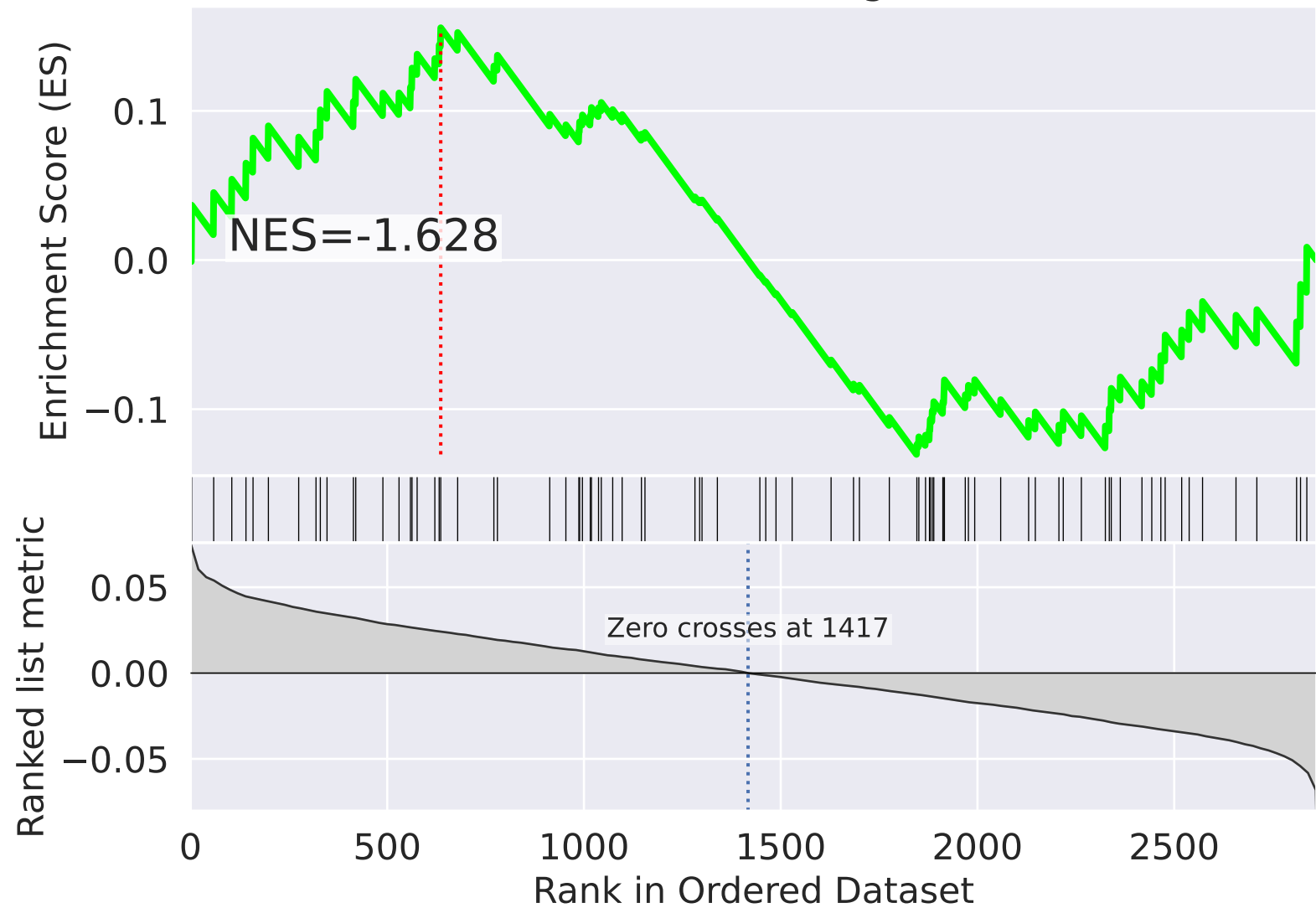
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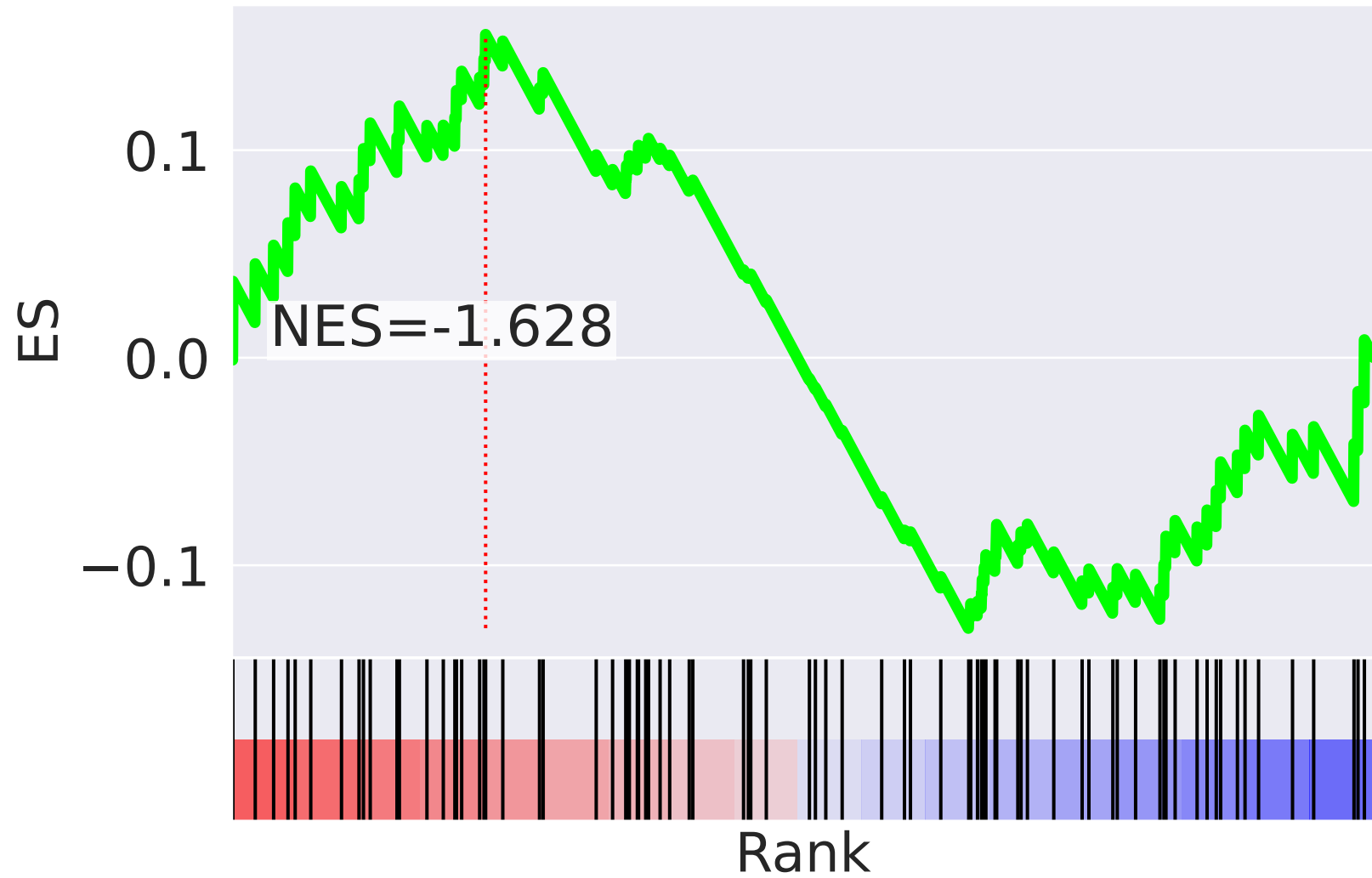
-5.696		protein ubiquitination (GO:0016567)
-5.585		cellular response to DNA damage stimulus (GO:0006974)
5.212		mitochondrial translational termination (GO:0070126)
5.158		mitochondrial translational elongation (GO:0070125)
5.019		transcription from RNA polymerase II promoter (GO:0006366)
-5.002		regulation of signal transduction by p53 class mediator (GO:1901796)
4.967		MAPK cascade (GO:0000165)
-4.813		sister chromatid cohesion (GO:0007062)
-4.166		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
4.140		mRNA splicing, via spliceosome (GO:0000398)
4.022		transcription initiation from RNA polymerase II promoter (GO:0006367)
-4.004		positive regulation of transcription, DNA-templated (GO:0045893)
-3.998		DNA replication (GO:0006260)
3.850		signal transduction (GO:0007165)
3.822		positive regulation of cell proliferation (GO:0008284)

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

mitochondrial translational elongation (GO:0070125)

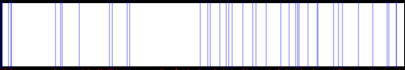
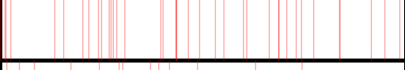

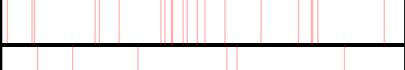
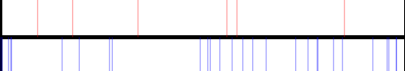
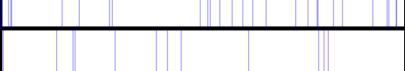


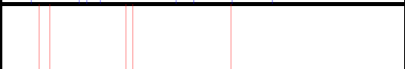

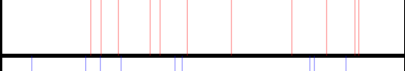
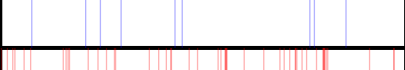
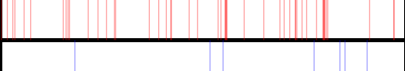




mitochondrial translational elongation (GO:0070125)



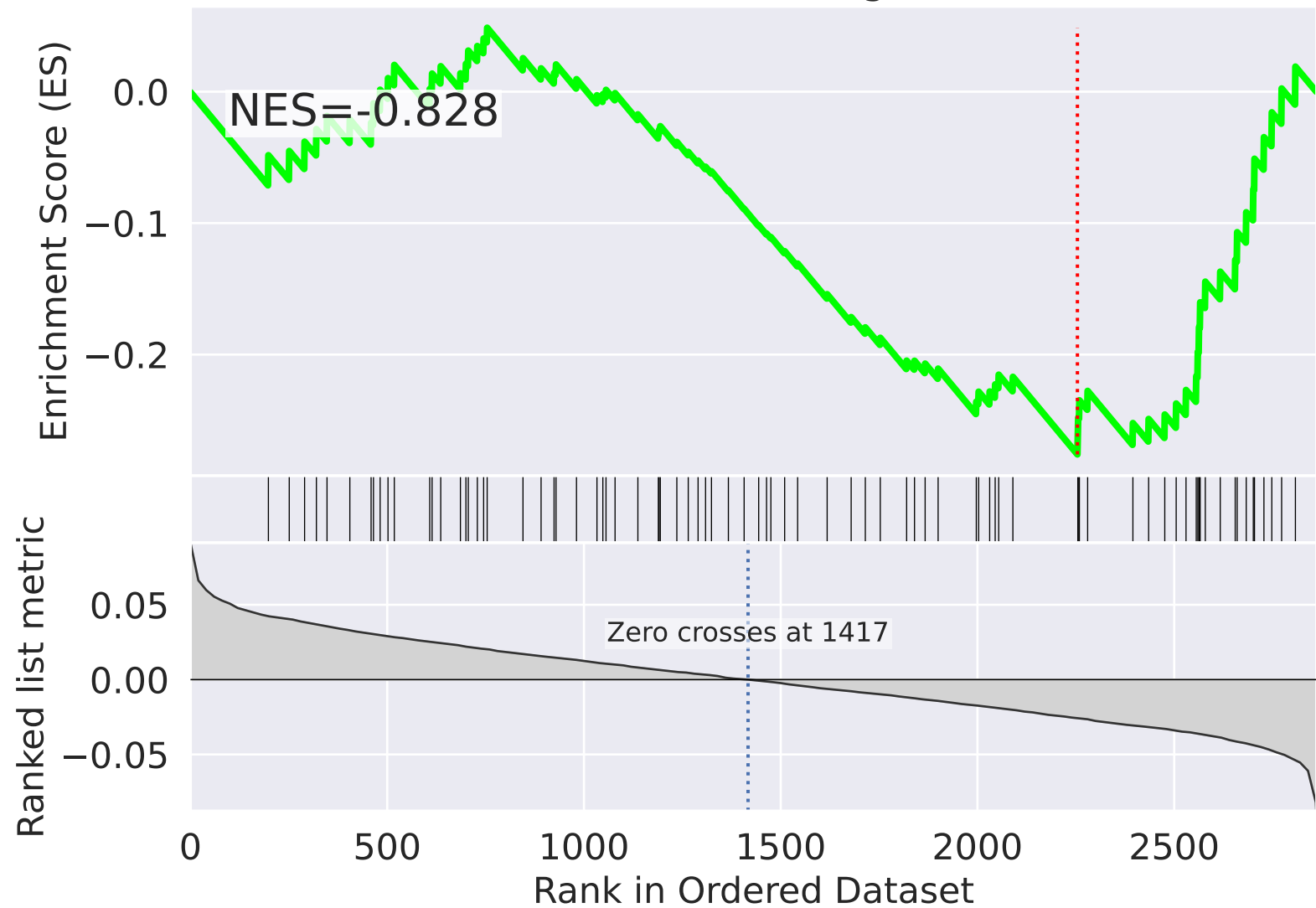
NES

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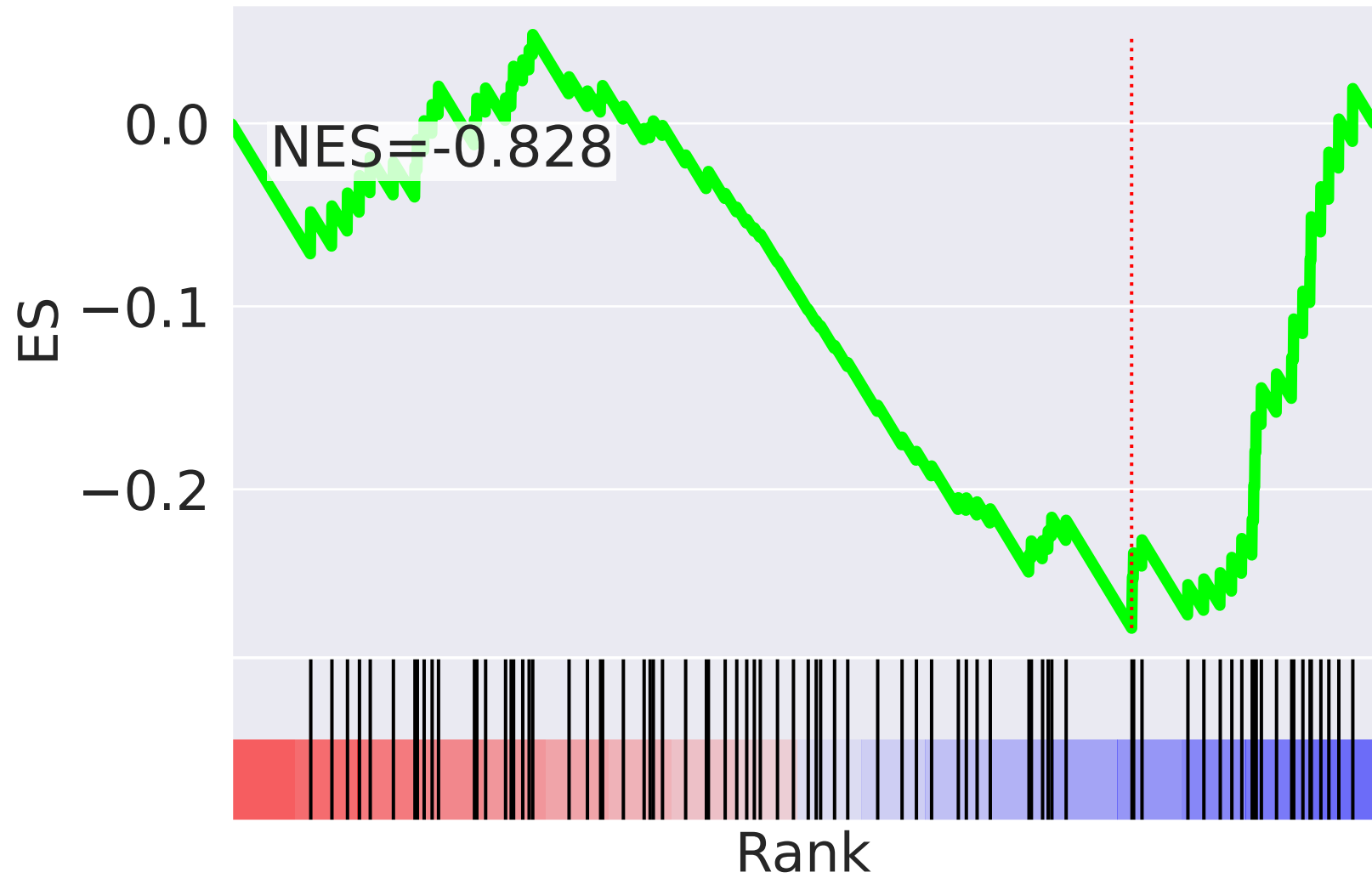
-3.164		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.996		protein sumoylation (GO:0016925)
2.763		transcription from RNA polymerase III promoter (GO:0006383)
2.550		positive regulation of type I interferon production (GO:0032481)
2.498		G2 DNA damage checkpoint (GO:0031572)
-2.493		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
-2.488		retrograde protein transport, ER to cytosol (GO:0030970)
2.456		epidermis development (GO:0008544)
-2.371		cellular respiration (GO:0045333)
2.299		regulation of protein catabolic process (GO:0042176)
-2.294		ERAD pathway (GO:0036503)
2.284		type I interferon signaling pathway (GO:0060337)
-2.246		mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122)
2.222		snRNA transcription from RNA polymerase II promoter (GO:0042795)
-2.207		base-excision repair (GO:0006284)

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)

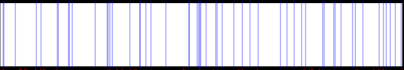

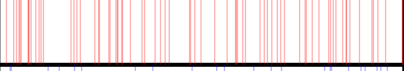
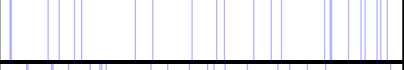
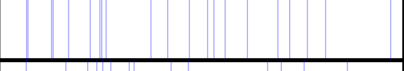

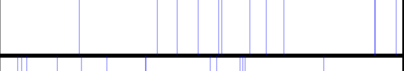



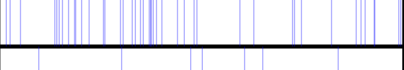
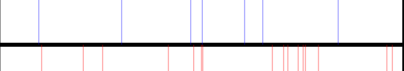
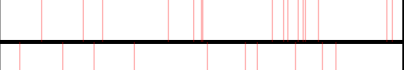
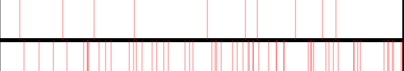
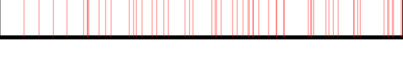


mitochondrial translational elongation (GO:0070125)



