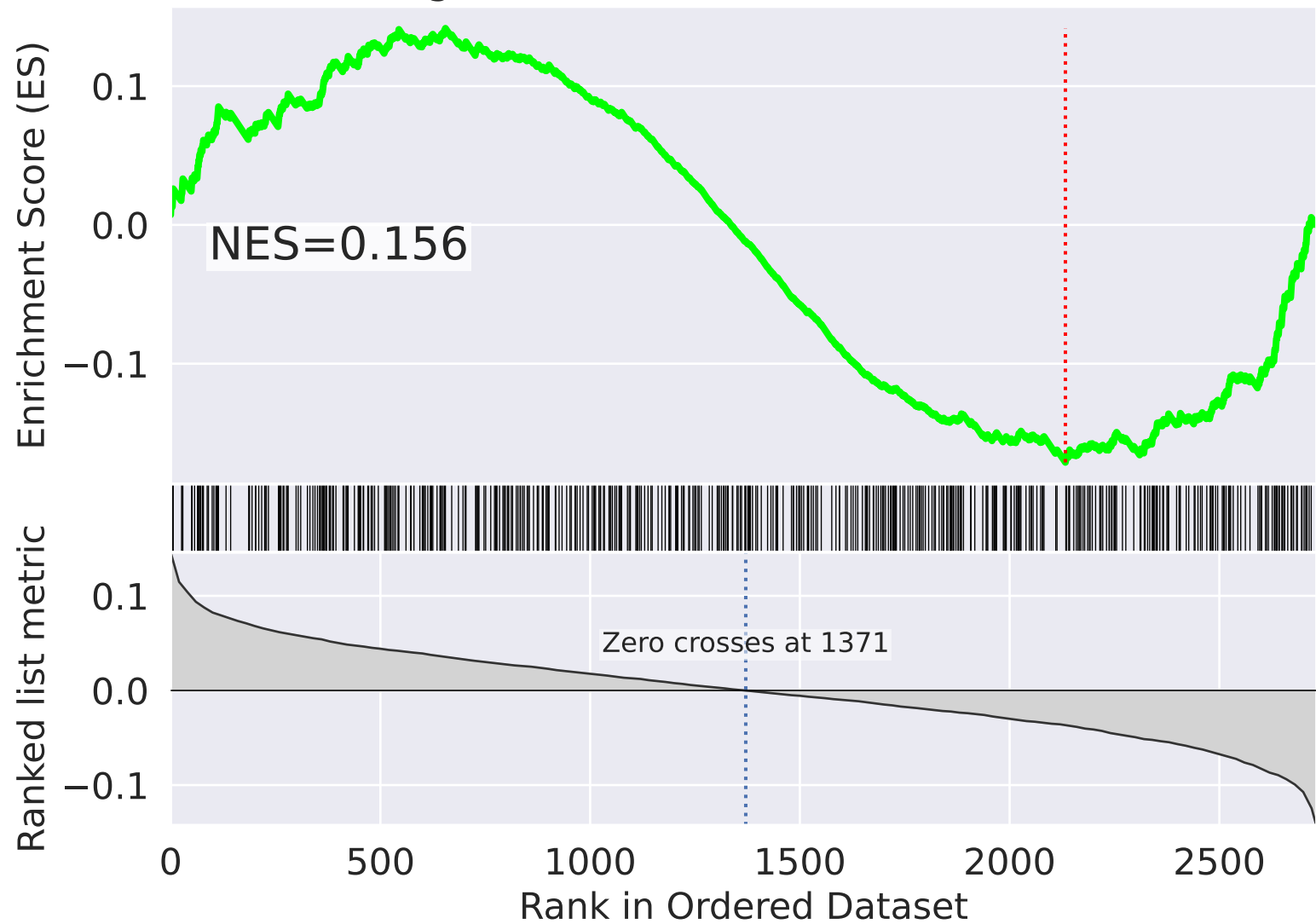
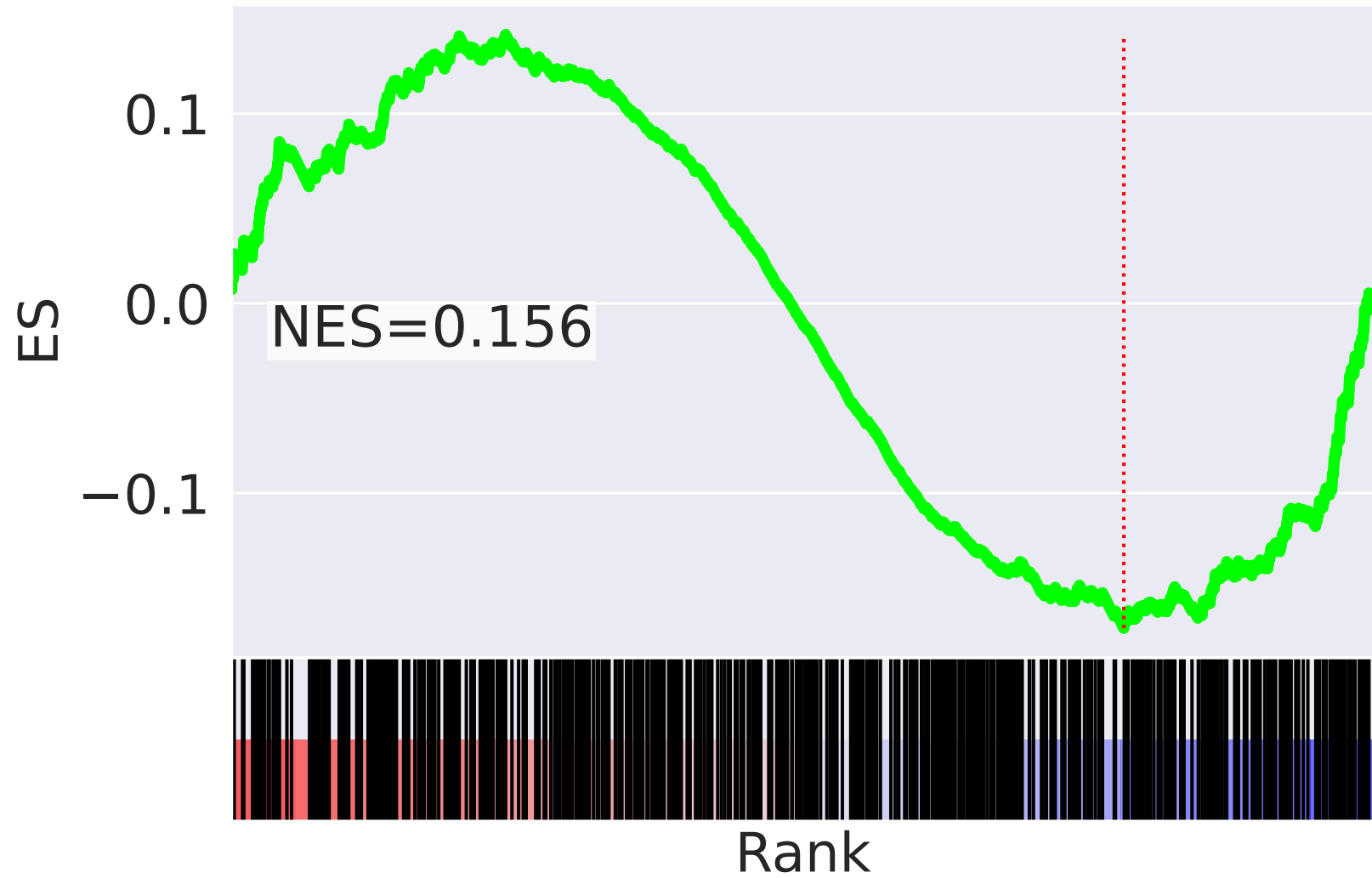



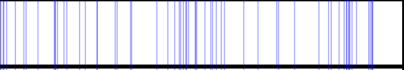
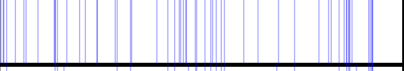
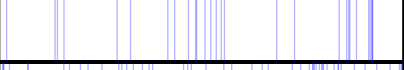
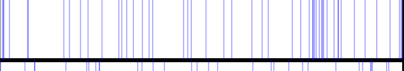

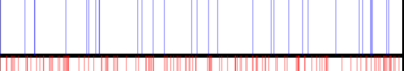
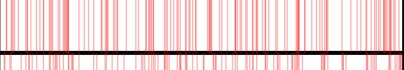
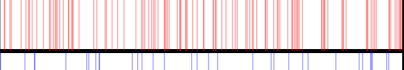
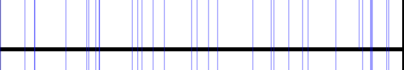
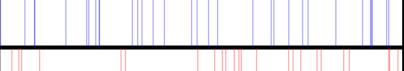
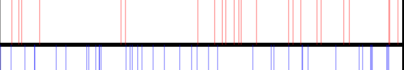
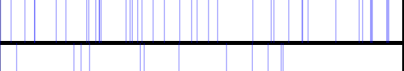

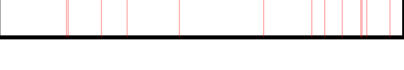
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=1$

Signal Transduction R-HSA-162582



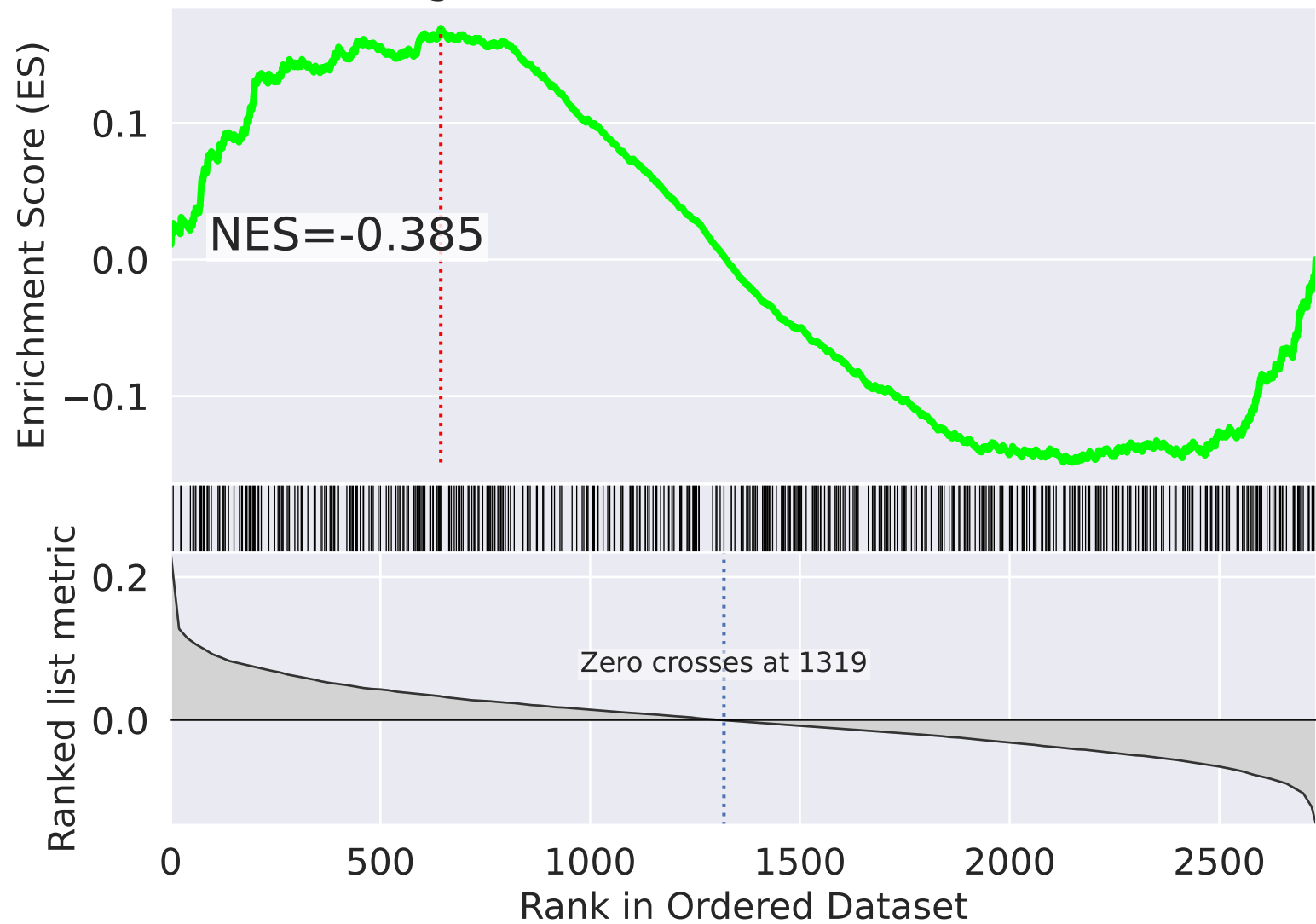
Signal Transduction R-HSA-162582



NES		SET
-5.310		rRNA Processing R-HSA-72312
-5.267		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-5.155		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.705		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-3.469		Protein Localization R-HSA-9609507
-3.399		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.399		Diseases Of DNA Repair R-HSA-9675135
3.245		HIV Infection R-HSA-162906
3.184		Transport Of Small Molecules R-HSA-382551
-3.087		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.073		Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
3.048		Metabolism Of Nucleotides R-HSA-15869
-3.037		HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-3.018		Cargo Trafficking To Periciliary Membrane R-HSA-5620920
2.945		MicroRNA (miRNA) Biogenesis R-HSA-203927

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=2$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

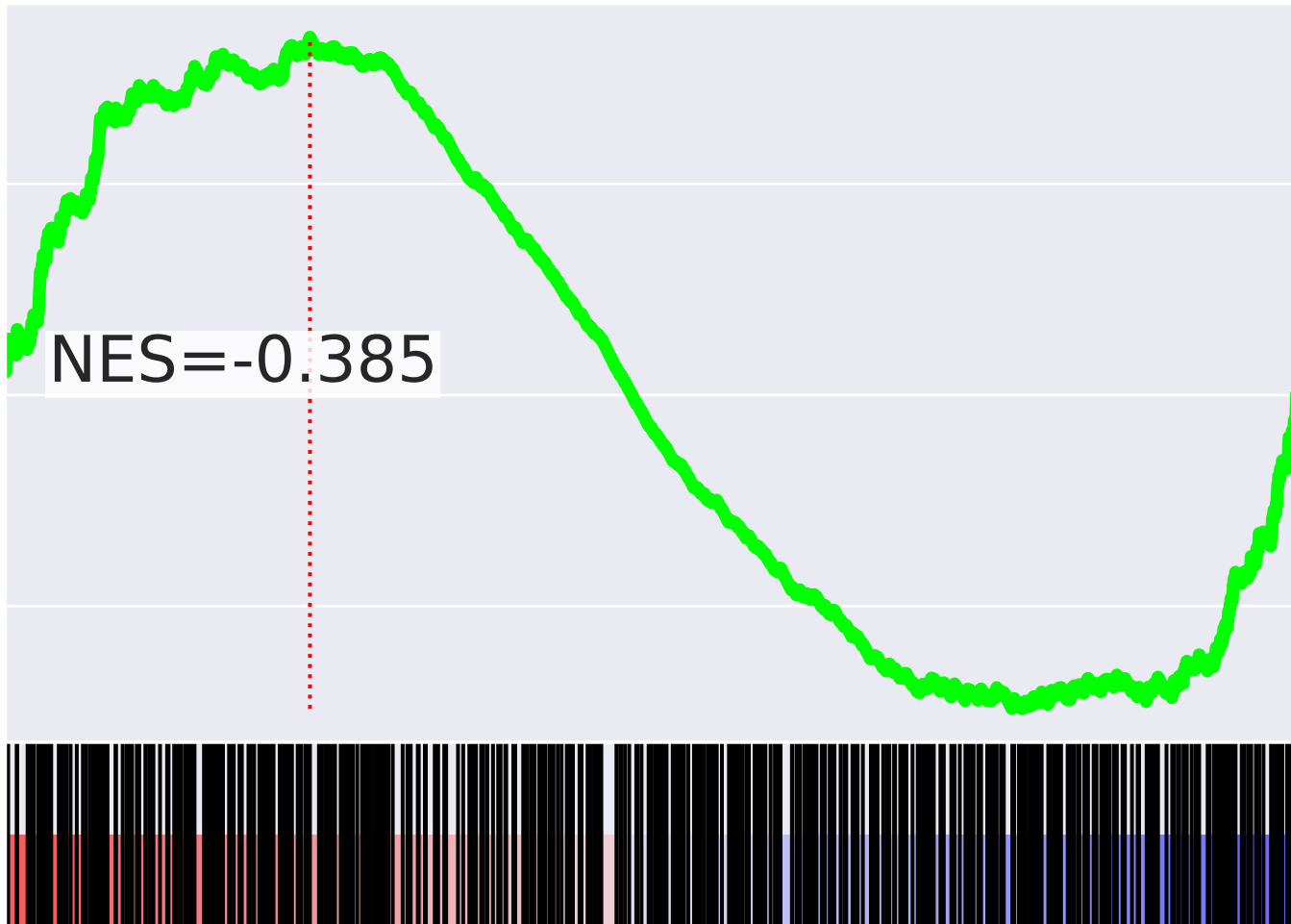
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0.0

-0.1

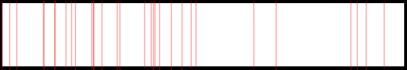
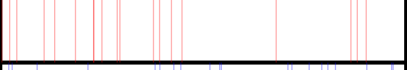
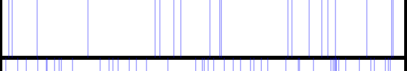
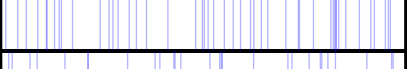

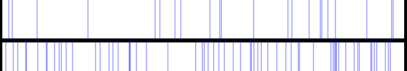
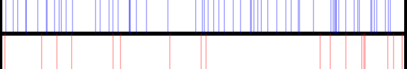

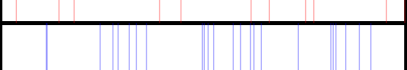
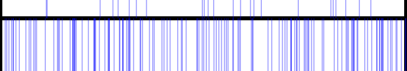

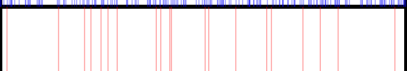



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Rank



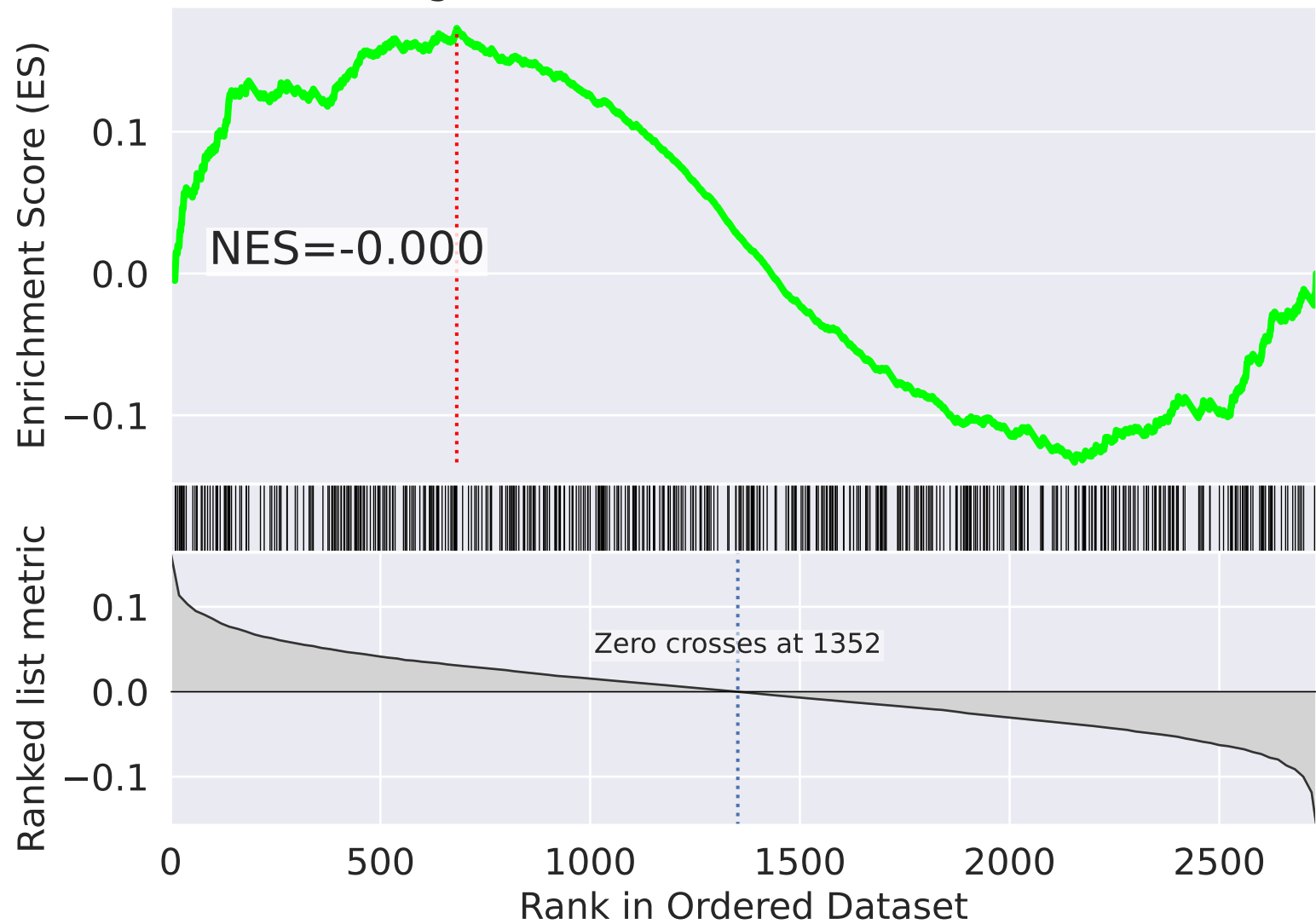
NES

SET

3.909		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.721		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
-3.703		FCGR3A-mediated Phagocytosis R-HSA-9664422
-3.388		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
-3.354		Fcgamma Receptor (FCGR) Dependent Phagocytosis R-HSA-2029480
-3.323		Regulation Of Actin Dynamics For Phagocytic Cup Formation R-HSA-2029482
-3.290		Nucleotide Excision Repair R-HSA-5696398
3.280		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
3.033		Nucleotide Biosynthesis R-HSA-8956320
-3.024		DNA Damage Recognition In GG-NER R-HSA-5696394
-2.879		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-2.856		Signaling By Rho GTPases R-HSA-194315
2.854		Biological Oxidations R-HSA-211859
2.791		Vitamin B5 (Pantothenate) Metabolism R-HSA-199220
-2.773		DNA Damage Bypass R-HSA-73893

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=3$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

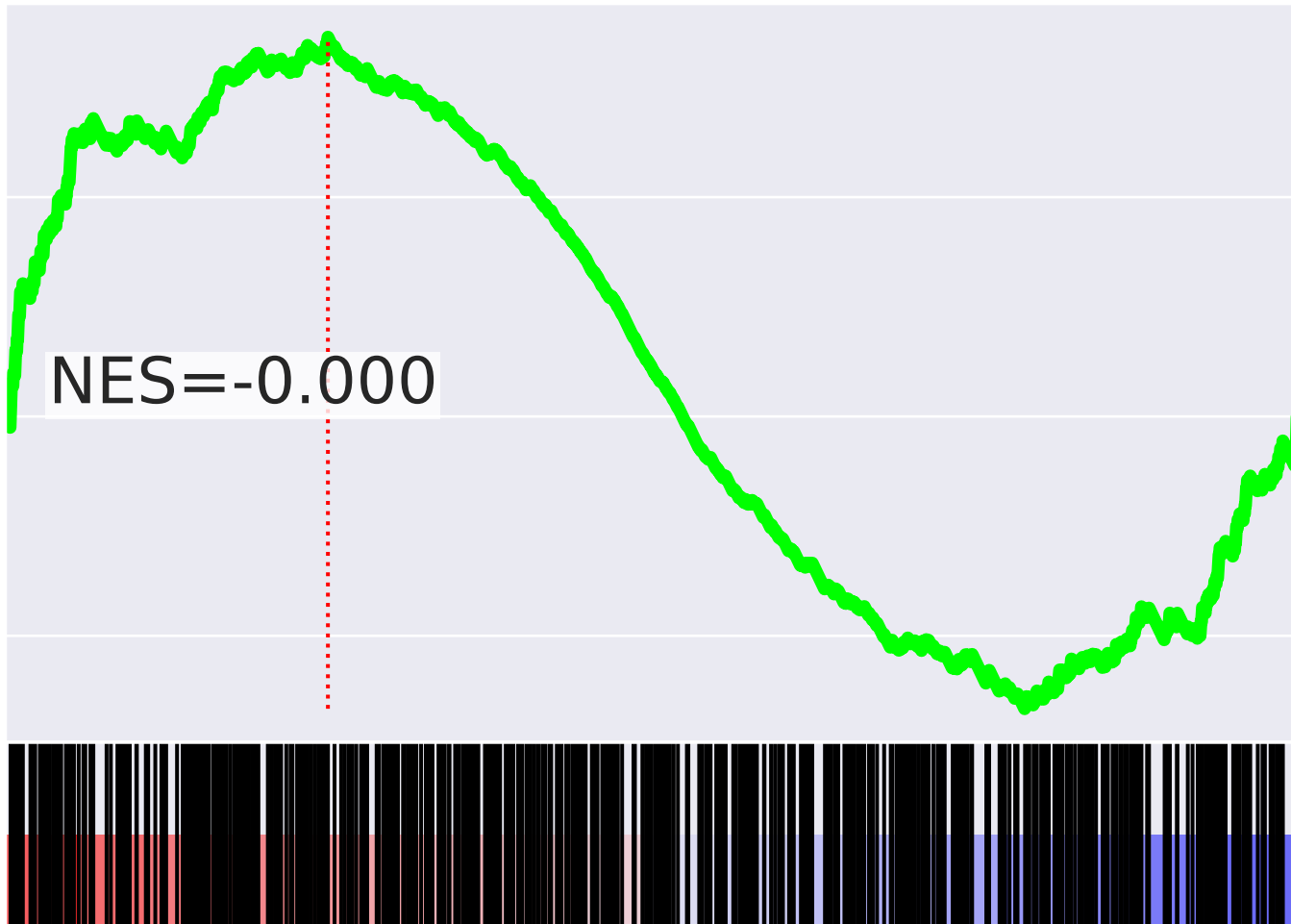
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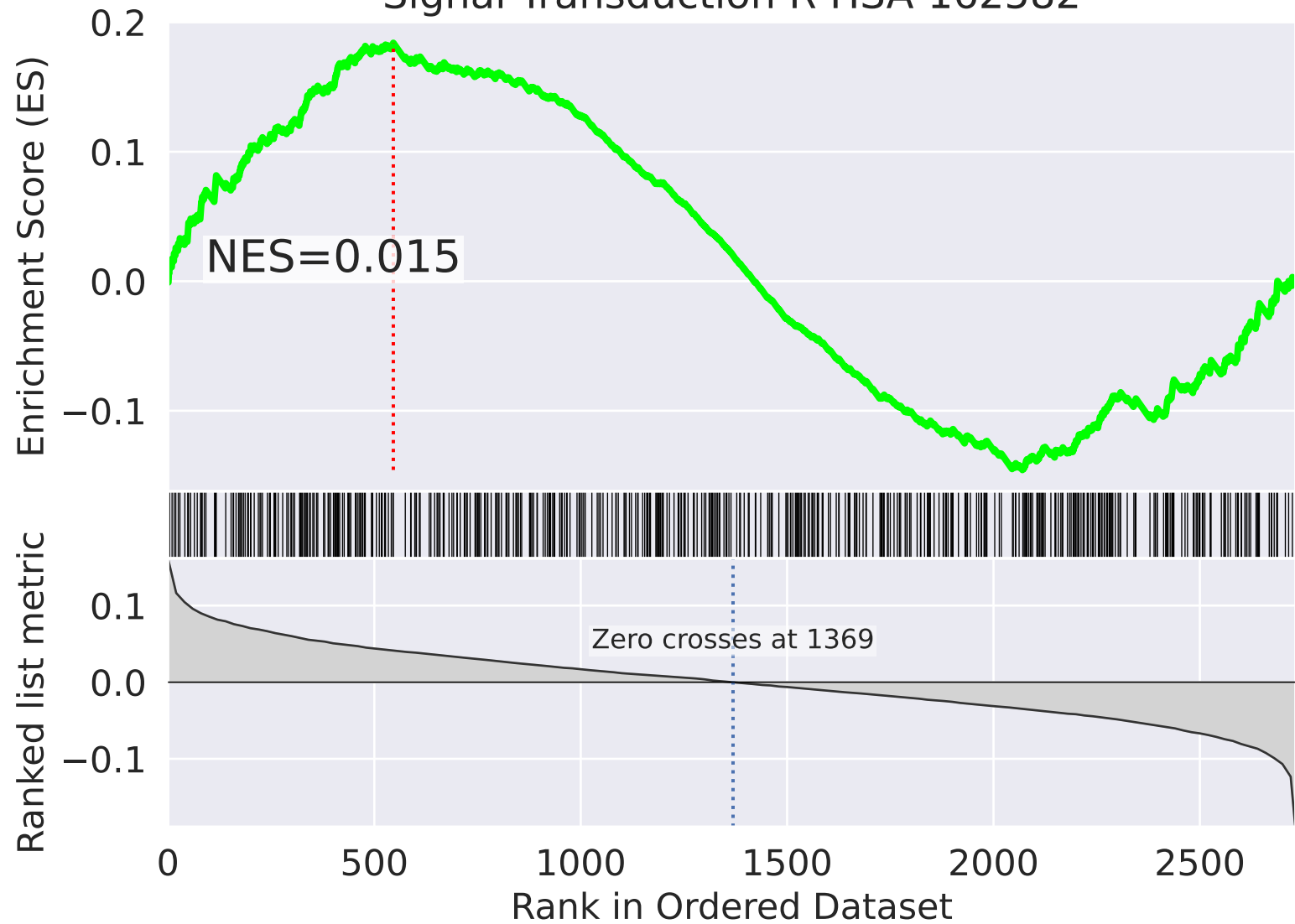
Rank



NES	SET
3.729	Homology Directed Repair R-HSA-5693538
3.594	HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
3.327	Diseases Of Mitotic Cell Cycle R-HSA-9675126
3.327	Aberrant Regulation Of Mitotic Cell Cycle Due To RB1 Defects R-HSA-9687139
3.217	DNA Double-Strand Break Repair R-HSA-5693532
3.200	Processing Of DNA Double-Strand Break Ends R-HSA-5693607
3.153	DNA Replication R-HSA-69306
3.124	Regulation Of TP53 Activity R-HSA-5633007
3.013	S Phase R-HSA-69242
3.009	Unfolded Protein Response (UPR) R-HSA-381119
2.934	DNA Repair R-HSA-73894
-2.919	Formation Of Early Elongation Complex R-HSA-113418
2.904	Activation Of ATR In Response To Replication Stress R-HSA-176187
2.901	Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
2.893	Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756

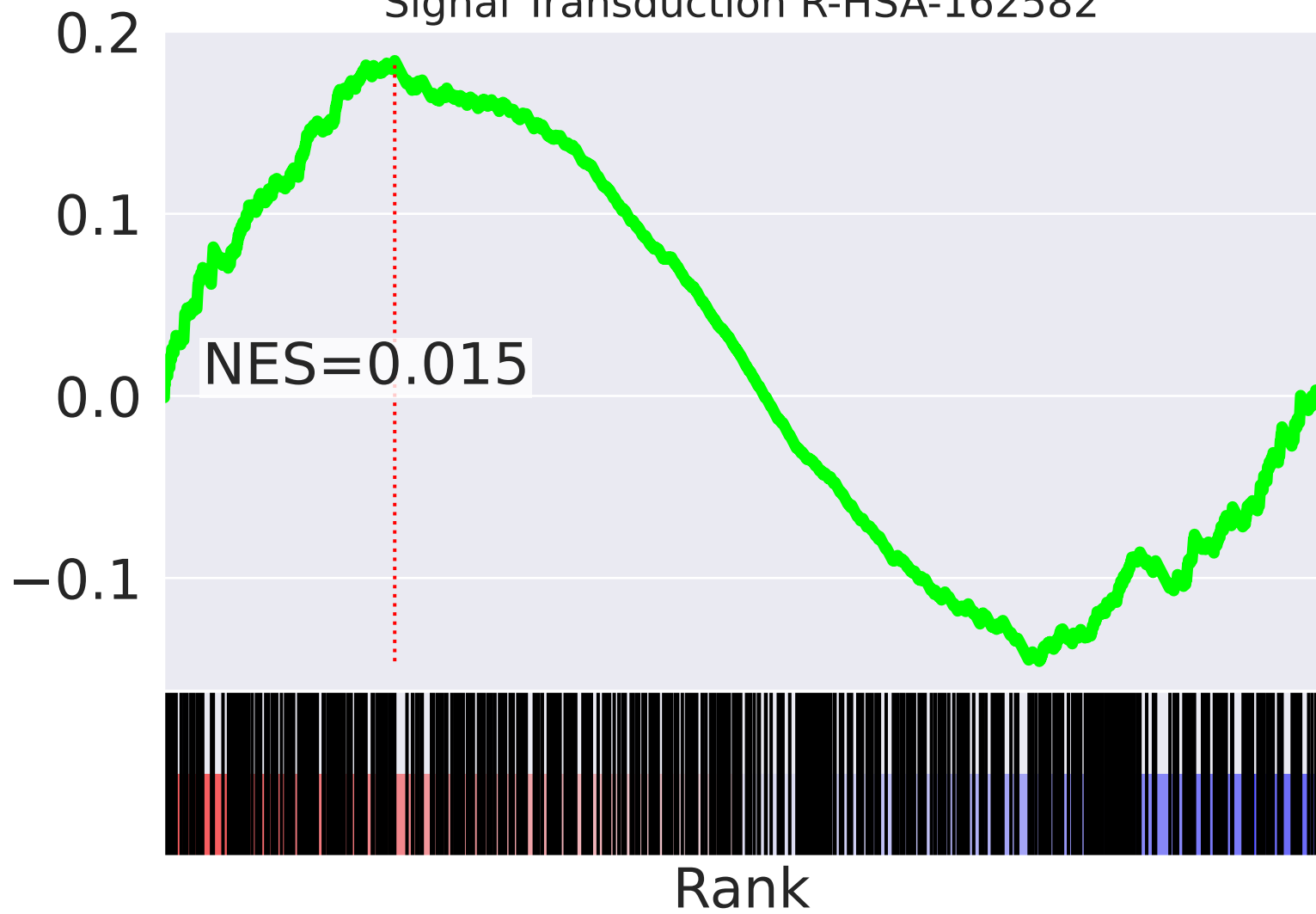
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=4$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

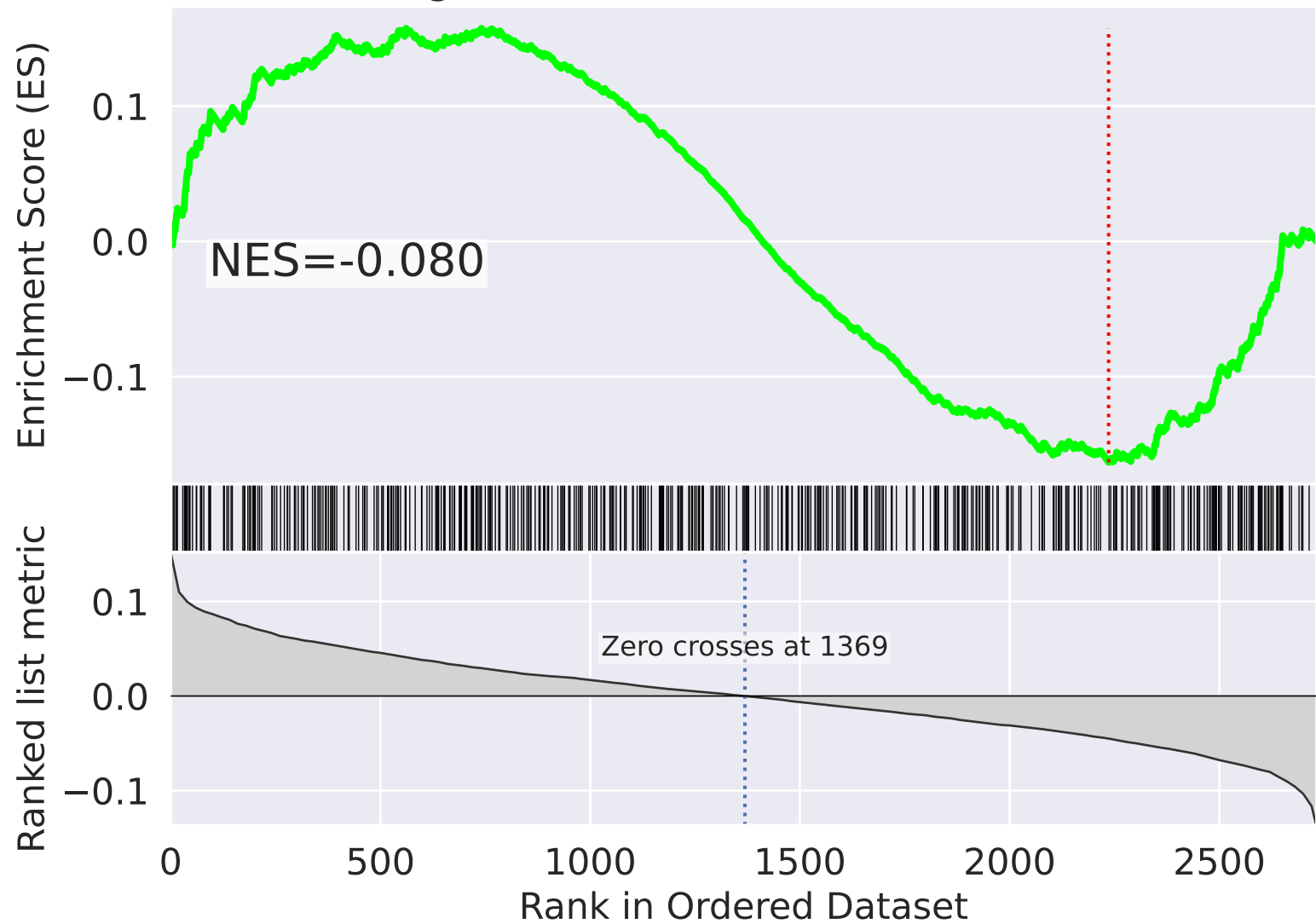
ES



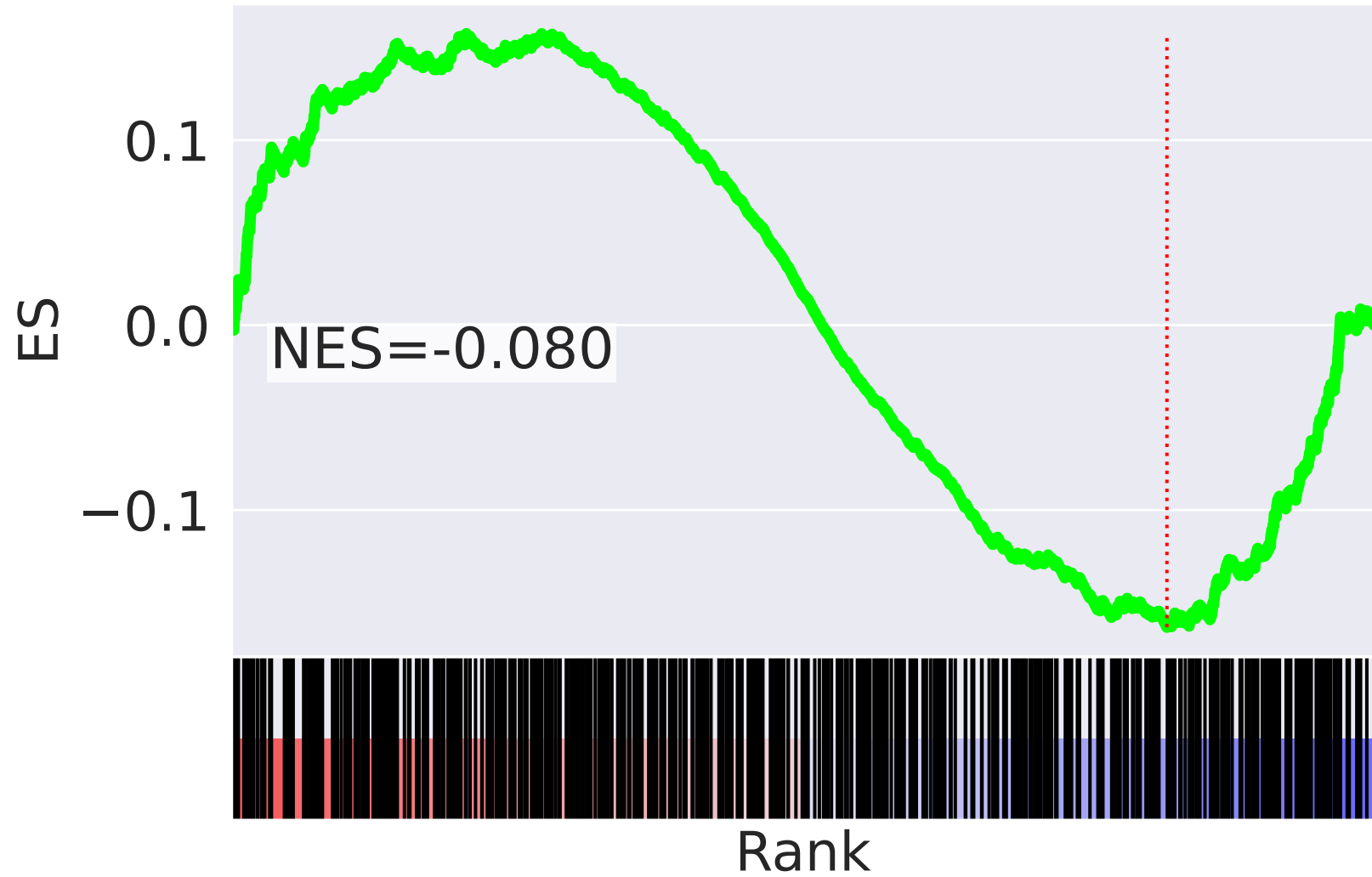
NES		SET
4.327		Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
-4.187		RNA Polymerase III Transcription Initiation R-HSA-76046
4.172		Cytokine Signaling In Immune System R-HSA-1280215
4.158		Cellular Response To Hypoxia R-HSA-1234174
4.118		Vif-mediated Degradation Of APOBEC3G R-HSA-180585
-4.064		RNA Polymerase III Abortive And Retractive Initiation R-HSA-749476
4.041		Oxygen-dependent Proline Hydroxylation Of Hypoxia-inducible Factor Alpha R-HSA-1234176
3.939		Signaling By NOTCH4 R-HSA-9013694
-3.871		Extension Of Telomeres R-HSA-180786
3.840		TNFR2 Non-Canonical NF-kB Pathway R-HSA-5668541
3.832		SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
3.819		Deubiquitination R-HSA-5688426
3.811		Interleukin-1 Family Signaling R-HSA-446652
3.808		Downstream Signaling Events Of B Cell Receptor (BCR) R-HSA-1168372
3.804		Regulation Of mRNA Stability By Proteins That Bind AU-rich Elements R-HSA-450531


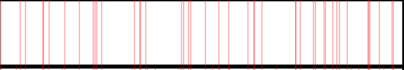
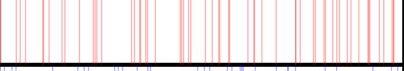
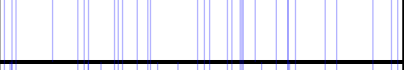
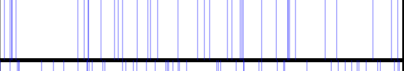
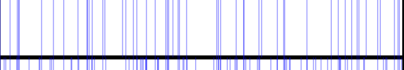
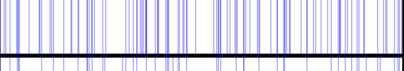
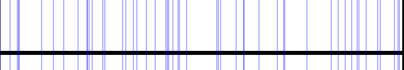
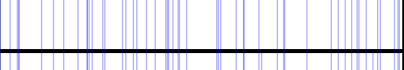
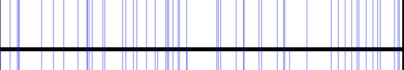
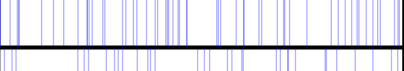
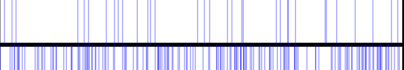
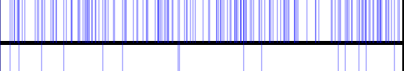

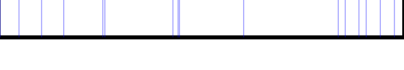
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=5$

Signal Transduction R-HSA-162582



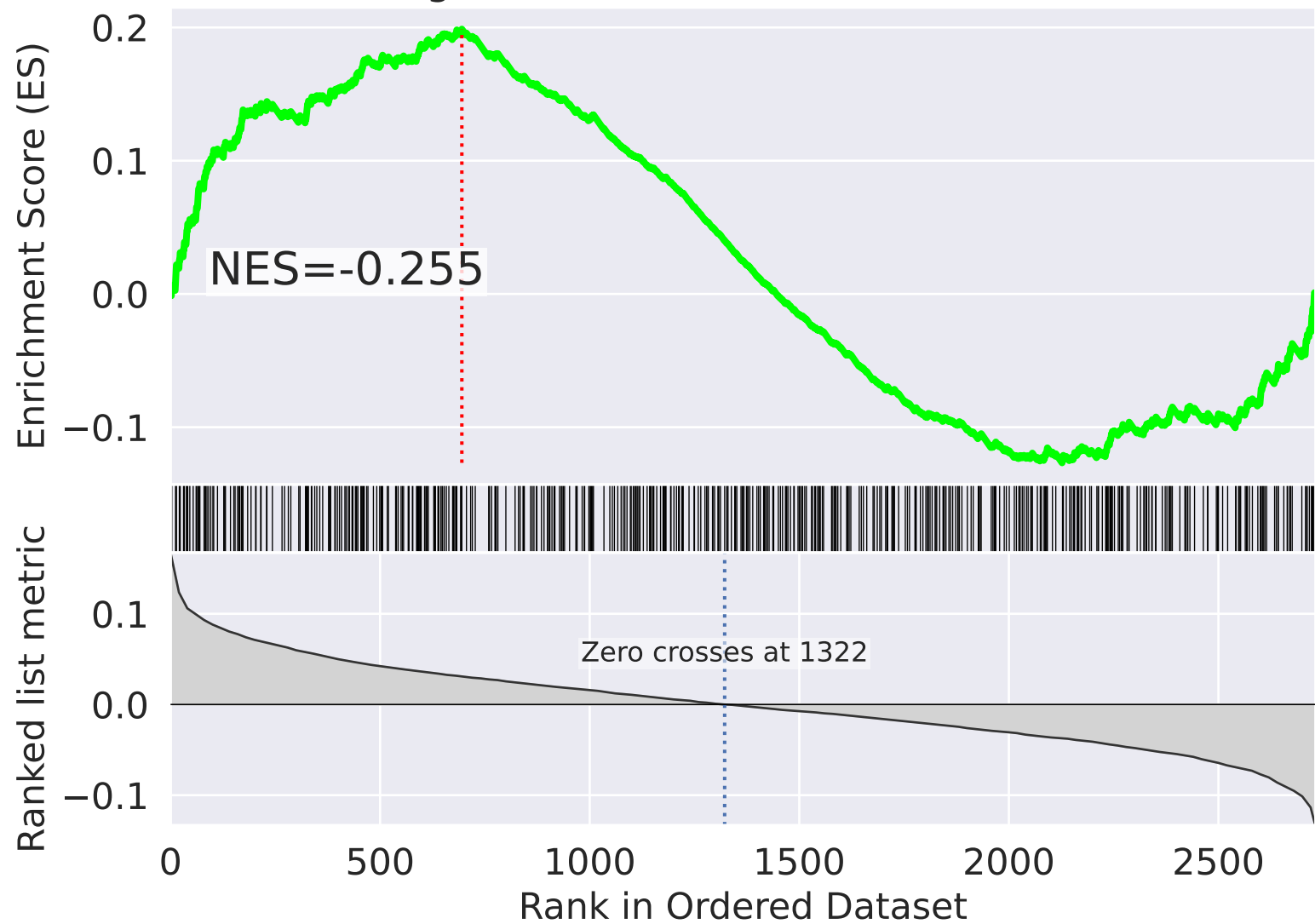
Signal Transduction R-HSA-162582



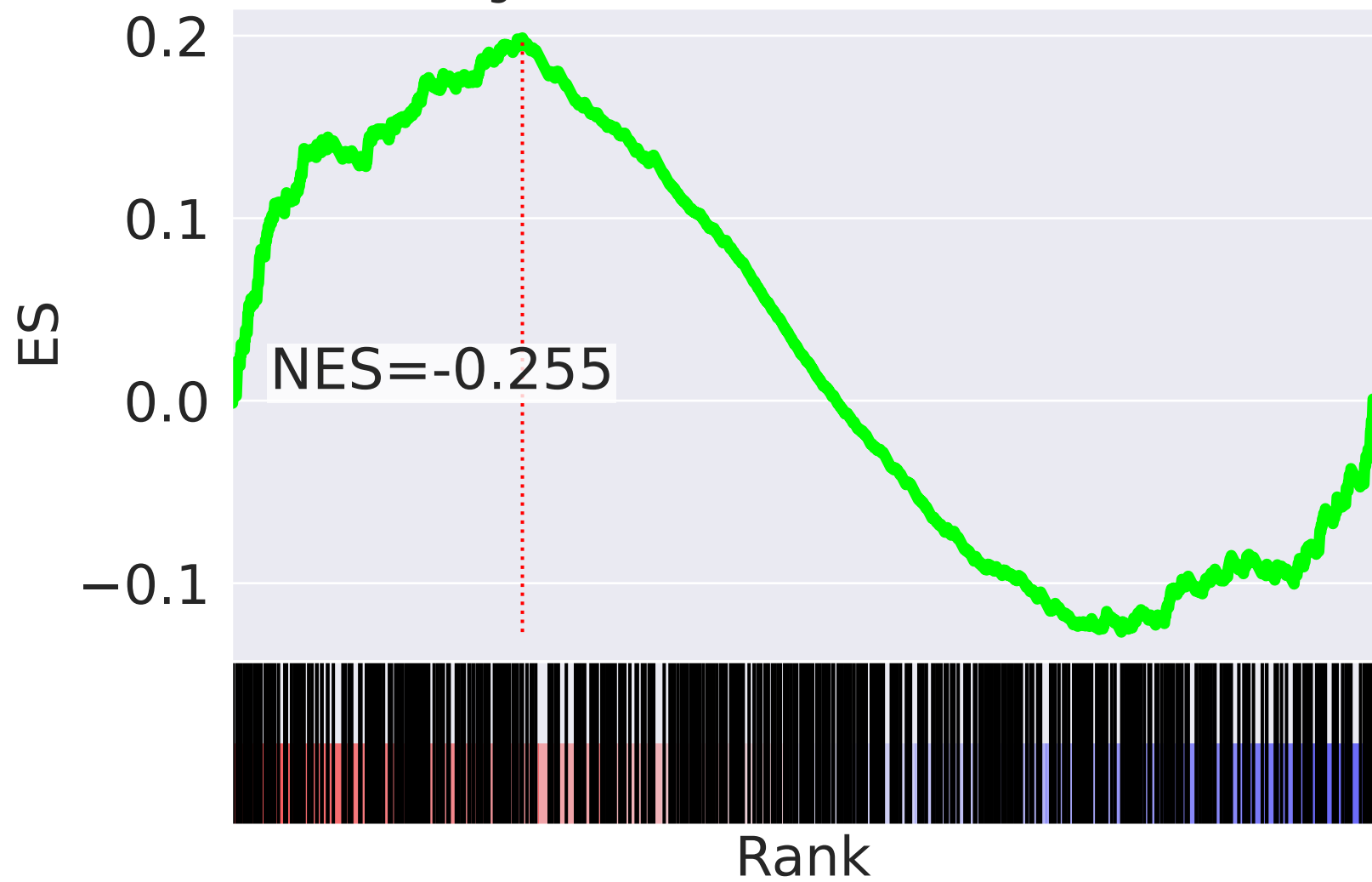
NES		SET
-3.997		Adaptive Immune System R-HSA-1280218
3.753		Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.544		RNA Polymerase II Pre-transcription Events R-HSA-674695
-3.307		AURKA Activation By TPX2 R-HSA-8854518
-3.289		Regulation Of PLK1 Activity At G2/M Transition R-HSA-2565942
-3.256		APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176409
-3.191		S Phase R-HSA-69242
-3.166		Cdc20:Phospho-APC/C Mediated Degradation Of Cyclin A R-HSA-174184
-3.166		APC:Cdc20 Mediated Degradation Of Cell Cycle Proteins Before Cycle Checkpoint Satisfied R-HSA-179419
-3.124		Activation Of APC/C And APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176814
-3.118		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
-3.098		Centrosome Maturation R-HSA-380287
-3.083		Cell Cycle Checkpoints R-HSA-69620
-3.078		APC/C:Cdc20 Mediated Degradation Of Cyclin B R-HSA-174048
-3.038		Inactivation Of APC/C Via Direct Inhibition Of APC/C Complex R-HSA-141430

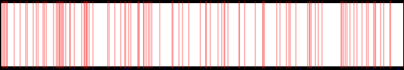



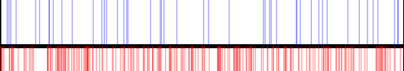


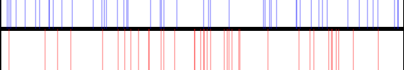
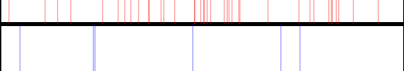
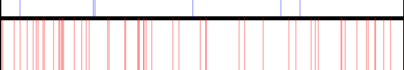
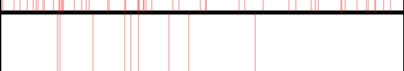
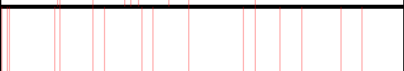

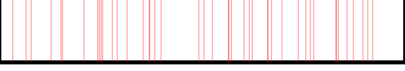

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=6$

Signal Transduction R-HSA-162582



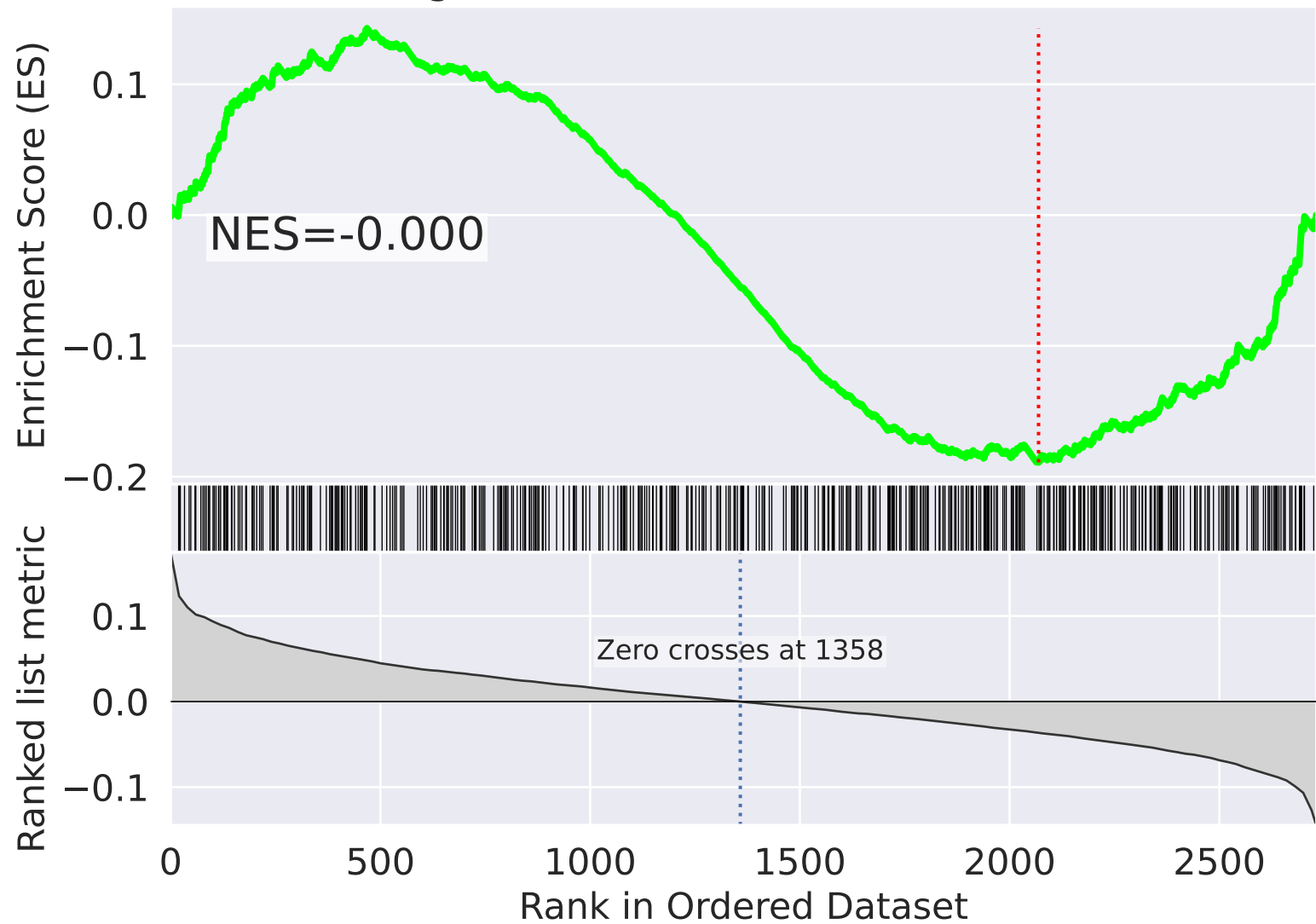
Signal Transduction R-HSA-162582



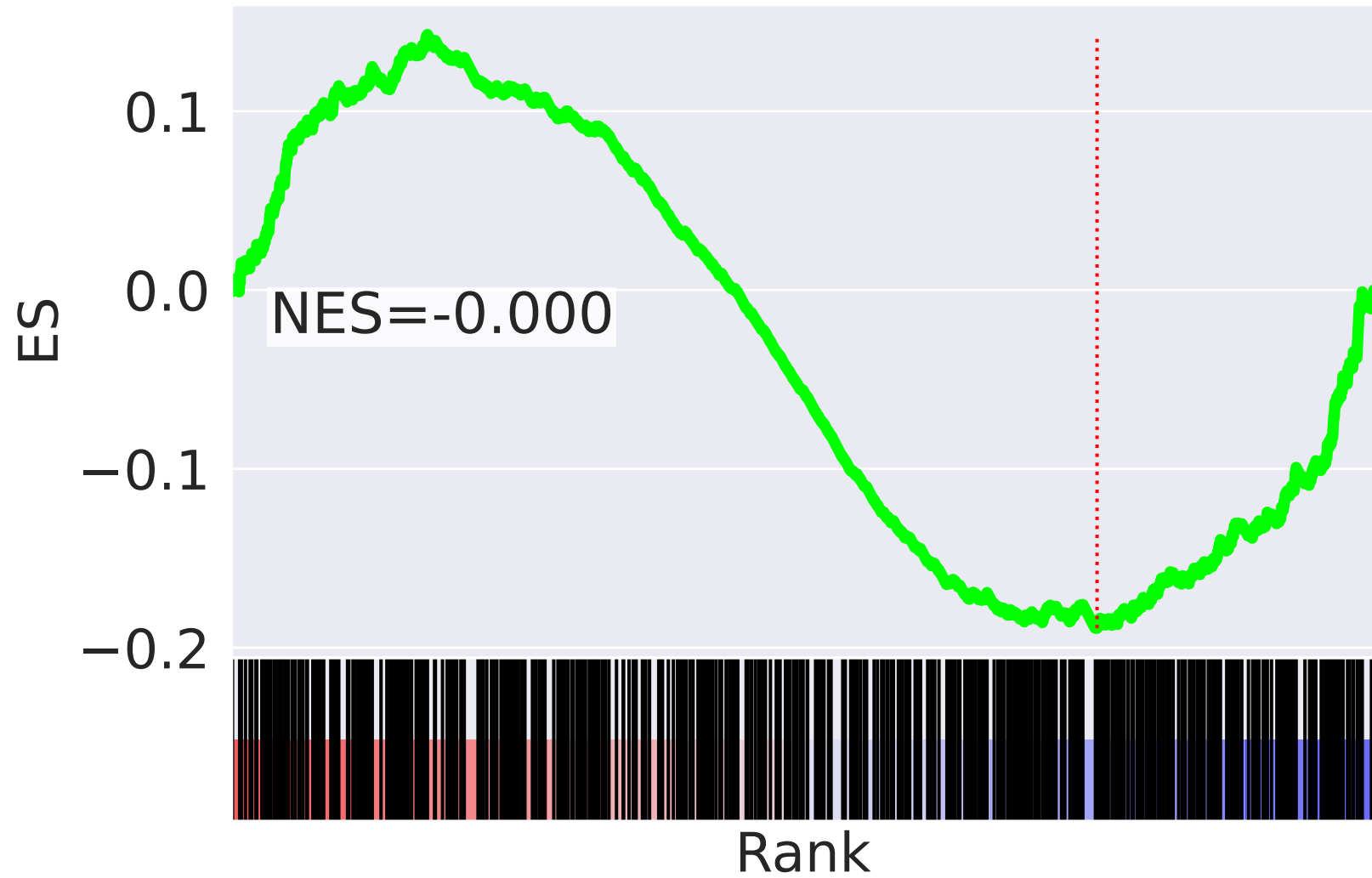
NES		SET
4.795		Chromatin Modifying Enzymes R-HSA-3247509
-3.977		COPII-mediated Vesicle Transport R-HSA-204005
-3.484		Rab Regulation Of Trafficking R-HSA-9007101
-3.440		RAB GEFs Exchange GTP For GDP On RABs R-HSA-8876198
-3.205		ER To Golgi Anterograde Transport R-HSA-199977
3.161		Developmental Biology R-HSA-1266738
-3.133		Cytosolic tRNA Aminoacylation R-HSA-379716
-2.991		Transport To Golgi And Subsequent Modification R-HSA-948021
2.957		Transcriptional Regulation By Small RNAs R-HSA-5578749
-2.954		E2F-enabled Inhibition Of Pre-Replication Complex Formation R-HSA-113507
2.916		HATs Acetylate Histones R-HSA-3214847
2.906		PRC2 Methylates Histones And DNA R-HSA-212300
2.851		Transcriptional Regulation By E2F6 R-HSA-8953750
2.843		PKMTs Methylate Histone Lysines R-HSA-3214841
2.840		Formation Of RNA Pol II Elongation Complex R-HSA-112382

