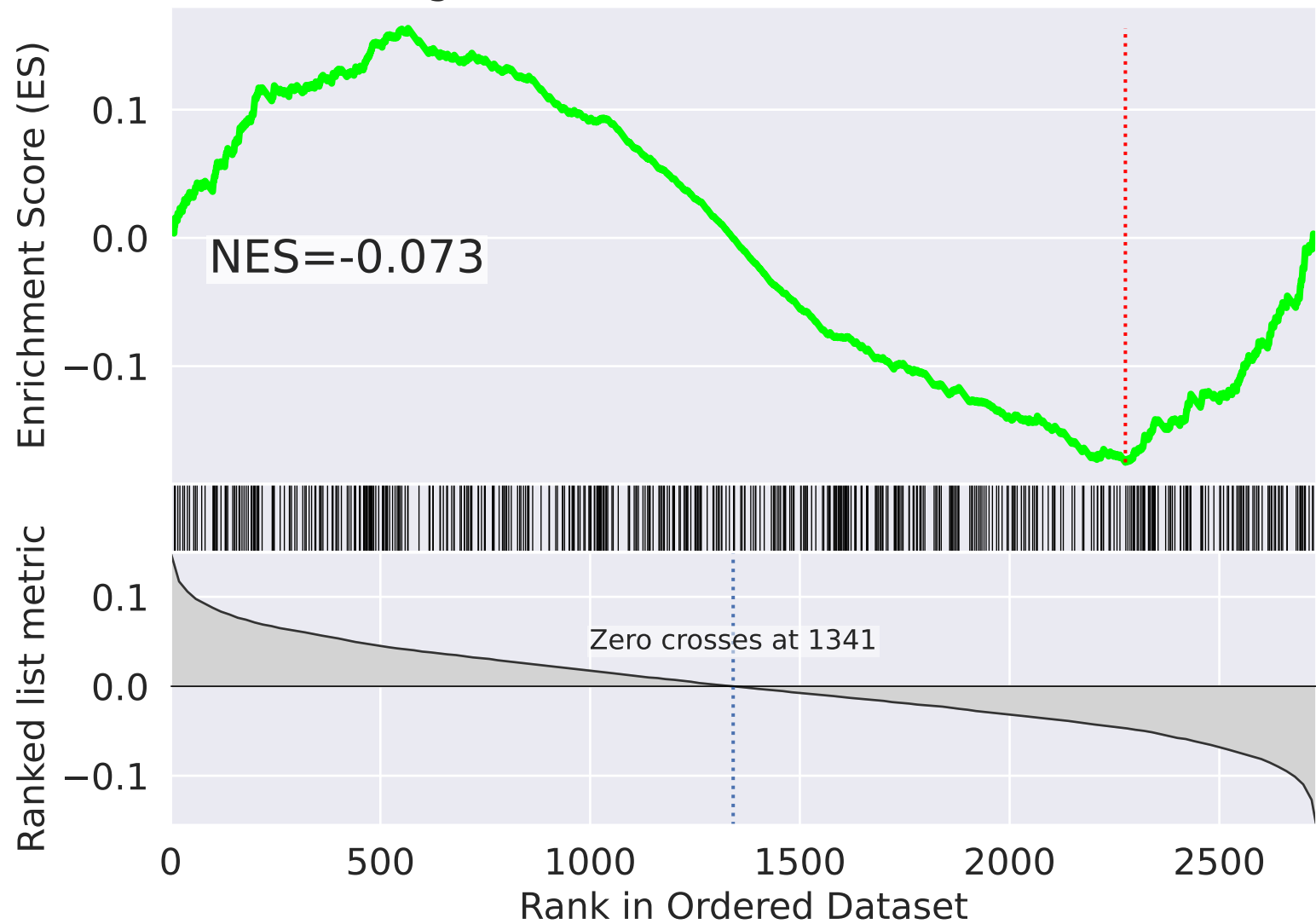
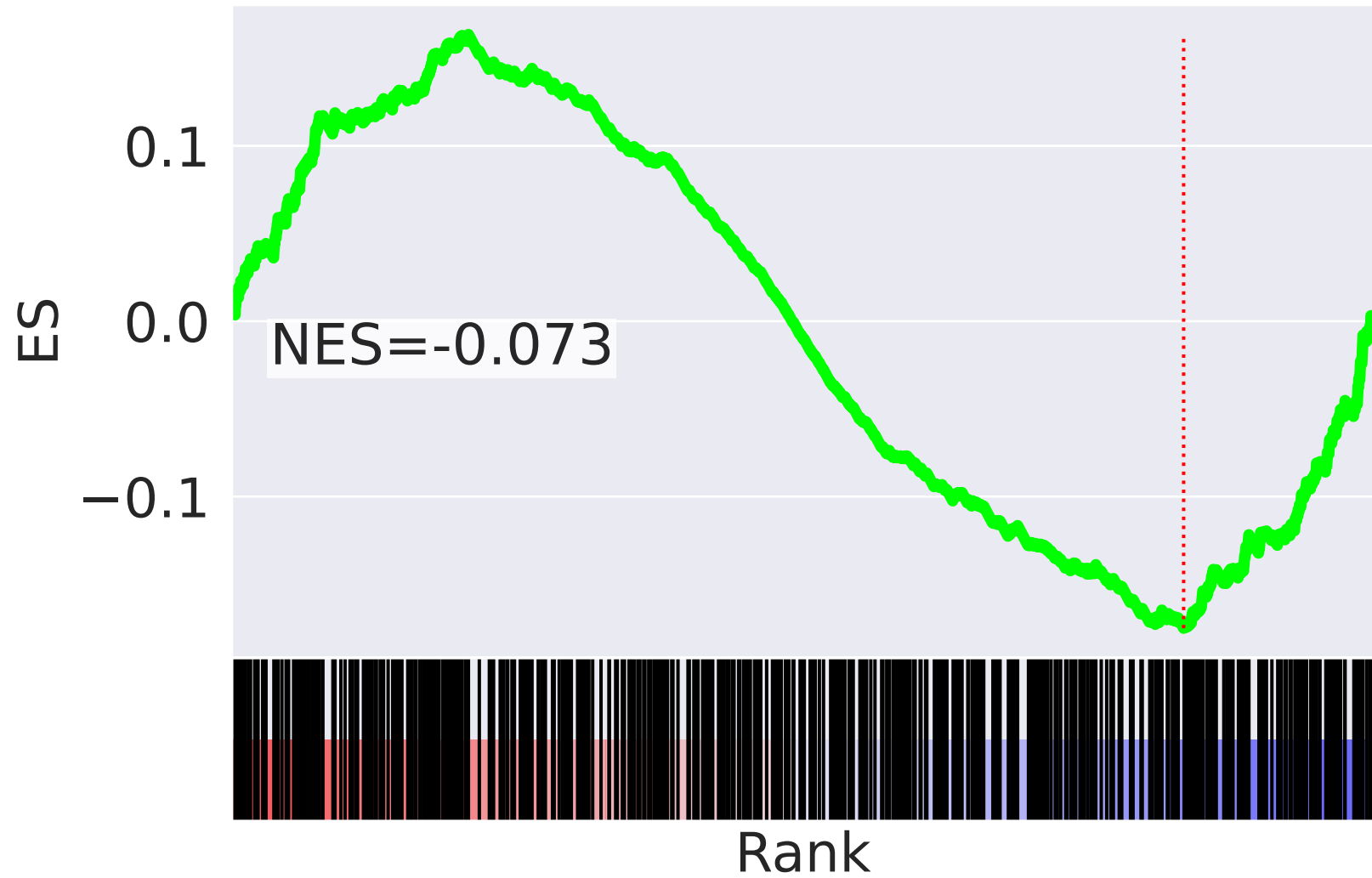



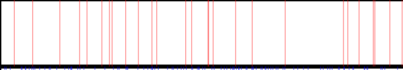
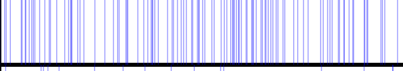
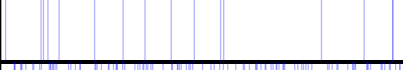
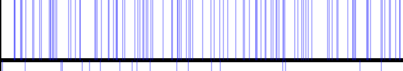
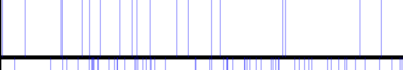
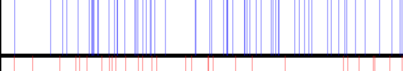
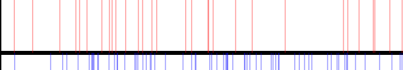
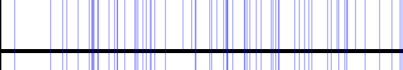
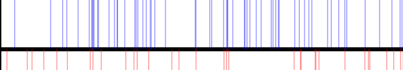
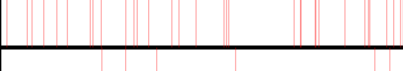


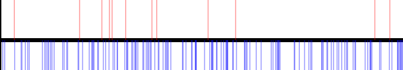

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=1$

Signal Transduction R-HSA-162582



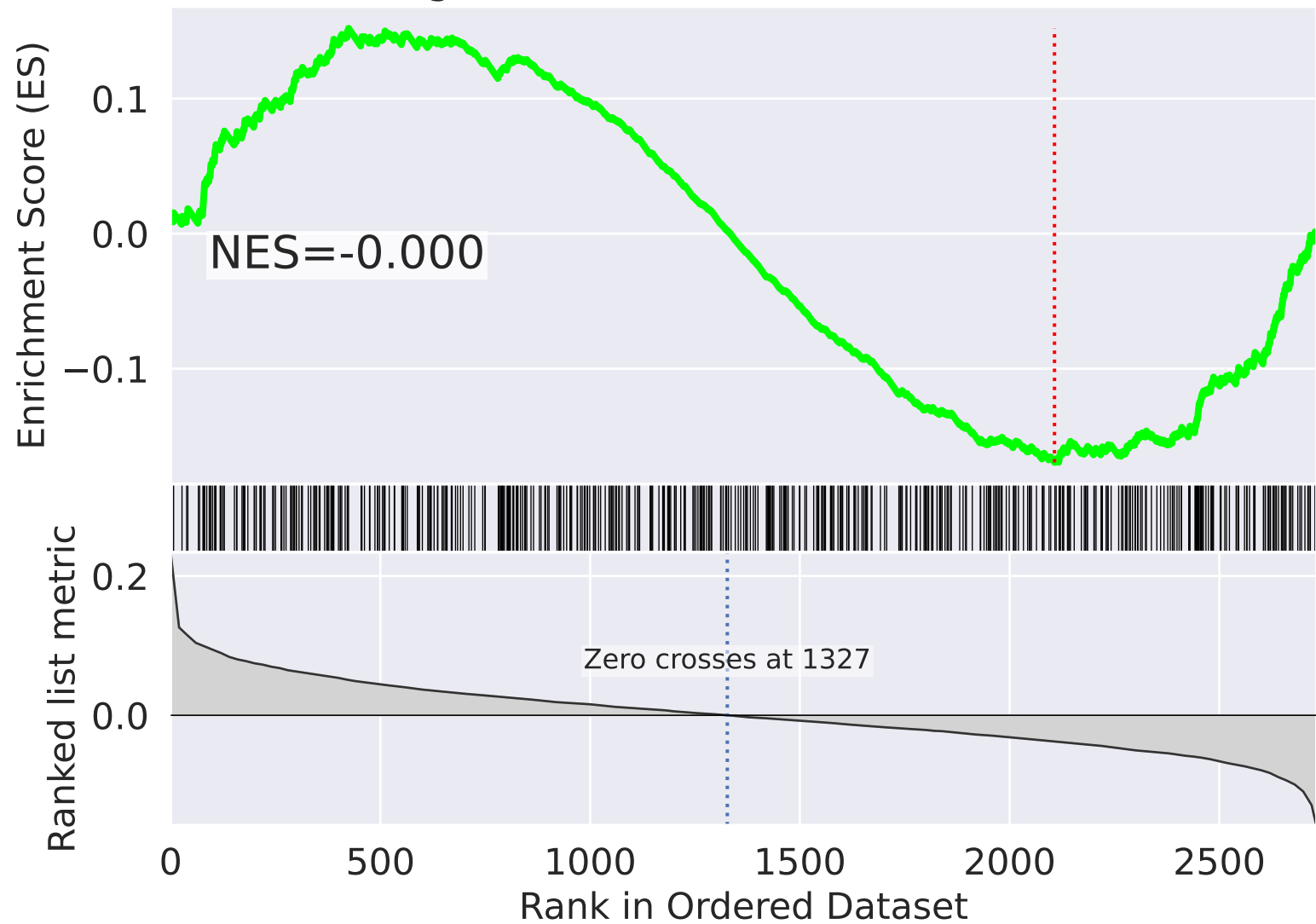
Signal Transduction R-HSA-162582



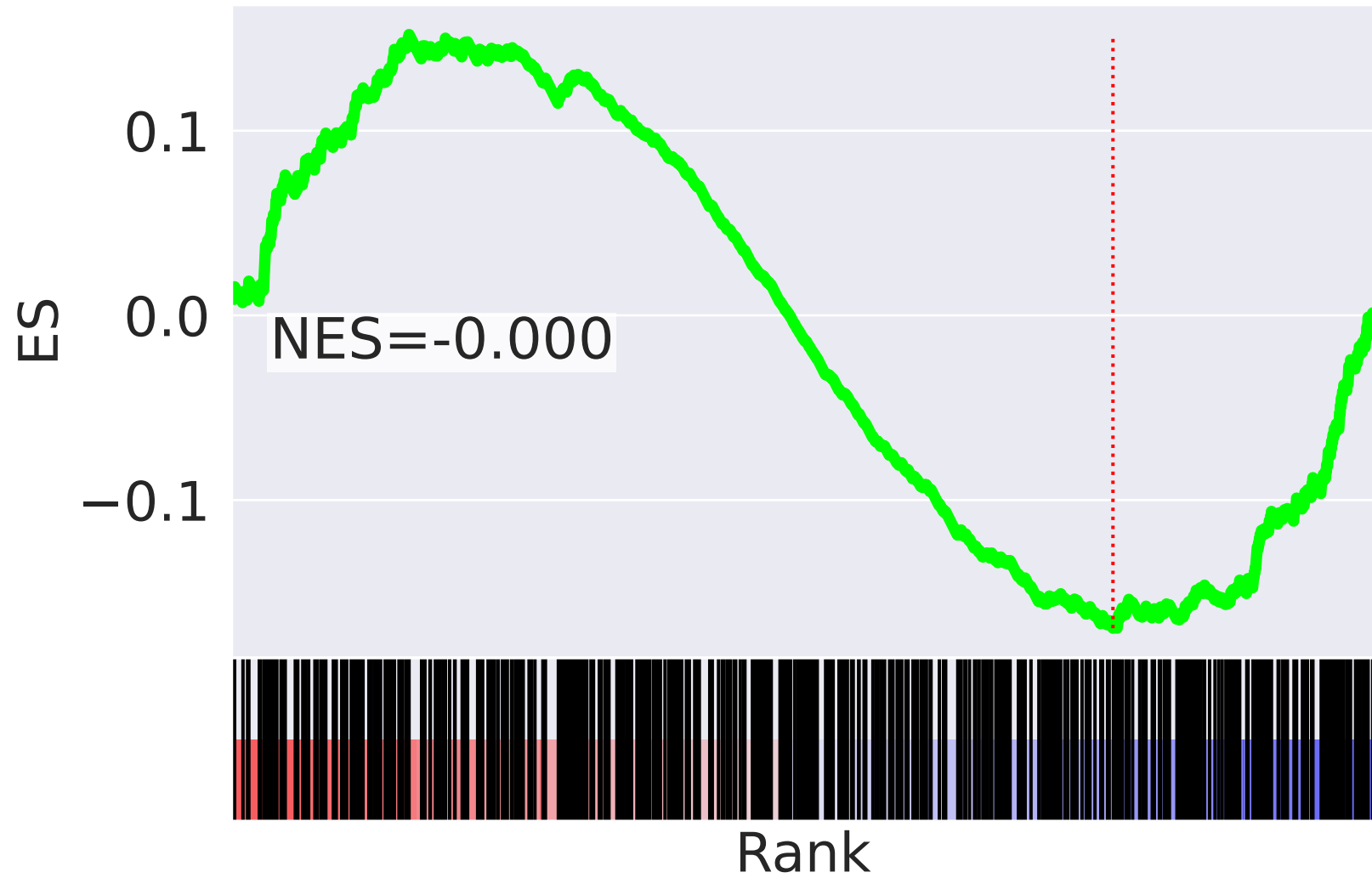
NES		SET
-3.023		Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
2.996		Chaperonin-mediated Protein Folding R-HSA-390466
-2.955		Deubiquitination R-HSA-5688426
-2.911		tRNA Modification In Nucleus And Cytosol R-HSA-6782315
-2.890		S Phase R-HSA-69242
-2.862		Cristae Formation R-HSA-8949613
-2.850		Homology Directed Repair R-HSA-5693538
2.799		Protein Folding R-HSA-391251
-2.704		DNA Double-Strand Break Repair R-HSA-5693532
-2.668		HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
2.650		Unfolded Protein Response (UPR) R-HSA-381119
2.641		BBSome-mediated Cargo-Targeting To Cilium R-HSA-5620922
2.627		Transcriptional Regulation By MECP2 R-HSA-8986944
2.588		Cooperation Of PDCL (PhLP1) And TRiC/CCT In G-protein Beta Folding R-HSA-6814122
-2.583		DNA Repair R-HSA-73894

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



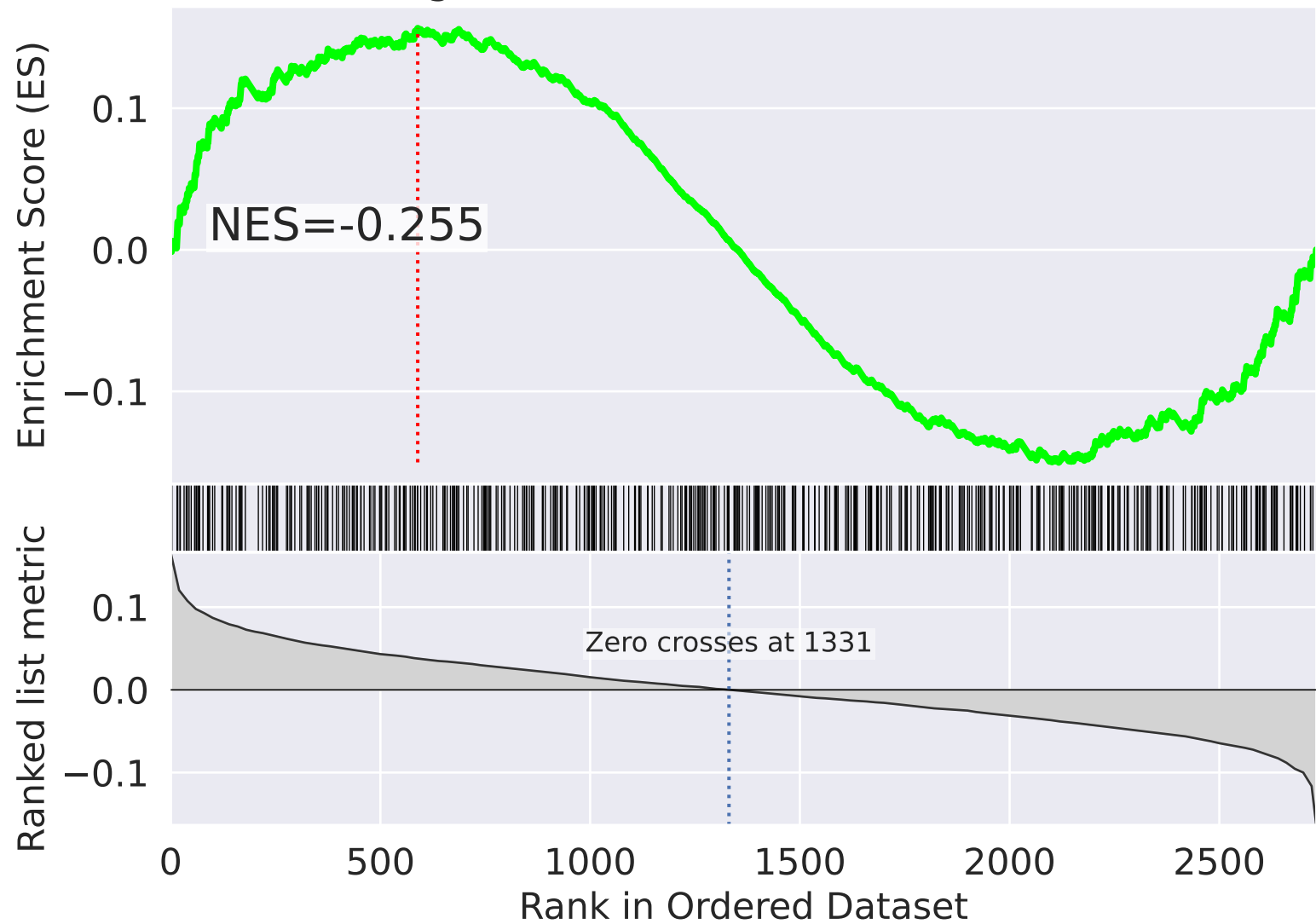
Signal Transduction R-HSA-162582



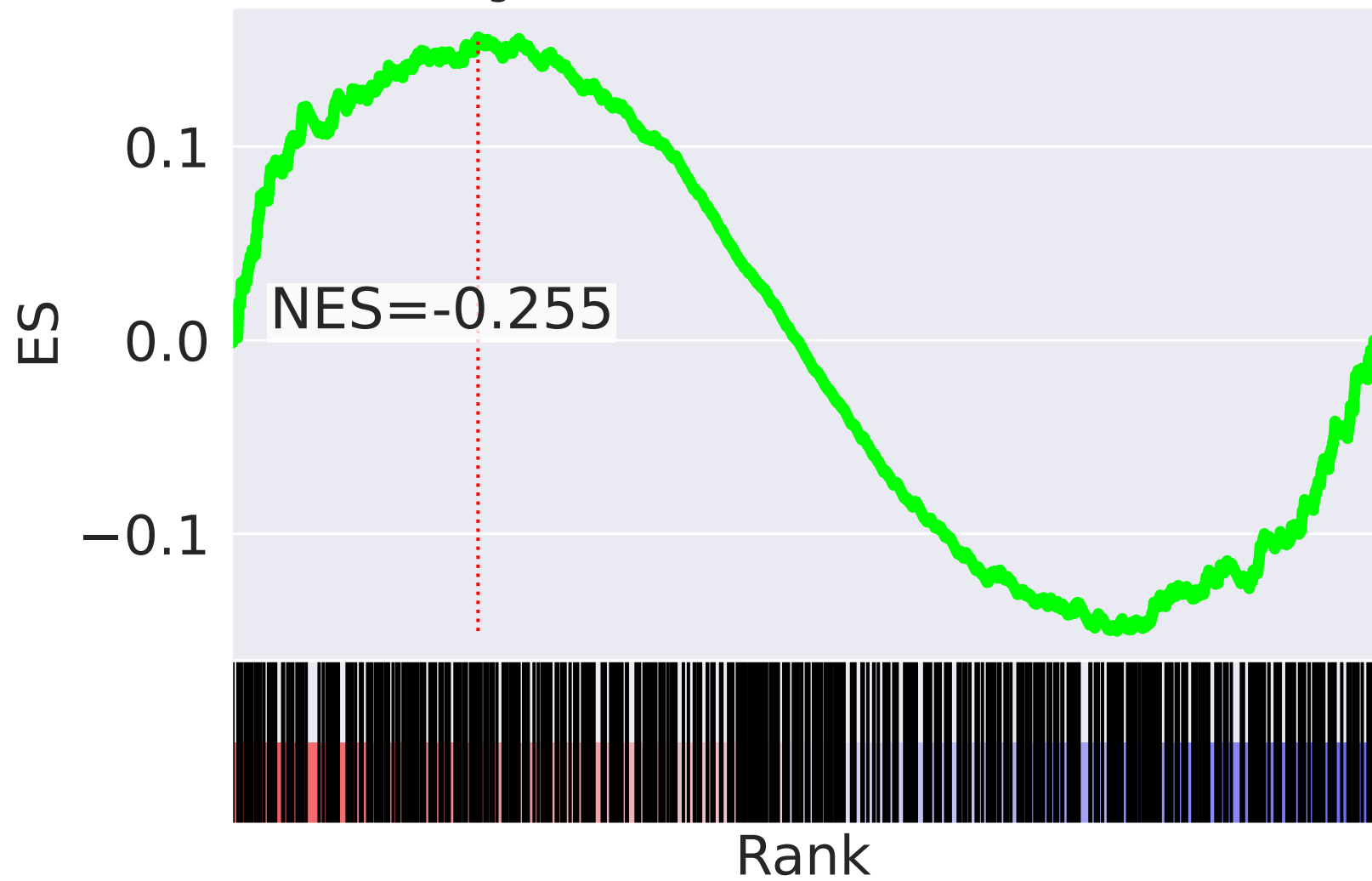
NES		SET
-3.793		Cristae Formation R-HSA-8949613
-3.689		Separation Of Sister Chromatids R-HSA-2467813
3.529		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
-3.448		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-3.410		SUMOylation Of RNA Binding Proteins R-HSA-4570464
3.410		Chromatin Modifying Enzymes R-HSA-3247509
-3.358		Nuclear Envelope Breakdown R-HSA-2980766
3.293		Metabolism Of Nucleotides R-HSA-15869
-3.288		Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
-3.268		Mitochondrial Protein Import R-HSA-1268020
-3.259		Mitotic Anaphase R-HSA-68882
-3.248		Mitotic Metaphase And Anaphase R-HSA-2555396
-3.231		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.226		RNA Polymerase II Pre-transcription Events R-HSA-674695
-3.208		SUMOylation Of DNA Replication Proteins R-HSA-4615885


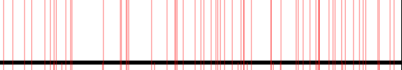
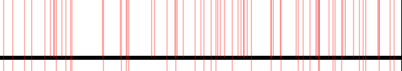
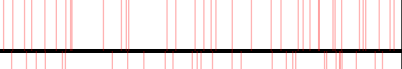
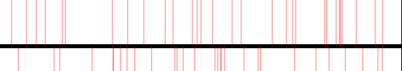
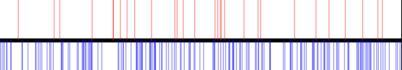
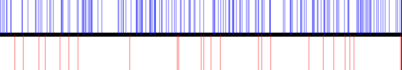

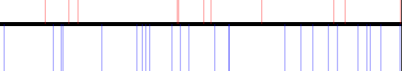

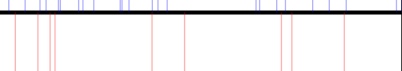
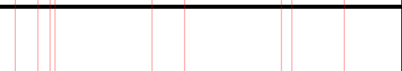
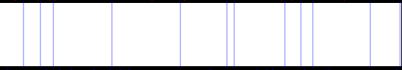