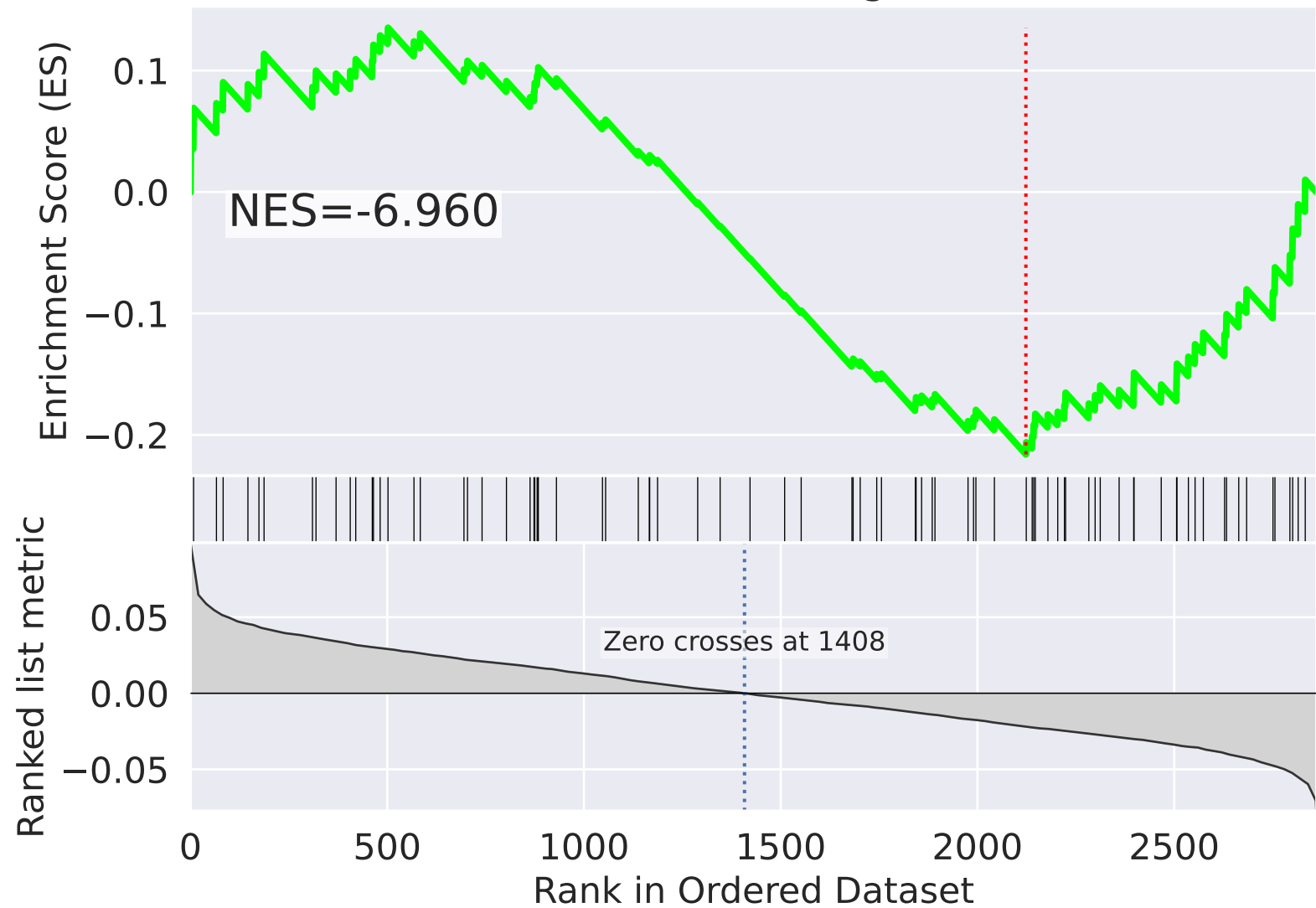
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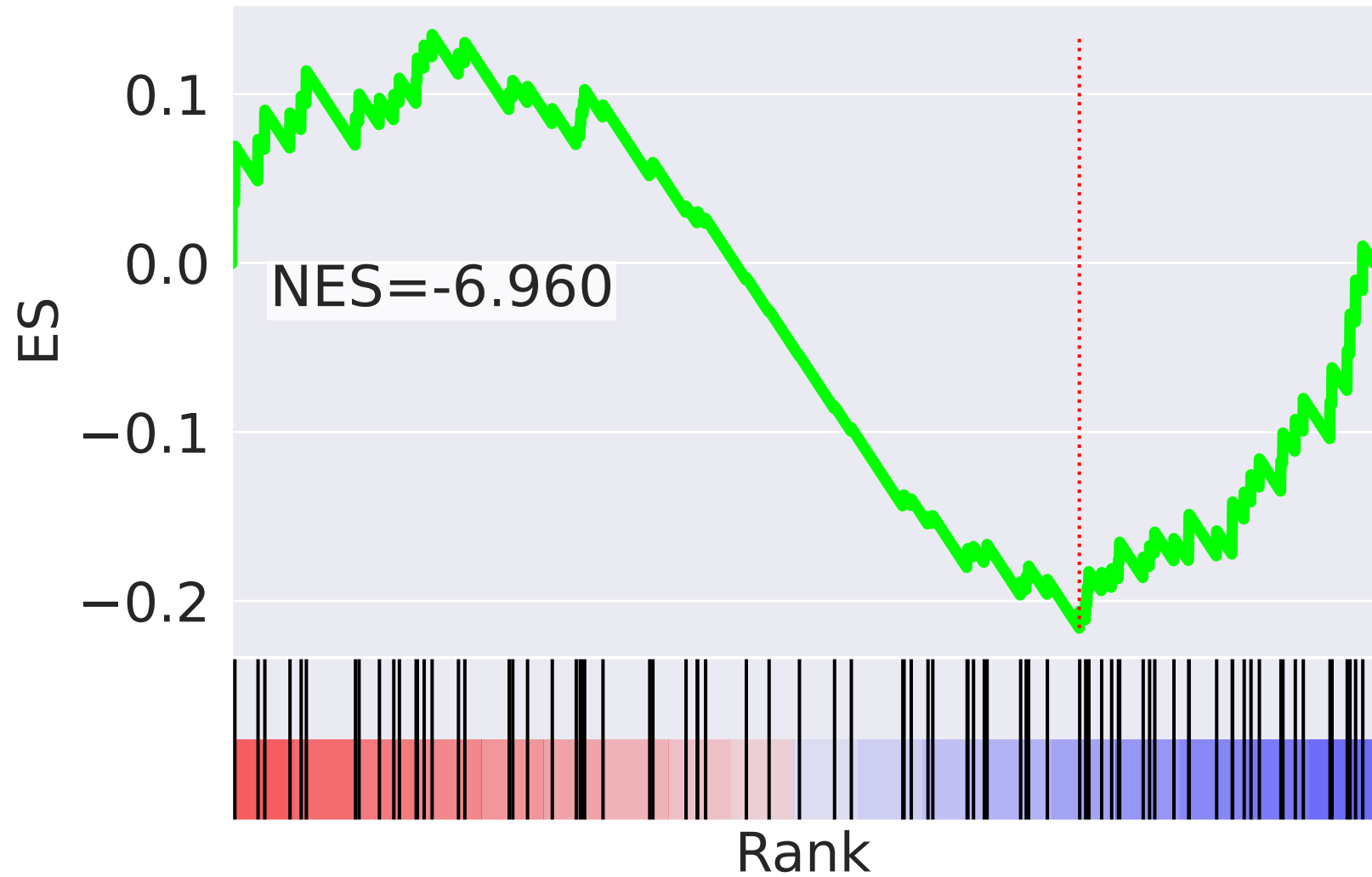
-2.985		membrane organization (GO:0061024)
2.975		chromatin remodeling (GO:0006338)
2.945		regulation of transcription, DNA-templated (GO:0006355)
-2.782		ubiquitin-dependent ERAD pathway (GO:0030433)
-2.677		DNA damage response, detection of DNA damage (GO:0042769)
-2.670		regulation of mitophagy (GO:1903146)
-2.648		protein N-linked glycosylation (GO:0006487)
-2.607		brain development (GO:0007420)
-2.589		positive regulation of DNA-directed DNA polymerase activity (GO:1900264)
-2.584		xenobiotic metabolic process (GO:0006805)
-2.583		transmembrane transport (GO:0055085)
-2.568		positive regulation of intracellular protein transport (GO:0090316)
2.545		RNA splicing, via transesterification reactions (GO:0000375)
2.507		positive regulation by host of viral transcription (GO:0043923)
2.495		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 $z=56$

mitochondrial translational elongation (GO:0070125)


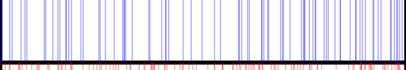
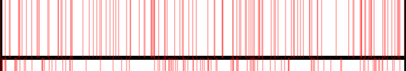

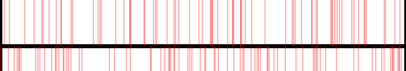
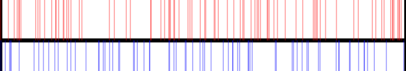
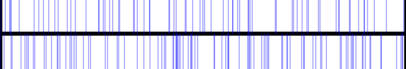
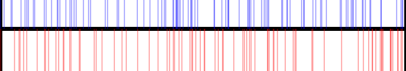
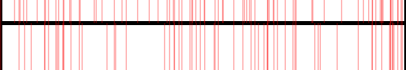
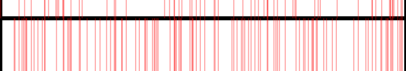
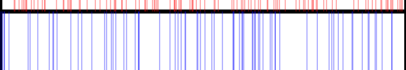
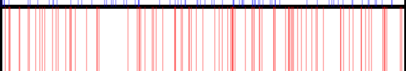

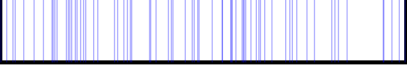



mitochondrial translational elongation (GO:0070125)



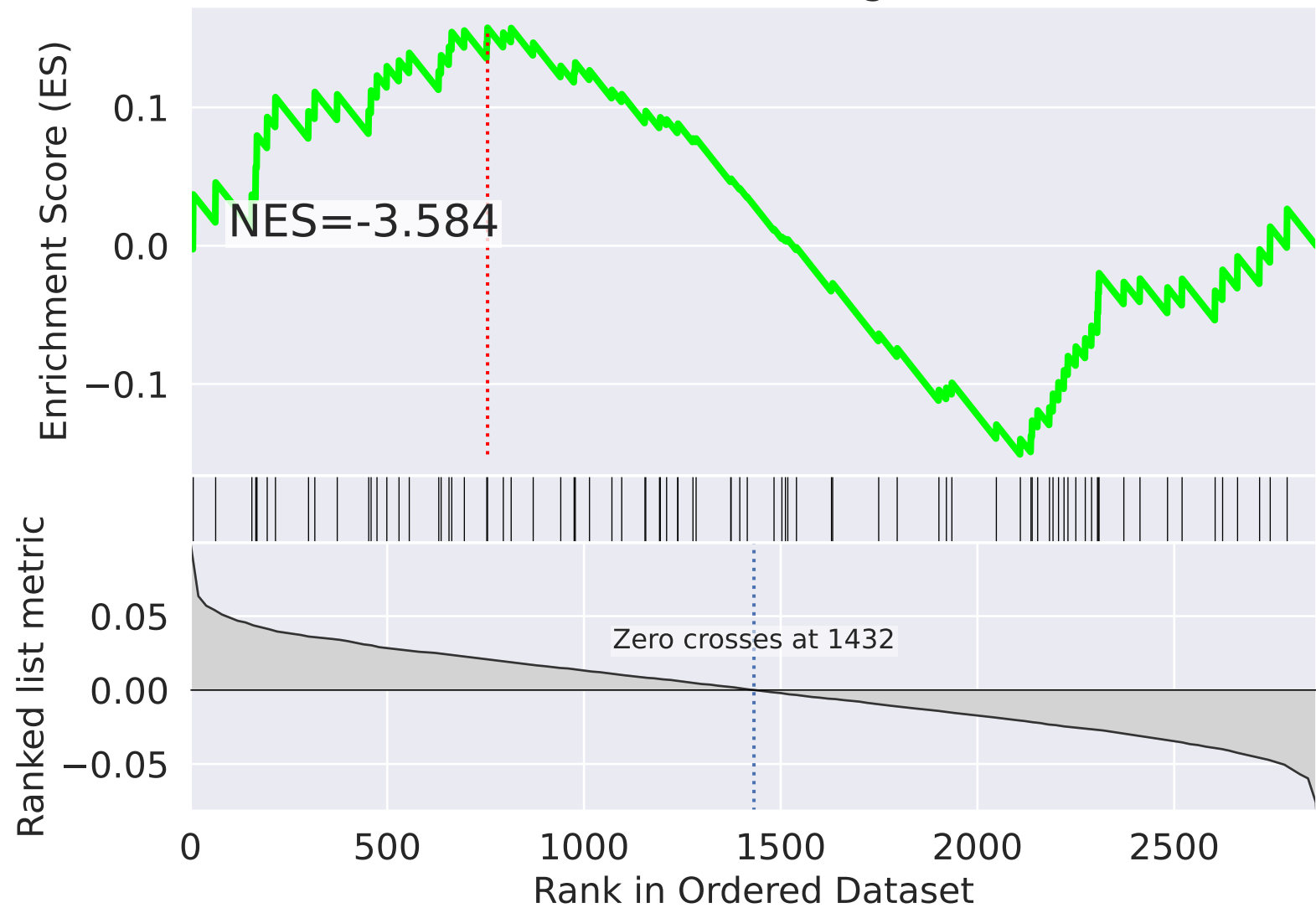
NES

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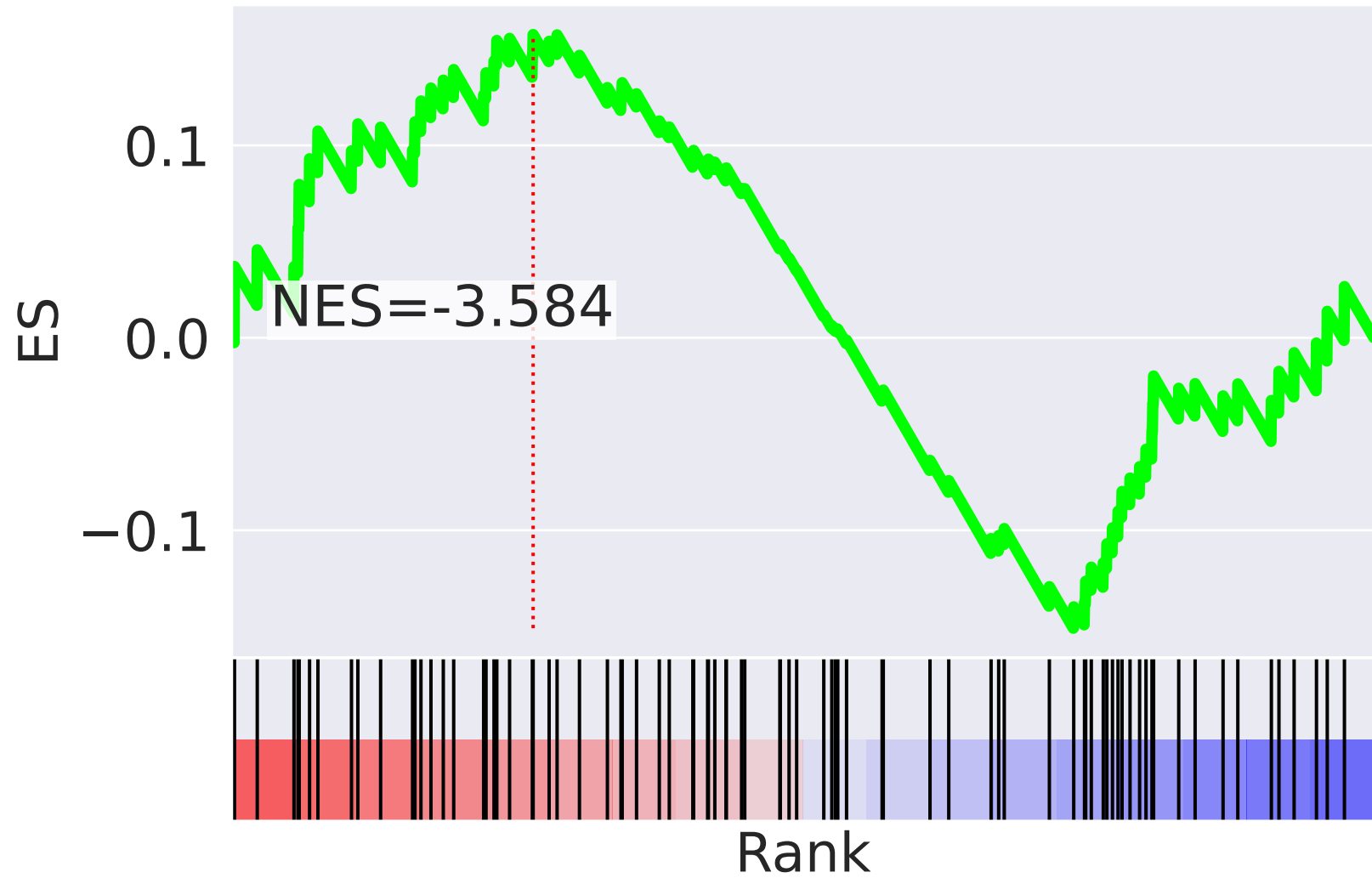
-6.960		mitochondrial translational elongation (GO:0070125)
-6.769		mitochondrial translational termination (GO:0070126)
5.959		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
5.201		transcription from RNA polymerase II promoter (GO:0006366)
4.792		regulation of transcription, DNA-templated (GO:0006355)
4.711		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-4.497		positive regulation of cell proliferation (GO:0008284)
-4.060		translation (GO:0006412)
4.009		post-translational protein modification (GO:0043687)
3.859		protein polyubiquitination (GO:0000209)
3.761		protein deubiquitination (GO:0016579)
-3.722		regulation of signal transduction by p53 class mediator (GO:1901796)
3.654		negative regulation of transcription, DNA-templated (GO:0045892)
-3.644		MAPK cascade (GO:0000165)
-3.479		protein phosphorylation (GO:0006468)

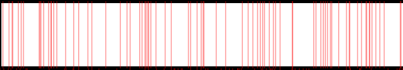
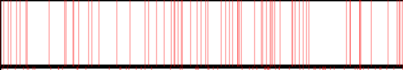
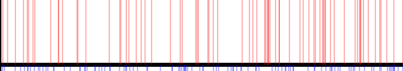
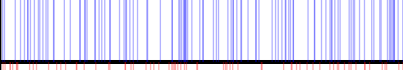
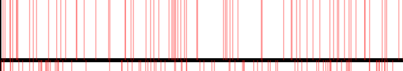
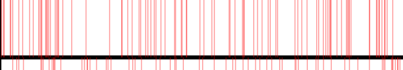
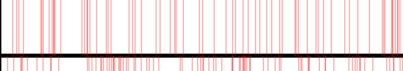
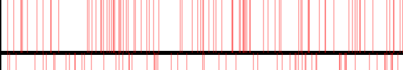
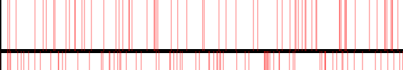
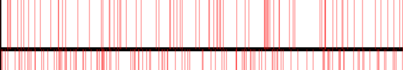
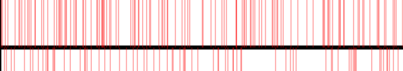
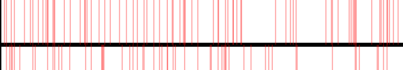
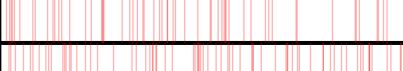
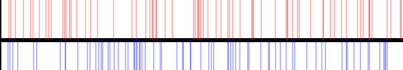
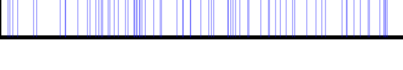
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=57$

mitochondrial translational elongation (GO:0070125)