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=7$

Signal Transduction R-HSA-162582



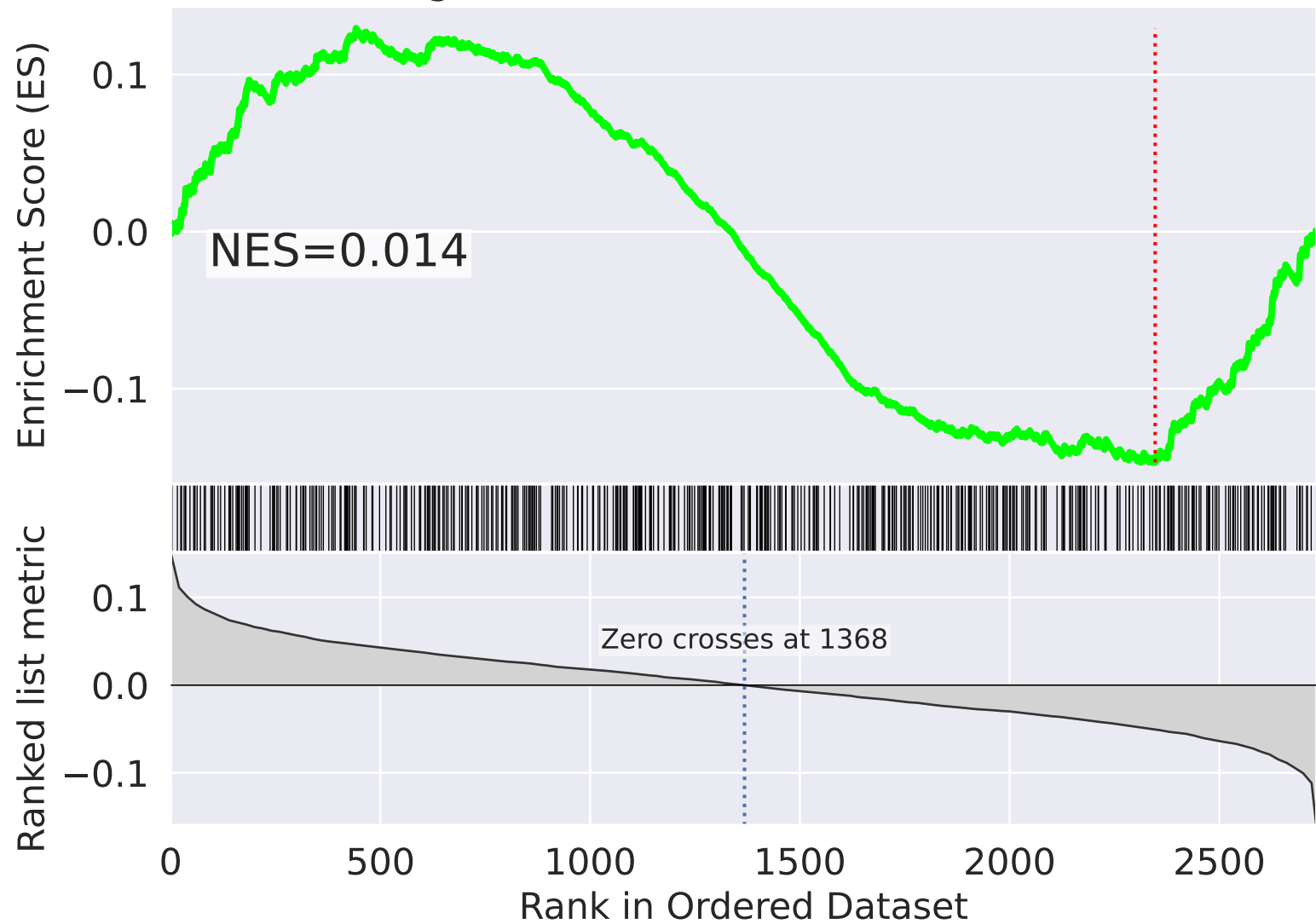
Signal Transduction R-HSA-162582



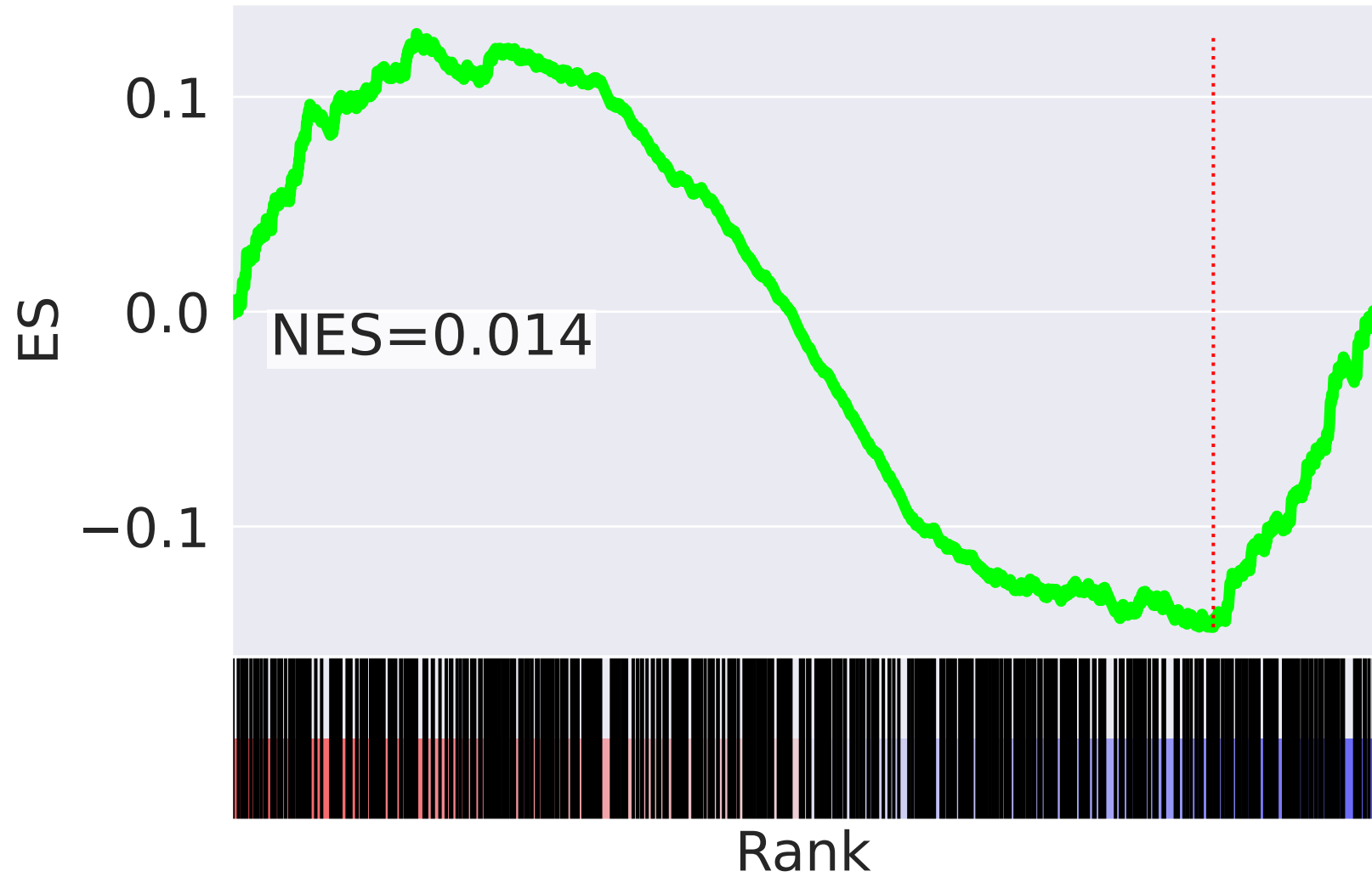
NES		SET
4.553		Transcriptional Regulation By RUNX1 R-HSA-8878171
-4.164		rRNA Processing R-HSA-72312
-4.069		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.010		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.929		RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
-3.483		Transport To Golgi And Subsequent Modification R-HSA-948021
-3.396		Asparagine N-linked Glycosylation R-HSA-446203
-3.374		ER To Golgi Anterograde Transport R-HSA-199977
3.286		Beta-catenin Independent WNT Signaling R-HSA-3858494
3.257		PCP/CE Pathway R-HSA-4086400
-3.212		Unfolded Protein Response (UPR) R-HSA-381119
3.164		HIV Infection R-HSA-162906
3.136		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.097		Signaling By WNT R-HSA-195721
3.075		Cellular Response To Chemical Stress R-HSA-9711123

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=8$

Signal Transduction R-HSA-162582



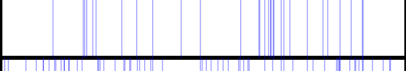
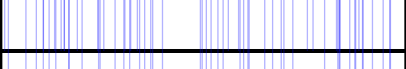
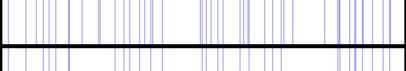
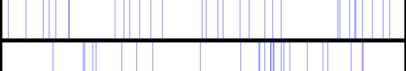

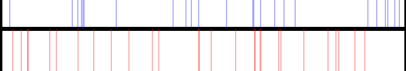
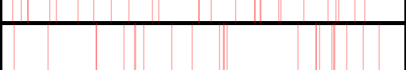
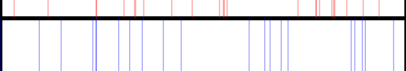

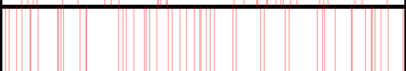





Signal Transduction R-HSA-162582



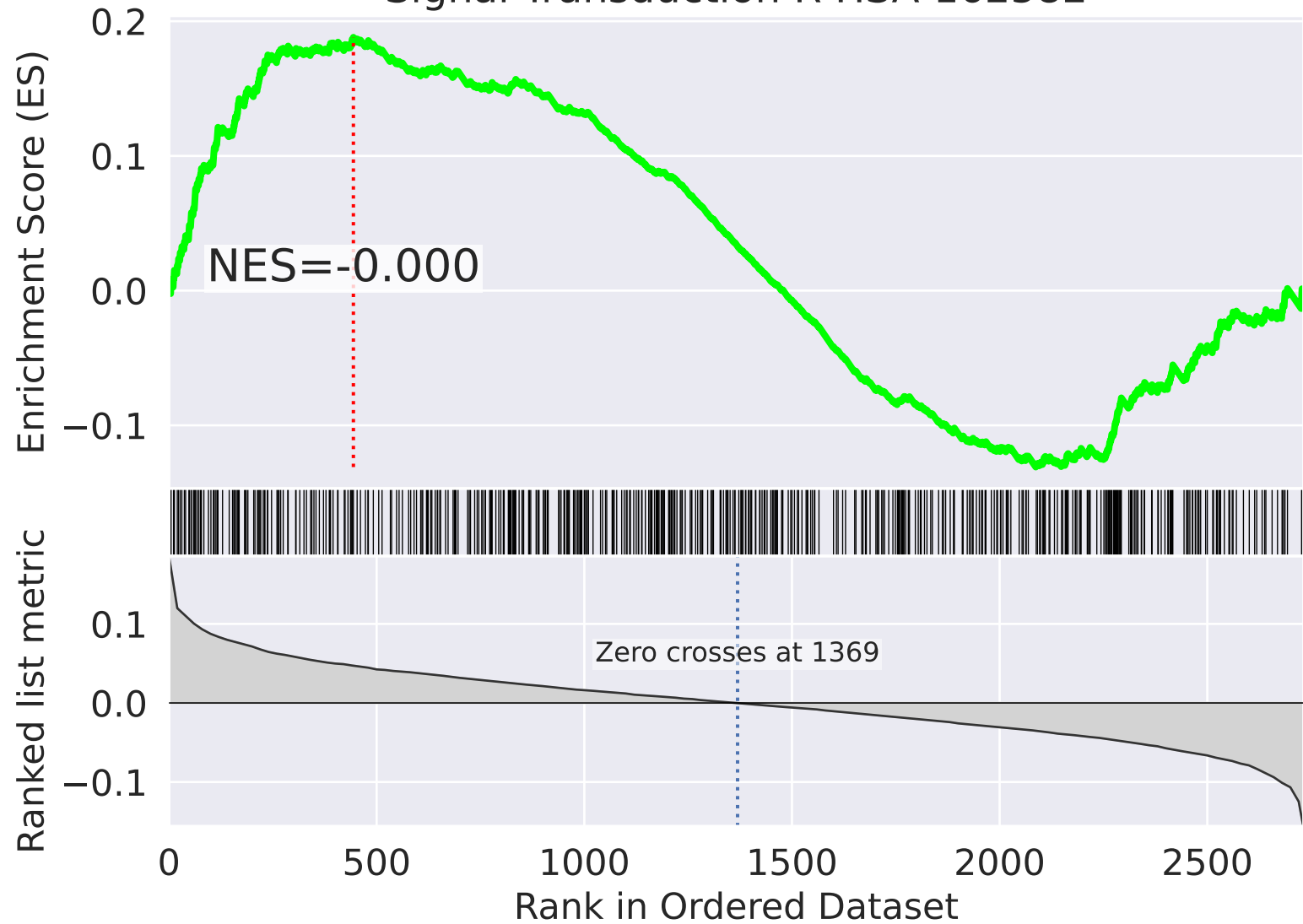
NES

SET

-4.489		Vesicle-mediated Transport R-HSA-5653656
-4.375		Membrane Trafficking R-HSA-199991
-3.527		Rab Regulation Of Trafficking R-HSA-9007101
-3.427		Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
-3.407		Golgi-to-ER Retrograde Transport R-HSA-8856688
-3.335		COPI-dependent Golgi-to-ER Retrograde Traffic R-HSA-6811434
-3.237		RAB GEFs Exchange GTP For GDP On RABs R-HSA-8876198
-2.998		Iron Uptake And Transport R-HSA-917937
2.920		Regulation Of PTEN Gene Transcription R-HSA-8943724
2.880		Metabolism Of Nucleotides R-HSA-15869
-2.863		COPII-mediated Vesicle Transport R-HSA-204005
2.632		Activation Of HOX Genes During Differentiation R-HSA-5619507
2.620		Protein Localization R-HSA-9609507
-2.617		Retrograde Transport At Trans-Golgi-Network R-HSA-6811440
2.594		Peptide Hormone Metabolism R-HSA-2980736

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=9$

Signal Transduction R-HSA-162582



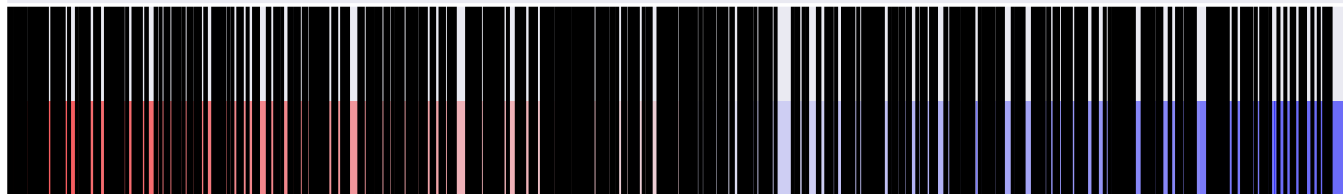
Signal Transduction R-HSA-162582

ES

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0.0
-0.1


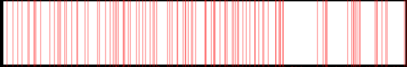
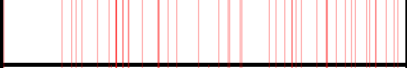
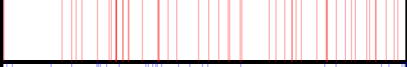
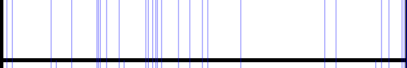
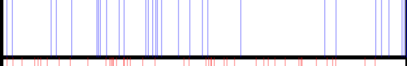
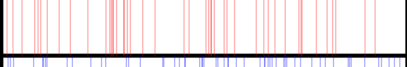
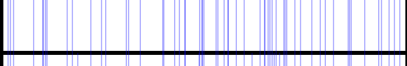
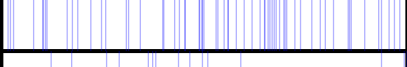
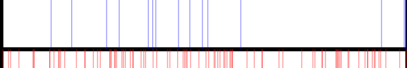
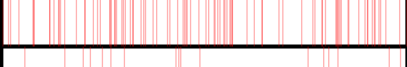


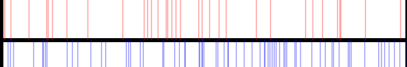
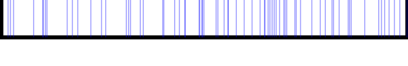
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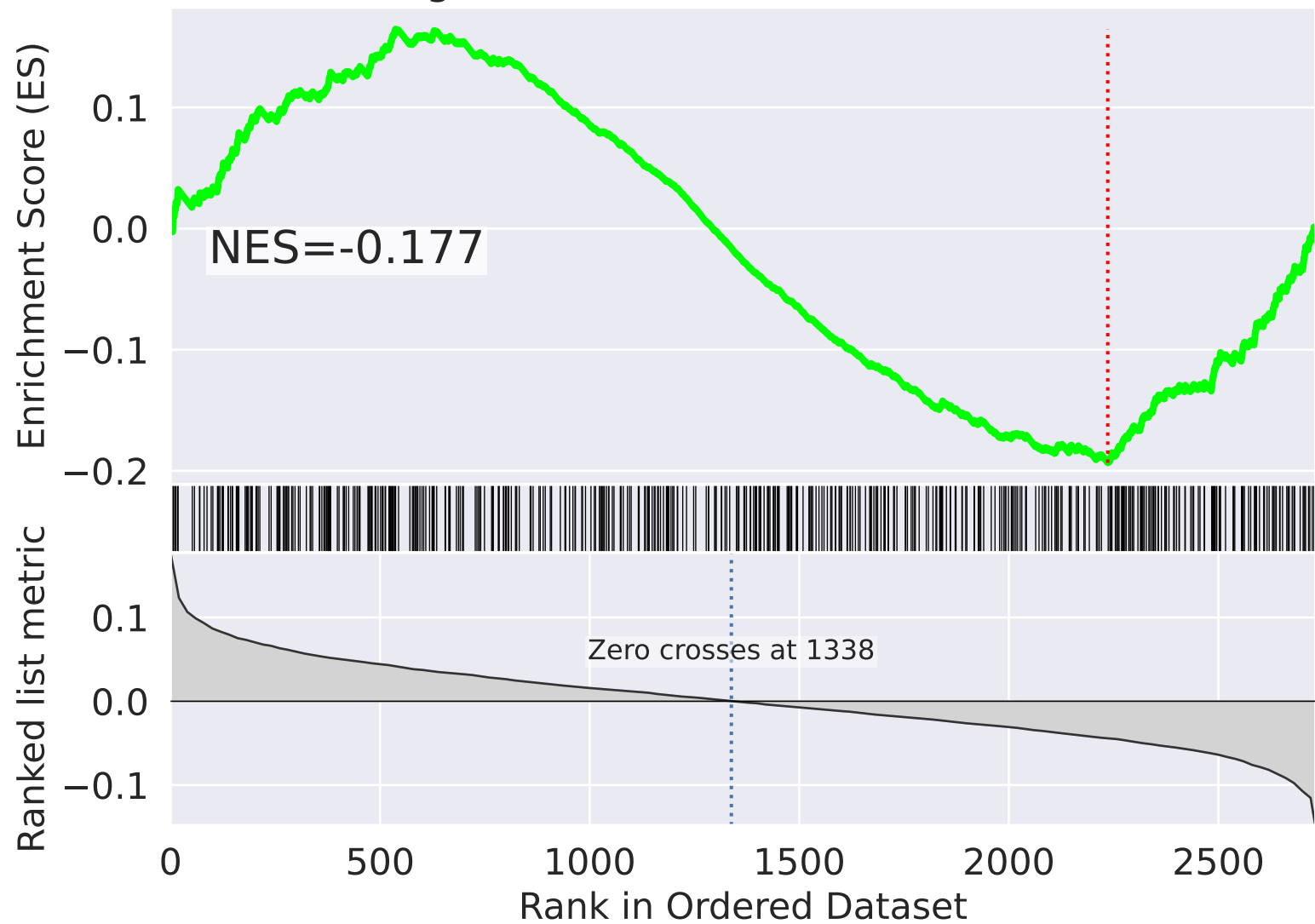
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SET

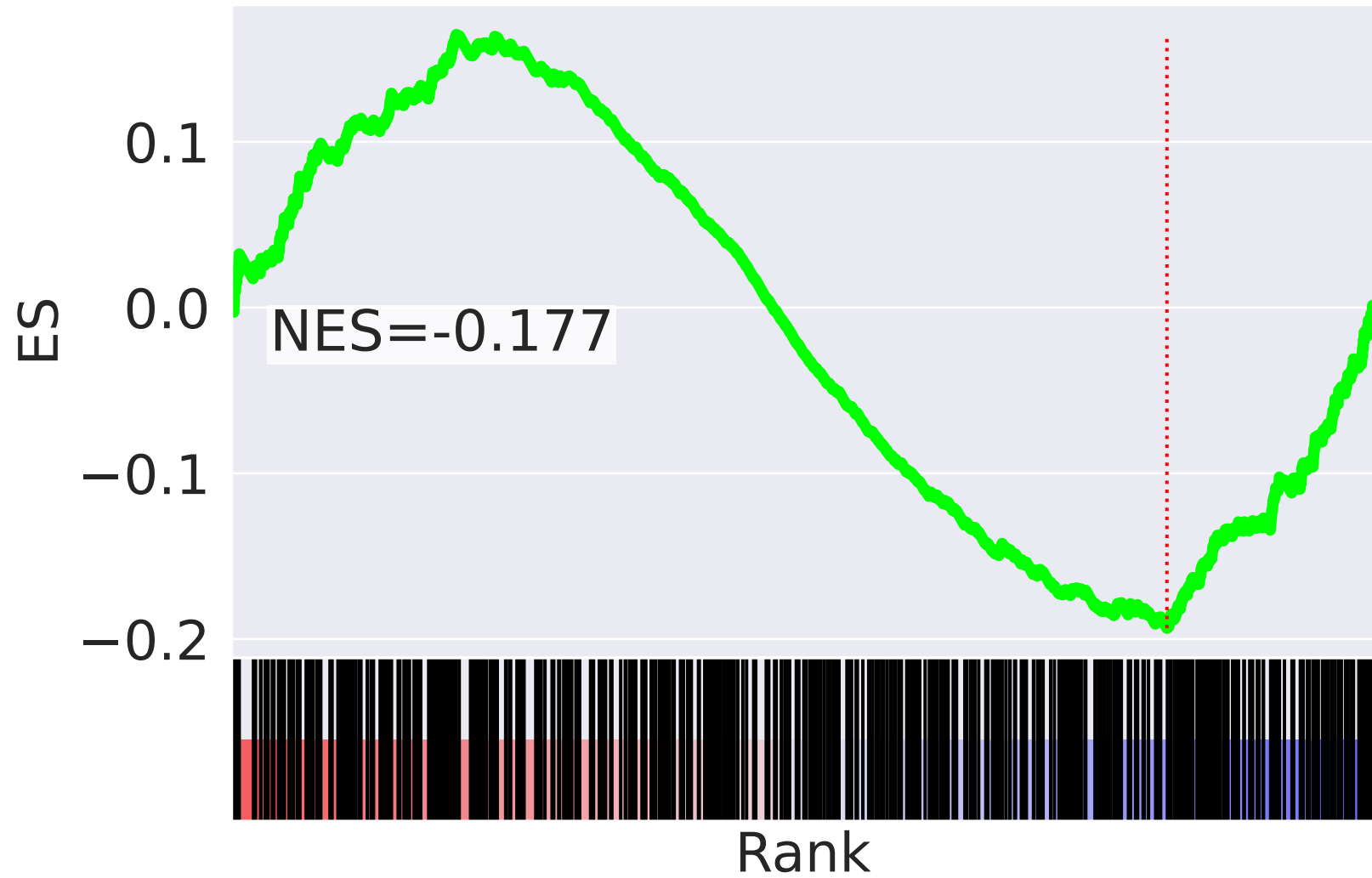
4.739		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
4.242		Chromatin Modifying Enzymes R-HSA-3247509
4.161		PPARA Activates Gene Expression R-HSA-1989781
3.959		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
-3.673		Chaperonin-mediated Protein Folding R-HSA-390466
-3.637		Protein Folding R-HSA-391251
3.628		Epigenetic Regulation Of Gene Expression R-HSA-212165
-3.528		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.212		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.156		Association Of TriC/CCT With Target Proteins During Biosynthesis R-HSA-390471
3.089		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.061		Translocation Of SLC2A4 (GLUT4) To Plasma Membrane R-HSA-1445148
3.018		CD28 Dependent PI3K/Akt Signaling R-HSA-389357
2.996		PI3K/AKT Signaling In Cancer R-HSA-2219528
-2.931		rRNA Processing R-HSA-72312


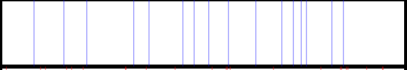
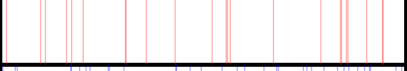
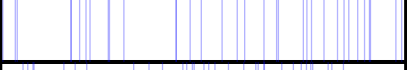
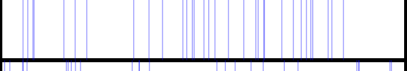
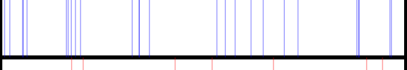
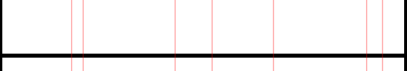
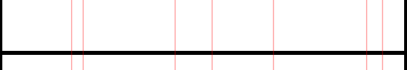
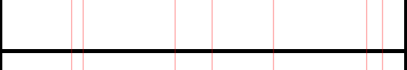
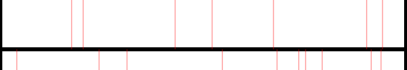

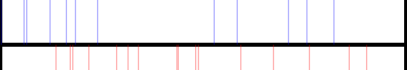
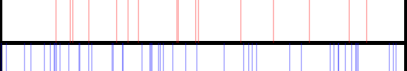
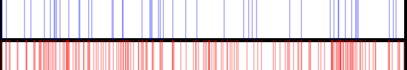
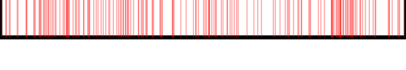
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=10$

Signal Transduction R-HSA-162582



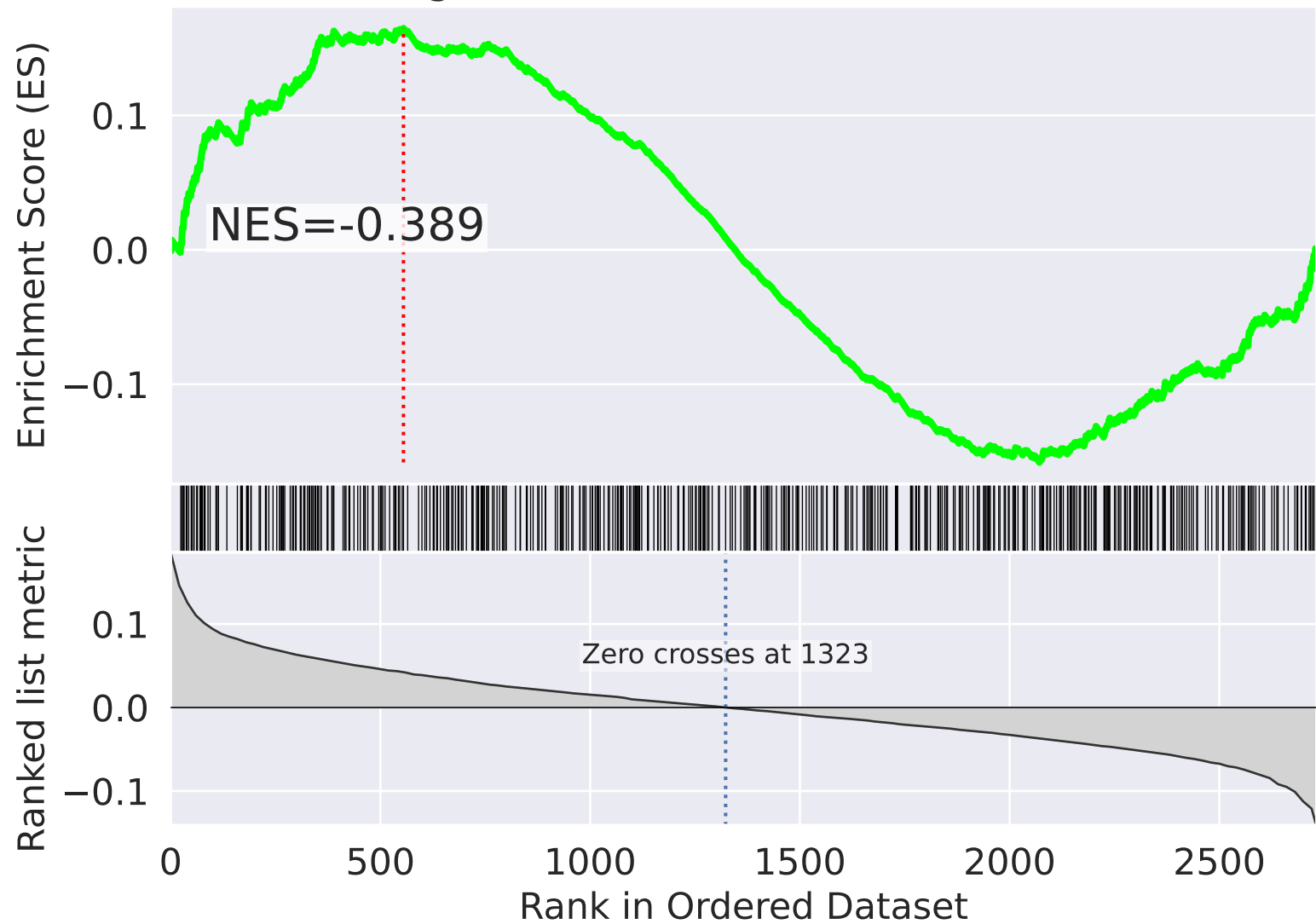
Signal Transduction R-HSA-162582



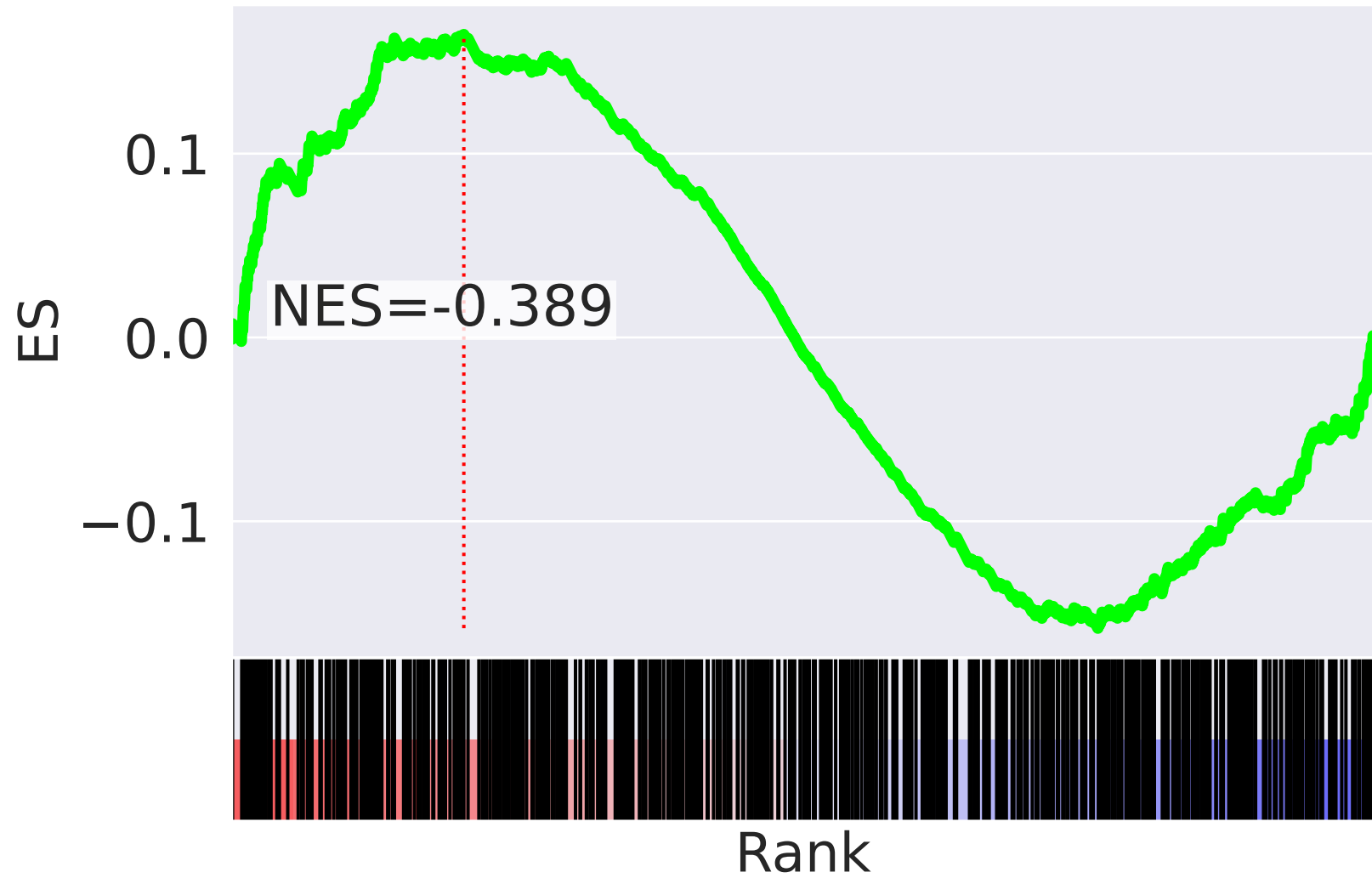
NES		SET
3.476		DNA Repair R-HSA-73894
-3.371		Cytosolic tRNA Aminoacylation R-HSA-379716
3.179		DNA Damage/Telomere Stress Induced Senescence R-HSA-2559586
-3.143		RAC1 GTPase Cycle R-HSA-9013149
-2.993		tRNA Aminoacylation R-HSA-379724
-2.813		RAB GEFs Exchange GTP For GDP On RABs R-HSA-8876198
2.771		Cleavage Of Damaged Purine R-HSA-110331
2.771		Cleavage Of Damaged Pyrimidine R-HSA-110329
2.771		Packaging Of Telomere Ends R-HSA-171306
2.771		Base-Excision Repair, AP Site Formation R-HSA-73929
2.755		Fatty acyl-CoA Biosynthesis R-HSA-75105
-2.745		VEGFR2 Mediated Vascular Permeability R-HSA-5218920
2.684		HDACs Deacetylate Histones R-HSA-3214815
-2.669		Cellular Response To Heat Stress R-HSA-3371556
2.633		Transcriptional Regulation By TP53 R-HSA-3700989

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=11$

Signal Transduction R-HSA-162582



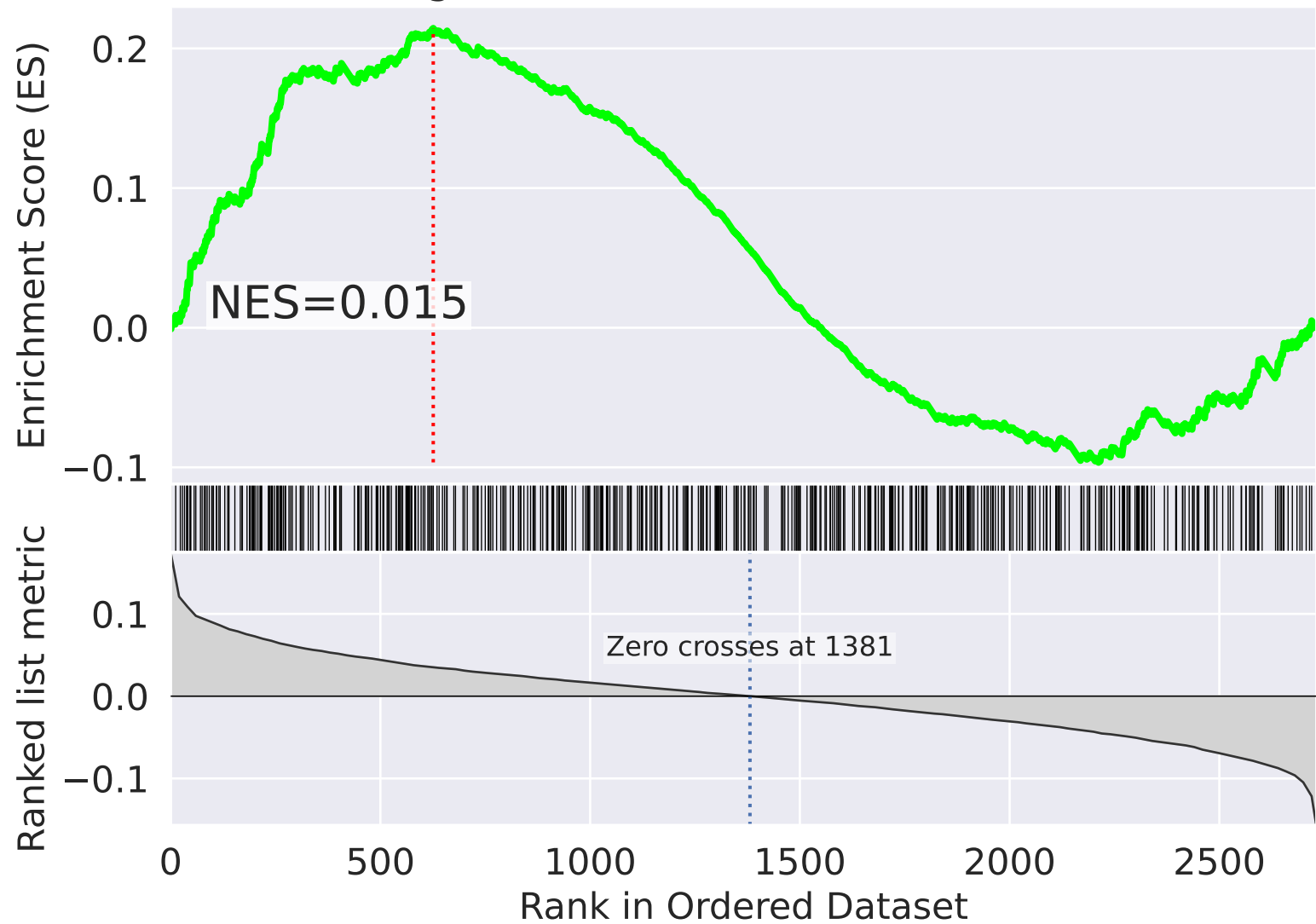
Signal Transduction R-HSA-162582



NES		SET
3.755		Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.706		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.610		Chromatin Modifying Enzymes R-HSA-3247509
2.997		Metabolism Of Porphyrins R-HSA-189445
2.997		Heme Biosynthesis R-HSA-189451
2.987		Protein Ubiquitination R-HSA-8852135
2.915		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
-2.910		Translesion Synthesis By Y Family DNA Polymerases Bypasses Lesions On DNA Template R-HSA-110313
2.902		E3 Ubiquitin Ligases Ubiquitinate Target Proteins R-HSA-8866654
-2.873		G2/M DNA Damage Checkpoint R-HSA-69473
-2.827		Lagging Strand Synthesis R-HSA-69186
-2.803		RHO GTPase Cycle R-HSA-9012999
2.775		Nucleotide-binding Domain, Leucine Rich Repeat Containing NLR Signaling Pathways R-HSA-168643
-2.729		MET Promotes Cell Motility R-HSA-8875878
-2.704		Mitochondrial Protein Import R-HSA-1268020

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=12$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.2

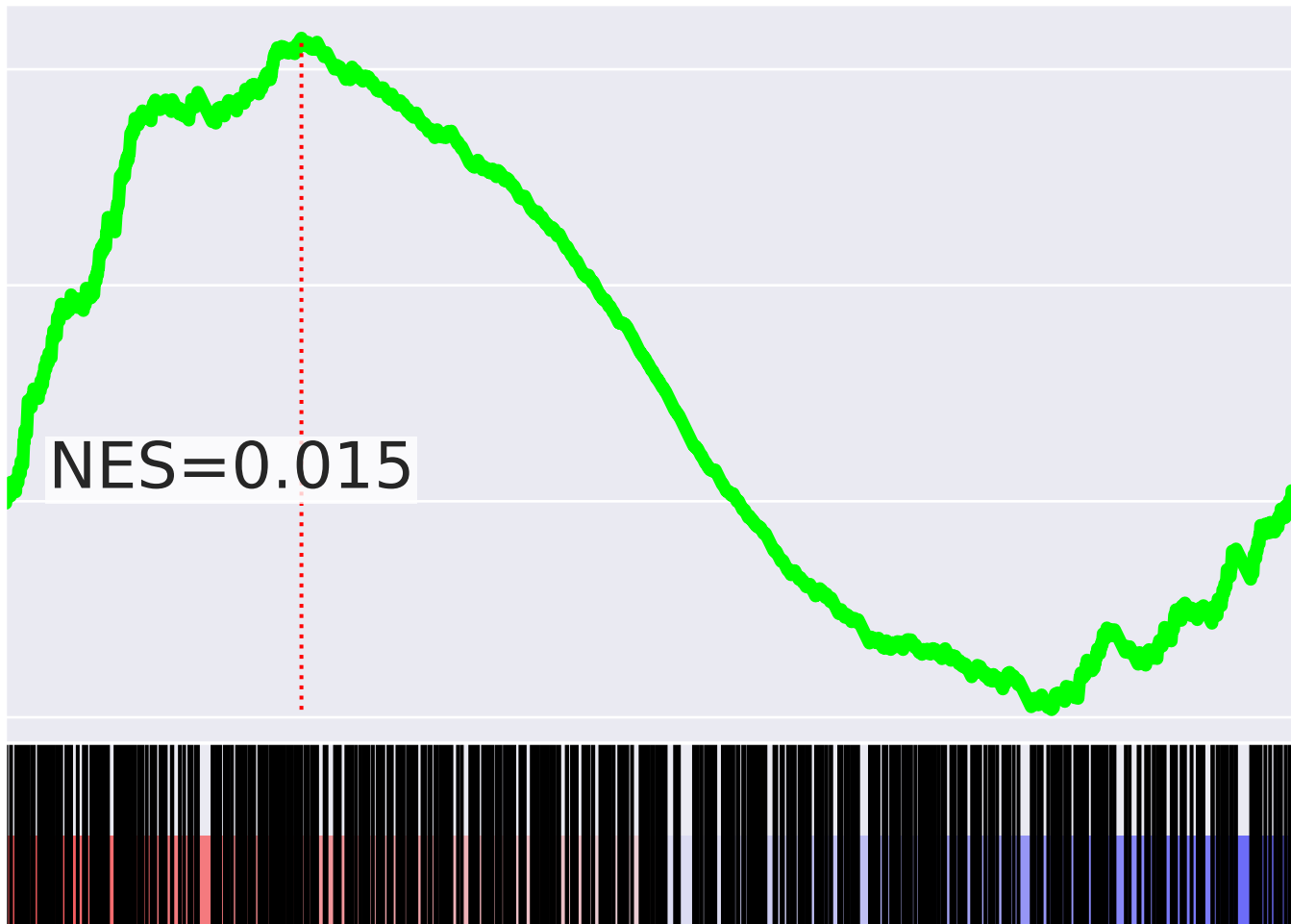
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0.0

-0.1

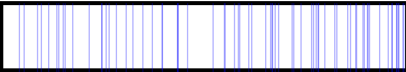
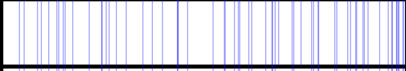
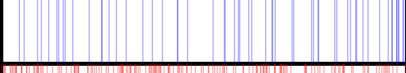
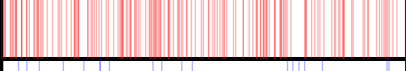

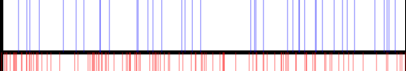
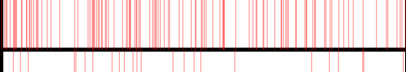
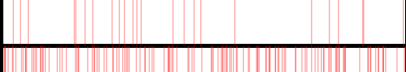
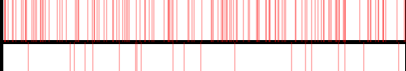
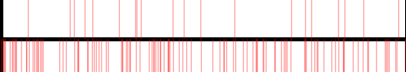
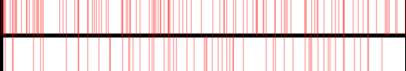
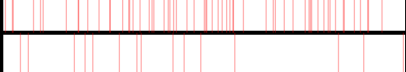
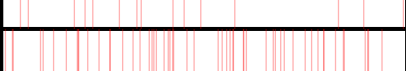
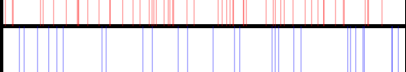

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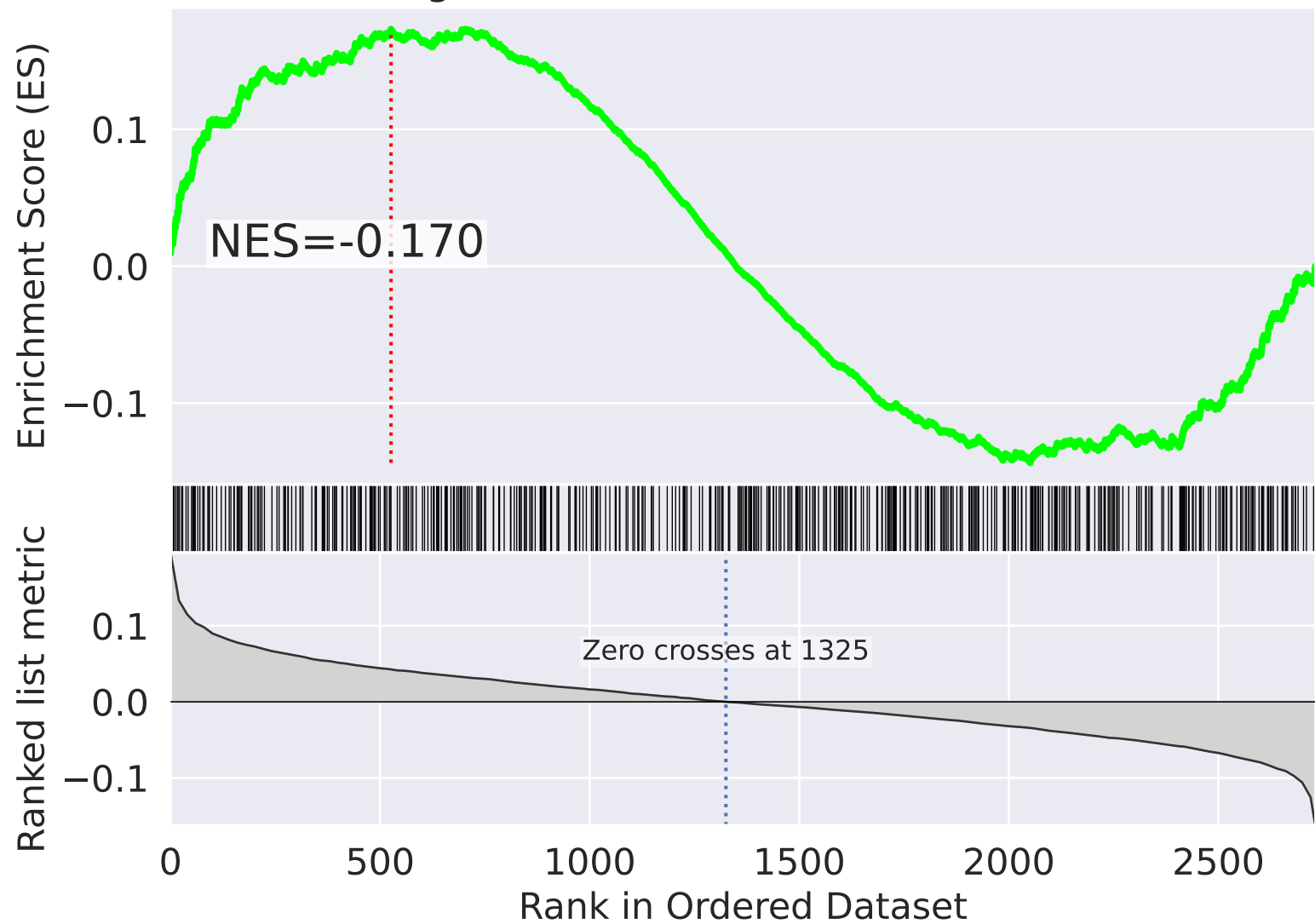
NES

SET

-5.937		rRNA Processing R-HSA-72312
-5.805		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-5.802		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.412		Cell Cycle Checkpoints R-HSA-69620
-3.705		Cristae Formation R-HSA-8949613
-3.633		Mitochondrial Biogenesis R-HSA-1592230
3.633		RHO GTPase Effectors R-HSA-195258
3.624		Iron Uptake And Transport R-HSA-917937
3.622		HIV Infection R-HSA-162906
3.604		Ion Channel Transport R-HSA-983712
3.427		Separation Of Sister Chromatids R-HSA-2467813
3.414		Fc Epsilon Receptor (FCERI) Signaling R-HSA-2454202
3.393		Transferrin Endocytosis And Recycling R-HSA-917977
3.387		Interleukin-1 Signaling R-HSA-9020702
-3.347		rRNA Modification In Nucleus And Cytosol R-HSA-6790901

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=13$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

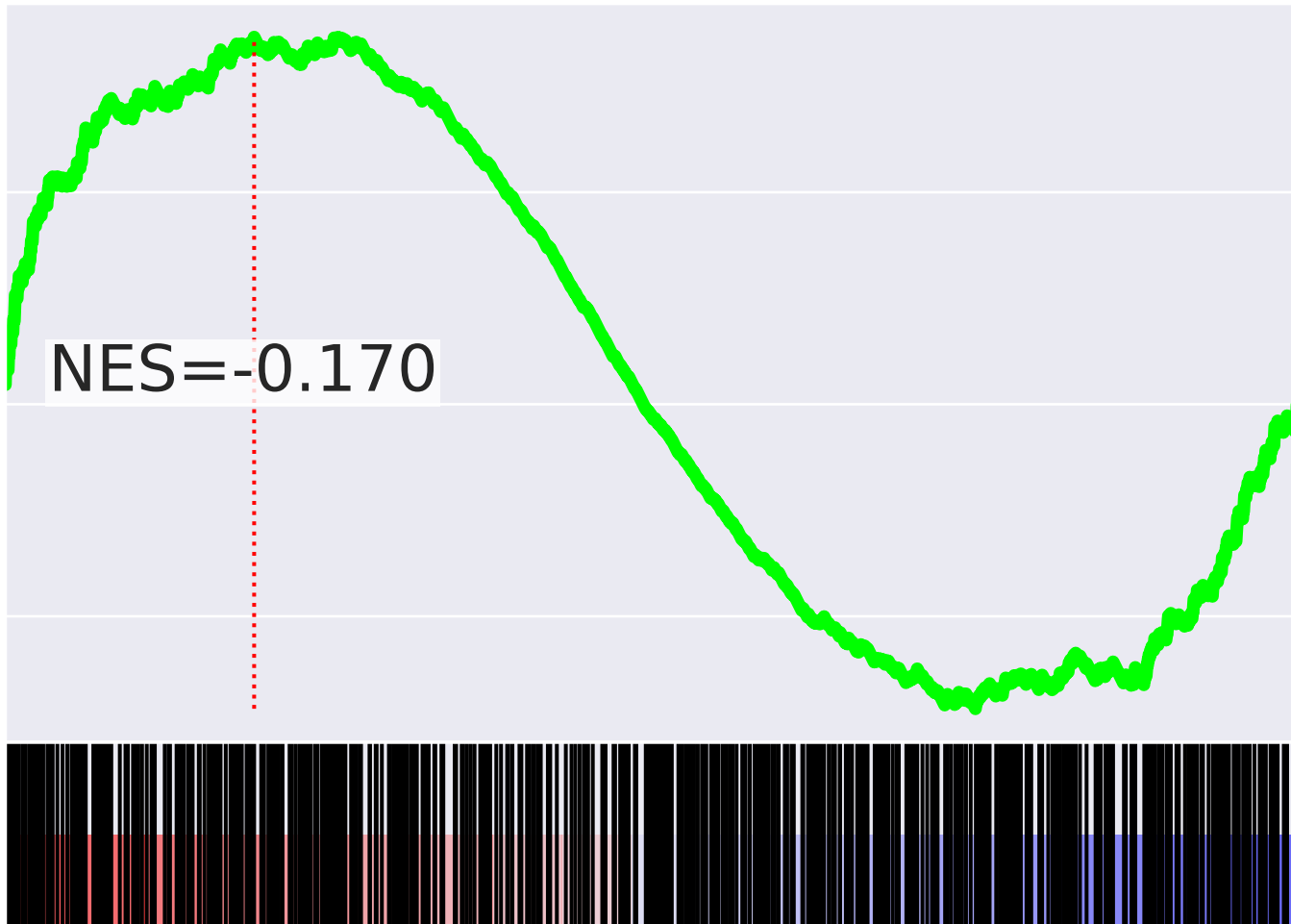
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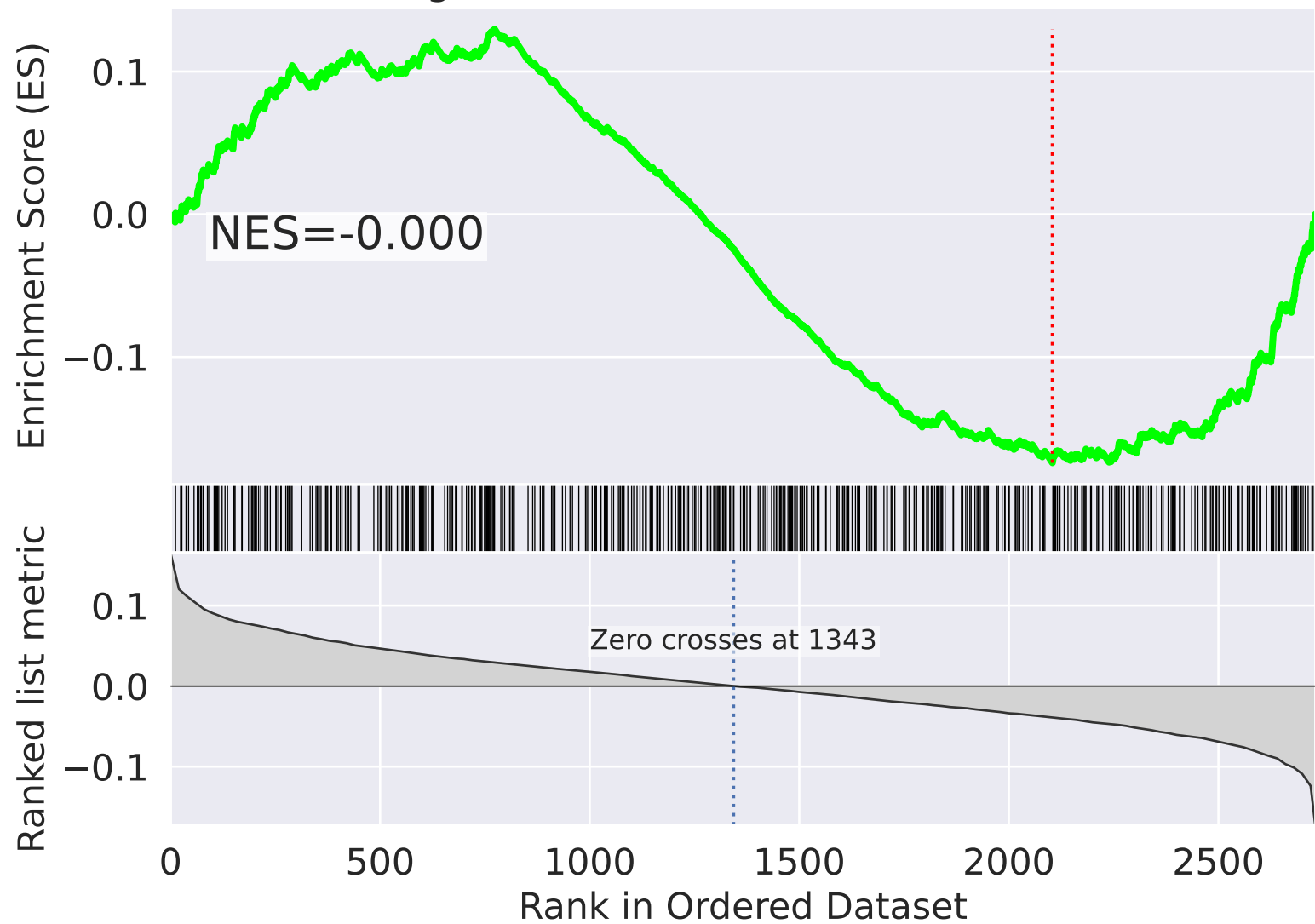
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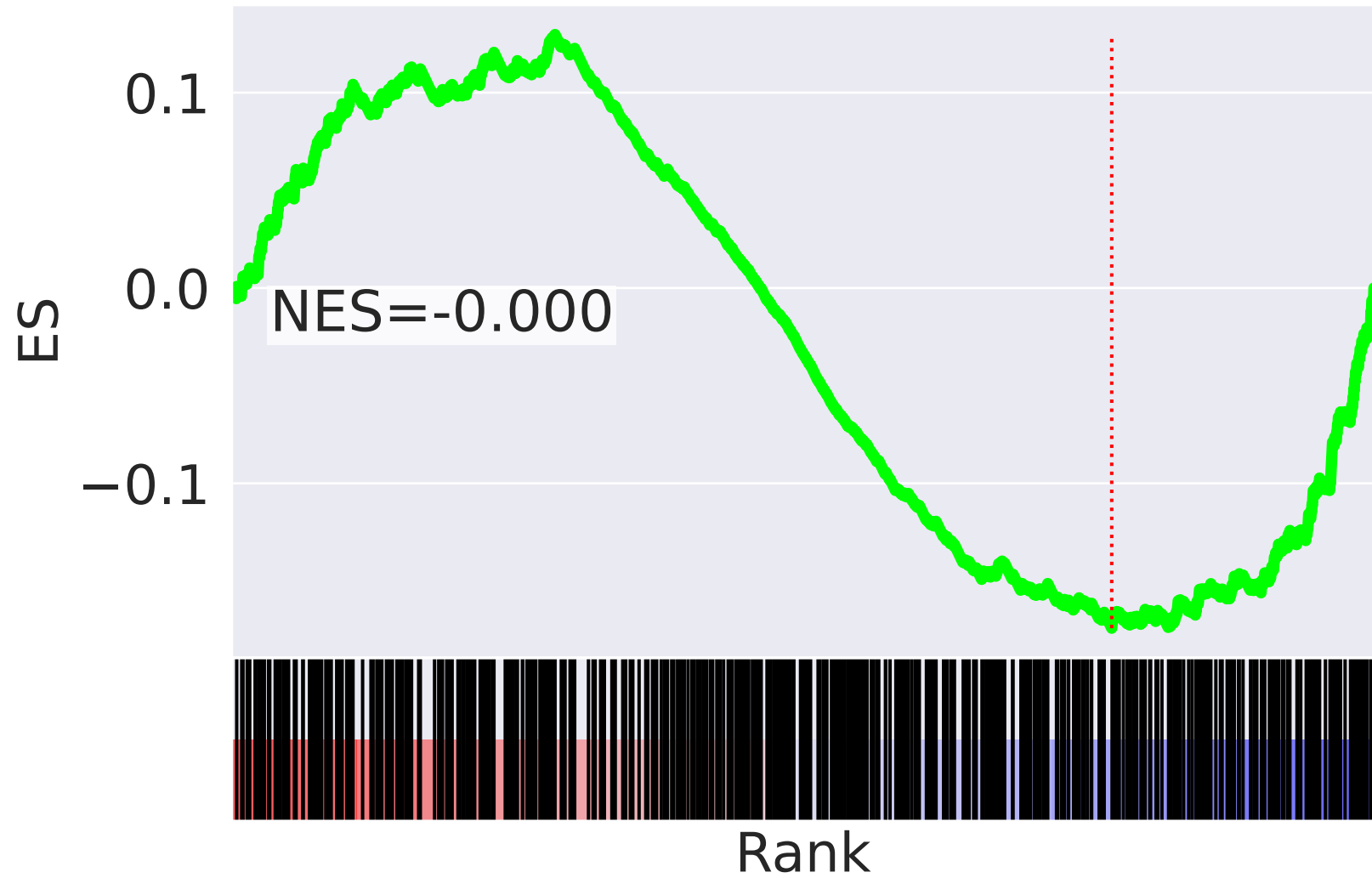
NES		SET
3.665		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.639		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.549		Respiratory Electron Transport R-HSA-611105
3.520		Nonhomologous End-Joining (NHEJ) R-HSA-5693571
-3.476		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.436		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.368		Metabolism Of Nucleotides R-HSA-15869
-3.324		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.297		DNA Double Strand Break Response R-HSA-5693606
3.262		Fanconi Anemia Pathway R-HSA-6783310
3.203		Recruitment And ATM-mediated Phosphorylation Of Repair And Signal Proteins At DNA Double Strand Breaks R-HSA-5693565
-3.126		rRNA Processing R-HSA-72312
-3.015		Interleukin-3, Interleukin-5 And GM-CSF Signaling R-HSA-512988
-2.979		Peroxisomal Protein Import R-HSA-9033241
2.897		Nucleotide Biosynthesis R-HSA-8956320