The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=3$

Signal Transduction R-HSA-162582



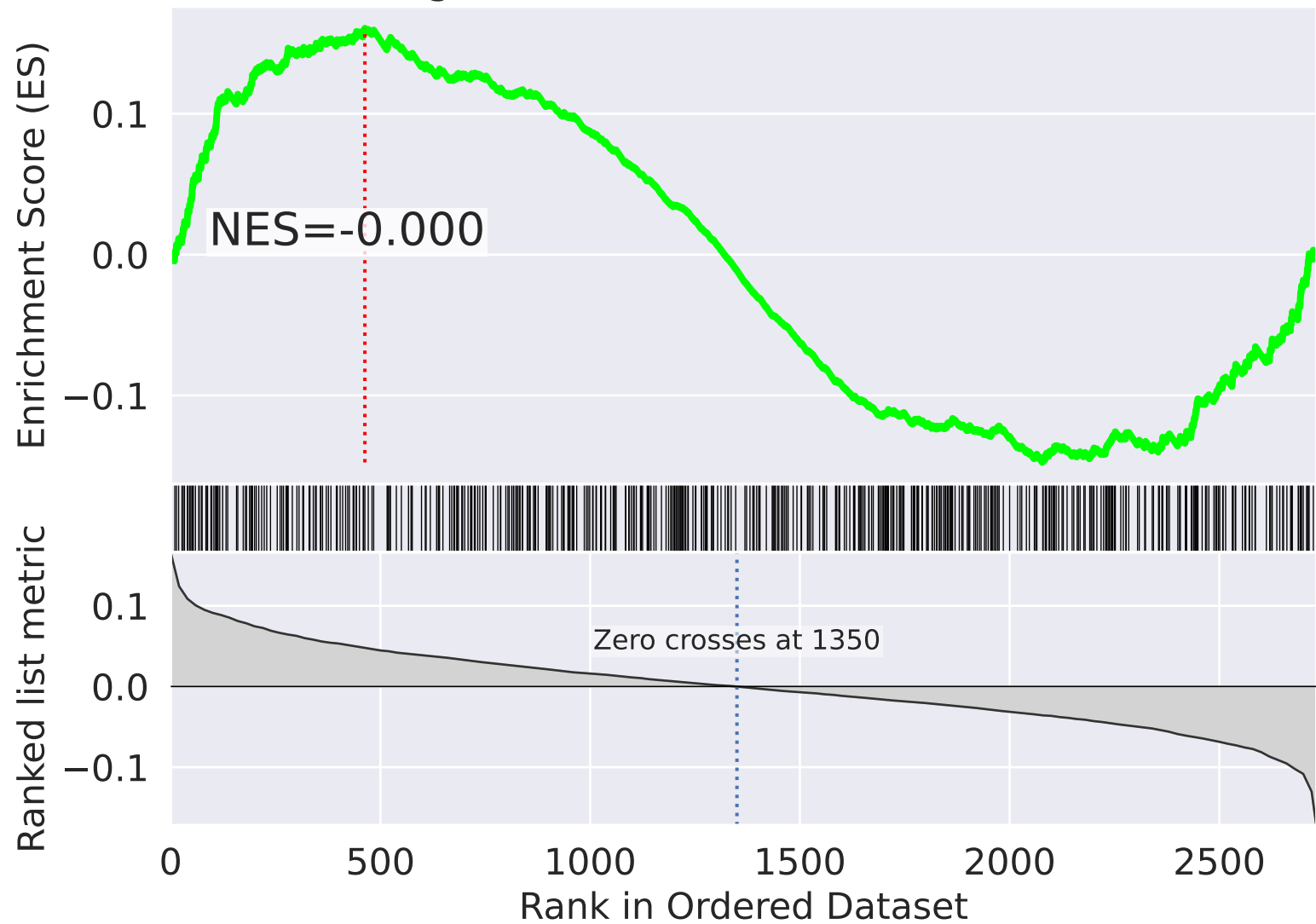
Signal Transduction R-HSA-162582



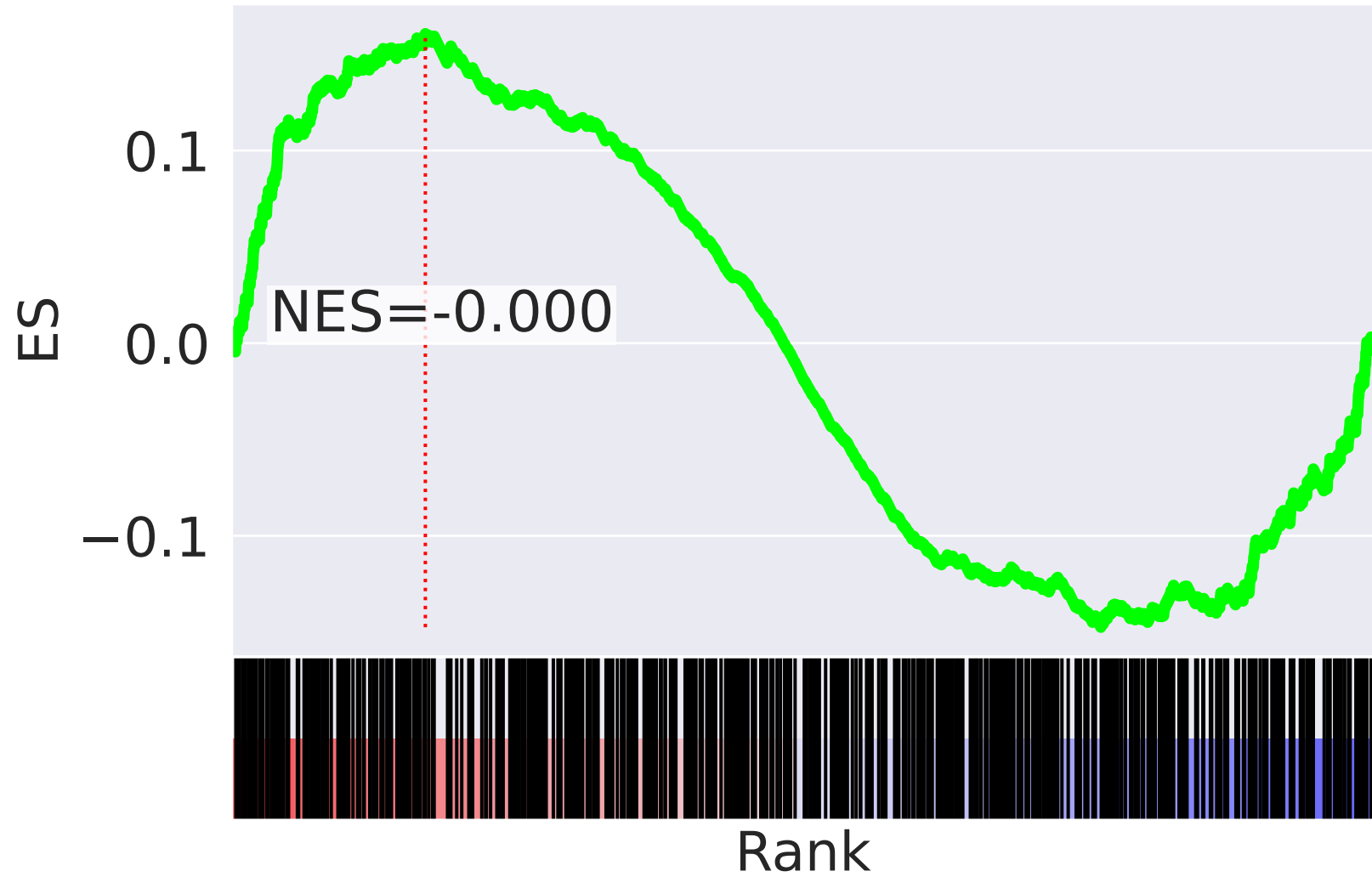
NES		SET
5.467		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.015		Respiratory Electron Transport R-HSA-611105
4.752		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.753		Complex I Biogenesis R-HSA-6799198
3.694		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.500		Cytoprotection By HMOX1 R-HSA-9707564
-3.376		Cell Cycle Checkpoints R-HSA-69620
3.351		Metabolism Of Nucleotides R-HSA-15869
3.291		Nucleotide Biosynthesis R-HSA-8956320
-3.168		Activation Of ATR In Response To Replication Stress R-HSA-176187
-3.090		Cell-Cell Communication R-HSA-1500931
3.082		Metabolism Of Porphyrins R-HSA-189445
3.082		Heme Biosynthesis R-HSA-189451
-2.980		Lagging Strand Synthesis R-HSA-69186
-2.958		Signaling By PDGF R-HSA-186797

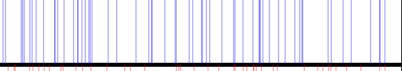
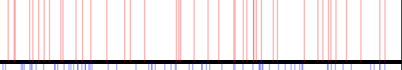
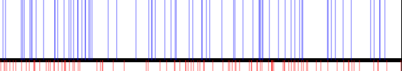
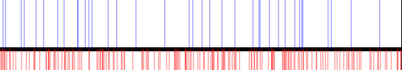
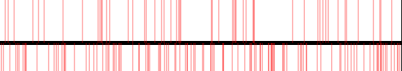
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=4$

Signal Transduction R-HSA-162582



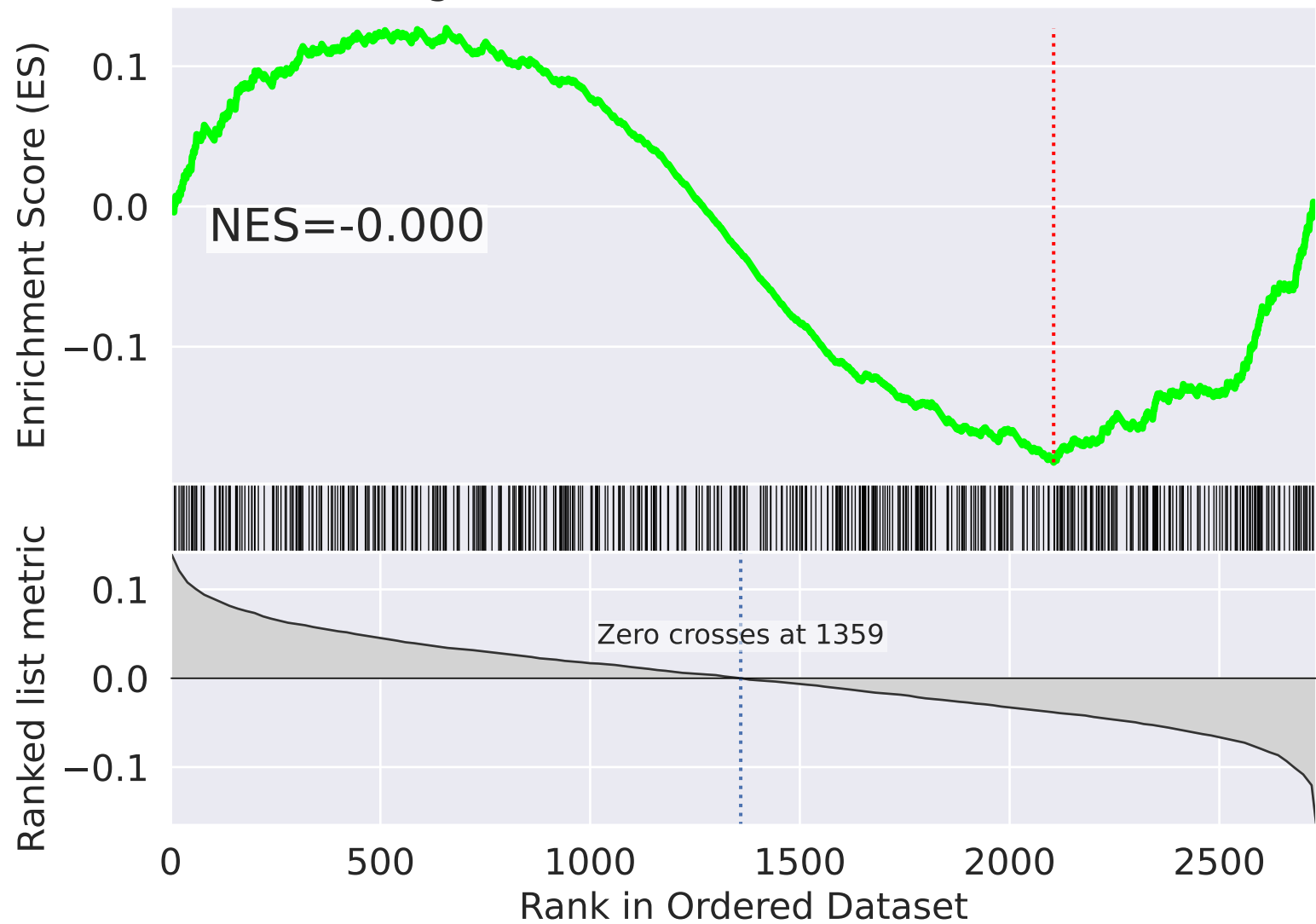
Signal Transduction R-HSA-162582



NES		SET
-3.876		Chromatin Modifying Enzymes R-HSA-3247509
-3.851		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.736		Respiratory Electron Transport R-HSA-611105
3.602		Nuclear Envelope (NE) Reassembly R-HSA-2995410
-3.527		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.492		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
3.264		Cytokine Signaling In Immune System R-HSA-1280215
3.251		Mitotic Metaphase And Anaphase R-HSA-2555396
3.251		Mitotic Anaphase R-HSA-68882
-3.224		Complex I Biogenesis R-HSA-6799198
3.040		Adaptive Immune System R-HSA-1280218
3.023		Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
2.977		Interferon Signaling R-HSA-913531
2.963		Nervous System Development R-HSA-9675108
2.962		Transport Of Mature Transcript To Cytoplasm R-HSA-72202

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

ES

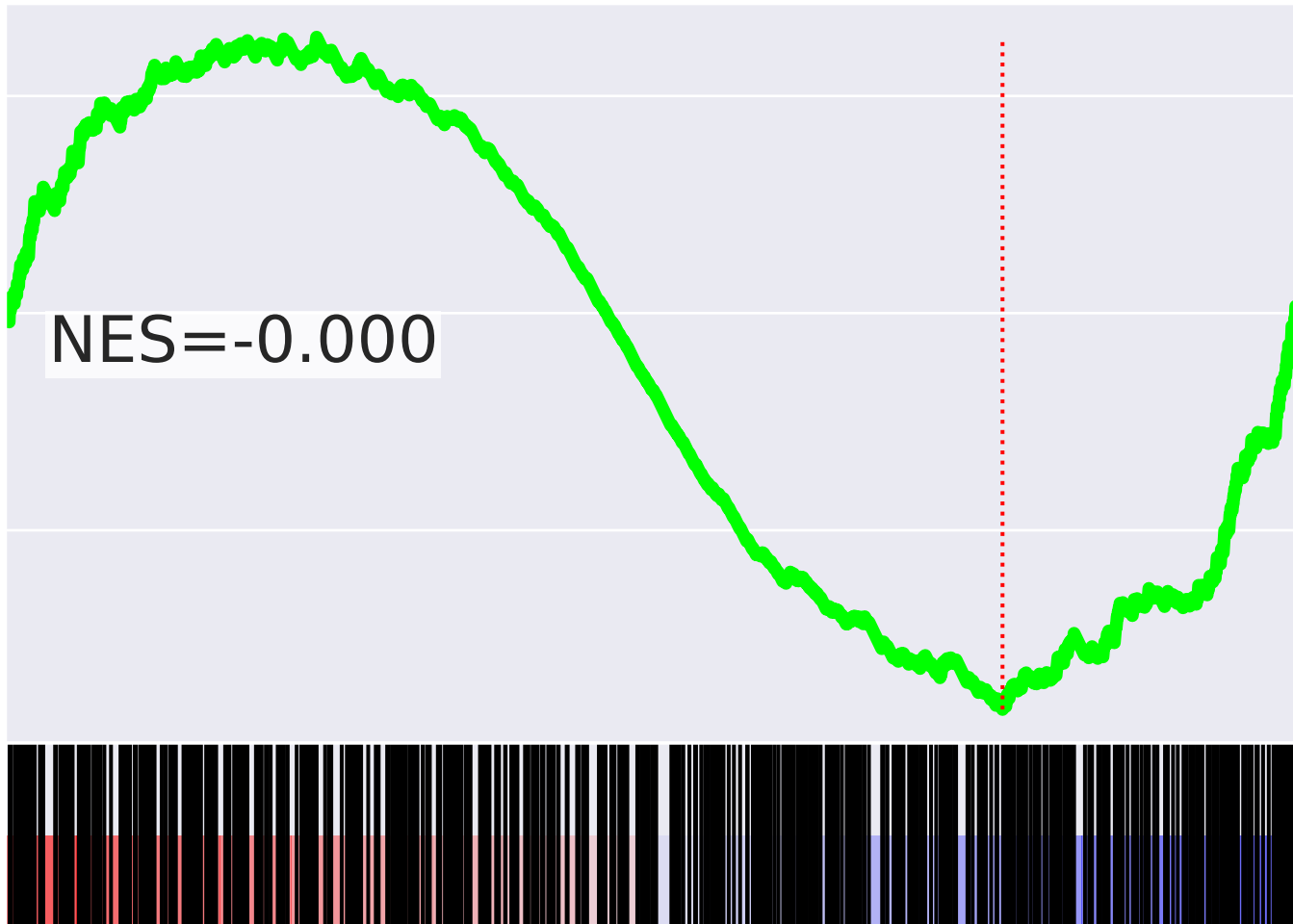
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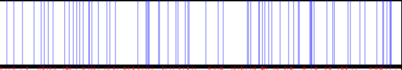
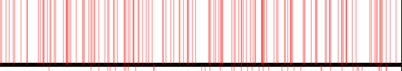



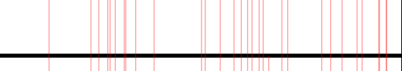



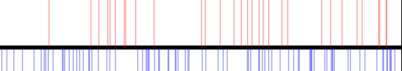
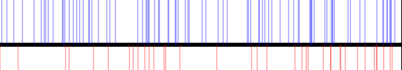
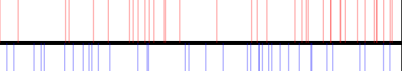
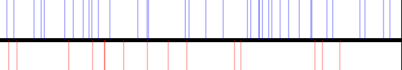

0.0

-0.1

NES=-0.000

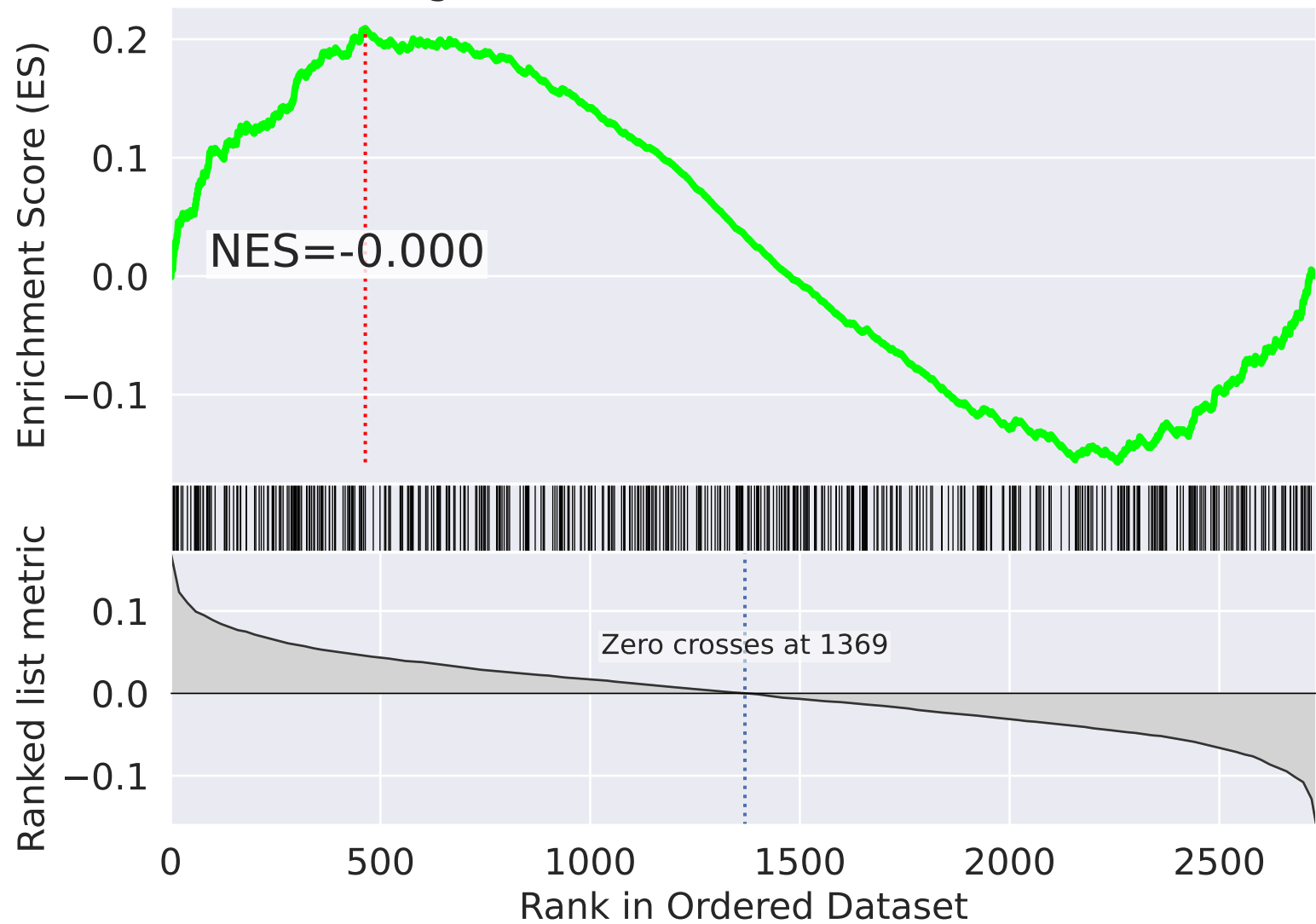
Rank



NES		SET
4.106		Toll Like Receptor 4 (TLR4) Cascade R-HSA-166016
-4.103		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.960		Signaling By Receptor Tyrosine Kinases R-HSA-9006934
3.933		Toll-like Receptor Cascades R-HSA-168898
3.869		Toll Like Receptor 3 (TLR3) Cascade R-HSA-168164
3.778		MyD88-independent TLR4 Cascade R-HSA-166166
3.727		MyD88 Cascade Initiated On Plasma Membrane R-HSA-975871
3.649		TRAF6 Mediated Induction Of NFkB And MAP Kinases Upon TLR7/8 Or 9 Activation R-HSA-975138
3.649		Toll Like Receptor 7/8 (TLR7/8) Cascade R-HSA-168181
3.649		MyD88:MAL(TIRAP) Cascade Initiated On Plasma Membrane R-HSA-166058
3.649		MyD88 Dependent Cascade Initiated On Endosome R-HSA-975155
-3.637		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.600		Factors Involved In Megakaryocyte Development And Platelet Production R-HSA-983231
-3.558		Complex I Biogenesis R-HSA-6799198
3.419		Cooperation Of Prefoldin And TriC/CCT In Actin And Tubulin Folding R-HSA-389958