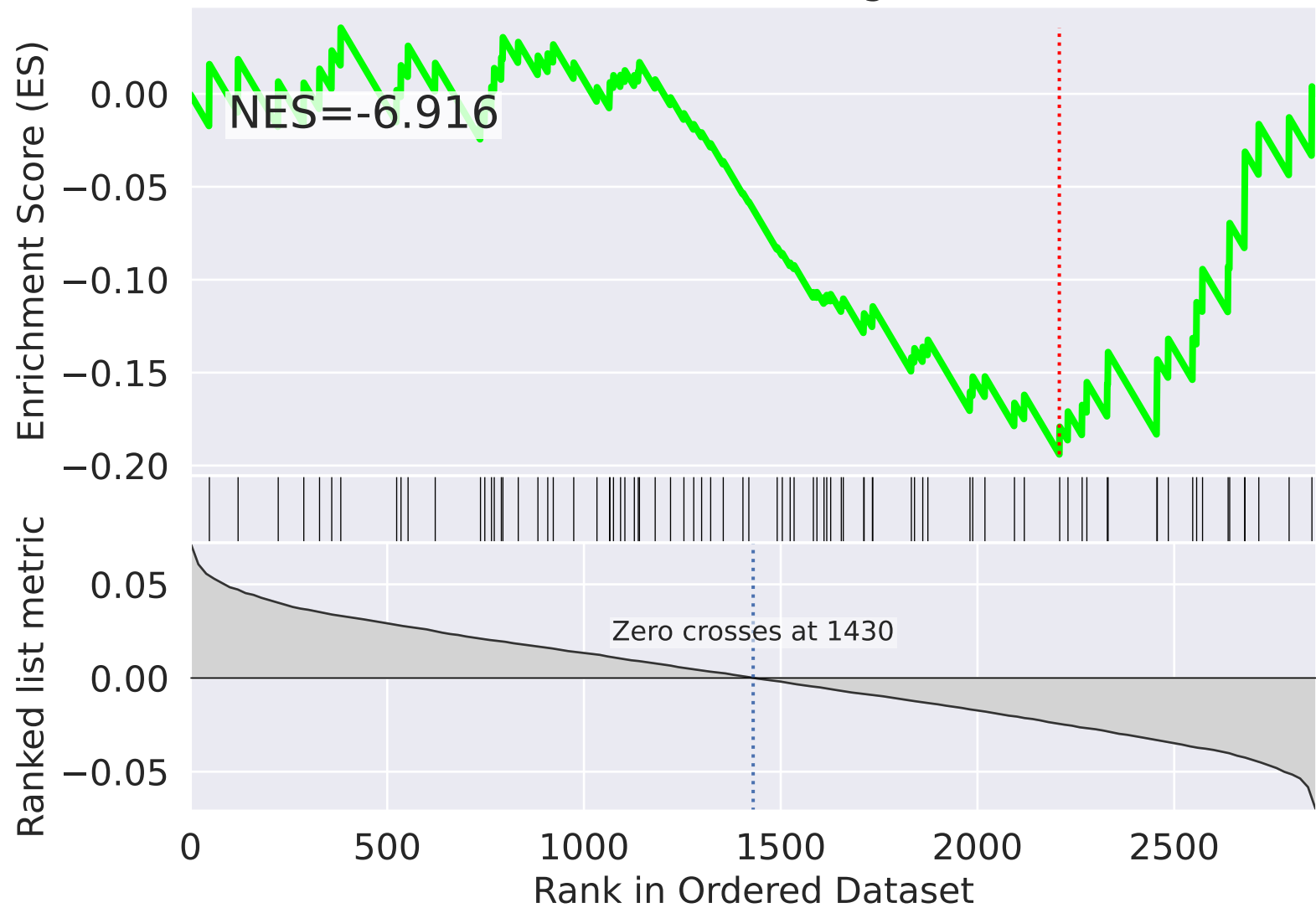
mitochondrial translational elongation (GO:0070125)



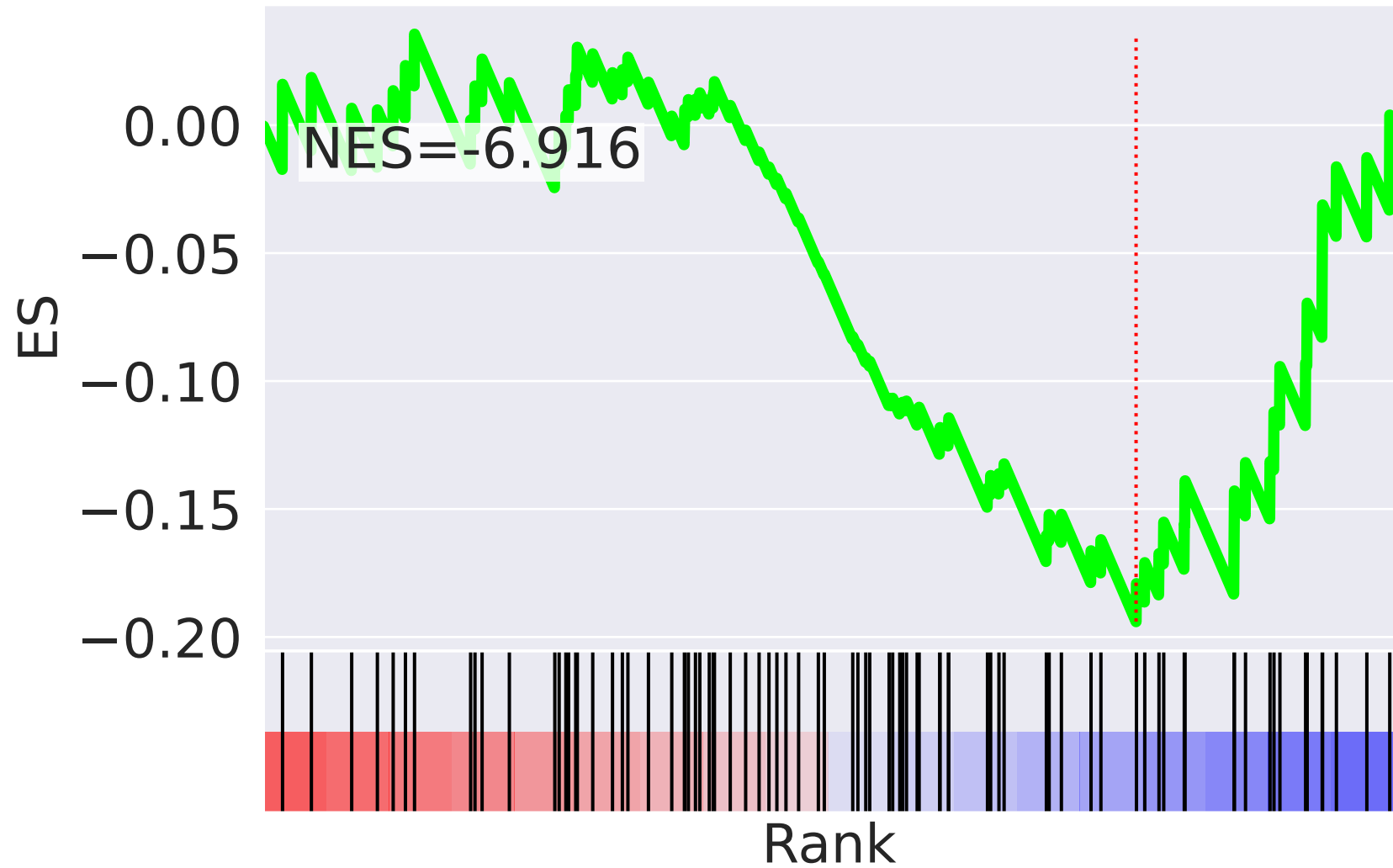
NES		SET
7.021		negative regulation of apoptotic process (GO:0043066)
5.932		protein phosphorylation (GO:0006468)
5.793		MAPK cascade (GO:0000165)
-5.548		rRNA processing (GO:0006364)
5.163		regulation of transcription, DNA-templated (GO:0006355)
4.916		negative regulation of transcription, DNA-templated (GO:0045892)
4.728		cellular response to DNA damage stimulus (GO:0006974)
4.385		neutrophil degranulation (GO:0043312)
4.178		DNA replication (GO:0006260)
4.142		post-translational protein modification (GO:0043687)
4.073		mRNA splicing, via spliceosome (GO:0000398)
4.029		viral transcription (GO:0019083)
3.999		mRNA export from nucleus (GO:0006406)
3.883		positive regulation of cell proliferation (GO:0008284)
-3.685		protein ubiquitination (GO:0016567)

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

mitochondrial translational elongation (GO:0070125)

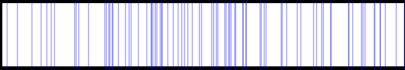
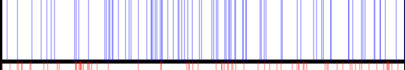
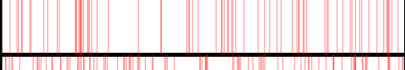
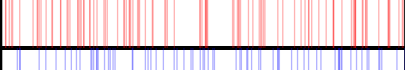
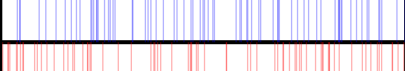
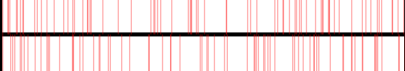
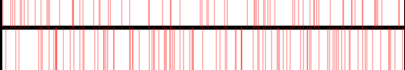
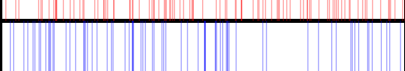
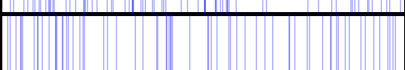

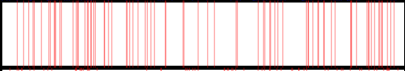
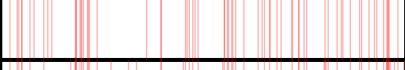
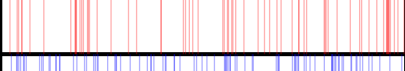
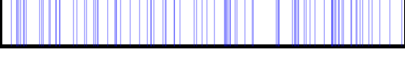



mitochondrial translational elongation (GO:0070125)



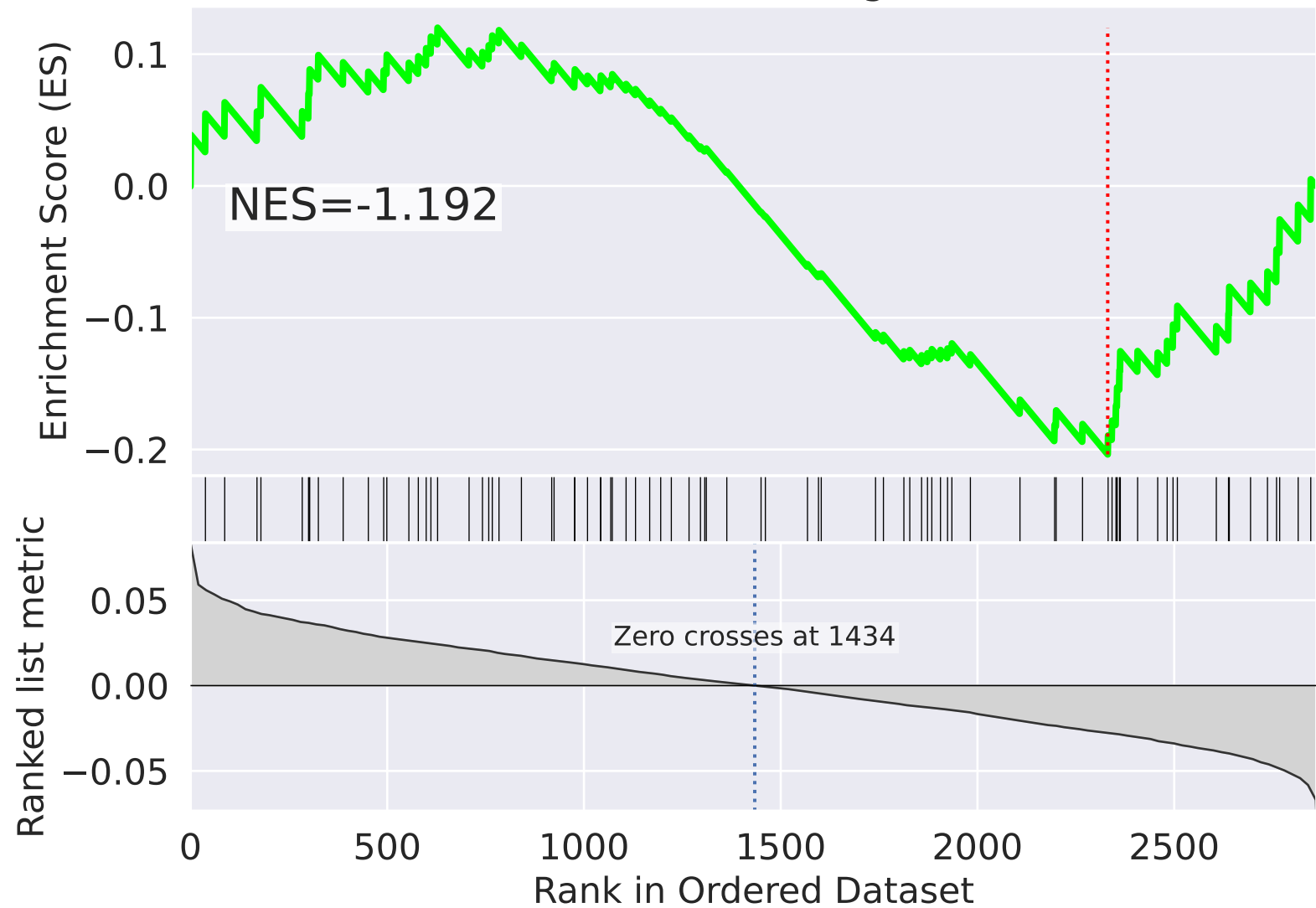
NES

SET

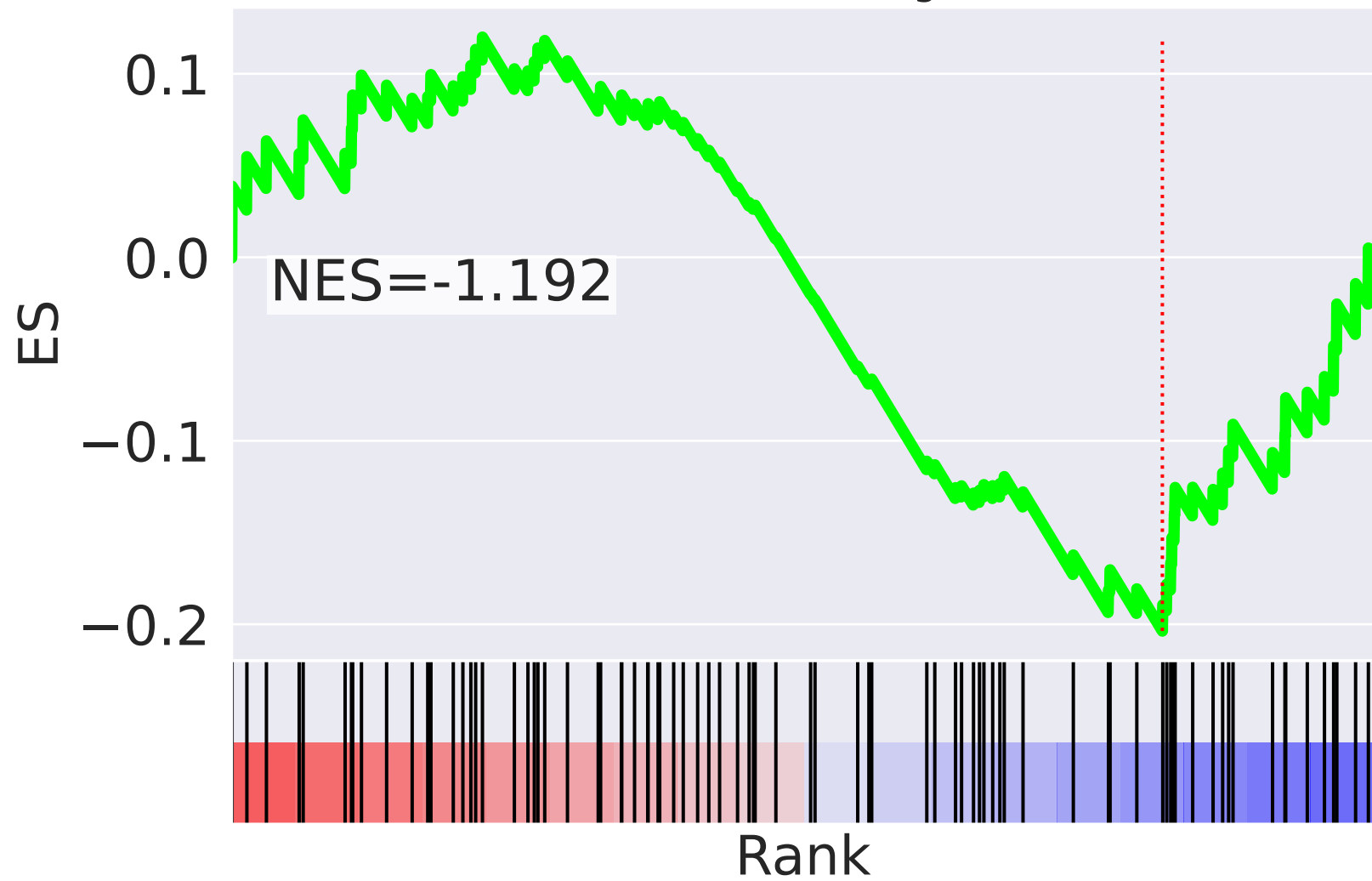
-6.916		mitochondrial translational elongation (GO:0070125)
-6.715		mitochondrial translational termination (GO:0070126)
5.085		viral transcription (GO:0019083)
4.813		signal transduction (GO:0007165)
-4.683		positive regulation of cell proliferation (GO:0008284)
4.557		protein ubiquitination (GO:0016567)
4.034		regulation of transcription, DNA-templated (GO:0006355)
3.541		regulation of transcription from RNA polymerase II promoter (GO:0006357)
-3.521		MAPK cascade (GO:0000165)
-3.355		transcription initiation from RNA polymerase II promoter (GO:0006367)
-3.299		sister chromatid cohesion (GO:0007062)
3.208		negative regulation of apoptotic process (GO:0043066)
3.083		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.073		translational initiation (GO:0006413)
-2.950		negative regulation of transcription, DNA-templated (GO:0045892)

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

mitochondrial translational elongation (GO:0070125)



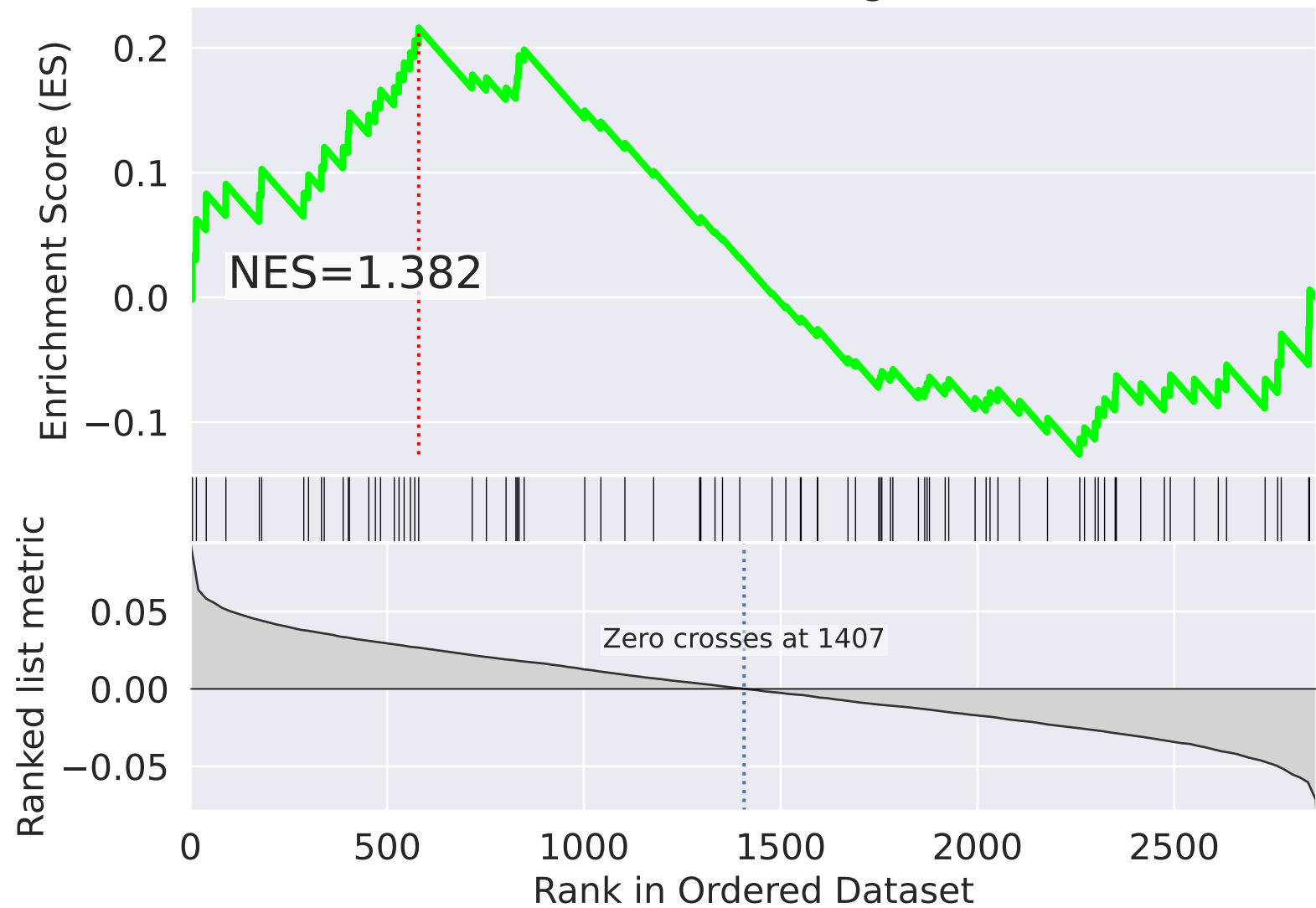
mitochondrial translational elongation (GO:0070125)