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=14$

Signal Transduction R-HSA-162582



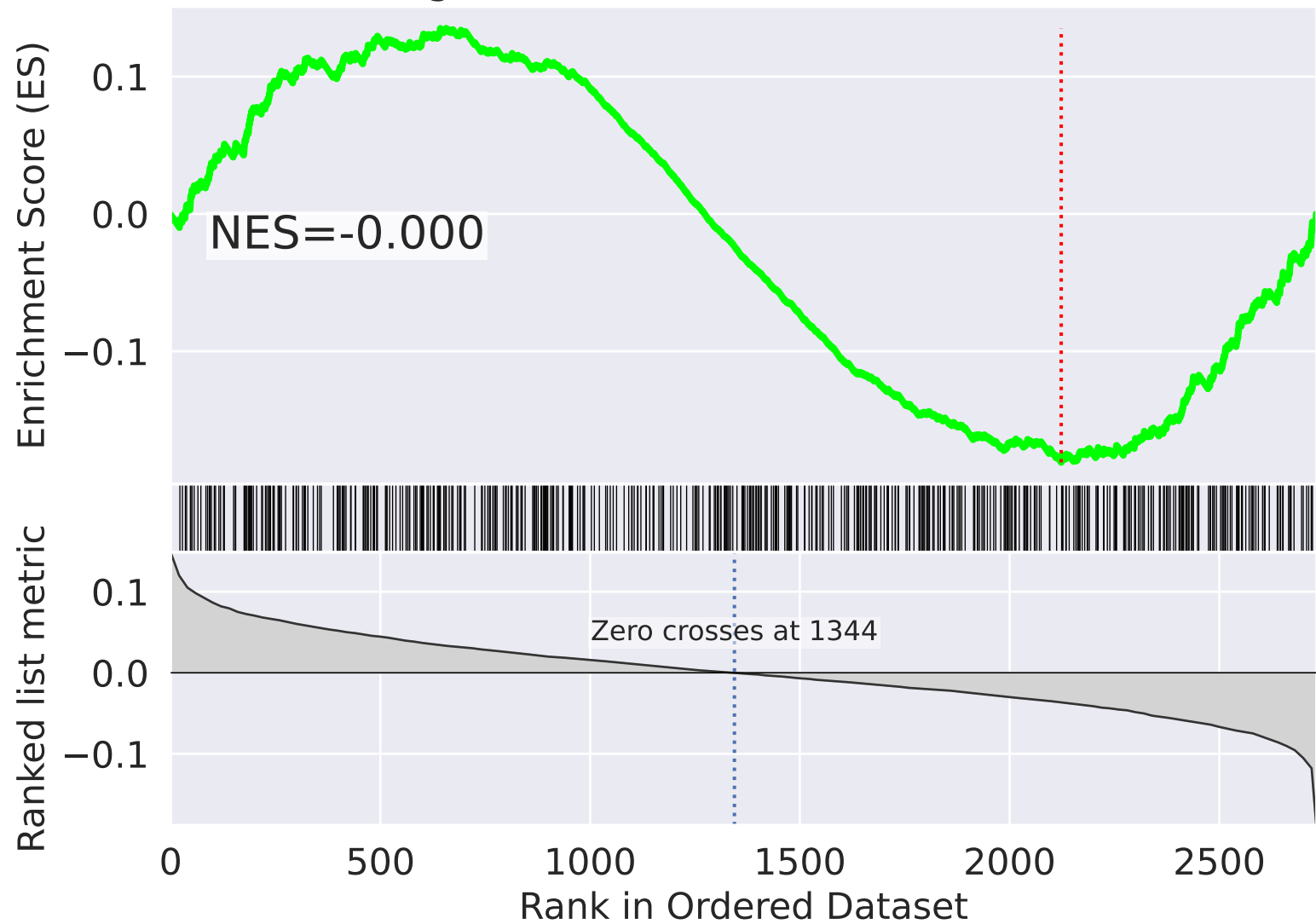
Signal Transduction R-HSA-162582



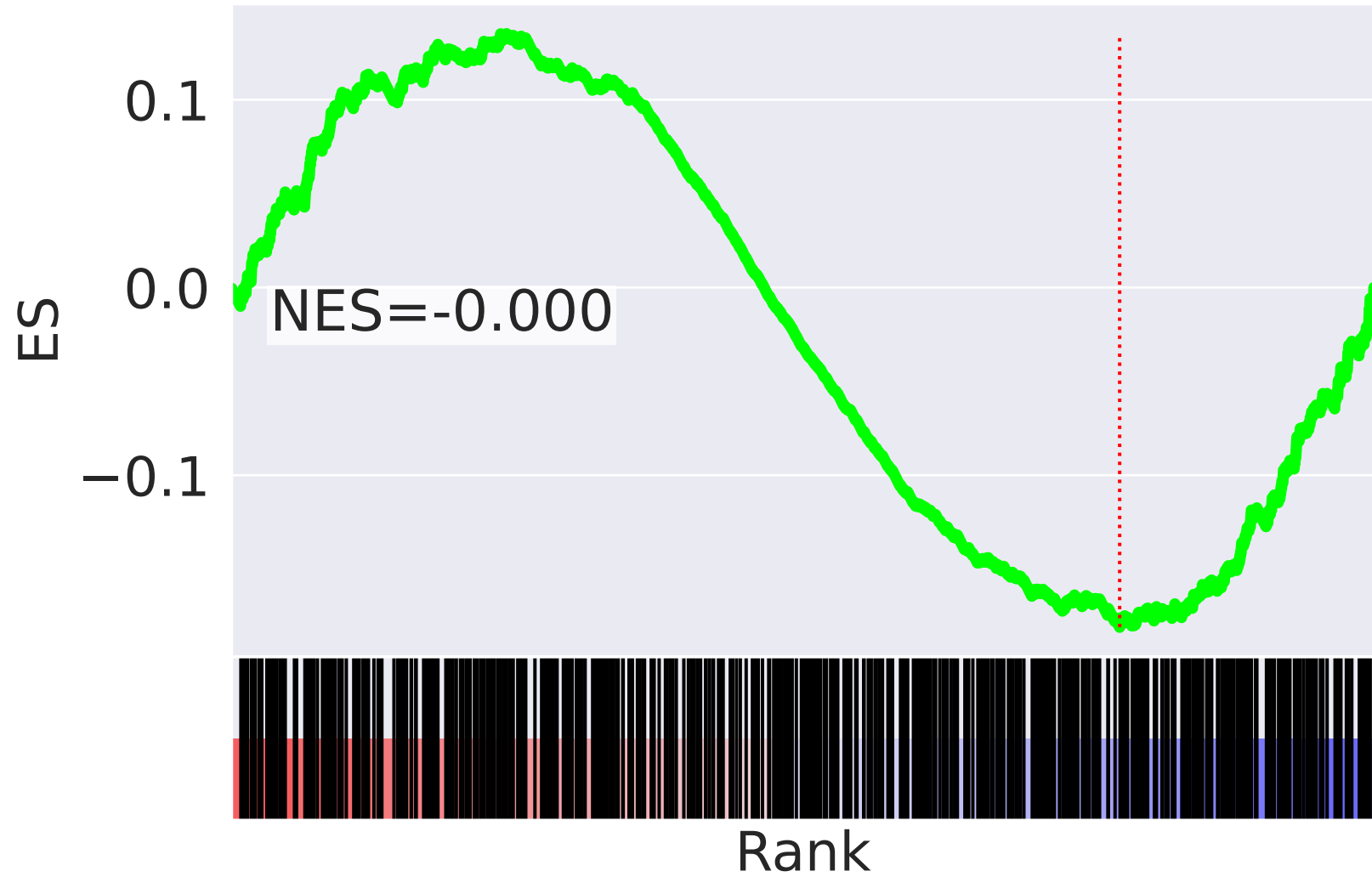
NES	SET
5.374	Signaling By WNT R-HSA-195721
5.032	PCP/CE Pathway R-HSA-4086400
4.935	Beta-catenin Independent WNT Signaling R-HSA-3858494
4.933	Metabolism Of Polyamines R-HSA-351202
4.910	Regulation Of RUNX2 Expression And Activity R-HSA-8939902
4.864	SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
4.848	Signaling By Hedgehog R-HSA-5358351
4.846	ER-Phagosome Pathway R-HSA-1236974
4.809	Downstream Signaling Events Of B Cell Receptor (BCR) R-HSA-1168372
4.769	NIK To Noncanonical NF-kB Signaling R-HSA-5676590
4.763	Regulation Of Ornithine Decarboxylase (ODC) R-HSA-350562
4.748	Activation Of NF-kappaB In B Cells R-HSA-1169091
4.739	Degradation Of Beta-Catenin By Destruction Complex R-HSA-195253
4.733	Ub-specific Processing Proteases R-HSA-5689880
4.697	ABC-family Proteins Mediated Transport R-HSA-382556

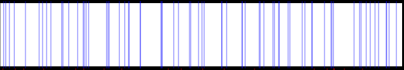
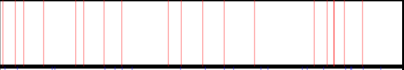

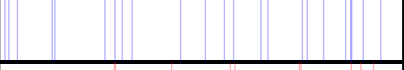
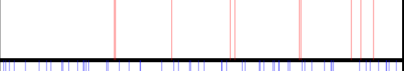
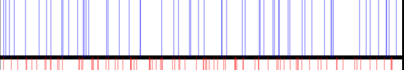
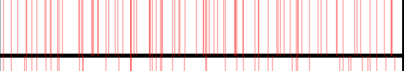
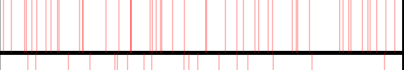
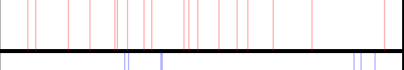
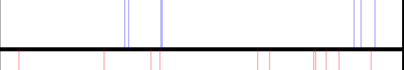



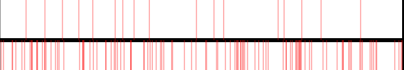
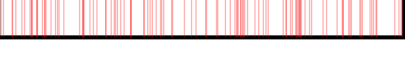
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=15$

Signal Transduction R-HSA-162582



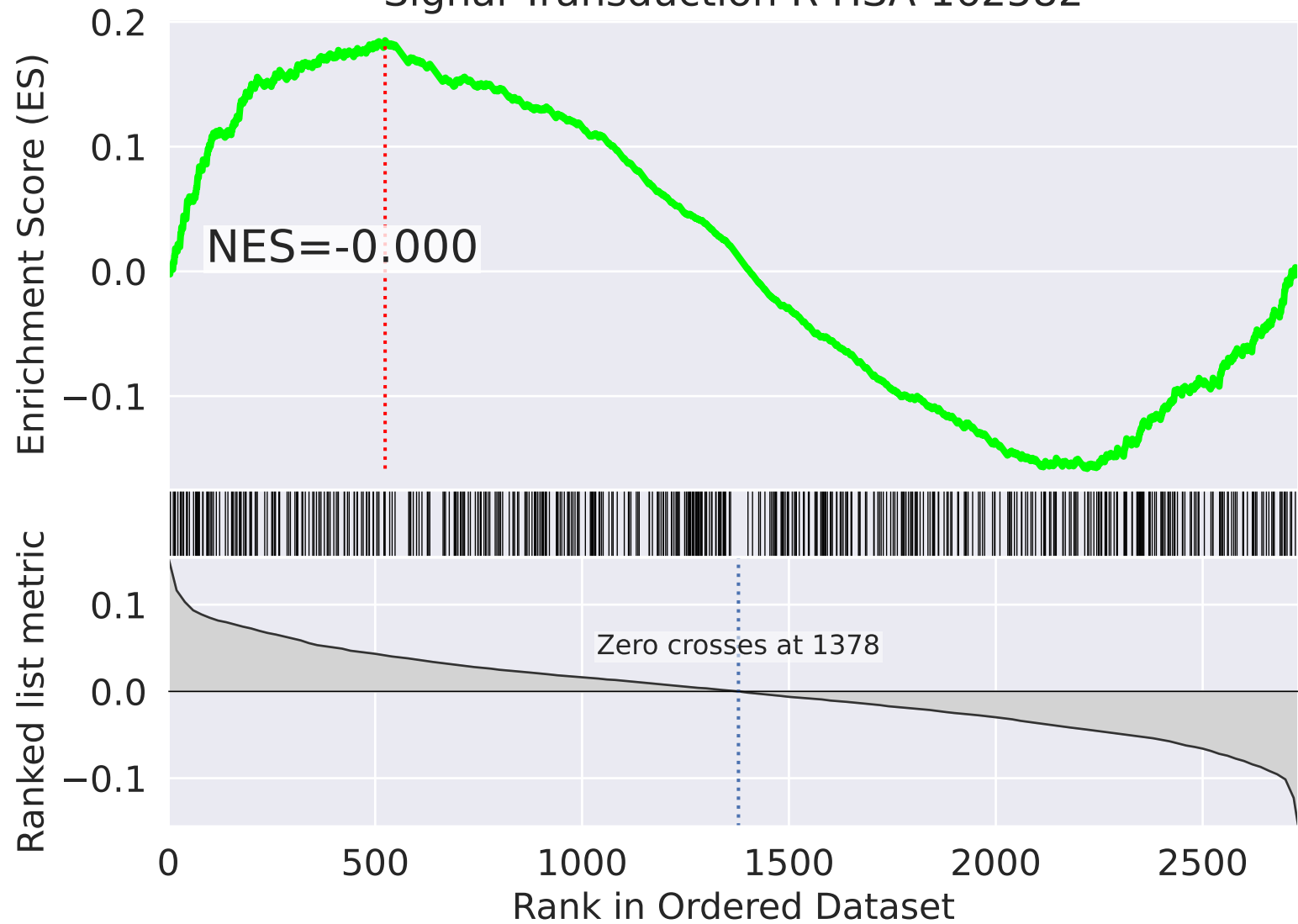
Signal Transduction R-HSA-162582



NES		SET
-3.419		rRNA Processing R-HSA-72312
3.183		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
-3.099		RNA Polymerase III Transcription Initiation R-HSA-76046
-3.084		RNA Polymerase III Abortive And Retractive Initiation R-HSA-749476
2.926		Transport Of Inorganic Cations/Anions And Amino Acids/Oligopeptides R-HSA-425393
-2.869		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
2.767		Transcriptional Regulation By RUNX1 R-HSA-8878171
2.756		Beta-catenin Independent WNT Signaling R-HSA-3858494
2.747		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-2.741		rRNA Processing In Mitochondrion R-HSA-8868766
2.739		Nucleotide Biosynthesis R-HSA-8956320
-2.725		RNA Polymerase III Transcription Initiation From Type 3 Promoter R-HSA-76071
2.707		Metabolism Of Vitamins And Cofactors R-HSA-196854
2.702		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
2.694		Transport Of Small Molecules R-HSA-382551

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=16$

Signal Transduction R-HSA-162582



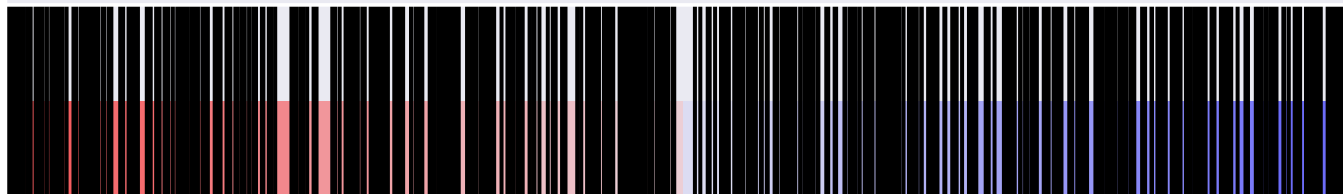
Signal Transduction R-HSA-162582

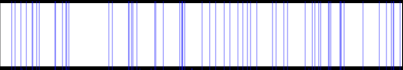
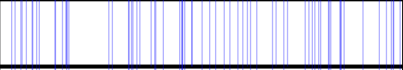
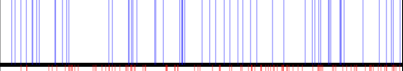
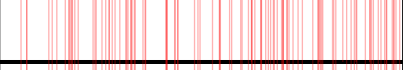
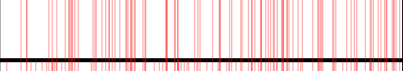
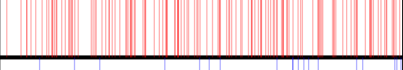
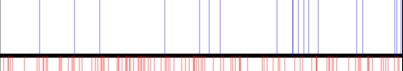
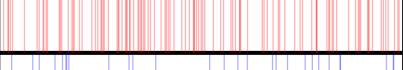
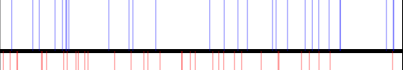
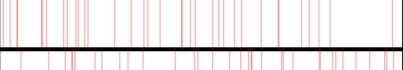
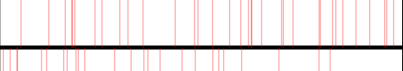
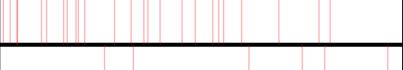
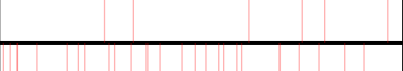
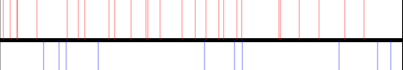
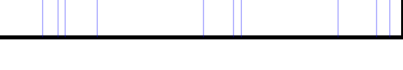
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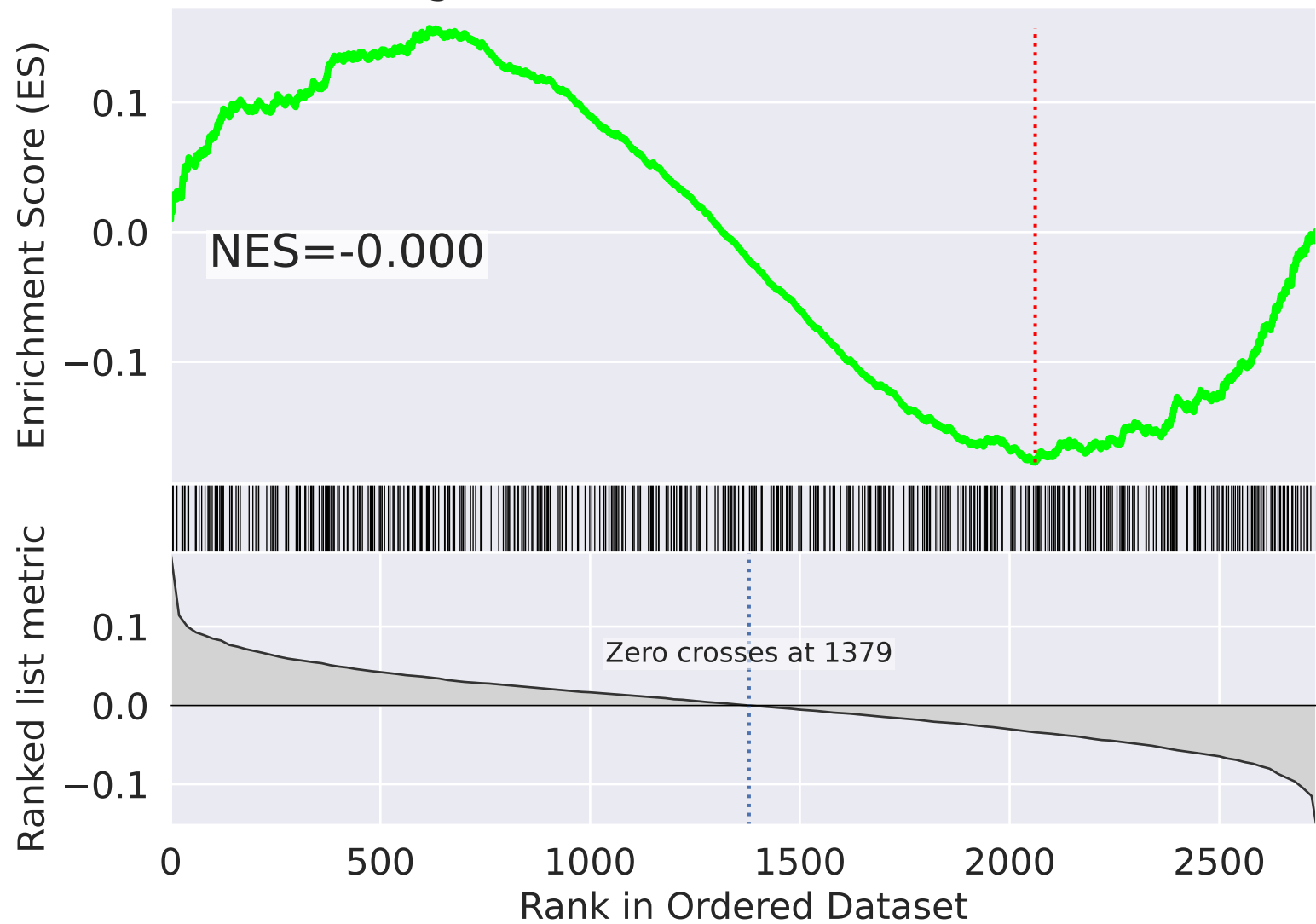
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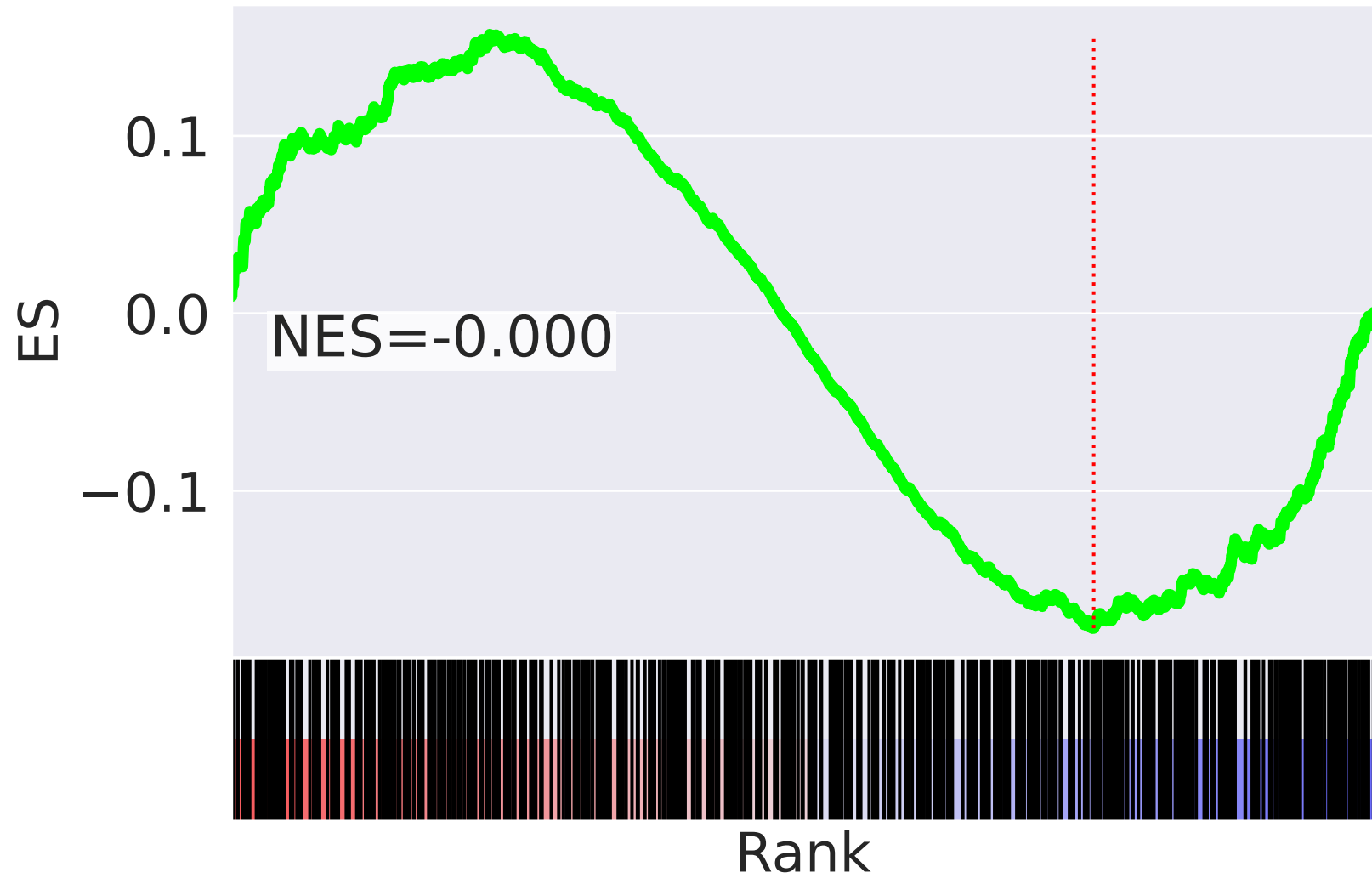
NES		SET
-5.602		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-5.522		rRNA Processing R-HSA-72312
-5.328		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.691		mRNA Splicing R-HSA-72172
4.487		mRNA Splicing - Major Pathway R-HSA-72163
4.262		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-3.154		Retrograde Transport At Trans-Golgi-Network R-HSA-6811440
3.094		Deubiquitination R-HSA-5688426
-3.056		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
2.979		Diseases Of Metabolism R-HSA-5668914
2.931		mRNA Splicing - Minor Pathway R-HSA-72165
2.900		Diseases Of Glycosylation R-HSA-3781865
2.891		SARS-CoV-2 Modulates Autophagy R-HSA-9754560
2.804		Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
-2.777		Fatty acyl-CoA Biosynthesis R-HSA-75105

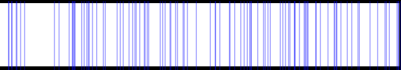
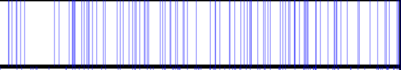
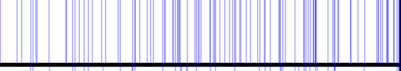
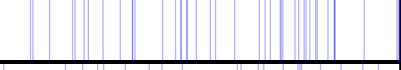


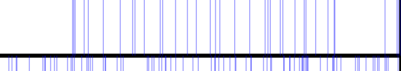
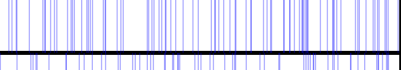
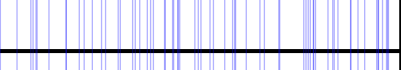
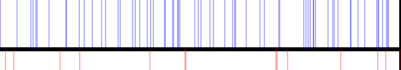


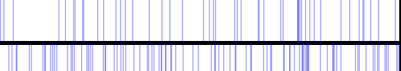
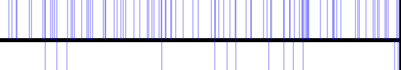
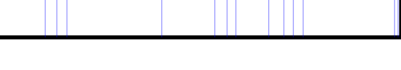
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=17$

Signal Transduction R-HSA-162582



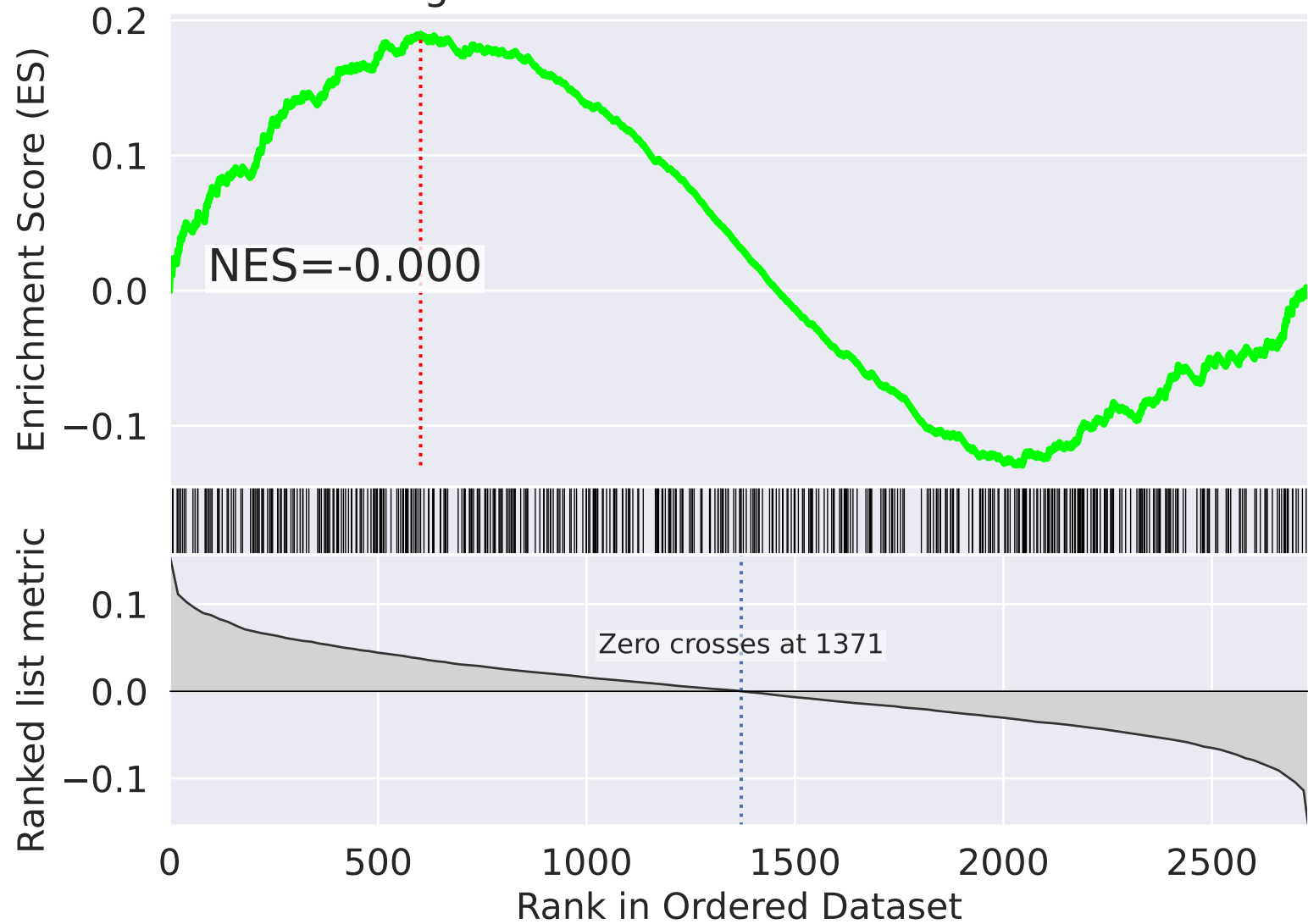
Signal Transduction R-HSA-162582



NES		SET
-3.883		Mitotic G2-G2/M Phases R-HSA-453274
-3.560		G2/M Transition R-HSA-69275
-3.512		Mitotic Prometaphase R-HSA-68877
-3.477		Cilium Assembly R-HSA-5617833
-3.319		COPII-mediated Vesicle Transport R-HSA-204005
-3.249		MET Promotes Cell Motility R-HSA-8875878
-3.076		Regulation Of PLK1 Activity At G2/M Transition R-HSA-2565942
-3.005		MAPK1/MAPK3 Signaling R-HSA-5684996
-2.969		EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
-2.969		Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
2.870		Inhibition Of DNA Recombination At Telomere R-HSA-9670095
-2.838		Signaling By Non-Receptor Tyrosine Kinases R-HSA-9006927
-2.834		ER To Golgi Anterograde Transport R-HSA-199977
-2.820		MAPK Family Signaling Cascades R-HSA-5683057
-2.747		Signaling To ERKs R-HSA-187687

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=18$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.2

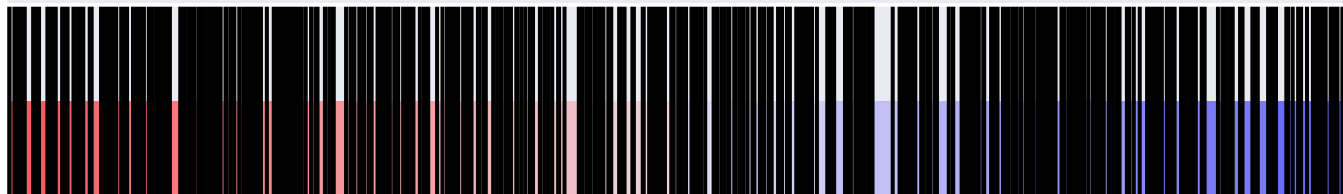
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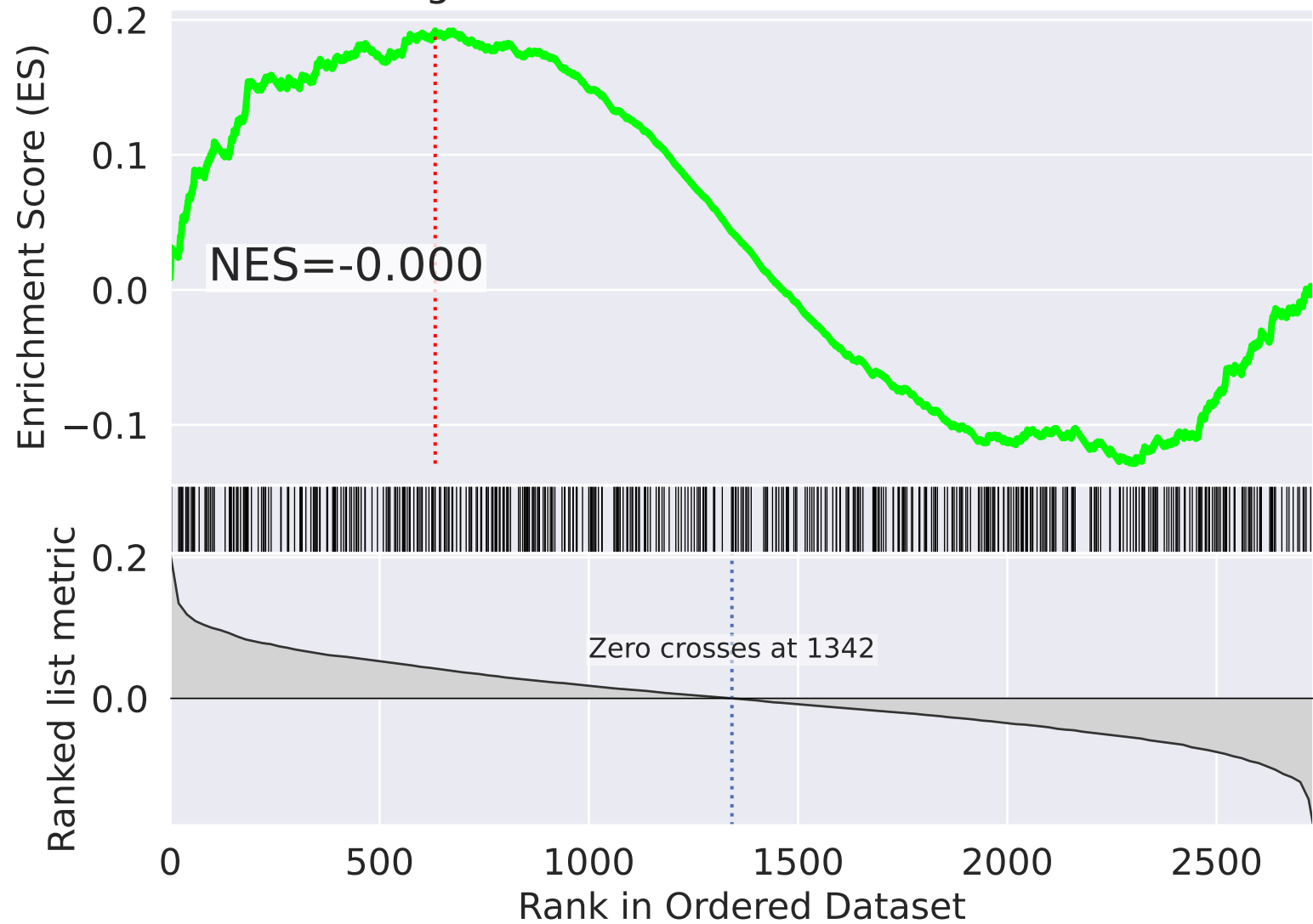
Rank



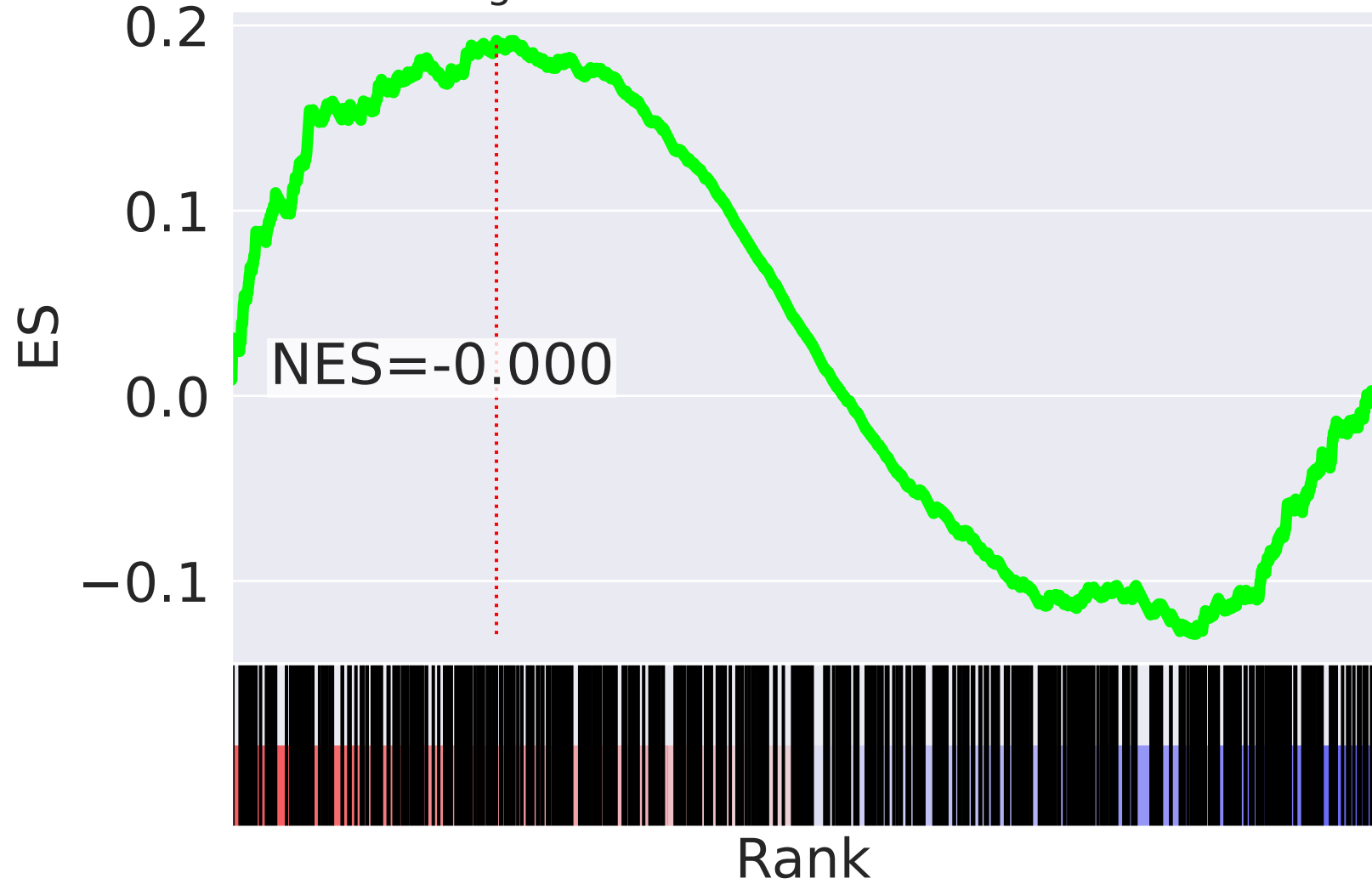
NES	SET
4.239	Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
3.763	Golgi-to-ER Retrograde Transport R-HSA-8856688
3.724	Transcriptional Regulation By RUNX1 R-HSA-8878171
3.661	COPI-dependent Golgi-to-ER Retrograde Traffic R-HSA-6811434
3.524	Regulation Of RUNX3 Expression And Activity R-HSA-8941858
3.472	Transport To Golgi And Subsequent Modification R-HSA-948021
3.464	ER To Golgi Anterograde Transport R-HSA-199977
3.399	Membrane Trafficking R-HSA-199991
3.367	Vesicle-mediated Transport R-HSA-5653656
3.347	RAF/MAP Kinase Cascade R-HSA-5673001
3.316	CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
3.302	Fc Epsilon Receptor (FCERI) Signaling R-HSA-2454202
3.301	ABC Transporter Disorders R-HSA-5619084
3.301	Defective CFTR Causes Cystic Fibrosis R-HSA-5678895
3.252	COPI-mediated Anterograde Transport R-HSA-6807878


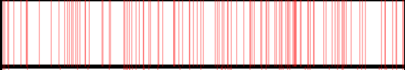
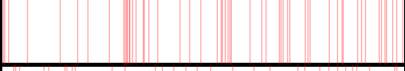
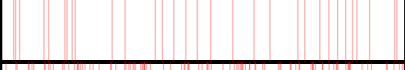
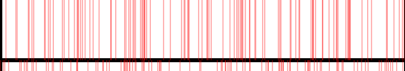
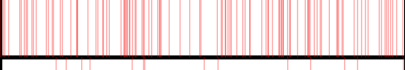
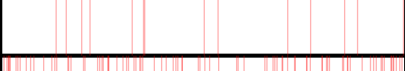
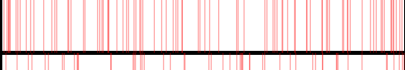
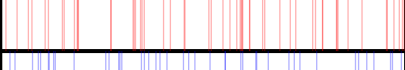
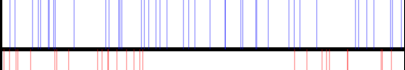
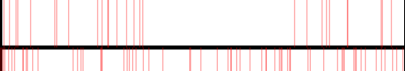
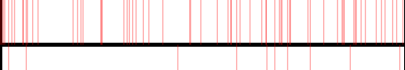
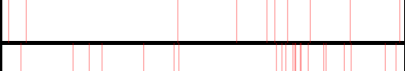
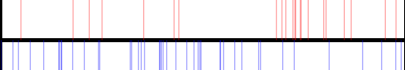
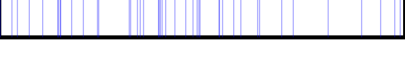
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=19$

Signal Transduction R-HSA-162582



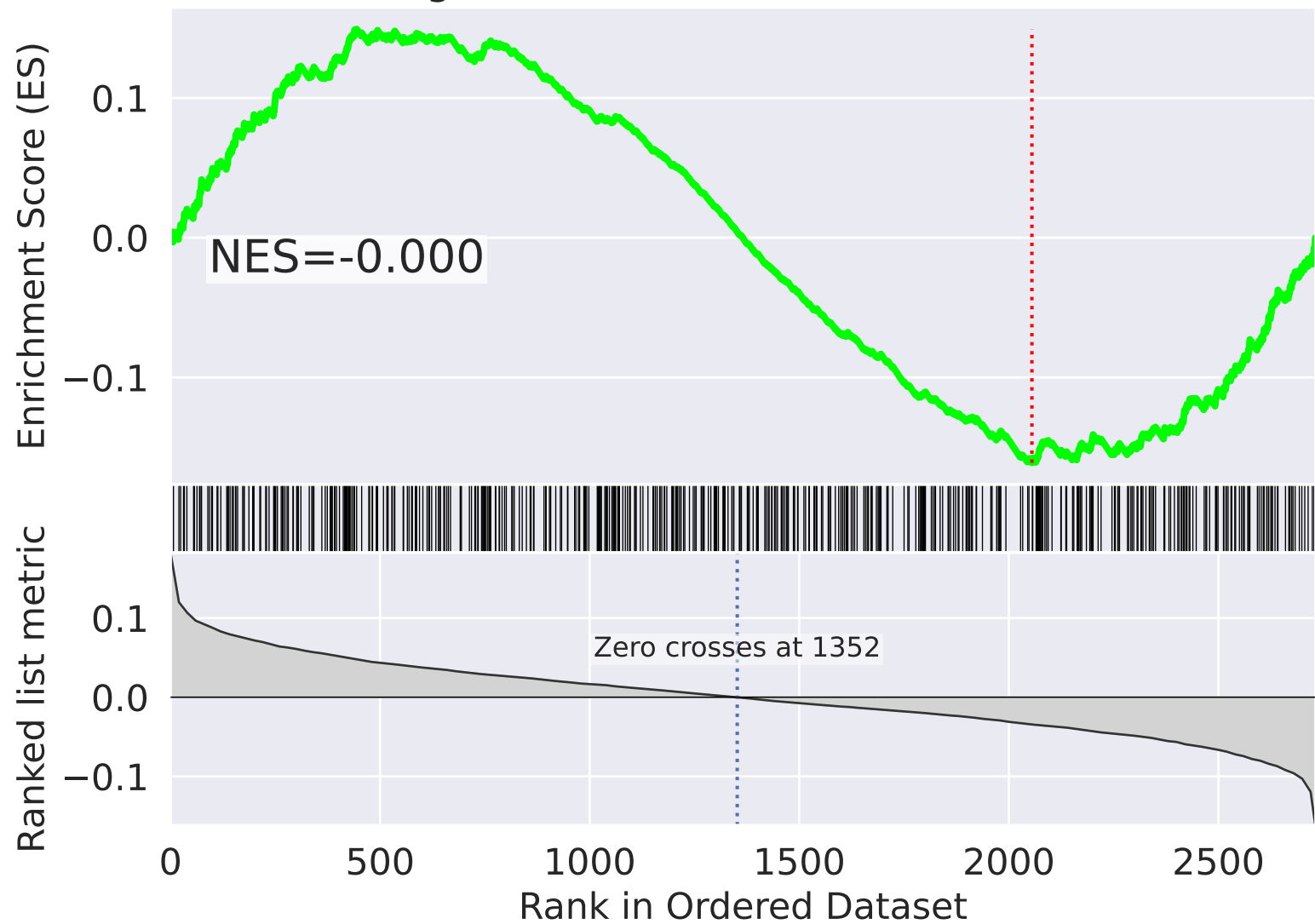
Signal Transduction R-HSA-162582



NES		SET
3.744		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.679		Transport Of Small Molecules R-HSA-382551
3.641		UCH Proteinases R-HSA-5689603
3.379		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.361		Chromatin Modifying Enzymes R-HSA-3247509
3.283		Deubiquitination R-HSA-5688426
3.241		Interferon Gamma Signaling R-HSA-877300
3.227		Asparagine N-linked Glycosylation R-HSA-446203
3.120		HATs Acetylate Histones R-HSA-3214847
-3.116		G2/M DNA Damage Checkpoint R-HSA-69473
3.089		Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
3.014		Disorders Of Transmembrane Transporters R-HSA-5619115
2.939		N-glycan Trimming In ER And Calnexin/Calreticulin Cycle R-HSA-532668
2.906		SLC-mediated Transmembrane Transport R-HSA-425407
-2.886		Cilium Assembly R-HSA-5617833

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=20$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

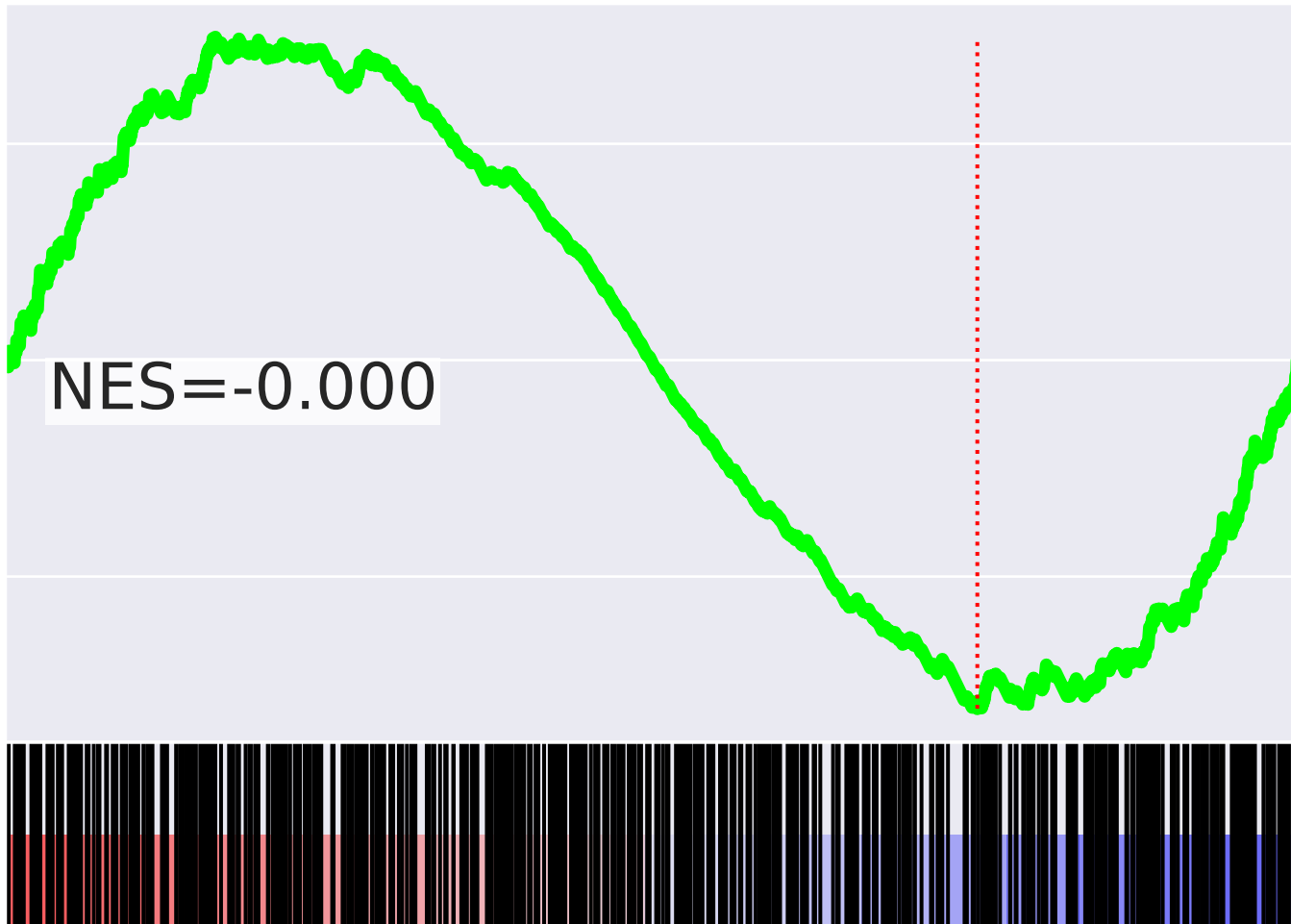
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0.0

-0.1

NES=-0.000

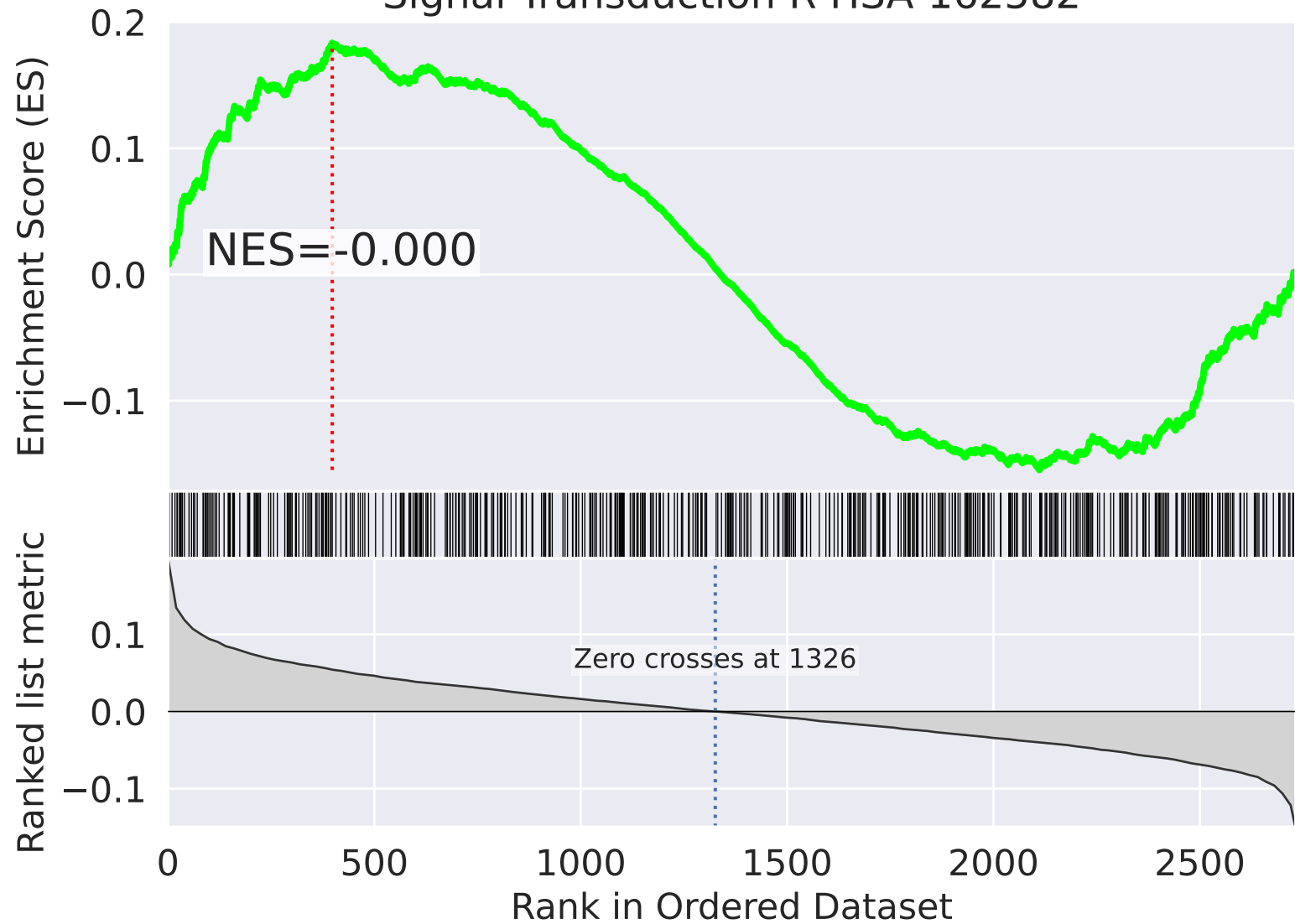
Rank



NES		SET
6.256		mRNA Splicing R-HSA-72172
6.079		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
6.069		mRNA Splicing - Major Pathway R-HSA-72163
5.374		Separation Of Sister Chromatids R-HSA-2467813
4.969		HIV Infection R-HSA-162906
4.836		M Phase R-HSA-68886
4.689		Disorders Of Transmembrane Transporters R-HSA-5619115
4.644		DNA Replication Pre-Initiation R-HSA-69002
4.589		G1/S DNA Damage Checkpoints R-HSA-69615
4.576		Mitotic Metaphase And Anaphase R-HSA-2555396
4.485		Mitotic Anaphase R-HSA-68882
4.461		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
4.439		SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
4.425		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
4.401		ER-Phagosome Pathway R-HSA-1236974

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=21$

Signal Transduction R-HSA-162582



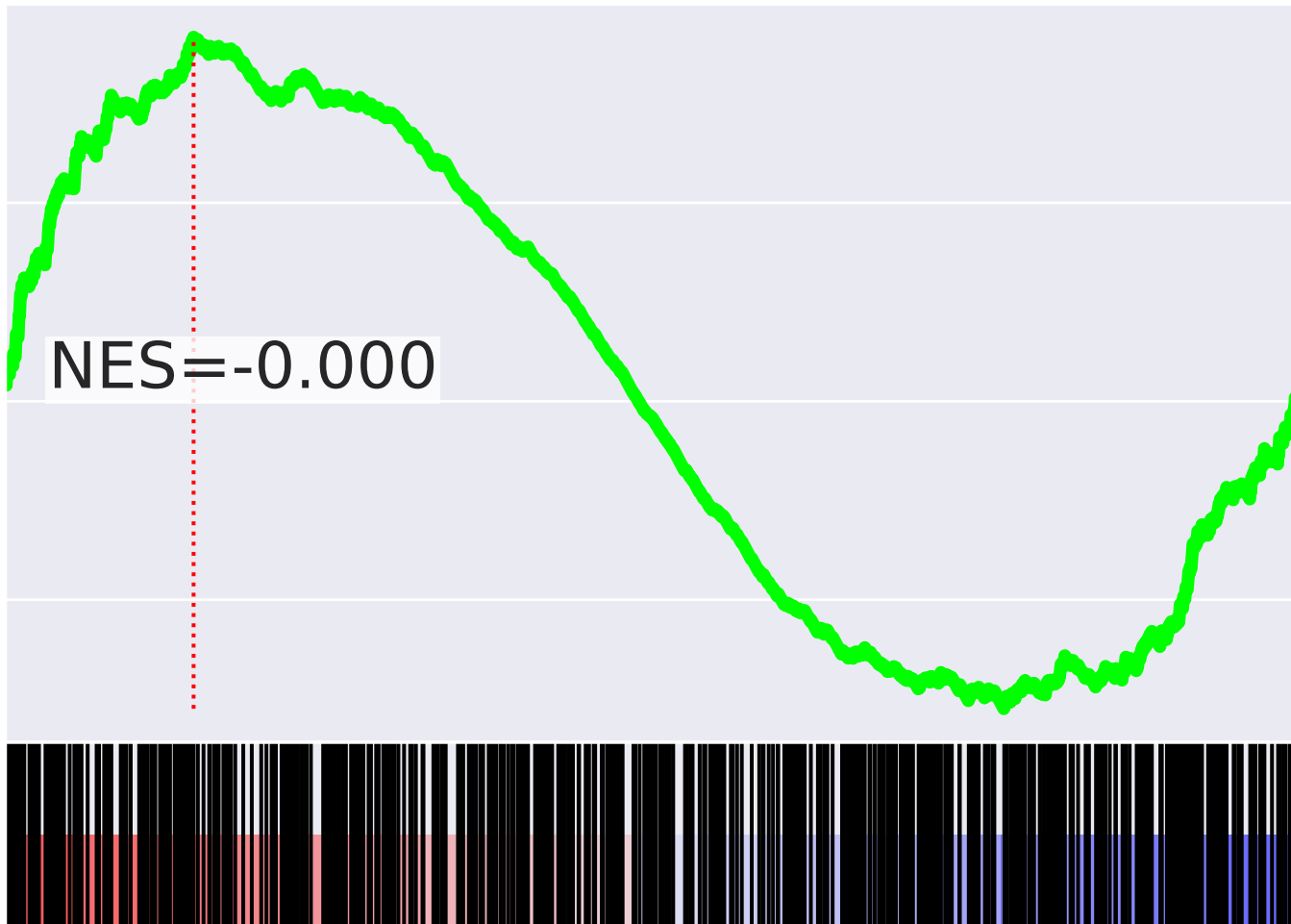
Signal Transduction R-HSA-162582

ES

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0.0
-0.1

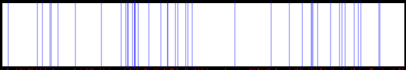
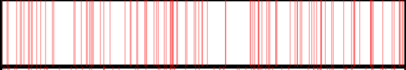
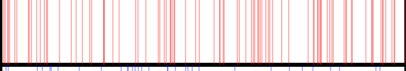
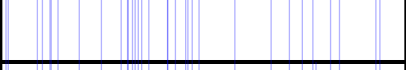
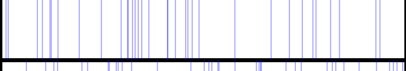
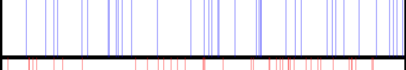
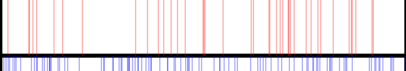
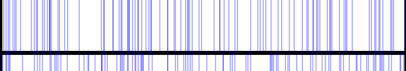
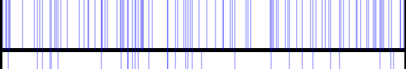
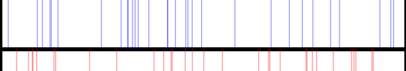
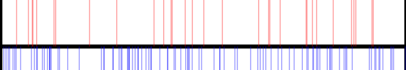
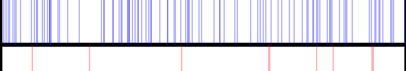
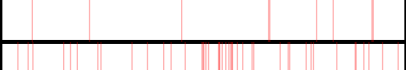
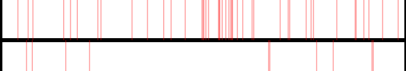
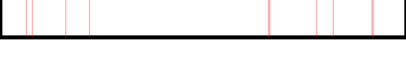
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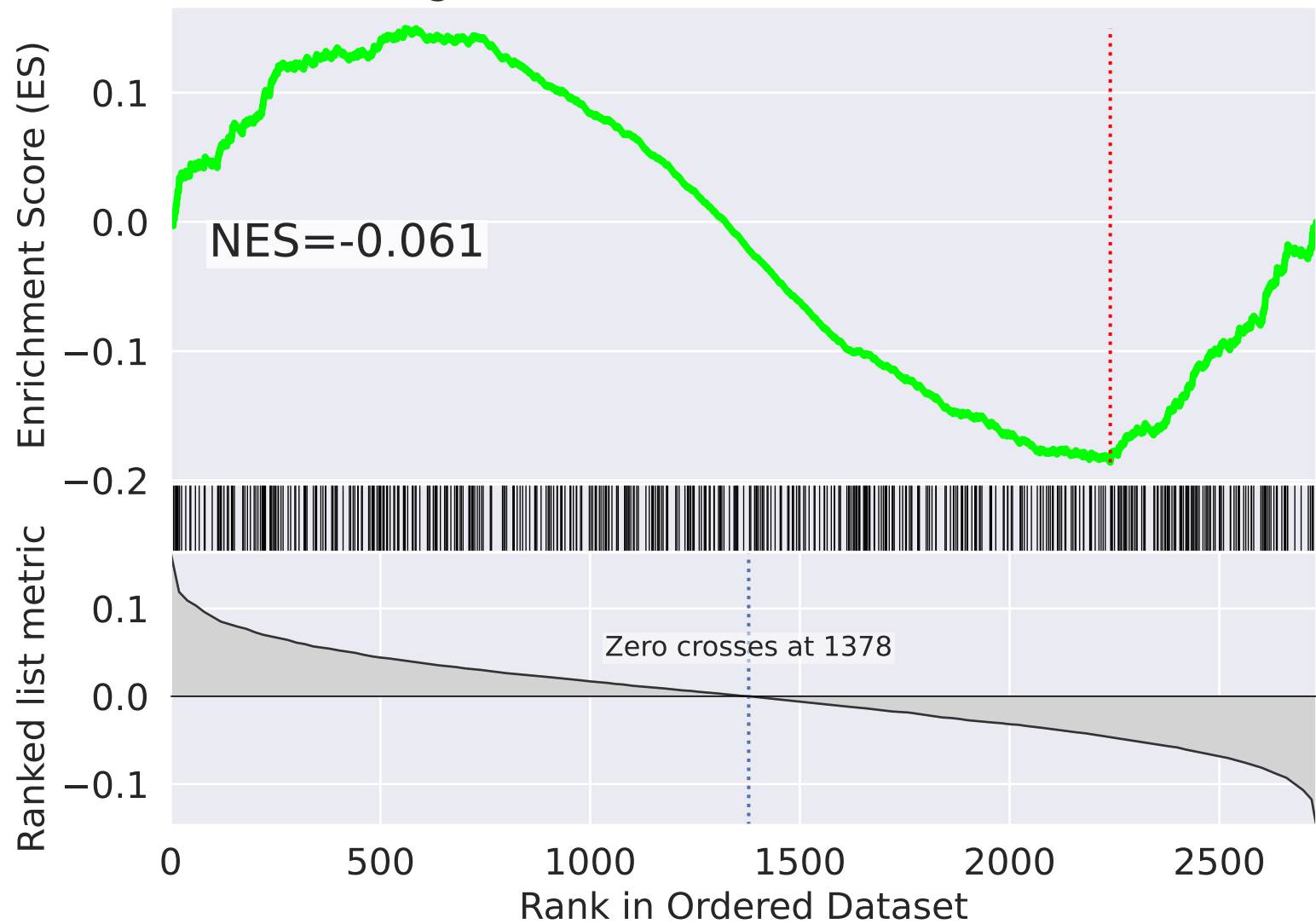
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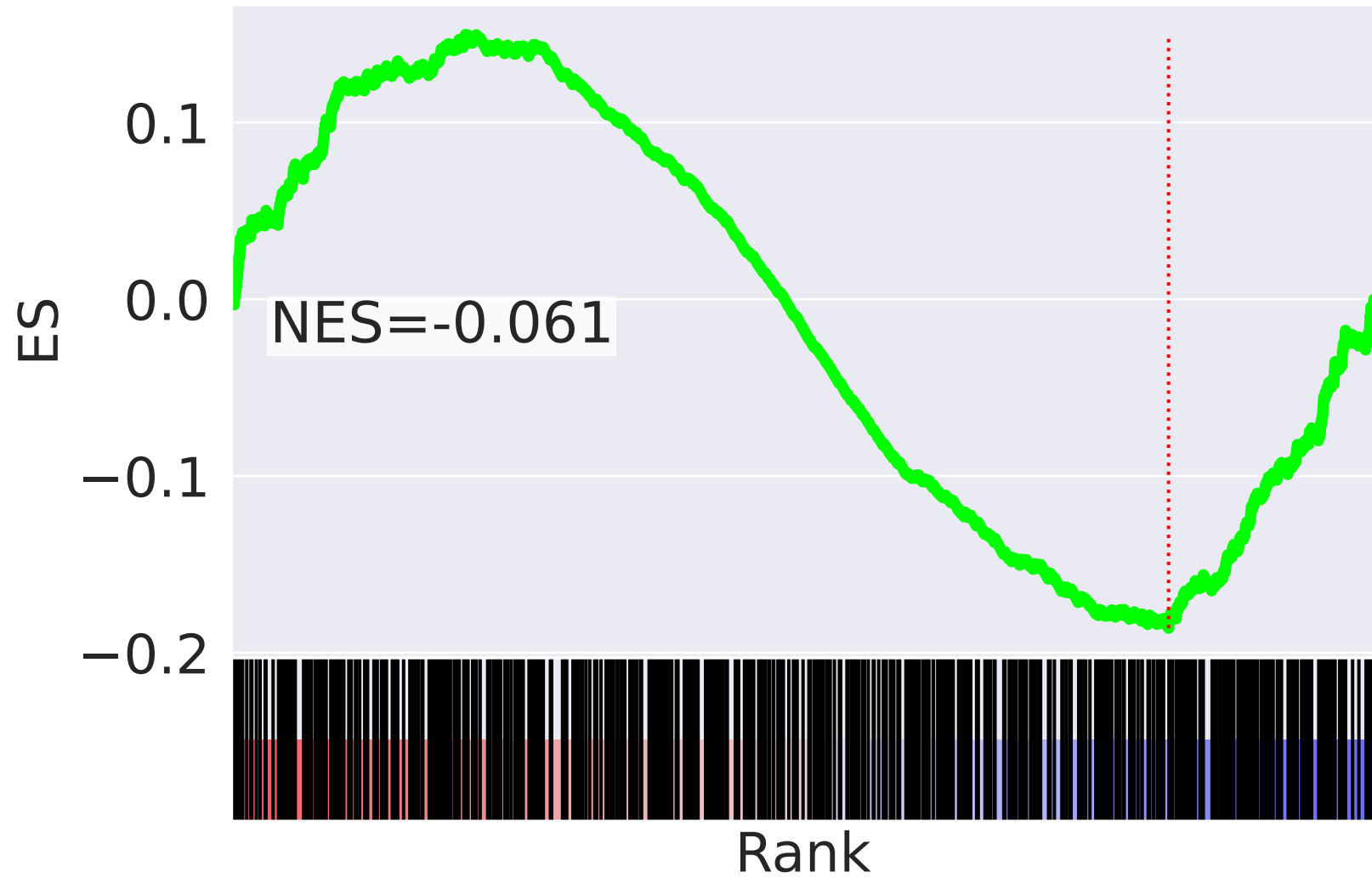
-3.576		Cilium Assembly R-HSA-5617833
3.541		Chromatin Modifying Enzymes R-HSA-3247509
3.496		Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.285		Centrosome Maturation R-HSA-380287
-3.257		Recruitment Of NuMA To Mitotic Centrosomes R-HSA-380320
-3.232		Complex I Biogenesis R-HSA-6799198
3.203		Estrogen-dependent Gene Expression R-HSA-9018519
-3.128		Mitotic G2-G2/M Phases R-HSA-453274
-3.099		Mitotic Prometaphase R-HSA-68877
-3.049		AURKA Activation By TPX2 R-HSA-8854518
2.985		Activation Of HOX Genes During Differentiation R-HSA-5619507
-2.964		G2/M Transition R-HSA-69275
2.947		PRC2 Methylates Histones And DNA R-HSA-212300
2.933		Formation Of RNA Pol II Elongation Complex R-HSA-112382
2.923		Defective Pyroptosis R-HSA-9710421