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



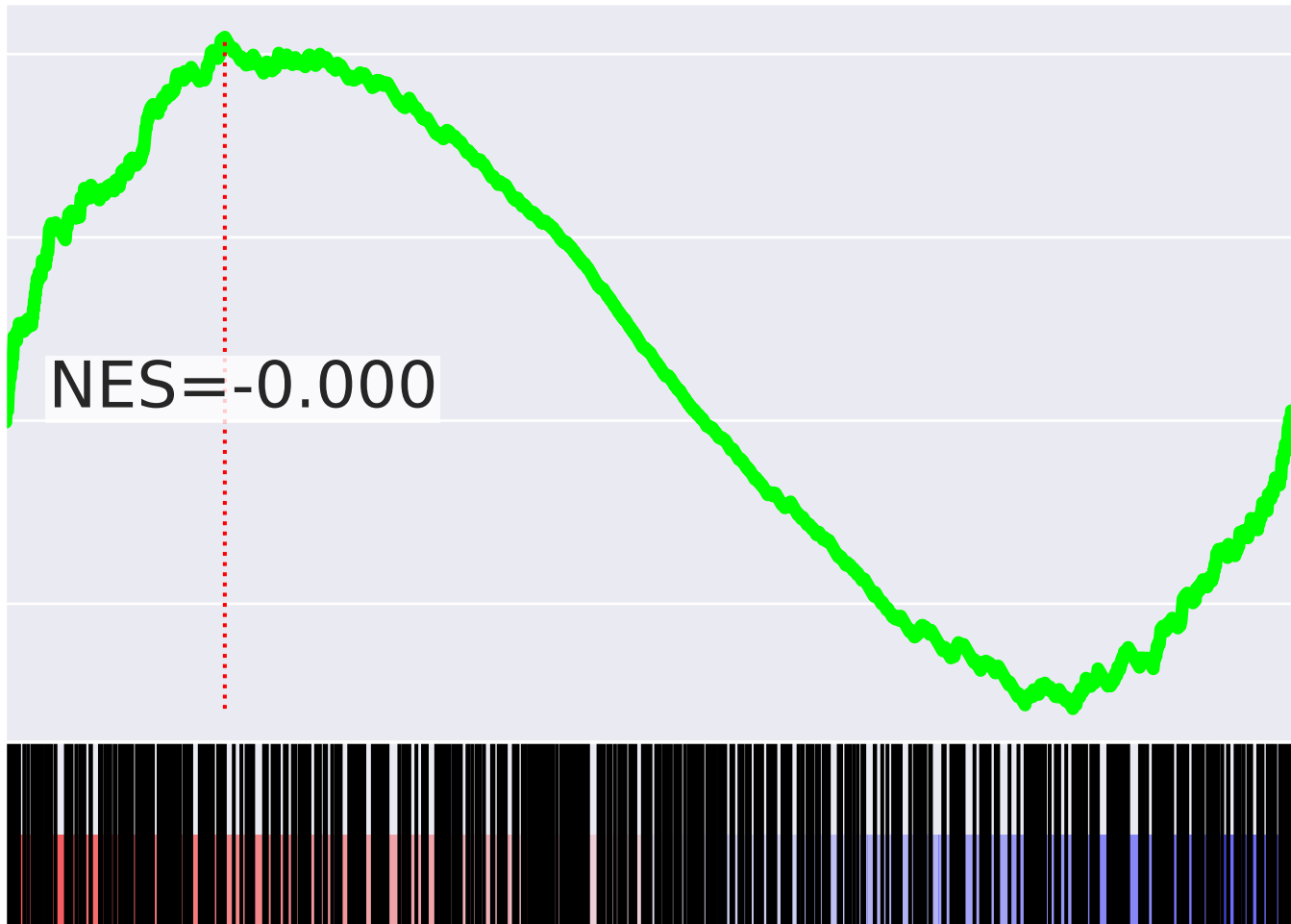
Signal Transduction R-HSA-162582

ES

0.2
0.1
0.0
-0.1

NES=-0.000

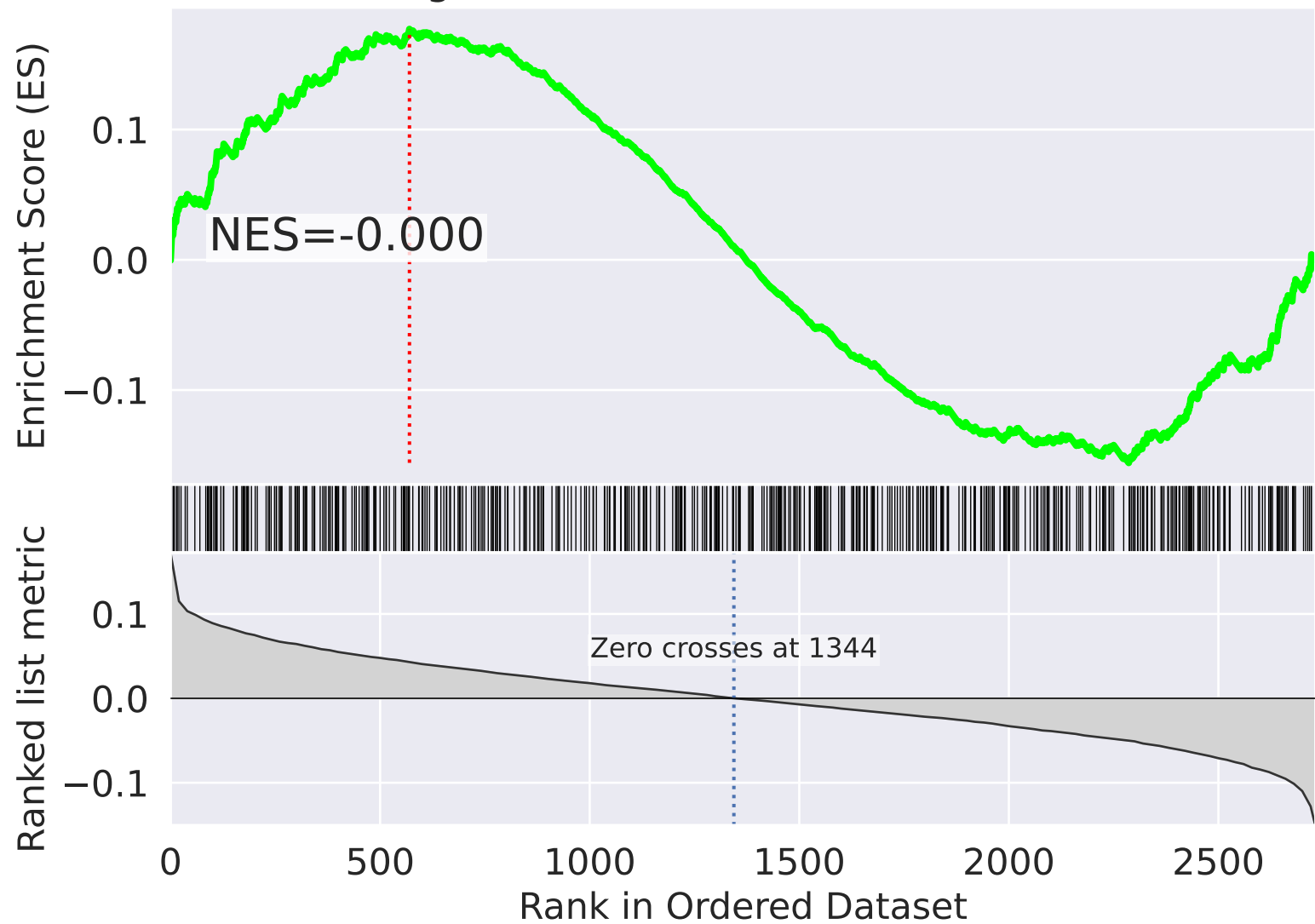
Rank



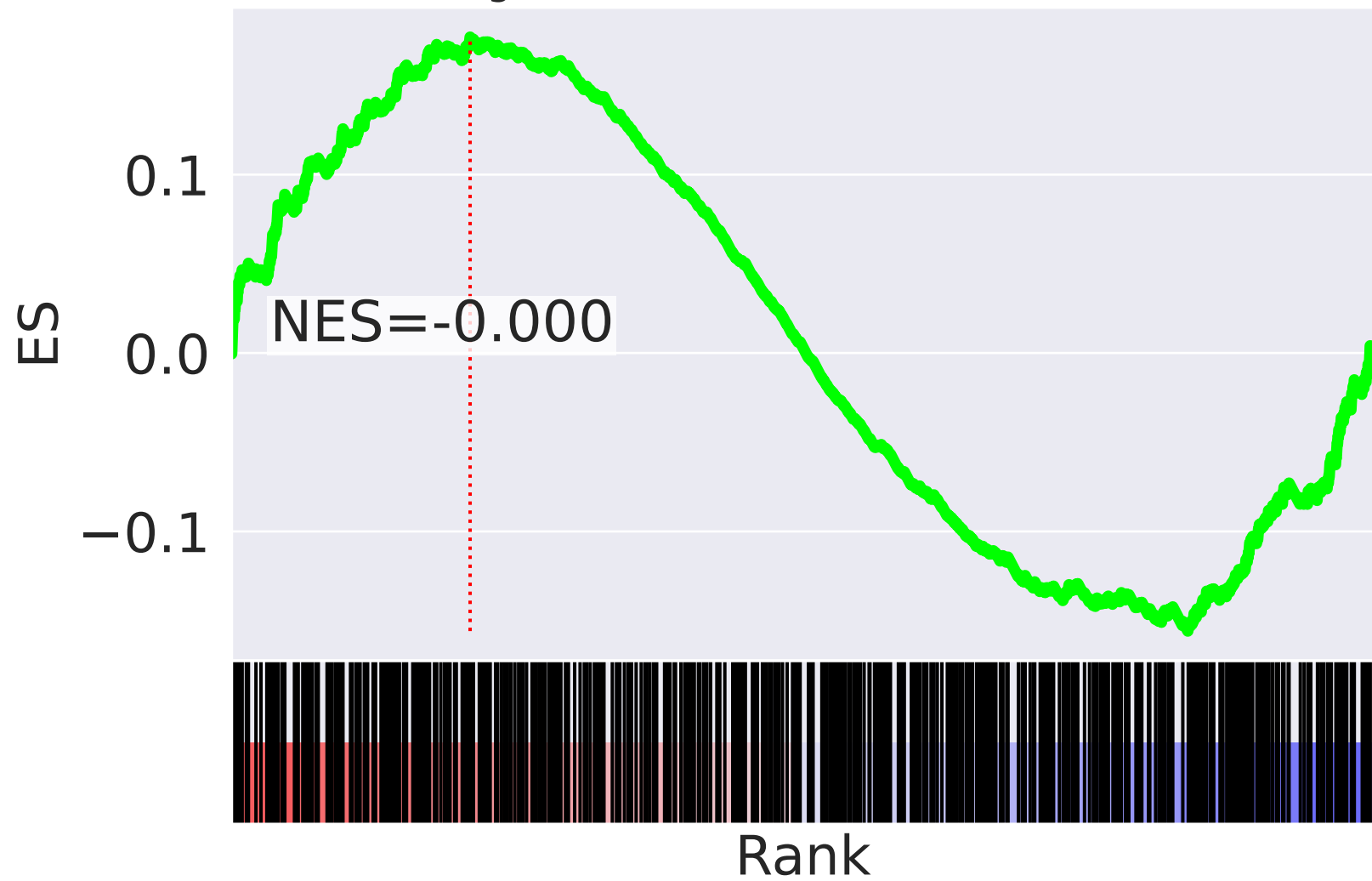
NES	SET
6.002	Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
5.675	mRNA Splicing R-HSA-72172
5.351	mRNA Splicing - Major Pathway R-HSA-72163
5.074	M Phase R-HSA-68886
4.761	Mitotic Metaphase And Anaphase R-HSA-2555396
4.674	Mitotic Anaphase R-HSA-68882
4.405	Separation Of Sister Chromatids R-HSA-2467813
4.247	Mitotic G2-G2/M Phases R-HSA-453274
4.115	G2/M Transition R-HSA-69275
3.884	Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
3.866	Neddylation R-HSA-8951664
3.824	HIV Infection R-HSA-162906
3.798	Host Interactions Of HIV Factors R-HSA-162909
3.776	Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
3.702	Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169

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



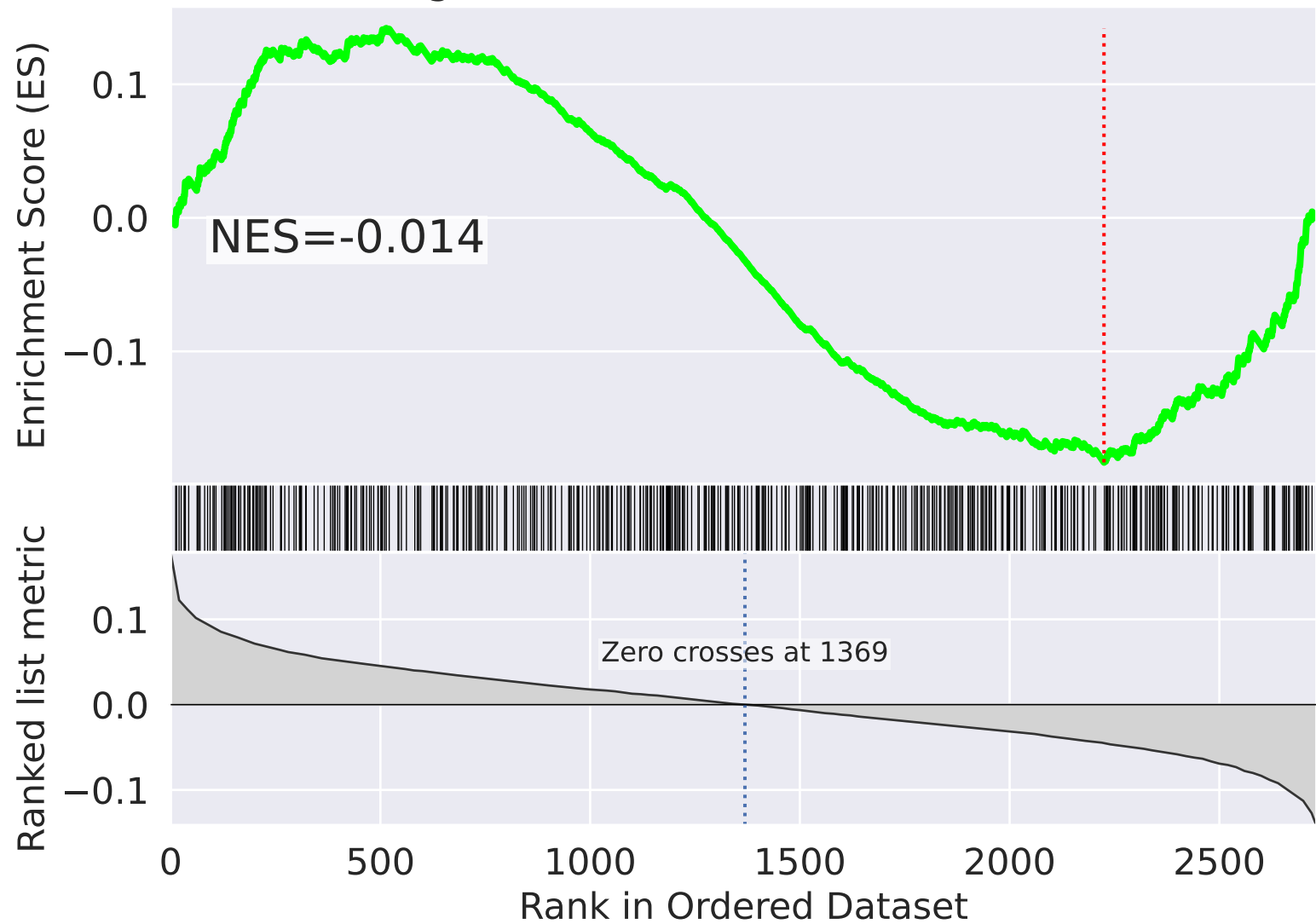
Signal Transduction R-HSA-162582



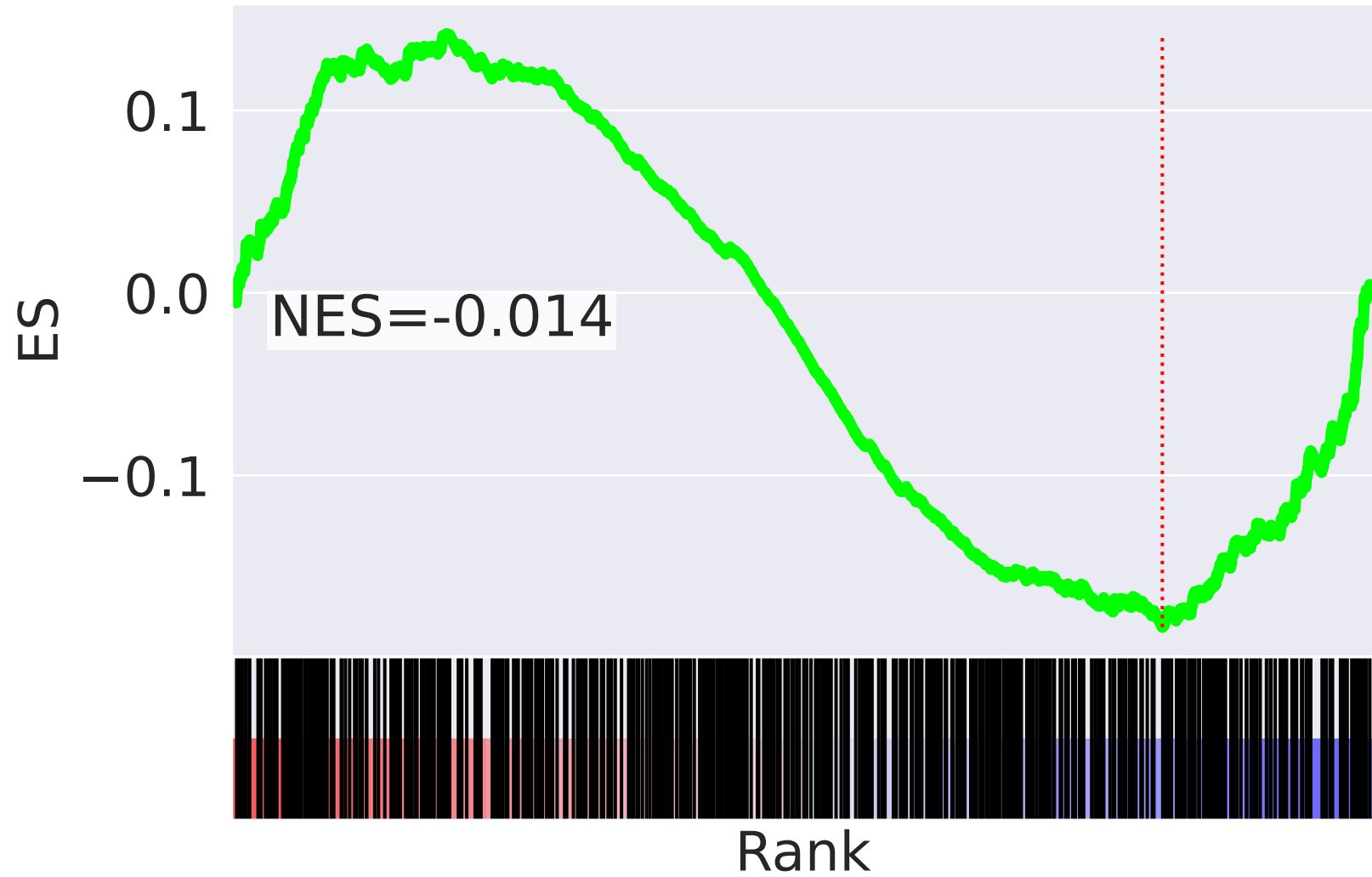
NES		SET
-4.322		rRNA Processing R-HSA-72312
-4.299		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.101		HIV Infection R-HSA-162906
-4.036		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.937		Interleukin-1 Signaling R-HSA-9020702
3.894		G1/S DNA Damage Checkpoints R-HSA-69615
3.854		S Phase R-HSA-69242
3.798		p53-Dependent G1 DNA Damage Response R-HSA-69563
3.740		Switching Of Origins To A Post-Replicative State R-HSA-69052
3.684		Mitotic G1 Phase And G1/S Transition R-HSA-453279
3.666		FCERI Mediated NF-kB Activation R-HSA-2871837
3.664		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
3.627		Nervous System Development R-HSA-9675108
3.620		Axon Guidance R-HSA-422475
3.593		Leishmania Infection R-HSA-9658195


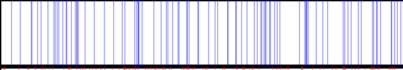
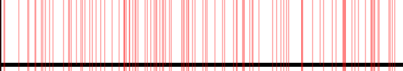
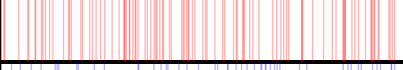
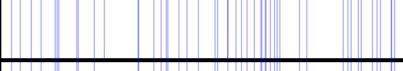
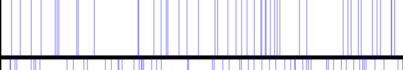
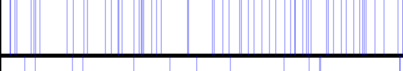

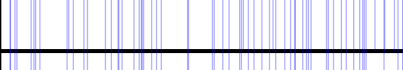
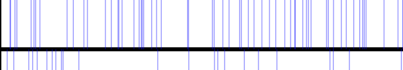
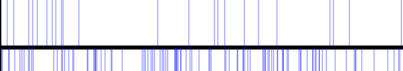
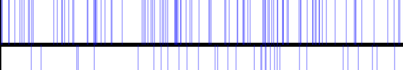
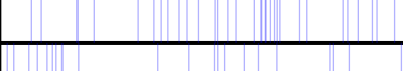


The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=8$

Signal Transduction R-HSA-162582



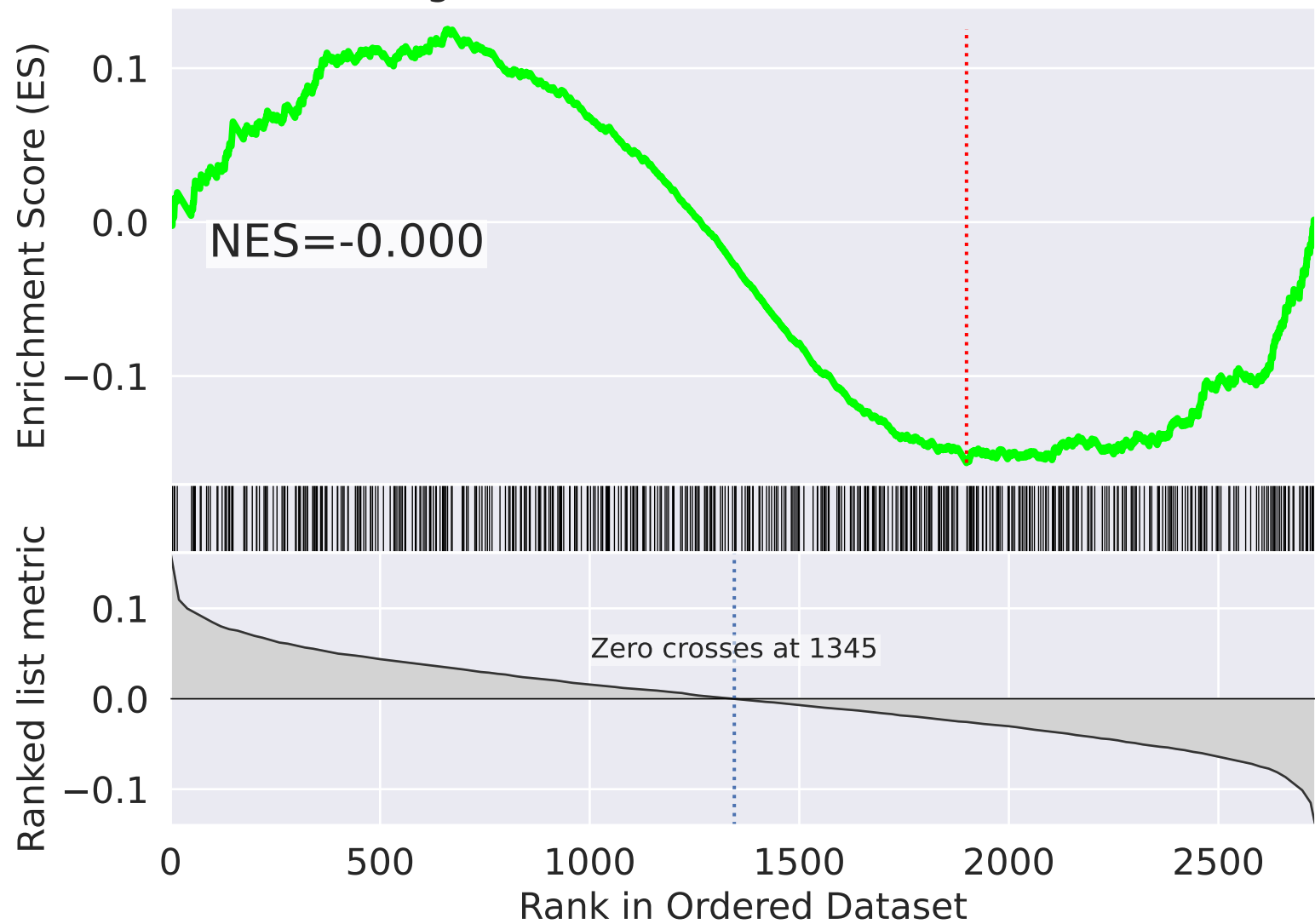
Signal Transduction R-HSA-162582



NES		SET
4.375		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-4.123		Asparagine N-linked Glycosylation R-HSA-446203
3.880		mRNA Splicing R-HSA-72172
3.854		mRNA Splicing - Major Pathway R-HSA-72163
-3.702		Transport To Golgi And Subsequent Modification R-HSA-948021
-3.511		ER To Golgi Anterograde Transport R-HSA-199977
-3.453		Homology Directed Repair R-HSA-5693538
-3.280		Cell Junction Organization R-HSA-446728
-3.240		DNA Double-Strand Break Repair R-HSA-5693532
-3.182		HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
-3.168		RNA Polymerase III Abortive And Retractive Initiation R-HSA-749476
-3.167		Intracellular Signaling By Second Messengers R-HSA-9006925
-3.111		COPI-mediated Anterograde Transport R-HSA-6807878
-3.040		RNA Polymerase III Transcription Initiation R-HSA-76046
-3.013		MAPK6/MAPK4 Signaling R-HSA-5687128

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

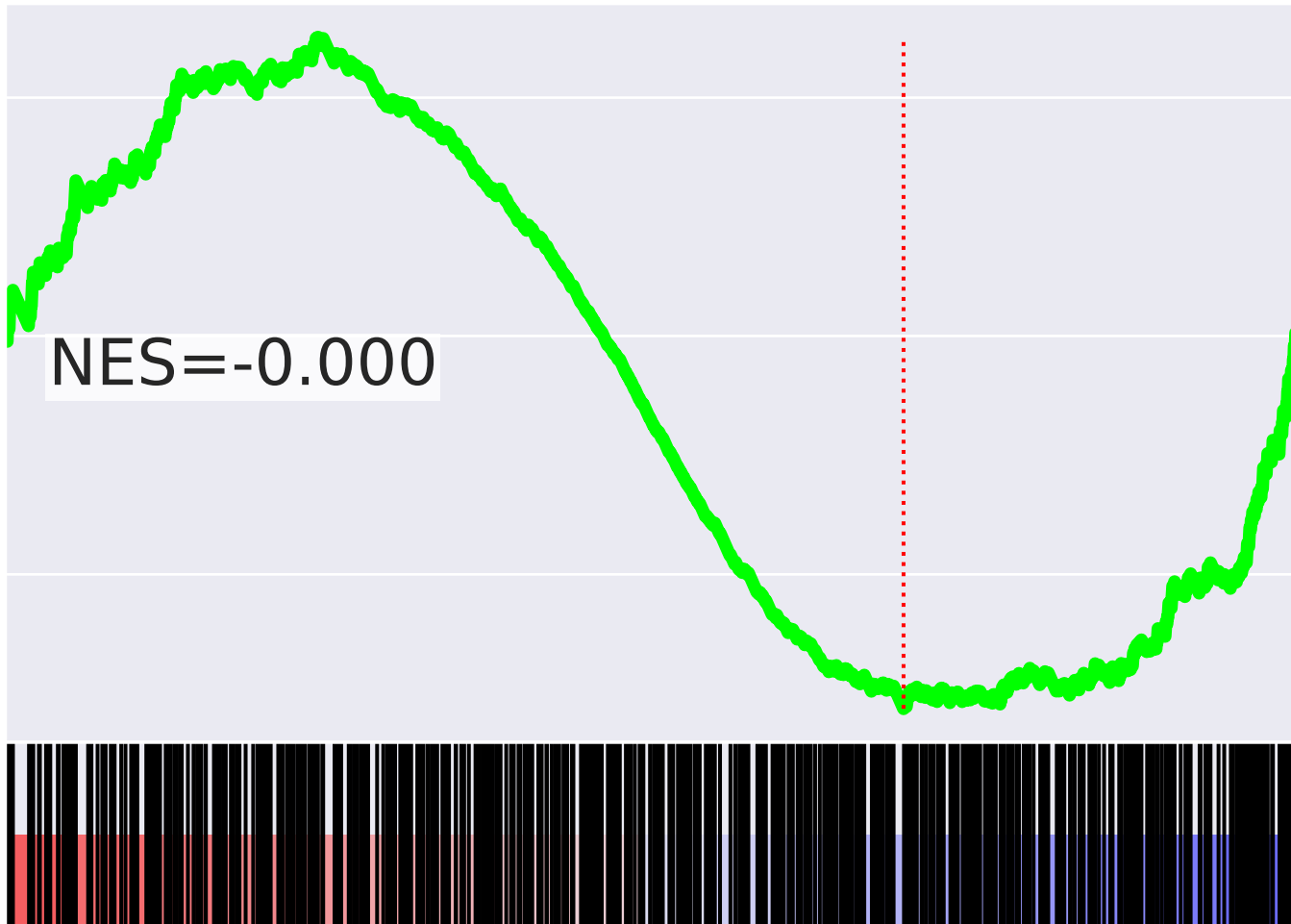
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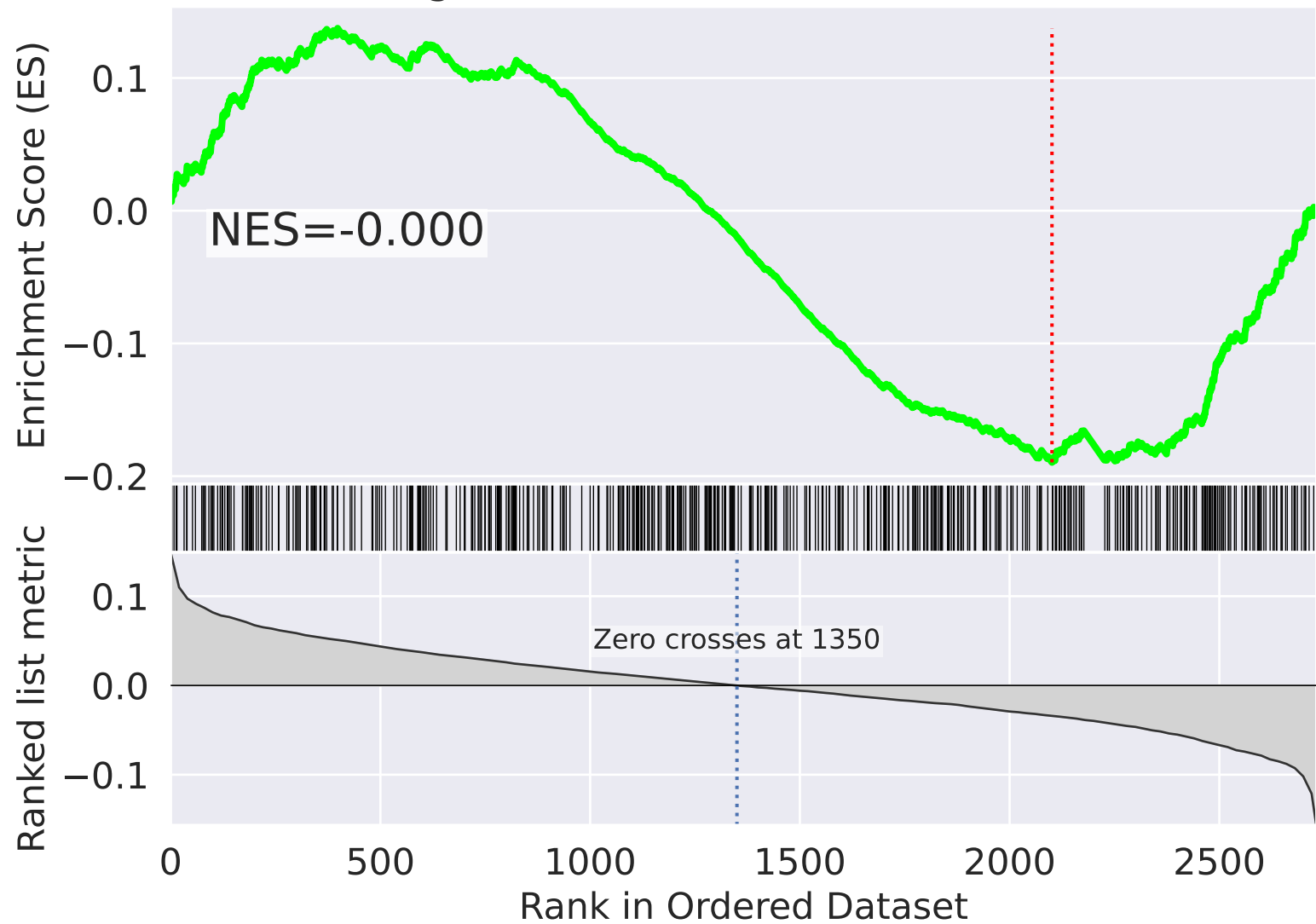
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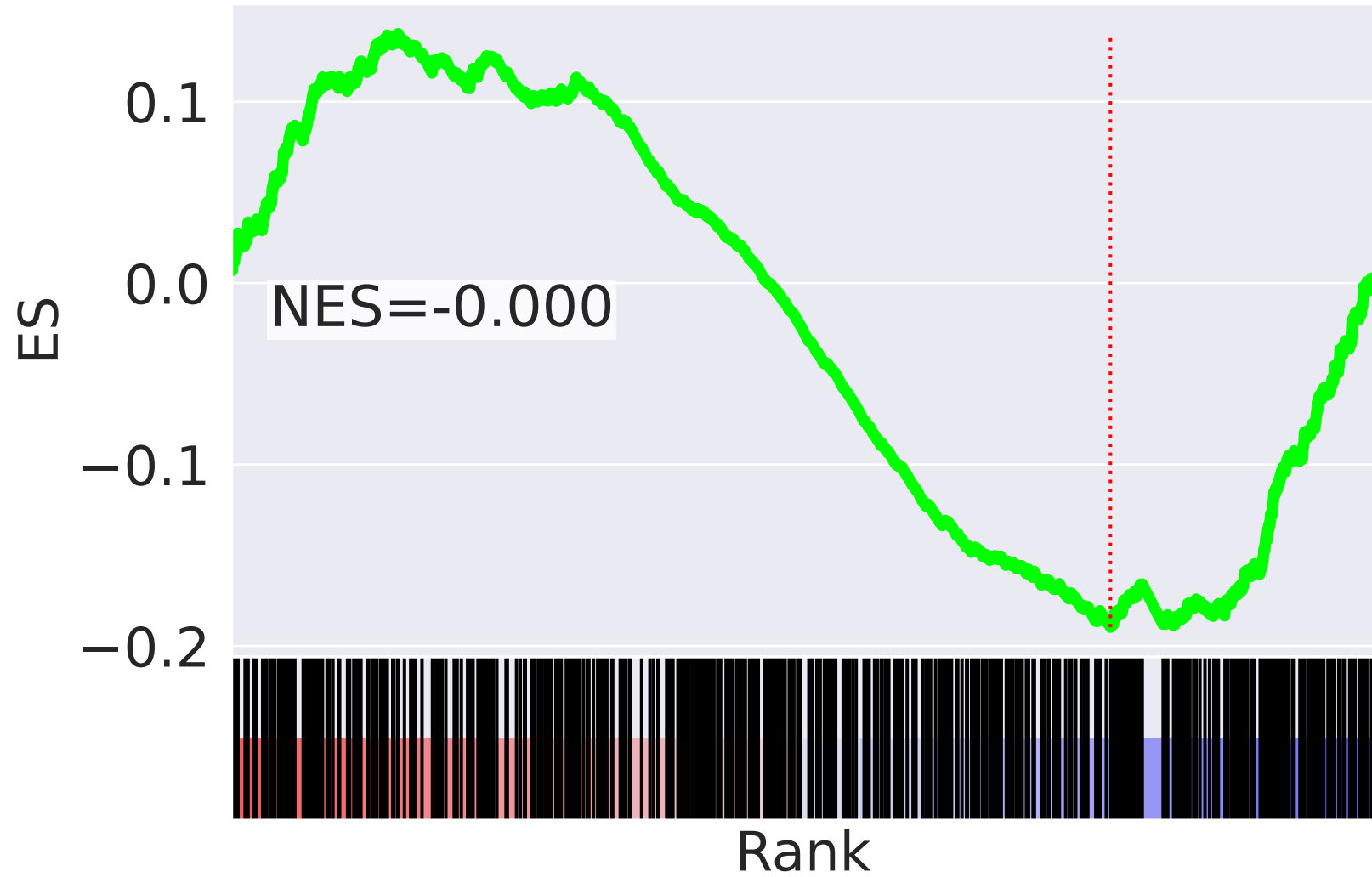
NES	SET
-3.443	G2/M DNA Damage Checkpoint R-HSA-69473
-3.395	Processing Of DNA Double-Strand Break Ends R-HSA-5693607
-3.109	HDR Thru Single Strand Annealing (SSA) R-HSA-5685938
-3.104	Impaired BRCA2 Binding To RAD51 R-HSA-9709570
-3.093	Nonhomologous End-Joining (NHEJ) R-HSA-5693571
-3.059	Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.032	Diseases Of DNA Repair R-HSA-9675135
-3.032	Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.016	HCMV Late Events R-HSA-9610379
-2.936	Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
-2.890	Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
-2.811	G2/M Checkpoints R-HSA-69481
-2.810	HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-2.751	Smooth Muscle Contraction R-HSA-445355
-2.749	DNA Double Strand Break Response R-HSA-5693606