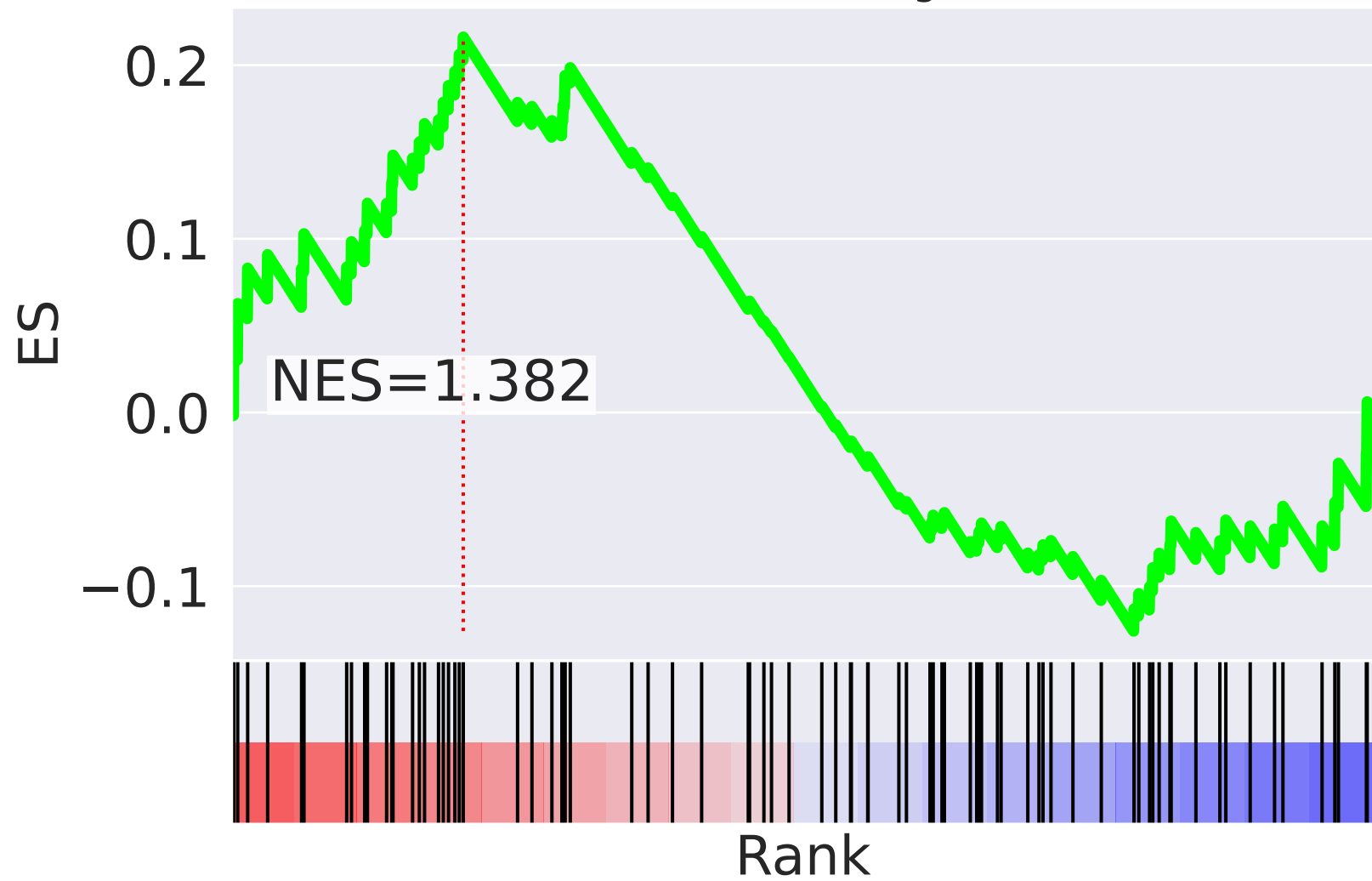
NES		SET
-2.819		male gonad development (GO:0008584)
2.776		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
-2.747		negative regulation of epidermal growth factor receptor signaling pathway (GO:0042059)
-2.714		positive regulation of cell cycle arrest (GO:0071158)
2.666		cellular protein modification process (GO:0006464)
2.596		nucleobase-containing small molecule interconversion (GO:0015949)
2.554		chromatin organization (GO:0006325)
-2.480		RNA export from nucleus (GO:0006405)
-2.405		membrane organization (GO:0061024)
-2.388		positive regulation of proteolysis (GO:0045862)
2.374		cellular response to epidermal growth factor stimulus (GO:0071364)
-2.272		endosomal transport (GO:0016197)
-2.232		positive regulation of gene expression (GO:0010628)
-2.224		positive regulation of mitotic metaphase/anaphase transition (GO:0045842)
-2.202		spliceosomal snRNP assembly (GO:0000387)

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

mitochondrial translational elongation (GO:0070125)



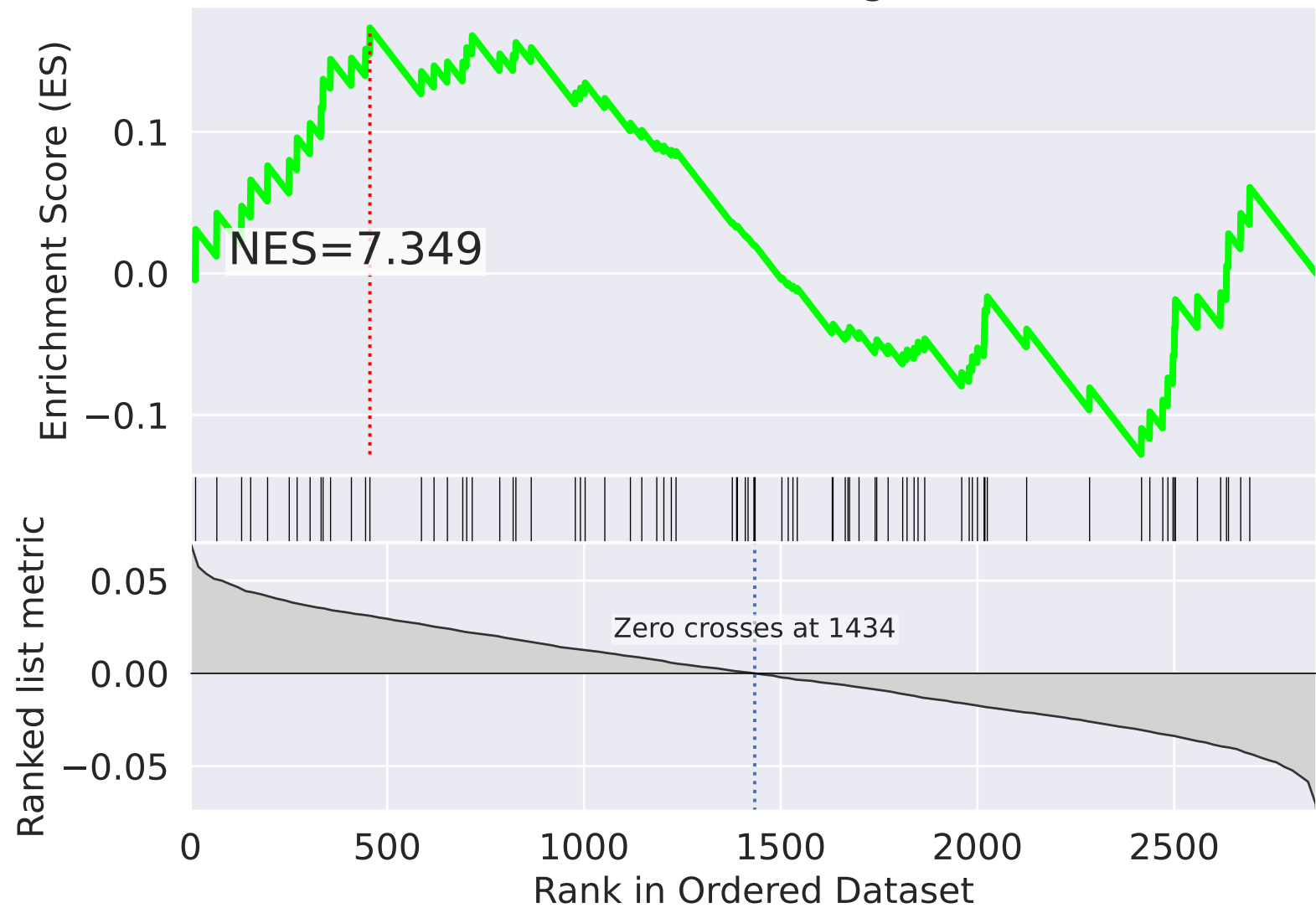
mitochondrial translational elongation (GO:0070125)



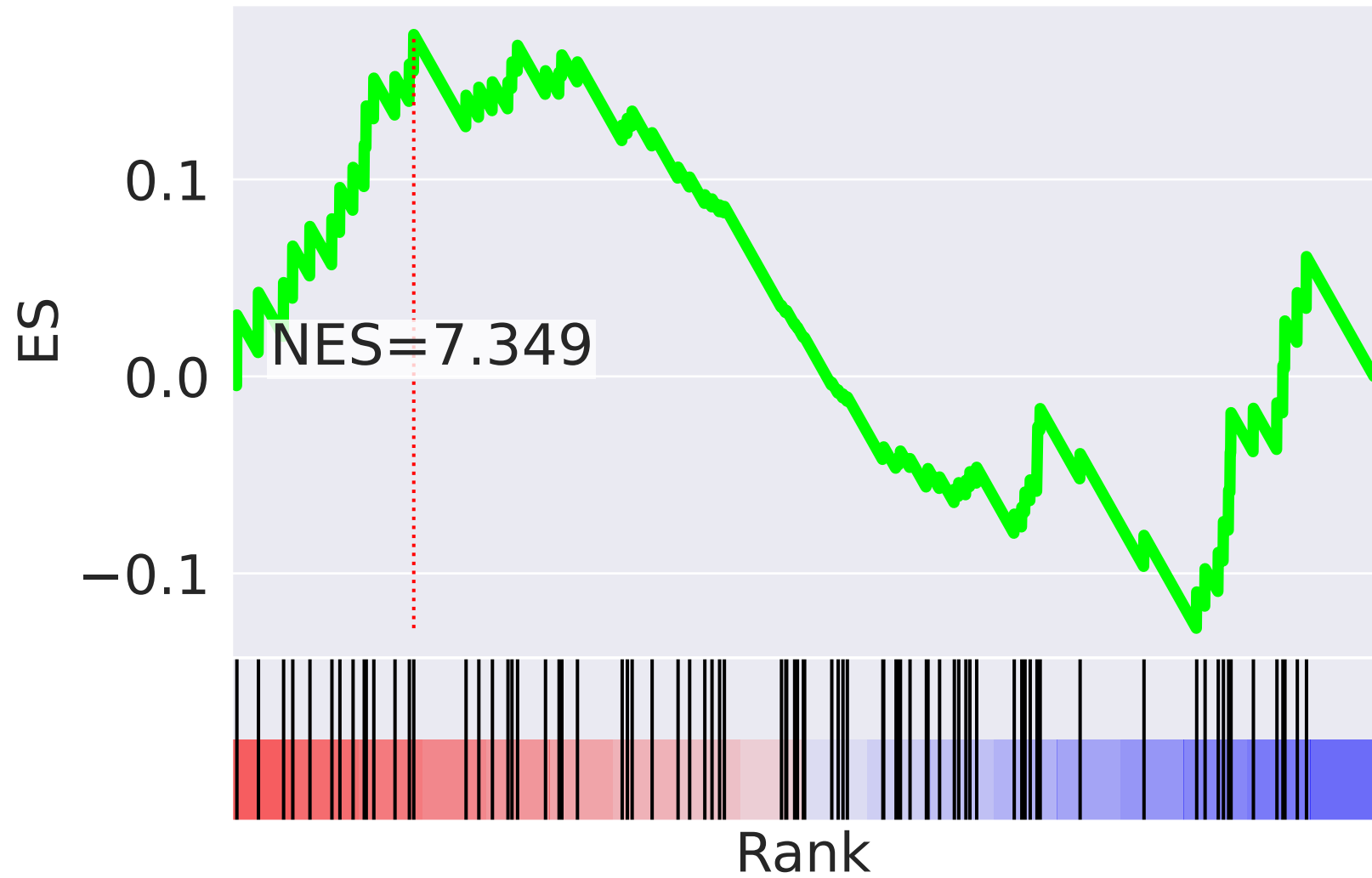
NES		SET
3.354		RNA secondary structure unwinding (GO:0010501)
-3.042		7-methylguanosine mRNA capping (GO:0006370)
-3.038		retrograde transport, endosome to Golgi (GO:0042147)
2.968		peptidyl-serine phosphorylation (GO:0018105)
2.907		positive regulation of TOR signaling (GO:0032008)
-2.834		regulation of gene silencing by miRNA (GO:0060964)
-2.713		G1/S transition of mitotic cell cycle (GO:0000082)
2.652		resolution of meiotic recombination intermediates (GO:0000712)
2.598		protein processing (GO:0016485)
2.590		phosphatidylinositol 3-kinase signaling (GO:0014065)
-2.587		regulation of transcription involved in G1/S transition of mitotic cell cycle (GO:0000083)
2.543		ribosomal large subunit biogenesis (GO:0042273)
-2.523		RNA metabolic process (GO:0016070)
-2.517		RNA export from nucleus (GO:0006405)
-2.485		somatic stem cell population maintenance (GO:0035019)

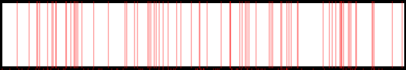
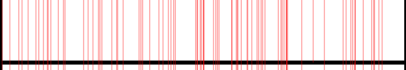
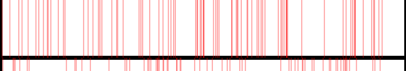
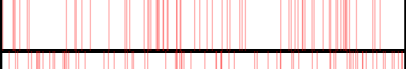
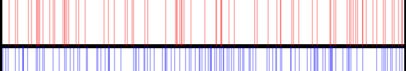
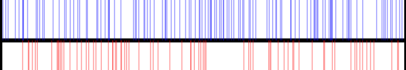
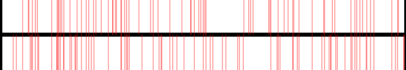
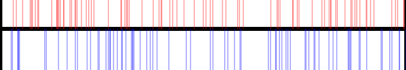
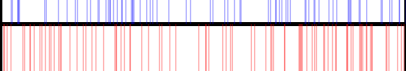
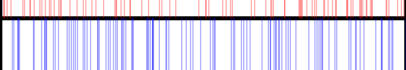
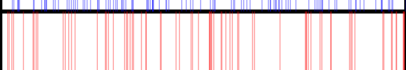
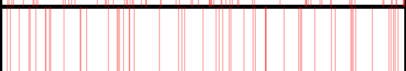

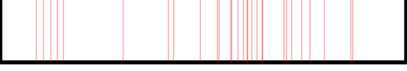

The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=61$

mitochondrial translational elongation (GO:0070125)



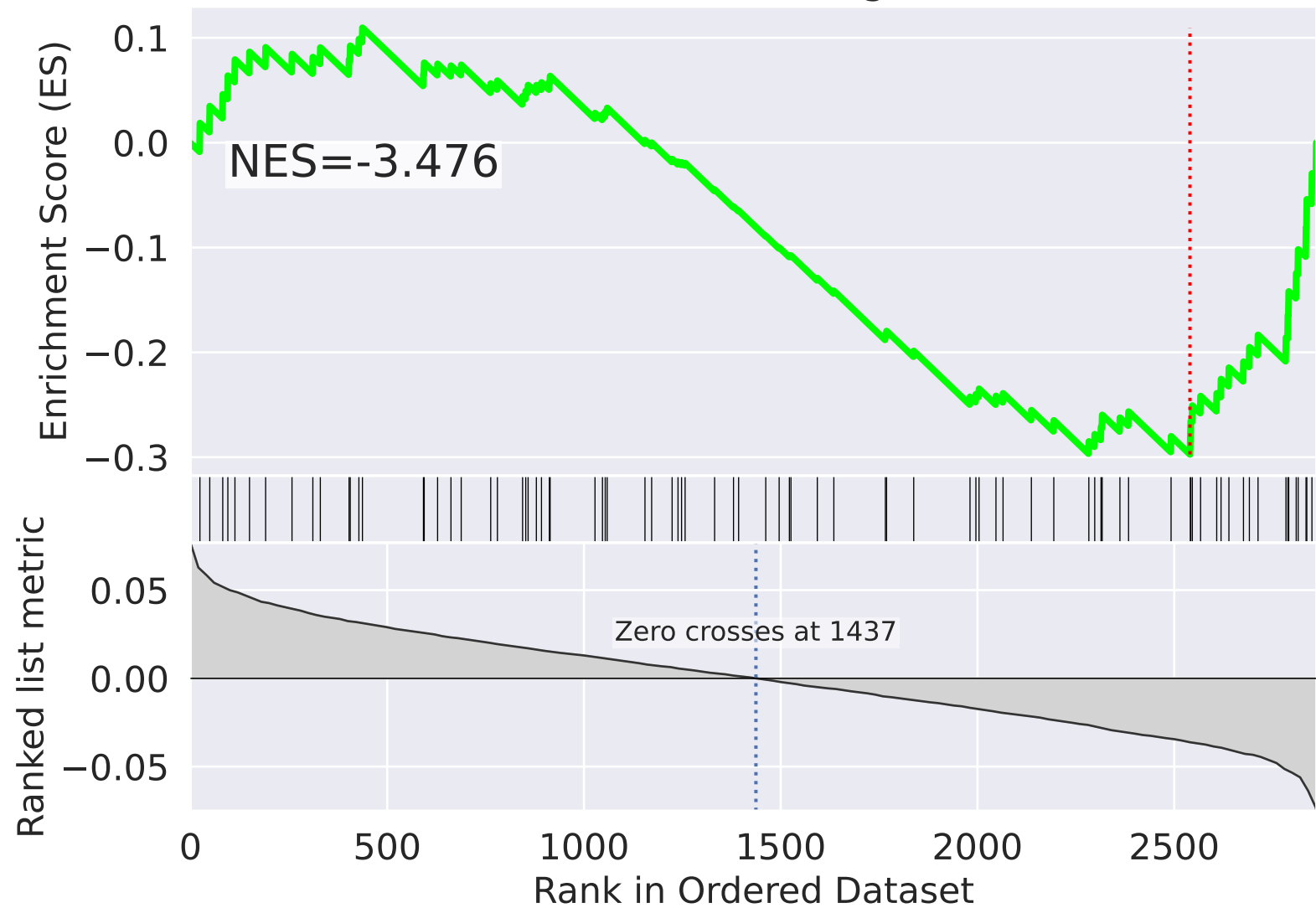
mitochondrial translational elongation (GO:0070125)