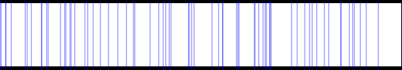
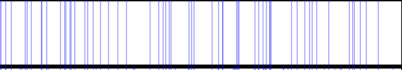
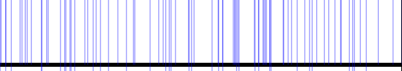
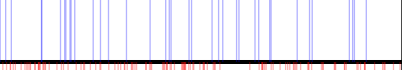
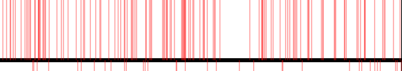

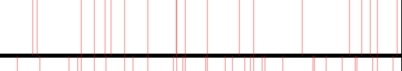
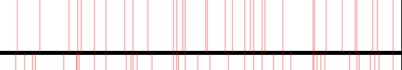
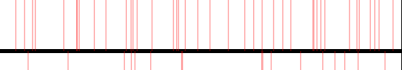
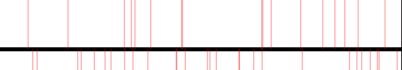
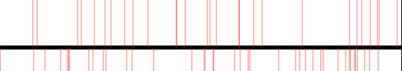
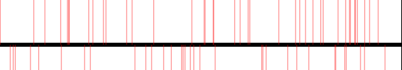
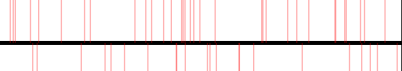

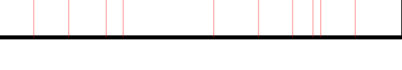
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=22$

Signal Transduction R-HSA-162582



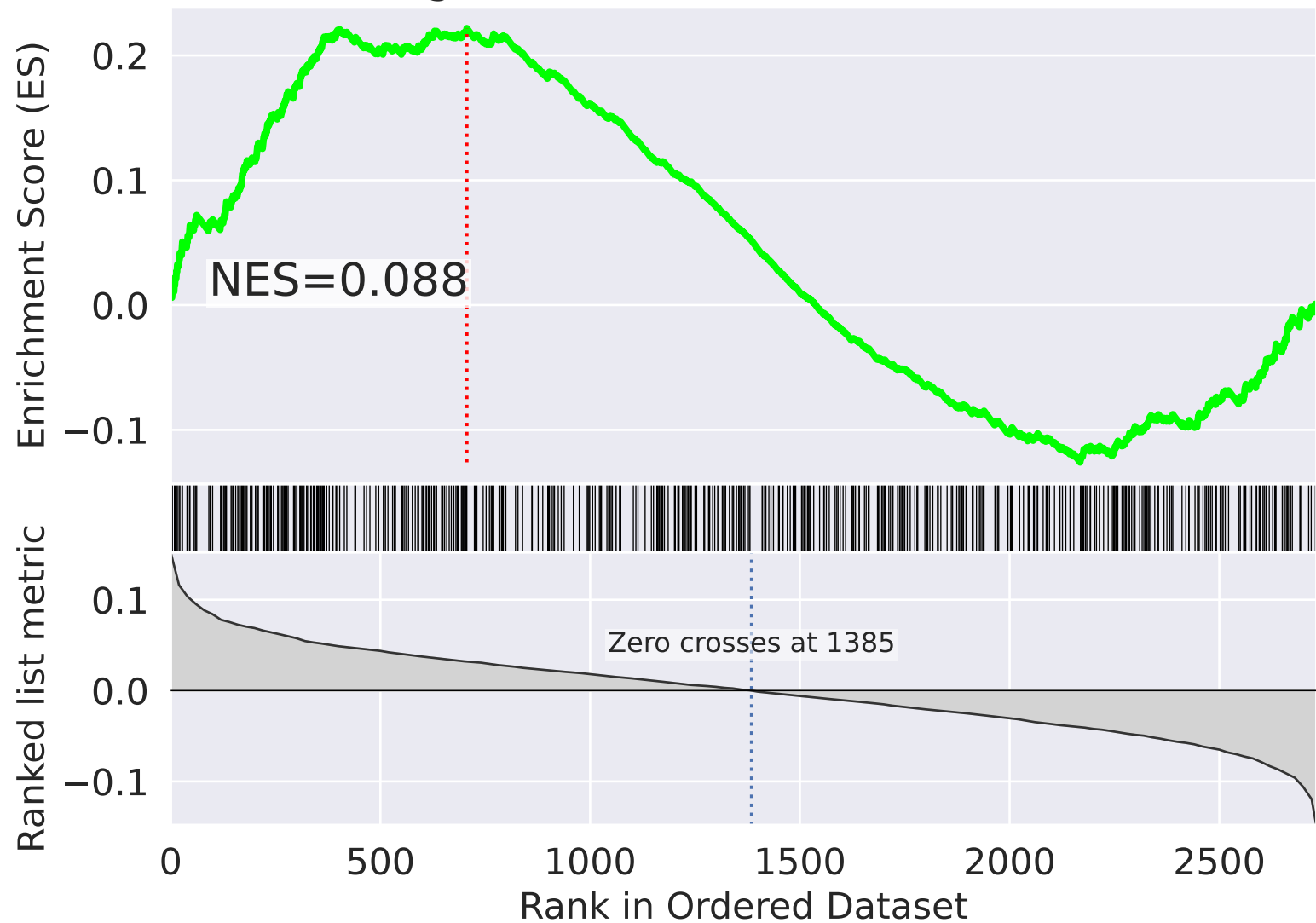
Signal Transduction R-HSA-162582



NES		SET
-5.727		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-5.511		Respiratory Electron Transport R-HSA-611105
-5.429		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-5.024		Complex I Biogenesis R-HSA-6799198
4.225		Metabolism Of Lipids R-HSA-556833
3.574		Leishmania Infection R-HSA-9658195
3.469		FCGR3A-mediated Phagocytosis R-HSA-9664422
3.328		VEGFA-VEGFR2 Pathway R-HSA-4420097
3.273		Platelet Activation, Signaling And Aggregation R-HSA-76002
3.074		Fatty Acid Metabolism R-HSA-8978868
3.037		Fcgamma Receptor (FCGR) Dependent Phagocytosis R-HSA-2029480
3.027		Signaling By TGF-beta Receptor Complex R-HSA-170834
2.974		Metabolism Of Steroids R-HSA-8957322
2.924		Regulation Of Actin Dynamics For Phagocytic Cup Formation R-HSA-2029482
2.919		Extracellular Matrix Organization R-HSA-1474244

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=23$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.2

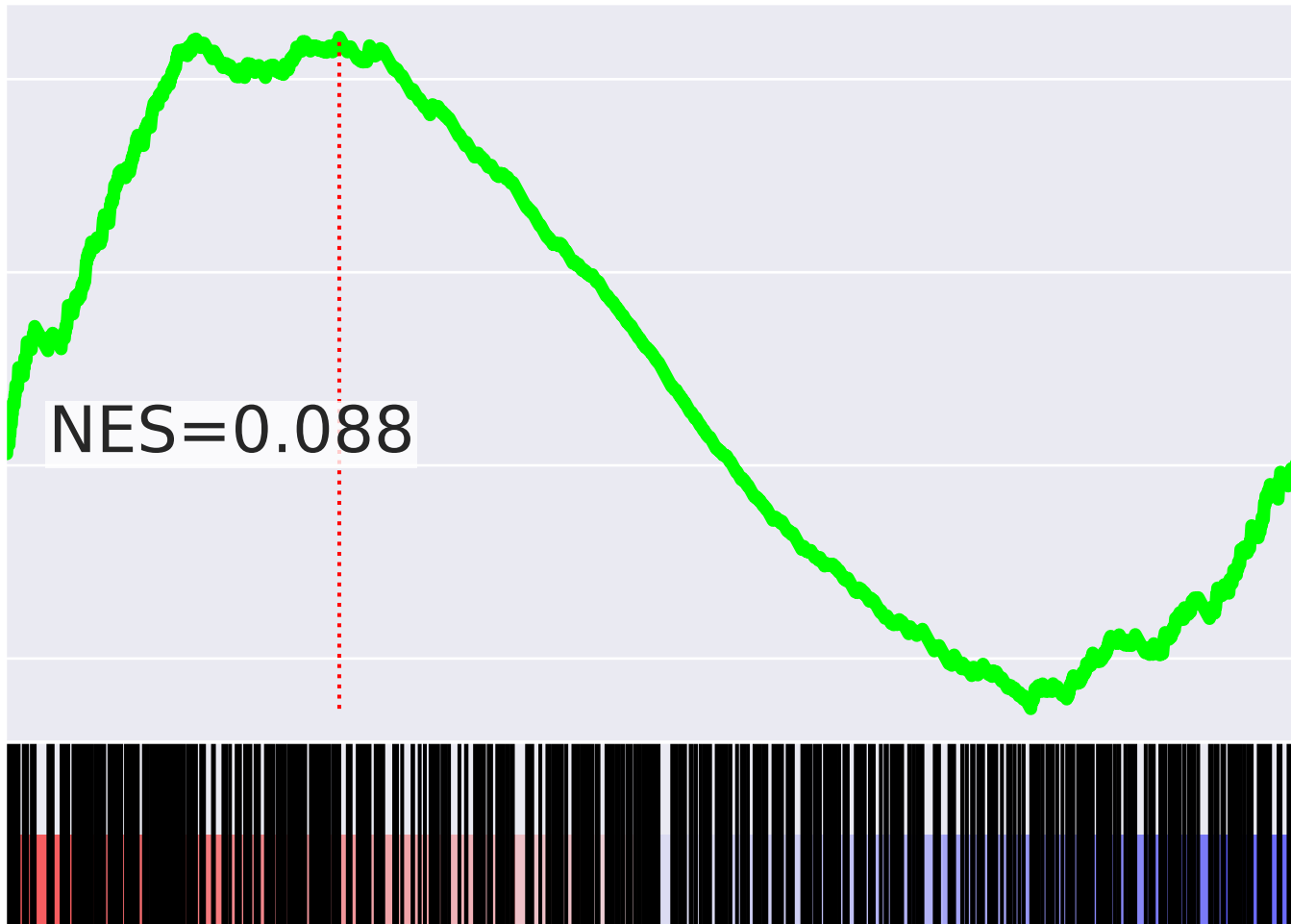
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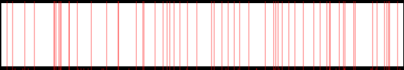
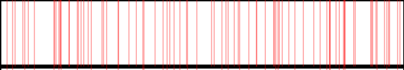
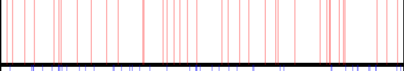
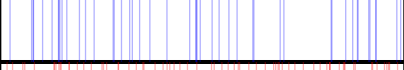
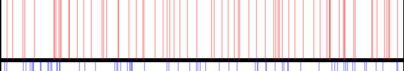
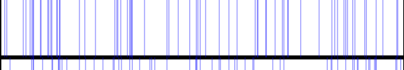
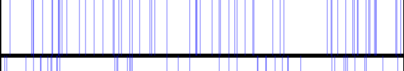
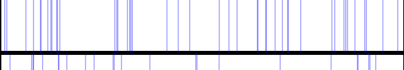
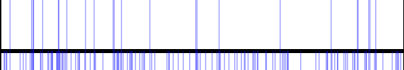
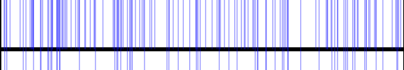
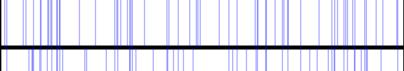

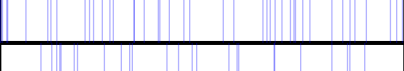

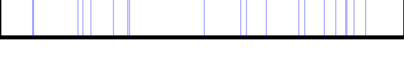
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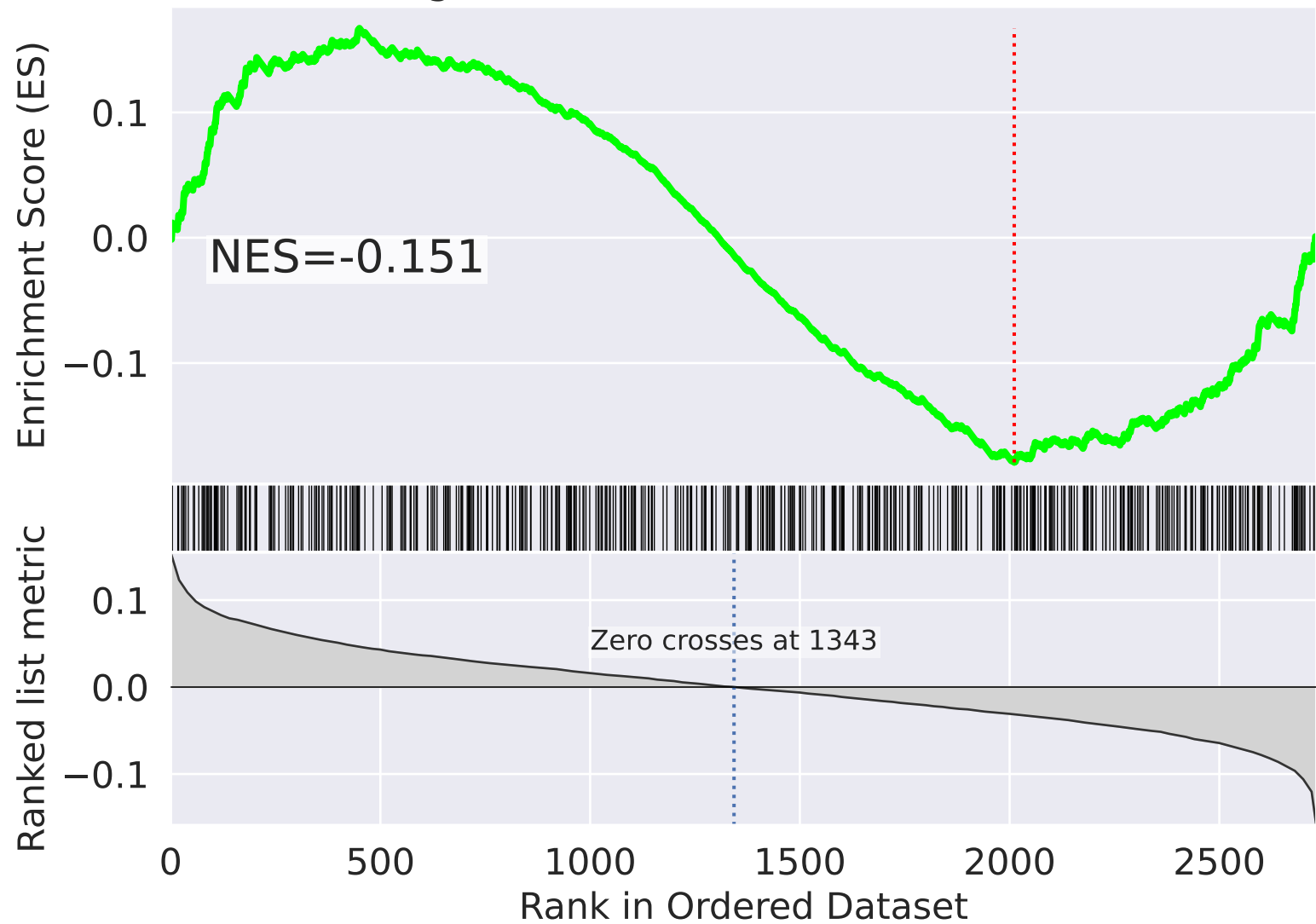
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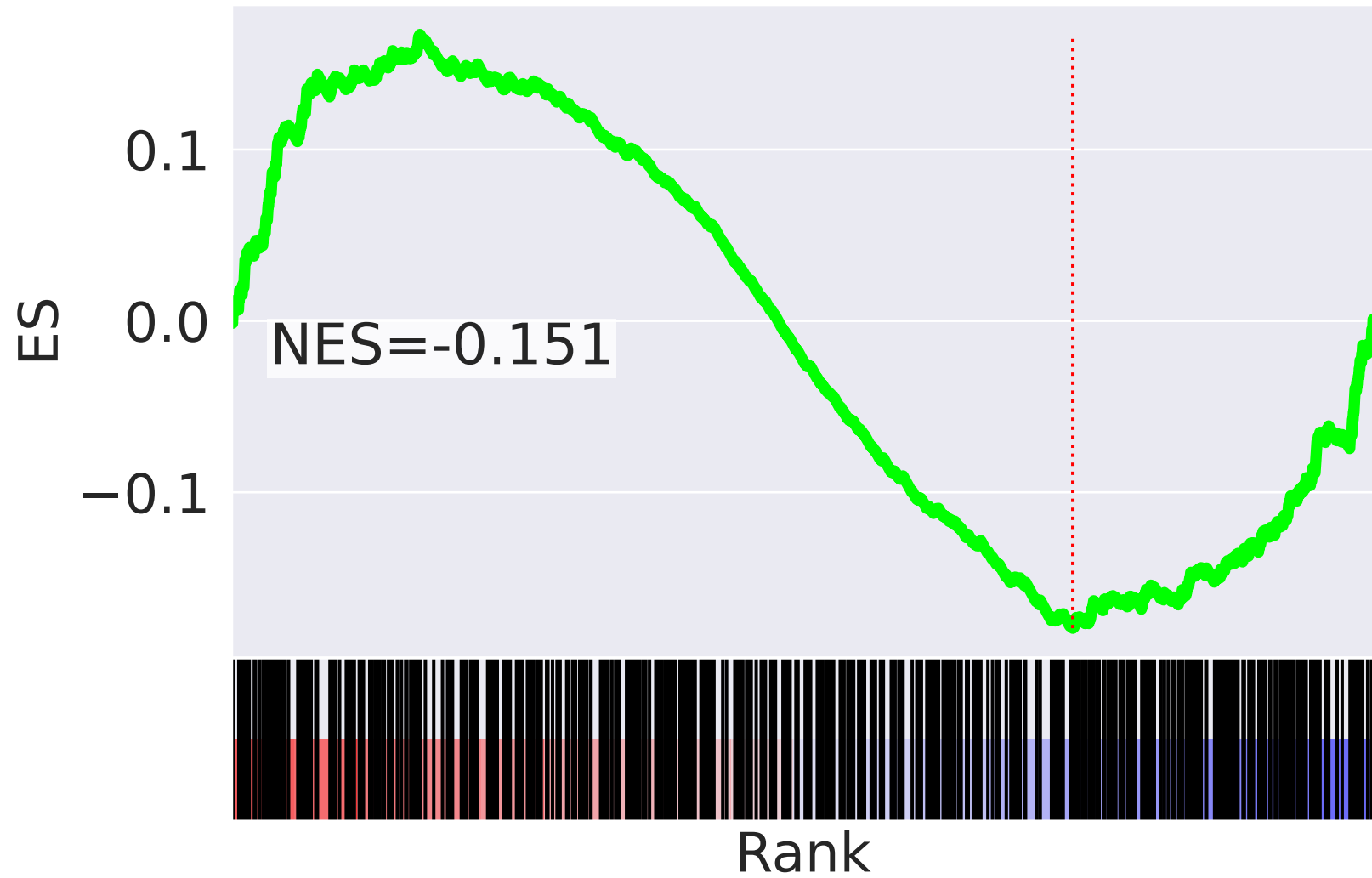
NES		SET
4.386		Respiratory Electron Transport R-HSA-611105
4.332		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.301		Complex I Biogenesis R-HSA-6799198
-4.282		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
4.176		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.849		DNA Double-Strand Break Repair R-HSA-5693532
-3.686		Nucleotide Excision Repair R-HSA-5696398
-3.622		Processing Of DNA Double-Strand Break Ends R-HSA-5693607
-3.573		DNA Damage Recognition In GG-NER R-HSA-5696394
-3.475		DNA Repair R-HSA-73894
-3.406		Homology Directed Repair R-HSA-5693538
-3.384		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
-3.337		SUMOylation Of DNA Damage Response And Repair Proteins R-HSA-3108214
-3.320		Activation Of ATR In Response To Replication Stress R-HSA-176187
-3.257		Selective Autophagy R-HSA-9663891

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=24$

Signal Transduction R-HSA-162582



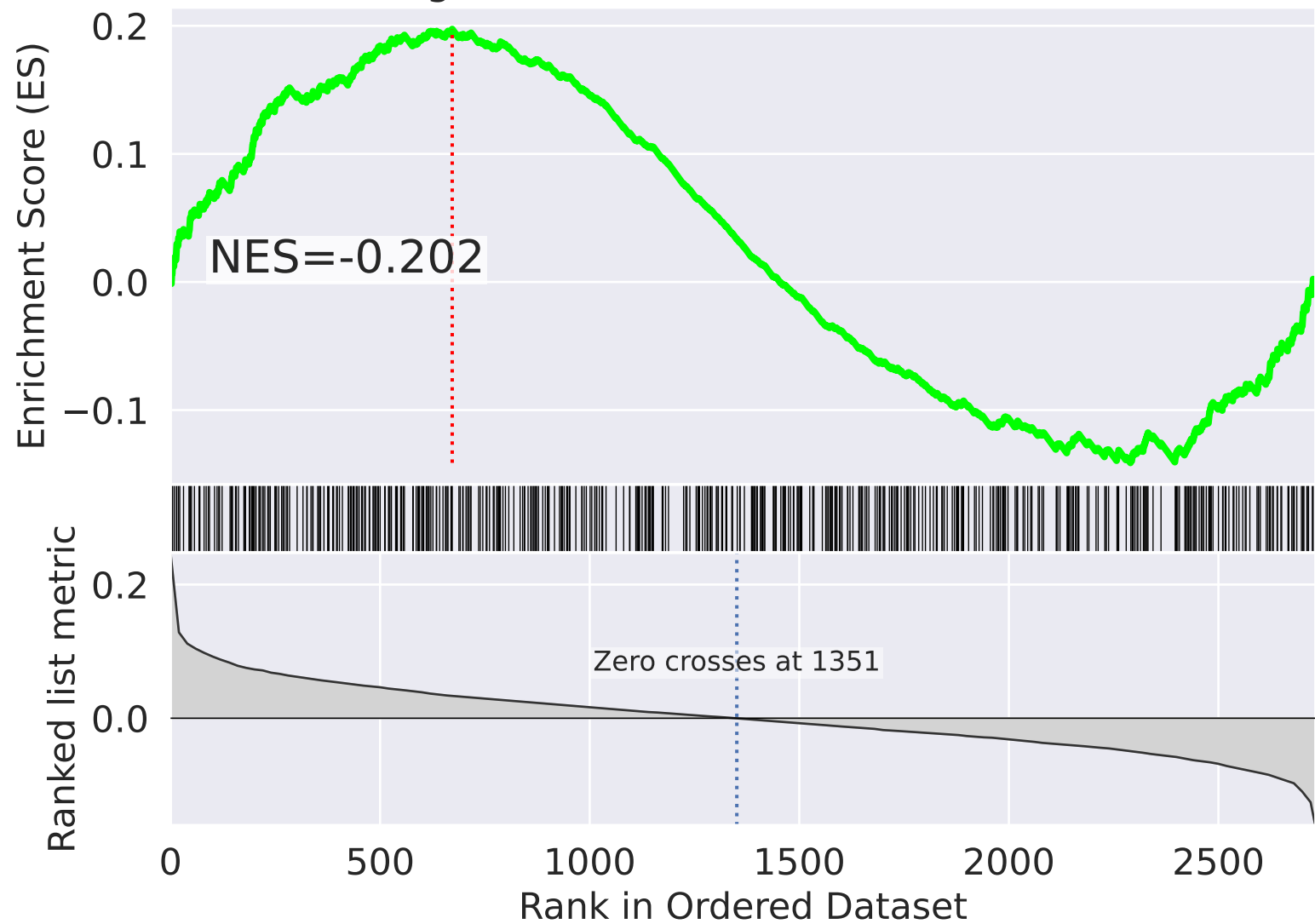
Signal Transduction R-HSA-162582



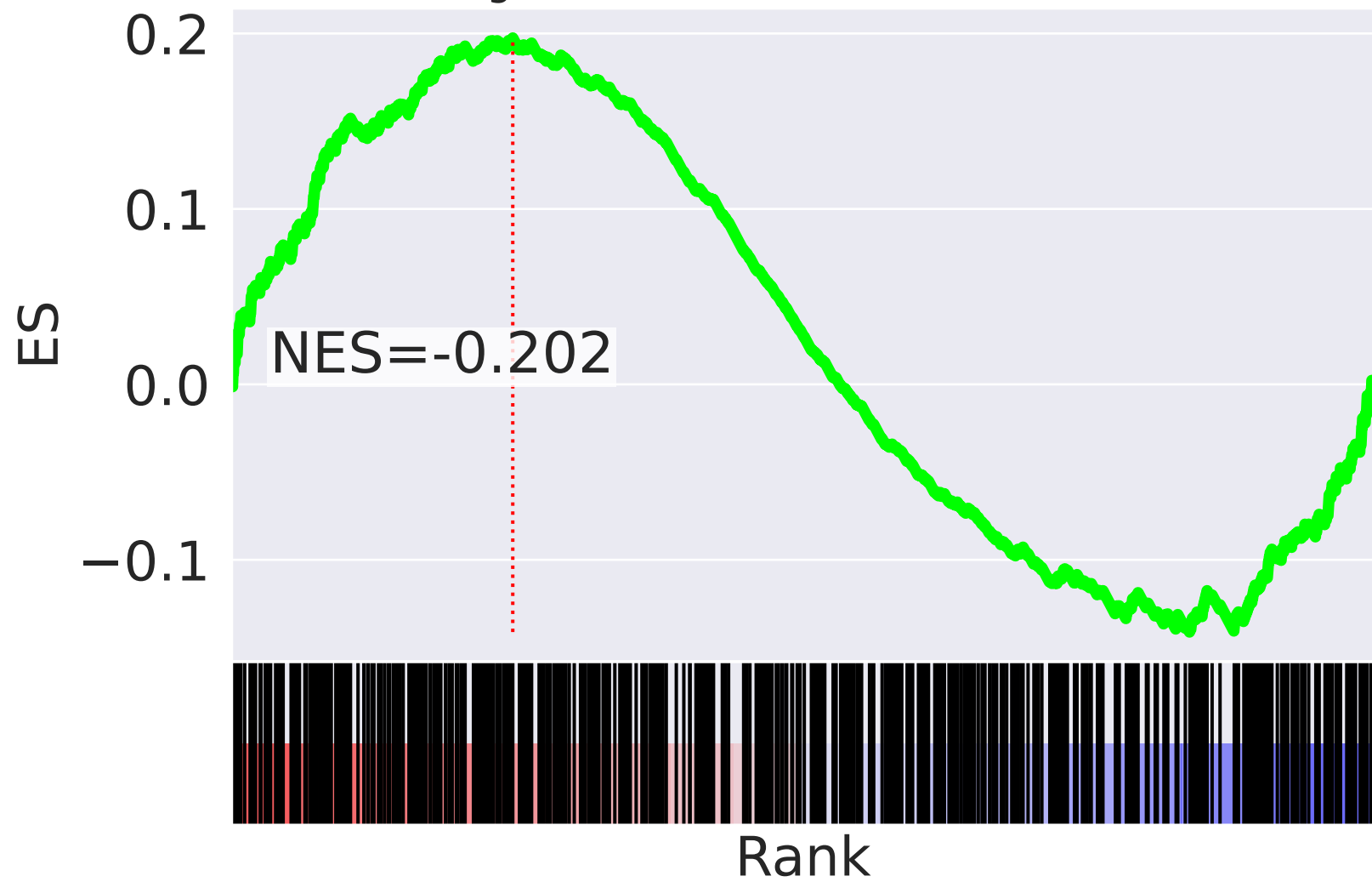
NES		SET
-3.746		tRNA Aminoacylation R-HSA-379724
-3.671		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
-3.545		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
-3.446		APC:Cdc20 Mediated Degradation Of Cell Cycle Proteins Before Cycle Checkpoint Satisfied R-HSA-179419
-3.446		Cdc20:Phospho-APC/C Mediated Degradation Of Cyclin A R-HSA-174184
3.439		Chromatin Modifying Enzymes R-HSA-3247509
-3.357		APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176409
-3.335		Activation Of APC/C And APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176814
3.307		HATs Acetylate Histones R-HSA-3214847
3.159		Base Excision Repair R-HSA-73884
-3.118		Mitotic Anaphase R-HSA-68882
-3.098		Mitotic Metaphase And Anaphase R-HSA-2555396
-3.071		HIV Infection R-HSA-162906
-3.028		Cyclin E Associated Events During G1/S Transition R-HSA-69202
-2.972		Cyclin A:Cdk2-associated Events At S Phase Entry R-HSA-69656

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=25$

Signal Transduction R-HSA-162582

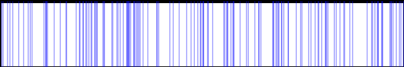
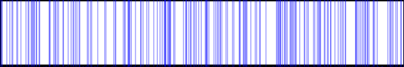
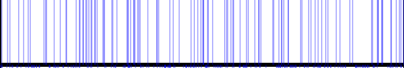
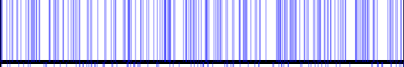
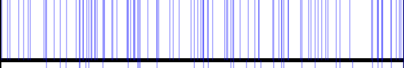
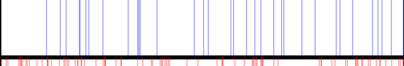
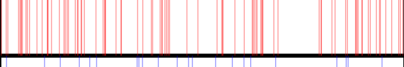
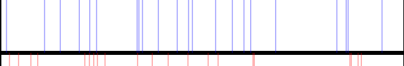
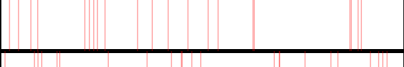
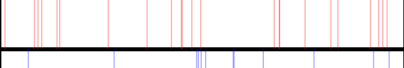
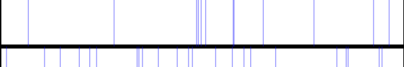
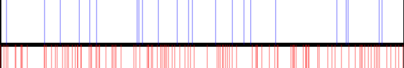
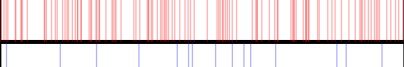
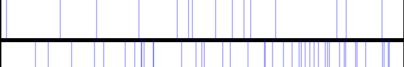
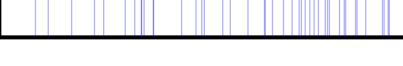


Signal Transduction R-HSA-162582



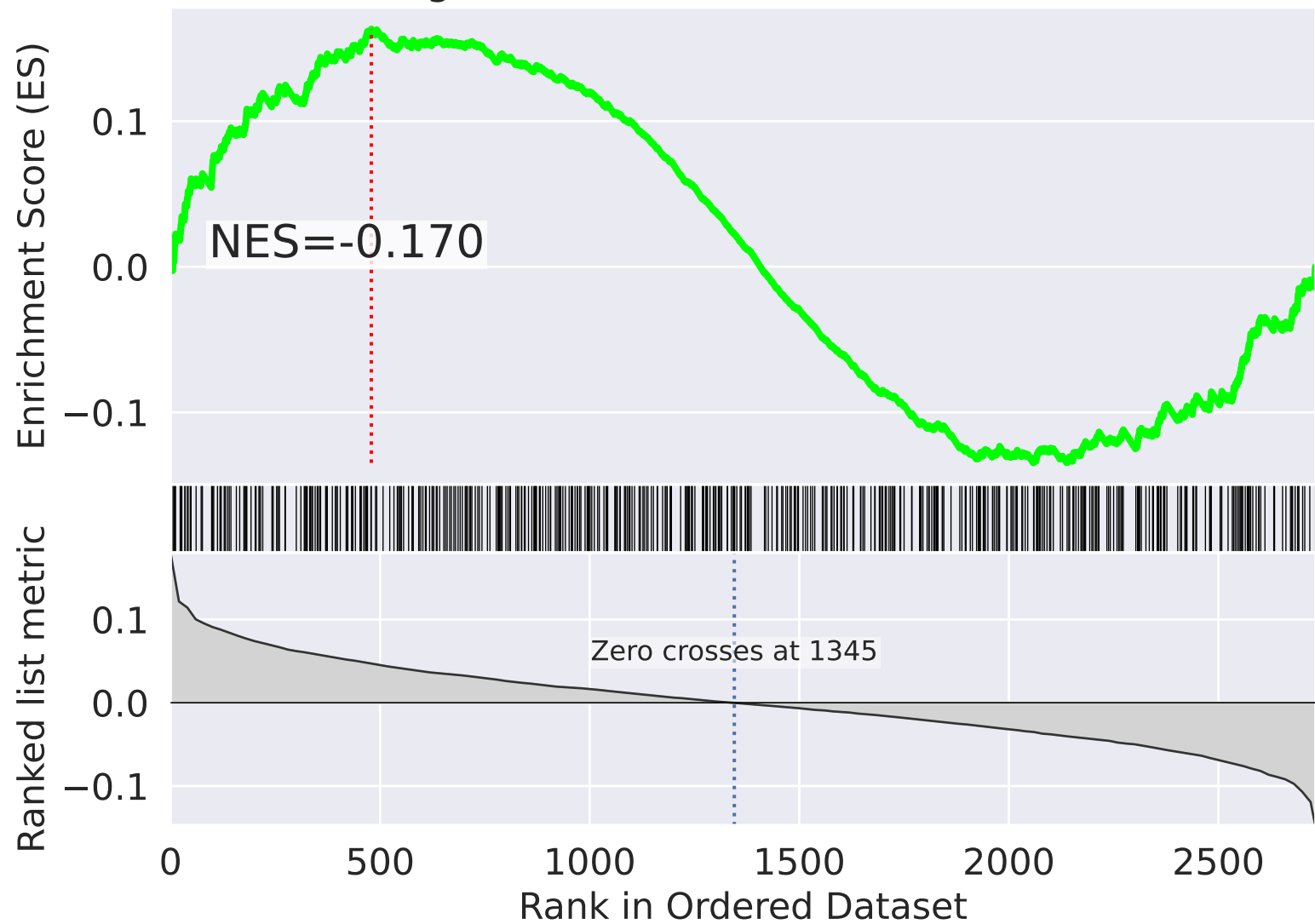
NES

SET

-4.021		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-3.472		Signaling By Rho GTPases R-HSA-194315
-3.458		mRNA Splicing R-HSA-72172
-3.309		Signaling By Rho GTPases, Miro GTPases And RHOBTB3 R-HSA-9716542
-3.301		mRNA Splicing - Major Pathway R-HSA-72163
-3.293		mRNA Splicing - Minor Pathway R-HSA-72165
3.174		Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.026		RNA Polymerase III Transcription Initiation R-HSA-76046
2.992		PKMTs Methylate Histone Lysines R-HSA-3214841
2.966		Metabolism Of Nucleotides R-HSA-15869
-2.920		mTORC1-mediated Signaling R-HSA-166208
-2.911		RNA Polymerase III Abortive And Retractive Initiation R-HSA-749476
2.910		Transport Of Small Molecules R-HSA-382551
-2.899		RNA Polymerase III Transcription Initiation From Type 3 Promoter R-HSA-76071
-2.872		G2/M DNA Damage Checkpoint R-HSA-69473

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=26$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

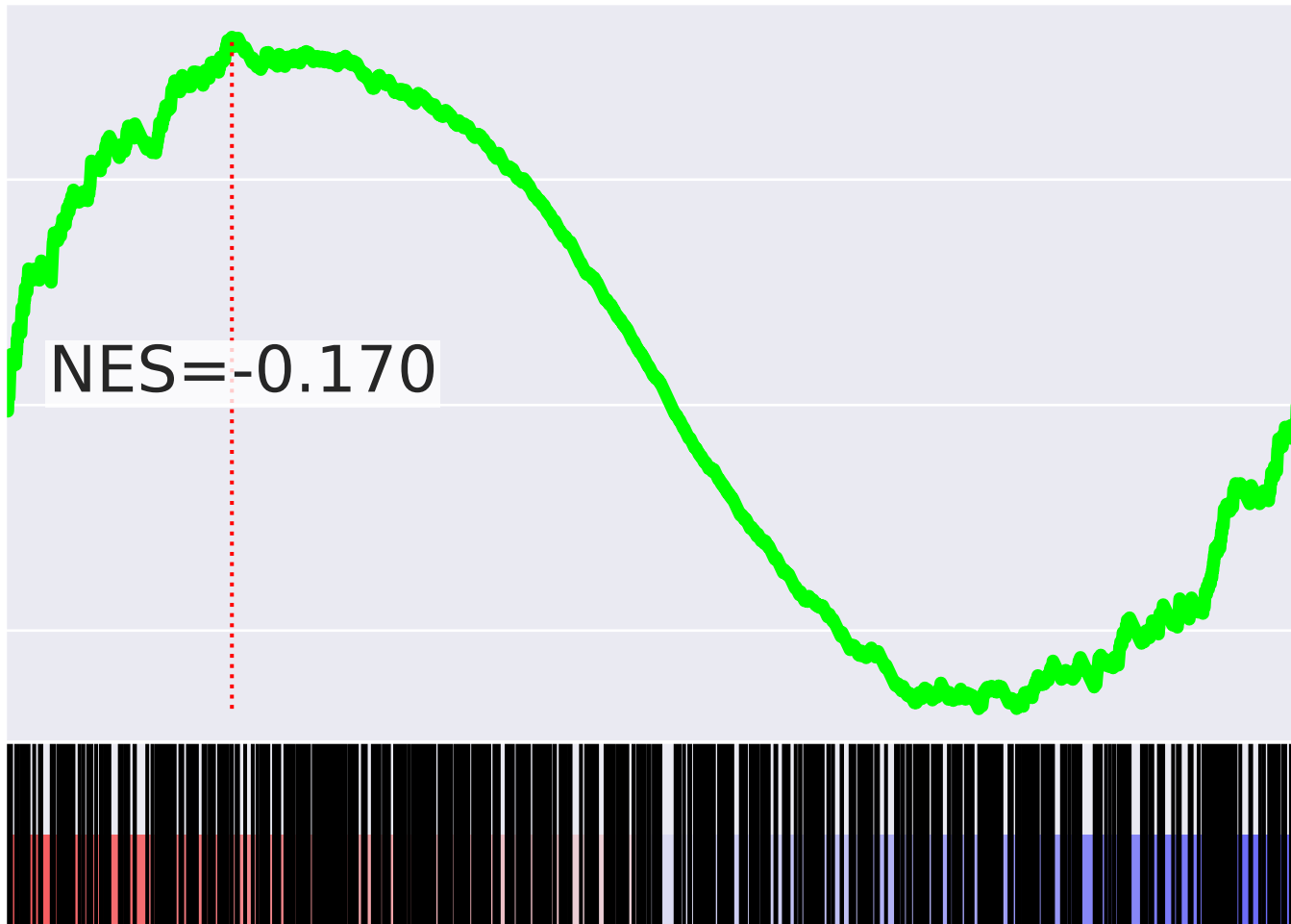
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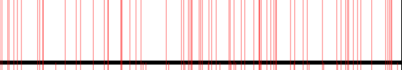
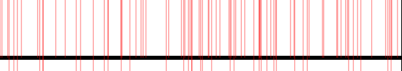
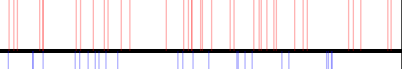
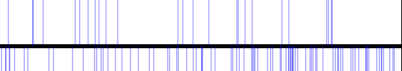
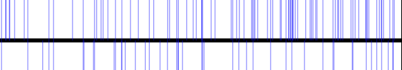
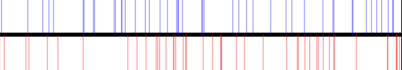
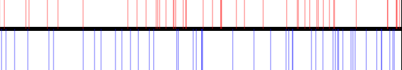
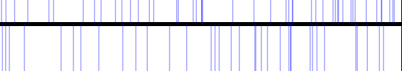
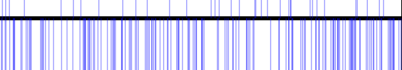
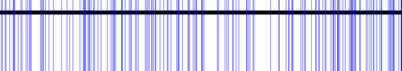
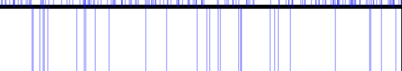



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-0.1

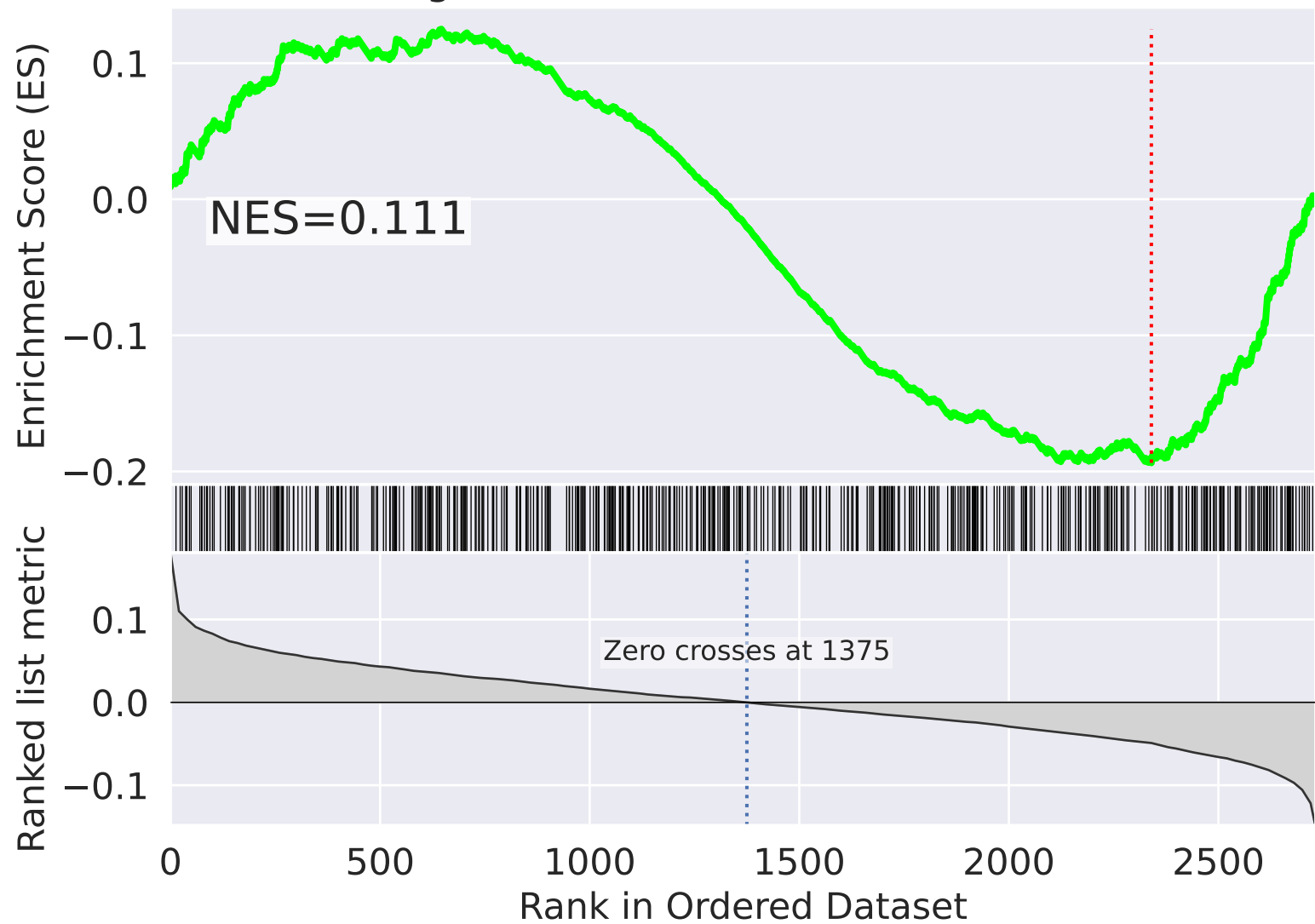
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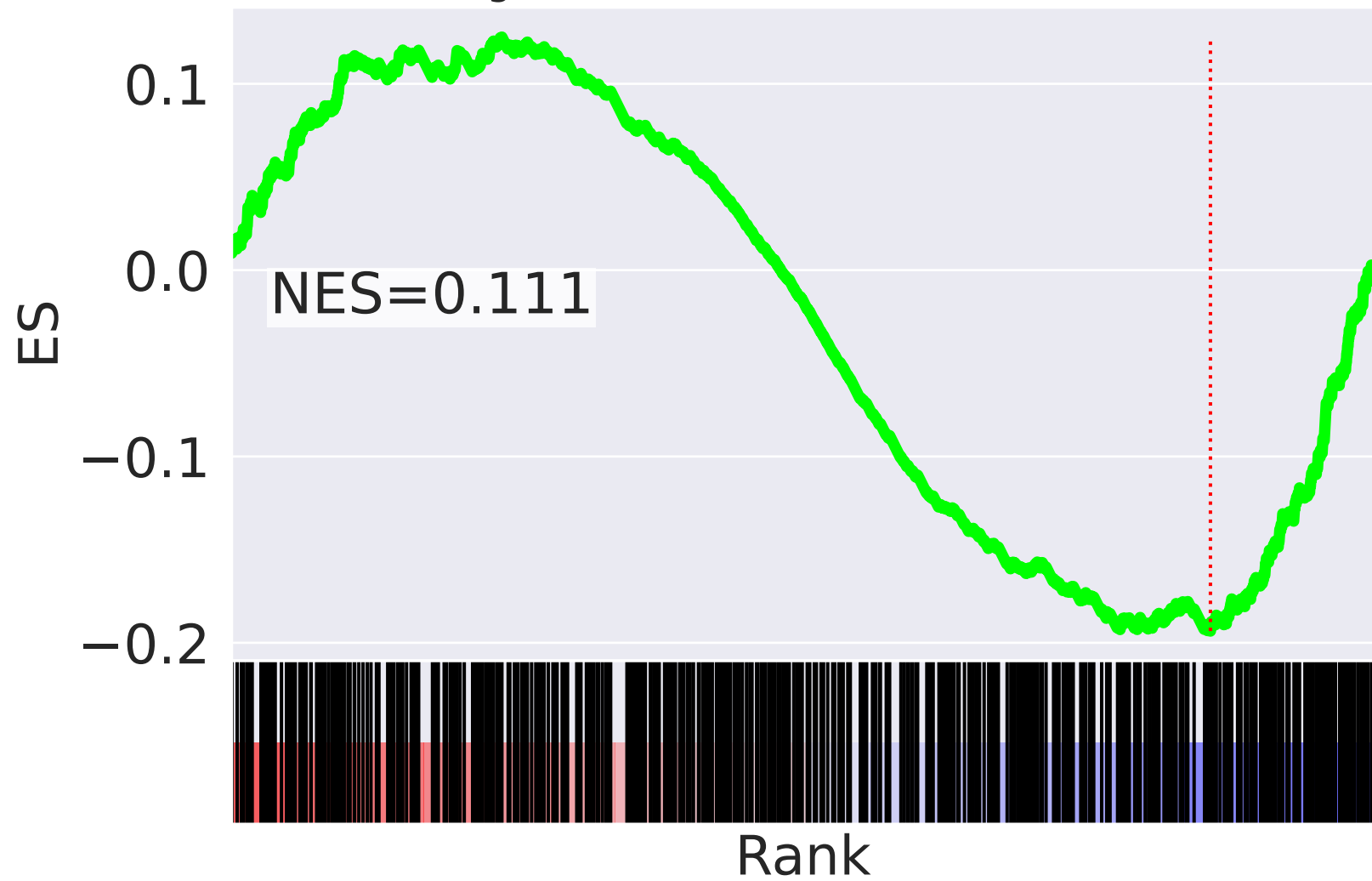
NES		SET
5.014		Respiratory Electron Transport R-HSA-611105
4.781		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.551		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.166		Complex I Biogenesis R-HSA-6799198
-4.062		Fanconi Anemia Pathway R-HSA-6783310
-3.639		Asparagine N-linked Glycosylation R-HSA-446203
-3.563		Golgi-to-ER Retrograde Transport R-HSA-8856688
3.525		Transcription Of HIV Genome R-HSA-167172
-3.193		ER To Golgi Anterograde Transport R-HSA-199977
-3.177		Diseases Of Metabolism R-HSA-5668914
-3.116		Membrane Trafficking R-HSA-199991
-3.052		Vesicle-mediated Transport R-HSA-5653656
-3.028		Extension Of Telomeres R-HSA-180786
3.010		DNA Damage/Telomere Stress Induced Senescence R-HSA-2559586
-3.006		COPII-mediated Vesicle Transport R-HSA-204005

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=27$

Signal Transduction R-HSA-162582



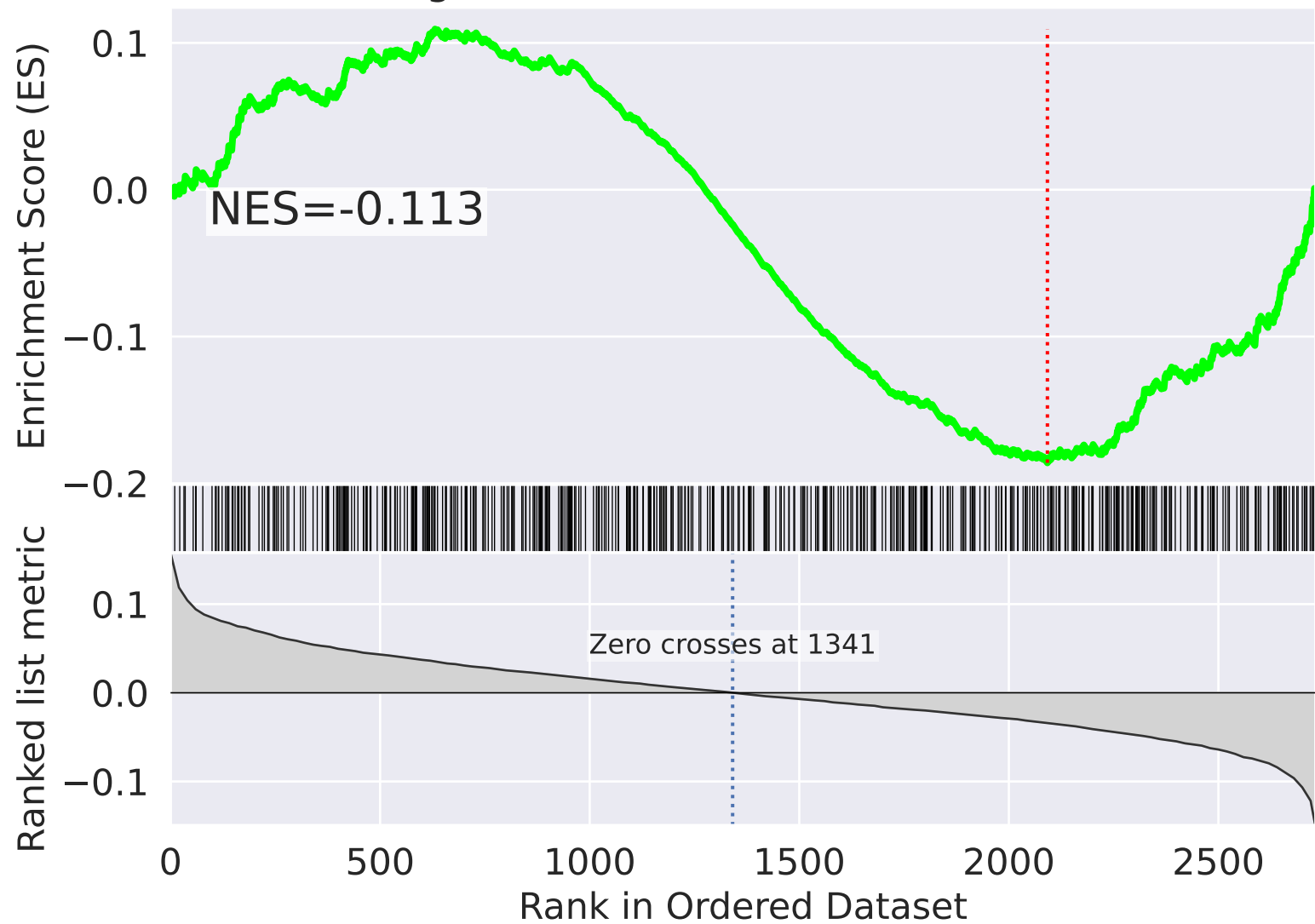
Signal Transduction R-HSA-162582



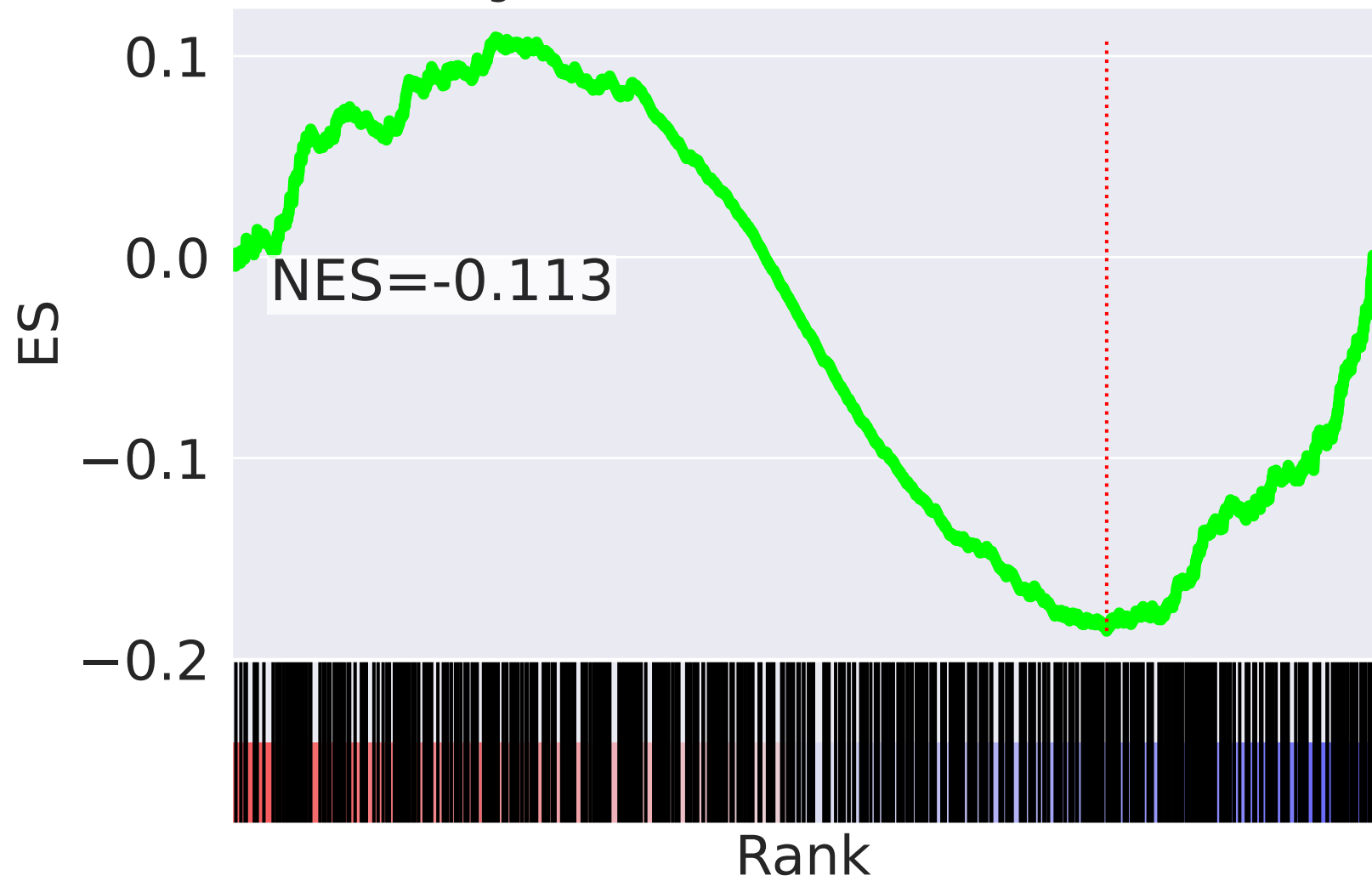
NES	SET
3.980	Respiratory Electron Transport R-HSA-611105
3.942	Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.557	Complex I Biogenesis R-HSA-6799198
3.199	Ubiquitin-dependent Degradation Of Cyclin D R-HSA-75815
3.199	Regulation Of PTEN Stability And Activity R-HSA-8948751
3.126	Metabolism Of Amino Acids And Derivatives R-HSA-71291
-3.107	tRNA Aminoacylation R-HSA-379724
3.104	Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.101	Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
3.077	RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
3.076	Citric Acid Cycle (TCA Cycle) R-HSA-71403
3.069	ER-Phagosome Pathway R-HSA-1236974
3.059	TNFR2 Non-Canonical NF-kB Pathway R-HSA-5668541
3.057	Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
3.050	Signaling By B Cell Receptor (BCR) R-HSA-983705

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=28$

Signal Transduction R-HSA-162582



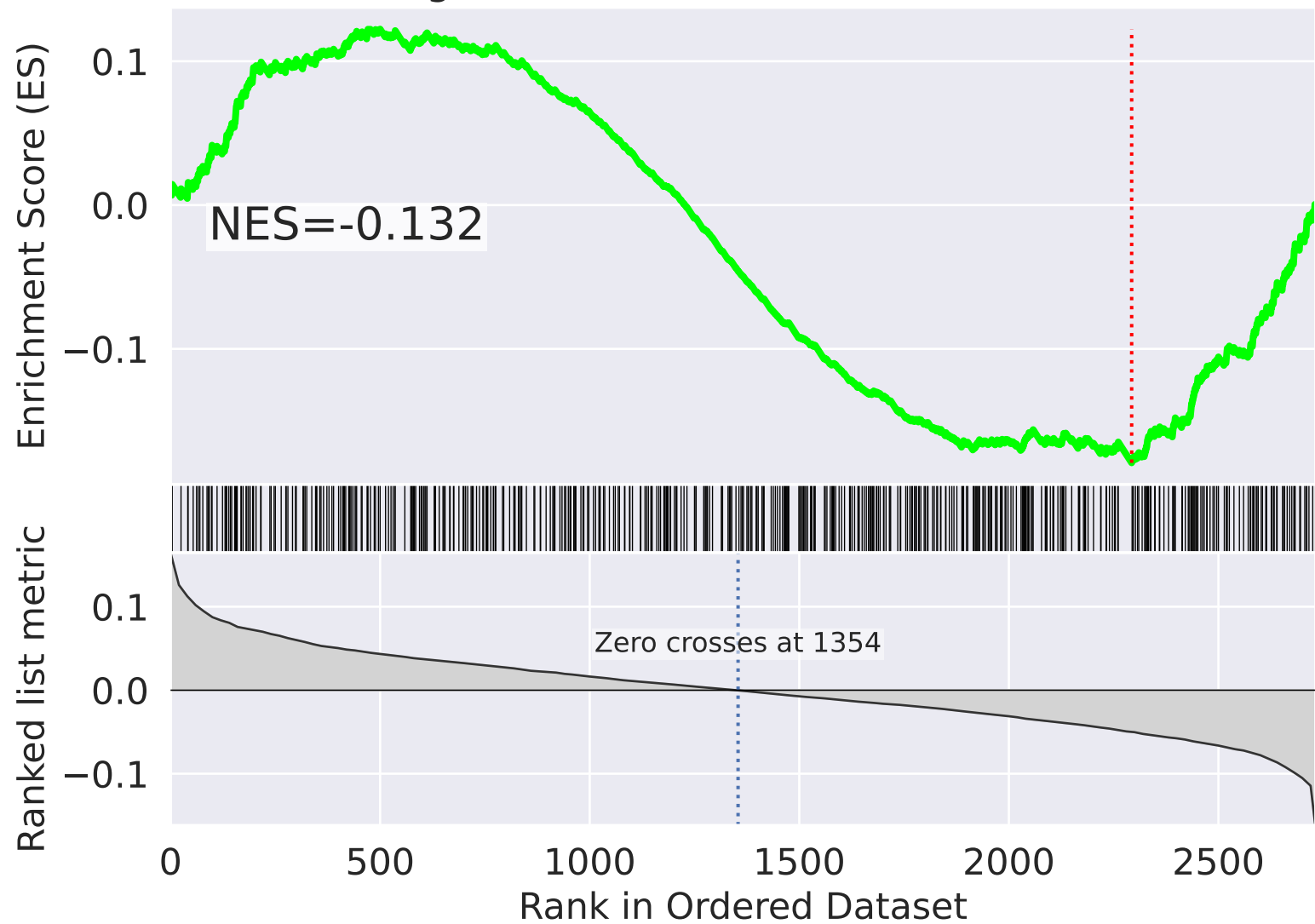
Signal Transduction R-HSA-162582



NES		SET
-3.437		Metabolism Of Non-Coding RNA R-HSA-194441
-3.345		Glycolysis R-HSA-70171
-3.317		SUMOylation Of DNA Damage Response And Repair Proteins R-HSA-3108214
-3.266		Metabolism Of Carbohydrates R-HSA-71387
-3.123		Glucose Metabolism R-HSA-70326
3.075		Respiratory Electron Transport R-HSA-611105
-3.011		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
-2.981		Golgi-to-ER Retrograde Transport R-HSA-8856688
-2.973		Cellular Response To Heat Stress R-HSA-3371556
-2.919		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
-2.915		HIV Life Cycle R-HSA-162587
-2.885		Nucleotide Excision Repair R-HSA-5696398
2.856		Synthesis Of PIPs At Late Endosome Membrane R-HSA-1660517
-2.842		Late Phase Of HIV Life Cycle R-HSA-162599
2.837		mRNA 3-End Processing R-HSA-72187

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=29$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