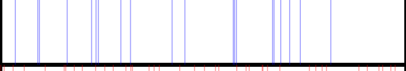
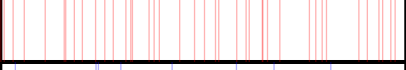
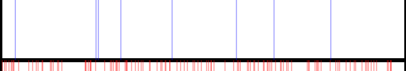
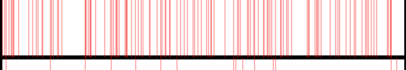

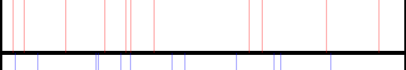
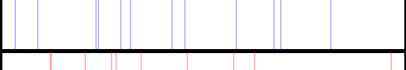
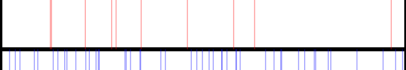
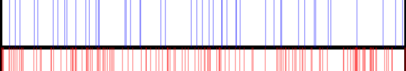
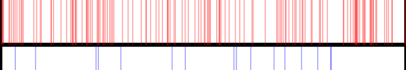

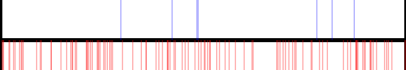
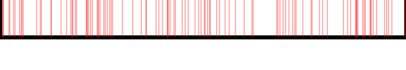
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=10$

Signal Transduction R-HSA-162582



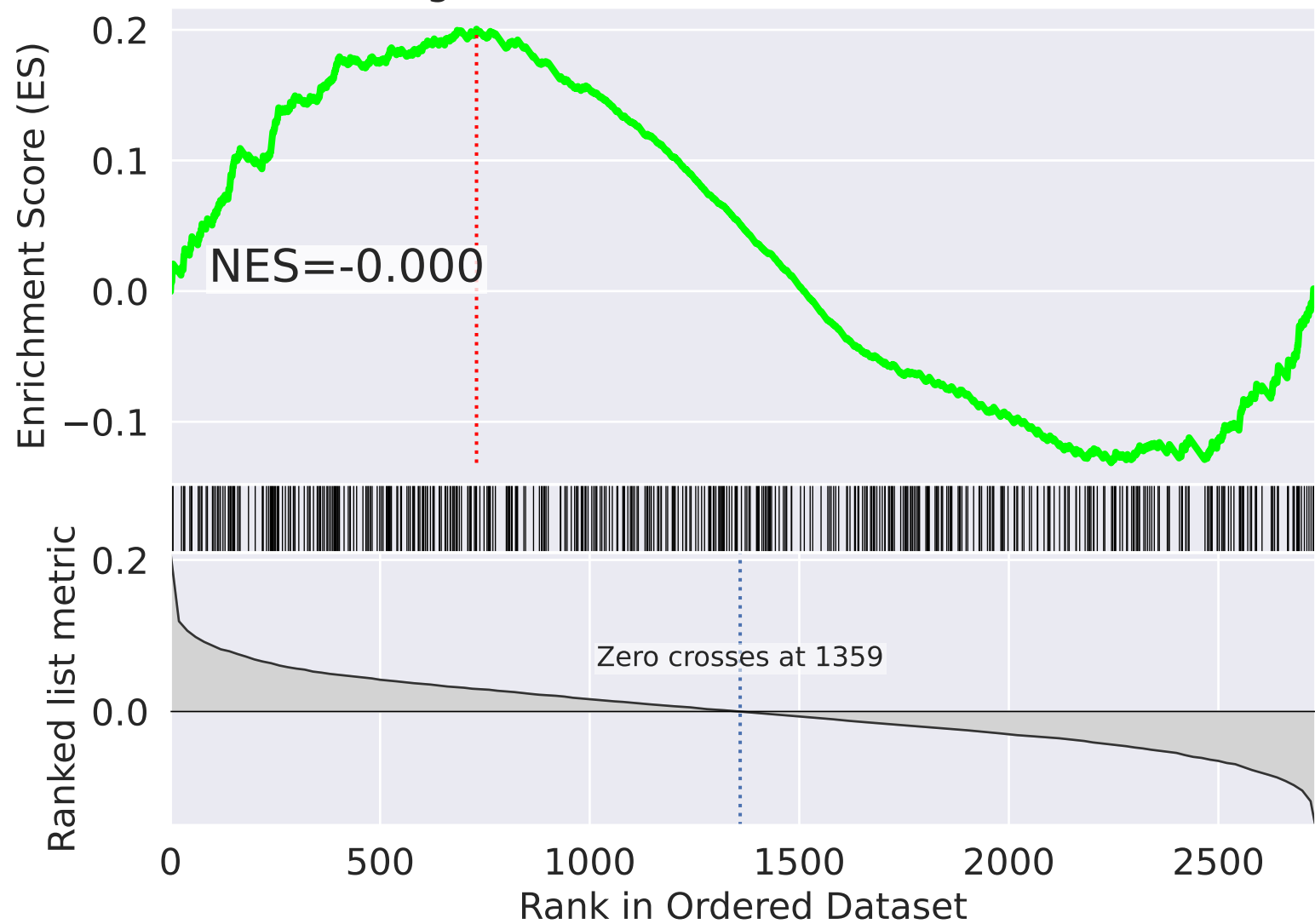
Signal Transduction R-HSA-162582



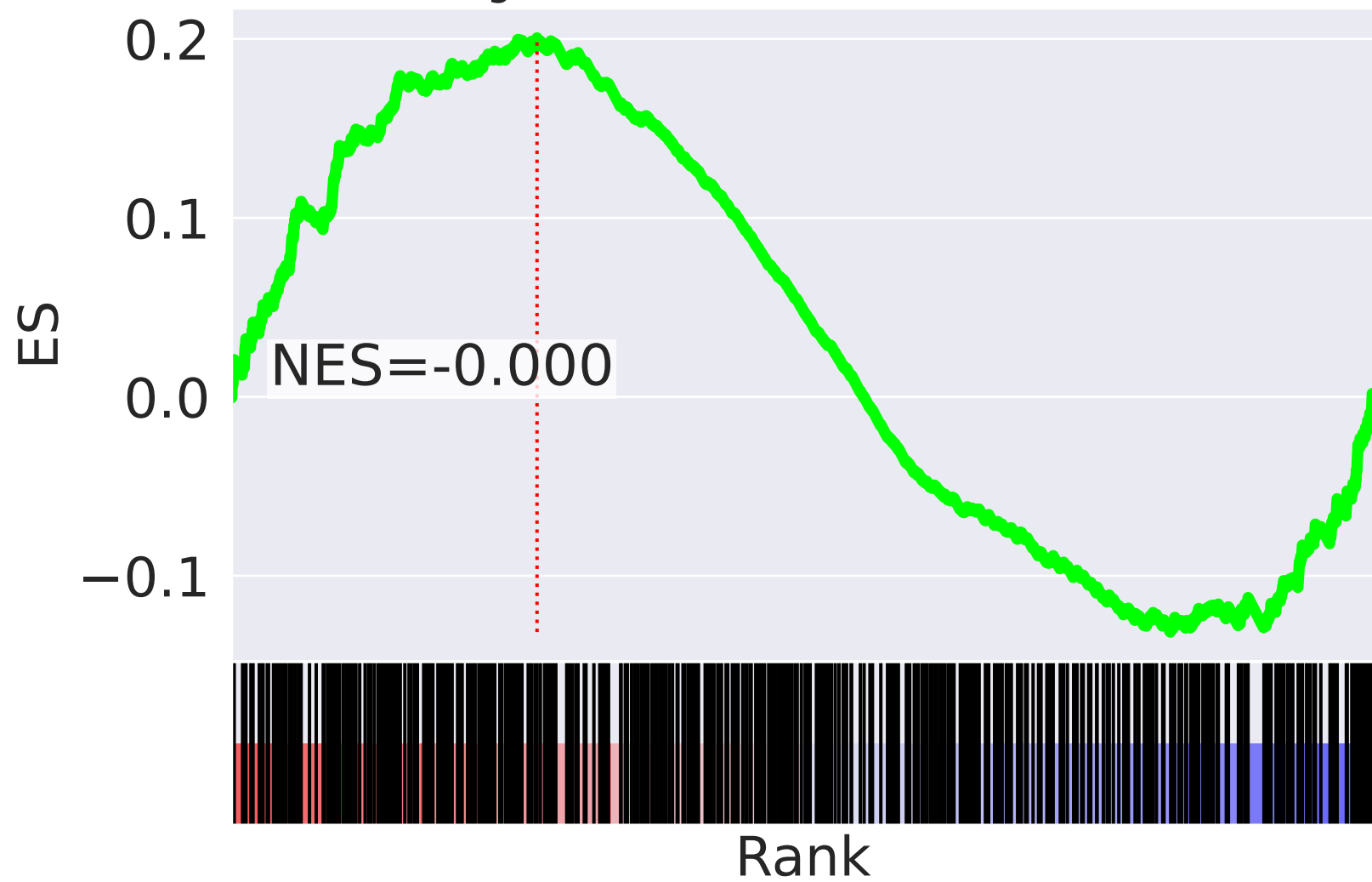
NES		SET
3.242		Cristae Formation R-HSA-8949613
-3.179		Activation Of ATR In Response To Replication Stress R-HSA-176187
-3.131		DNA Strand Elongation R-HSA-69190
3.104		Mitochondrial Biogenesis R-HSA-1592230
-2.975		Leading Strand Synthesis R-HSA-69109
2.809		Signaling By Interleukins R-HSA-449147
2.718		Signaling By CSF3 (G-CSF) R-HSA-9674555
2.701		Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
-2.701		Lagging Strand Synthesis R-HSA-69186
2.683		Interleukin-2 Family Signaling R-HSA-451927
-2.664		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
2.637		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-2.622		Polymerase Switching On C-strand Of Telomere R-HSA-174411
-2.611		Inhibition Of Replication Initiation Of Damaged DNA By RB1/E2F1 R-HSA-113501
2.543		mRNA Splicing R-HSA-72172

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



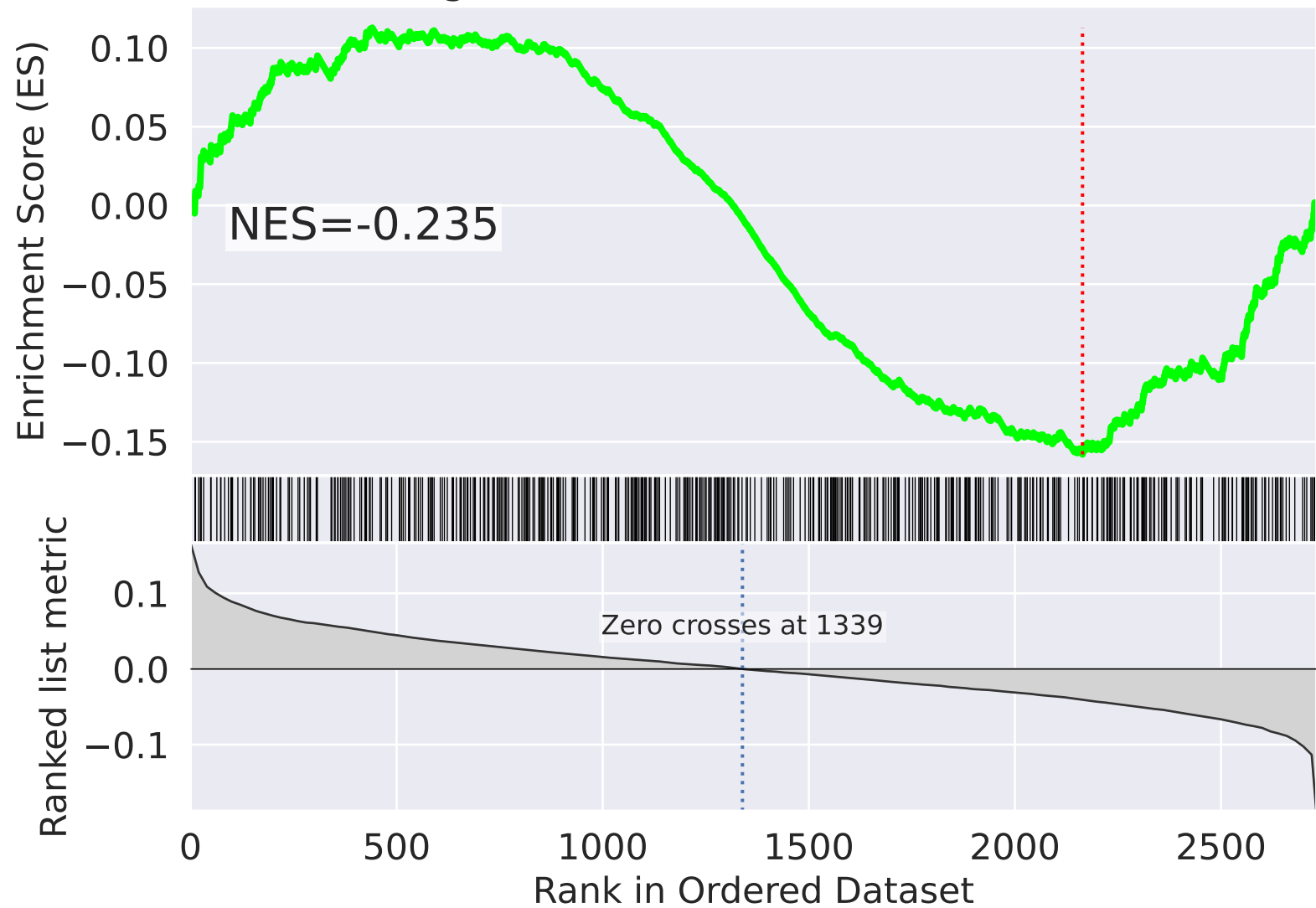
Signal Transduction R-HSA-162582



NES		SET
3.923		Transcriptional Regulation By TP53 R-HSA-3700989
3.703		Fanconi Anemia Pathway R-HSA-6783310
3.533		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.196		TP53 Regulates Metabolic Genes R-HSA-5628897
-3.157		Metabolism Of Lipids R-HSA-556833
3.028		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
3.022		Respiratory Electron Transport R-HSA-611105
2.944		Transcriptional Regulation By RUNX1 R-HSA-8878171
2.808		Metabolism Of Amino Acids And Derivatives R-HSA-71291
2.796		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-2.756		RHO GTPases Activate WASPs And WAVES R-HSA-5663213
-2.738		Glycosaminoglycan Metabolism R-HSA-1630316
2.735		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
2.733		TP53 Regulates Transcription Of DNA Repair Genes R-HSA-6796648
-2.670		Metabolism Of Carbohydrates R-HSA-71387

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



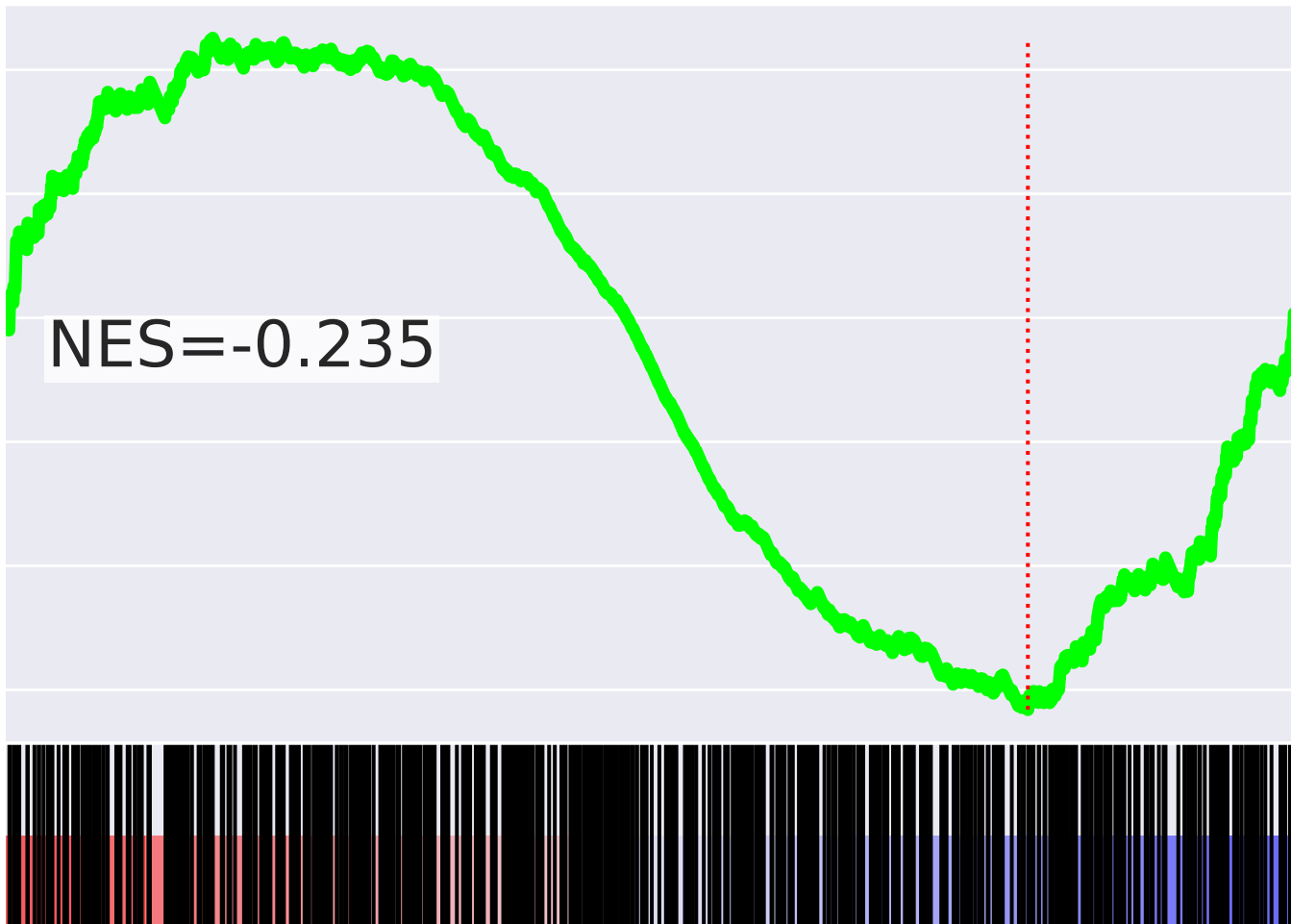
Signal Transduction R-HSA-162582

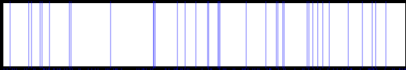
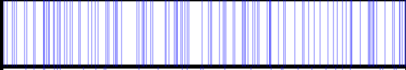
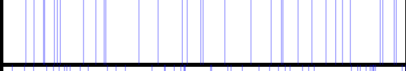
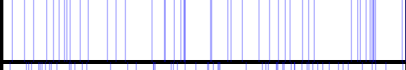
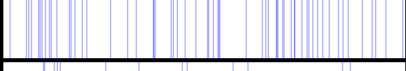

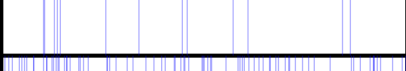
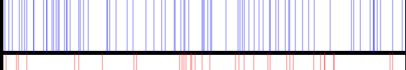
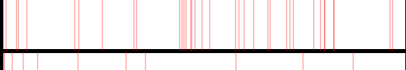
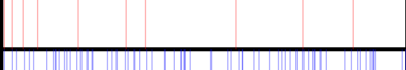
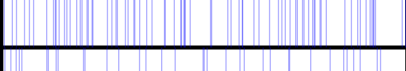

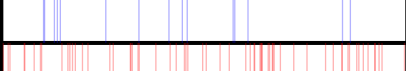
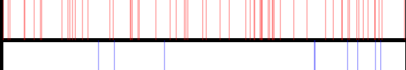
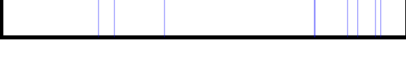
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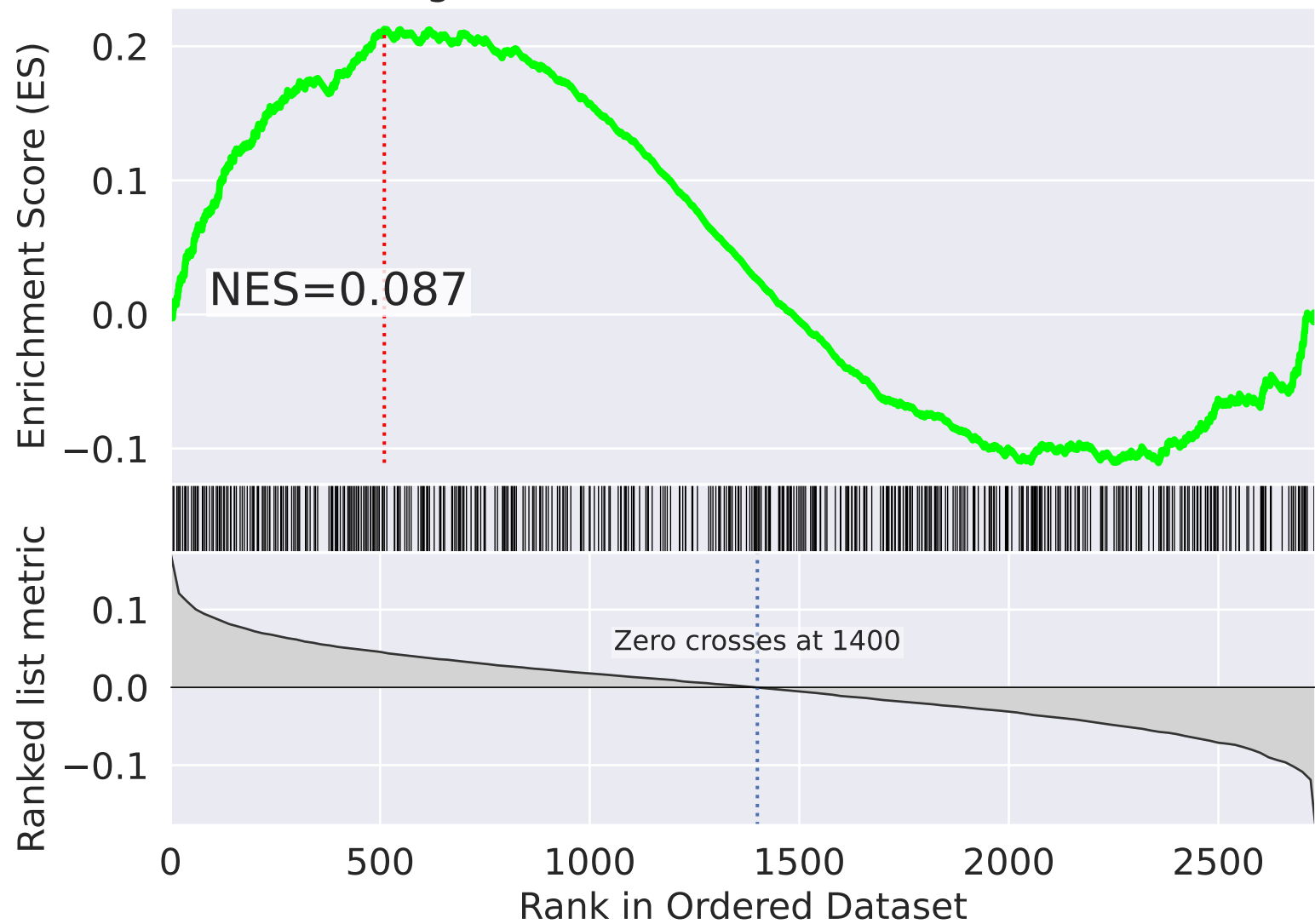
Rank



NES		SET
-3.859		Complex I Biogenesis R-HSA-6799198
-3.530		Transport Of Small Molecules R-HSA-382551
-3.325		Amino Acids Regulate mTORC1 R-HSA-9639288
-3.097		Signaling By NOTCH4 R-HSA-9013694
-3.064		Respiratory Electron Transport R-HSA-611105
-3.002		ROS And RNS Production In Phagocytes R-HSA-1222556
-3.002		Insulin Receptor Recycling R-HSA-77387
-2.817		Host Interactions Of HIV Factors R-HSA-162909
2.810		Potential Therapeutics For SARS R-HSA-9679191
2.790		Cell-cell Junction Organization R-HSA-421270
-2.750		Signaling By NOTCH R-HSA-157118
-2.746		Nuclear Envelope Breakdown R-HSA-2980766
-2.730		Transferrin Endocytosis And Recycling R-HSA-917977
2.709		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-2.659		Nuclear Signaling By ERBB4 R-HSA-1251985