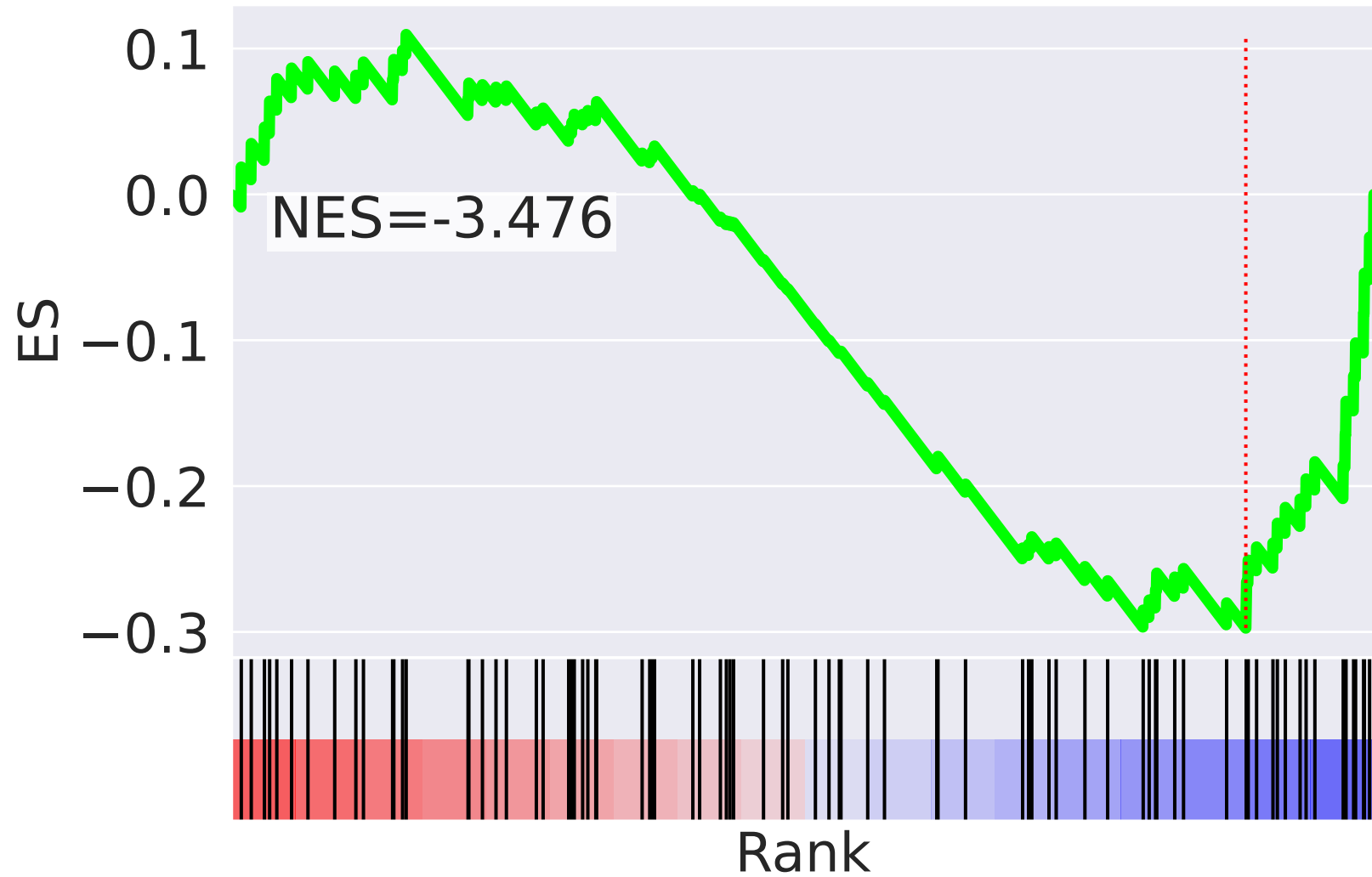
NES		SET
inf		regulation of signal transduction by p53 class mediator (GO:1901796)
7.532		mitochondrial translational termination (GO:0070126)
7.349		mitochondrial translational elongation (GO:0070125)
5.350		DNA replication (GO:0006260)
4.558		negative regulation of apoptotic process (GO:0043066)
-4.208		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
4.052		MAPK cascade (GO:0000165)
3.954		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-3.942		viral transcription (GO:0019083)
3.673		neutrophil degranulation (GO:0043312)
-3.659		rRNA processing (GO:0006364)
3.571		protein ubiquitination (GO:0016567)
3.532		membrane organization (GO:0061024)
3.434		regulation of transcription from RNA polymerase II promoter (GO:0006357)
3.419		mitochondrial translation (GO:0032543)



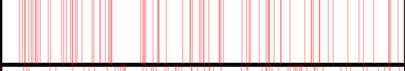
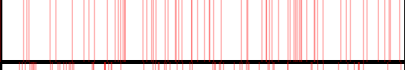
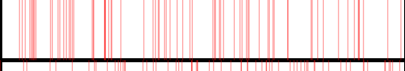
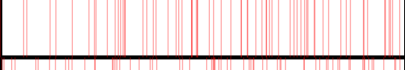
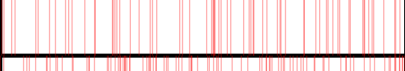
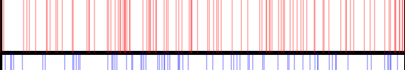
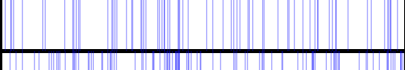
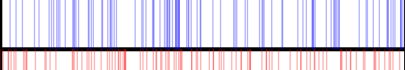
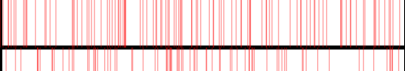
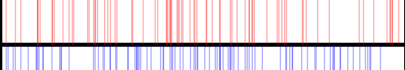
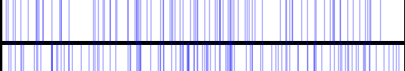
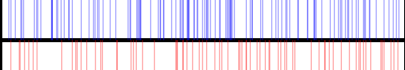
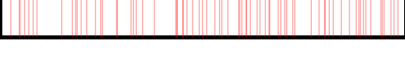
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=62$

mitochondrial translational elongation (GO:0070125)



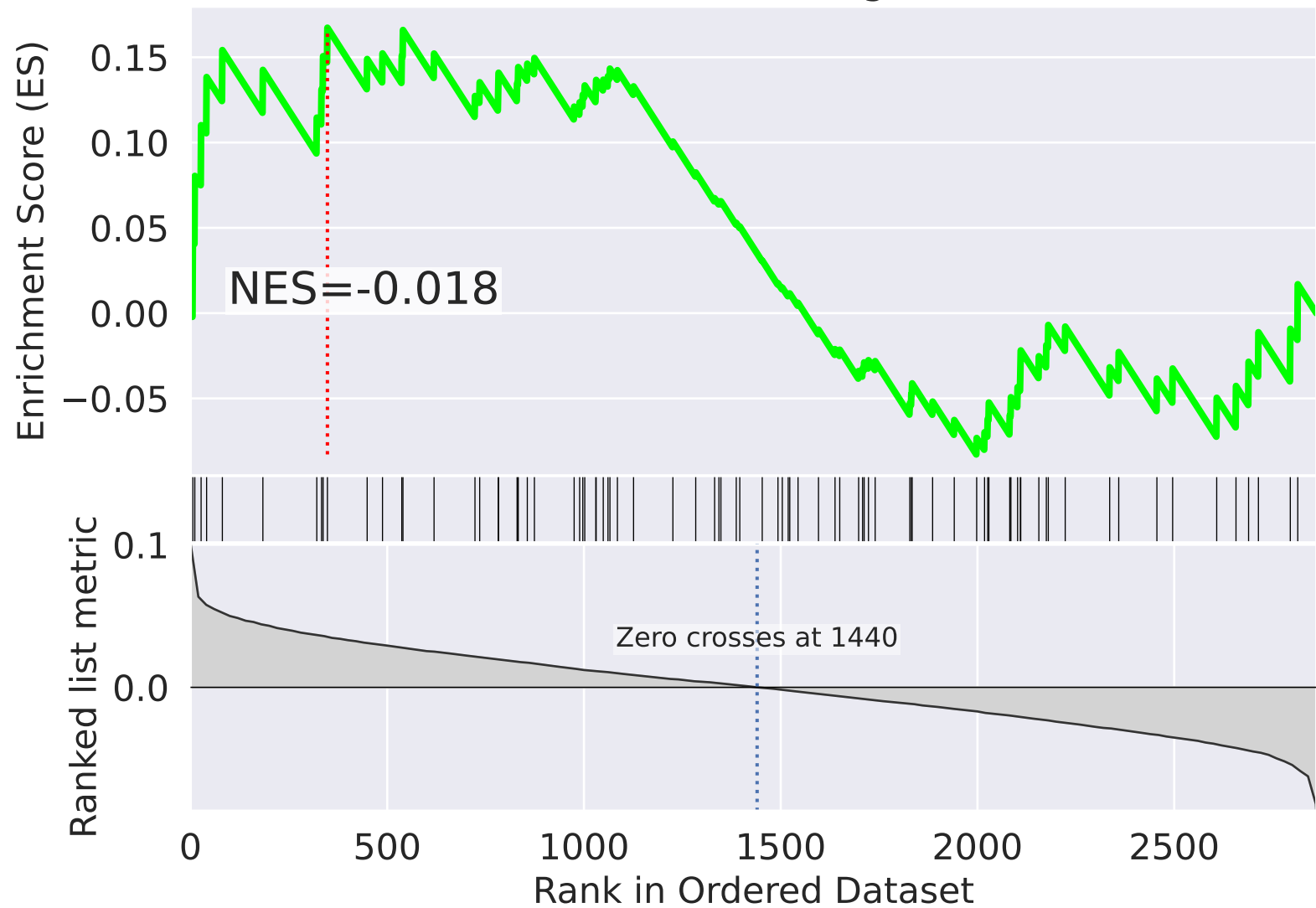
mitochondrial translational elongation (GO:0070125)



NES		SET
inf		viral transcription (GO:0019083)
6.345		post-translational protein modification (GO:0043687)
6.232		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
6.170		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
5.910		MAPK cascade (GO:0000165)
5.887		translational initiation (GO:0006413)
5.526		sister chromatid cohesion (GO:0007062)
5.274		translation (GO:0006412)
-5.069		protein phosphorylation (GO:0006468)
-4.928		signal transduction (GO:0007165)
4.801		rRNA processing (GO:0006364)
4.685		negative regulation of apoptotic process (GO:0043066)
-4.445		negative regulation of transcription, DNA-templated (GO:0045892)
-4.404		negative regulation of transcription from RNA polymerase II promoter (GO:0000122)
4.231		protein ubiquitination (GO:0016567)

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

mitochondrial translational elongation (GO:0070125)



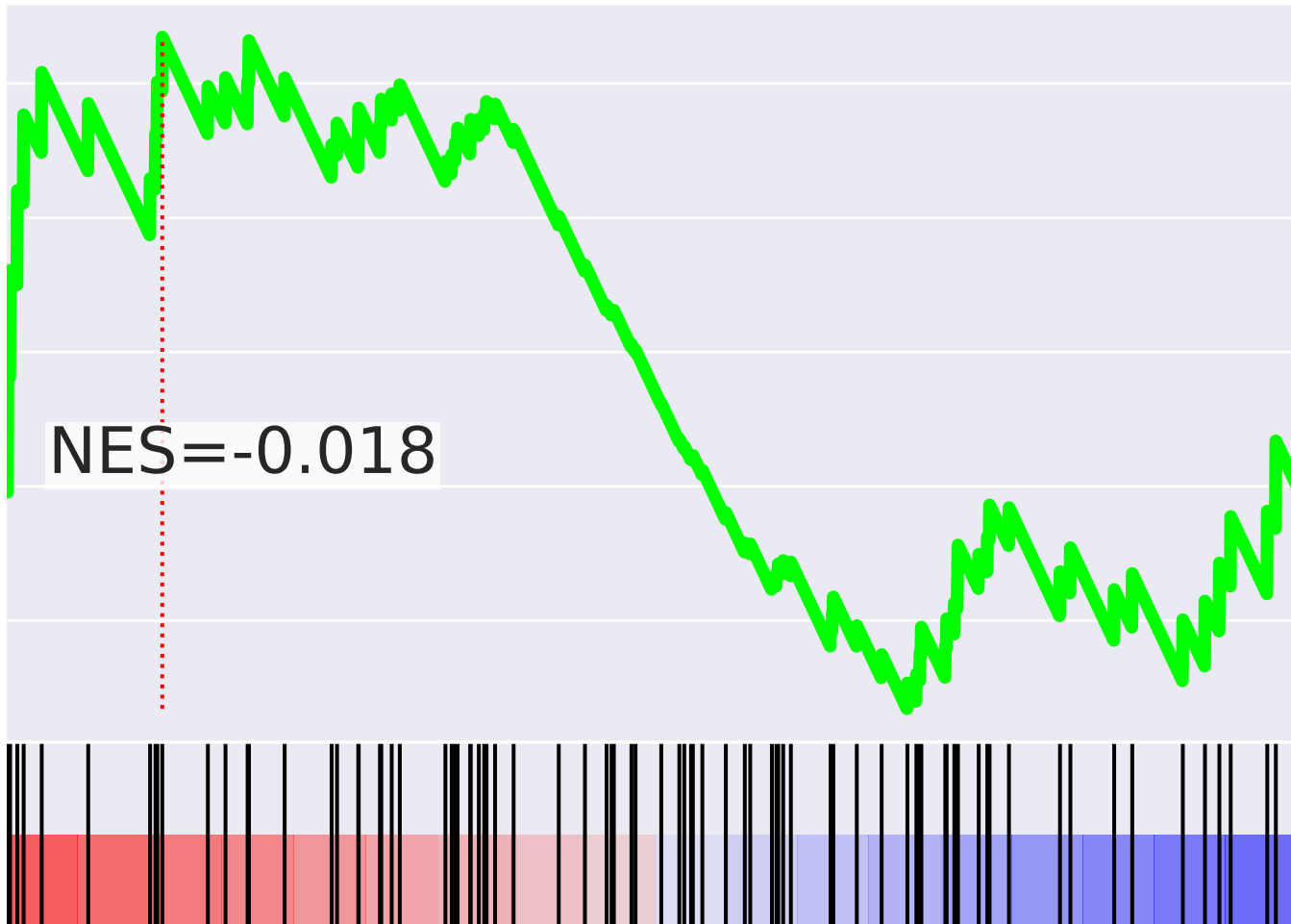
mitochondrial translational elongation (GO:0070125)

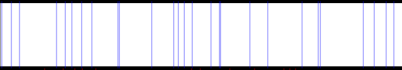

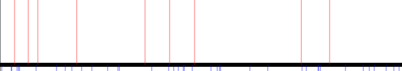
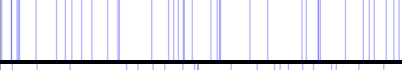





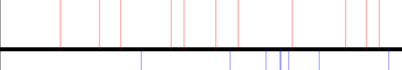



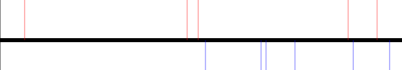

ES

0.15
0.10
0.05
0.00
-0.05

NES=-0.018

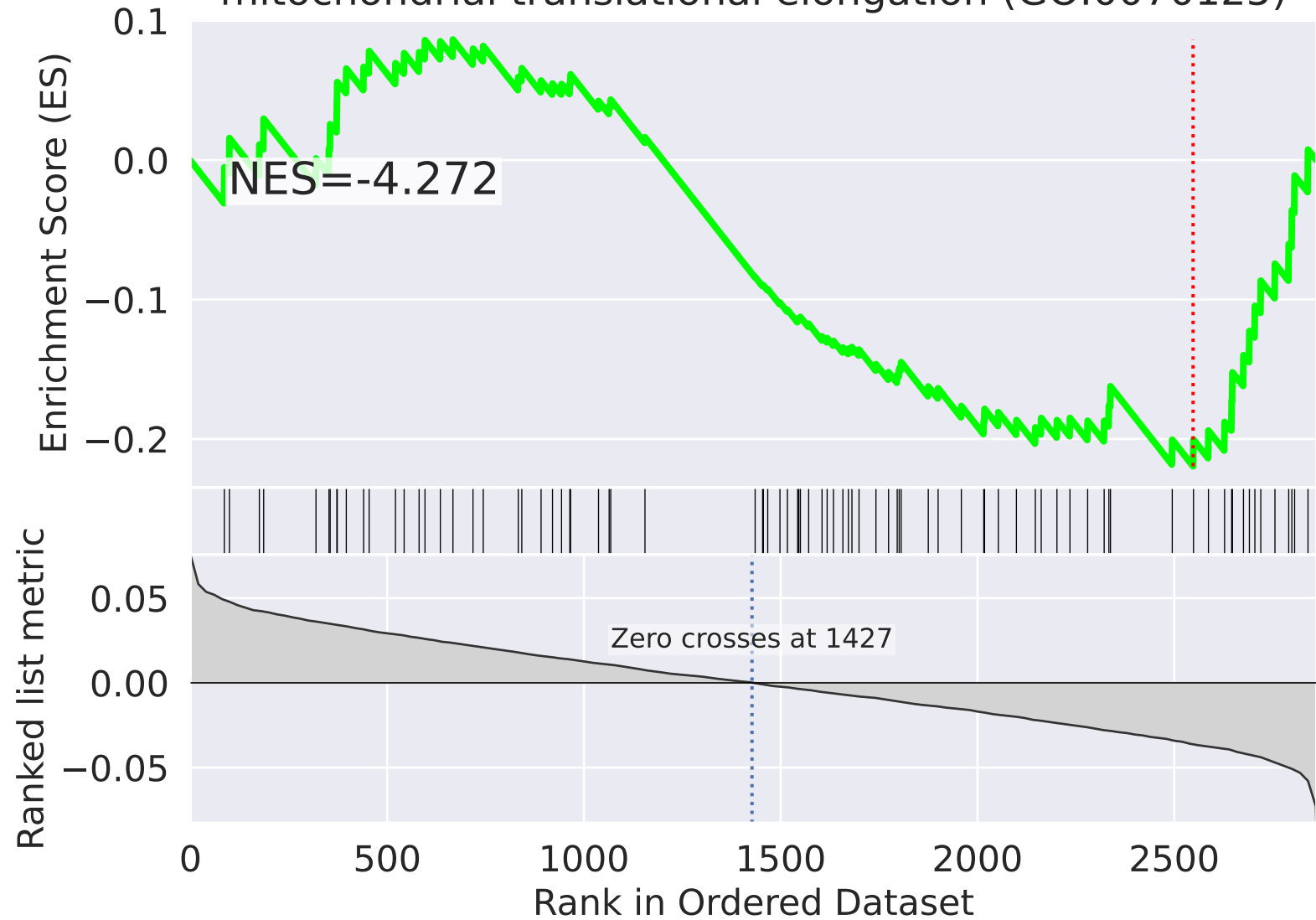
Rank



NES		SET
-3.018		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.828		tRNA aminoacylation for protein translation (GO:0006418)
2.823		central nervous system development (GO:0007417)
-2.648		mitochondrial respiratory chain complex I assembly (GO:0032981)
-2.625		transforming growth factor beta receptor signaling pathway (GO:0007179)
-2.602		DNA damage response, detection of DNA damage (GO:0042769)
-2.599		miRNA metabolic process (GO:0010586)
-2.552		translesion synthesis (GO:0019985)
2.495		negative regulation of TOR signaling (GO:0032007)
2.484		regulation of circadian rhythm (GO:0042752)
-2.437		regulation of GTPase activity (GO:0043087)
-2.432		regulation of transcription involved in G1/S transition of mitotic cell cycle (GO:0000083)
2.410		humoral immune response (GO:0006959)
2.371		cellular defense response (GO:0006968)
-2.349		negative regulation of Ras protein signal transduction (GO:0046580)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)