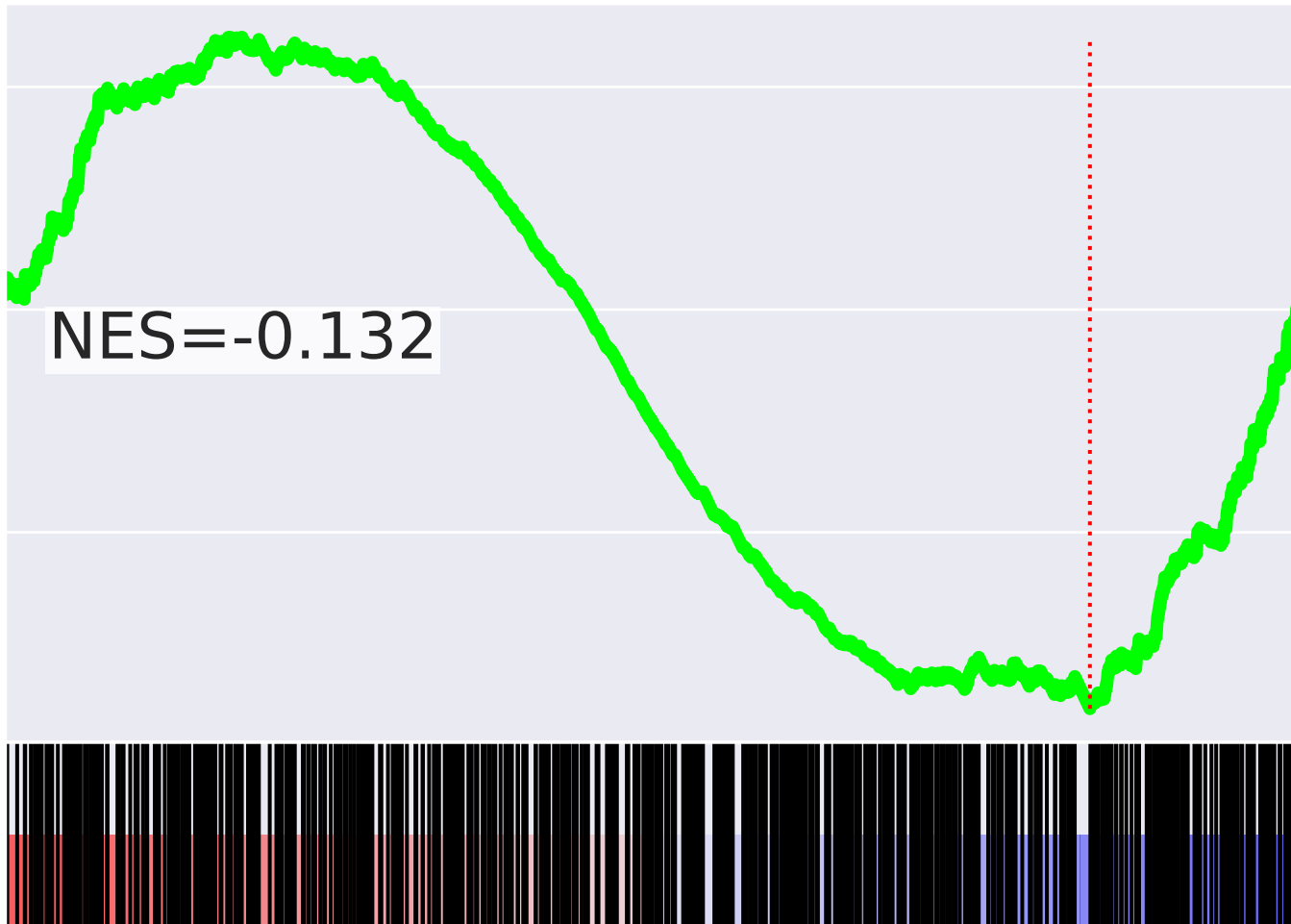
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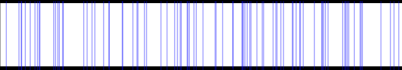
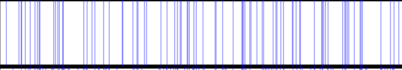
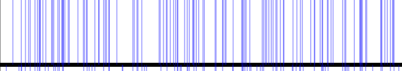
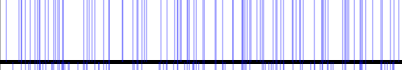
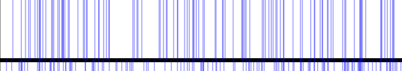
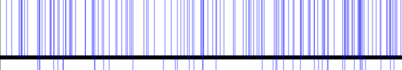
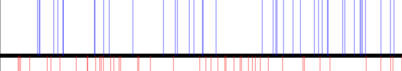
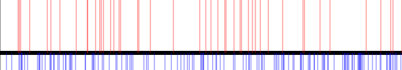
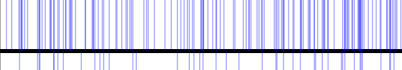
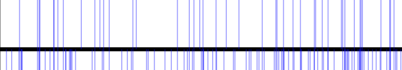
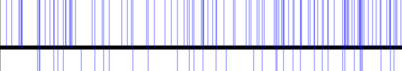
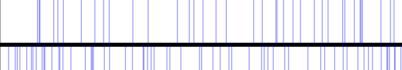
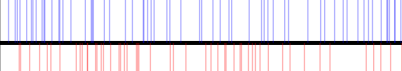
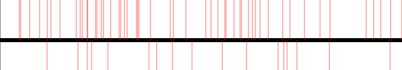

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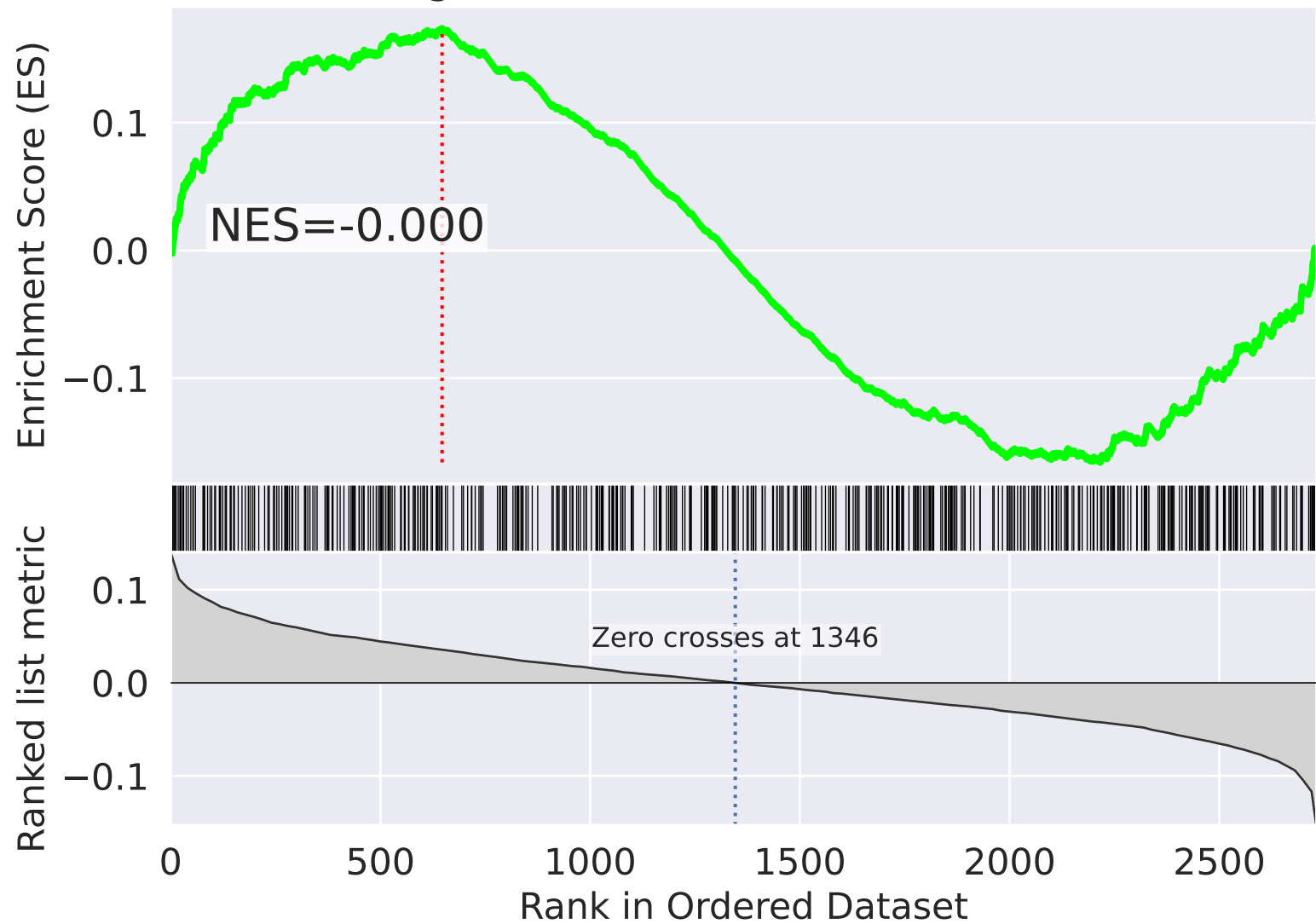
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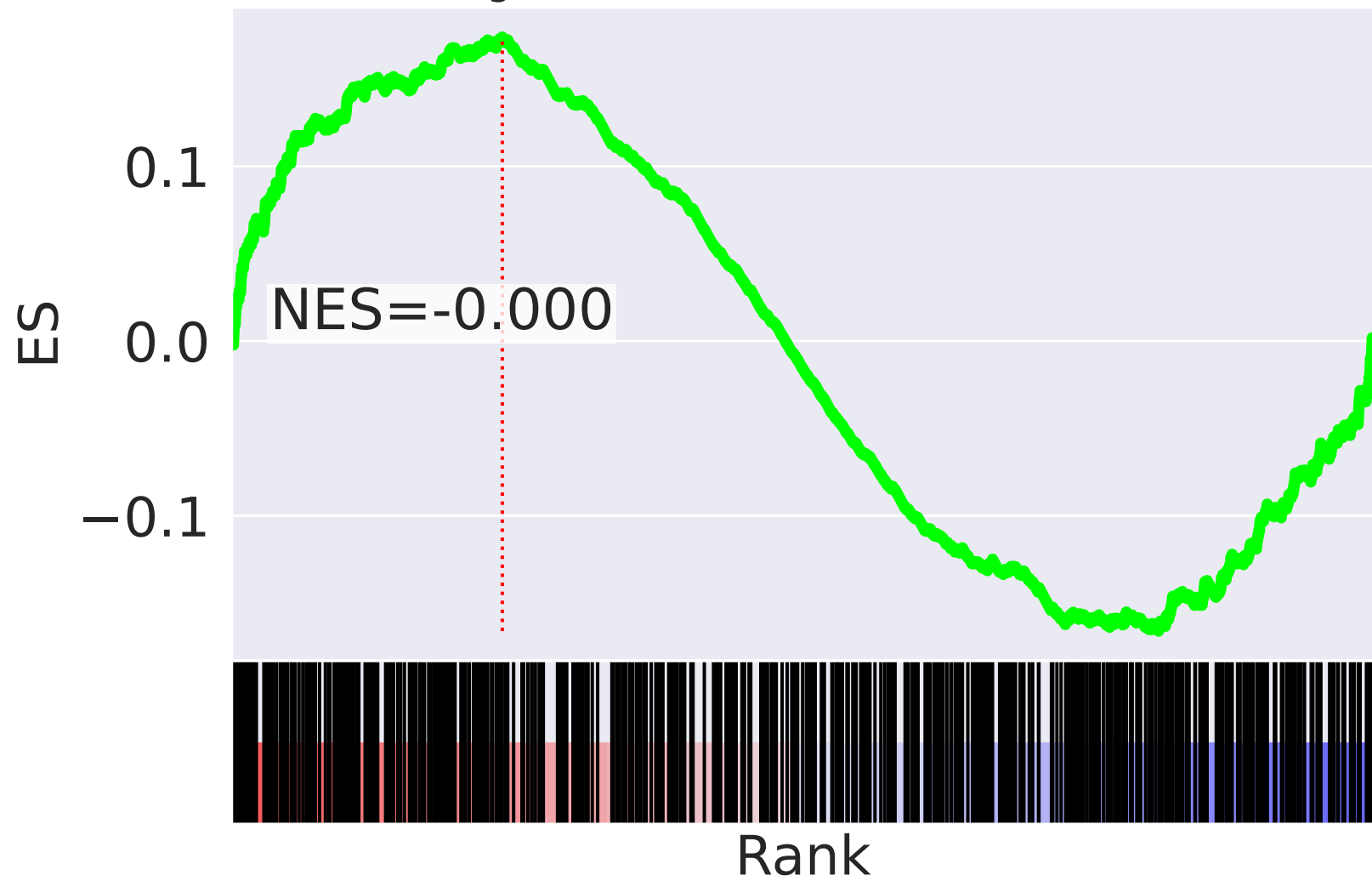
NES		SET
-4.223		MAPK1/MAPK3 Signaling R-HSA-5684996
-4.024		RAF/MAP Kinase Cascade R-HSA-5673001
-3.890		Nervous System Development R-HSA-9675108
-3.688		MAPK Family Signaling Cascades R-HSA-5683057
-3.608		Axon Guidance R-HSA-422475
-3.600		Mitotic Metaphase And Anaphase R-HSA-2555396
-3.480		Oxygen-dependent Proline Hydroxylation Of Hypoxia-inducible Factor Alpha R-HSA-1234176
3.464		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
-3.435		Mitotic Anaphase R-HSA-68882
-3.412		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
-3.198		Separation Of Sister Chromatids R-HSA-2467813
-3.174		SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
-3.159		tRNA Processing R-HSA-72306
3.158		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
3.157		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243


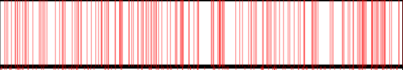
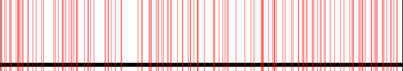
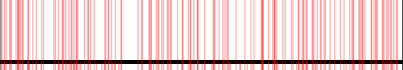
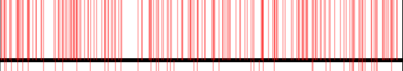
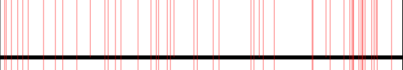
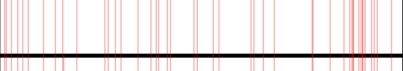
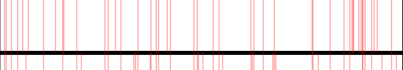
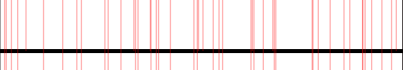
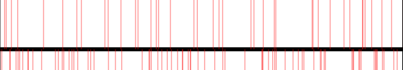
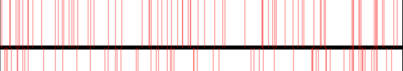
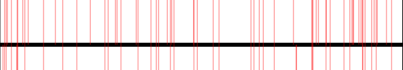
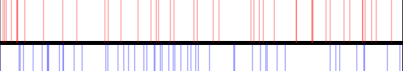
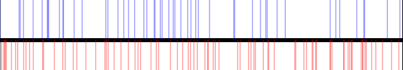
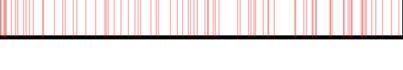
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=30$

Signal Transduction R-HSA-162582



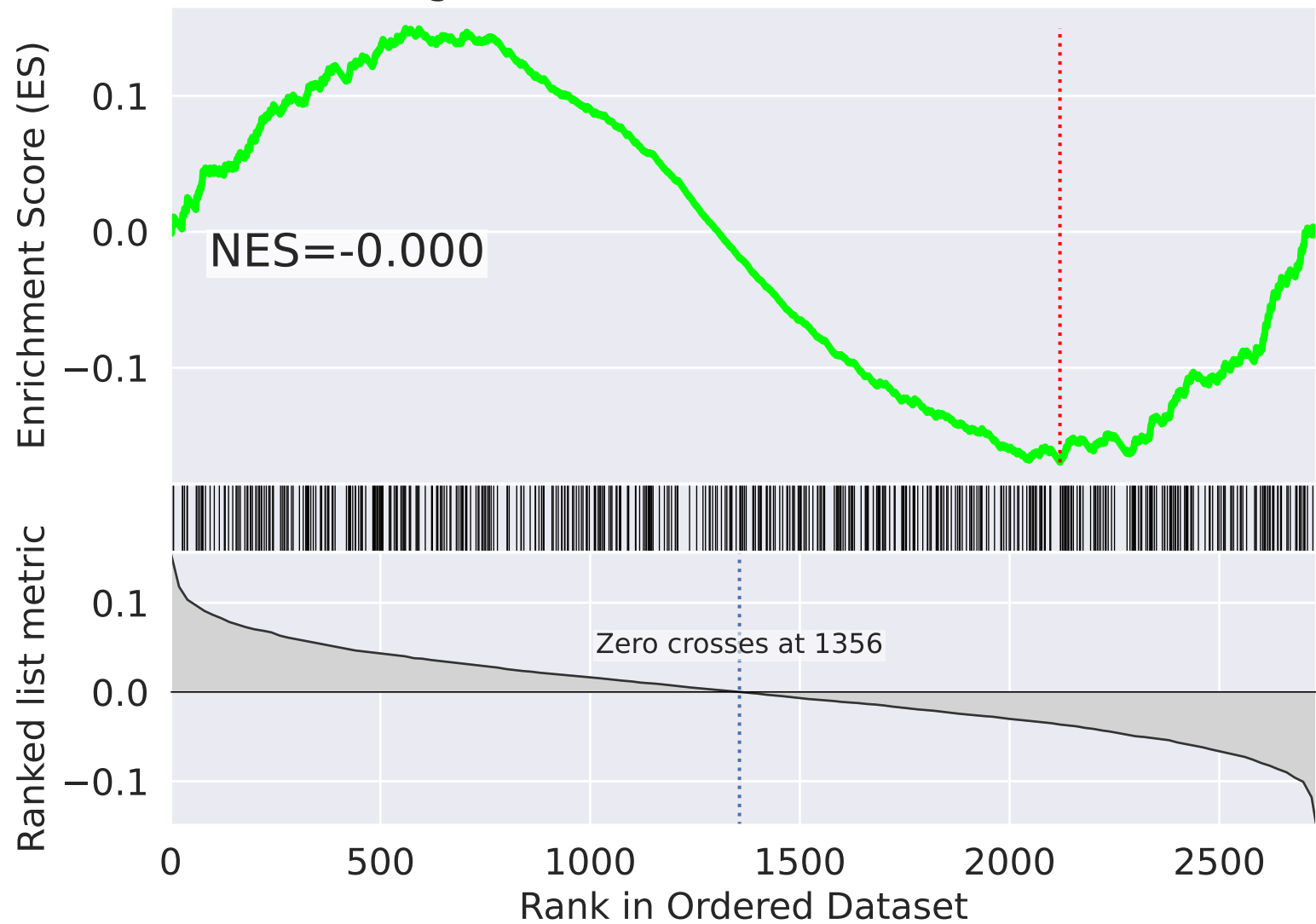
Signal Transduction R-HSA-162582



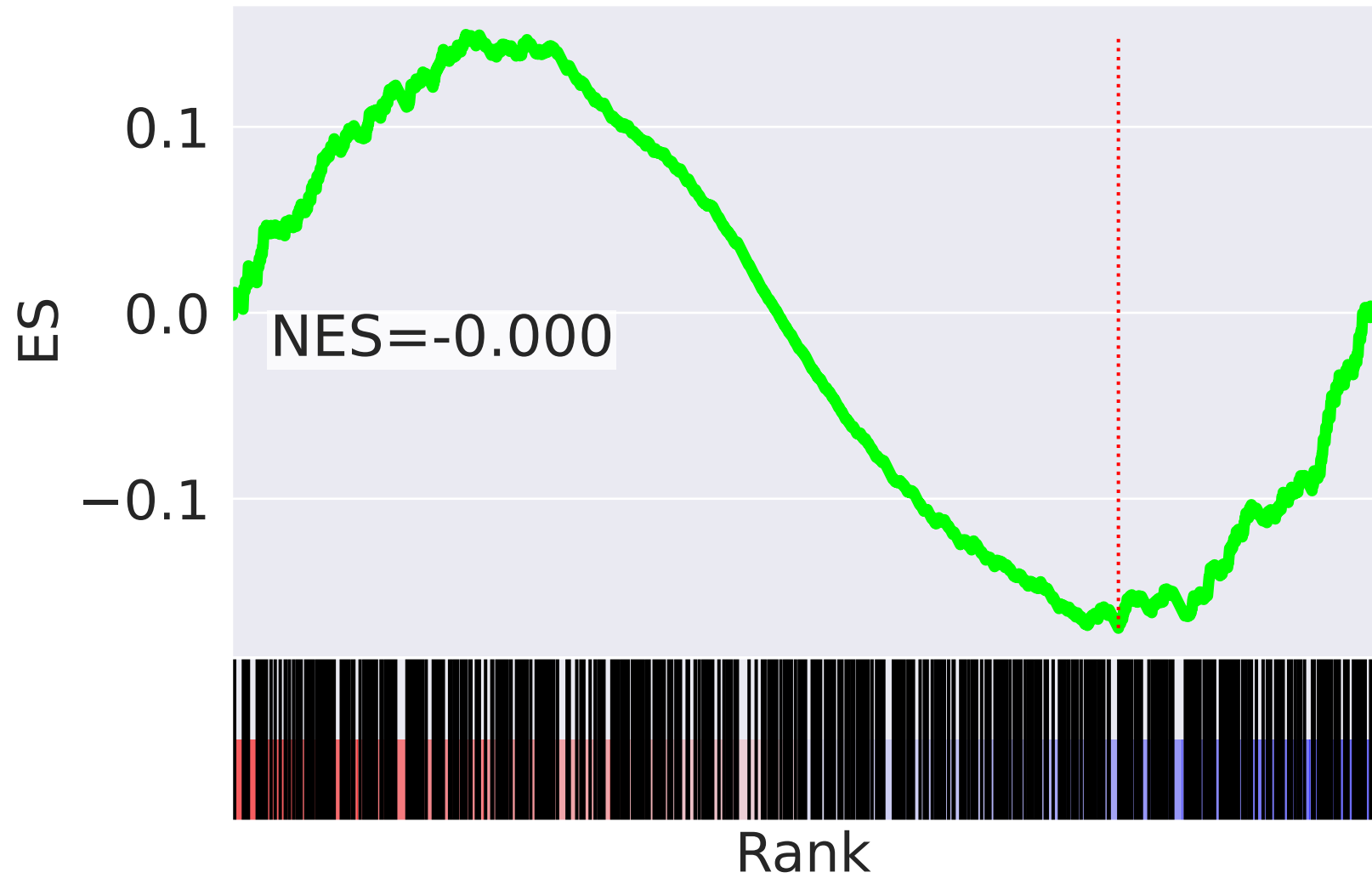
NES		SET
5.376		Separation Of Sister Chromatids R-HSA-2467813
4.708		Adaptive Immune System R-HSA-1280218
4.641		Mitotic Anaphase R-HSA-68882
4.565		Mitotic Metaphase And Anaphase R-HSA-2555396
4.552		M Phase R-HSA-68886
4.382		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
3.993		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
3.979		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
3.978		Beta-catenin Independent WNT Signaling R-HSA-3858494
3.930		PCP/CE Pathway R-HSA-4086400
3.918		Mitotic Spindle Checkpoint R-HSA-69618
3.797		Switching Of Origins To A Post-Replicative State R-HSA-69052
3.773		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
-3.767		Protein Localization R-HSA-9609507
3.757		RAF/MAP Kinase Cascade R-HSA-5673001


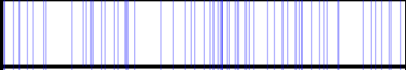
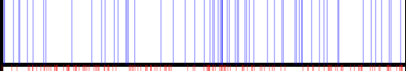
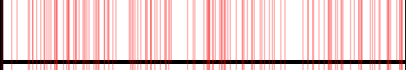
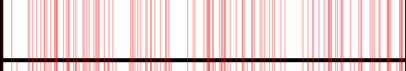
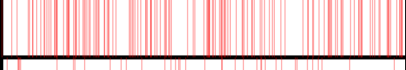
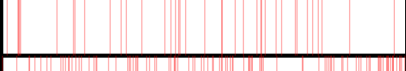
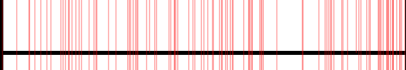
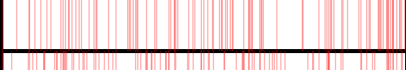
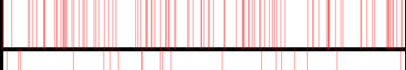
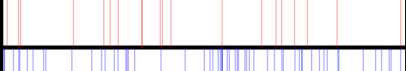
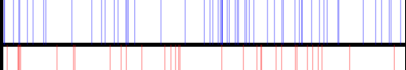
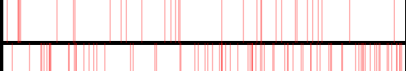
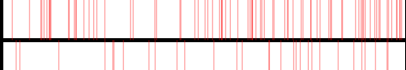

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=31$

Signal Transduction R-HSA-162582



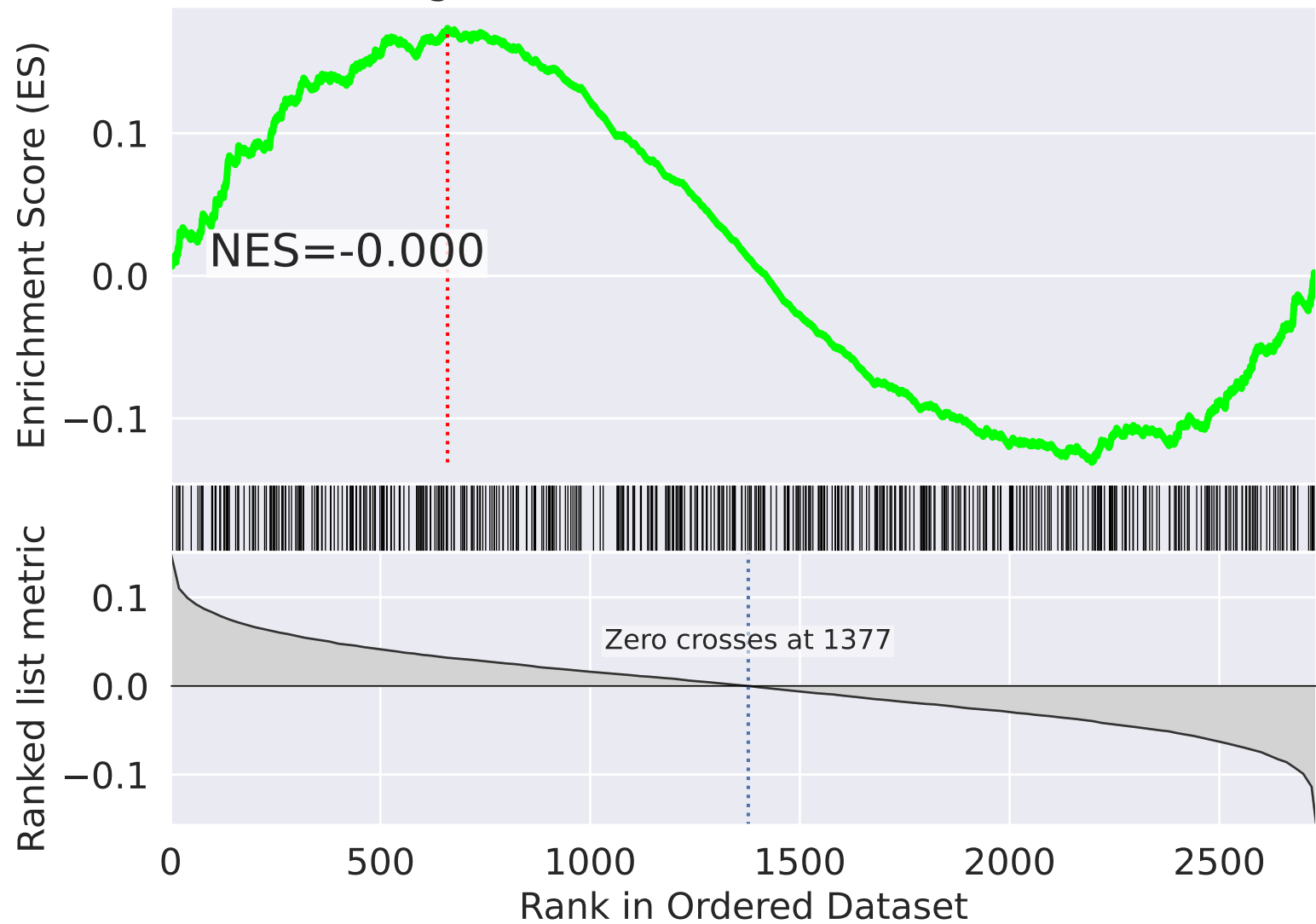
Signal Transduction R-HSA-162582



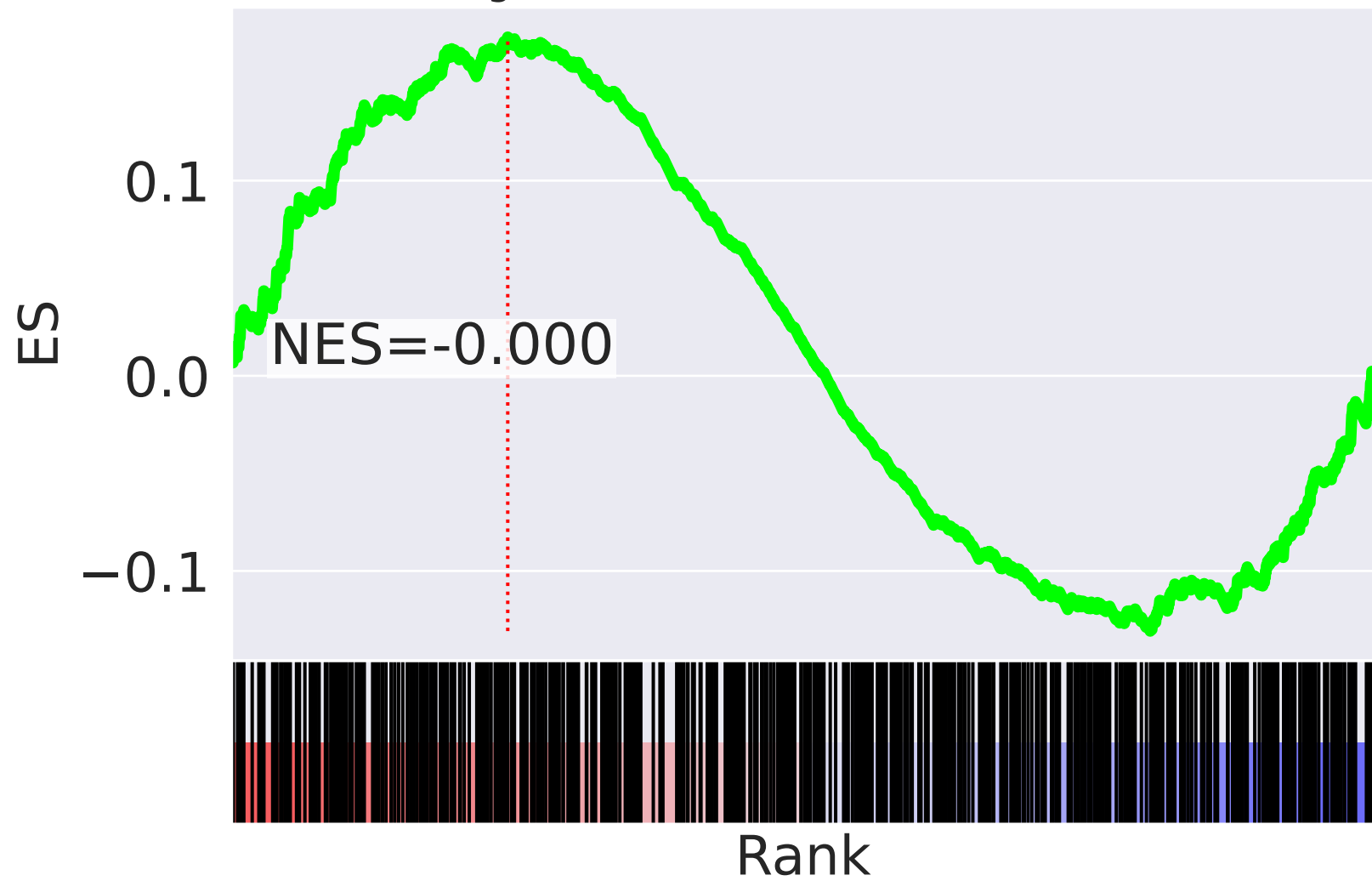
NES		SET
4.132		M Phase R-HSA-68886
-4.045		rRNA Processing R-HSA-72312
-3.943		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.888		Mitotic Anaphase R-HSA-68882
3.886		Separation Of Sister Chromatids R-HSA-2467813
3.851		Mitotic Metaphase And Anaphase R-HSA-2555396
3.676		Cellular Response To Starvation R-HSA-9711097
3.667		Mitotic G2-G2/M Phases R-HSA-453274
3.565		G2/M Transition R-HSA-69275
3.542		Mitotic Prometaphase R-HSA-68877
3.525		Ion Channel Transport R-HSA-983712
-3.517		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.462		Amino Acids Regulate mTORC1 R-HSA-9639288
3.418		RAF/MAP Kinase Cascade R-HSA-5673001
3.337		COPI-dependent Golgi-to-ER Retrograde Traffic R-HSA-6811434

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=32$

Signal Transduction R-HSA-162582

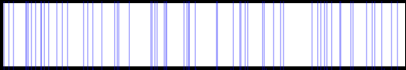
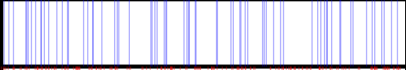
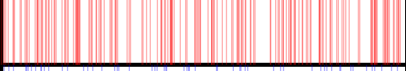
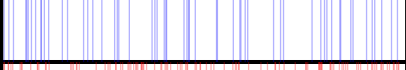
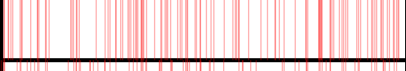
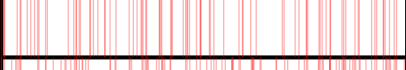
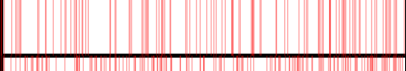
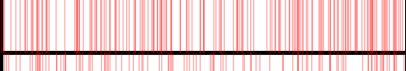
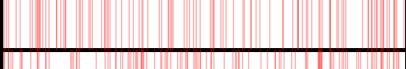
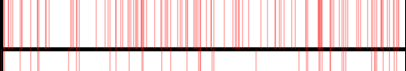
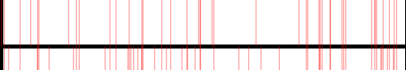
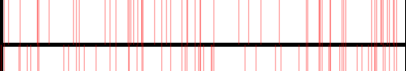
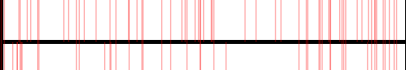
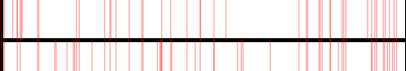



Signal Transduction R-HSA-162582



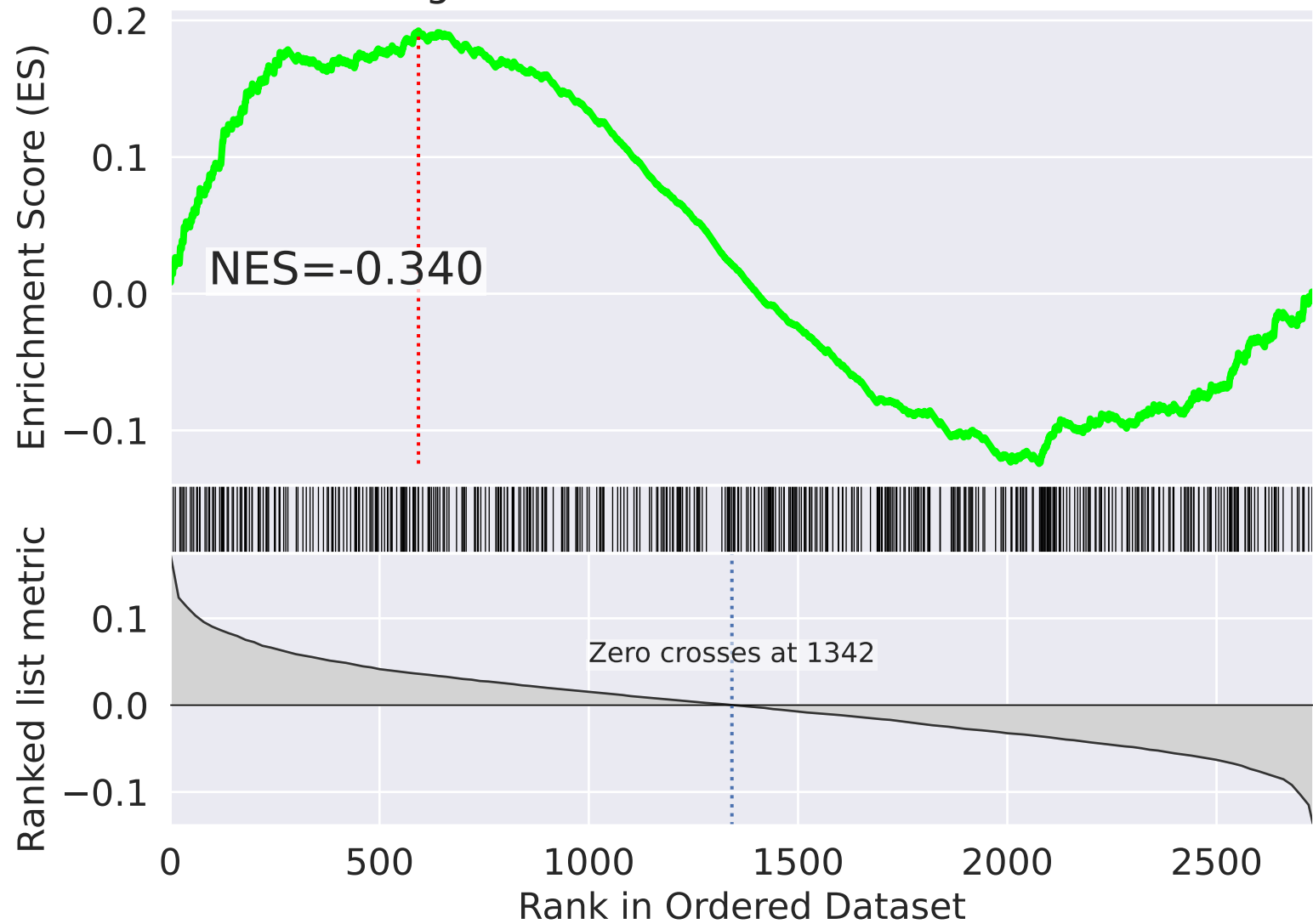
NES

SET

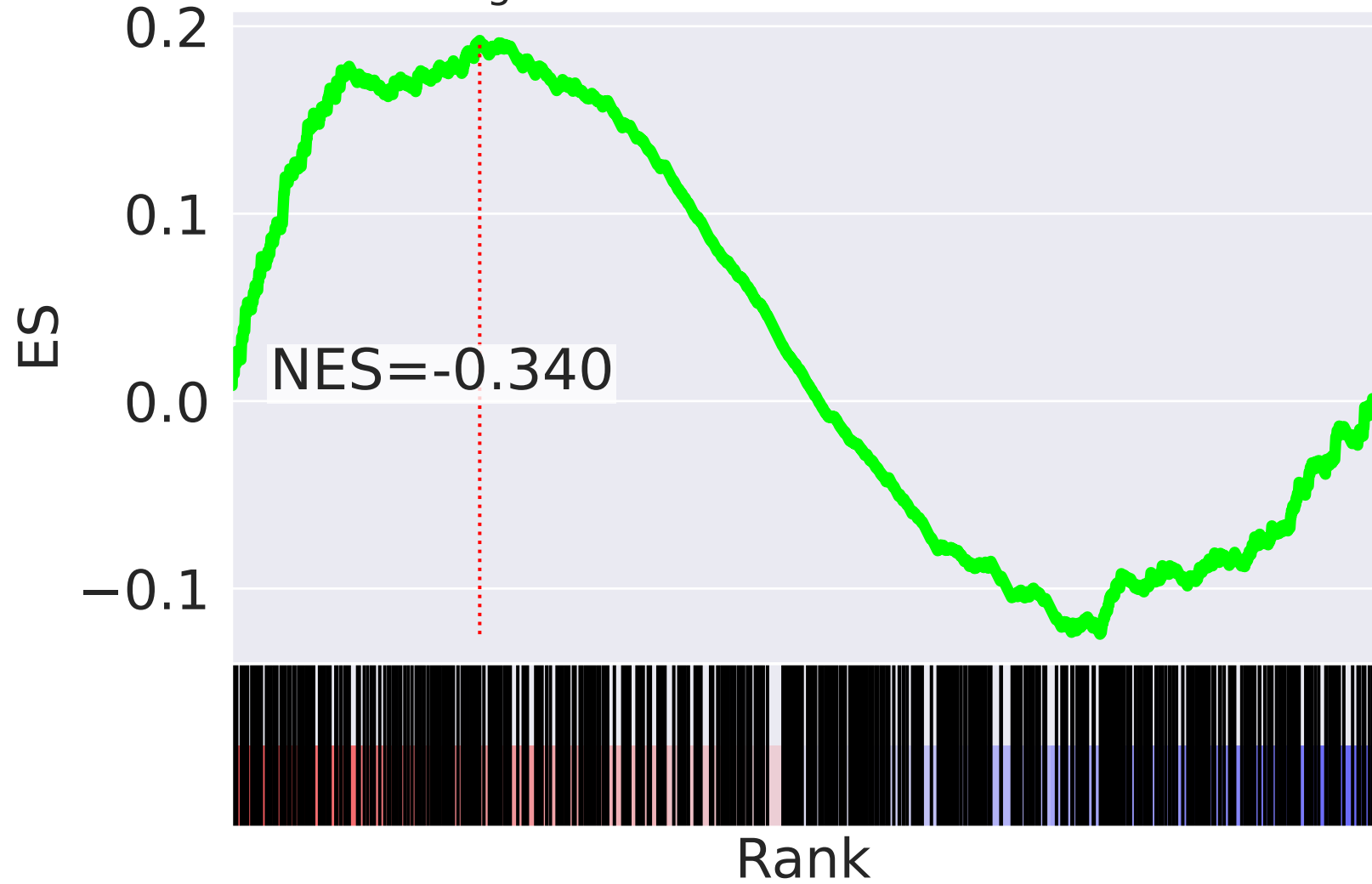
-5.630		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-5.570		rRNA Processing R-HSA-72312
5.567		Adaptive Immune System R-HSA-1280218
-5.249		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
5.060		Axon Guidance R-HSA-422475
5.054		Signaling By WNT R-HSA-195721
4.999		Transport Of Small Molecules R-HSA-382551
4.986		Cytokine Signaling In Immune System R-HSA-1280215
4.886		Deubiquitination R-HSA-5688426
4.828		Nervous System Development R-HSA-9675108
4.814		Regulation Of RUNX2 Expression And Activity R-HSA-8939902
4.785		Signaling By ROBO Receptors R-HSA-376176
4.772		Transcriptional Regulation By RUNX2 R-HSA-8878166
4.767		Signaling By NOTCH4 R-HSA-9013694
4.643		C-type Lectin Receptors (CLRs) R-HSA-5621481



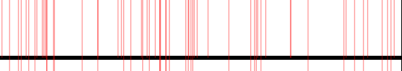
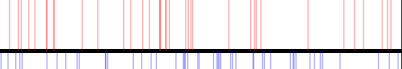
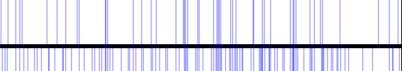
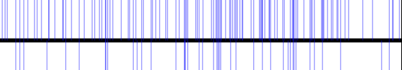
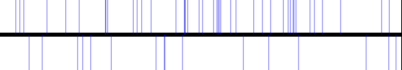
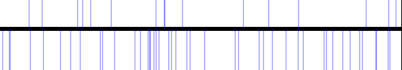
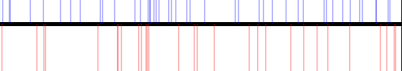
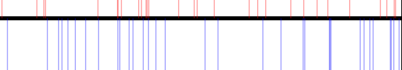


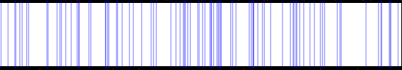


The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=33$

Signal Transduction R-HSA-162582



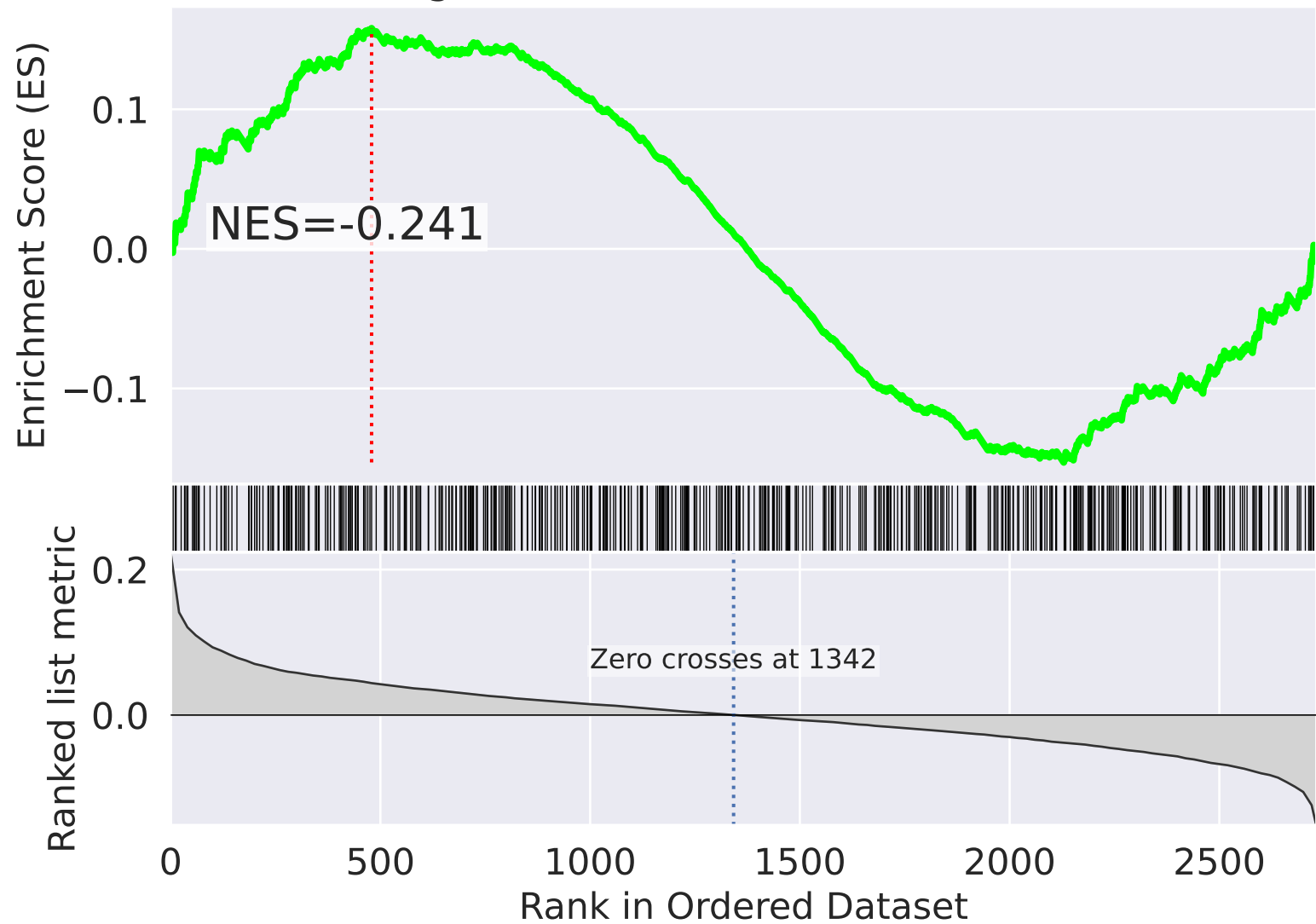
Signal Transduction R-HSA-162582



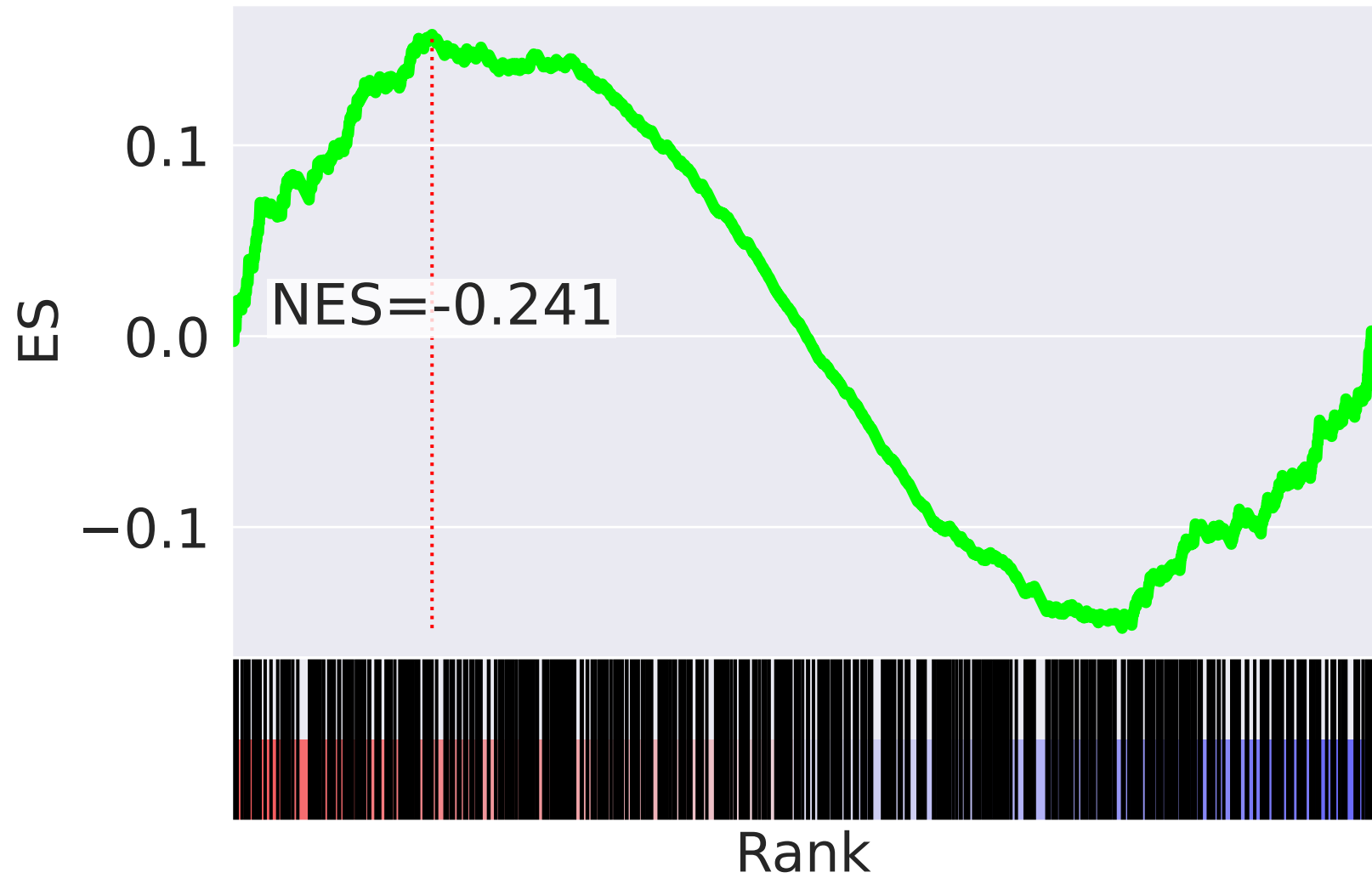
NES		SET
7.390		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
7.320		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
7.192		Respiratory Electron Transport R-HSA-611105
6.254		Complex I Biogenesis R-HSA-6799198
-3.301		RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
-3.132		Transport Of Small Molecules R-HSA-382551
-3.062		Regulation Of RUNX2 Expression And Activity R-HSA-8939902
-3.014		Polymerase Switching On C-strand Of Telomere R-HSA-174411
-2.945		Golgi-to-ER Retrograde Transport R-HSA-8856688
2.895		Cytoprotection By HMOX1 R-HSA-9707564
-2.825		Deadenylation-dependent mRNA Decay R-HSA-429914
2.794		Metabolism Of Cofactors R-HSA-8978934
2.757		Mitochondrial tRNA Aminoacylation R-HSA-379726
-2.755		Transcriptional Regulation By RUNX1 R-HSA-8878171
2.652		Ubiquinol Biosynthesis R-HSA-2142789

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=34$

Signal Transduction R-HSA-162582



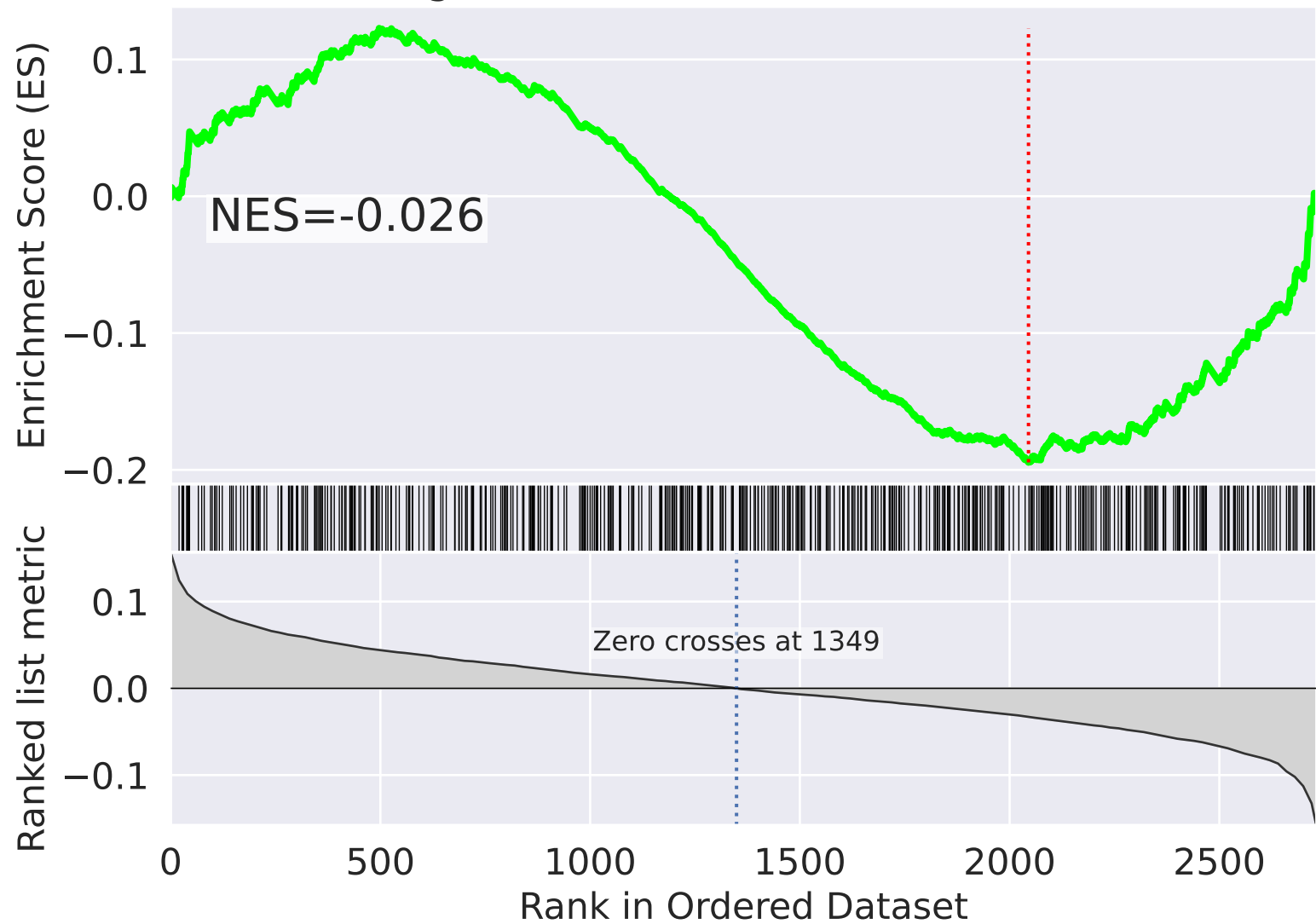
Signal Transduction R-HSA-162582



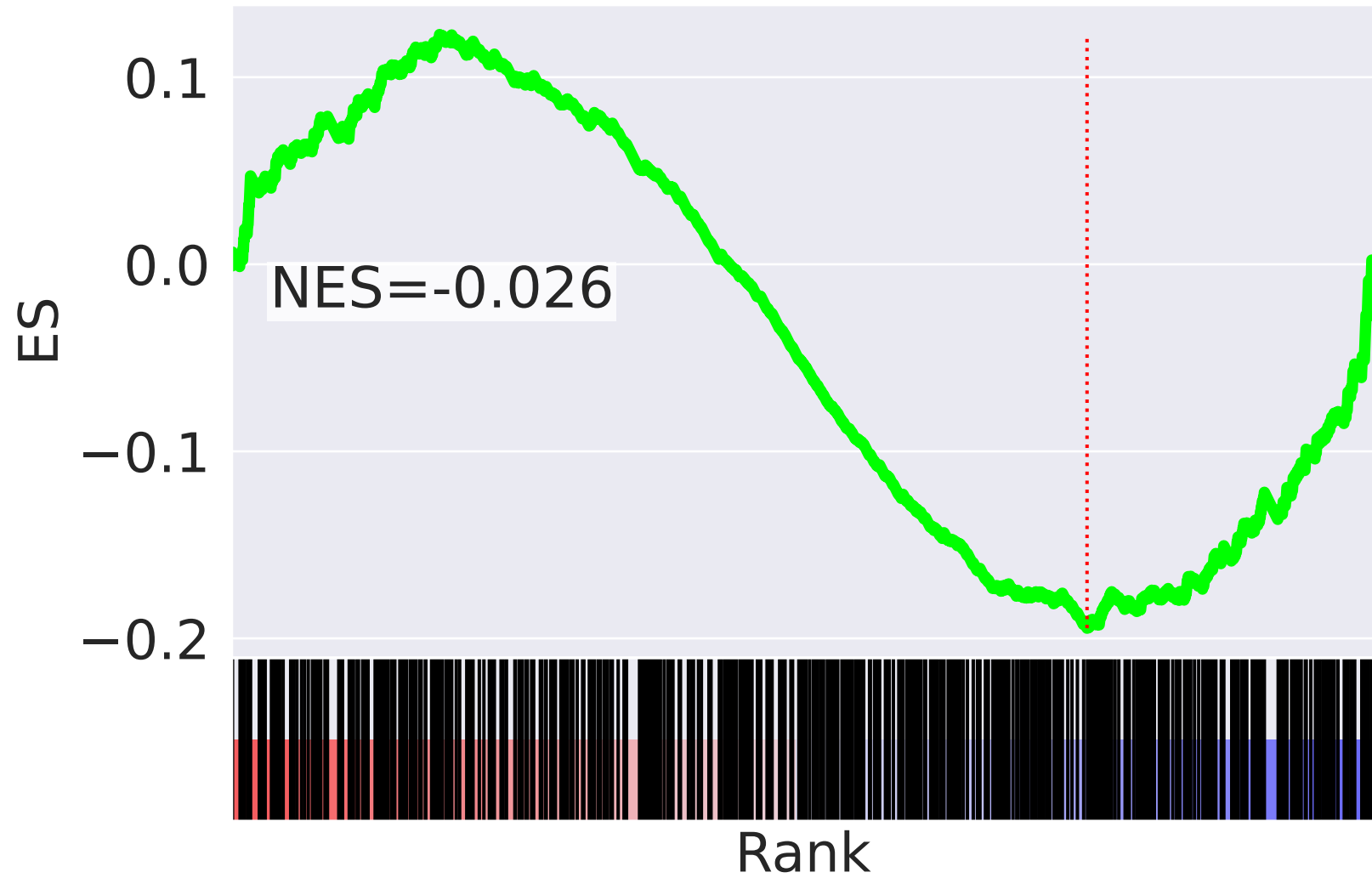
NES		SET
-4.471		rRNA Processing R-HSA-72312
-4.346		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.171		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-4.069		Complex I Biogenesis R-HSA-6799198
3.463		Metabolism Of Nucleotides R-HSA-15869
-3.359		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.352		Respiratory Electron Transport R-HSA-611105
-3.304		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-3.187		Mitotic G2-G2/M Phases R-HSA-453274
-3.144		G2/M Transition R-HSA-69275
3.097		Nucleotide Biosynthesis R-HSA-8956320
3.078		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
-3.071		RNA Polymerase I Transcription Termination R-HSA-73863
-3.030		RNA Polymerase I Transcription Initiation R-HSA-73762
2.812		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=35$