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

0.2

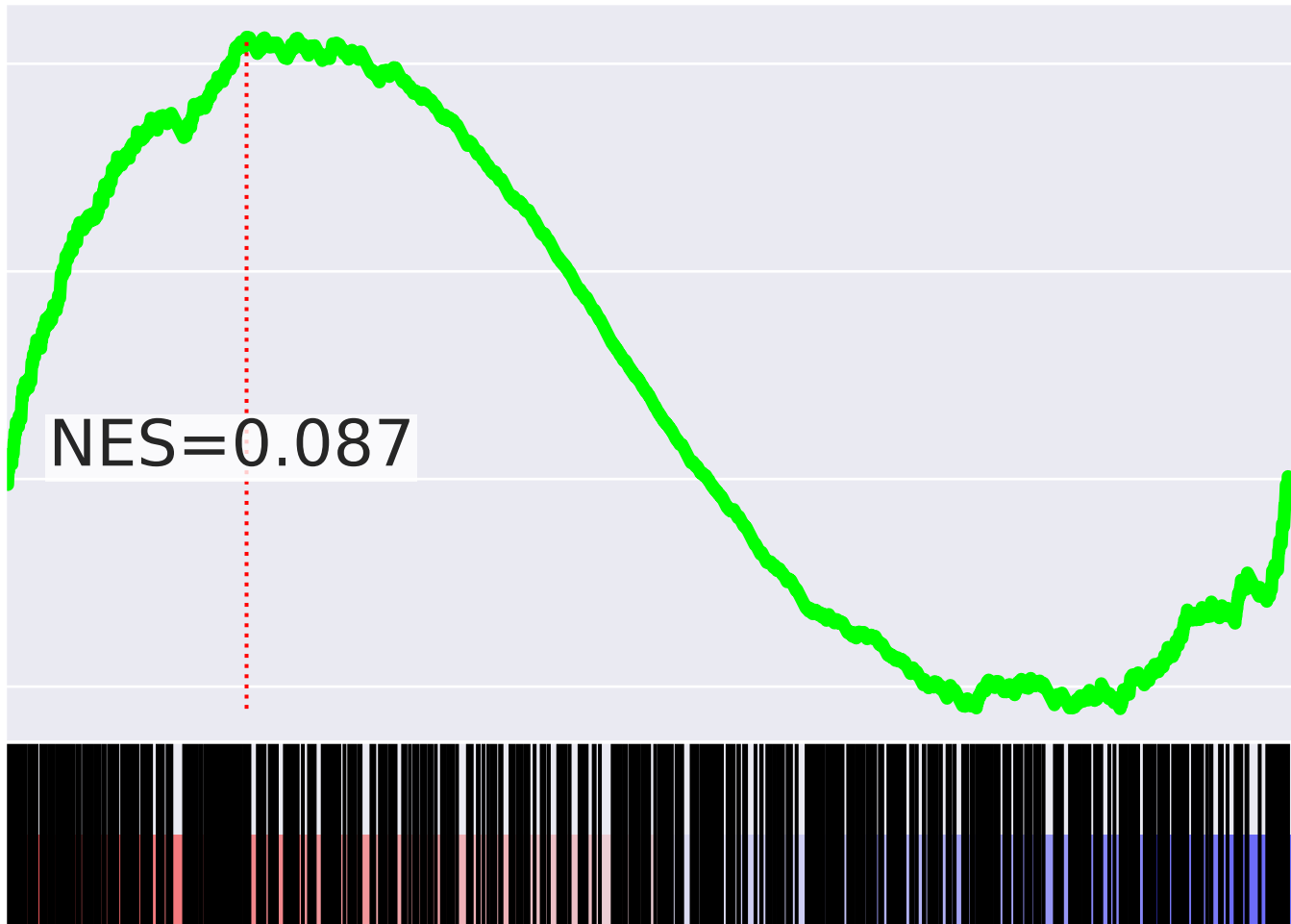
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0.0

-0.1

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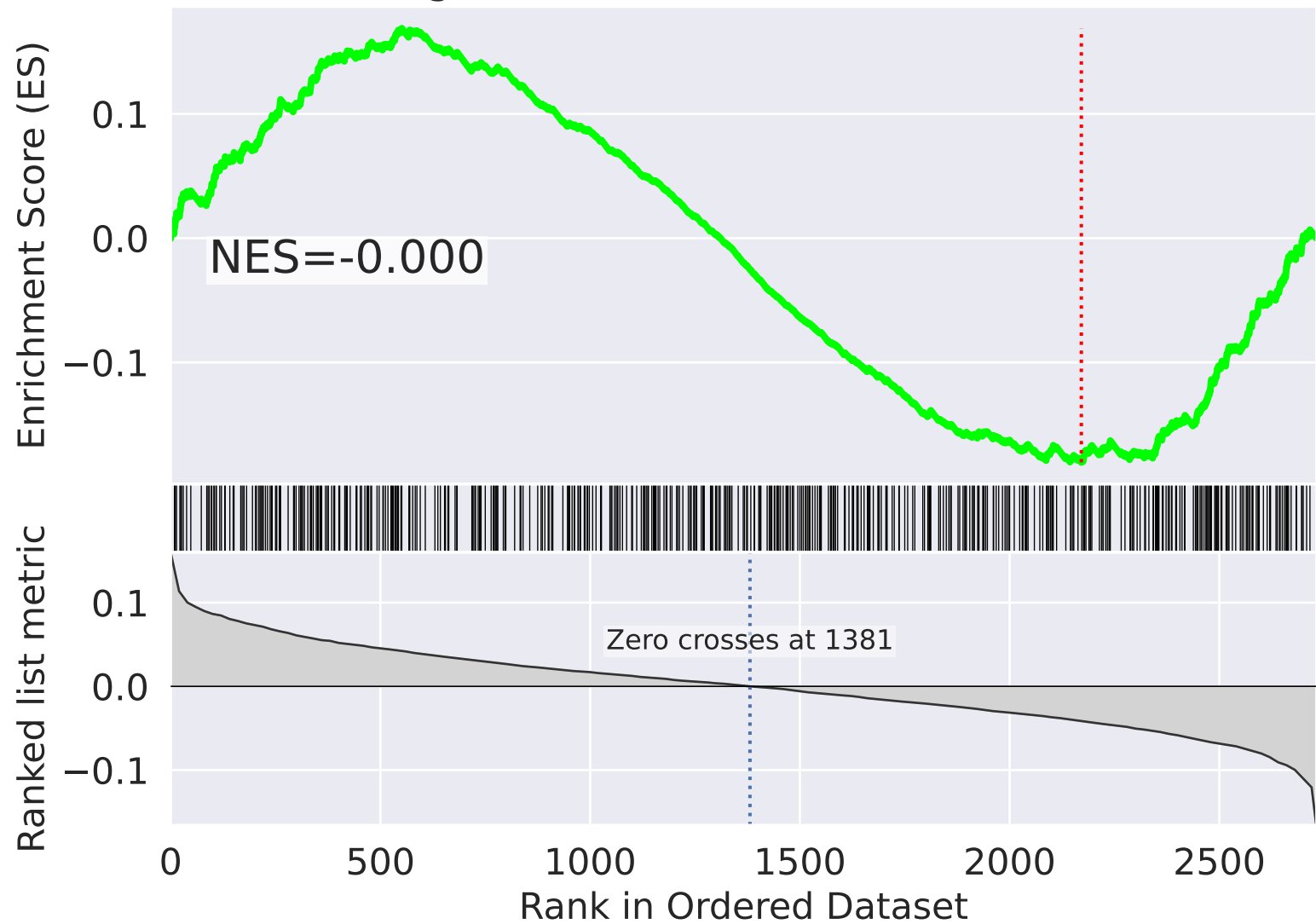
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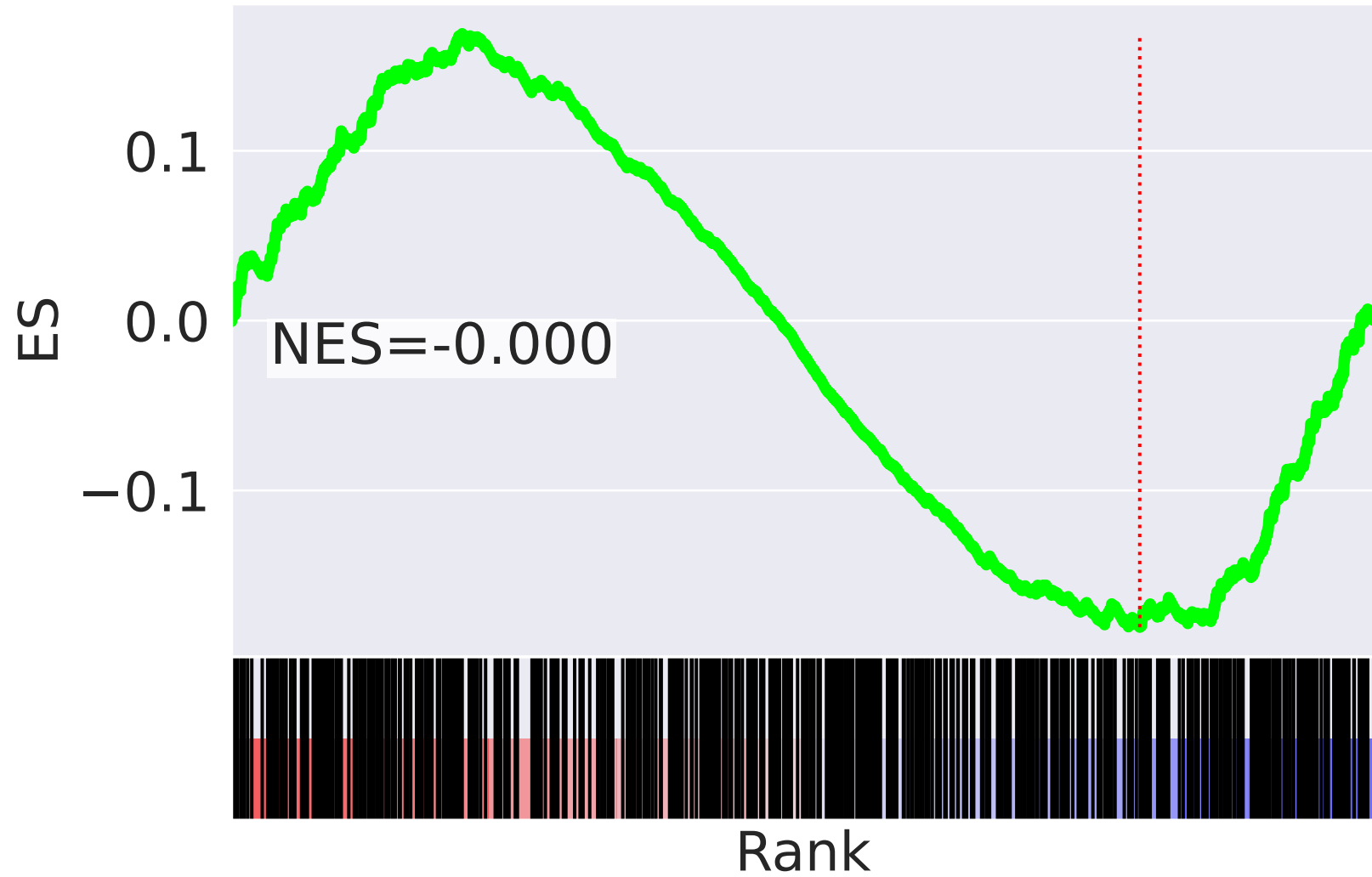
NES	SET
5.460	Intracellular Signaling By Second Messengers R-HSA-9006925
5.094	Transport Of Small Molecules R-HSA-382551
5.075	PIP3 Activates AKT Signaling R-HSA-1257604
4.987	Deubiquitination R-HSA-5688426
4.950	Beta-catenin Independent WNT Signaling R-HSA-3858494
-4.949	rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.893	Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.841	PTEN Regulation R-HSA-6807070
4.839	MAPK6/MAPK4 Signaling R-HSA-5687128
4.670	UCH Proteinases R-HSA-5689603
4.662	Regulation Of PTEN Stability And Activity R-HSA-8948751
4.563	G1/S Transition R-HSA-69206
4.561	Signaling By WNT R-HSA-195721
4.561	Transcriptional Regulation By RUNX1 R-HSA-8878171
4.559	Transcriptional Regulation By RUNX3 R-HSA-8878159

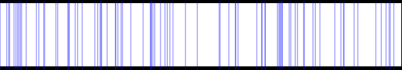
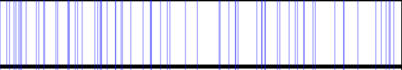
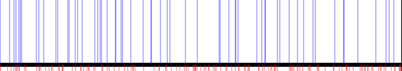
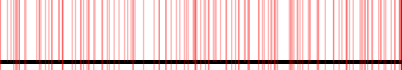
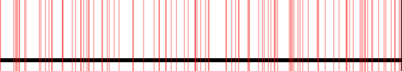
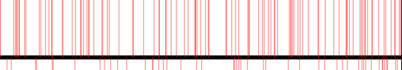

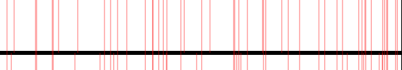
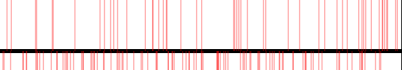
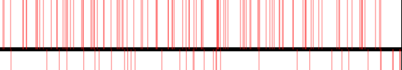
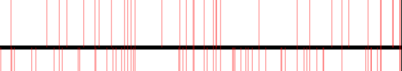
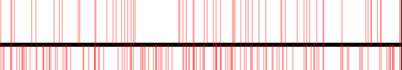

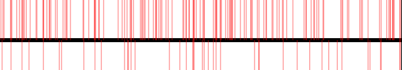
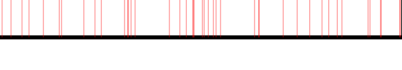
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=14$

Signal Transduction R-HSA-162582



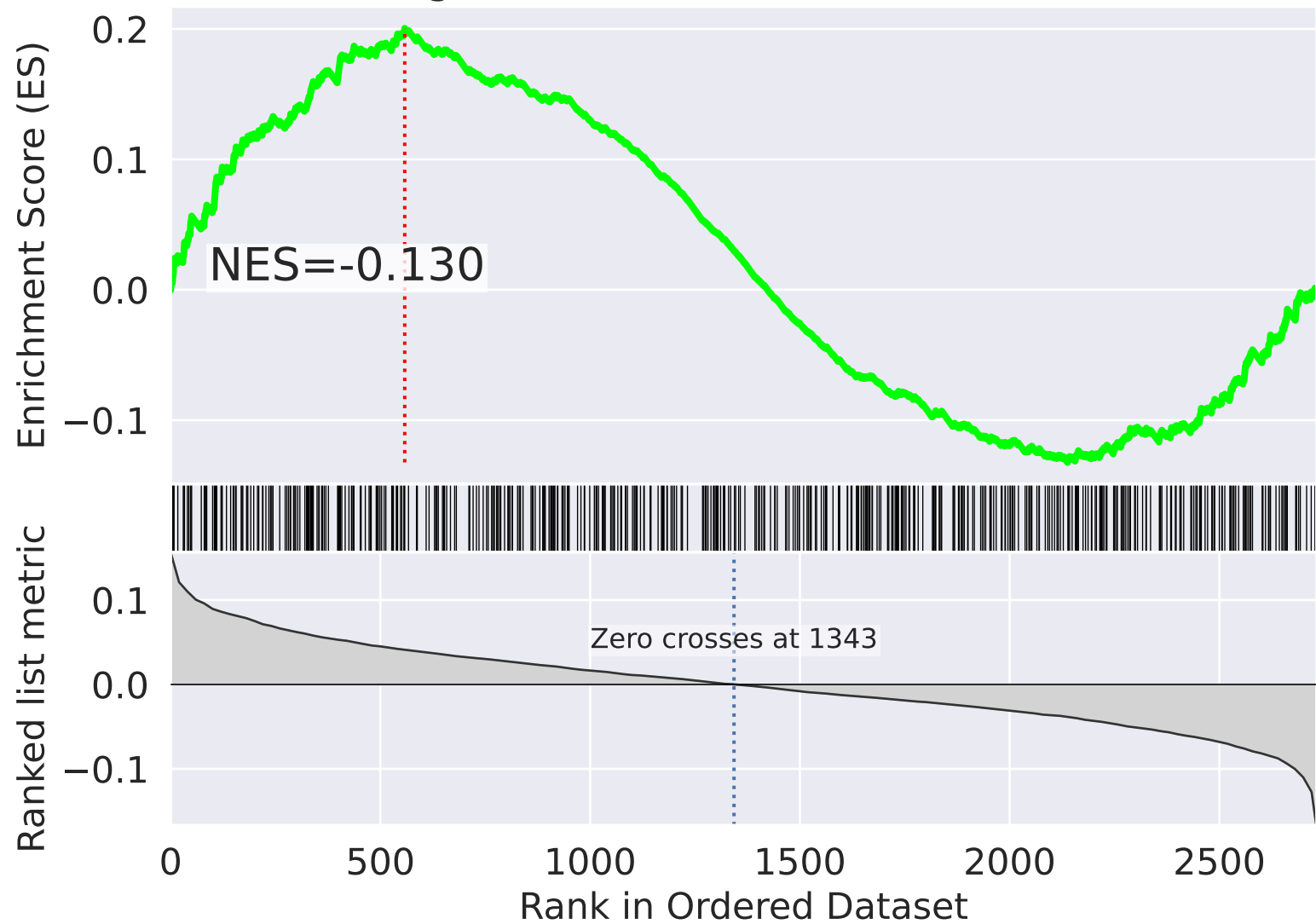
Signal Transduction R-HSA-162582



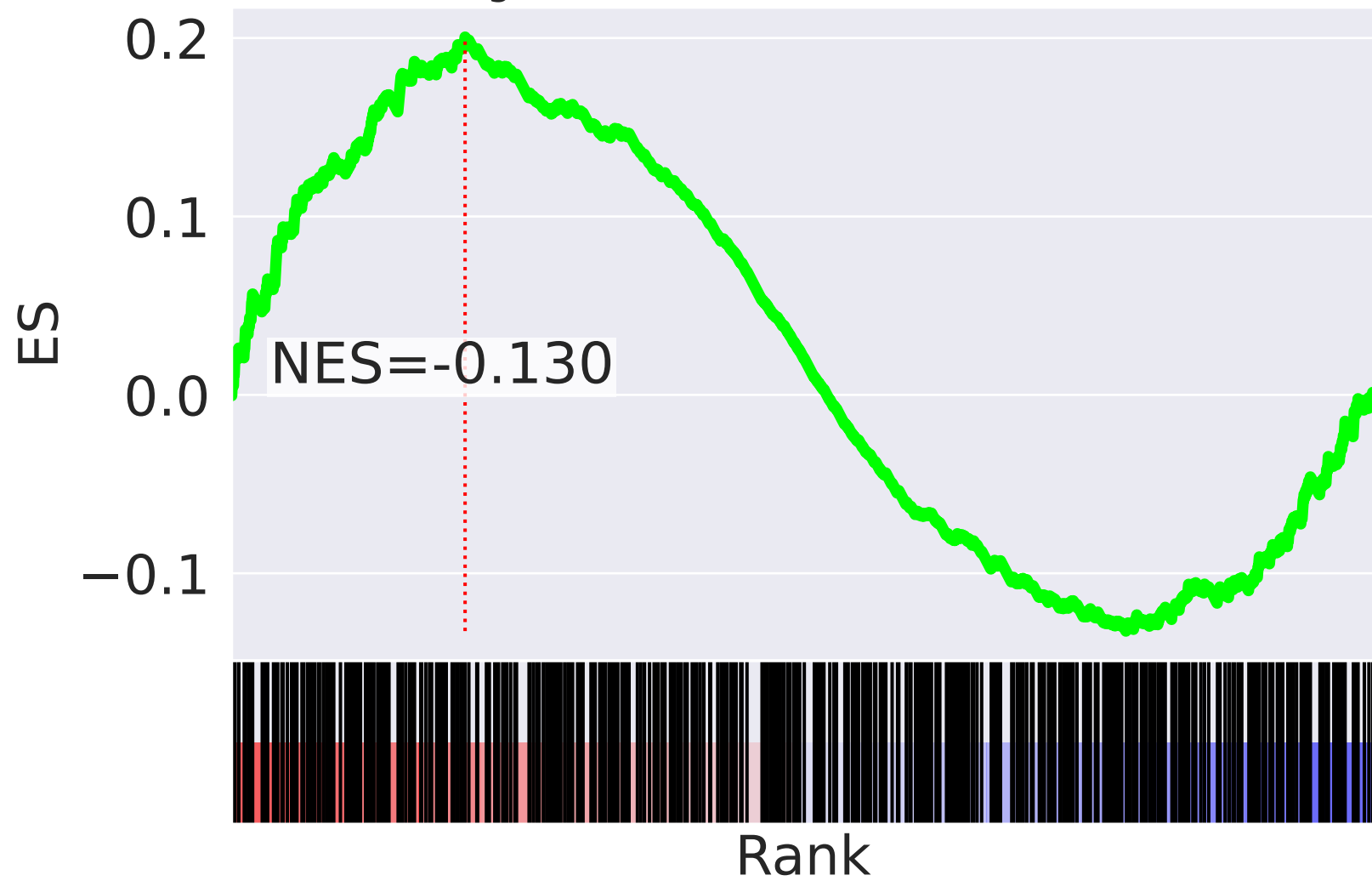
NES		SET
-5.719		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-5.551		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-4.836		Respiratory Electron Transport R-HSA-611105
4.772		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.634		mRNA Splicing R-HSA-72172
4.575		mRNA Splicing - Major Pathway R-HSA-72163
4.097		PPARA Activates Gene Expression R-HSA-1989781
4.062		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
3.919		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
3.744		S Phase R-HSA-69242
3.658		Nuclear Envelope Breakdown R-HSA-2980766
3.609		HCMV Infection R-HSA-9609646
3.584		Mitotic Anaphase R-HSA-68882
3.509		Mitotic Metaphase And Anaphase R-HSA-2555396
3.216		SUMOylation Of DNA Damage Response And Repair Proteins R-HSA-3108214

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



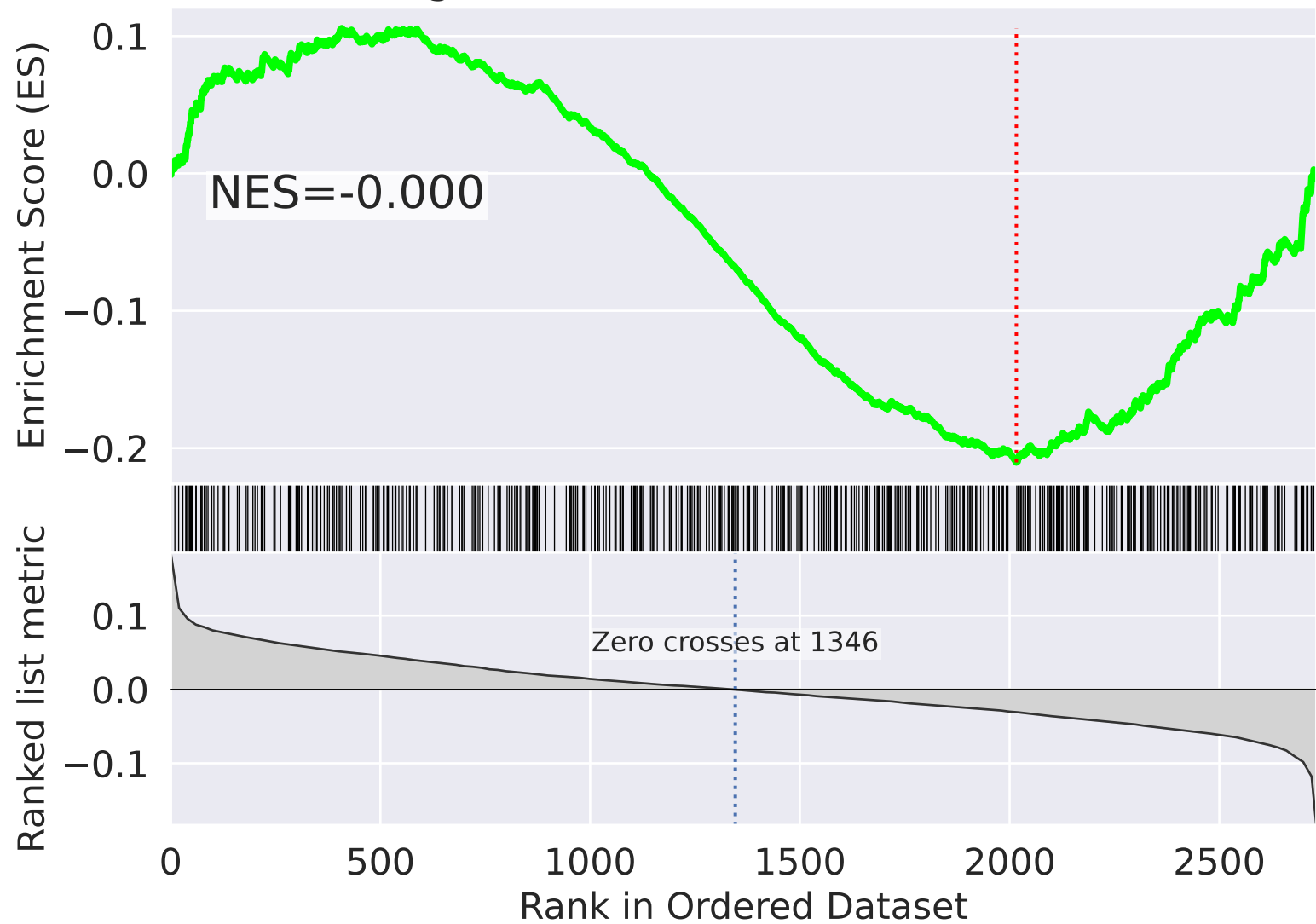
Signal Transduction R-HSA-162582



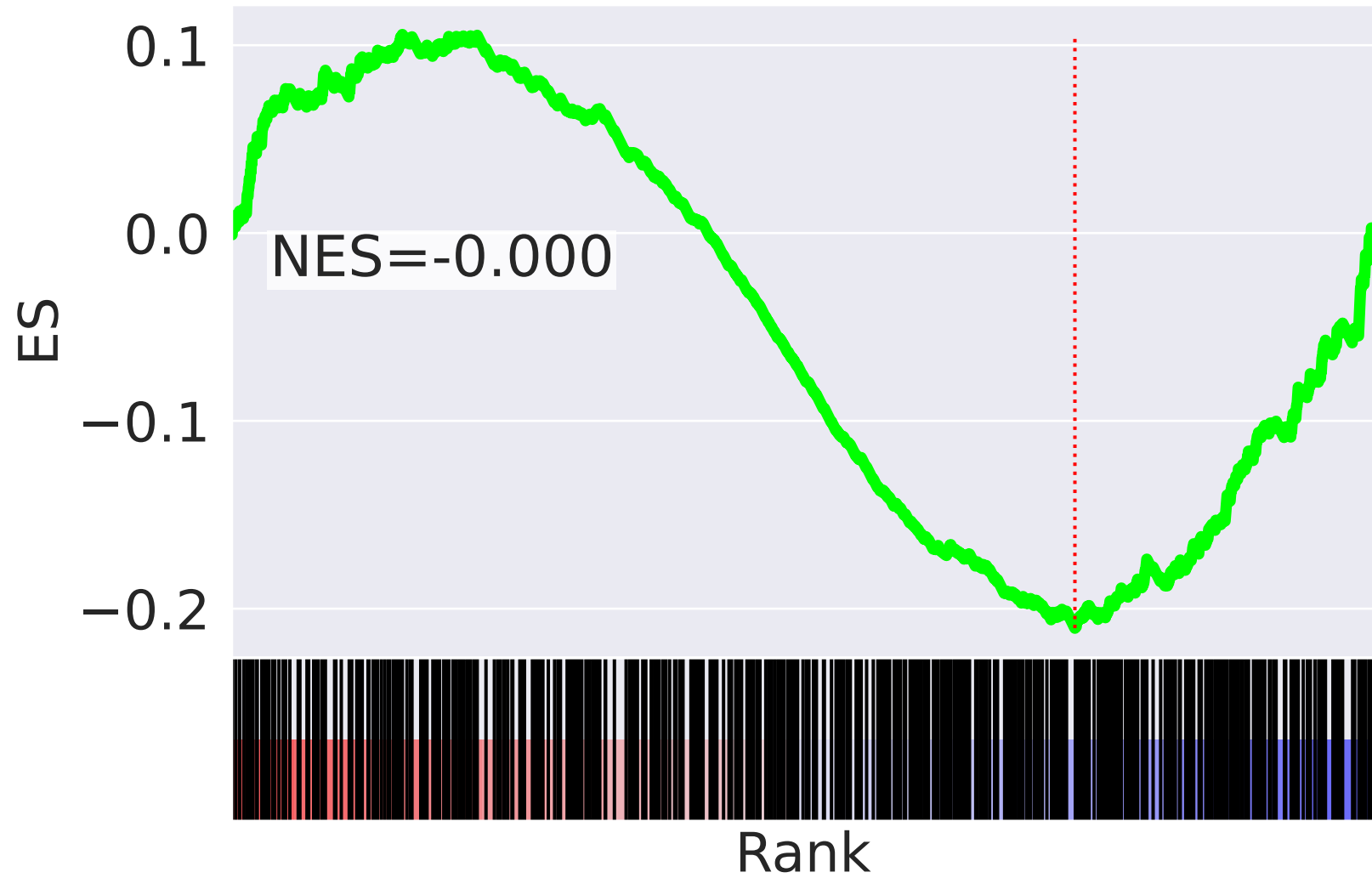
NES	SET
-4.622	Mitotic Anaphase R-HSA-68882
-4.542	Mitotic Metaphase And Anaphase R-HSA-2555396
-4.291	Separation Of Sister Chromatids R-HSA-2467813
-3.879	Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
-3.866	APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
-3.812	mRNA Splicing R-HSA-72172
-3.758	APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
-3.625	Cell Cycle Checkpoints R-HSA-69620
-3.483	mRNA Splicing - Major Pathway R-HSA-72163
-3.470	M Phase R-HSA-68886
-3.442	Phosphorylation Of APC/C R-HSA-176412
-3.402	Activation Of APC/C And APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176814
-3.261	Conversion From APC/C:Cdc20 To APC/C:Cdh1 In Late Anaphase R-HSA-176407
-3.253	Cdc20:Phospho-APC/C Mediated Degradation Of Cyclin A R-HSA-174184
-3.253	APC:Cdc20 Mediated Degradation Of Cell Cycle Proteins Before Cycle Checkpoint Satisfied R-HSA-179419