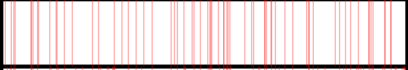
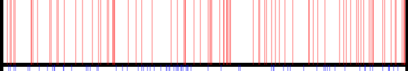
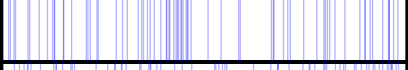
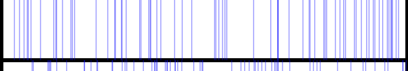
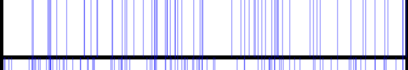
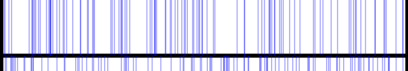
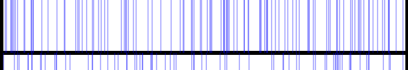
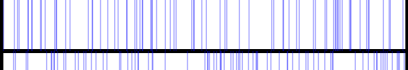
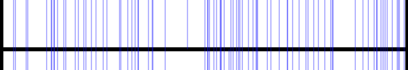
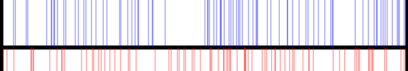
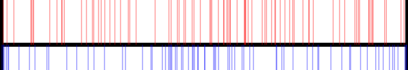
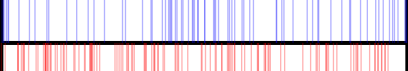
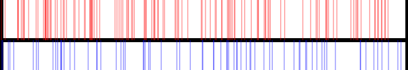
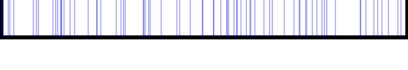
ES

0.1
0.0
-0.1
-0.2

NES=-4.272

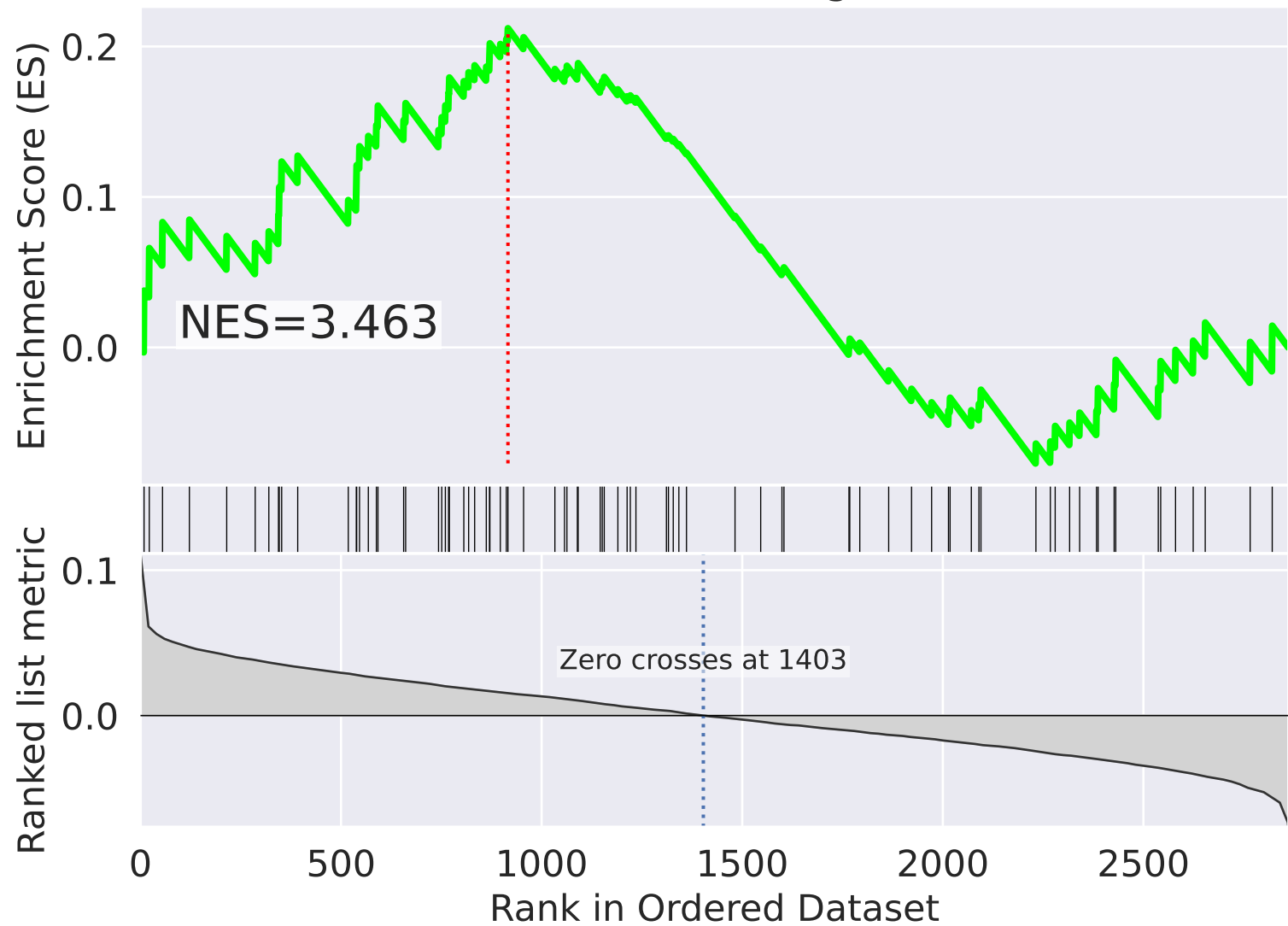
Rank



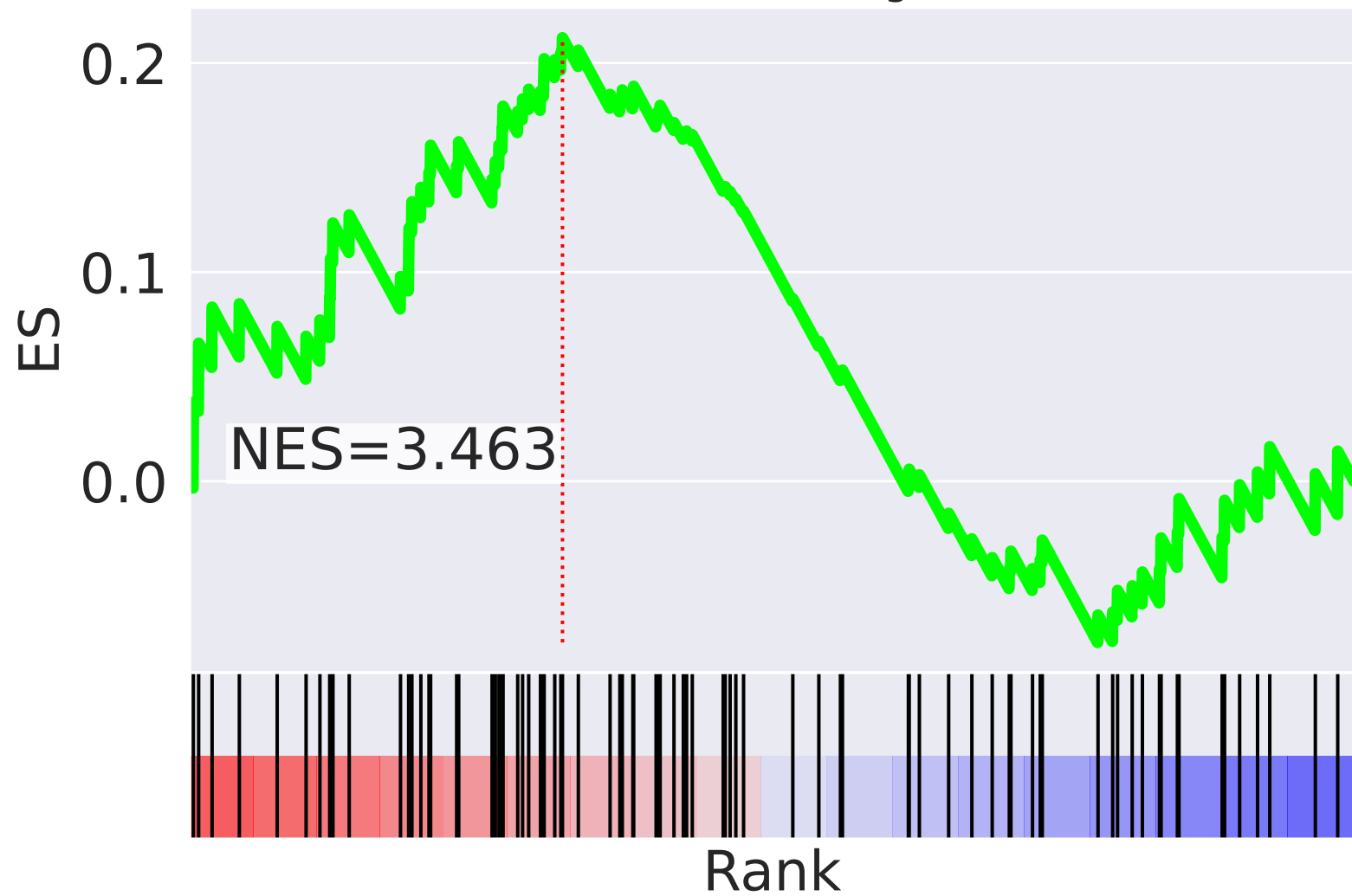
NES		SET
6.602		protein ubiquitination (GO:0016567)
5.768		protein polyubiquitination (GO:0000209)
5.037		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-4.989		positive regulation of cell proliferation (GO:0008284)
-4.939		cellular response to DNA damage stimulus (GO:0006974)
-4.681		transcription initiation from RNA polymerase II promoter (GO:0006367)
-4.597		transcription from RNA polymerase II promoter (GO:0006366)
-4.557		protein deubiquitination (GO:0016579)
-4.395		regulation of signal transduction by p53 class mediator (GO:1901796)
-4.356		mitochondrial translational termination (GO:0070126)
-4.272		mitochondrial translational elongation (GO:0070125)
4.219		post-translational protein modification (GO:0043687)
-4.089		viral transcription (GO:0019083)
4.031		mRNA splicing, via spliceosome (GO:0000398)
-3.980		regulation of transcription, DNA-templated (GO:0006355)

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

mitochondrial translational elongation (GO:0070125)

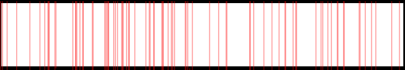
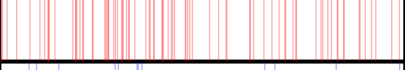
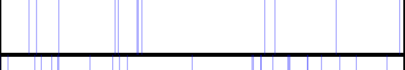
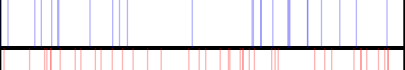
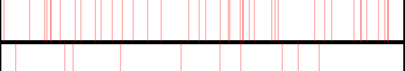
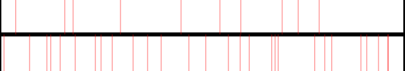






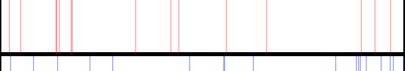




mitochondrial translational elongation (GO:0070125)



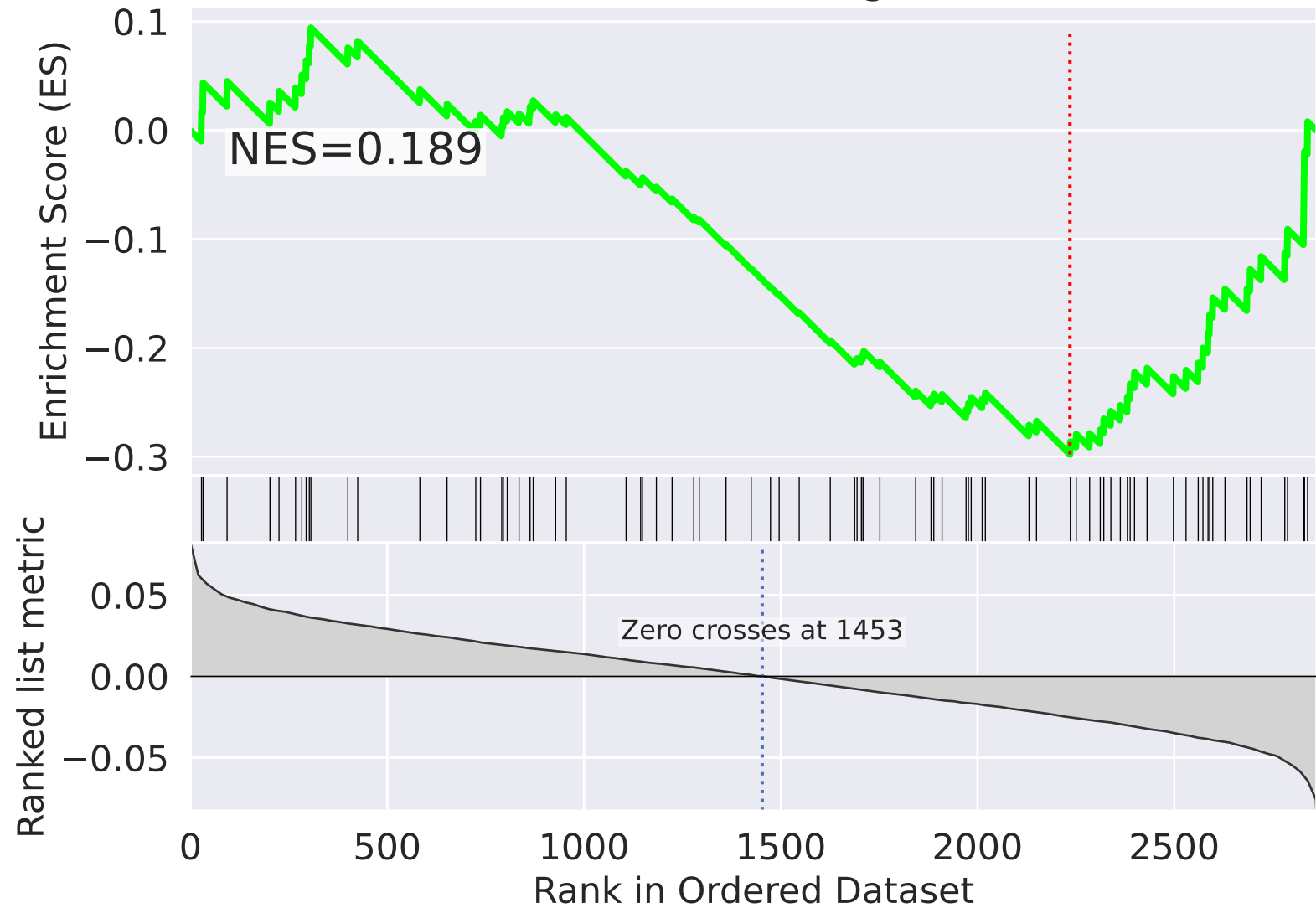
NES

SET

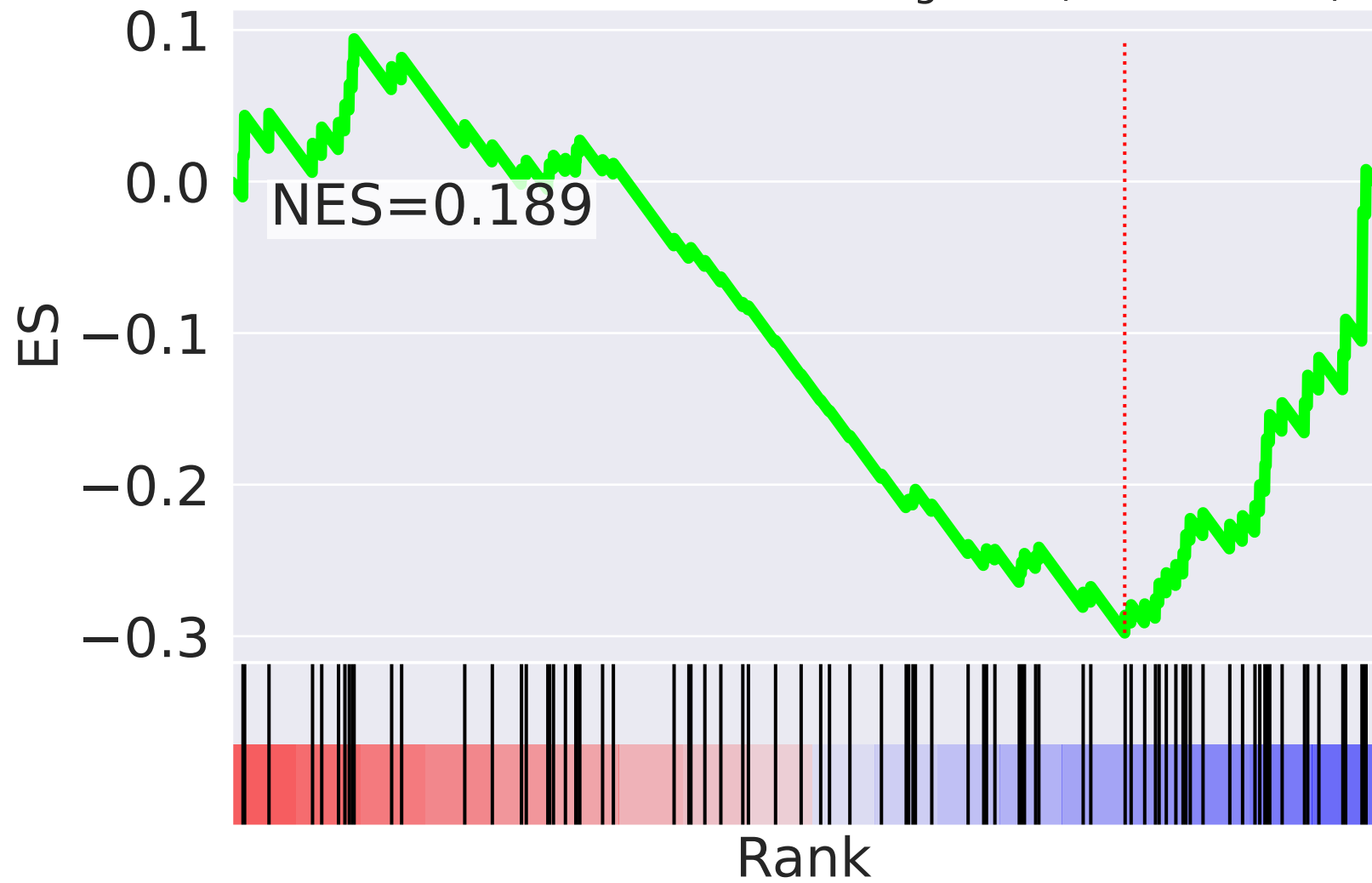
3.646		mitochondrial translational termination (GO:0070126)
3.463		mitochondrial translational elongation (GO:0070125)
-3.140		establishment of protein localization (GO:0045184)
-3.103		Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)
2.994		mitochondrial respiratory chain complex I assembly (GO:0032981)
2.964		nucleosome disassembly (GO:0006337)
2.944		mitochondrial electron transport, NADH to ubiquinone (GO:0006120)
2.875		skeletal muscle tissue development (GO:0007519)
2.863		nervous system development (GO:0007399)
-2.817		mitotic spindle organization (GO:0007052)
-2.806		movement of cell or subcellular component (GO:0006928)
-2.747		positive regulation of angiogenesis (GO:0045766)
-2.682		ESCRT III complex disassembly (GO:1904903)
2.657		tricarboxylic acid cycle (GO:0006099)
-2.612		epidermal growth factor receptor signaling pathway (GO:0007173)