Signal Transduction R-HSA-162582



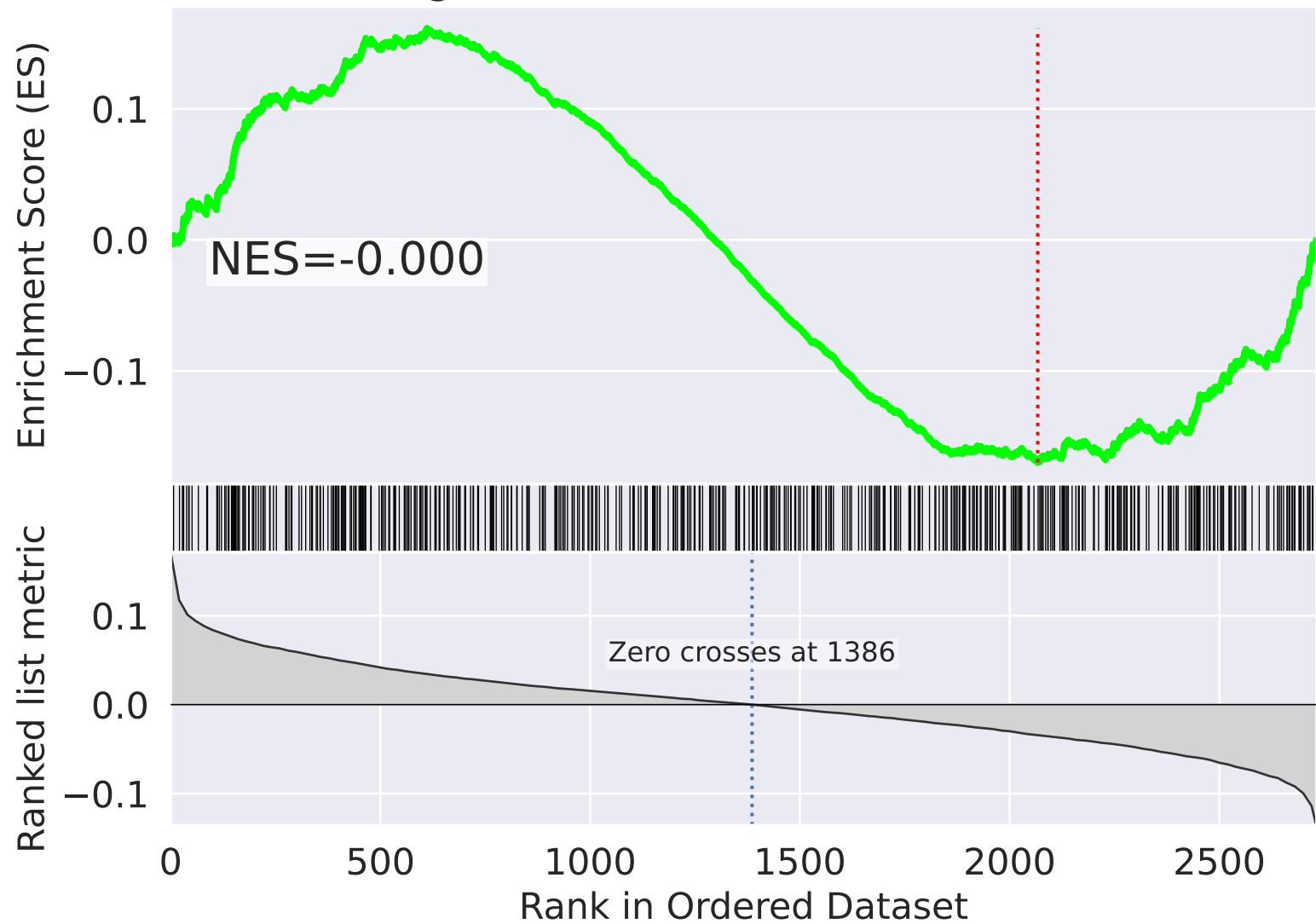
Signal Transduction R-HSA-162582



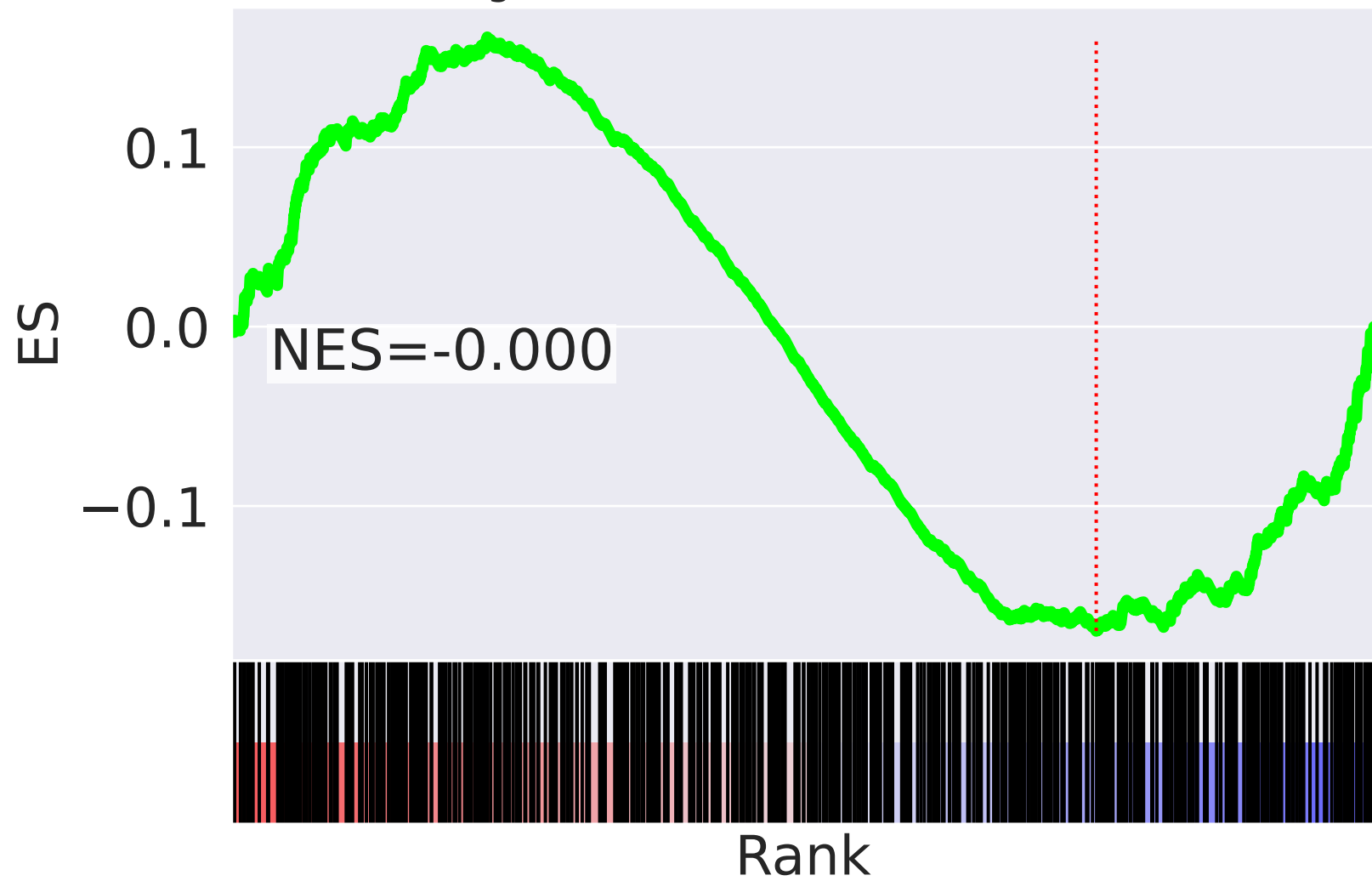
NES		SET
-4.354		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.816		Platelet Activation, Signaling And Aggregation R-HSA-76002
3.805		Asparagine N-linked Glycosylation R-HSA-446203
3.796		VEGFA-VEGFR2 Pathway R-HSA-4420097
-3.685		Respiratory Electron Transport R-HSA-611105
-3.317		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.248		Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
3.248		Leishmania Infection R-HSA-9658195
3.217		Metabolism Of Lipids R-HSA-556833
3.206		Signaling By GPCR R-HSA-372790
3.206		GPCR Downstream Signaling R-HSA-388396
-3.151		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
3.114		COPI-mediated Anterograde Transport R-HSA-6807878
-3.110		Cyclin E Associated Events During G1/S Transition R-HSA-69202
3.034		Integrin Signaling R-HSA-354192

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=36$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582



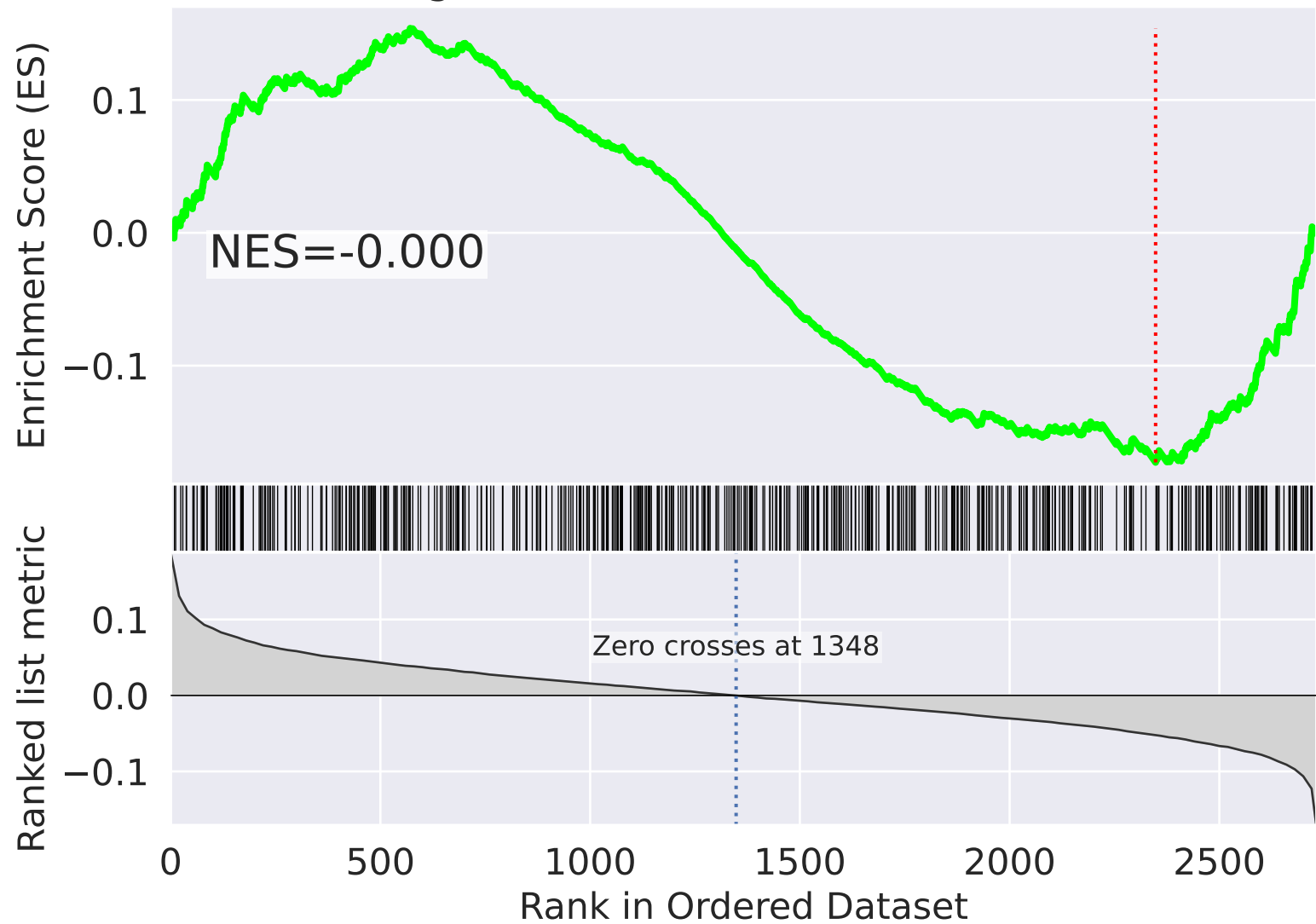
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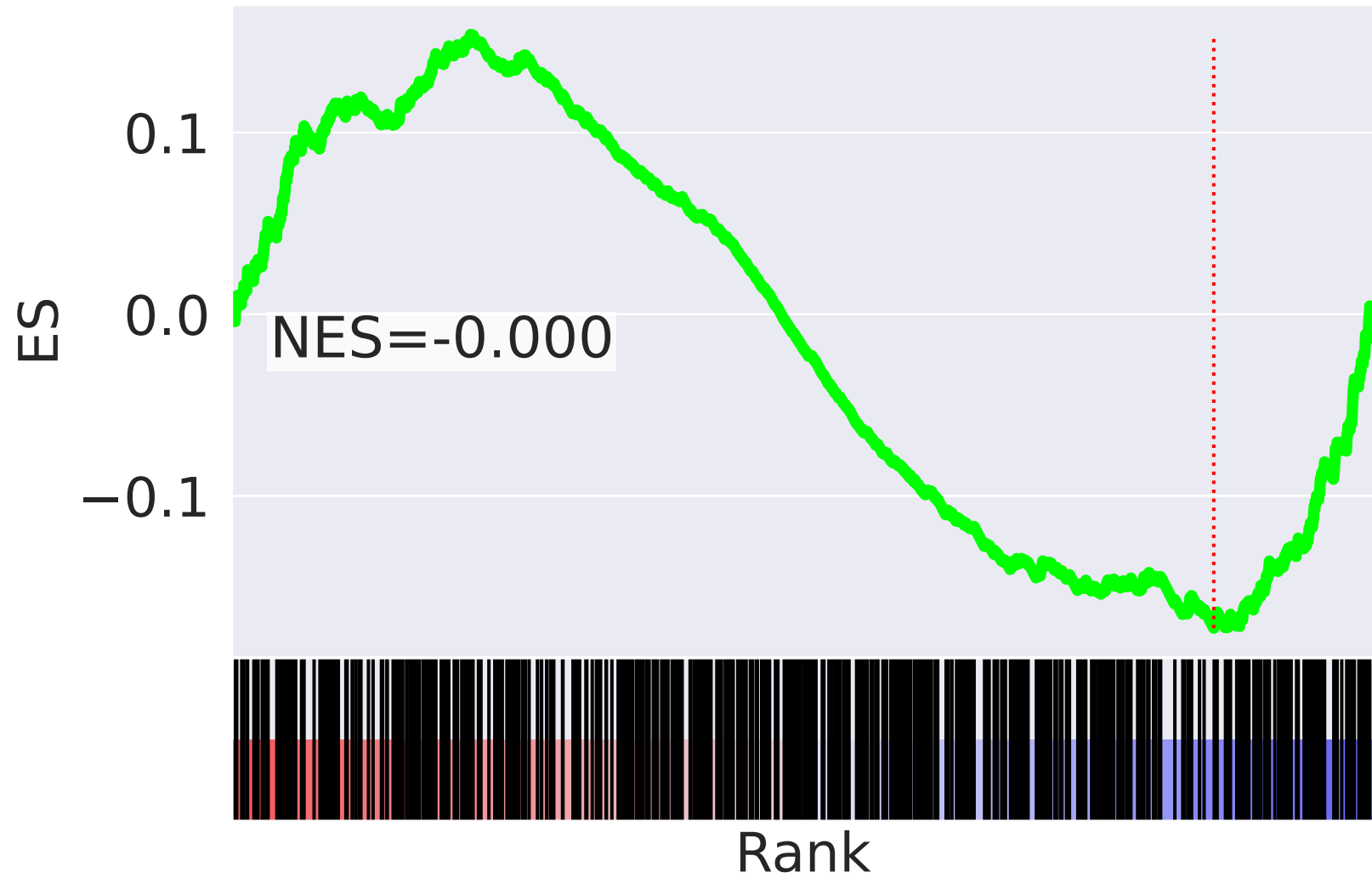
5.964		mRNA Splicing - Major Pathway R-HSA-72163
5.880		mRNA Splicing R-HSA-72172
5.341		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.543		FCERI Mediated NF-kB Activation R-HSA-2871837
4.537		Downstream TCR Signaling R-HSA-202424
4.504		TCR Signaling R-HSA-202403
4.465		Regulation Of PTEN Stability And Activity R-HSA-8948751
4.460		Antigen processing-Cross Presentation R-HSA-1236975
4.446		Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
4.431		KEAP1-NFE2L2 Pathway R-HSA-9755511
4.422		Signaling By Hedgehog R-HSA-5358351
4.350		ER-Phagosome Pathway R-HSA-1236974
4.342		Hh Mutants Abrogate Ligand Secretion R-HSA-5387390
4.342		Hedgehog Ligand Biogenesis R-HSA-5358346
4.342		Hh Mutants Are Degraded By ERAD R-HSA-5362768

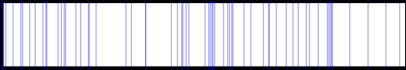
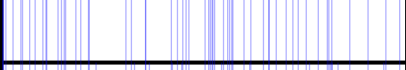
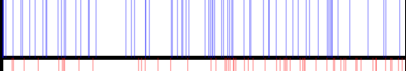
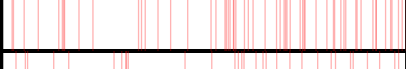
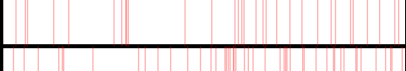
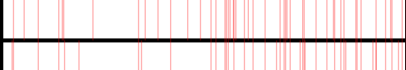
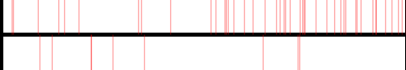
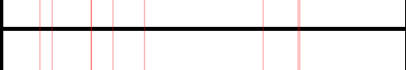

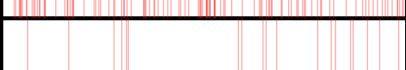
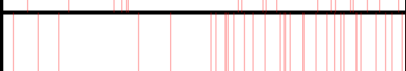
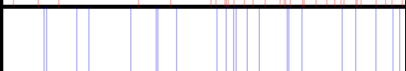

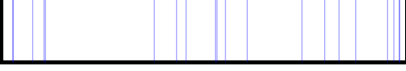

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=37$

Signal Transduction R-HSA-162582



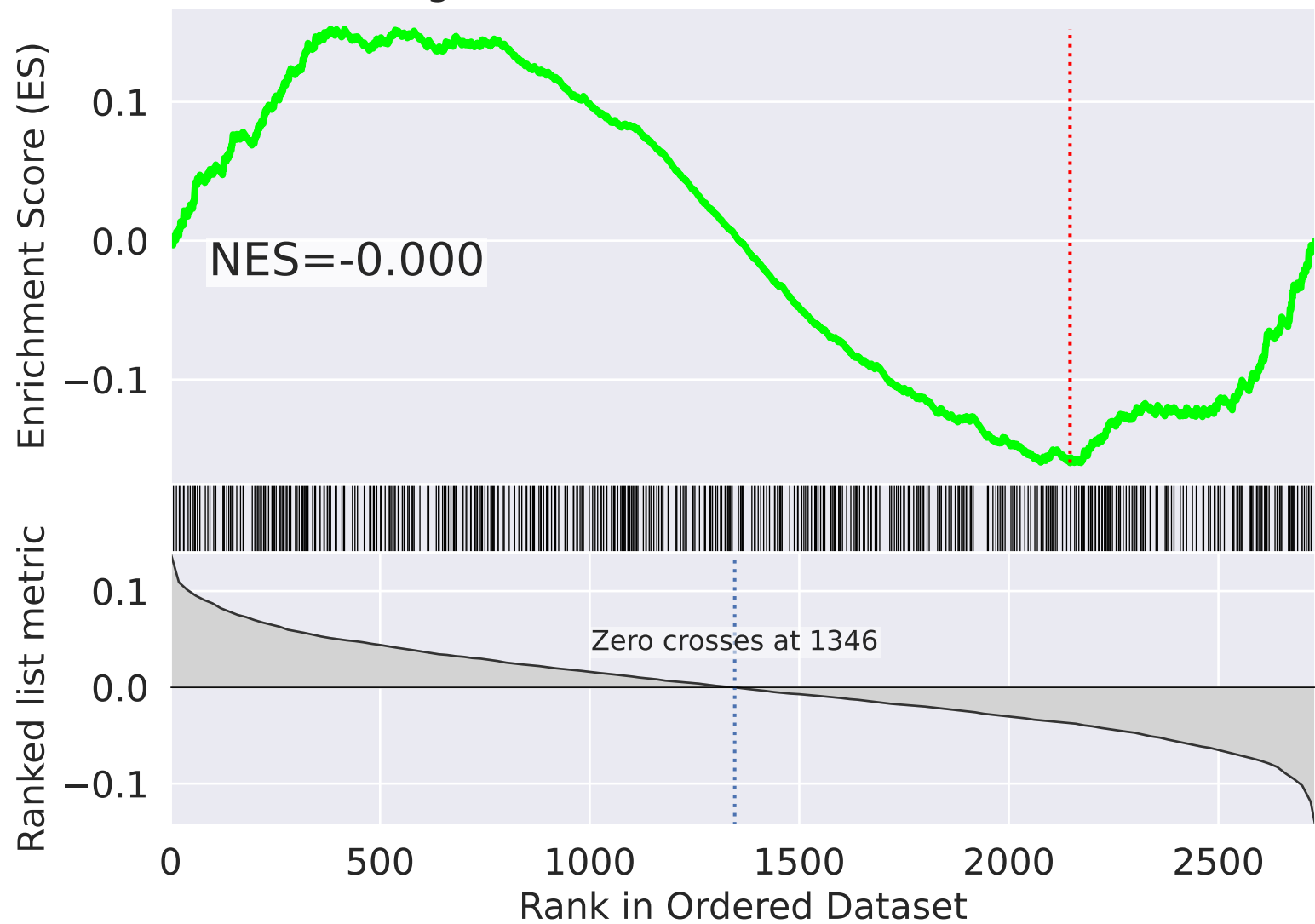
Signal Transduction R-HSA-162582



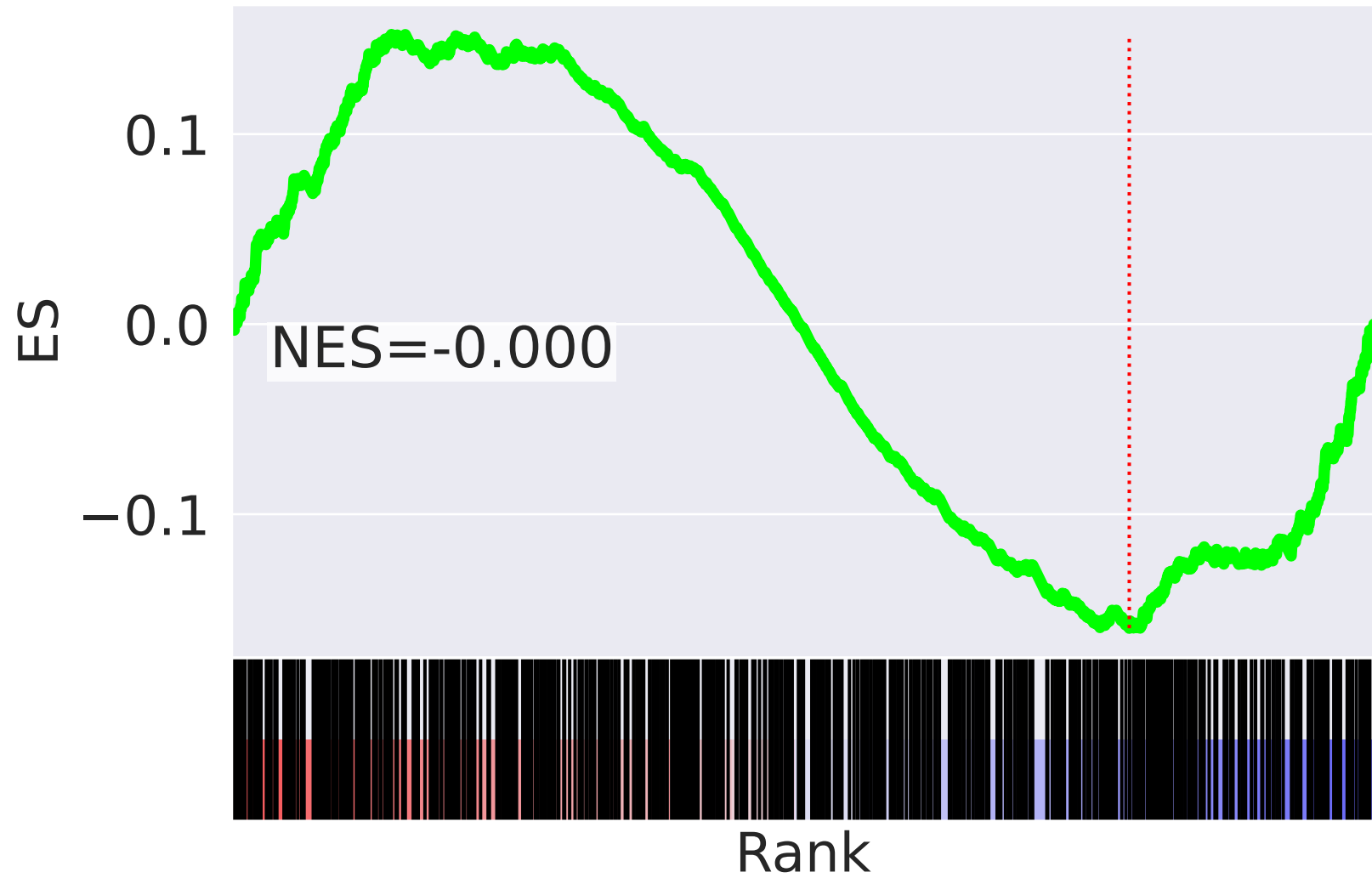
NES		SET
-4.039		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.022		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.895		rRNA Processing R-HSA-72312
3.561		RNA Polymerase II Pre-transcription Events R-HSA-674695
3.480		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.315		Transcription Of HIV Genome R-HSA-167172
3.217		Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.143		Heme Biosynthesis R-HSA-189451
3.143		Metabolism Of Porphyrins R-HSA-189445
3.139		Transport Of Small Molecules R-HSA-382551
3.098		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
2.993		Formation Of HIV Elongation Complex In Absence Of HIV Tat R-HSA-167152
-2.992		Signaling By ERBB2 R-HSA-1227986
2.979		Ion Channel Transport R-HSA-983712
-2.941		Signaling By Non-Receptor Tyrosine Kinases R-HSA-9006927

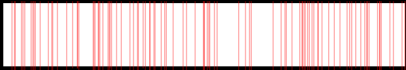
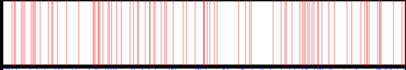
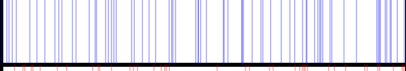

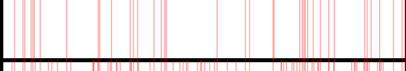
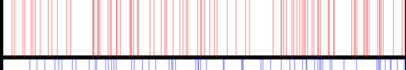
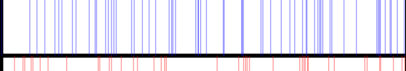
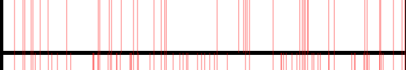
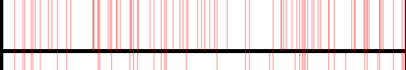
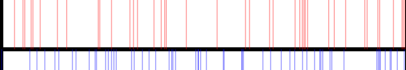
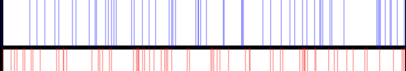
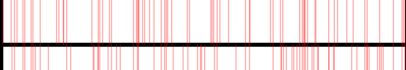
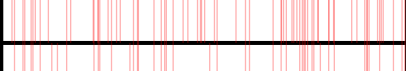


The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=38$

Signal Transduction R-HSA-162582



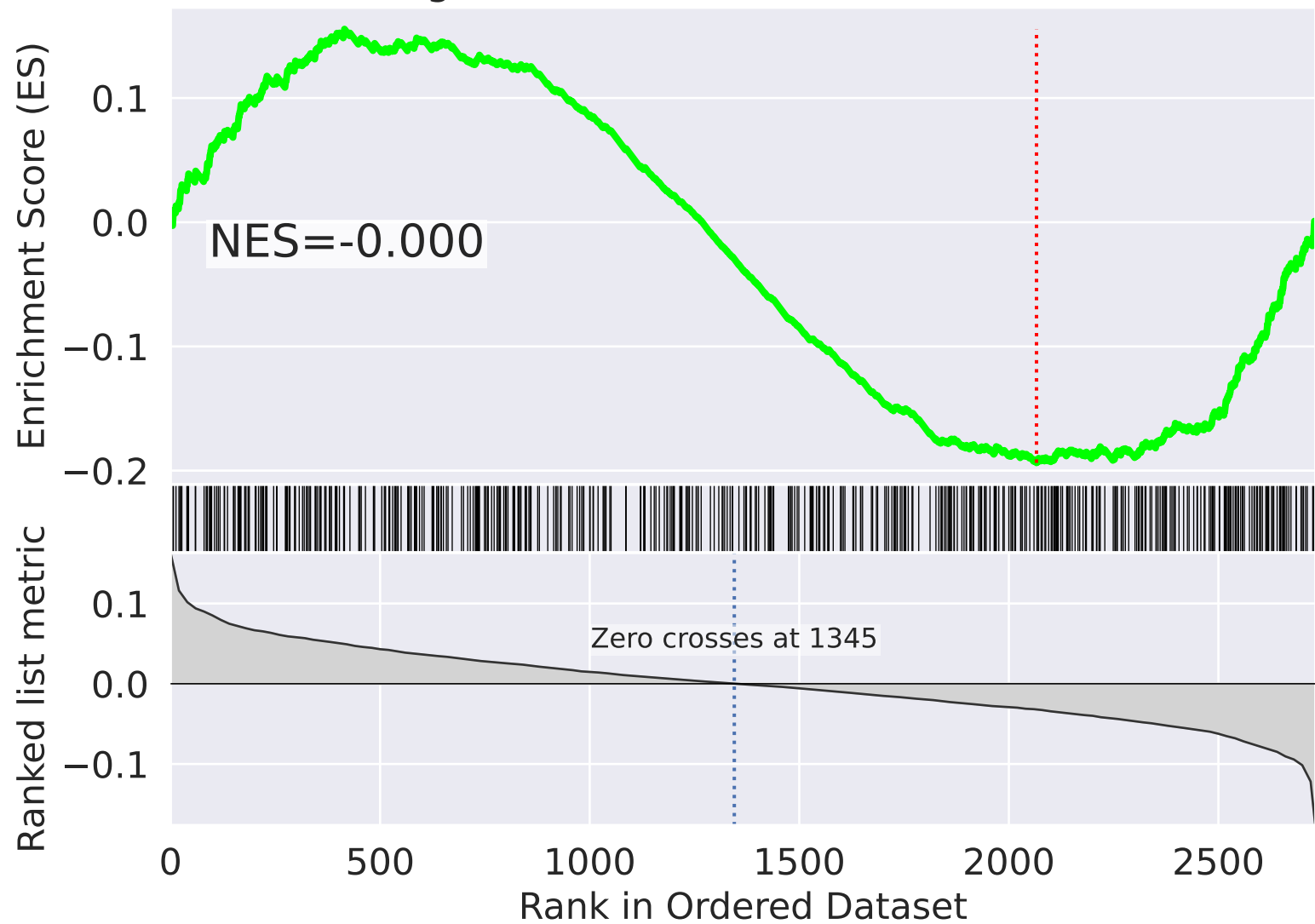
Signal Transduction R-HSA-162582



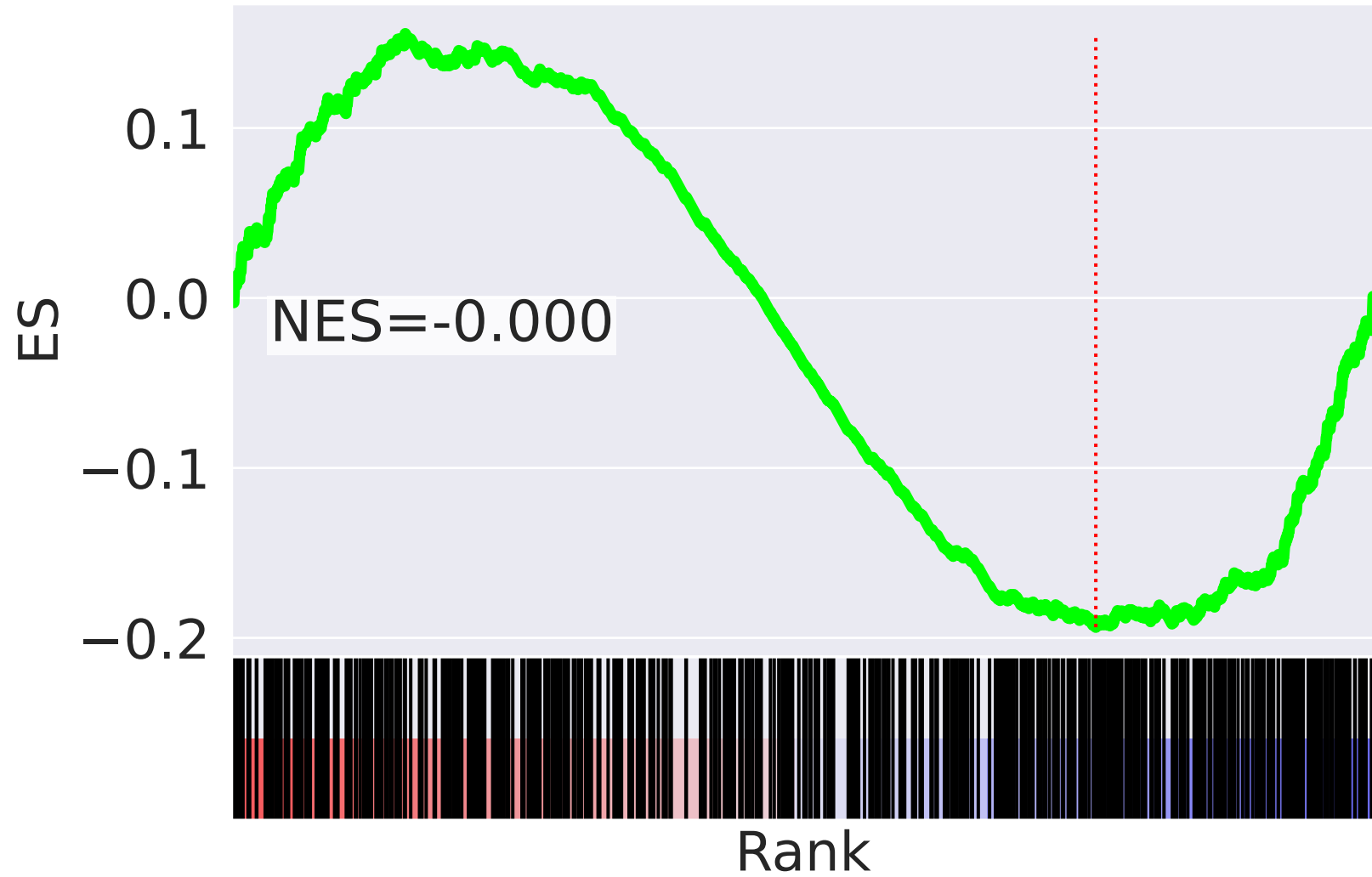
NES		SET
3.863		Mitotic G1 Phase And G1/S Transition R-HSA-453279
3.746		G1/S Transition R-HSA-69206
-3.735		rRNA Processing R-HSA-72312
3.637		TNFR2 Non-Canonical NF-kB Pathway R-HSA-5668541
3.584		Regulation Of RAS By GAPs R-HSA-5658442
3.565		DNA Replication R-HSA-69306
-3.561		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.516		Role Of GTSE1 In G2/M Progression After G2 Checkpoint R-HSA-8852276
3.507		Synthesis Of DNA R-HSA-69239
3.446		Dectin-1 Mediated Noncanonical NF-kB Signaling R-HSA-5607761
-3.441		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.439		Metabolism Of Amino Acids And Derivatives R-HSA-71291
3.407		DNA Replication Pre-Initiation R-HSA-69002
3.399		Orc1 Removal From Chromatin R-HSA-68949
3.392		ABC-family Proteins Mediated Transport R-HSA-382556

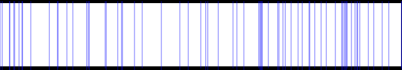
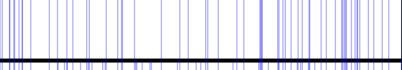
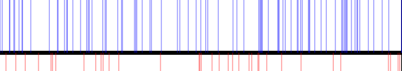
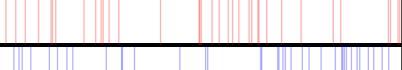

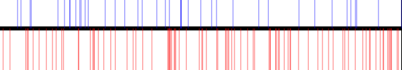
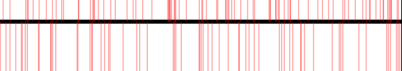
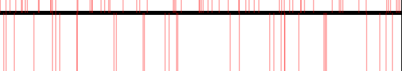

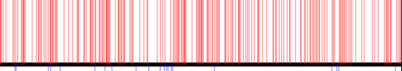

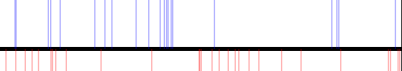
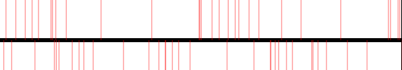
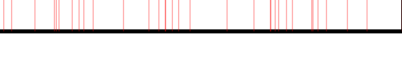

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=39$

Signal Transduction R-HSA-162582



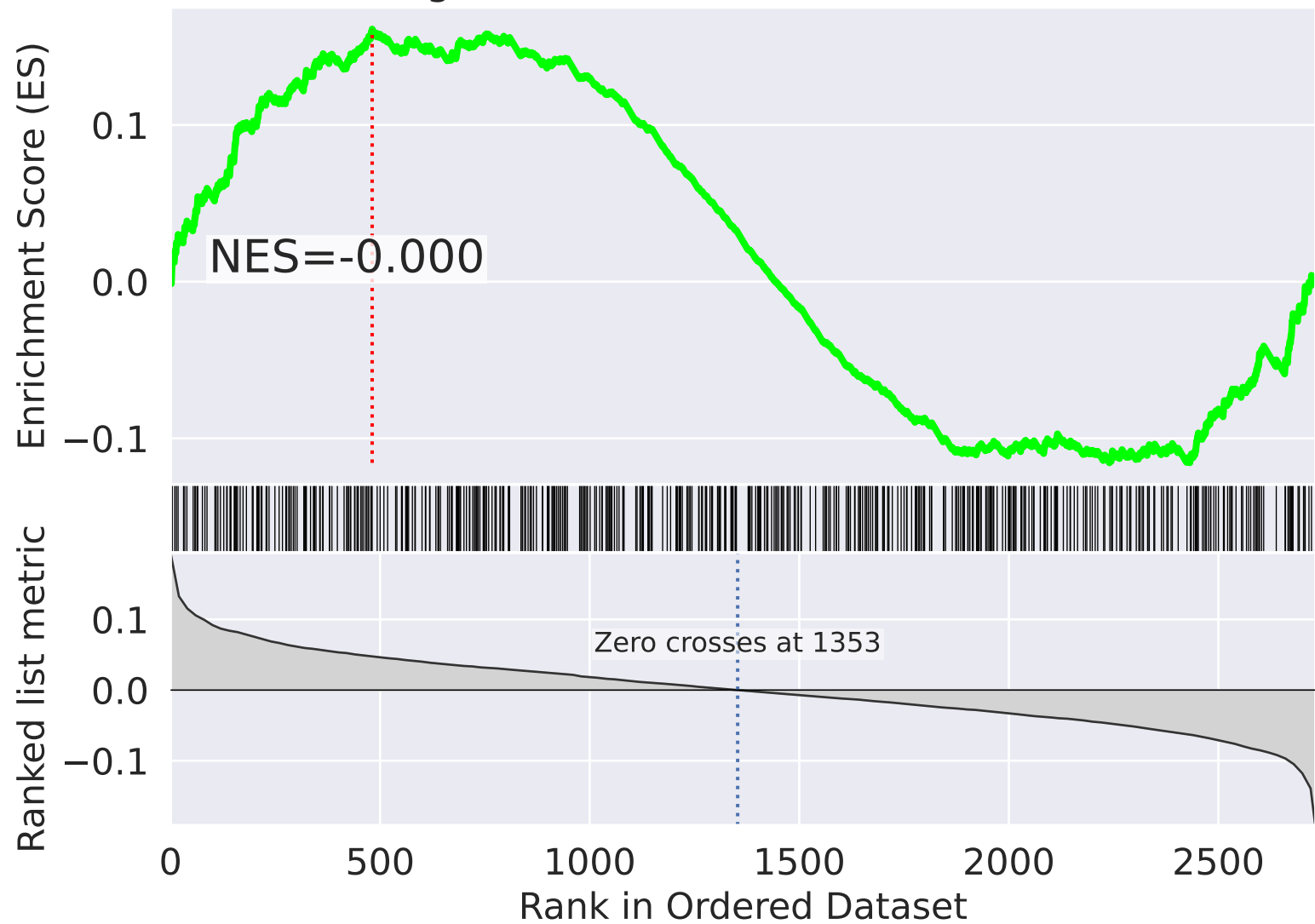
Signal Transduction R-HSA-162582



NES		SET
-5.467		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-4.717		Respiratory Electron Transport R-HSA-611105
-4.292		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.637		Nuclear Envelope Breakdown R-HSA-2980766
-3.591		Complex I Biogenesis R-HSA-6799198
-3.558		Mitochondrial Biogenesis R-HSA-1592230
3.554		Asparagine N-linked Glycosylation R-HSA-446203
3.539		Disorders Of Transmembrane Transporters R-HSA-5619115
3.398		Amino Acids Regulate mTORC1 R-HSA-9639288
-3.366		Impaired BRCA2 Binding To PALB2 R-HSA-9709603
3.354		M Phase R-HSA-68886
-3.350		Resolution Of D-Loop Structures R-HSA-5693537
-3.350		Resolution Of D-loop Structures Thru Holliday Junction Intermediates R-HSA-5693568
3.348		SUMOylation Of RNA Binding Proteins R-HSA-4570464
3.290		VEGFA-VEGFR2 Pathway R-HSA-4420097

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=40$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

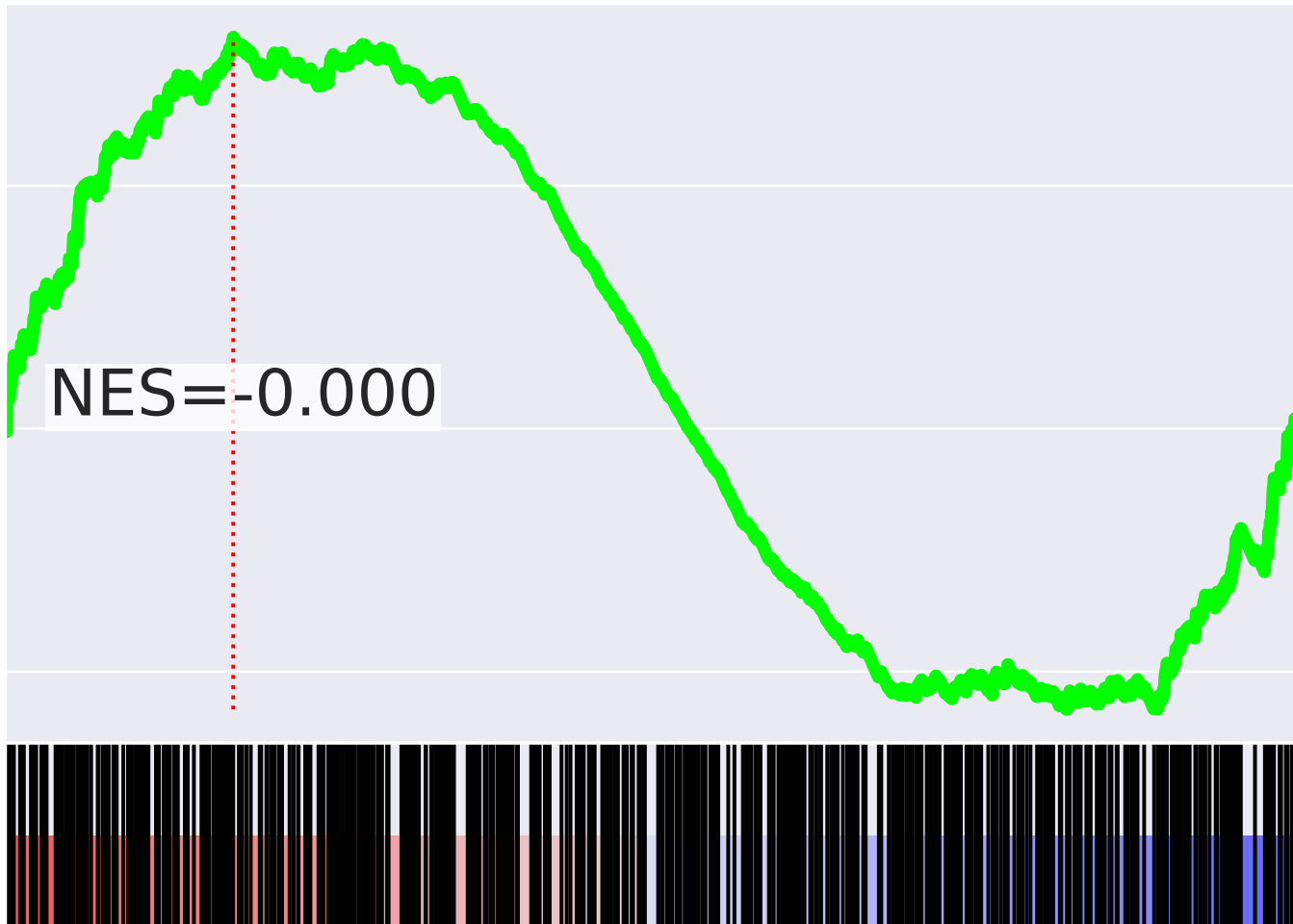
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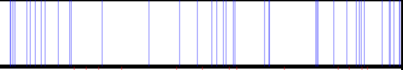
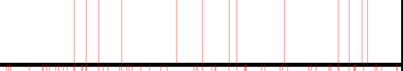
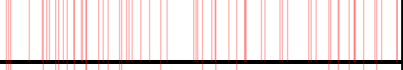
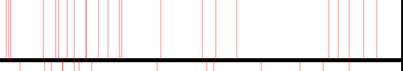
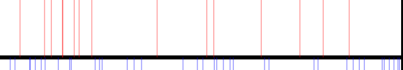
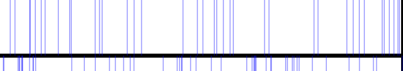
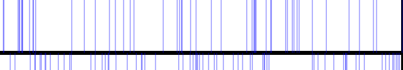
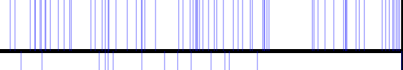
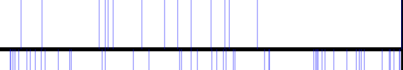
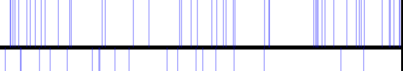


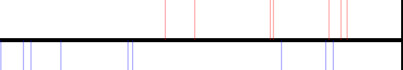
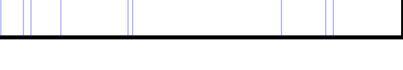
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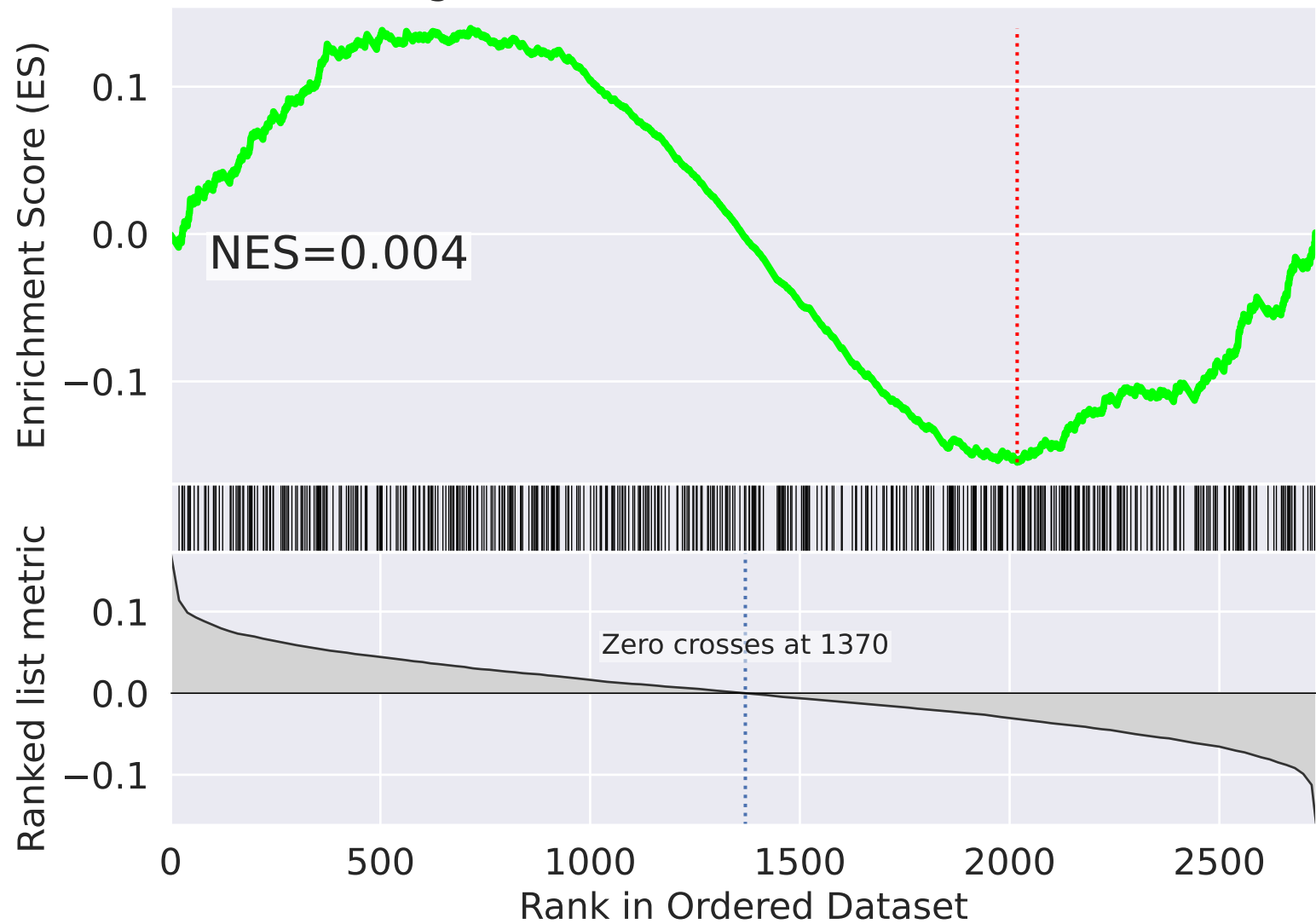
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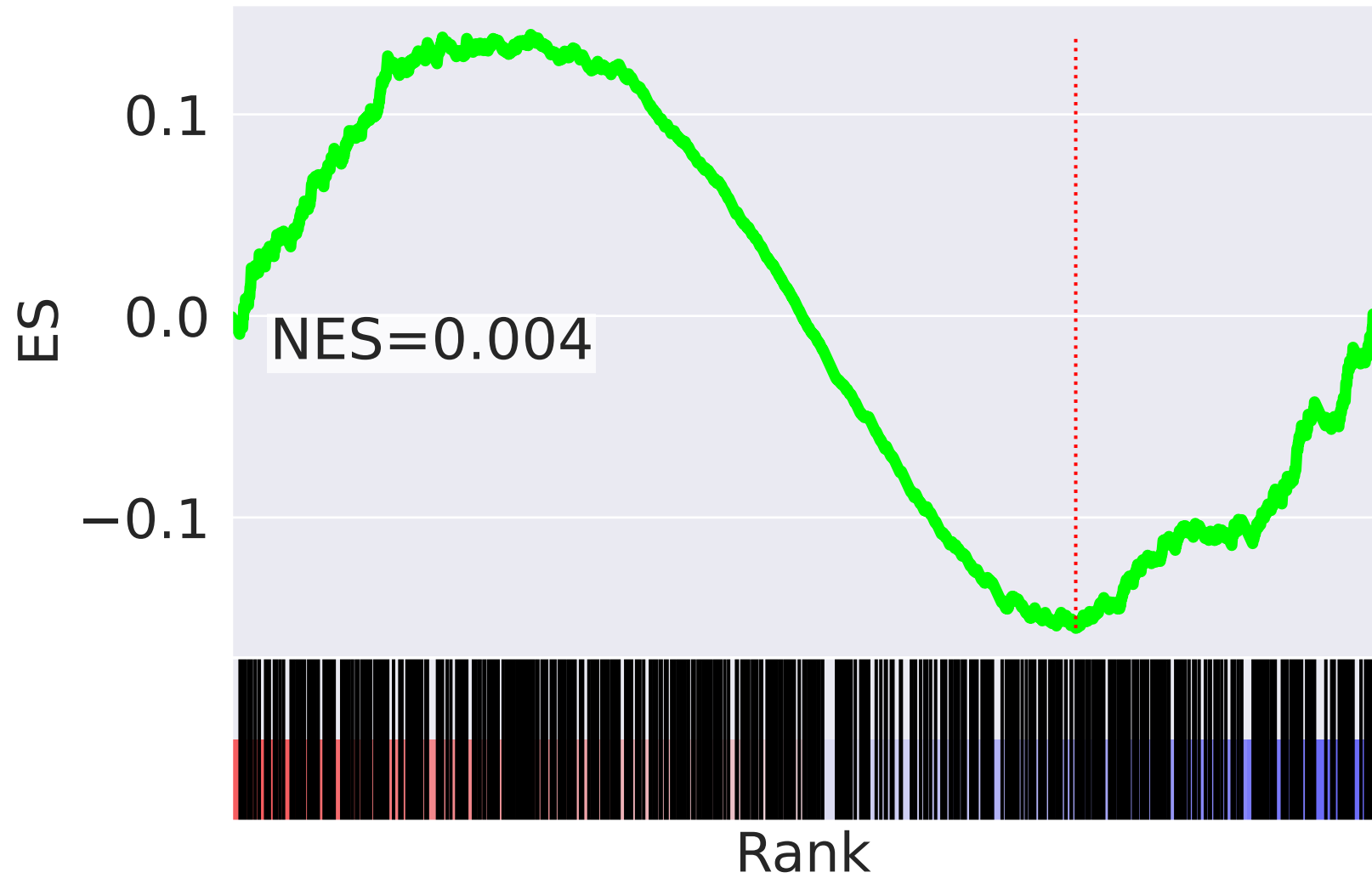
NES		SET
-2.988		SARS-CoV-2 Infection R-HSA-9694516
-2.882		Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
2.849		Meiotic Synapsis R-HSA-1221632
2.709		Cellular Senescence R-HSA-2559583
2.682		DNA Damage/Telomere Stress Induced Senescence R-HSA-2559586
2.668		HDACs Deacetylate Histones R-HSA-3214815
-2.600		Metabolism Of Non-Coding RNA R-HSA-194441
-2.572		Protein Localization R-HSA-9609507
-2.556		SARS-CoV-2-host Interactions R-HSA-9705683
-2.544		Transcriptional Regulation By AP-2 (TFAP2) Family Of Transcription Factors R-HSA-8864260
-2.521		Cellular Response To Heat Stress R-HSA-3371556
-2.469		Signaling By Non-Receptor Tyrosine Kinases R-HSA-9006927
-2.457		Downregulation Of ERBB2:ERBB3 Signaling R-HSA-1358803
2.426		Gluconeogenesis R-HSA-70263
-2.380		Gamma Carboxylation, Hypusine Formation And Arylsulfatase Activation R-HSA-163841

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=41$

Signal Transduction R-HSA-162582



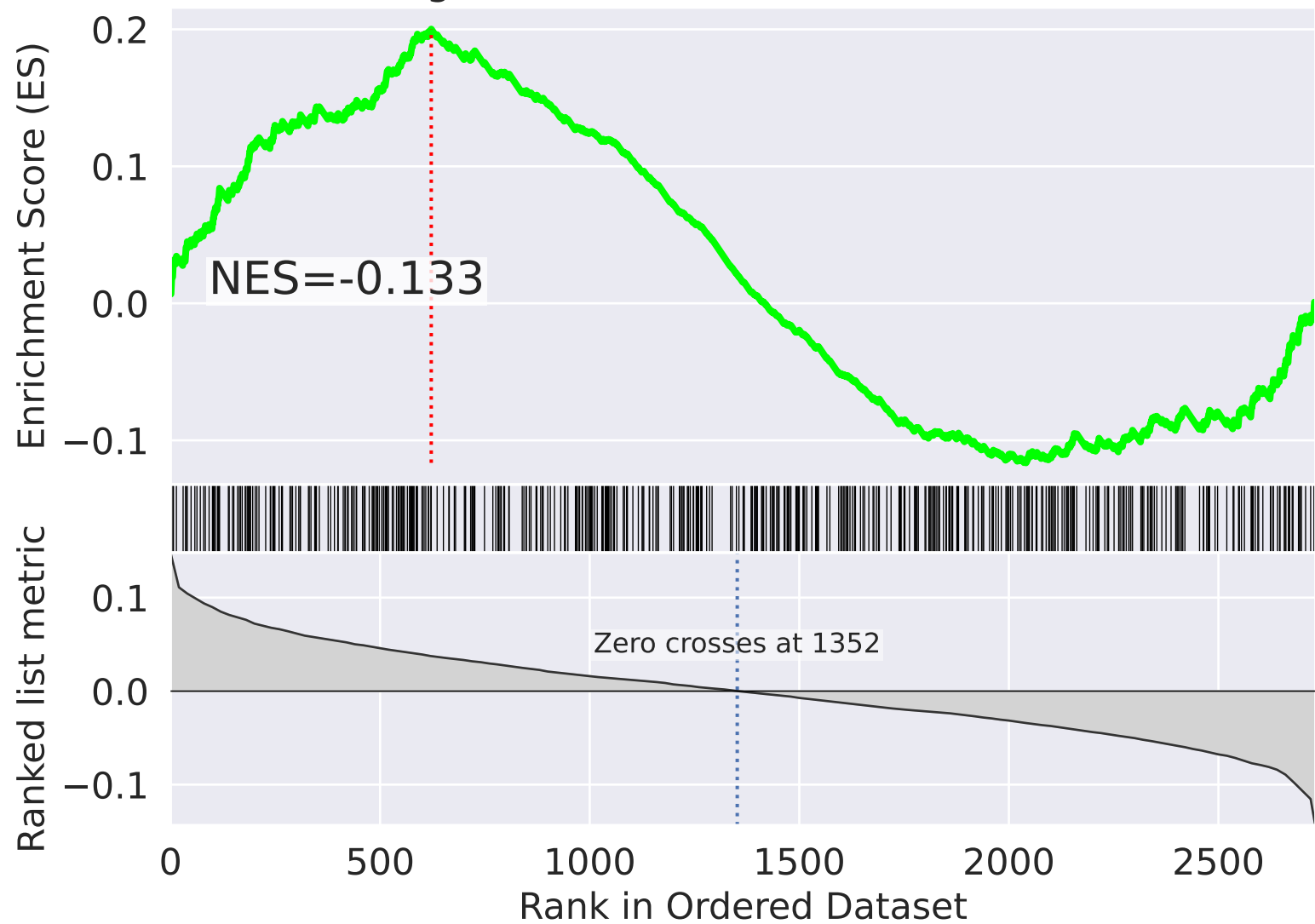
Signal Transduction R-HSA-162582



NES		SET
3.857		TCF Dependent Signaling In Response To WNT R-HSA-201681
3.843		Regulation Of PTEN Stability And Activity R-HSA-8948751
3.674		Orc1 Removal From Chromatin R-HSA-68949
3.651		Deubiquitination R-HSA-5688426
3.587		DNA Replication R-HSA-69306
3.564		Negative Regulation Of NOTCH4 Signaling R-HSA-9604323
3.563		Vif-mediated Degradation Of APOBEC3G R-HSA-180585
-3.558		Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
3.552		Hedgehog On State R-HSA-5632684
3.520		Degradation Of AXIN R-HSA-4641257
3.450		Transcriptional Regulation By RUNX2 R-HSA-8878166
3.406		ABC-family Proteins Mediated Transport R-HSA-382556
3.403		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.380		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
3.315		Signaling By WNT R-HSA-195721

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=42$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.2

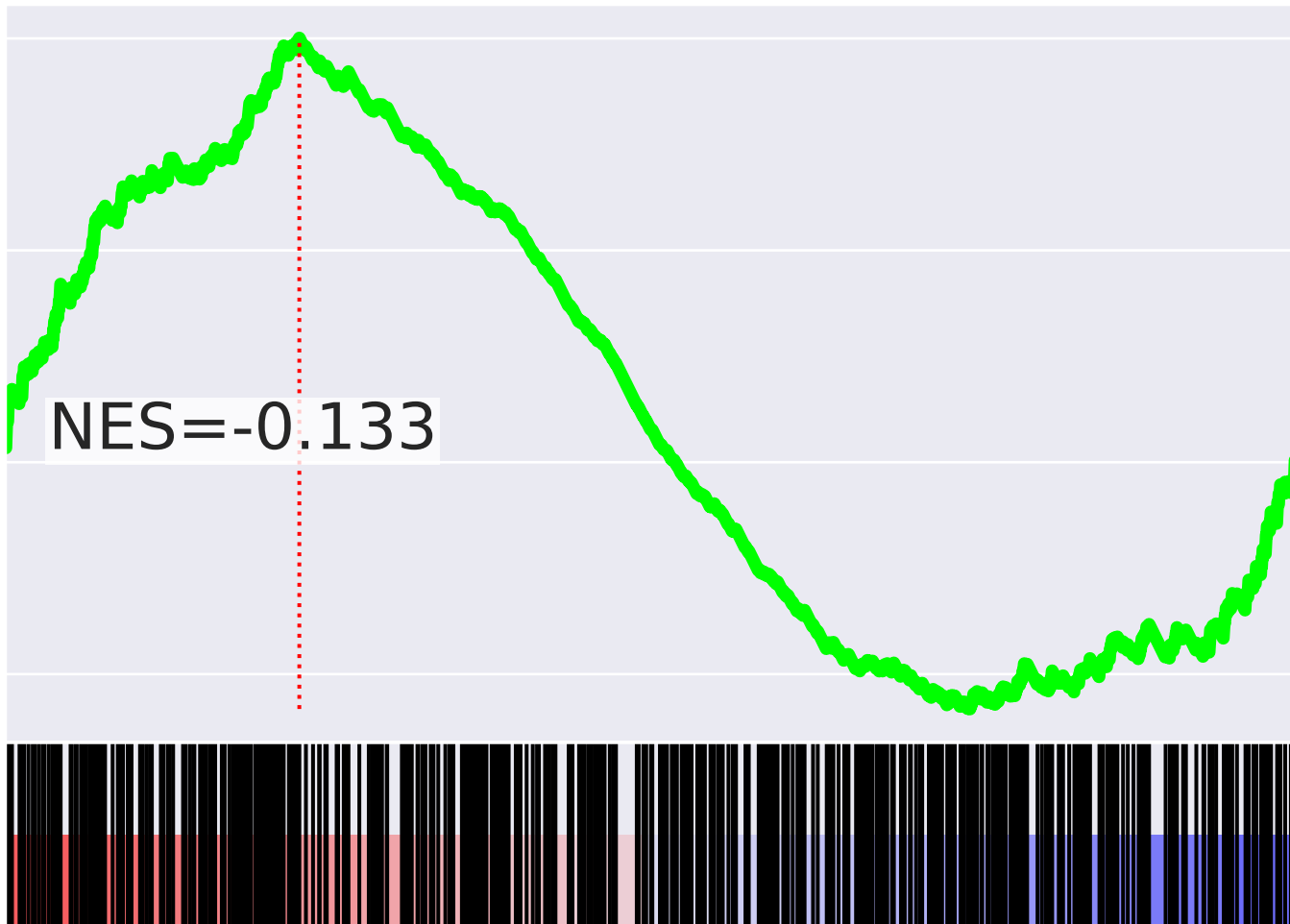
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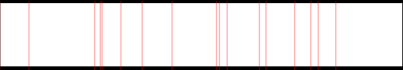
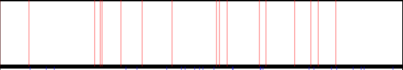
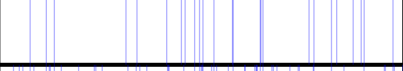
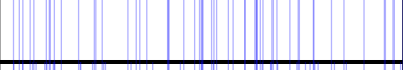
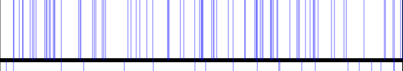

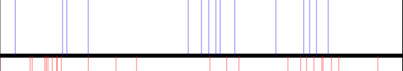

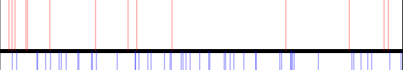
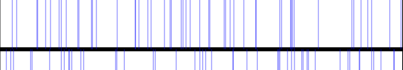
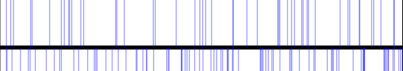
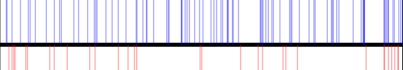