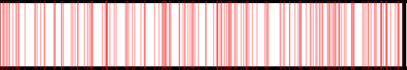
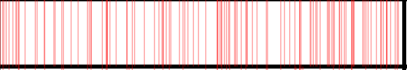
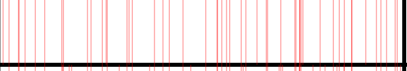
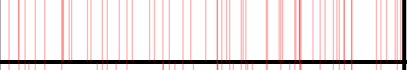
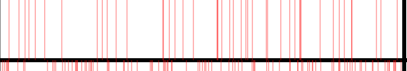
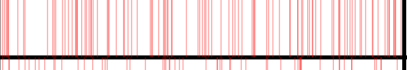
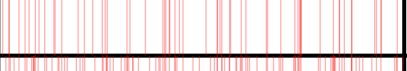
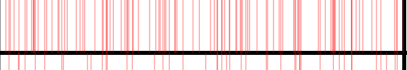
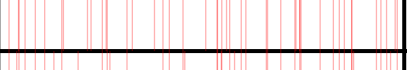
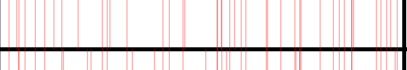
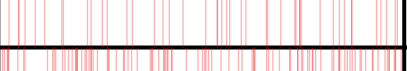
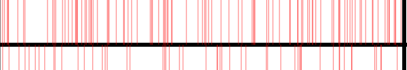
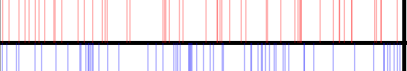
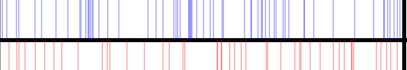
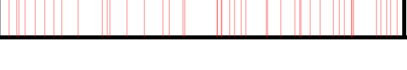
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=16$

Signal Transduction R-HSA-162582



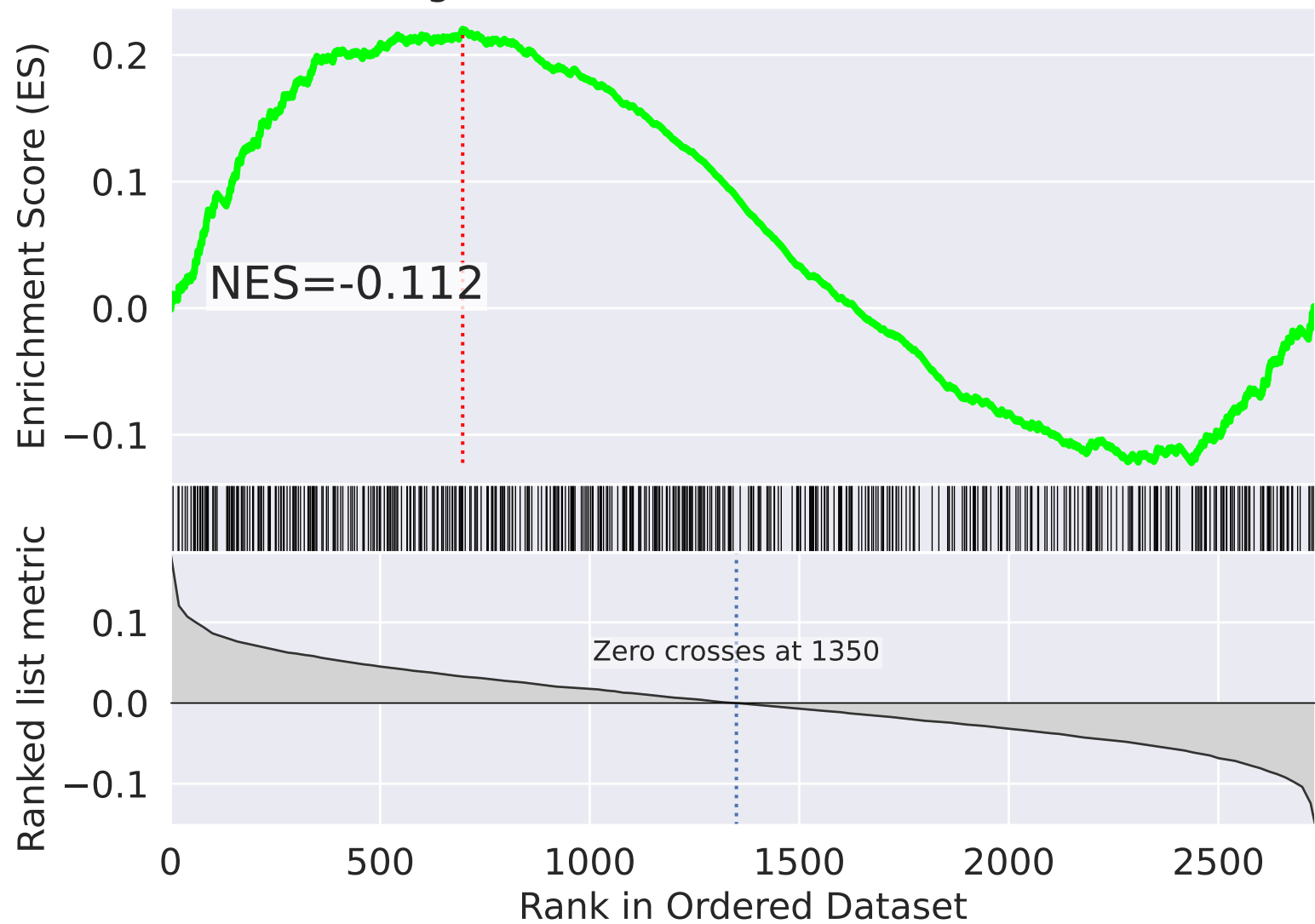
Signal Transduction R-HSA-162582



NES		SET
5.179		Adaptive Immune System R-HSA-1280218
4.781		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
4.407		APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
4.320		Assembly Of Pre-Replicative Complex R-HSA-68867
4.264		Cellular Response To Hypoxia R-HSA-1234174
4.228		mRNA Splicing R-HSA-72172
4.218		C-type Lectin Receptors (CLRs) R-HSA-5621481
4.211		Deubiquitination R-HSA-5688426
4.173		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
4.128		ER-Phagosome Pathway R-HSA-1236974
4.081		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
4.019		mRNA Splicing - Major Pathway R-HSA-72163
4.017		CLEC7A (Dectin-1) Signaling R-HSA-5607764
-3.984		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.970		Antigen processing-Cross Presentation R-HSA-1236975

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

ES

0.2

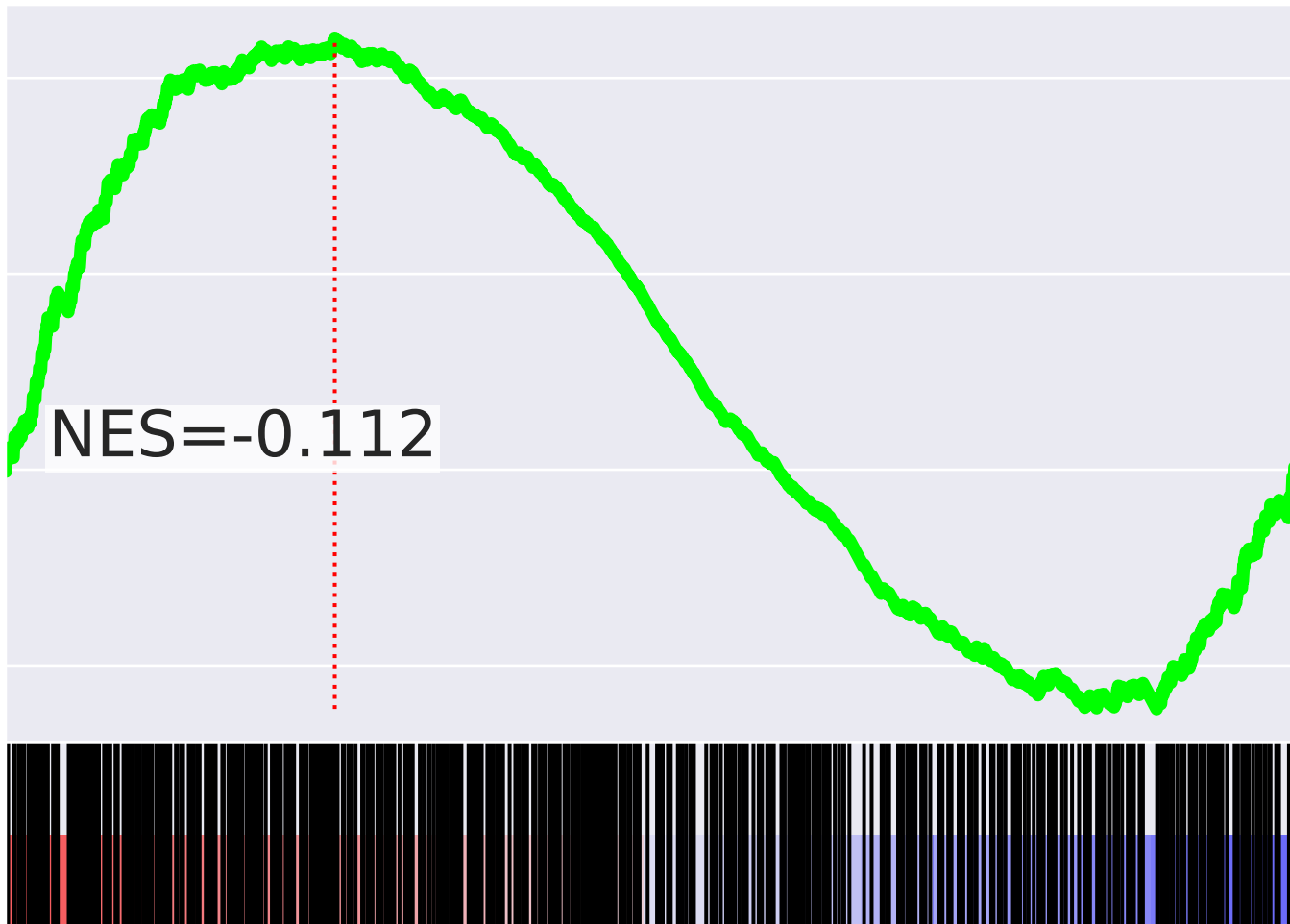
0.1

0.0

-0.1

NES=-0.112

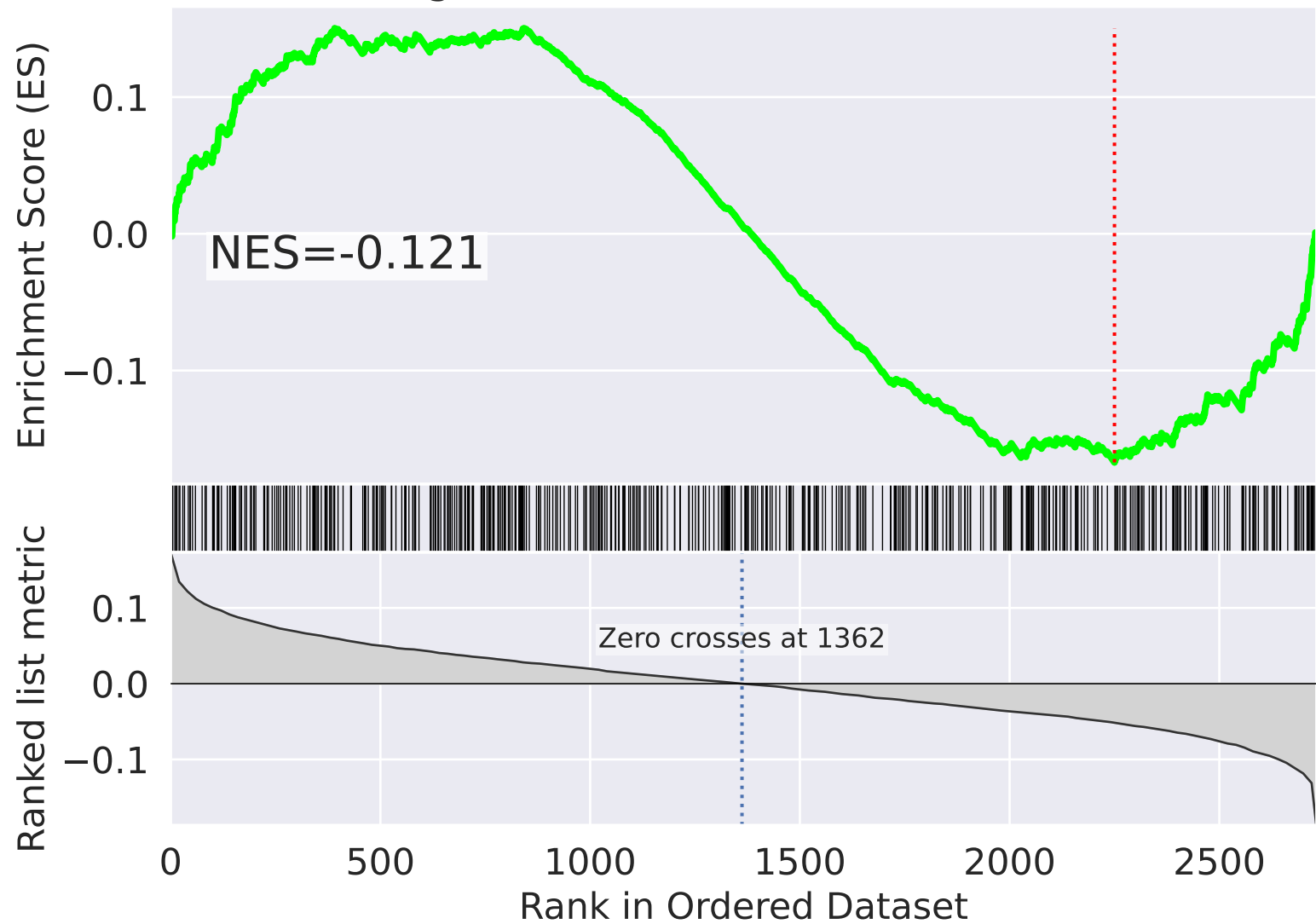
Rank



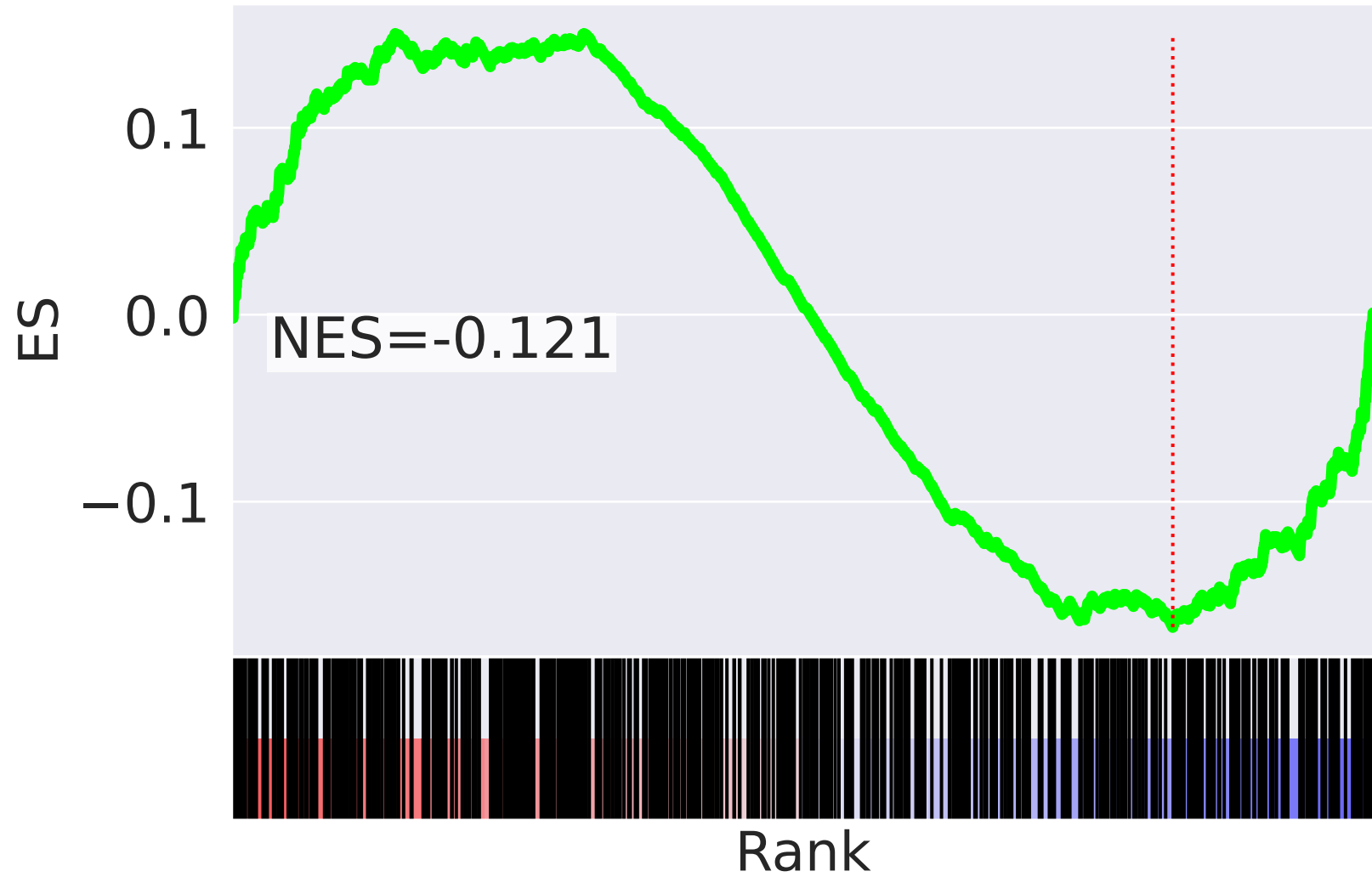
NES		SET
-3.345		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
3.335		Metabolism Of Porphyrins R-HSA-189445
3.335		Heme Biosynthesis R-HSA-189451
-3.108		RNA Polymerase I Transcription Initiation R-HSA-73762
-3.070		Diseases Associated With N-glycosylation Of Proteins R-HSA-3781860
3.068		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
-3.018		Endosomal Sorting Complex Required For Transport (ESCRT) R-HSA-917729
2.929		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
2.927		GPVI-mediated Activation Cascade R-HSA-114604
-2.844		Budding And Maturation Of HIV Virion R-HSA-162588
2.802		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
-2.801		RNA Polymerase I Promoter Clearance R-HSA-73854
-2.801		RNA Polymerase I Transcription R-HSA-73864
2.785		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-2.723		DNA Damage Recognition In GG-NER R-HSA-5696394

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



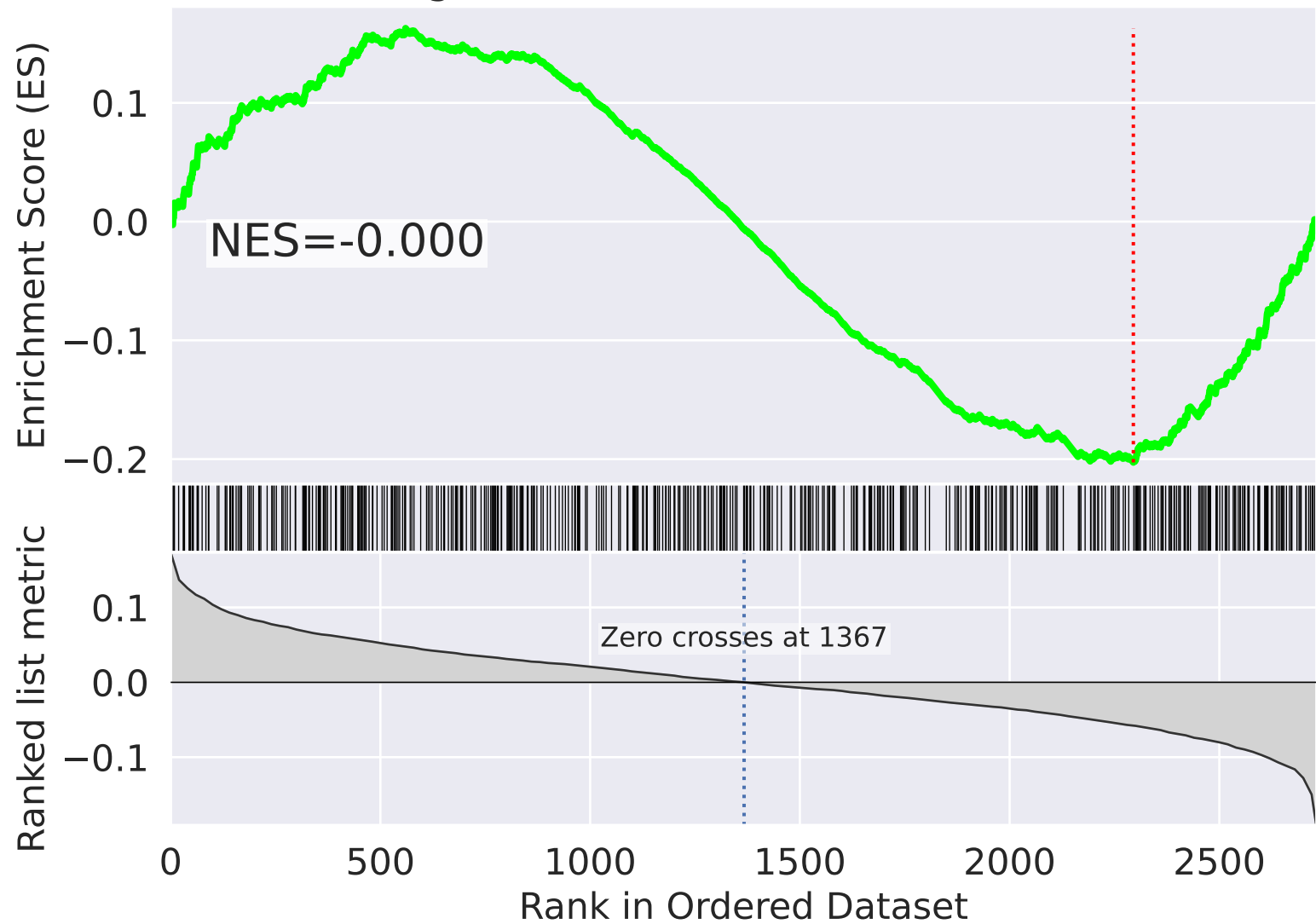
Signal Transduction R-HSA-162582



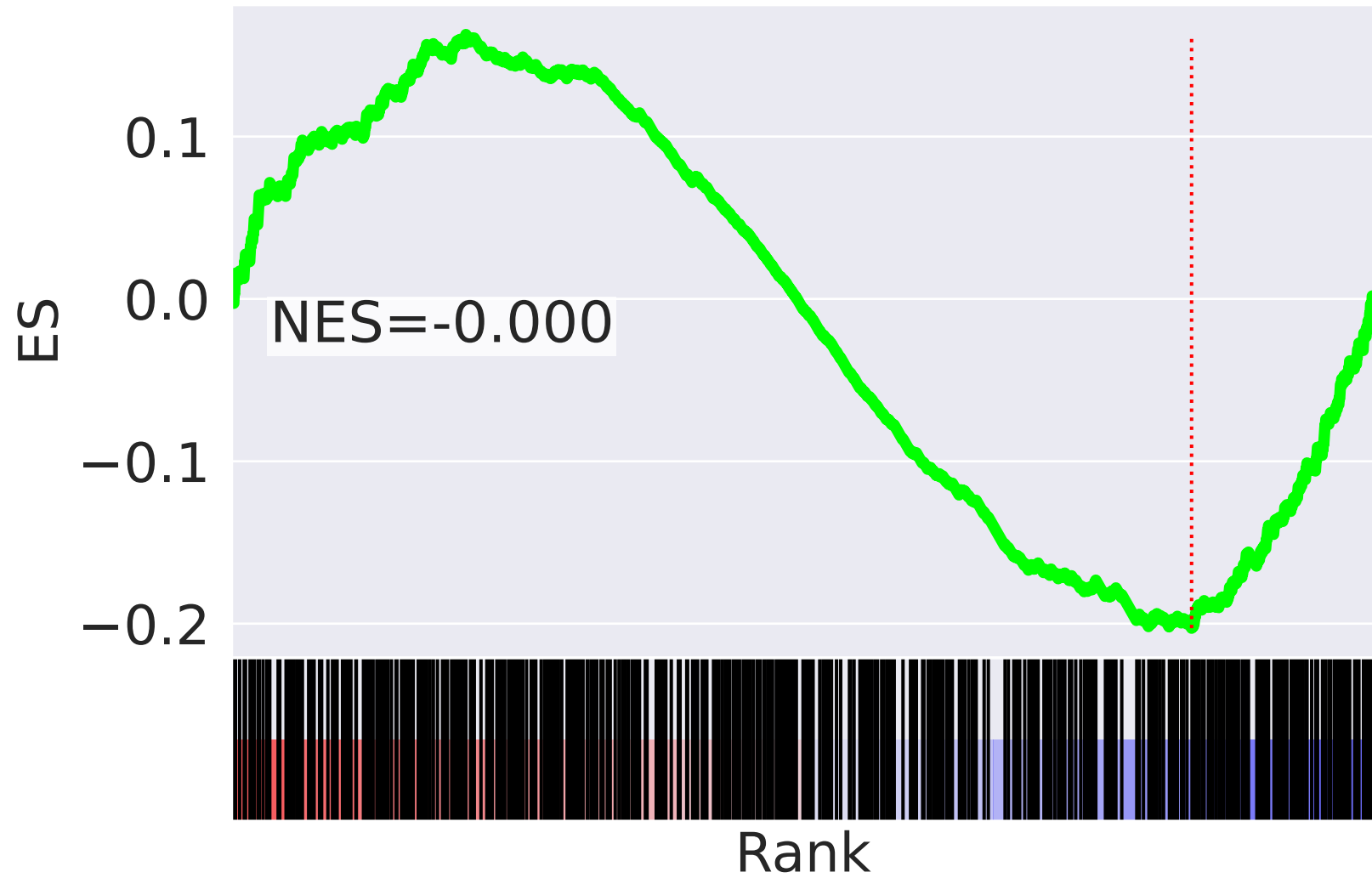
NES	SET
-4.117	Mitotic Prometaphase R-HSA-68877
-4.044	RHO GTPase Effectors R-HSA-195258
-3.949	Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
-3.949	EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
-3.775	Separation Of Sister Chromatids R-HSA-2467813
-3.742	Resolution Of Sister Chromatid Cohesion R-HSA-2500257
-3.740	RHO GTPases Activate Formins R-HSA-5663220
-3.541	Mitotic Spindle Checkpoint R-HSA-69618
-3.472	Cell Cycle Checkpoints R-HSA-69620
-3.440	Mitotic Metaphase And Anaphase R-HSA-2555396
-3.439	Mitotic Anaphase R-HSA-68882
-3.175	Signaling By Rho GTPases R-HSA-194315
-3.006	Signaling By Rho GTPases, Miro GTPases And RHOBTB3 R-HSA-9716542
-2.806	mRNA Splicing R-HSA-72172
-2.622	Negative Regulation Of MAPK Pathway R-HSA-5675221