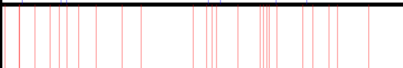




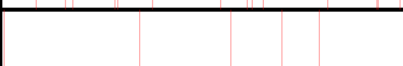
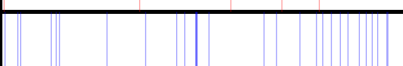

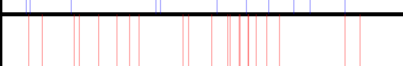


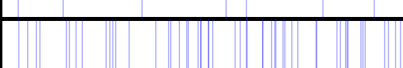
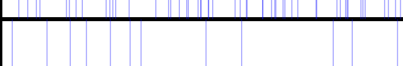
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=66$

mitochondrial translational elongation (GO:0070125)



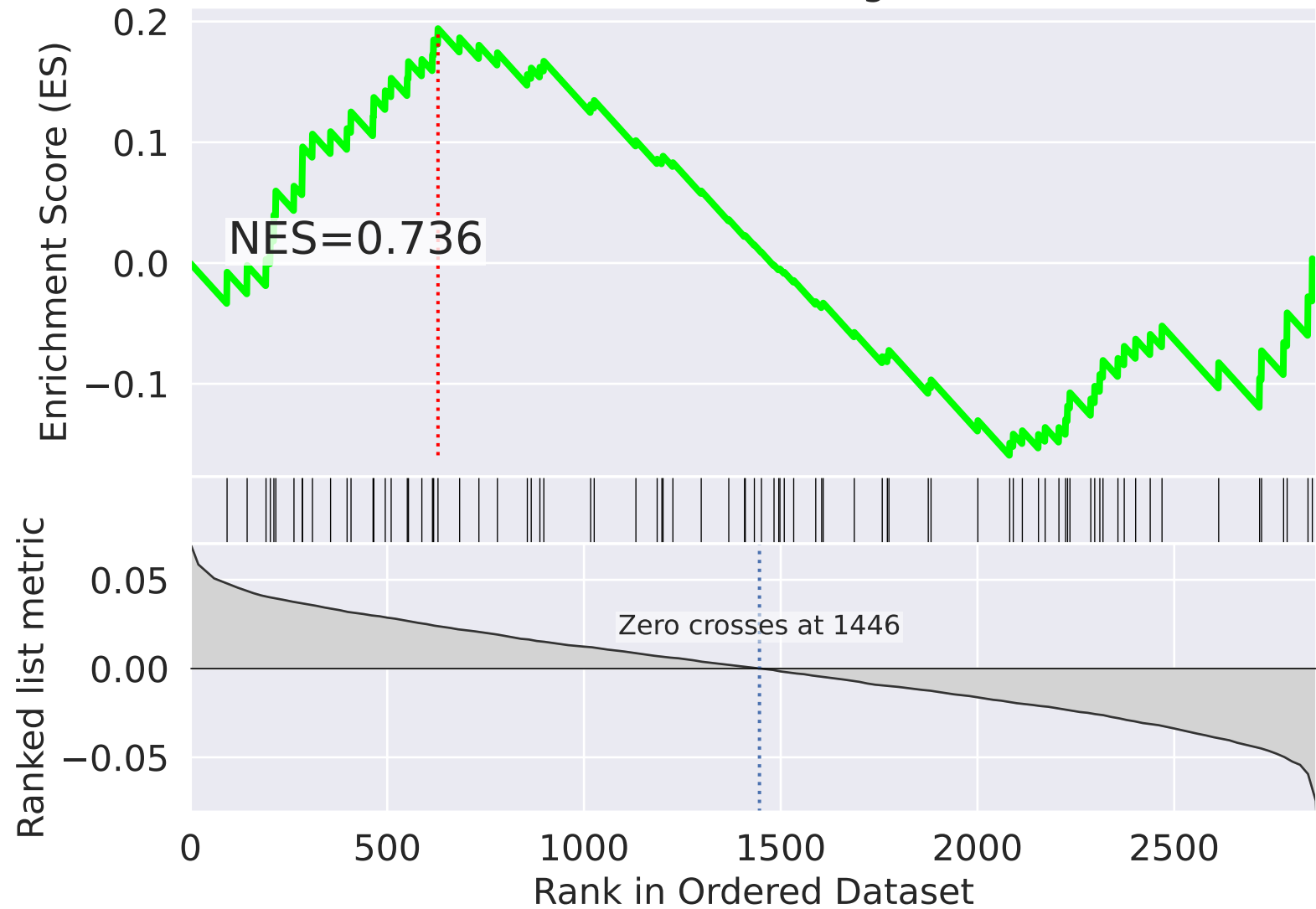
mitochondrial translational elongation (GO:0070125)



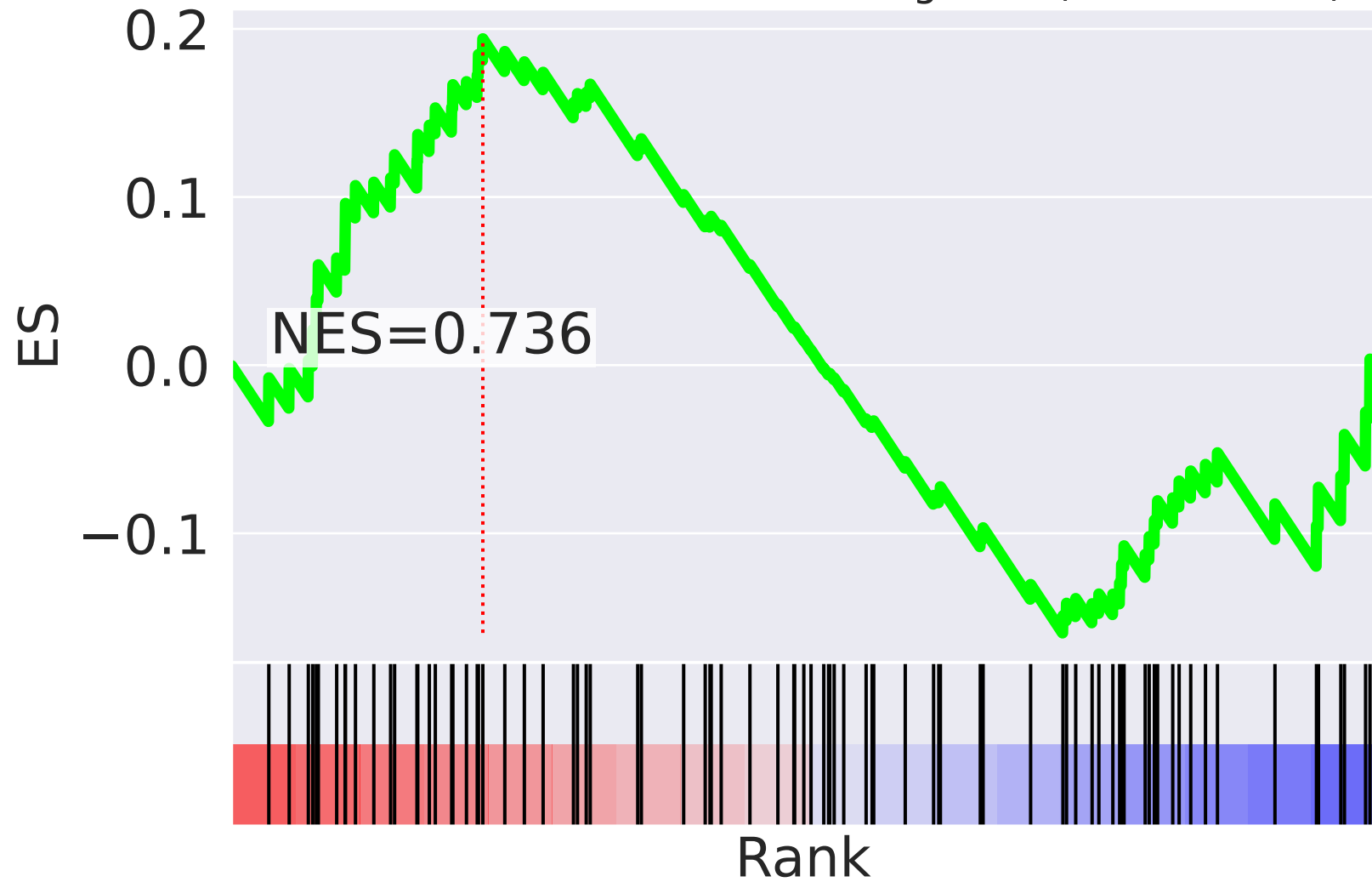
NES		SET
3.021		microtubule cytoskeleton organization (GO:0000226)
-2.776		negative regulation of fibroblast proliferation (GO:0048147)
2.729		positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)
-2.700		RNA splicing, via transesterification reactions (GO:0000375)
-2.669		cellular response to gamma radiation (GO:0071480)
-2.665		Notch signaling pathway (GO:0007219)
2.592		intra-Golgi vesicle-mediated transport (GO:0006891)
2.588		negative regulation of tyrosine phosphorylation of STAT protein (GO:0042532)
-2.573		histone H3 acetylation (GO:0043966)
-2.492		cell division (GO:0051301)
2.485		movement of cell or subcellular component (GO:0006928)
-2.472		positive regulation of mitochondrial translation (GO:0070131)
-2.442		attachment of mitotic spindle microtubules to kinetochore (GO:0051315)
-2.430		G1/S transition of mitotic cell cycle (GO:0000082)
-2.353		spliceosomal complex assembly (GO:0000245)

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

mitochondrial translational elongation (GO:0070125)



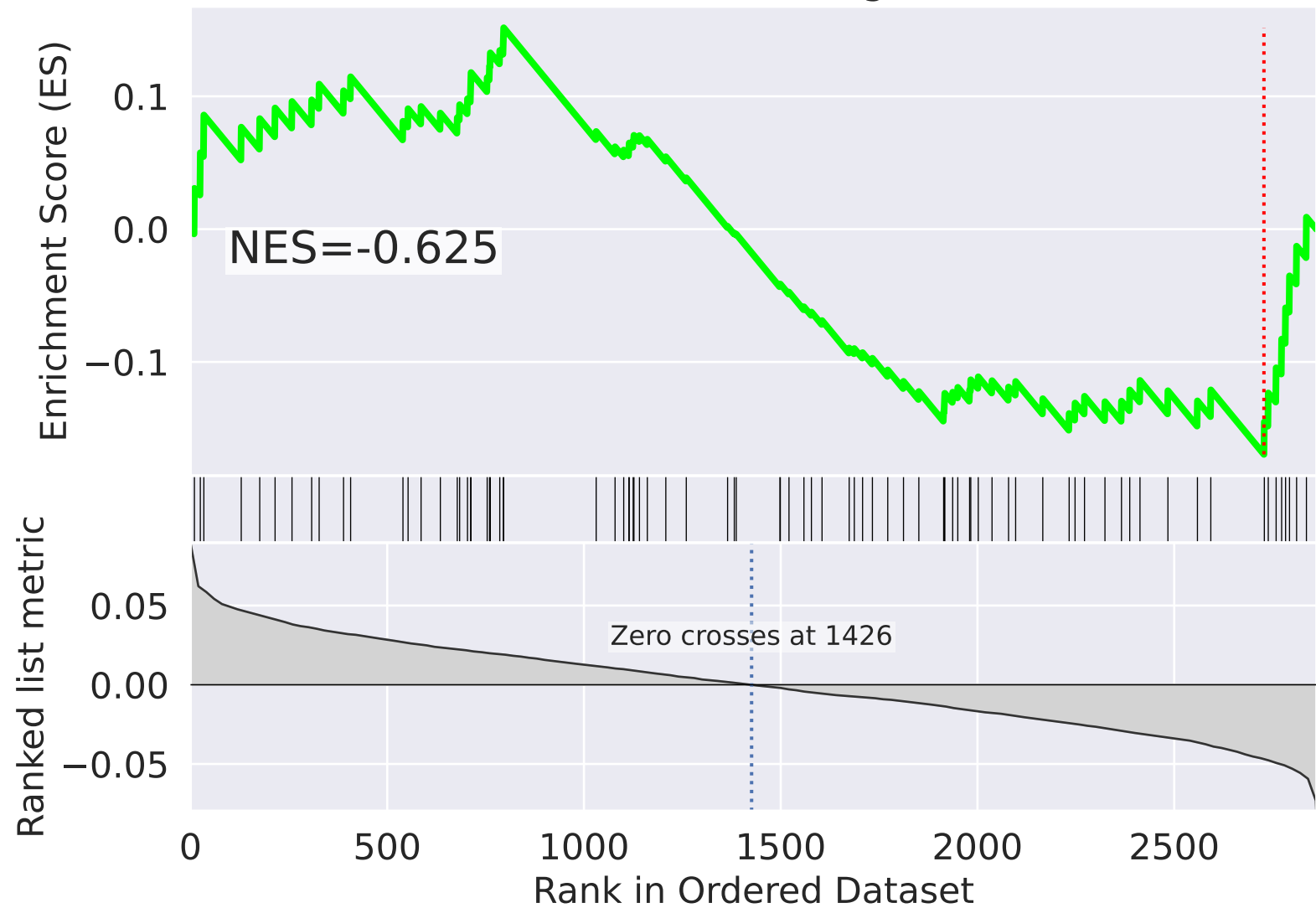
mitochondrial translational elongation (GO:0070125)



NES		SET
3.577		beta-catenin-TCF complex assembly (GO:1904837)
-2.692		substrate adhesion-dependent cell spreading (GO:0034446)
2.676		cellular response to oxidative stress (GO:0034599)
2.655		negative regulation of gene expression, epigenetic (GO:0045814)
-2.541		positive regulation of phosphatidylinositol 3-kinase signaling (GO:0014068)
2.517		cellular iron ion homeostasis (GO:0006879)
2.509		interstrand cross-link repair (GO:0036297)
2.487		histone H2B ubiquitination (GO:0033523)
-2.459		extrinsic apoptotic signaling pathway in absence of ligand (GO:0097192)
-2.455		cellular response to transforming growth factor beta stimulus (GO:0071560)
-2.430		regulation of defense response to virus by virus (GO:0050690)
2.271		Notch signaling pathway (GO:0007219)
2.266		cellular response to UV (GO:0034644)
2.247		regulation of transcription from RNA polymerase I promoter (GO:0006356)
2.212		TOR signaling (GO:0031929)

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

mitochondrial translational elongation (GO:0070125)



mitochondrial translational elongation (GO:0070125)

ES

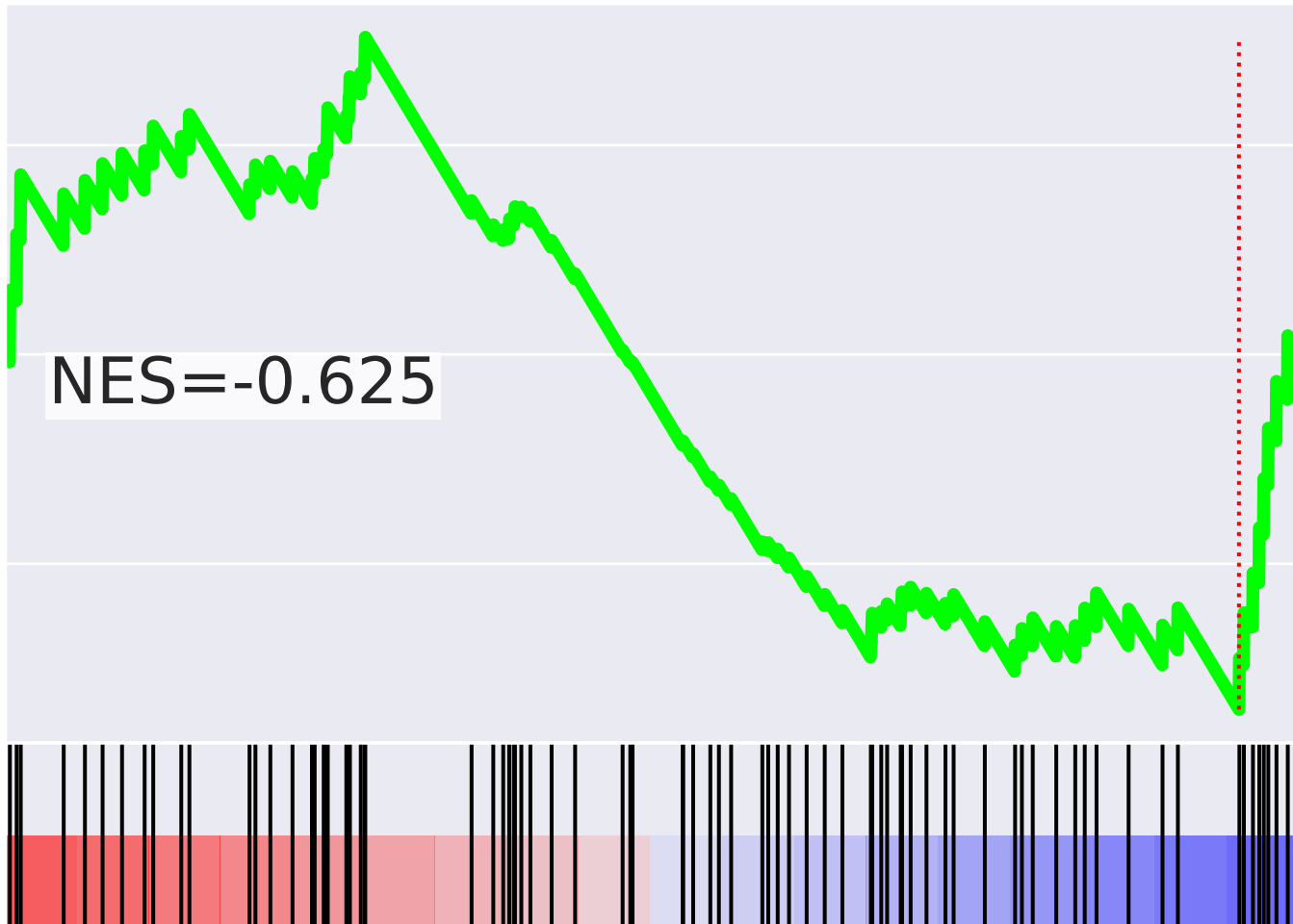
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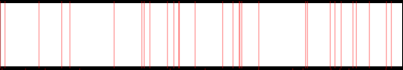


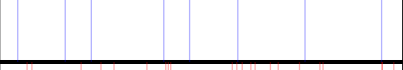


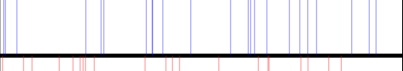
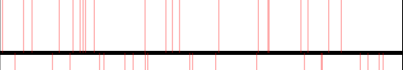

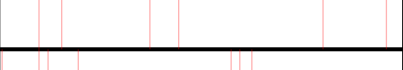
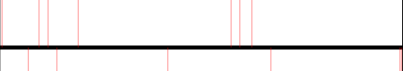

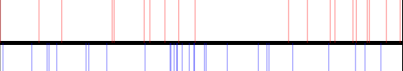
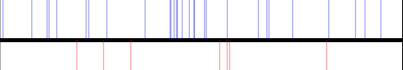
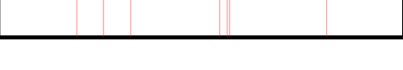
0.0