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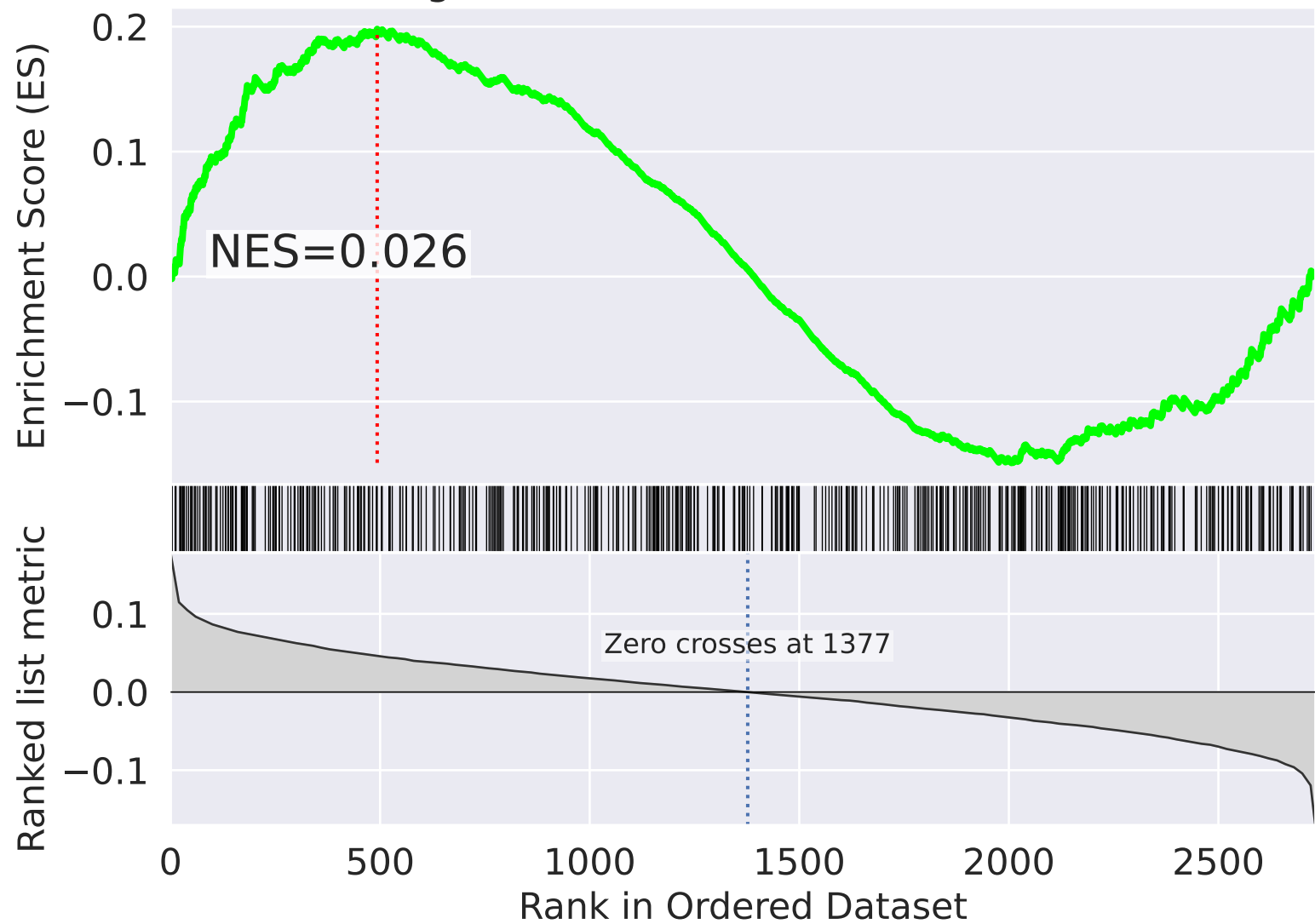
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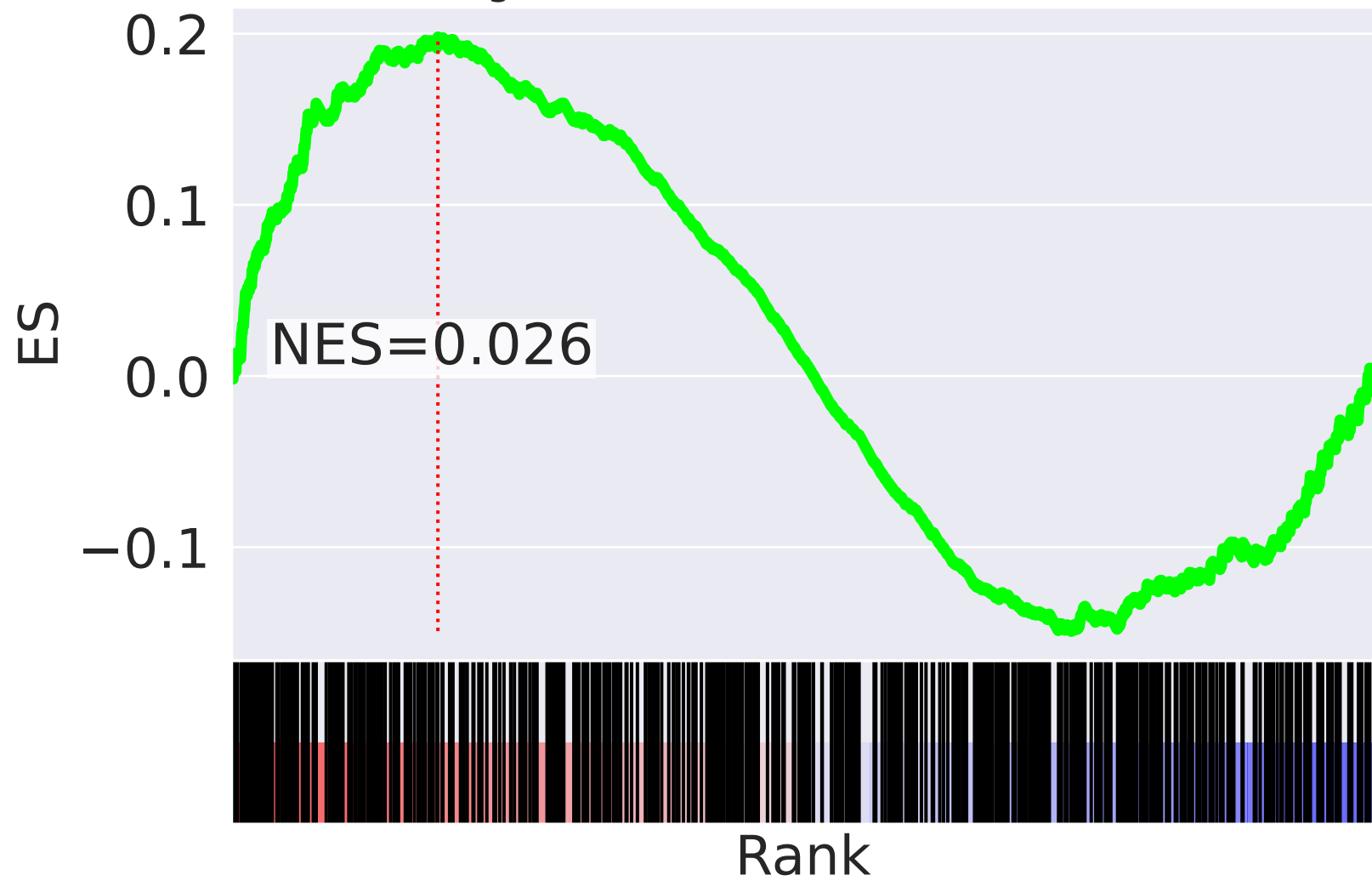
NES		SET
3.505		IRE1alpha Activates Chaperones R-HSA-381070
3.505		XBP1(S) Activates Chaperone Genes R-HSA-381038
-3.340		Activation Of ATR In Response To Replication Stress R-HSA-176187
-3.036		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
-2.808		Regulation Of TP53 Activity R-HSA-5633007
-2.679		Selective Autophagy R-HSA-9663891
-2.652		Interleukin-12 Family Signaling R-HSA-447115
2.648		Fanconi Anemia Pathway R-HSA-6783310
2.642		Inhibition Of DNA Recombination At Telomere R-HSA-9670095
-2.623		Protein Localization R-HSA-9609507
-2.582		Macroautophagy R-HSA-1632852
-2.568		G2/M Checkpoints R-HSA-69481
2.501		Activation Of HOX Genes During Differentiation R-HSA-5619507
-2.460		mRNA Decay By 5 To 3 Exoribonuclease R-HSA-430039
-2.420		Insertion Of Tail-Anchored Proteins Into Endoplasmic Reticulum Membrane R-HSA-9609523

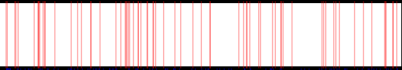
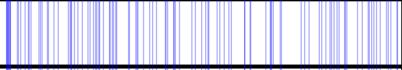
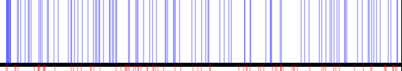
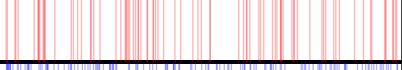
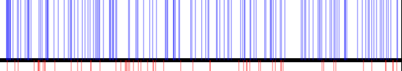
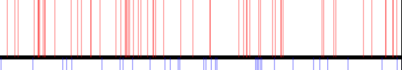
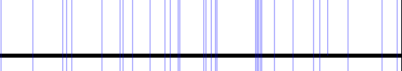
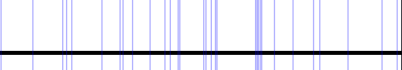
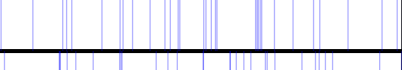
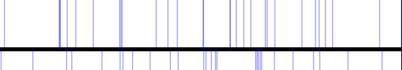
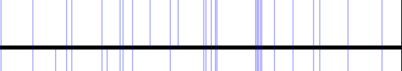
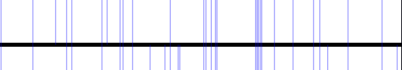
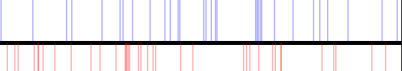
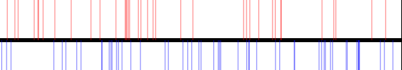
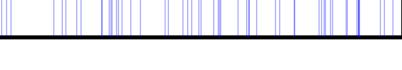
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=43$

Signal Transduction R-HSA-162582



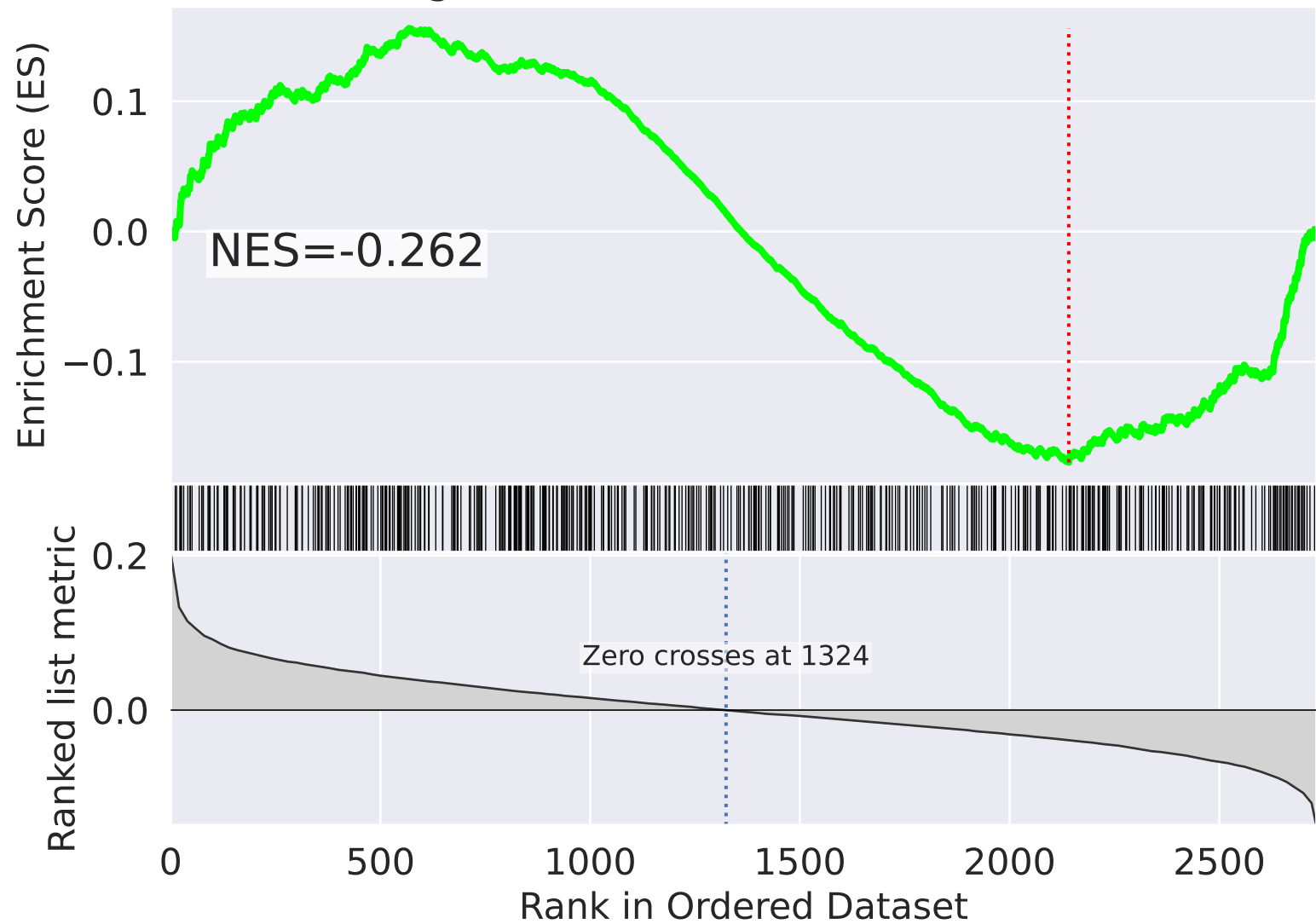
Signal Transduction R-HSA-162582



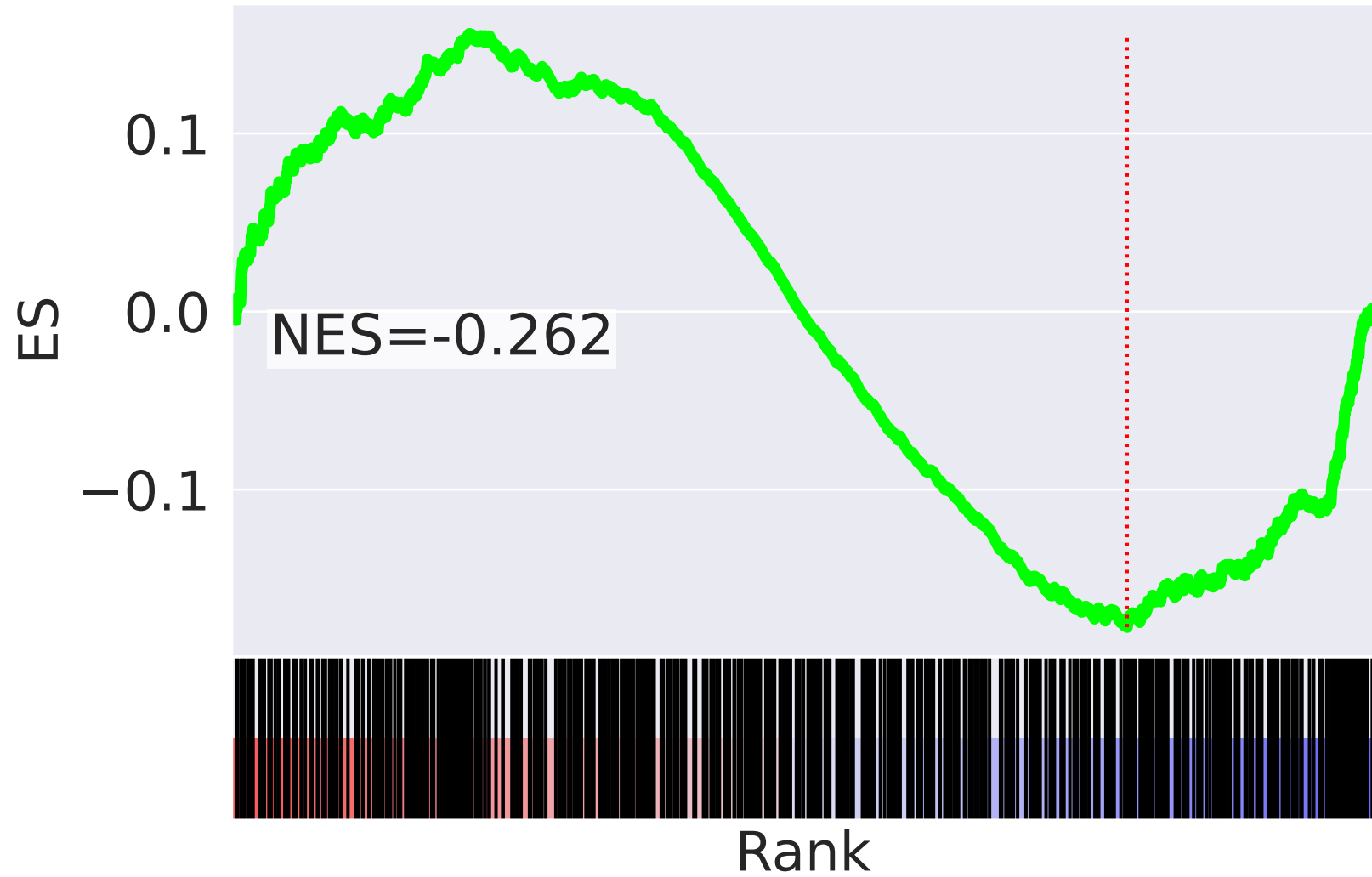
NES		SET
3.689		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.688		mRNA Splicing R-HSA-72172
-3.653		mRNA Splicing - Major Pathway R-HSA-72163
3.558		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.420		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
3.320		Respiratory Electron Transport R-HSA-611105
-3.283		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.218		Diseases Of DNA Repair R-HSA-9675135
-3.218		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.208		Rab Regulation Of Trafficking R-HSA-9007101
-3.187		Impaired BRCA2 Binding To RAD51 R-HSA-9709570
-3.112		HDR Thru Single Strand Annealing (SSA) R-HSA-5685938
-3.020		Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
3.008		Complex I Biogenesis R-HSA-6799198
-3.000		Autophagy R-HSA-9612973

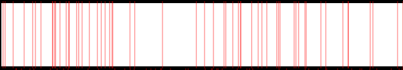
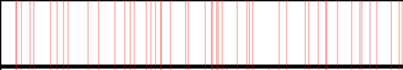
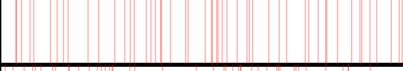
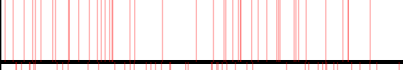
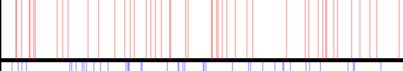
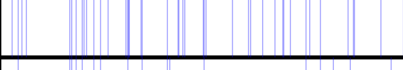
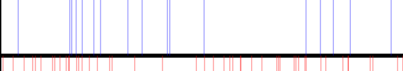
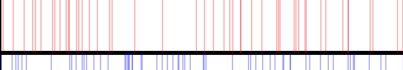
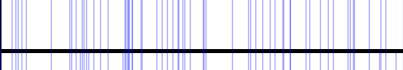
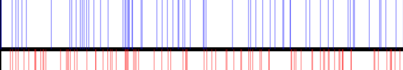
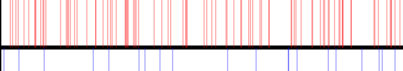
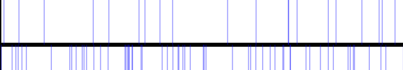
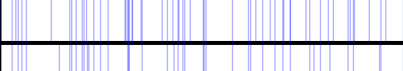

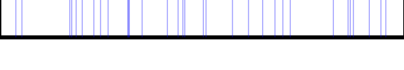
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=44$

Signal Transduction R-HSA-162582



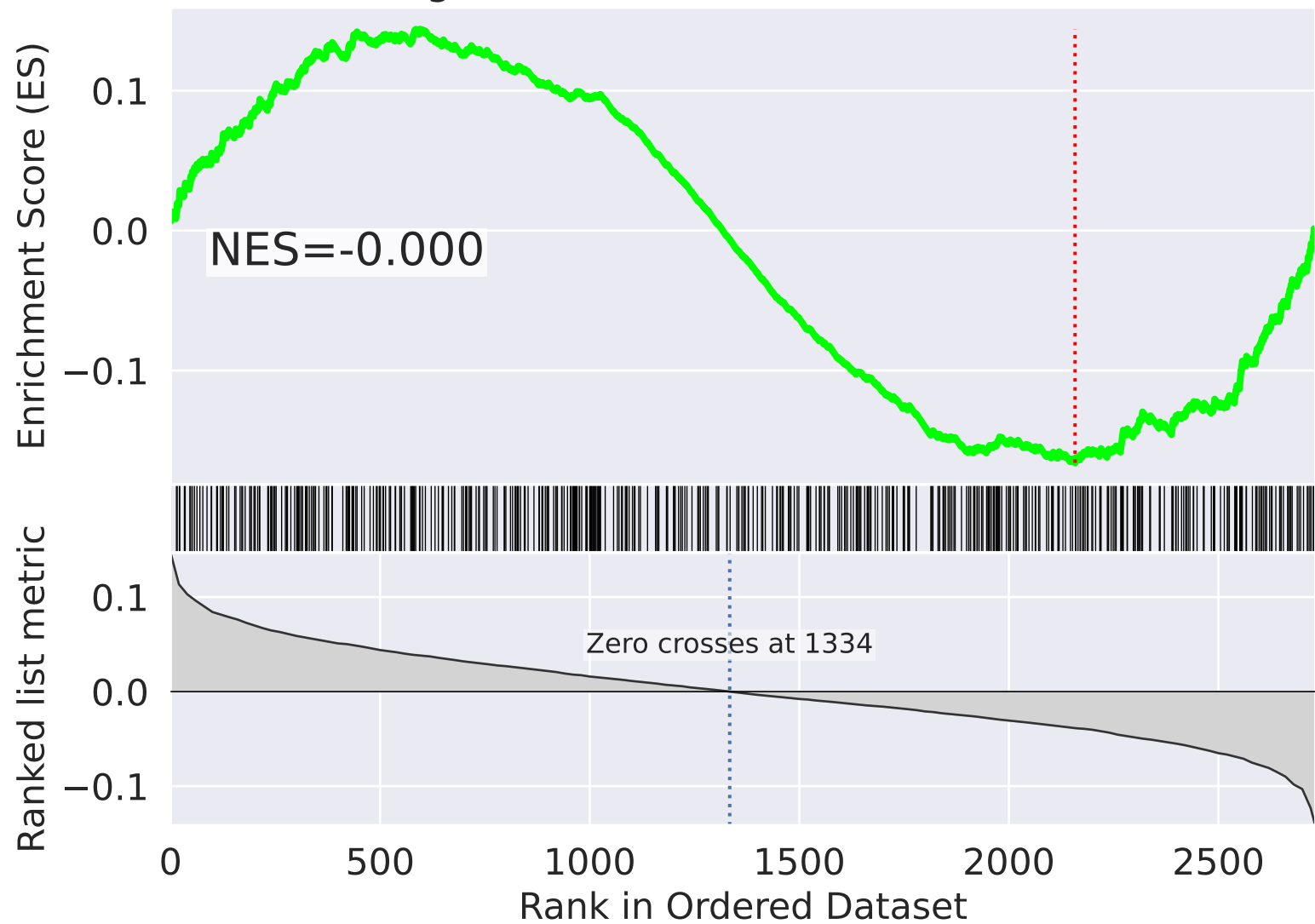
Signal Transduction R-HSA-162582



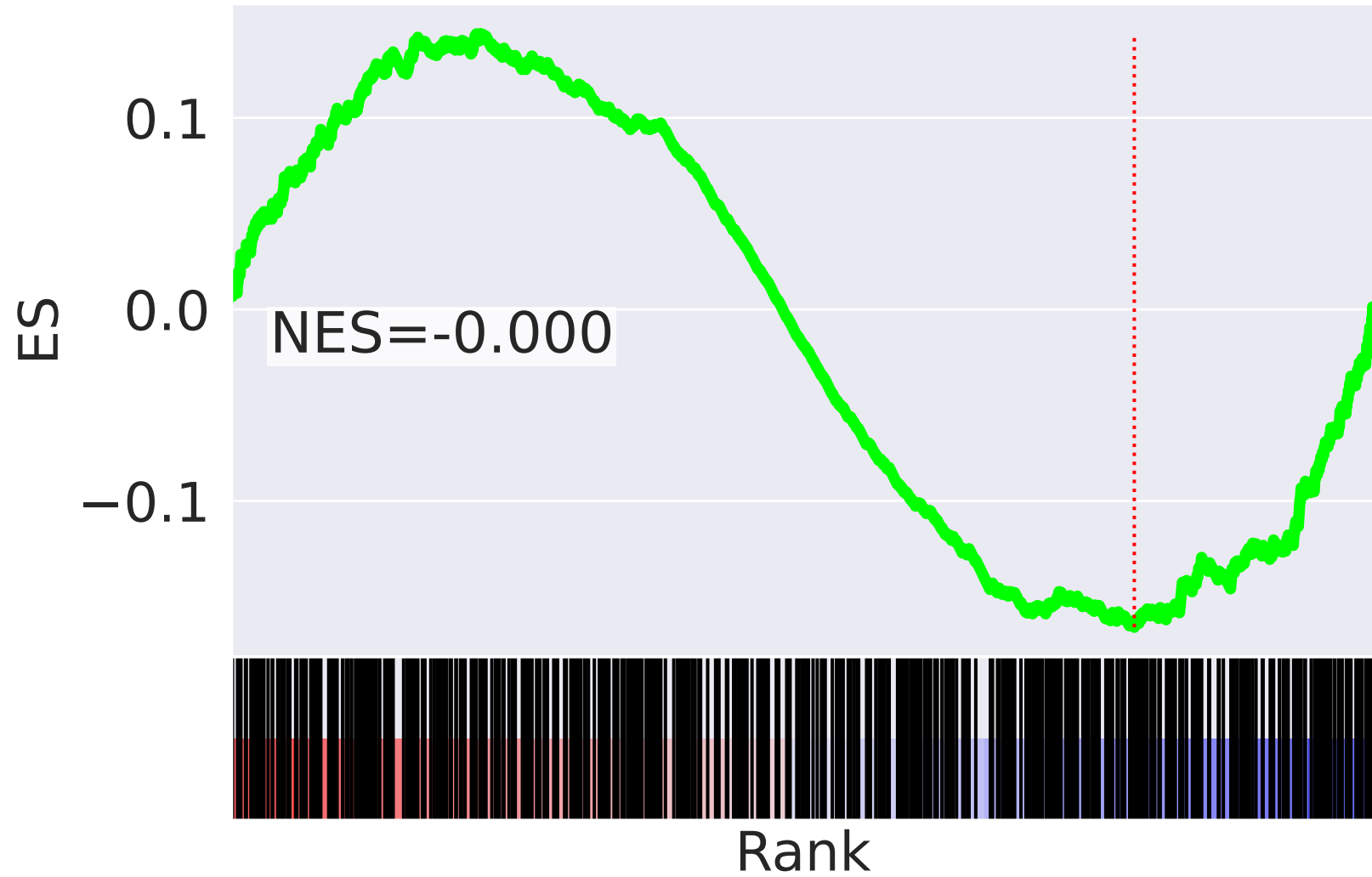
NES		SET
4.154		RNA Polymerase II Pre-transcription Events R-HSA-674695
3.810		PPARA Activates Gene Expression R-HSA-1989781
3.669		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
3.625		Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.537		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
-3.439		Processing Of DNA Double-Strand Break Ends R-HSA-5693607
-3.386		Meiotic Recombination R-HSA-912446
3.372		Transcription Of HIV Genome R-HSA-167172
-3.358		Homology Directed Repair R-HSA-5693538
-3.299		DNA Double-Strand Break Repair R-HSA-5693532
3.297		Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.257		FCGR3A-mediated Phagocytosis R-HSA-9664422
-3.234		HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
-3.164		G2/M DNA Damage Checkpoint R-HSA-69473
-3.079		Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=45$

Signal Transduction R-HSA-162582



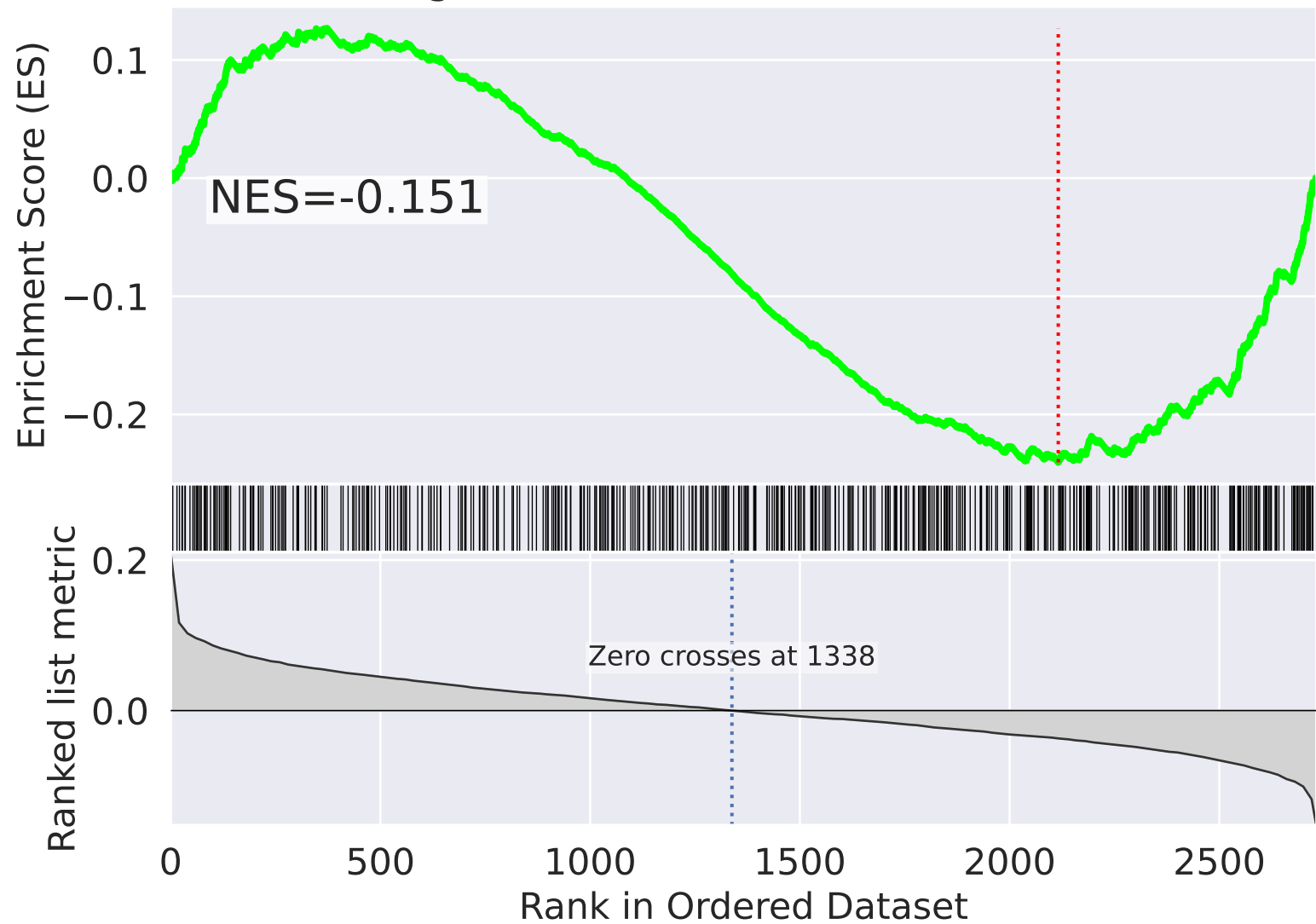
Signal Transduction R-HSA-162582



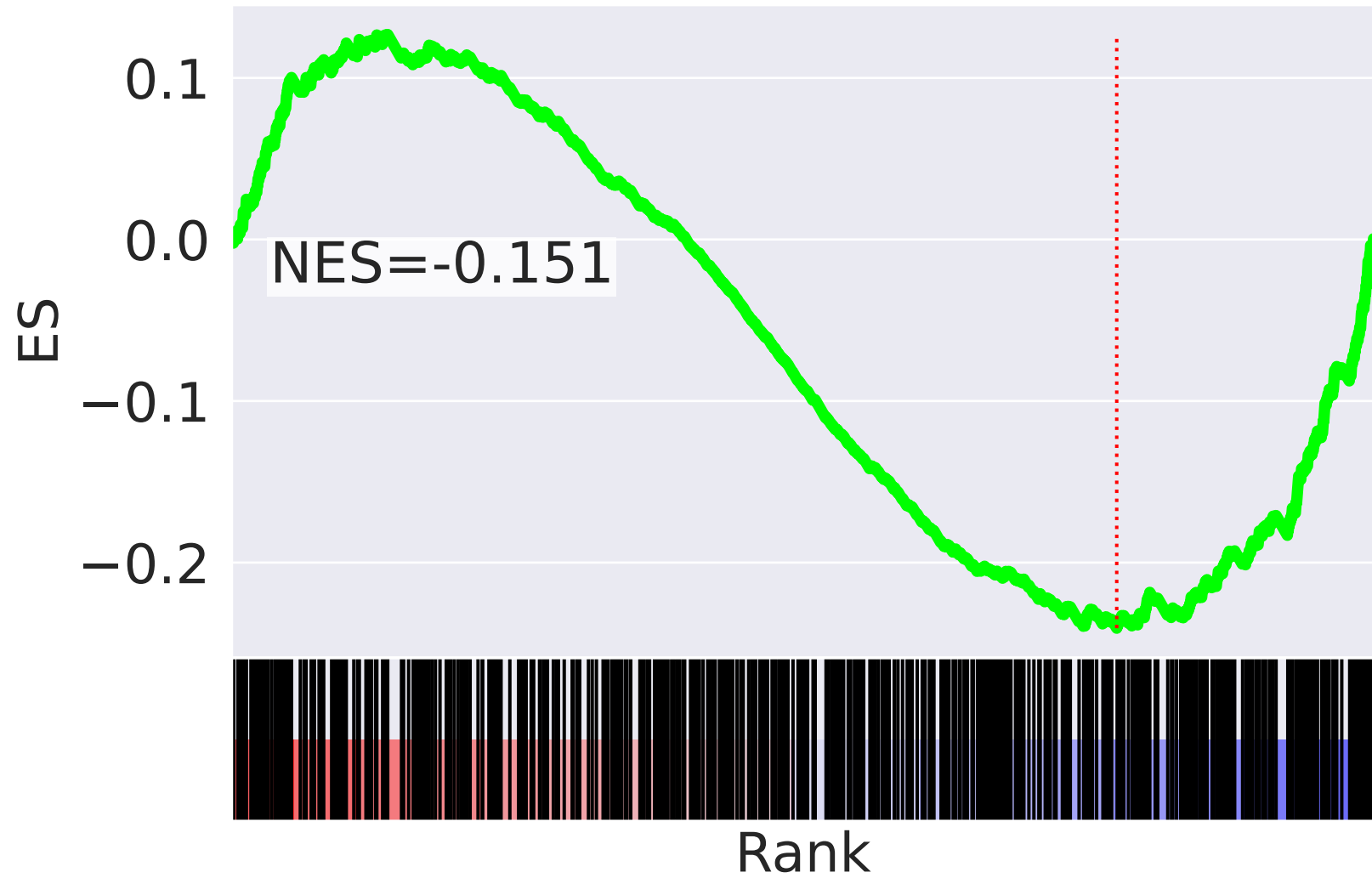
NES	SET
3.986	Transcriptional Regulation By RUNX1 R-HSA-8878171
3.957	Deubiquitination R-HSA-5688426
3.903	Signaling By ROBO Receptors R-HSA-376176
3.888	Hedgehog On State R-HSA-5632684
3.869	Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
3.861	Signaling By Hedgehog R-HSA-5358351
3.827	UCH Proteinases R-HSA-5689603
3.783	Cellular Response To Hypoxia R-HSA-1234174
3.776	ABC-family Proteins Mediated Transport R-HSA-382556
3.695	Degradation Of AXIN R-HSA-4641257
3.659	PTEN Regulation R-HSA-6807070
3.655	Hh Mutants Abrogate Ligand Secretion R-HSA-5387390
3.655	Hedgehog Ligand Biogenesis R-HSA-5358346
3.655	Hh Mutants Are Degraded By ERAD R-HSA-5362768
3.653	ABC Transporter Disorders R-HSA-5619084

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=46$

Signal Transduction R-HSA-162582



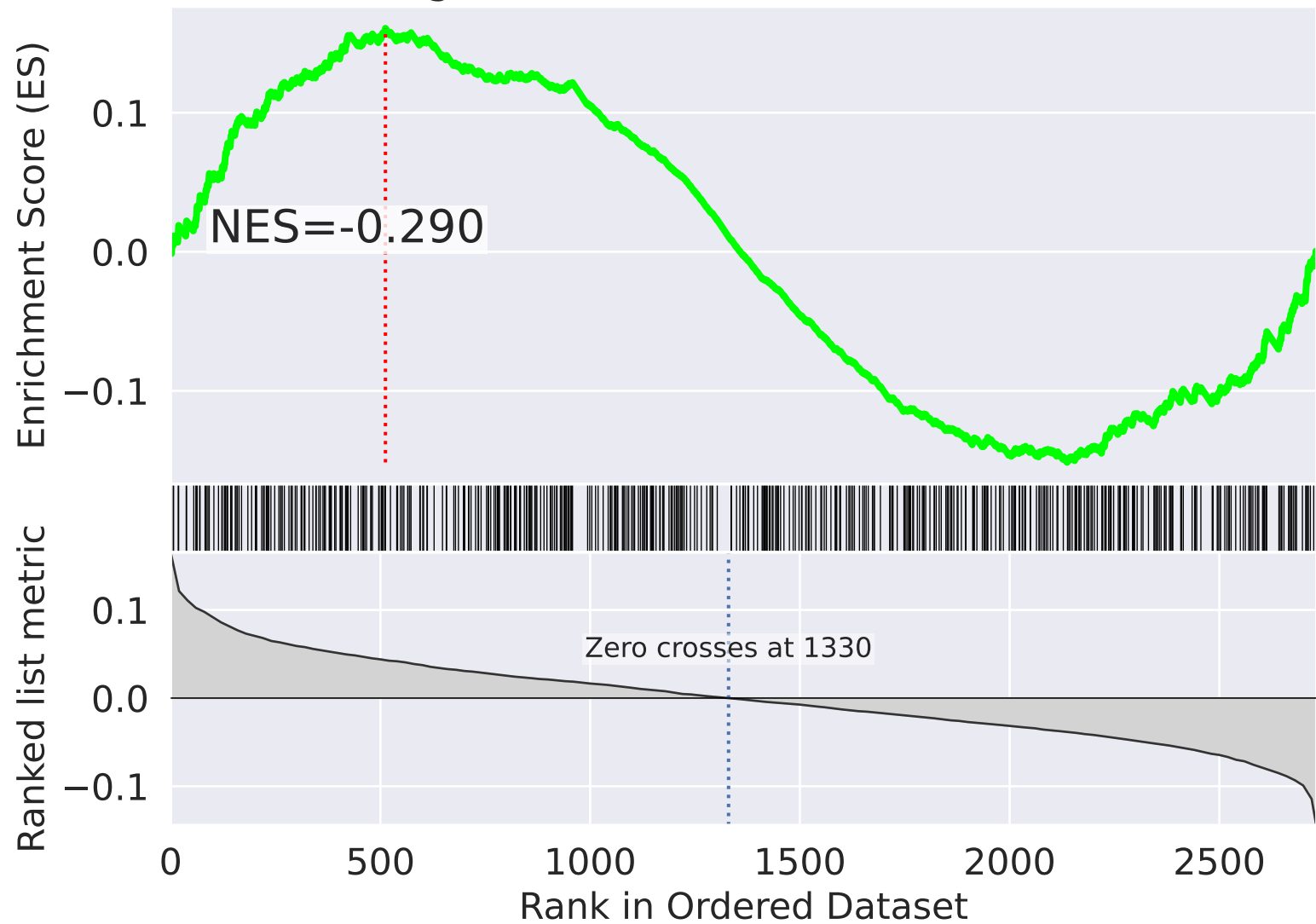
Signal Transduction R-HSA-162582



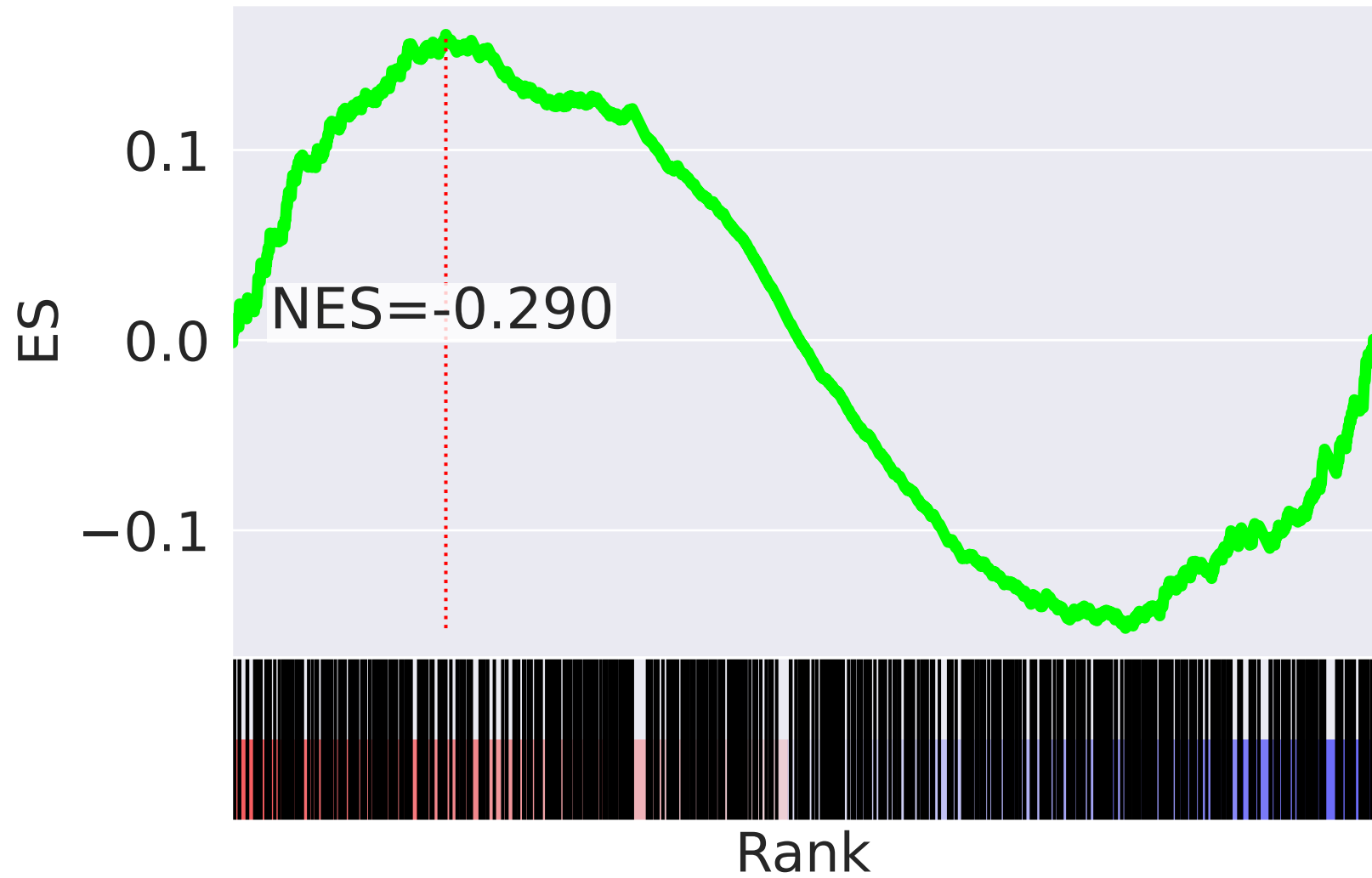
NES	SET
5.636	Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
5.502	HIV Infection R-HSA-162906
5.071	mRNA Splicing R-HSA-72172
4.988	mRNA Splicing - Major Pathway R-HSA-72163
4.912	Synthesis Of DNA R-HSA-69239
4.857	S Phase R-HSA-69242
4.673	Disorders Of Transmembrane Transporters R-HSA-5619115
4.650	SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
4.649	HIV Life Cycle R-HSA-162587
4.648	Late Phase Of HIV Life Cycle R-HSA-162599
4.574	Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
4.561	Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
4.477	G1/S DNA Damage Checkpoints R-HSA-69615
4.457	DNA Replication R-HSA-69306
4.444	Switching Of Origins To A Post-Replicative State R-HSA-69052

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=47$

Signal Transduction R-HSA-162582



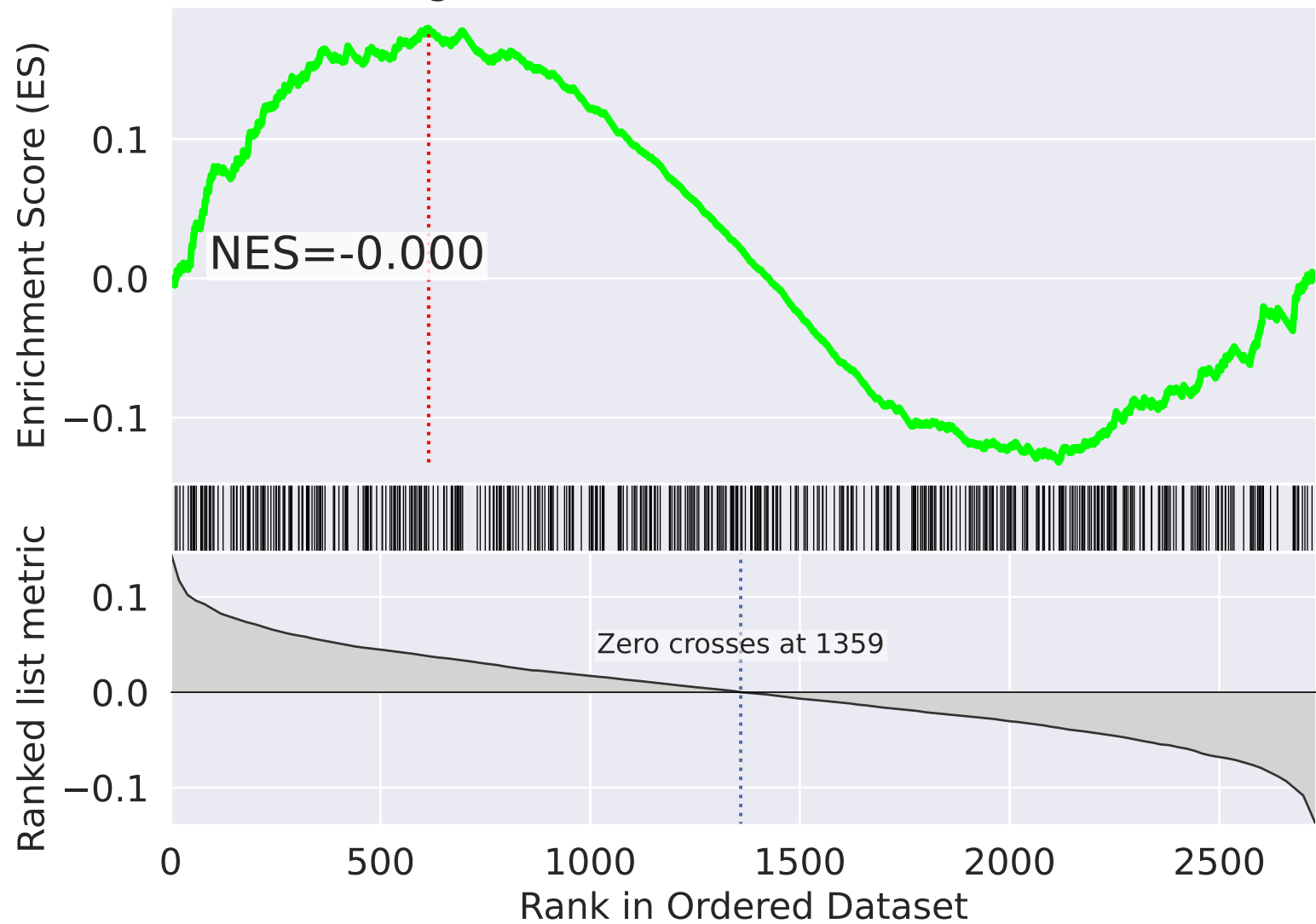
Signal Transduction R-HSA-162582



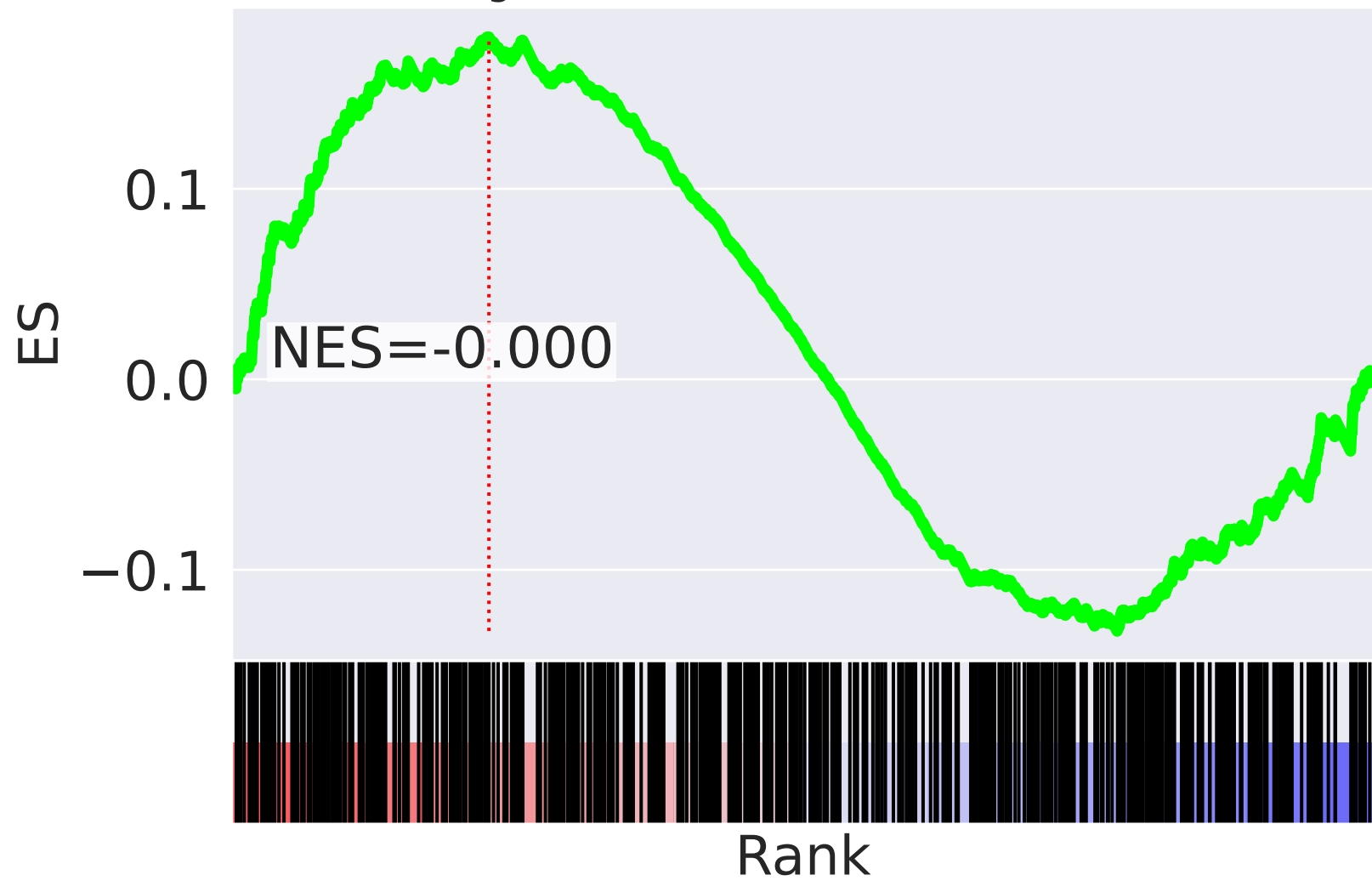
NES		SET
-3.365		rRNA Processing R-HSA-72312
-3.326		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.300		Telomere C-strand (Lagging Strand) Synthesis R-HSA-174417
3.105		Transcriptional Regulation By Small RNAs R-HSA-5578749
-3.102		Complex I Biogenesis R-HSA-6799198
-3.088		Association Of TriC/CCT With Target Proteins During Biosynthesis R-HSA-390471
-3.054		DNA Strand Elongation R-HSA-69190
3.017		Diseases Of Metabolism R-HSA-5668914
2.971		Late Phase Of HIV Life Cycle R-HSA-162599
2.892		Transport Of Mature Transcript To Cytoplasm R-HSA-72202
2.888		HIV Infection R-HSA-162906
2.837		Influenza Infection R-HSA-168255
2.835		Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
2.787		Transcriptional Regulation By RUNX1 R-HSA-8878171
2.785		HIV Life Cycle R-HSA-162587

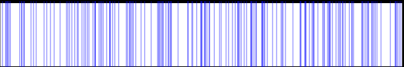


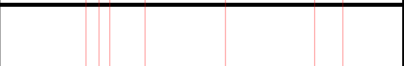
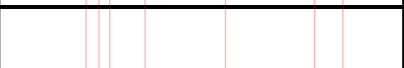
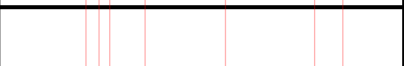
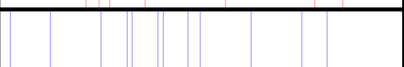


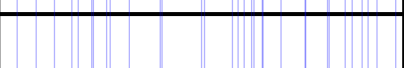
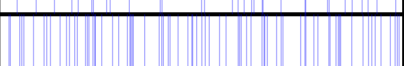
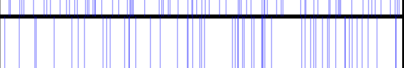
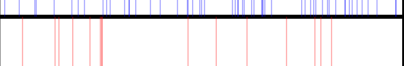
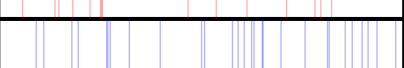

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=48$

Signal Transduction R-HSA-162582



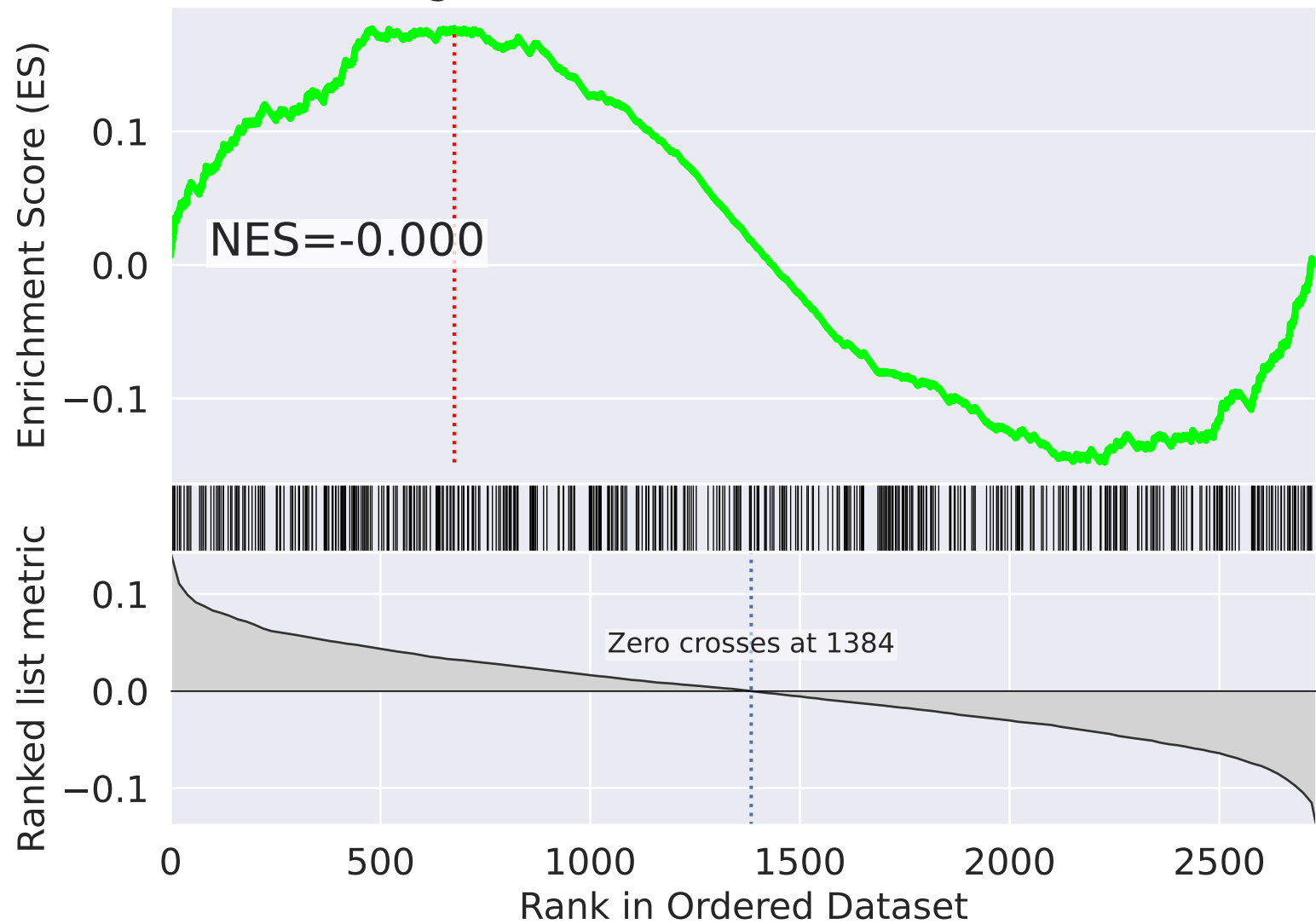
Signal Transduction R-HSA-162582



NES		SET
-3.051		Cell Cycle Checkpoints R-HSA-69620
-2.828		COPII-mediated Vesicle Transport R-HSA-204005
2.655		Base-Excision Repair, AP Site Formation R-HSA-73929
2.655		Cleavage Of Damaged Purine R-HSA-110331
2.655		Cleavage Of Damaged Pyrimidine R-HSA-110329
2.655		Packaging Of Telomere Ends R-HSA-171306
-2.635		Negative Regulation Of MAPK Pathway R-HSA-5675221
-2.629		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-2.583		Diseases Of DNA Repair R-HSA-9675135
-2.583		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-2.557		Mitotic Spindle Checkpoint R-HSA-69618
-2.517		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
2.499		SRP-dependent Cotranslational Protein Targeting To Membrane R-HSA-1799339
-2.469		HDR Thru Single Strand Annealing (SSA) R-HSA-5685938
-2.448		Impaired BRCA2 Binding To RAD51 R-HSA-9709570

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=49$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

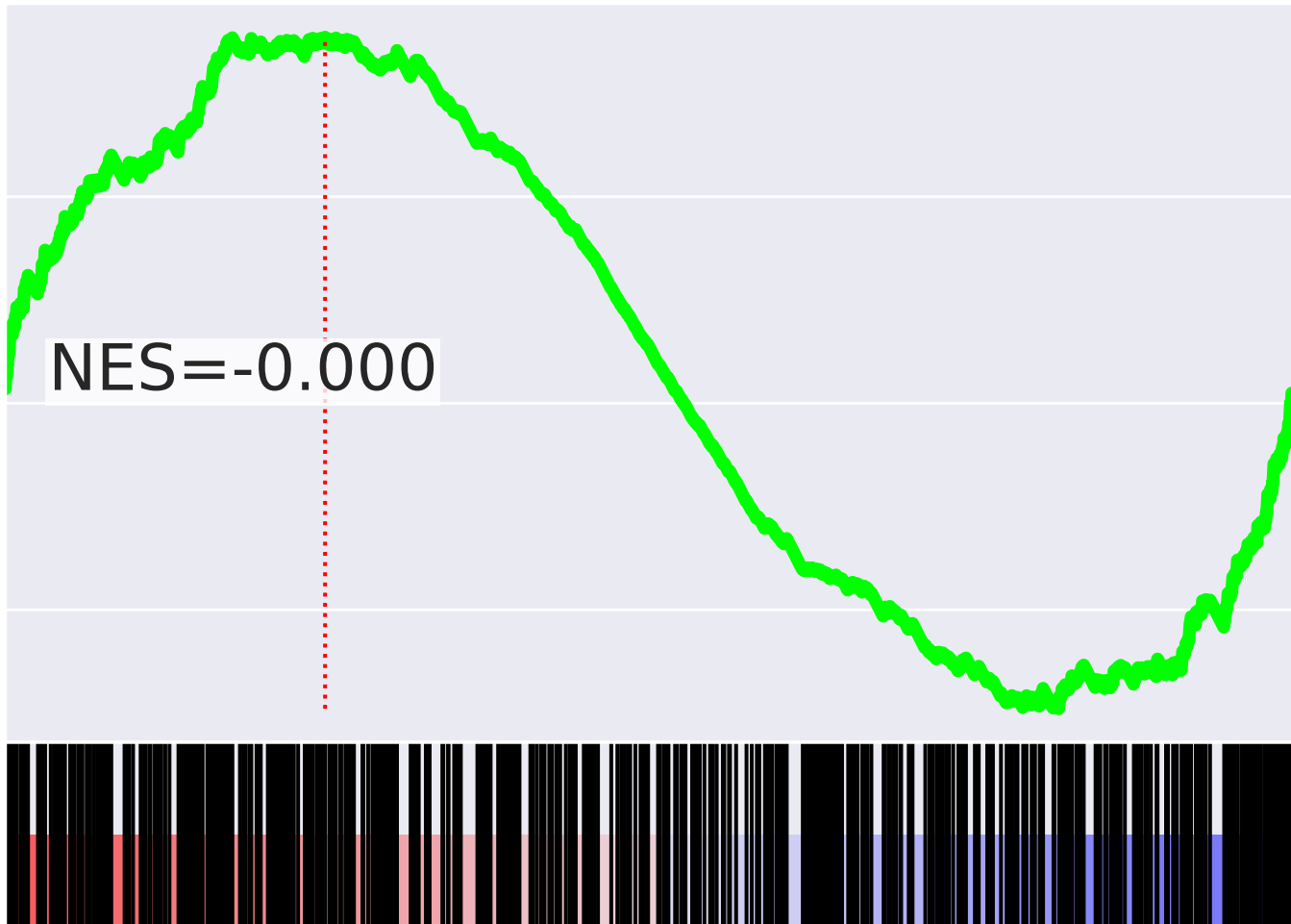
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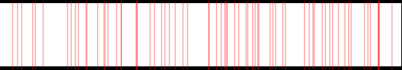
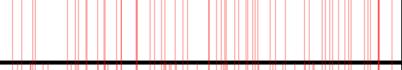
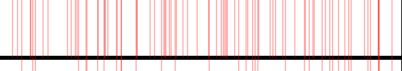

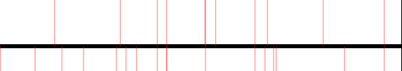
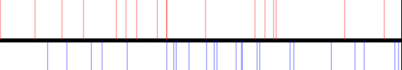

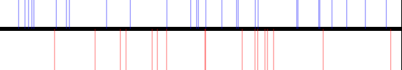
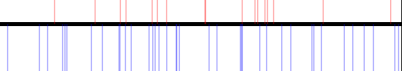
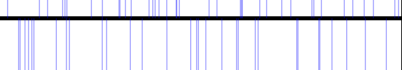
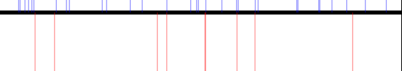
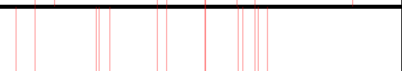