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



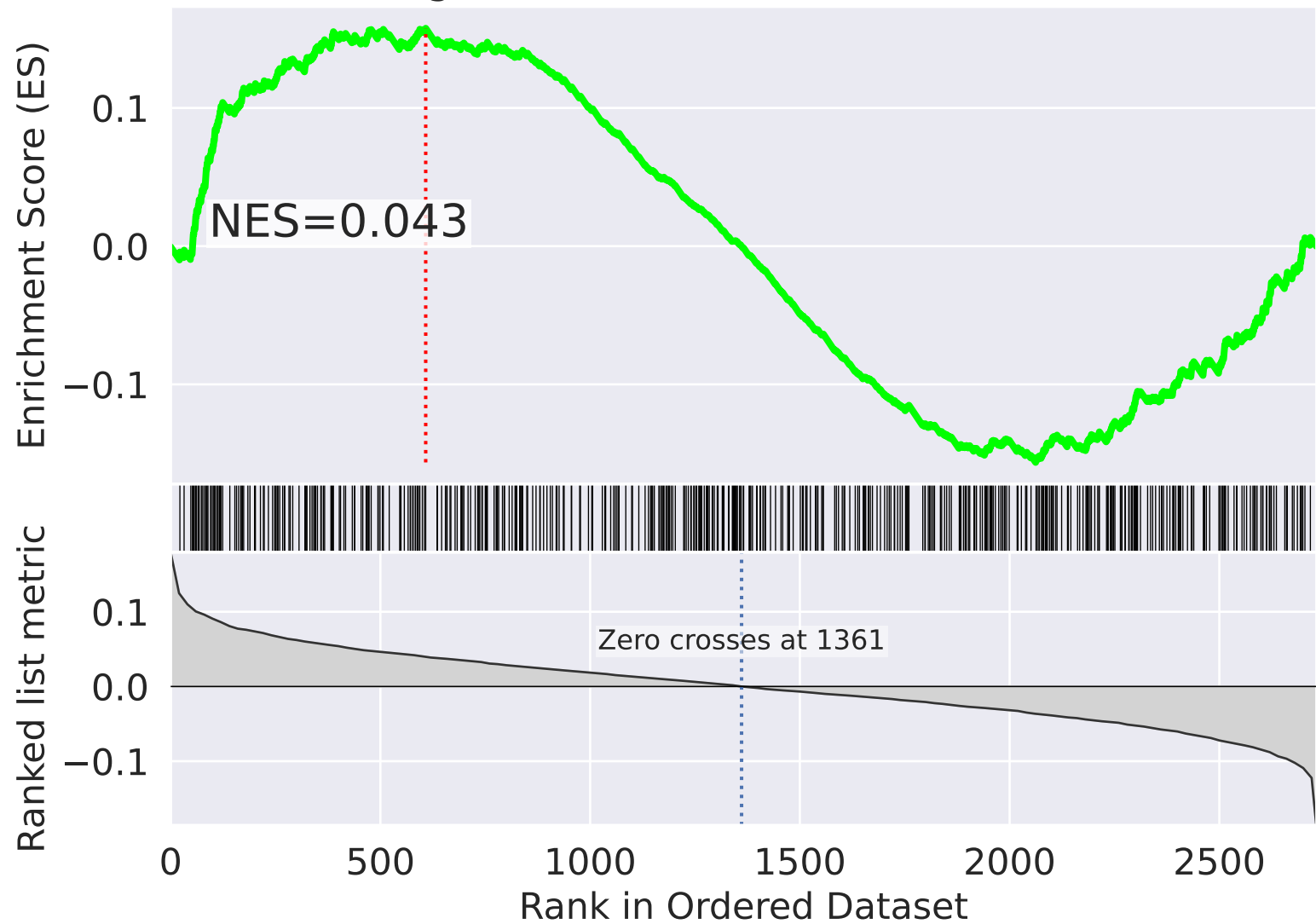
Signal Transduction R-HSA-162582



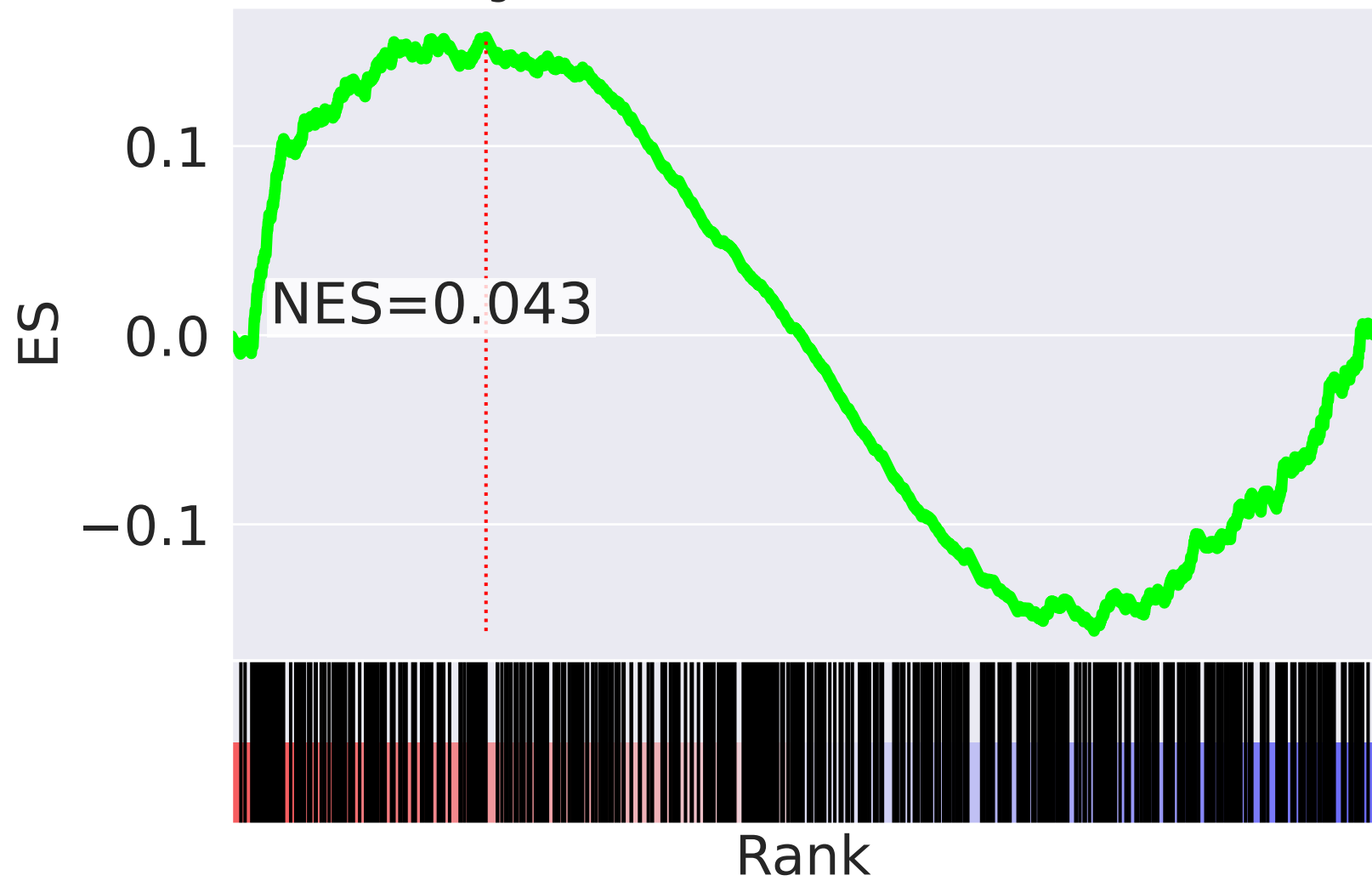
NES		SET
-6.092		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-5.823		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-5.521		Respiratory Electron Transport R-HSA-611105
-4.665		Complex I Biogenesis R-HSA-6799198
3.987		Leishmania Infection R-HSA-9658195
3.658		FCGR3A-mediated Phagocytosis R-HSA-9664422
-3.649		Iron Uptake And Transport R-HSA-917937
-3.639		ROS And RNS Production In Phagocytes R-HSA-1222556
-3.639		Insulin Receptor Recycling R-HSA-77387
3.636		Asparagine N-linked Glycosylation R-HSA-446203
-3.623		Transport Of Small Molecules R-HSA-382551
-3.493		Transferrin Endocytosis And Recycling R-HSA-917977
-3.313		Ion Channel Transport R-HSA-983712
3.306		RHO GTPases Activate WASPs And WAVES R-HSA-5663213
-3.262		Cellular Response To Starvation R-HSA-9711097




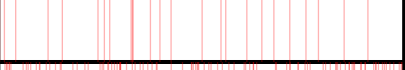
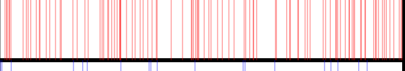


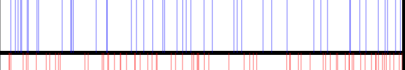
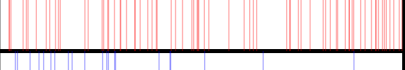



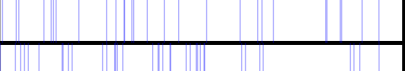
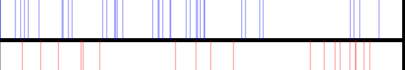

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=20$

Signal Transduction R-HSA-162582



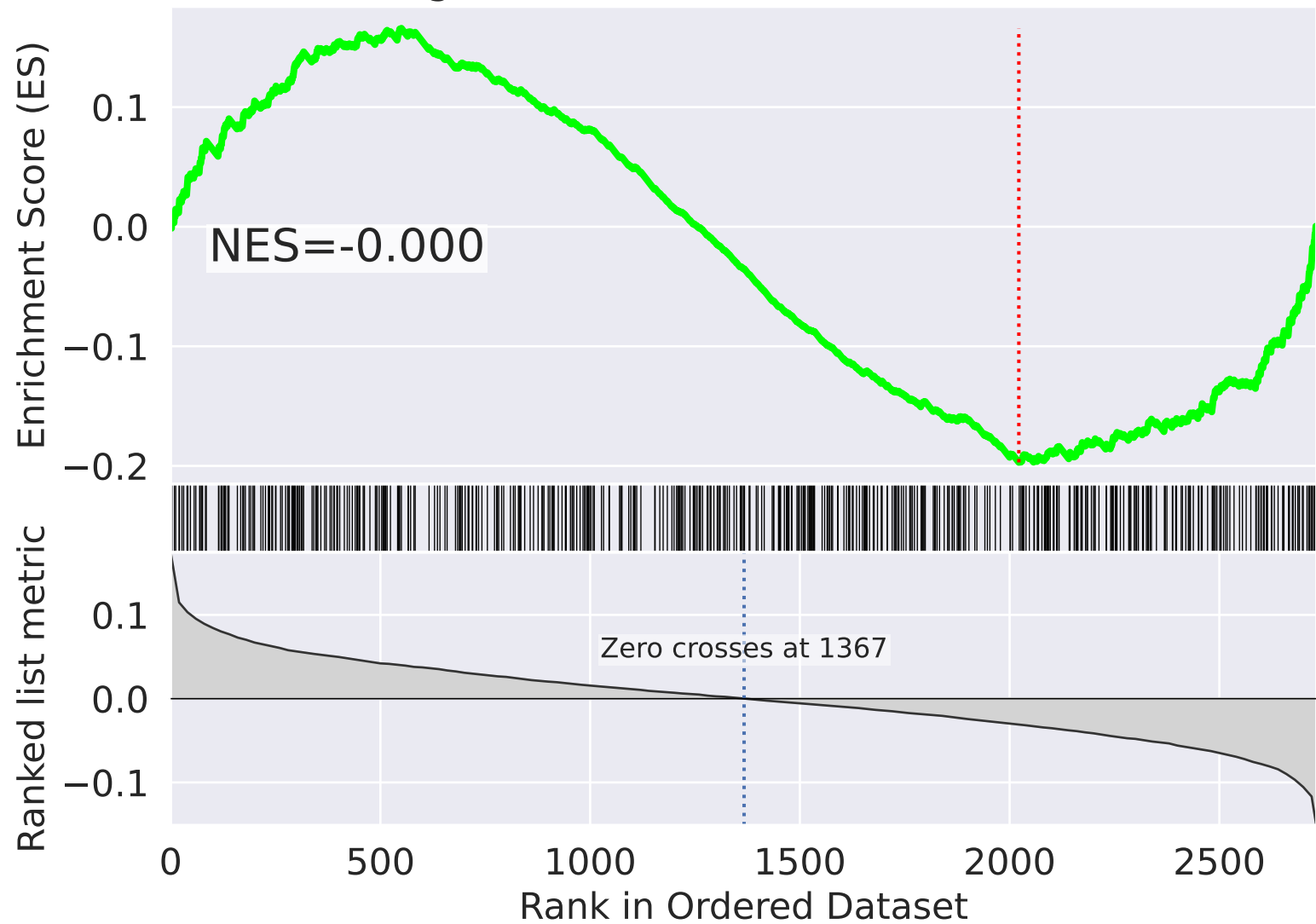
Signal Transduction R-HSA-162582



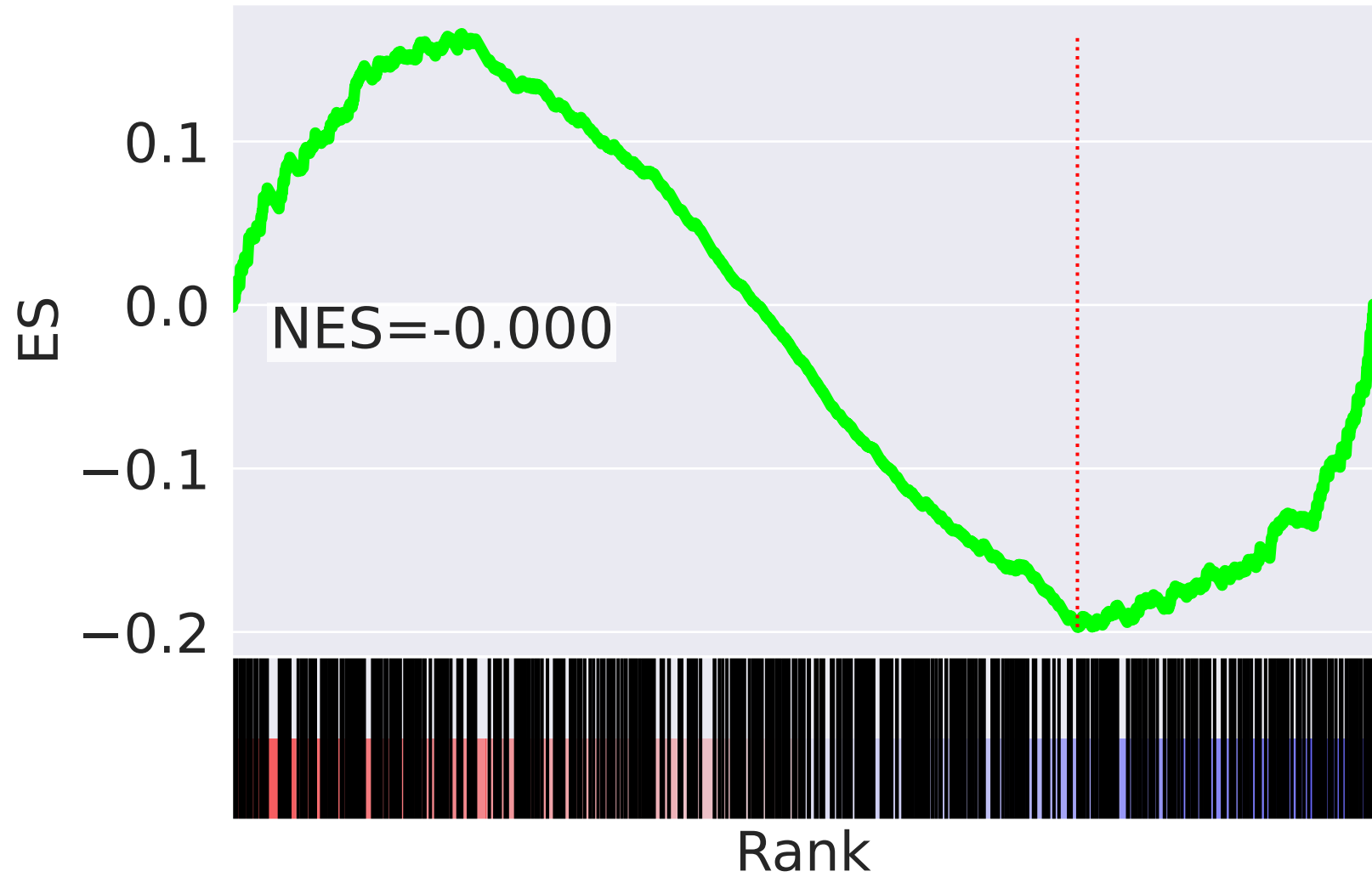
NES		SET
4.629		RHO GTPase Effectors R-HSA-195258
-3.523		Metabolism Of Nucleotides R-HSA-15869
-3.370		Nucleotide Biosynthesis R-HSA-8956320
3.367		Diseases Of Glycosylation R-HSA-3781865
3.207		Mitotic Prometaphase R-HSA-68877
-3.123		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
-2.949		Purine Ribonucleoside Monophosphate Biosynthesis R-HSA-73817
-2.946		Epigenetic Regulation Of Gene Expression R-HSA-212165
2.939		RHO GTPases Activate Formins R-HSA-5663220
-2.918		Translesion Synthesis By Y Family DNA Polymerases Bypasses Lesions On DNA Template R-HSA-110313
-2.854		DNA Damage Bypass R-HSA-73893
-2.794		Diseases Of Programmed Cell Death R-HSA-9645723
-2.783		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-2.777		Dual Incision In TC-NER R-HSA-6782135
2.760		FCGR3A-mediated Phagocytosis R-HSA-9664422

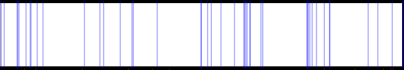

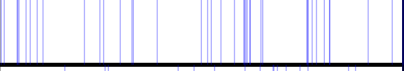
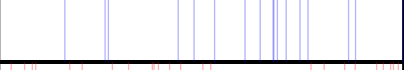


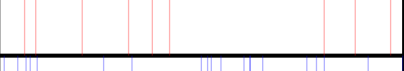
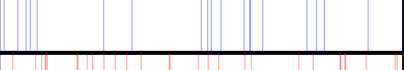
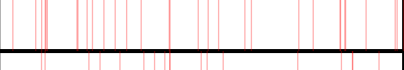
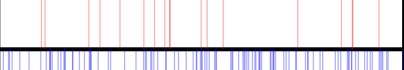
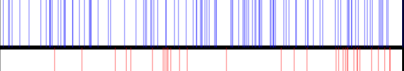
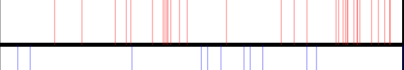
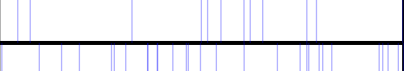
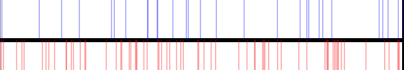
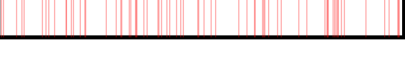
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=21$

Signal Transduction R-HSA-162582



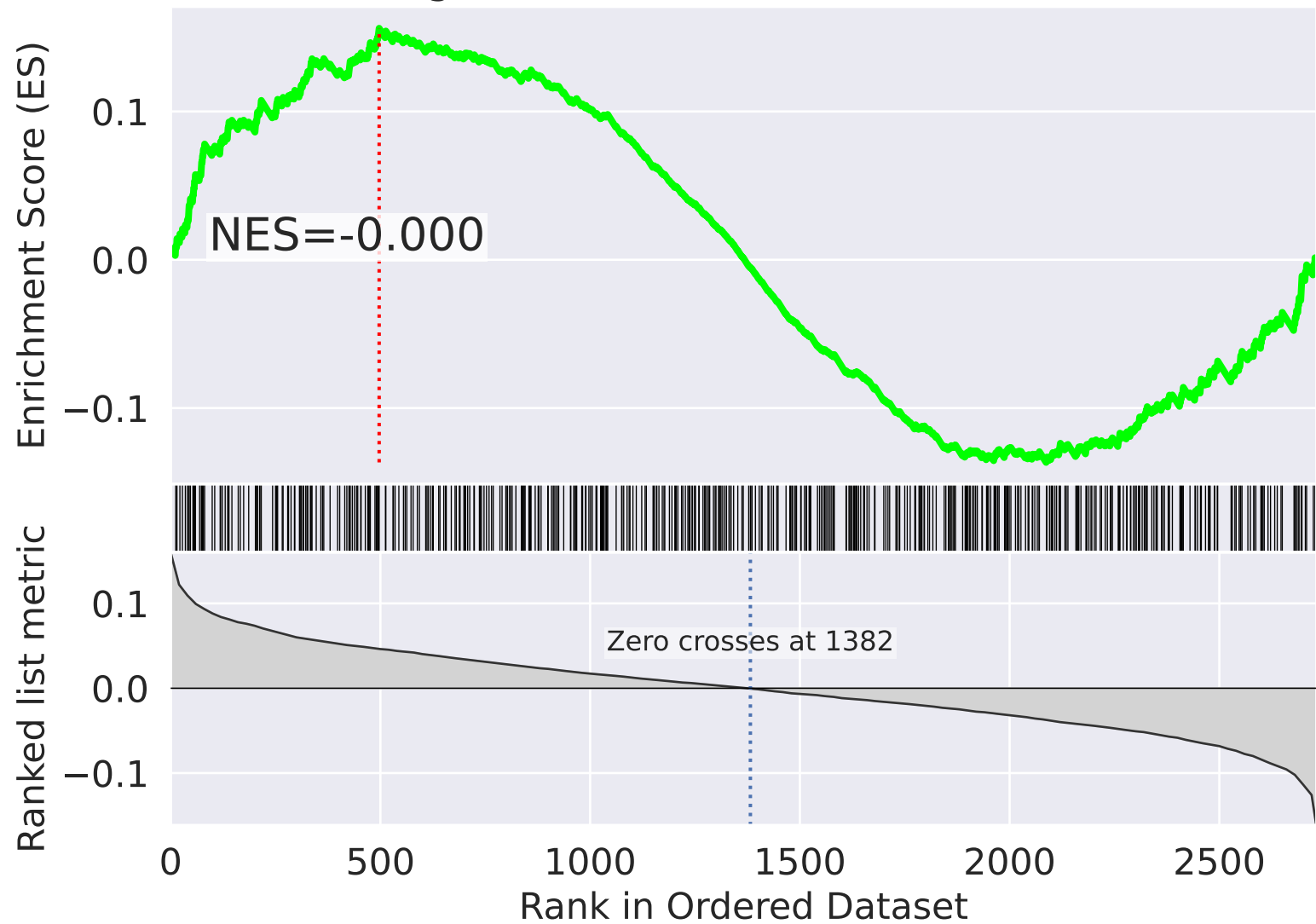
Signal Transduction R-HSA-162582



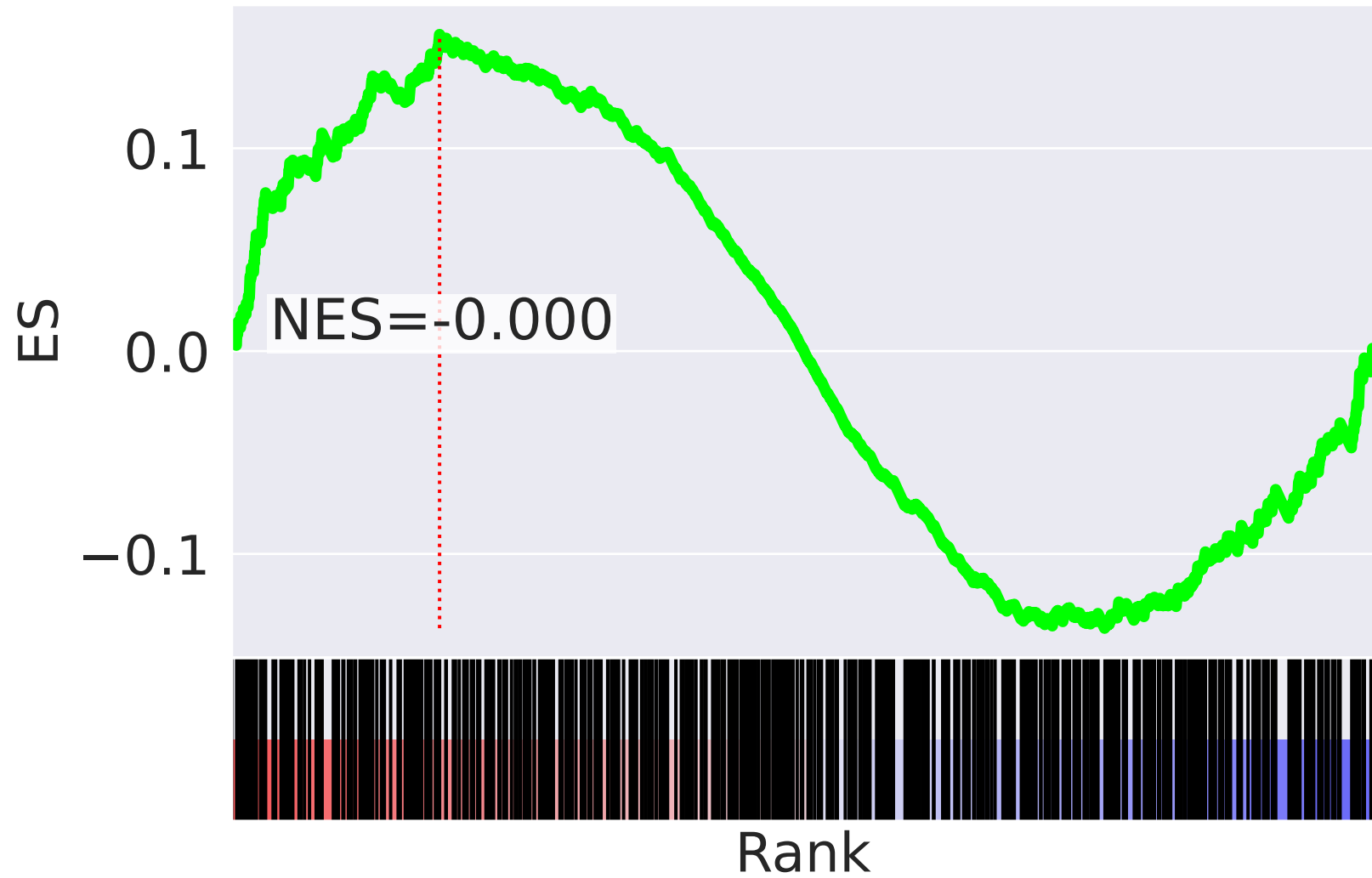
NES		SET
-4.067		Signaling By TGFB Family Members R-HSA-9006936
3.613		Nucleotide Biosynthesis R-HSA-8956320
-3.512		Signaling By TGF-beta Receptor Complex R-HSA-170834
-3.369		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
3.353		Metabolism Of Nucleotides R-HSA-15869
3.264		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.200		Purine Ribonucleoside Monophosphate Biosynthesis R-HSA-73817
-3.169		TGF-beta Receptor Signaling Activates SMADs R-HSA-2173789
3.138		Metabolism Of Vitamins And Cofactors R-HSA-196854
2.961		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-2.948		Chromatin Modifying Enzymes R-HSA-3247509
2.894		tRNA Aminoacylation R-HSA-379724
-2.834		Downregulation Of TGF-beta Receptor Signaling R-HSA-2173788
-2.817		Oxidative Stress Induced Senescence R-HSA-2559580
2.792		Metabolism Of Amino Acids And Derivatives R-HSA-71291


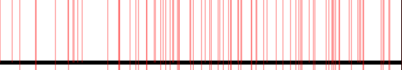
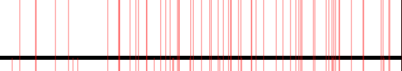
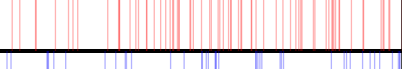
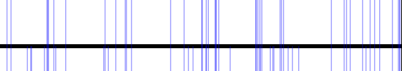
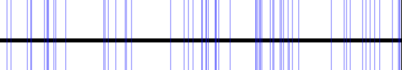
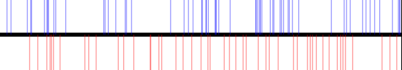
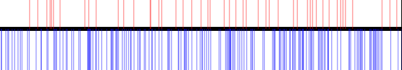
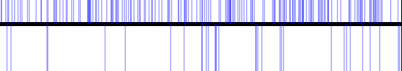

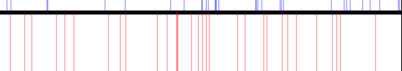
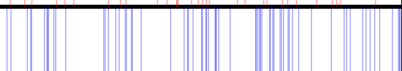