-0.1

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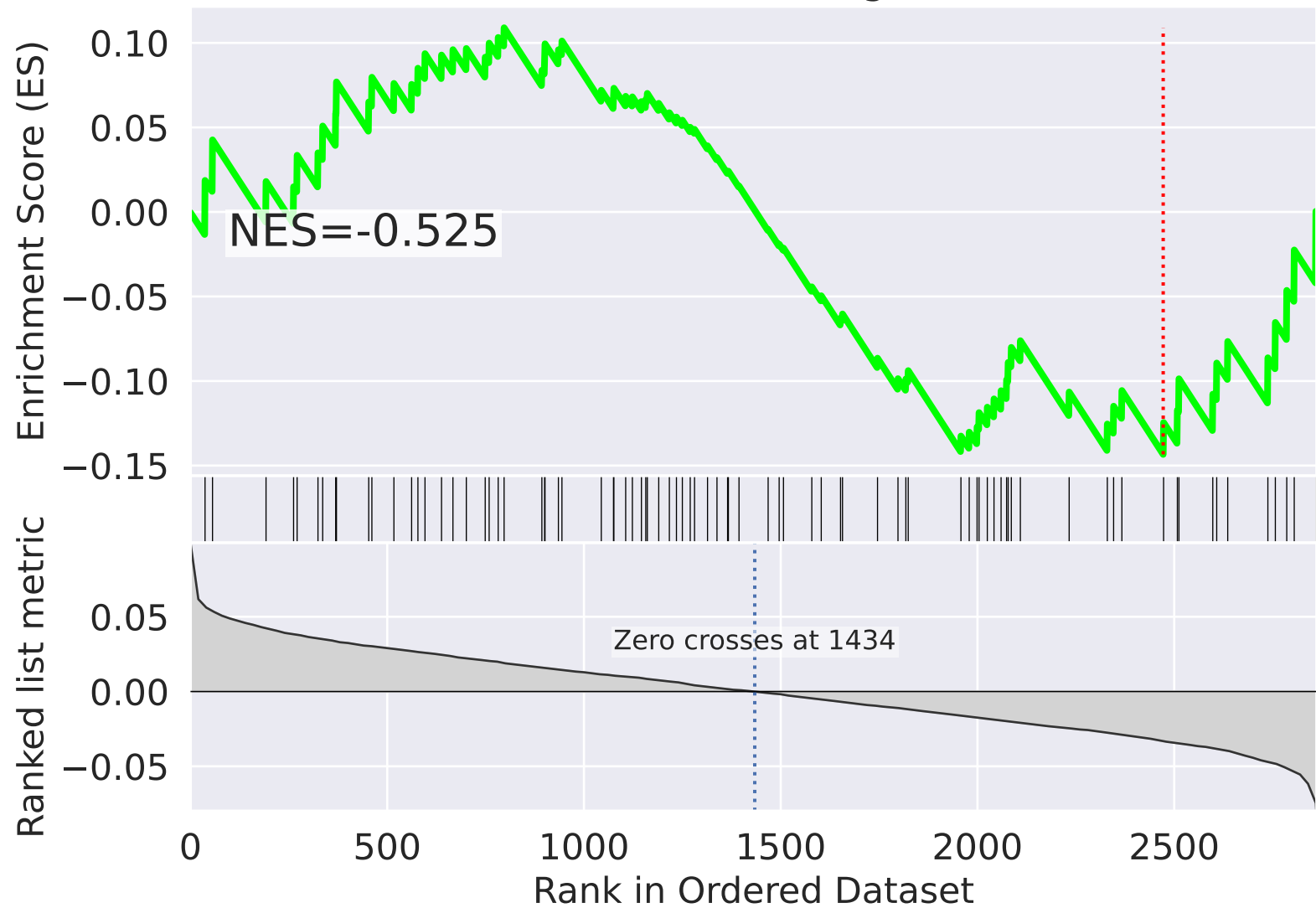
Rank



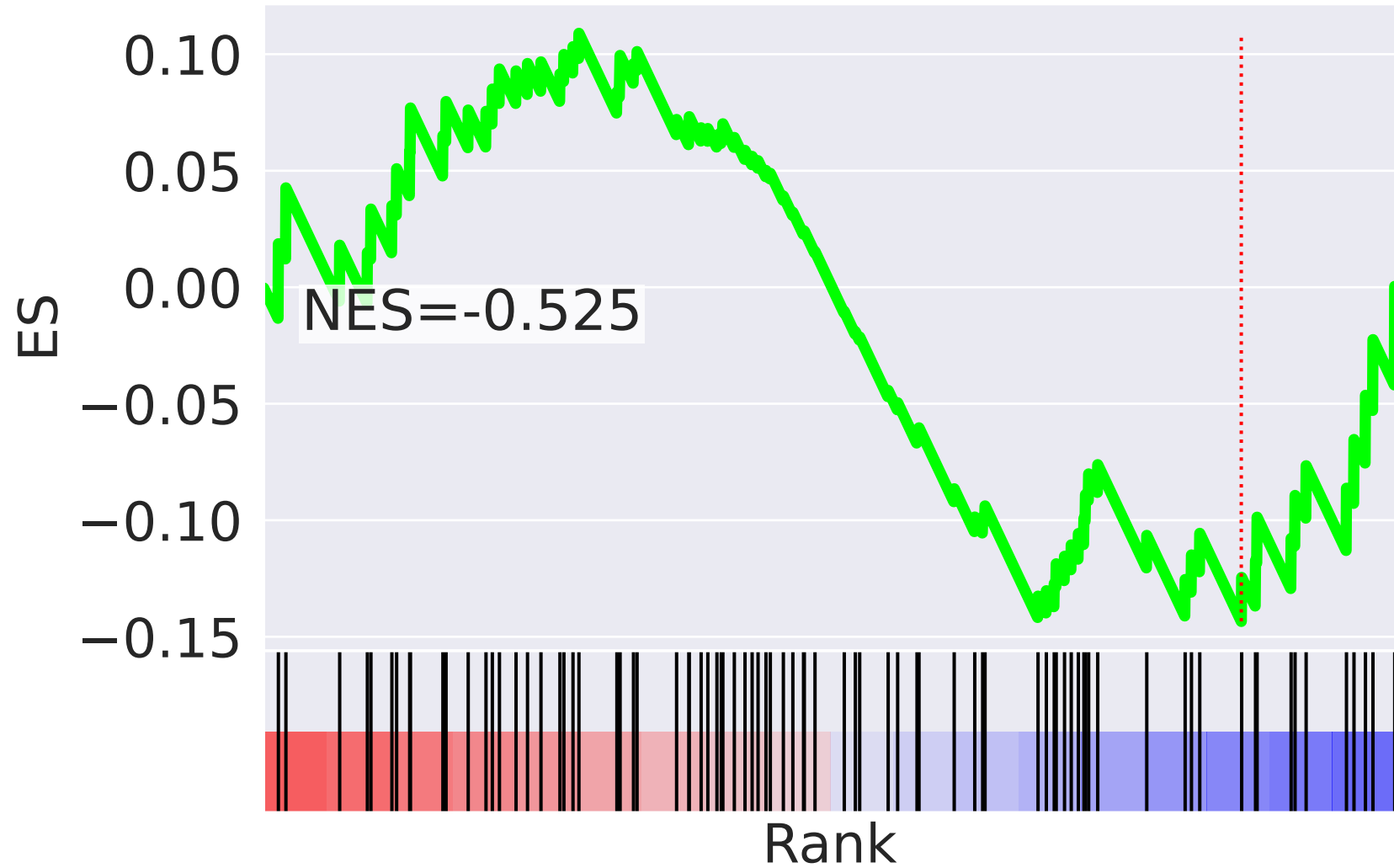
NES		SET
2.722		antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886)
2.637		cellular iron ion homeostasis (GO:0006879)
2.573		maturation of LSU-rRNA (GO:0000470)
-2.559		xenobiotic metabolic process (GO:0006805)
2.396		movement of cell or subcellular component (GO:0006928)
2.306		cellular defense response (GO:0006968)
-2.306		mitochondrion organization (GO:0007005)
2.304		telomere maintenance via recombination (GO:0000722)
2.297		regulation of cholesterol biosynthetic process (GO:0045540)
2.269		low-density lipoprotein particle receptor catabolic process (GO:0032802)
2.229		receptor internalization (GO:0031623)
2.225		negative regulation of fat cell differentiation (GO:0045599)
2.207		microtubule-based movement (GO:0007018)
-2.183		interstrand cross-link repair (GO:0036297)
2.183		protein localization to kinetochore (GO:0034501)



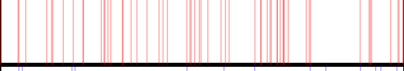


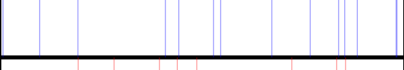





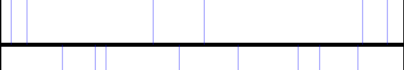

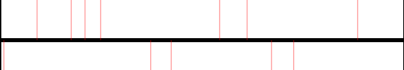
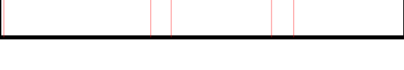
The three following figures visualize the negative control gene set enrichment analysis results for mitochondrial translational elongation (GO:0070125) in the latent dimension $z=69$

mitochondrial translational elongation (GO:0070125)



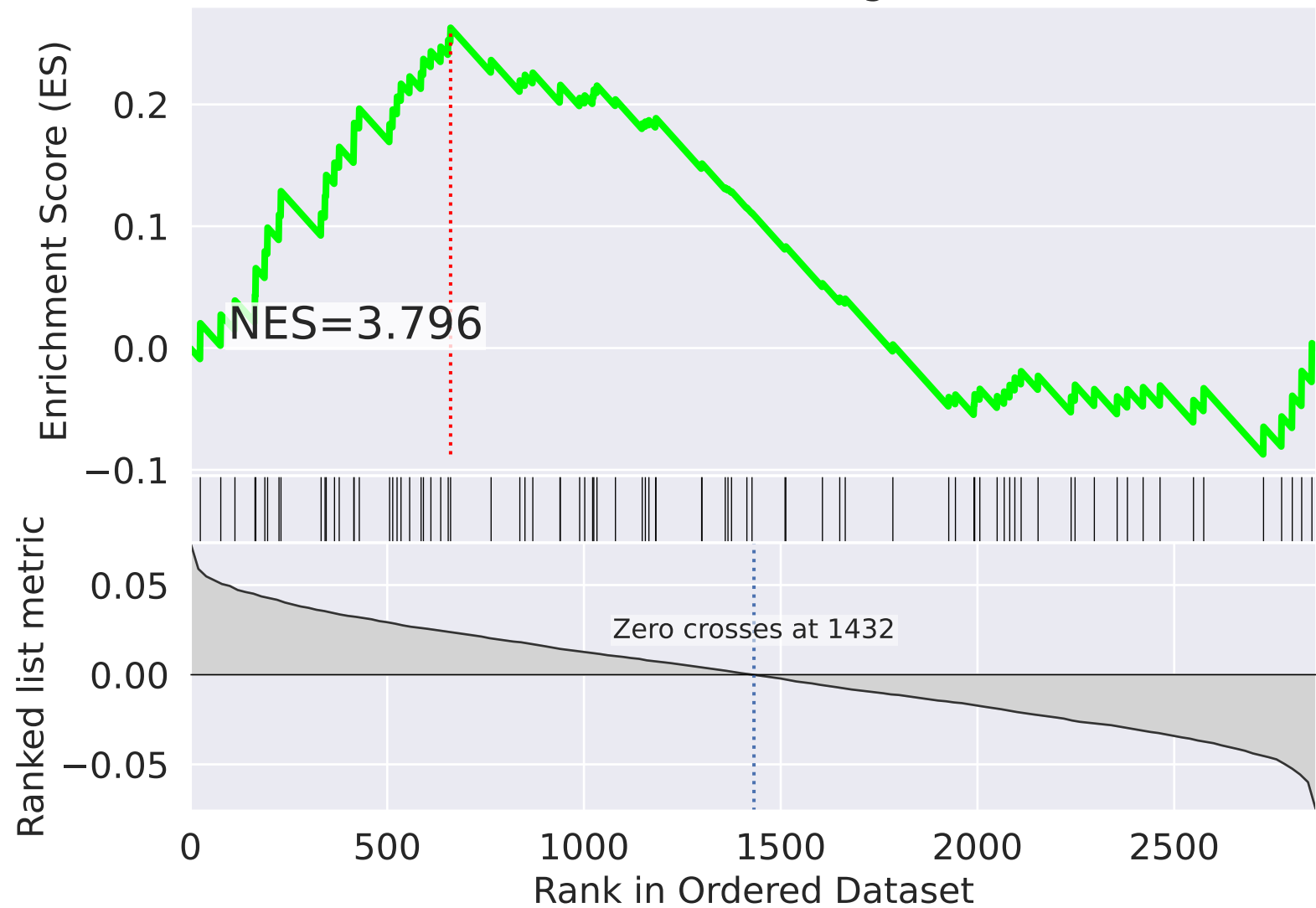
mitochondrial translational elongation (GO:0070125)



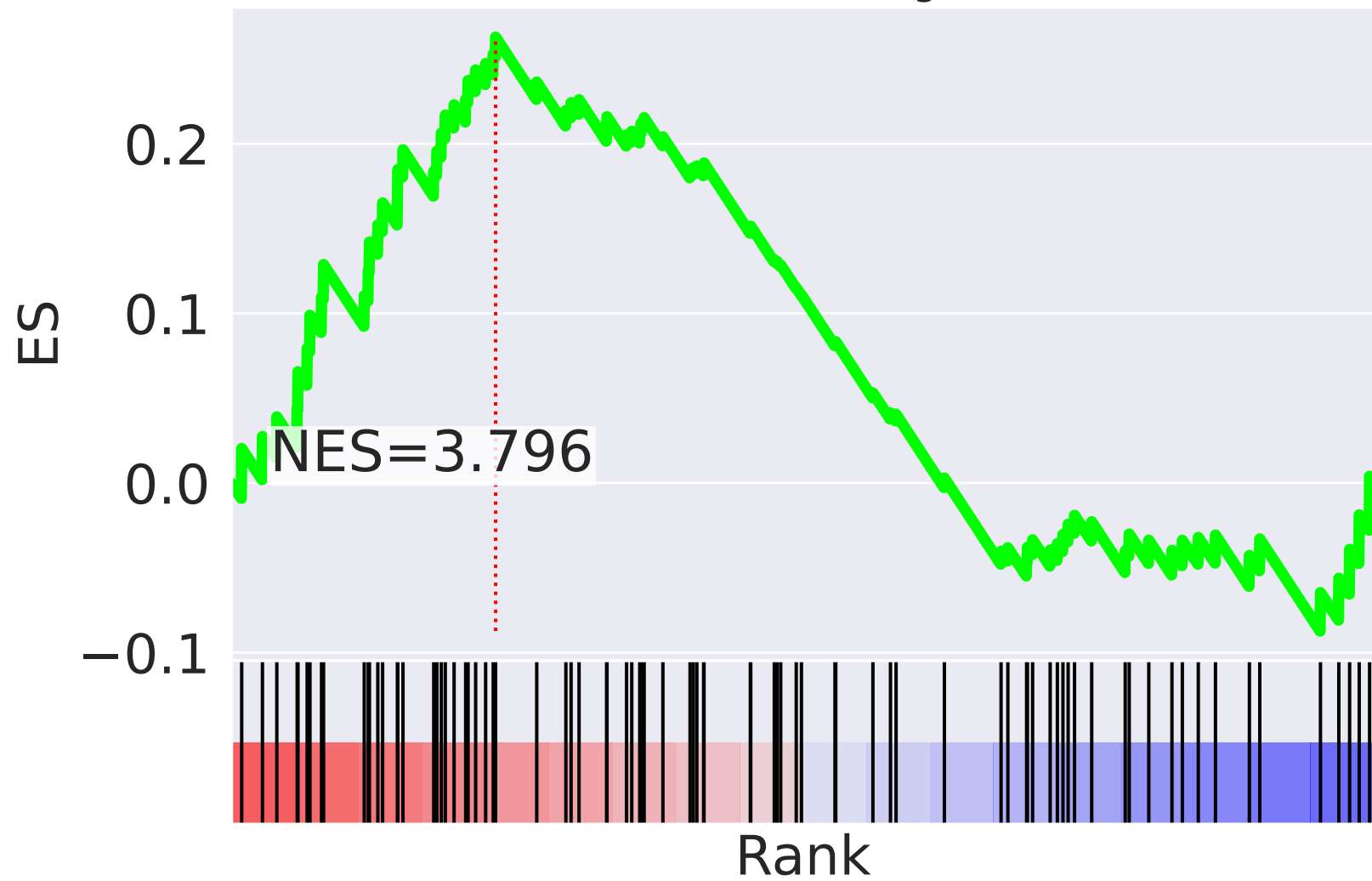
NES		SET
2.956		G-protein coupled receptor signaling pathway (GO:0007186)
-2.938		protein neddylation (GO:0045116)
2.808		mRNA export from nucleus (GO:0006406)
-2.782		Notch signaling pathway (GO:0007219)
2.750		female pregnancy (GO:0007565)
-2.641		nucleotide-excision repair, DNA gap filling (GO:0006297)
2.636		regulation of DNA replication (GO:0006275)
-2.610		negative regulation of protein kinase activity (GO:0006469)
-2.520		DNA metabolic process (GO:0006259)
-2.512		base-excision repair (GO:0006284)
2.499		type I interferon signaling pathway (GO:0060337)
-2.469		positive regulation of lamellipodium assembly (GO:0010592)
-2.465		activation of protein kinase activity (GO:0032147)
2.449		negative regulation of autophagy (GO:0010507)
2.437		negative regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045736)

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

mitochondrial translational elongation (GO:0070125)

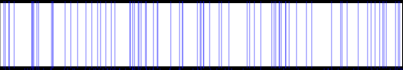
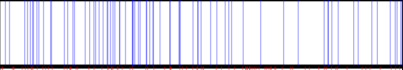
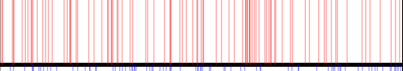
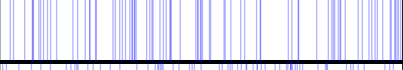
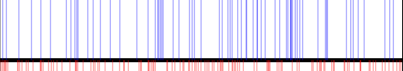
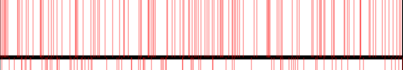
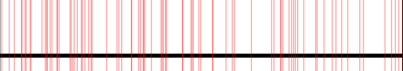
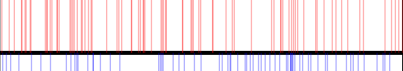
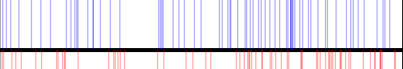
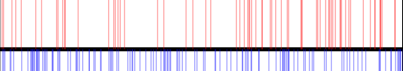
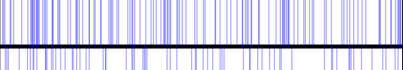
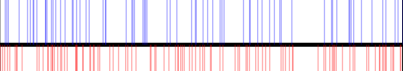
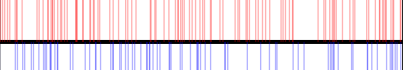
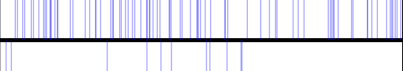



mitochondrial translational elongation (GO:0070125)



NES

SET

-5.034		negative regulation of apoptotic process (GO:0043066)
-5.026		MAPK cascade (GO:0000165)
4.612		negative regulation of transcription, DNA-templated (GO:0045892)
-4.328		proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)
-4.069		nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)
3.908		mRNA splicing, via spliceosome (GO:0000398)
3.896		mitochondrial translational termination (GO:0070126)
3.796		mitochondrial translational elongation (GO:0070125)
-3.751		translational initiation (GO:0006413)
3.538		sister chromatid cohesion (GO:0007062)
-3.530		positive regulation of transcription, DNA-templated (GO:0045893)
-3.525		protein phosphorylation (GO:0006468)
3.447		transcription from RNA polymerase II promoter (GO:0006366)
-3.312		post-translational protein modification (GO:0043687)
-3.194		negative regulation of cell migration (GO:0030336)