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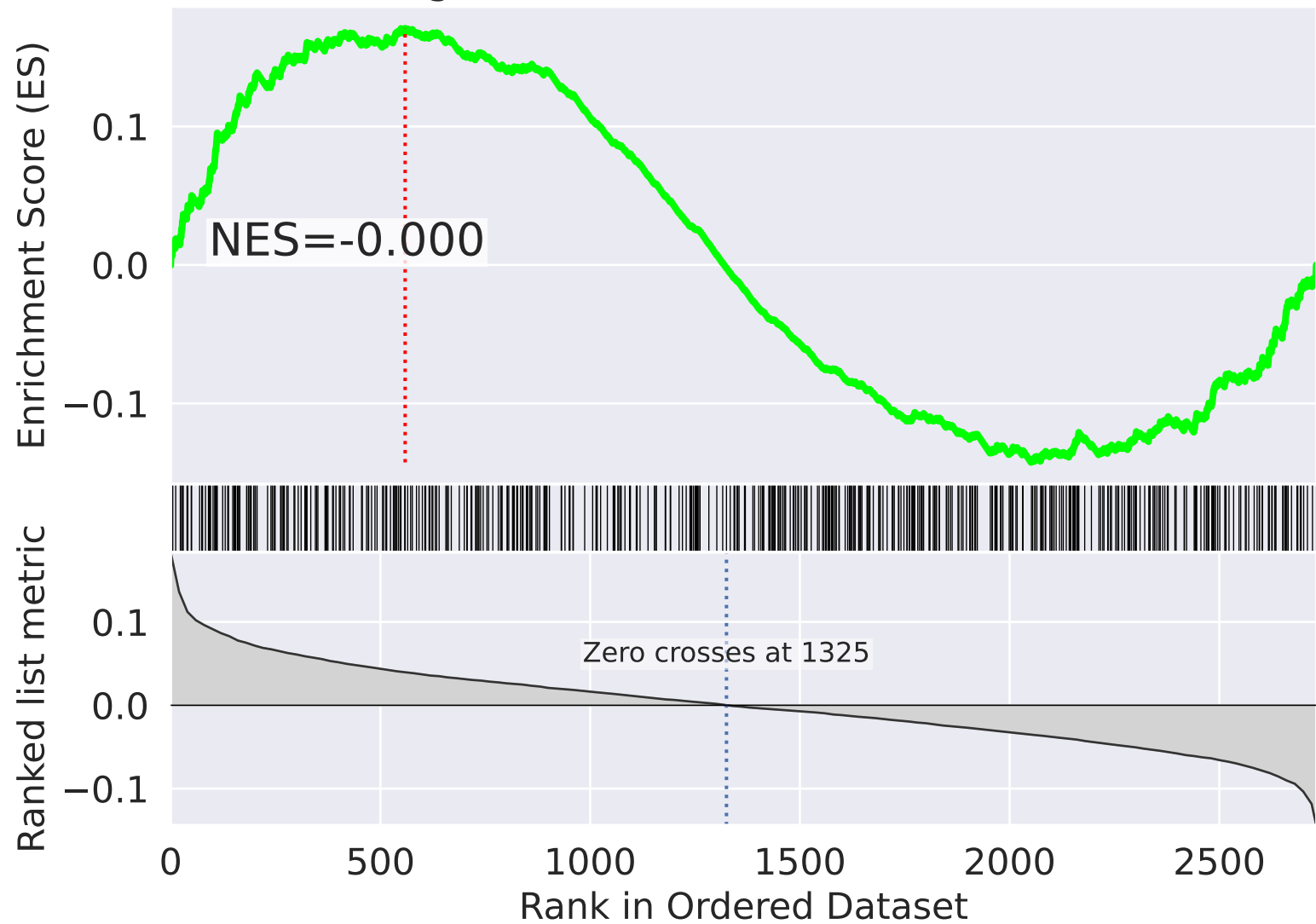
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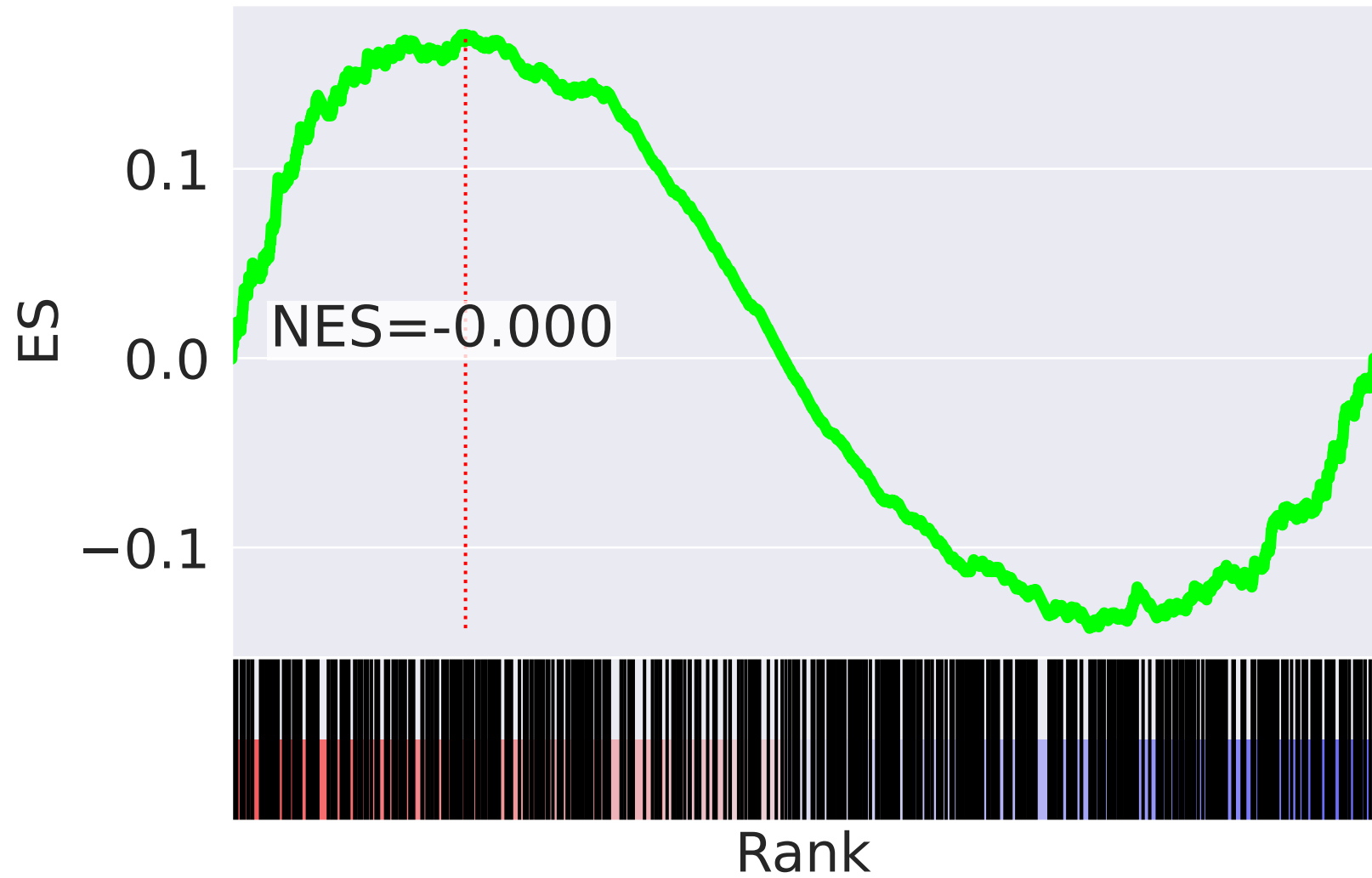
NES		SET
5.794		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.458		Respiratory Electron Transport R-HSA-611105
5.431		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.060		Complex I Biogenesis R-HSA-6799198
3.152		RET Signaling R-HSA-8853659
3.144		Signaling By ERBB4 R-HSA-1236394
-3.117		Iron Uptake And Transport R-HSA-917937
-3.099		Chaperonin-mediated Protein Folding R-HSA-390466
3.089		Constitutive Signaling By Aberrant PI3K In Cancer R-HSA-2219530
-3.085		Cellular Response To Starvation R-HSA-9711097
-3.020		Protein Folding R-HSA-391251
2.941		FLT3 Signaling In Disease R-HSA-9682385
2.890		Signaling By PDGF R-HSA-186797
-2.889		Amino Acids Regulate mTORC1 R-HSA-9639288
-2.884		Endosomal Sorting Complex Required For Transport (ESCRT) R-HSA-917729

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=50$

Signal Transduction R-HSA-162582



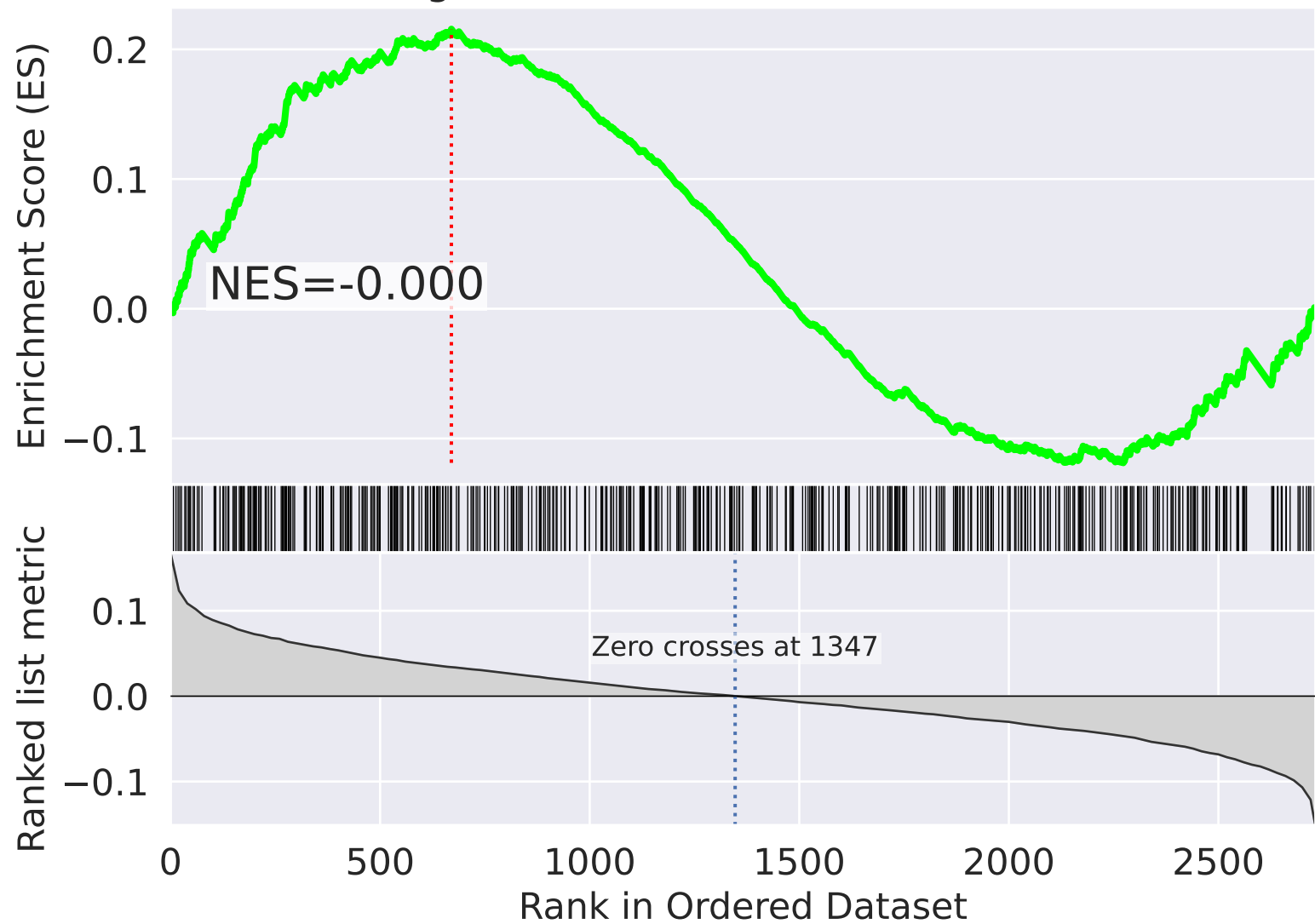
Signal Transduction R-HSA-162582



NES		SET
3.865		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
3.603		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.540		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
3.448		Metabolism Of Lipids R-HSA-556833
-3.338		Mitotic Prometaphase R-HSA-68877
3.286		ESR-mediated Signaling R-HSA-8939211
3.276		RUNX1 Regulates Genes Involved In Megakaryocyte Differentiation And Platelet Function R-HSA-8936459
-3.265		Complex I Biogenesis R-HSA-6799198
3.176		Estrogen-dependent Gene Expression R-HSA-9018519
-3.121		Cilium Assembly R-HSA-5617833
2.954		Signaling By Nuclear Receptors R-HSA-9006931
2.954		MTOR Signaling R-HSA-165159
2.947		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
-2.904		Resolution Of Sister Chromatid Cohesion R-HSA-2500257
-2.883		Regulation Of PLK1 Activity At G2/M Transition R-HSA-2565942

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=51$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.2

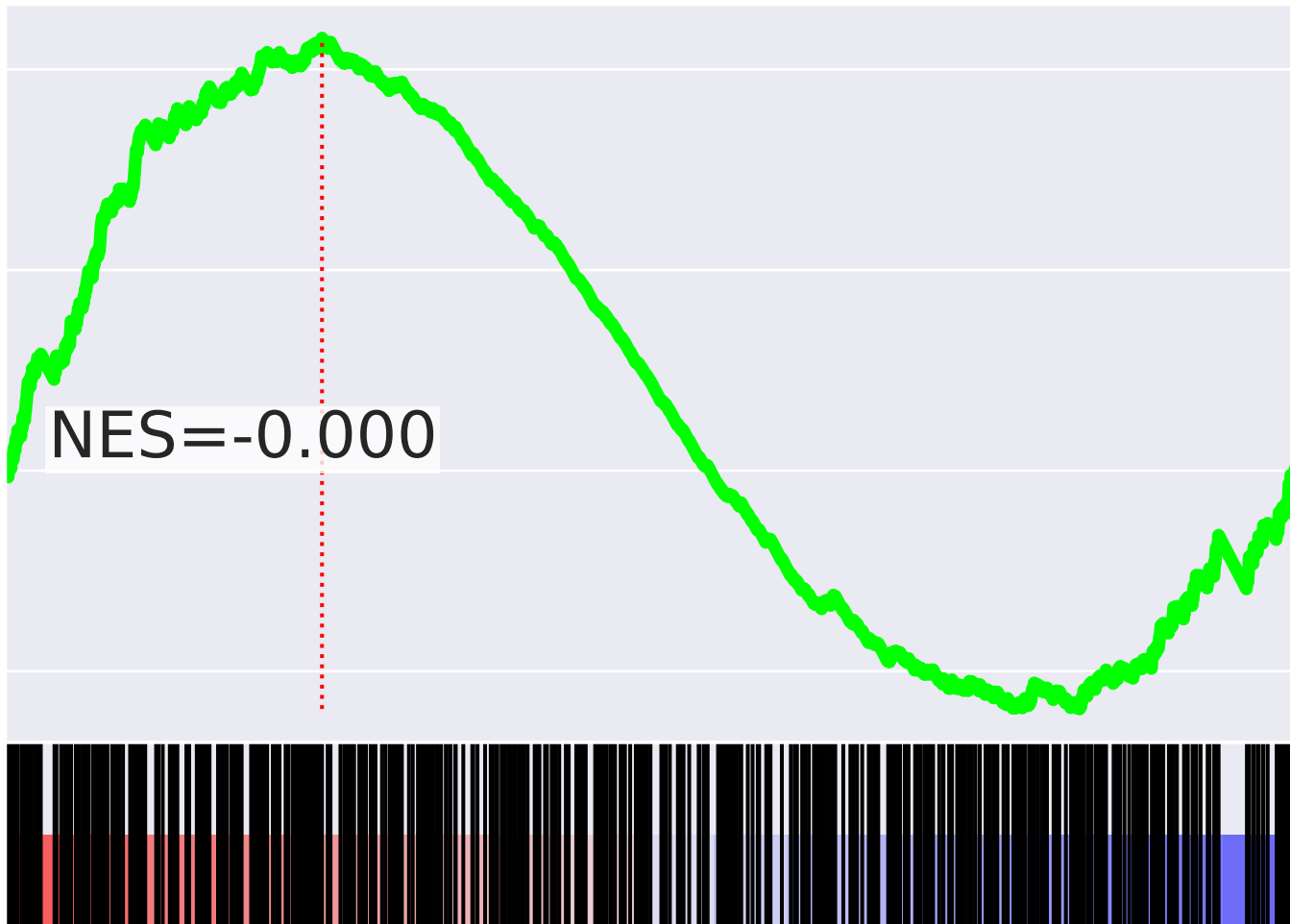
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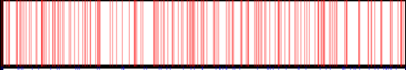
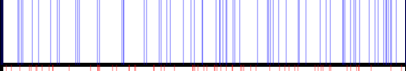
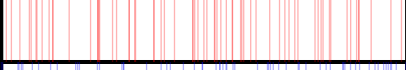
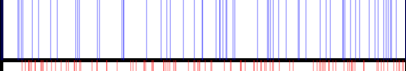
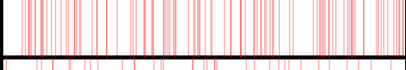
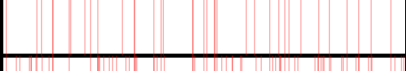
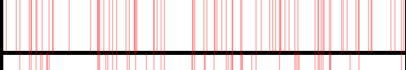
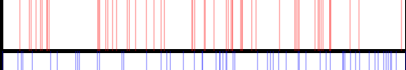
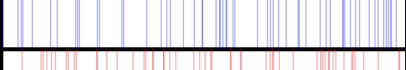
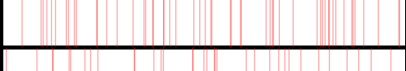
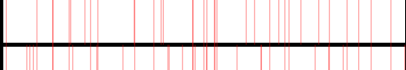
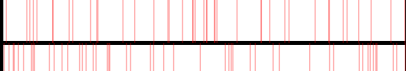
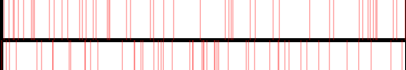
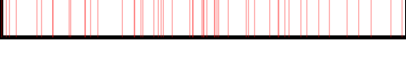
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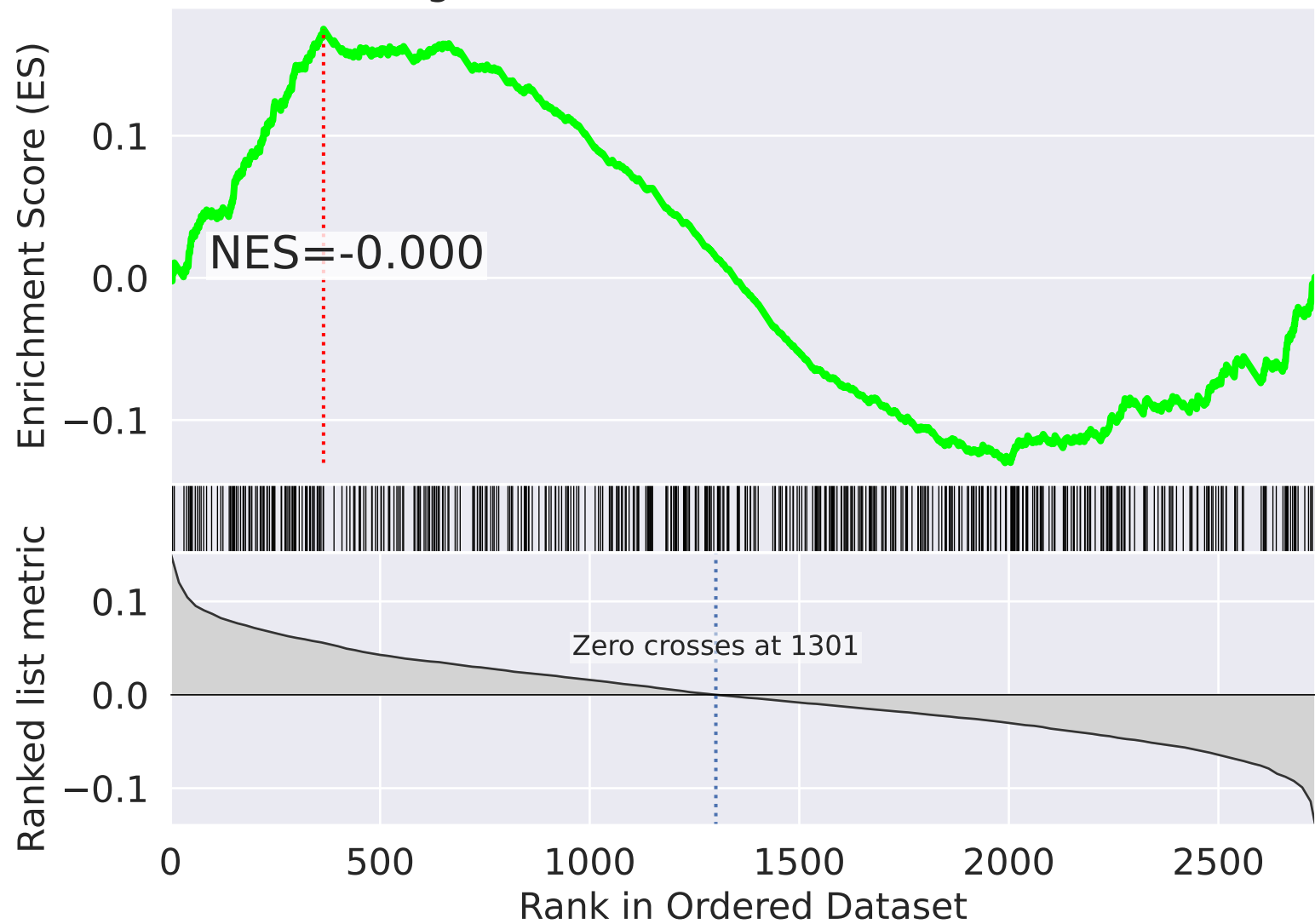
Rank



NES		SET
5.136		Deubiquitination R-HSA-5688426
5.079		Cytokine Signaling In Immune System R-HSA-1280215
-5.034		rRNA Processing R-HSA-72312
4.828		Disorders Of Transmembrane Transporters R-HSA-5619115
-4.762		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.492		Chromatin Modifying Enzymes R-HSA-3247509
4.459		Antiviral Mechanism By IFN-stimulated Genes R-HSA-1169410
4.426		Host Interactions Of HIV Factors R-HSA-162909
4.426		UCH Proteinases R-HSA-5689603
-4.402		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.315		HATs Acetylate Histones R-HSA-3214847
4.302		ISG15 Antiviral Mechanism R-HSA-1169408
4.288		Gene Silencing By RNA R-HSA-211000
4.270		PPARA Activates Gene Expression R-HSA-1989781
4.241		Interferon Signaling R-HSA-913531

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=52$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

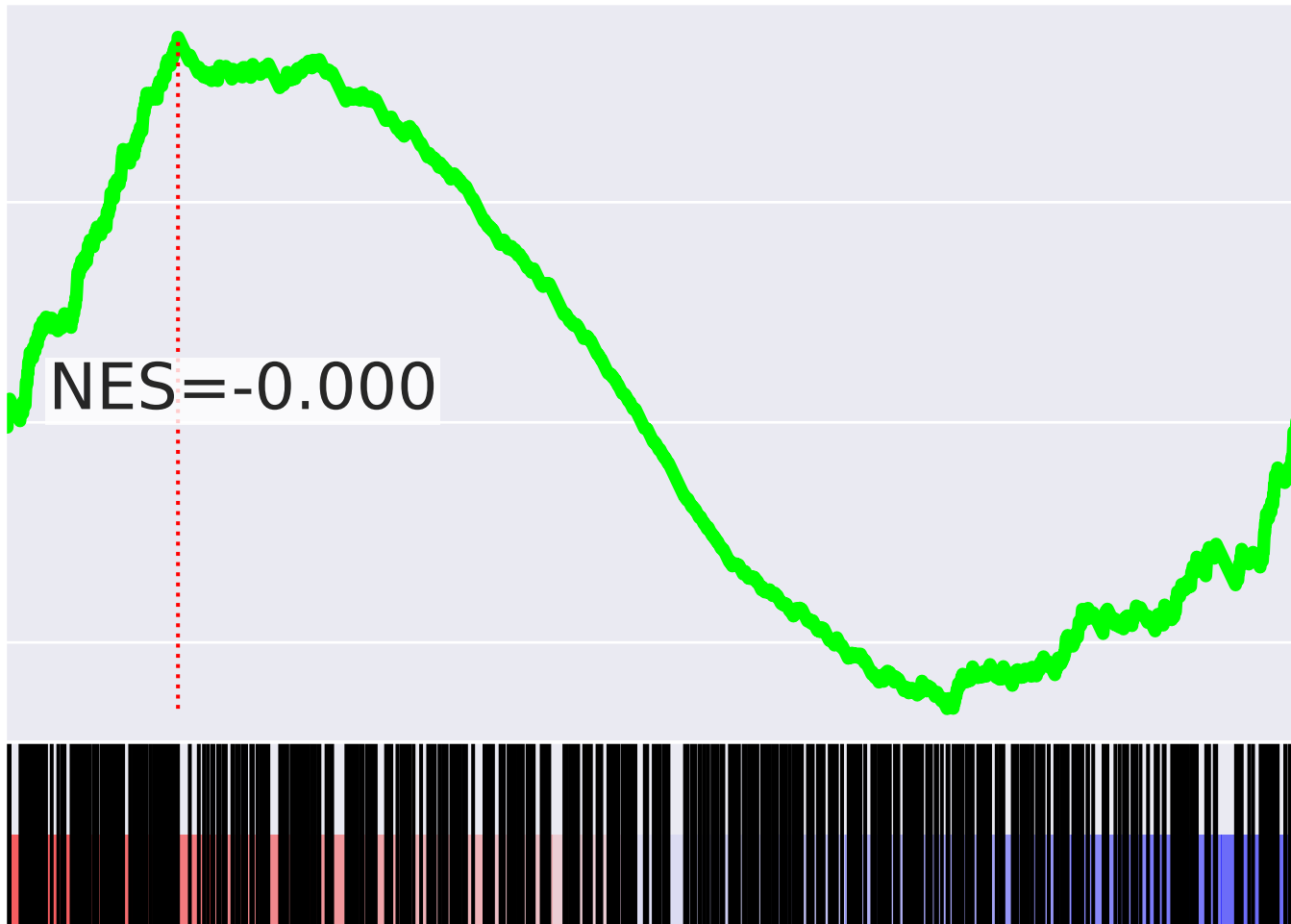
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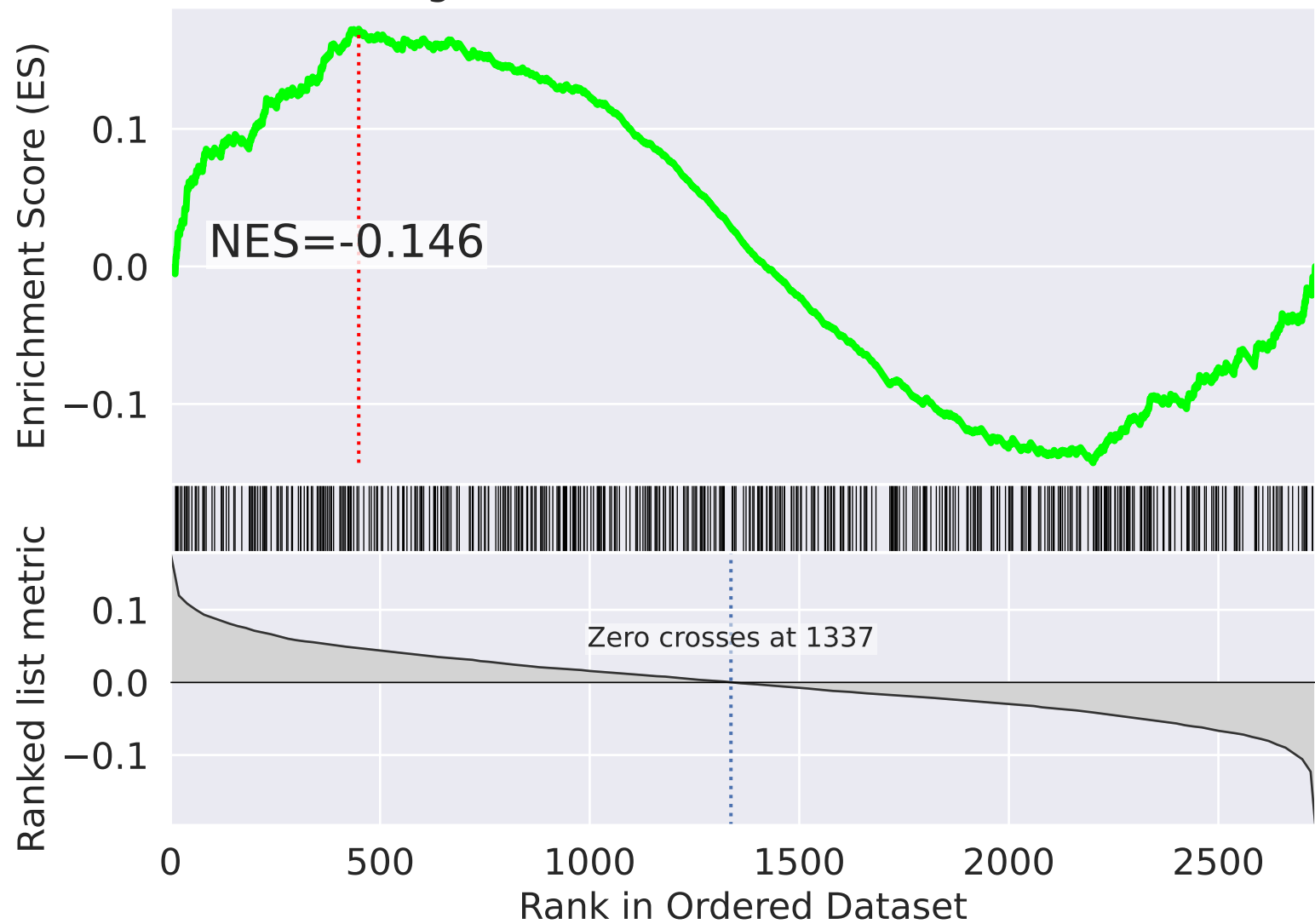
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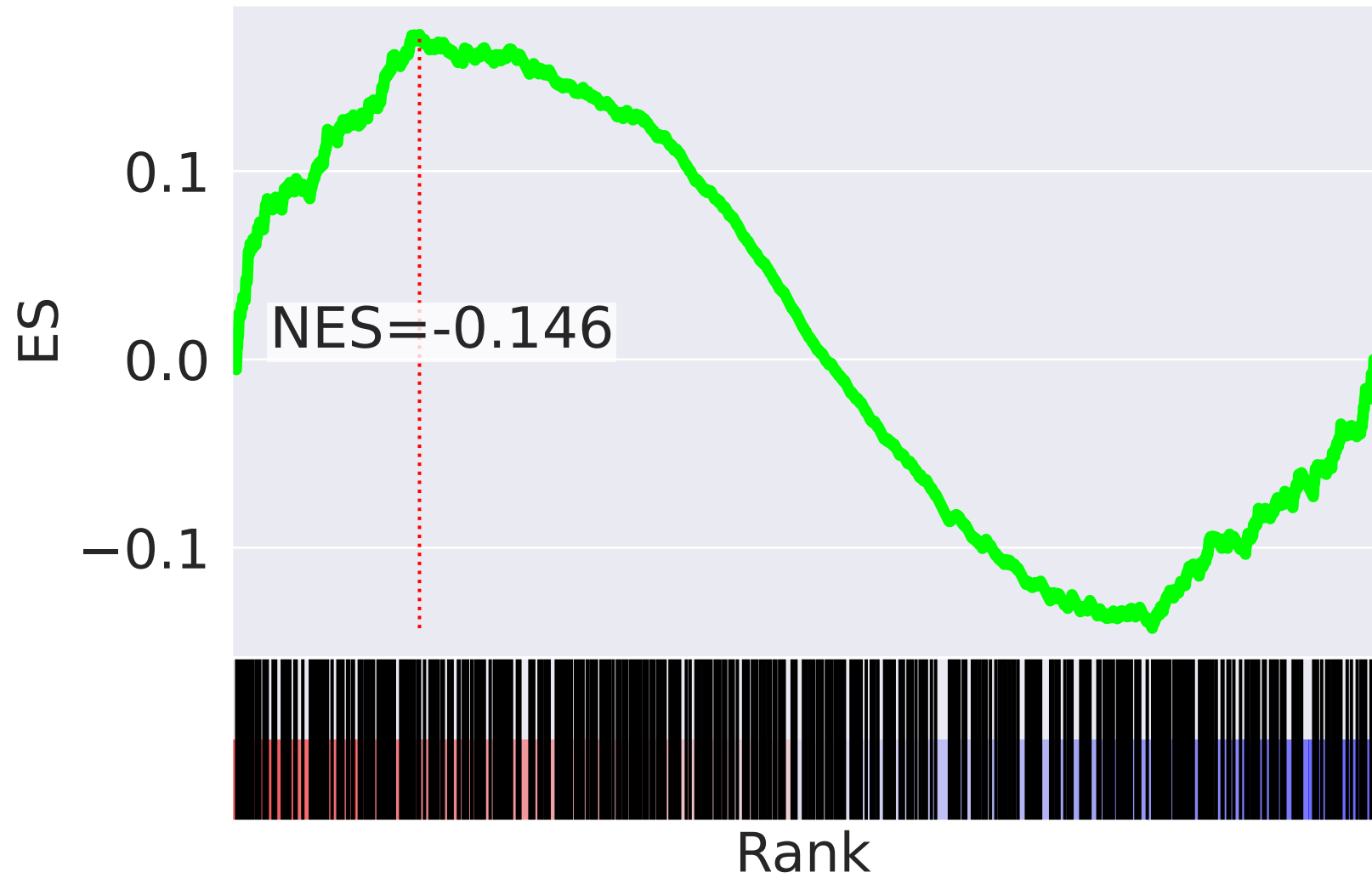
NES	SET
4.998	APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
4.988	APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
4.983	Separation Of Sister Chromatids R-HSA-2467813
4.967	Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
4.944	CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
4.770	Signaling By Hedgehog R-HSA-5358351
4.685	Signaling By ROBO Receptors R-HSA-376176
4.554	Hedgehog On State R-HSA-5632684
4.541	Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
4.533	M Phase R-HSA-68886
4.507	Adaptive Immune System R-HSA-1280218
4.487	Beta-catenin Independent WNT Signaling R-HSA-3858494
4.483	Nervous System Development R-HSA-9675108
4.481	Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
4.436	Hedgehog Off State R-HSA-5610787

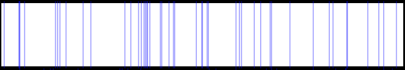

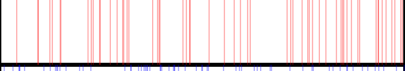
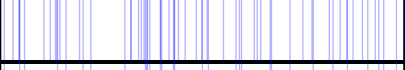
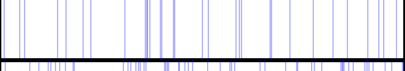
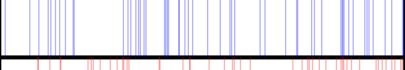
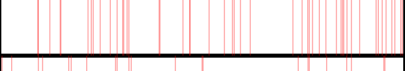
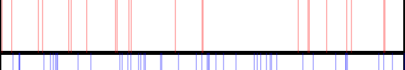
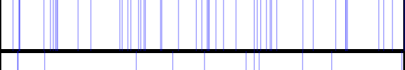

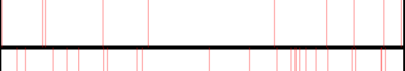
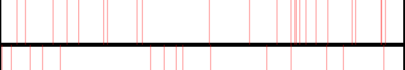
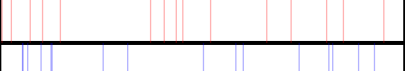
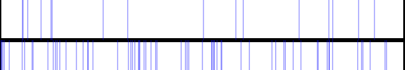
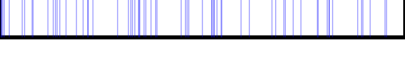
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=53$

Signal Transduction R-HSA-162582



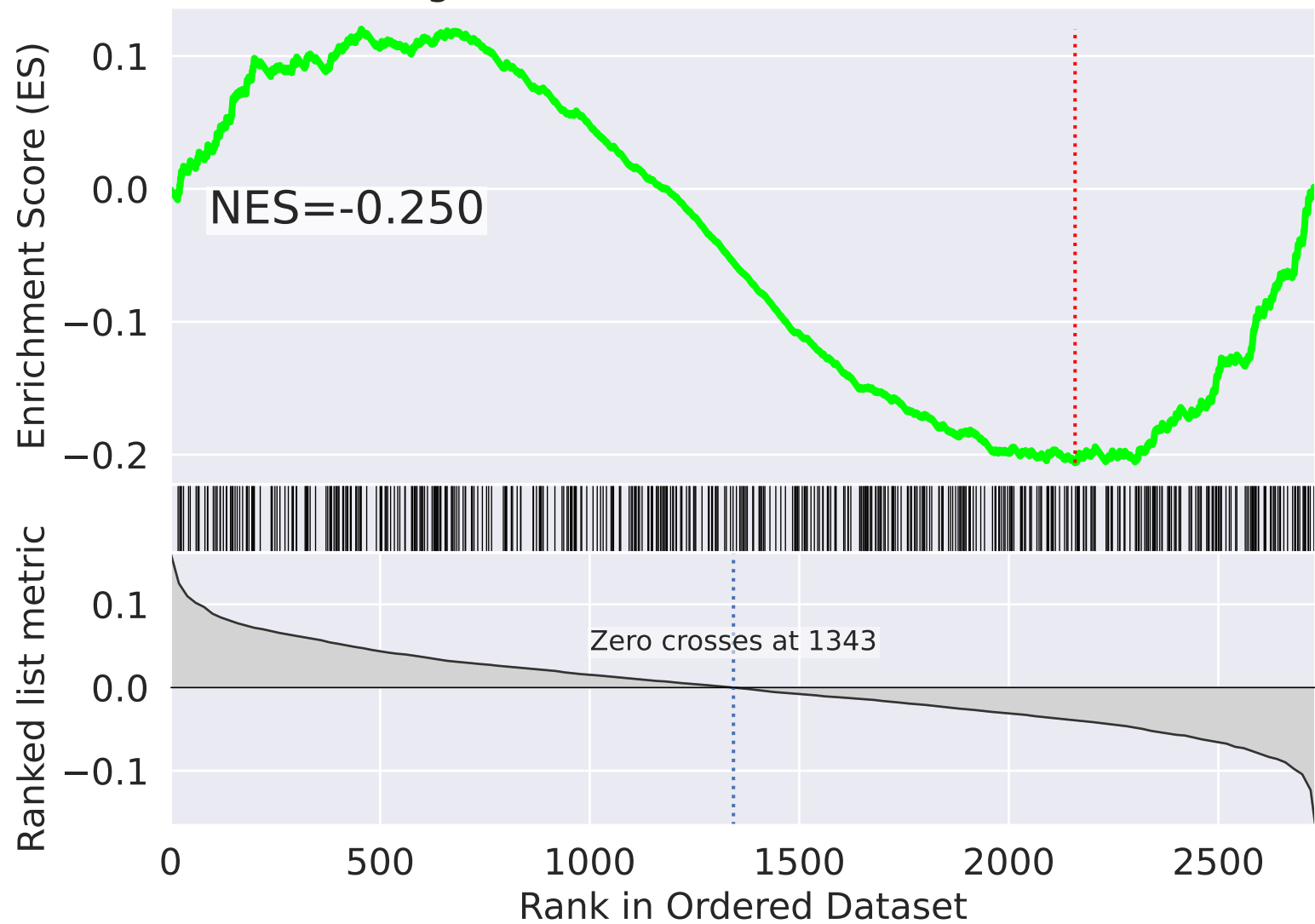
Signal Transduction R-HSA-162582



NES		SET
-3.450		Golgi-to-ER Retrograde Transport R-HSA-8856688
-3.317		COPII-mediated Vesicle Transport R-HSA-204005
3.113		RNA Polymerase II Pre-transcription Events R-HSA-674695
-3.016		Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
-3.001		COPI-dependent Golgi-to-ER Retrograde Traffic R-HSA-6811434
-2.915		Autophagy R-HSA-9612973
2.873		Transcription Of HIV Genome R-HSA-167172
2.815		B-WICH Complex Positively Regulates rRNA Expression R-HSA-5250924
-2.806		ER To Golgi Anterograde Transport R-HSA-199977
-2.785		RHOF GTPase Cycle R-HSA-9035034
2.780		Defective Pyroptosis R-HSA-9710421
2.767		Metabolism Of Nucleotides R-HSA-15869
2.741		RHO GTPases Activate PKNs R-HSA-5625740
-2.735		Cytosolic tRNA Aminoacylation R-HSA-379716
-2.699		Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=54$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

0.1

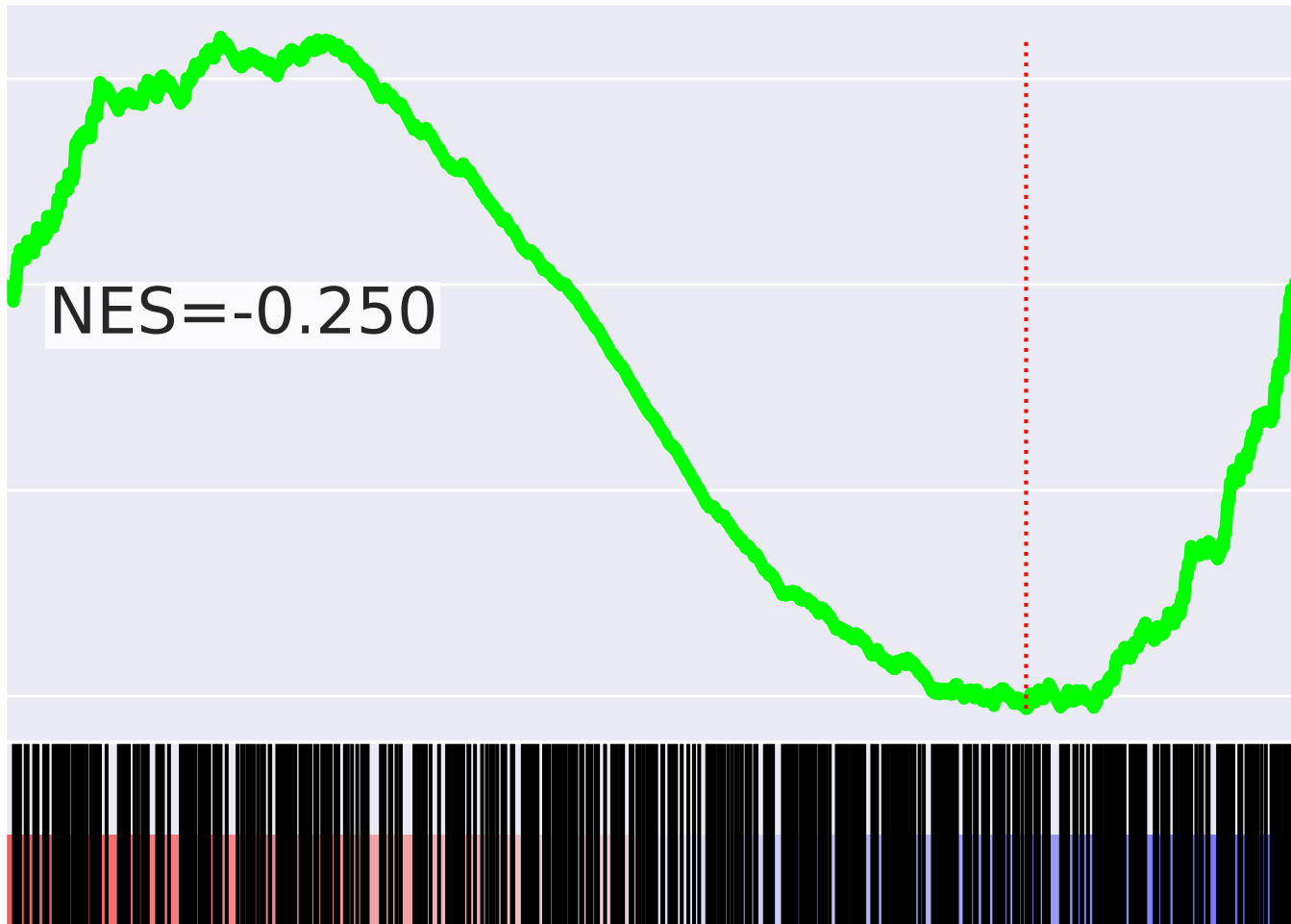
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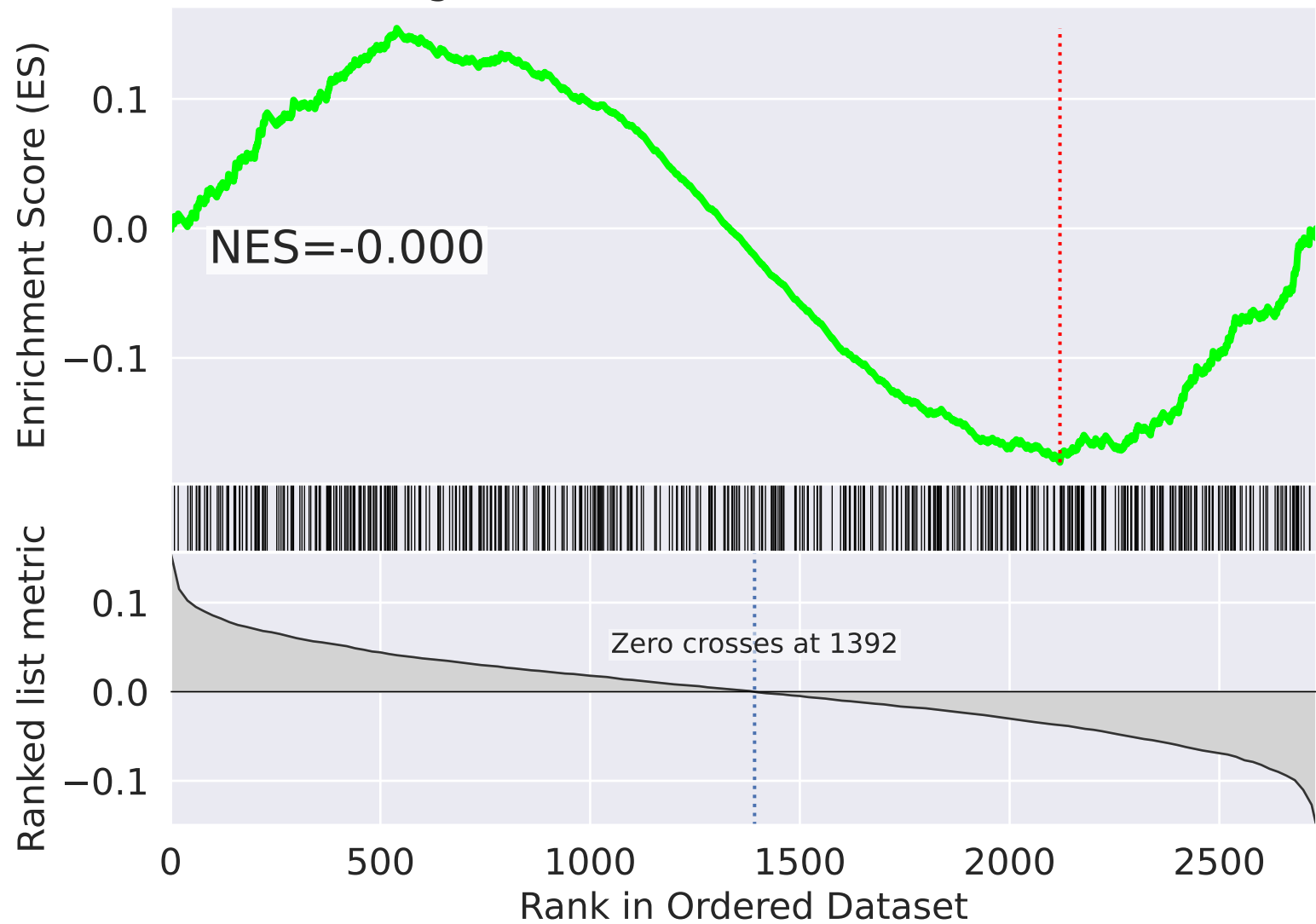
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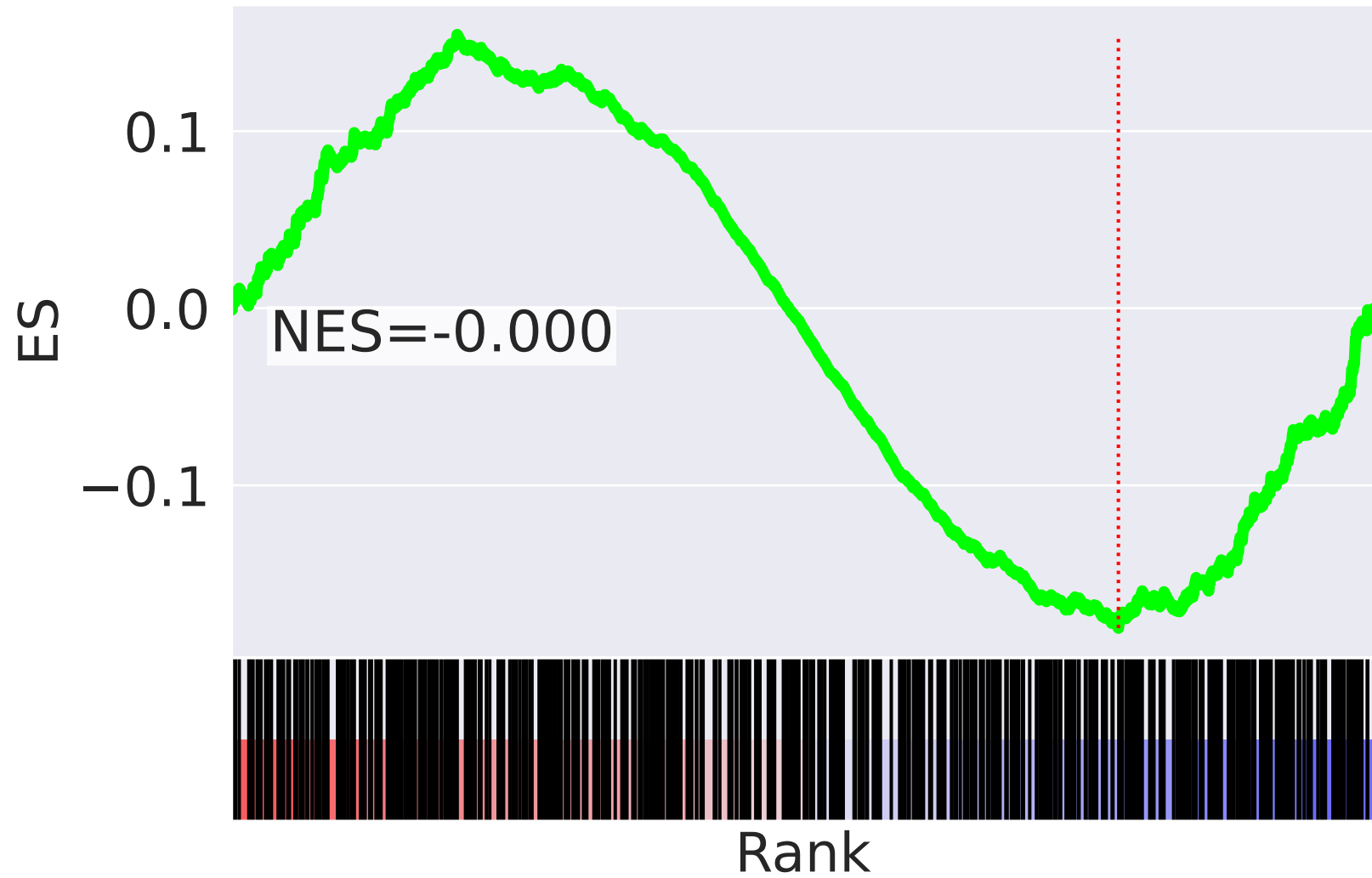
NES	SET
6.062	Respiratory Electron Transport R-HSA-611105
6.019	Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.699	Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.461	Complex I Biogenesis R-HSA-6799198
3.834	Fanconi Anemia Pathway R-HSA-6783310
-3.729	Metabolism Of Carbohydrates R-HSA-71387
-3.597	PPARA Activates Gene Expression R-HSA-1989781
-3.490	Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
-3.481	Cell-Cell Communication R-HSA-1500931
3.323	Mitochondrial tRNA Aminoacylation R-HSA-379726
3.266	TP53 Regulates Metabolic Genes R-HSA-5628897
-3.137	Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
-3.133	PERK Regulates Gene Expression R-HSA-381042
-3.130	rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.077	ATF4 Activates Genes In Response To Endoplasmic Reticulum Stress R-HSA-380994

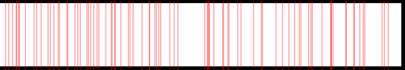
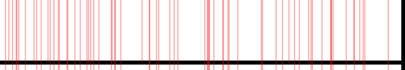
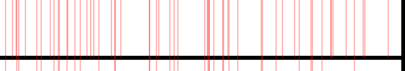
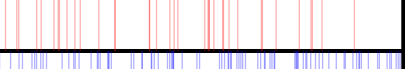
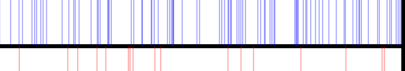


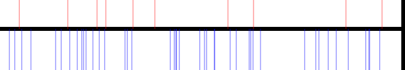
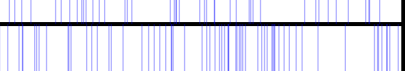
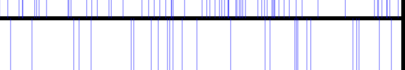

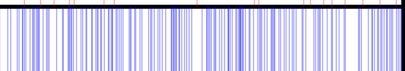

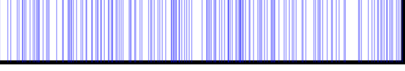

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=55$

Signal Transduction R-HSA-162582



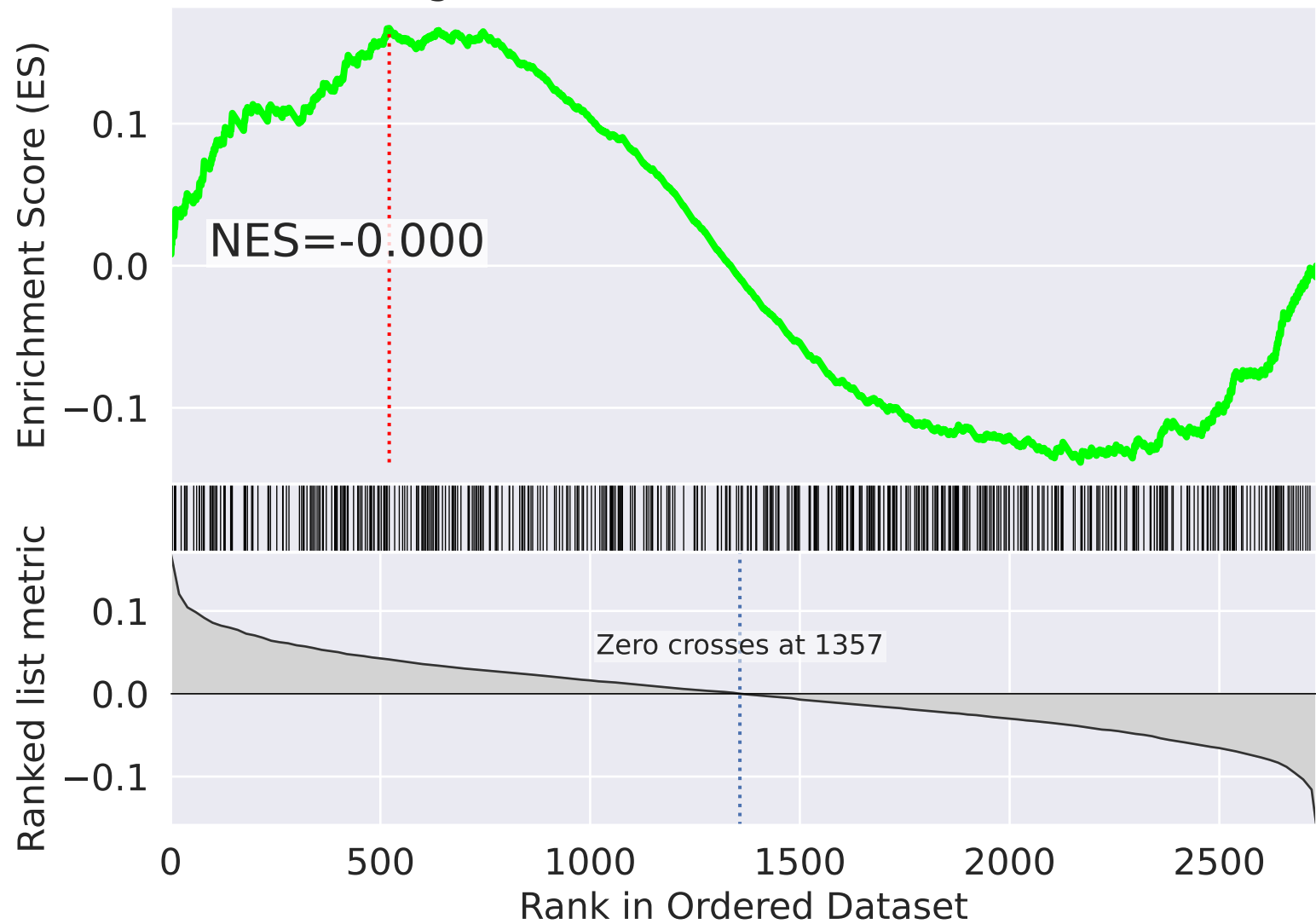
Signal Transduction R-HSA-162582



NES		SET
4.704		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.165		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.086		Respiratory Electron Transport R-HSA-611105
4.014		Complex I Biogenesis R-HSA-6799198
-3.316		Asparagine N-linked Glycosylation R-HSA-446203
3.248		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-3.139		NOTCH1 Intracellular Domain Regulates Transcription R-HSA-2122947
3.086		Citric Acid Cycle (TCA Cycle) R-HSA-71403
-3.084		Nuclear Envelope (NE) Reassembly R-HSA-2995410
-3.061		Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
-3.033		Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
3.006		Signaling By FGFR2 In Disease R-HSA-5655253
-2.888		Vesicle-mediated Transport R-HSA-5653656
-2.873		Retrograde Transport At Trans-Golgi-Network R-HSA-6811440
-2.808		Membrane Trafficking R-HSA-199991

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=56$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

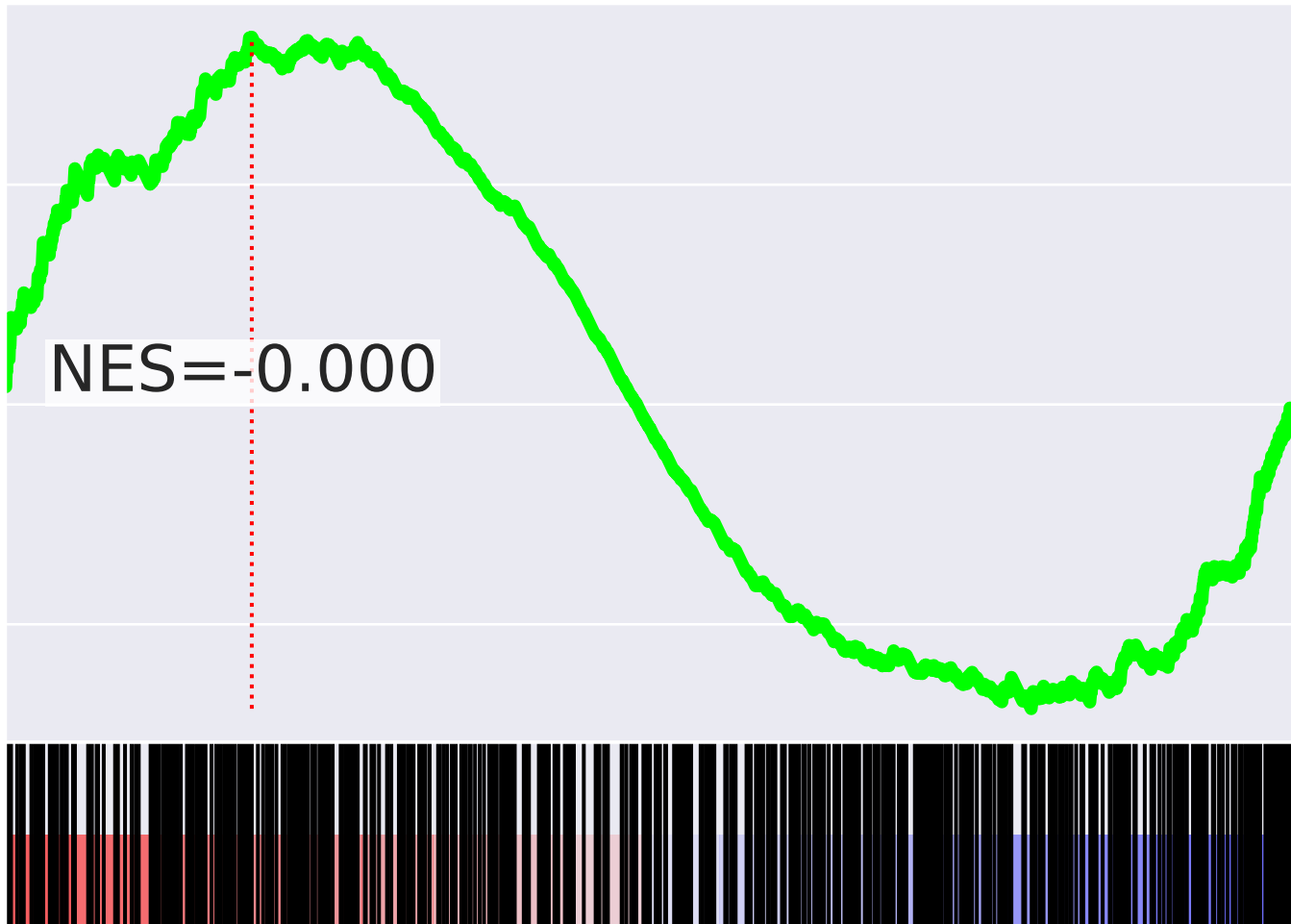
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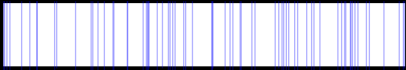
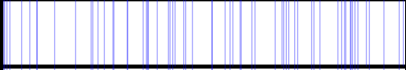
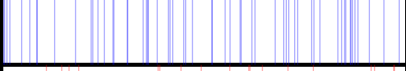
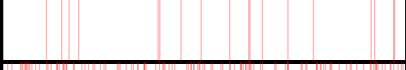
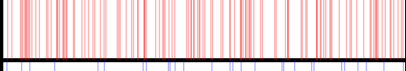
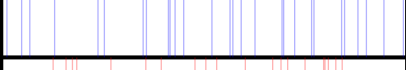
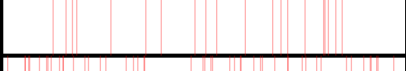
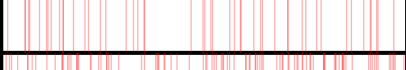
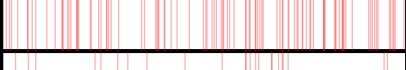
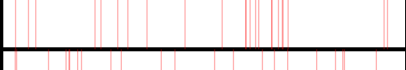
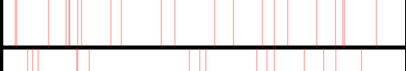
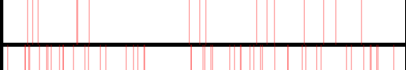
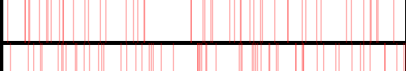
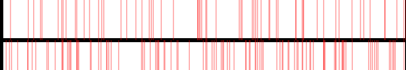
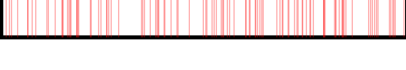
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Rank



NES		SET
-5.139		rRNA Processing R-HSA-72312
-5.001		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.949		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.385		FOXO-mediated Transcription R-HSA-9614085
3.286		Metabolism Of Lipids R-HSA-556833
-3.189		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
3.186		Diseases Of Programmed Cell Death R-HSA-9645723
3.102		PPARA Activates Gene Expression R-HSA-1989781
3.043		PIP3 Activates AKT Signaling R-HSA-1257604
2.986		Cell Surface Interactions At Vascular Wall R-HSA-202733
2.980		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
2.976		Transcriptional Regulation By E2F6 R-HSA-8953750
2.975		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
2.958		HCMV Infection R-HSA-9609646
2.934		Intracellular Signaling By Second Messengers R-HSA-9006925