The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=22$

Signal Transduction R-HSA-162582



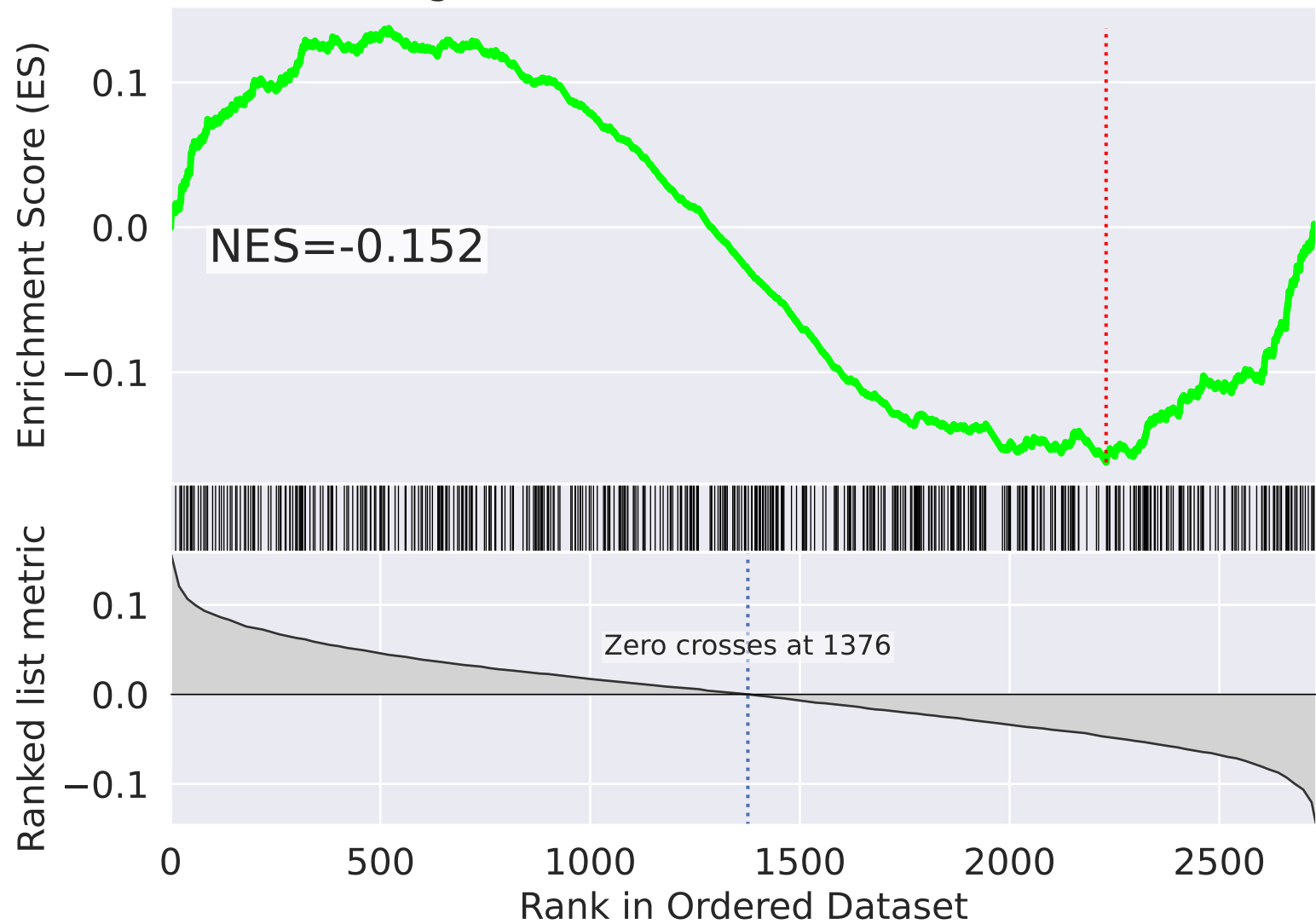
Signal Transduction R-HSA-162582



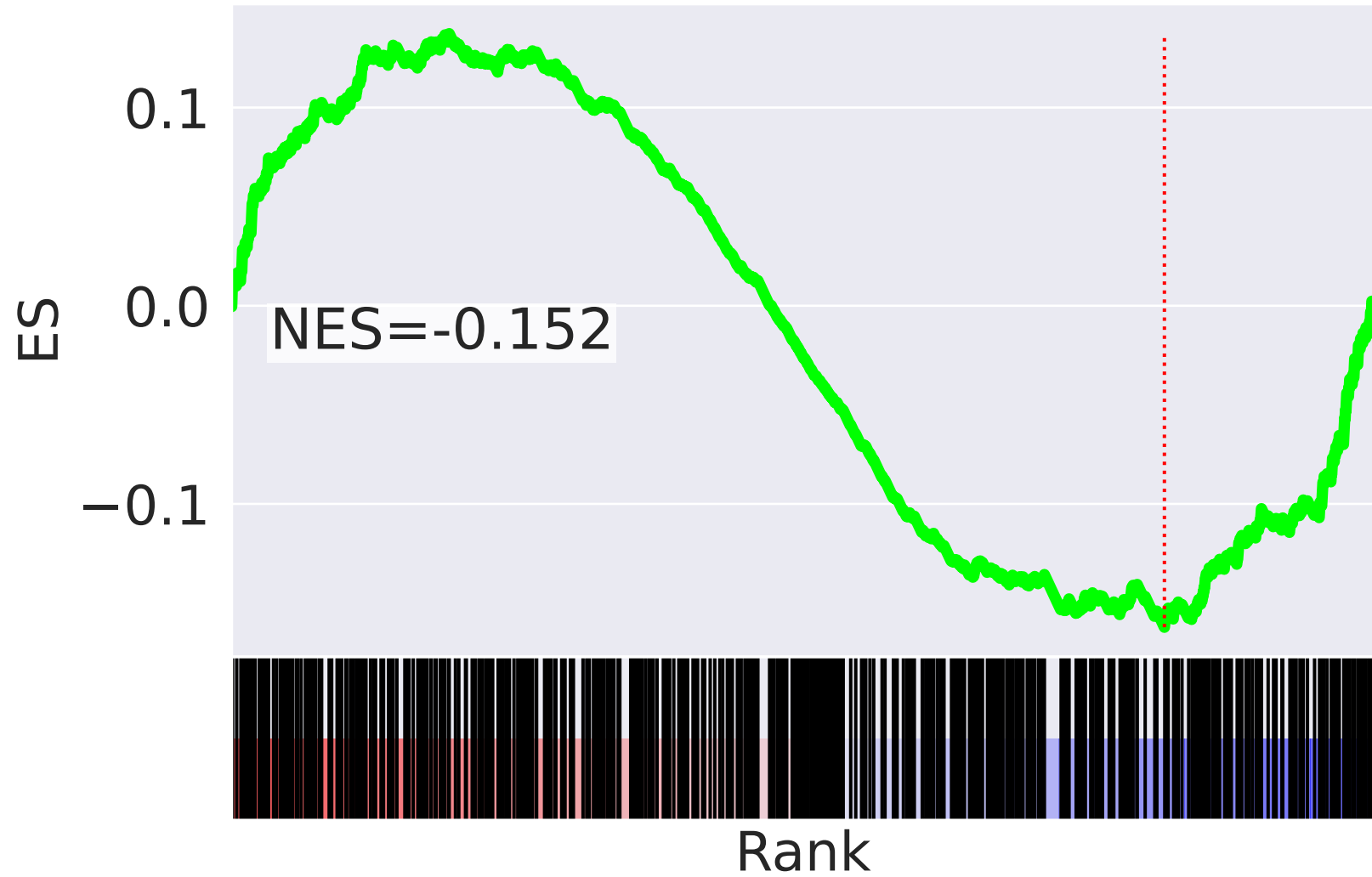
NES		SET
-4.334		DNA Repair R-HSA-73894
4.231		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.826		Respiratory Electron Transport R-HSA-611105
3.800		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.738		HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-3.562		HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
-3.513		Homology Directed Repair R-HSA-5693538
3.494		Transcription Of HIV Genome R-HSA-167172
-3.409		Adaptive Immune System R-HSA-1280218
-3.168		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.168		Diseases Of DNA Repair R-HSA-9675135
3.145		Metabolism Of Vitamins And Cofactors R-HSA-196854
-3.081		DNA Double-Strand Break Repair R-HSA-5693532
3.057		Metabolism Of Cofactors R-HSA-8978934
-3.039		Fanconi Anemia Pathway R-HSA-6783310

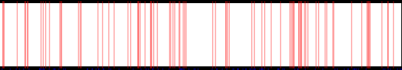
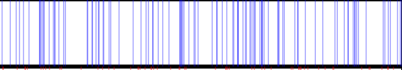
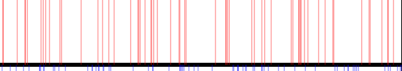
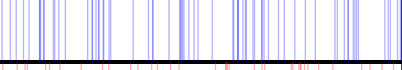
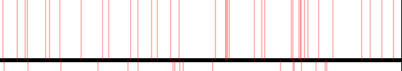
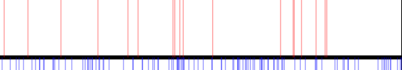
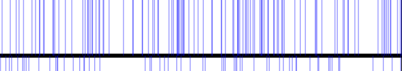
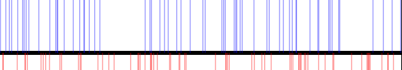
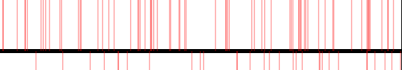
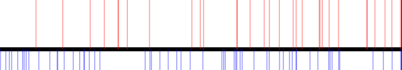
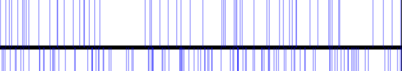
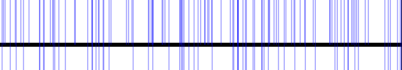
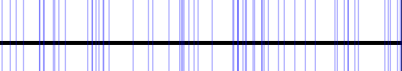
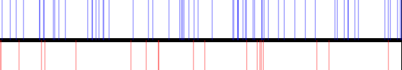

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=23$

Signal Transduction R-HSA-162582



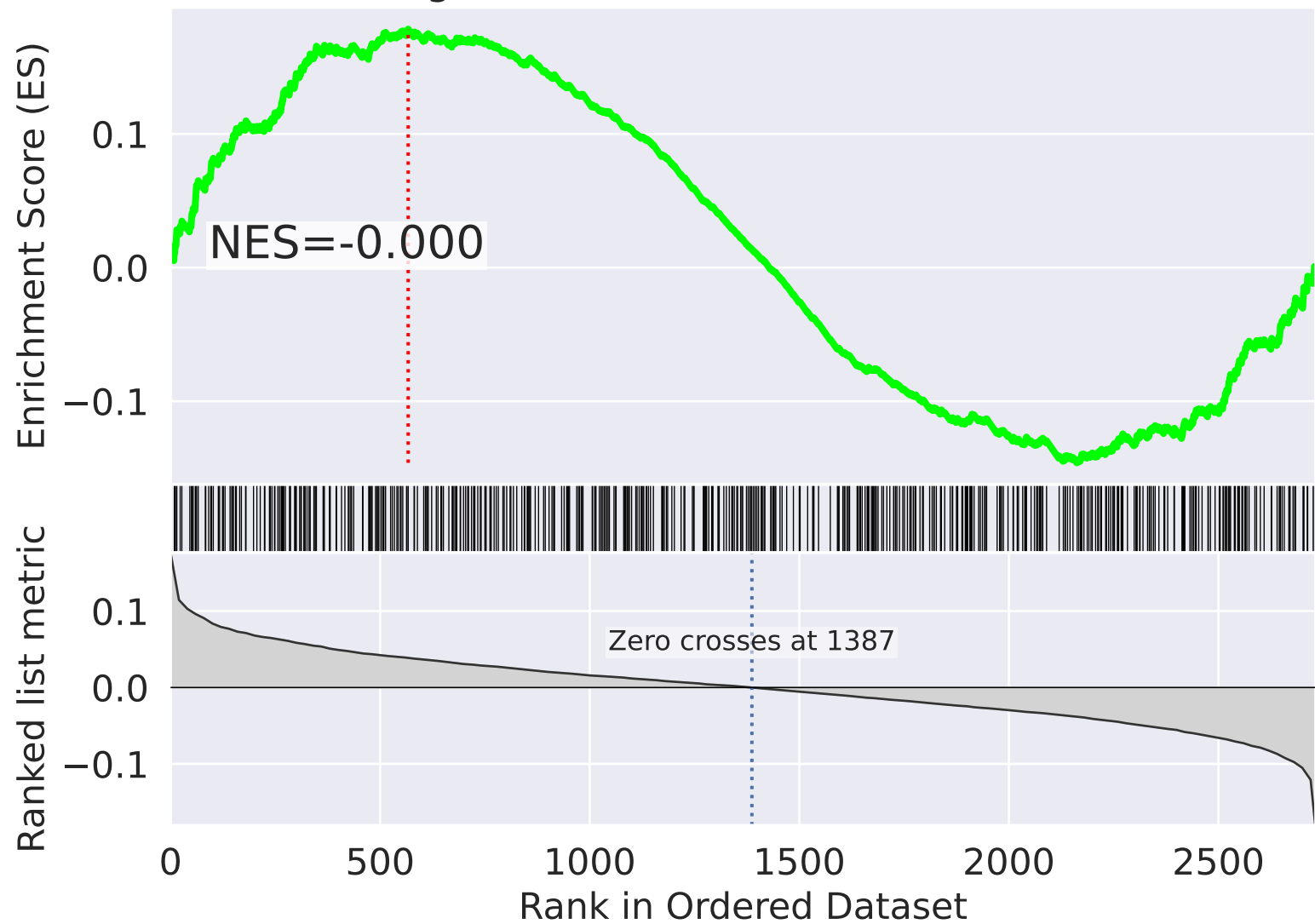
Signal Transduction R-HSA-162582



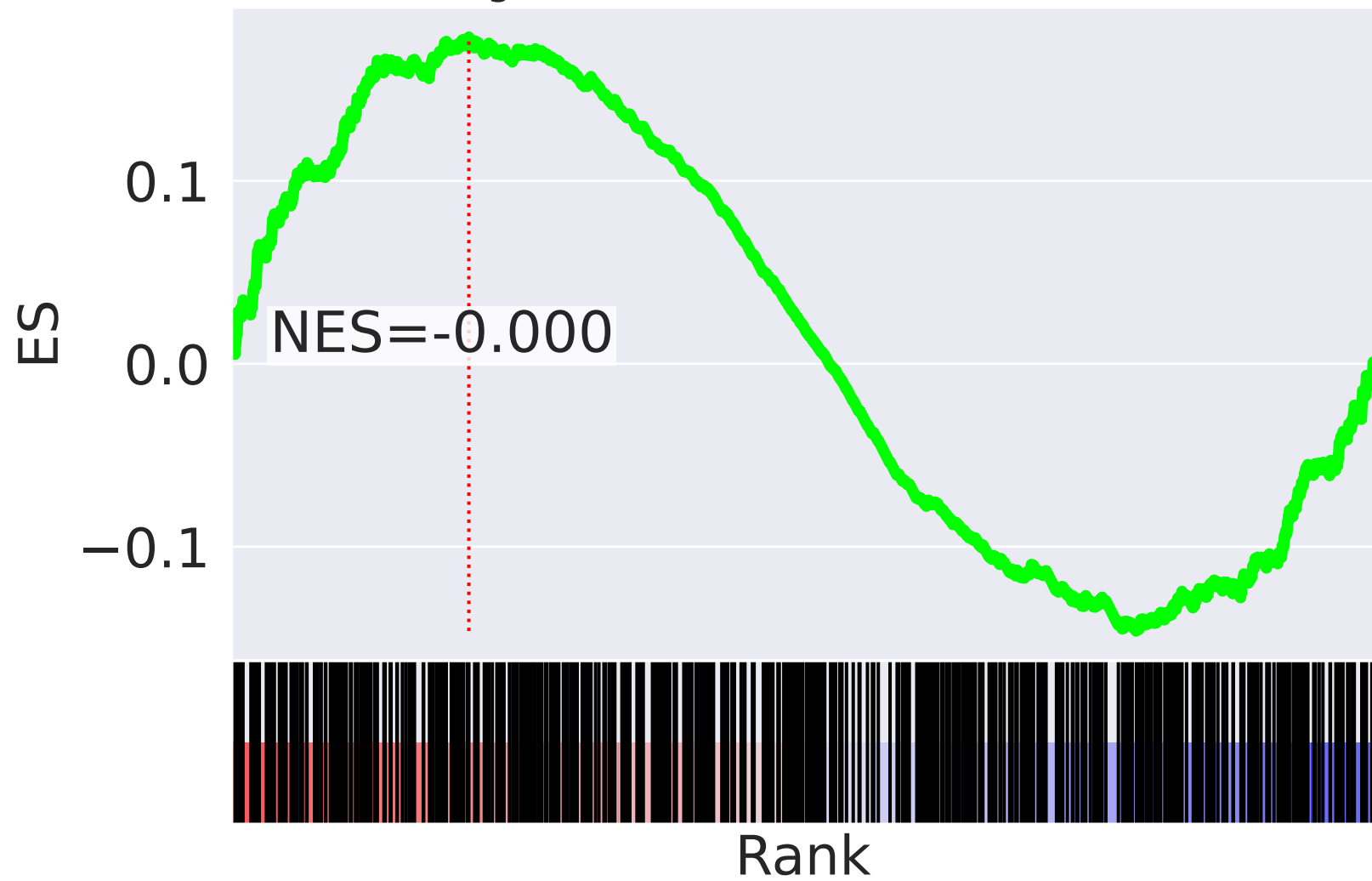
NES		SET
4.808		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-4.497		Mitotic Prometaphase R-HSA-68877
4.179		Respiratory Electron Transport R-HSA-611105
-3.730		Resolution Of Sister Chromatid Cohesion R-HSA-2500257
3.701		Complex I Biogenesis R-HSA-6799198
3.604		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-3.499		RHO GTPase Effectors R-HSA-195258
-3.402		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.365		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.292		Metabolism Of Vitamins And Cofactors R-HSA-196854
-3.263		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.237		Separation Of Sister Chromatids R-HSA-2467813
-3.211		Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
-3.211		EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
3.150		Diseases Of Programmed Cell Death R-HSA-9645723

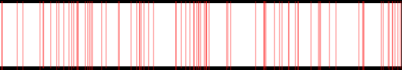
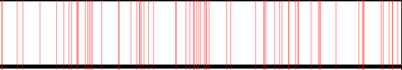
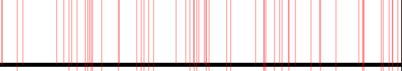
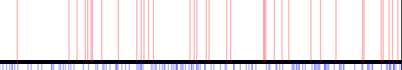
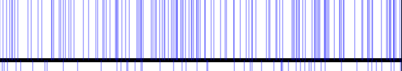
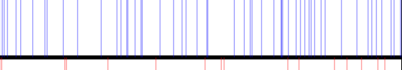
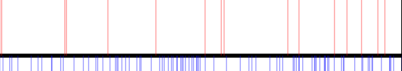
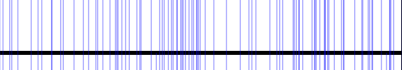
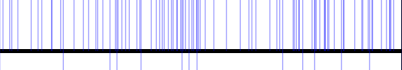
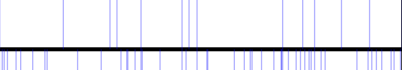
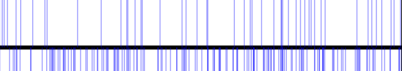
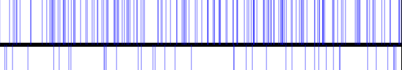
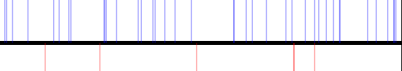
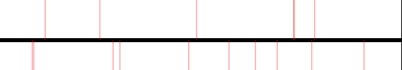
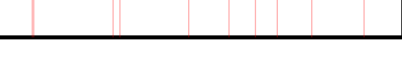
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=24$

Signal Transduction R-HSA-162582



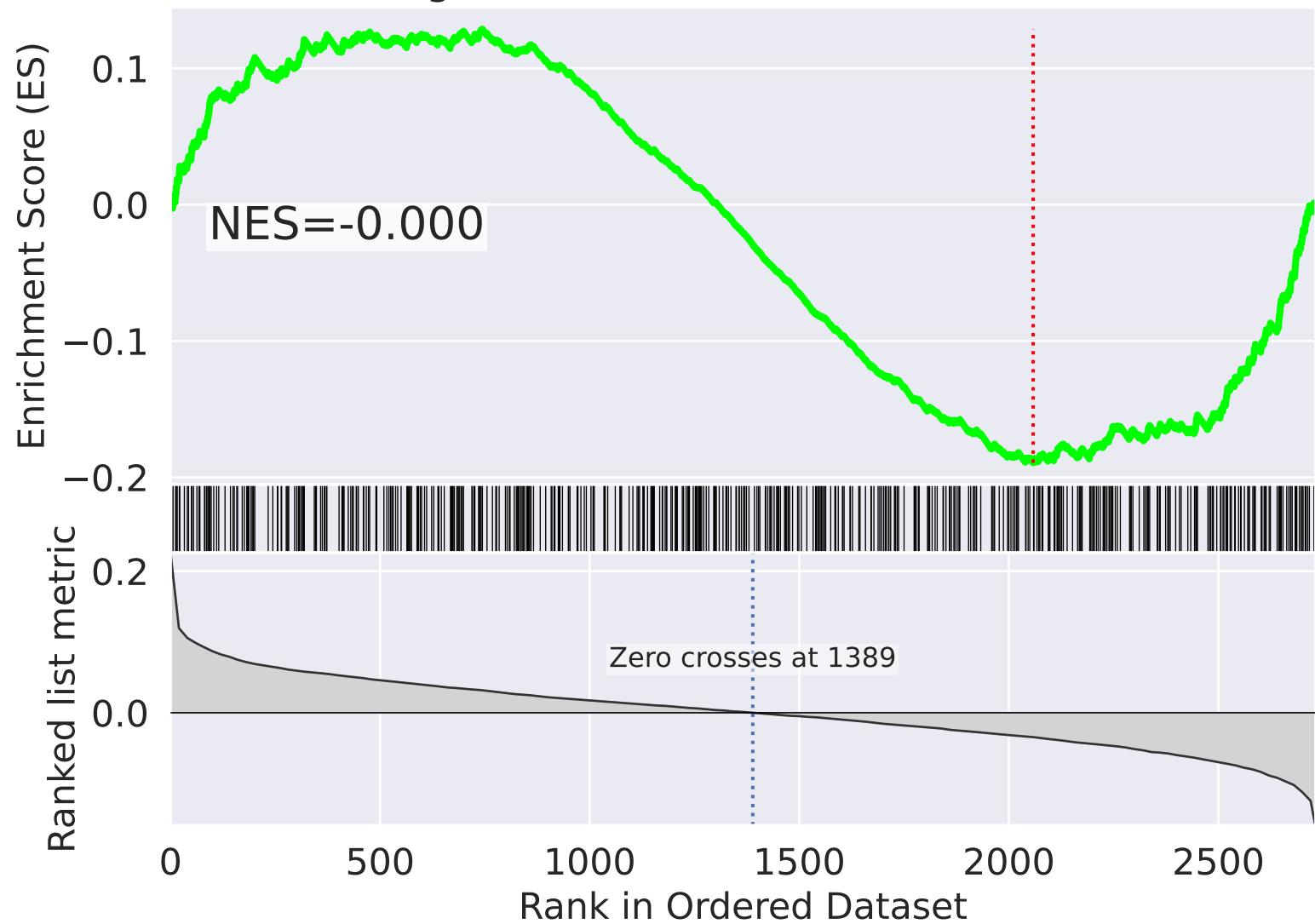
Signal Transduction R-HSA-162582



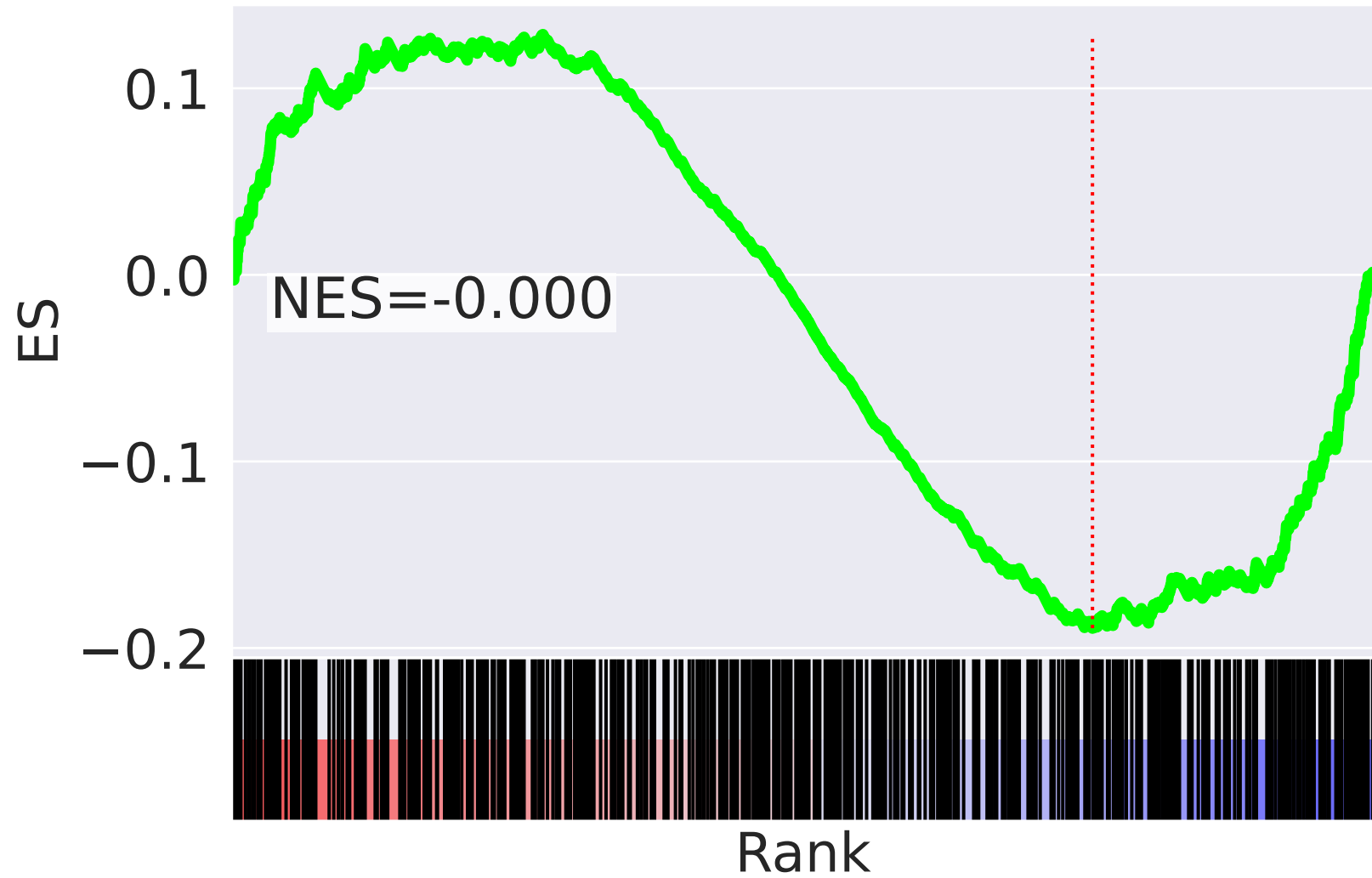
NES		SET
5.892		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.724		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.305		Respiratory Electron Transport R-HSA-611105
4.631		Complex I Biogenesis R-HSA-6799198
-3.595		HIV Infection R-HSA-162906
-3.459		Autophagy R-HSA-9612973
3.292		tRNA Modification In Nucleus And Cytosol R-HSA-6782315
-3.185		Late Phase Of HIV Life Cycle R-HSA-162599
-3.125		HIV Life Cycle R-HSA-162587
-2.976		Budding And Maturation Of HIV Virion R-HSA-162588
-2.955		Macroautophagy R-HSA-1632852
-2.910		Membrane Trafficking R-HSA-199991
-2.845		Regulation Of RAS By GAPs R-HSA-5658442
2.798		Nonsense Mediated Decay (NMD) Independent Of Exon Junction Complex (EJC) R-HSA-975956
2.755		Mitochondrial Translation R-HSA-5368287



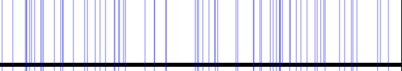
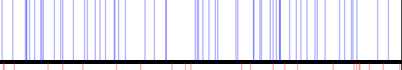
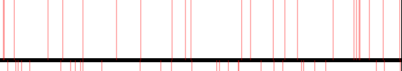
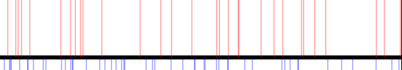
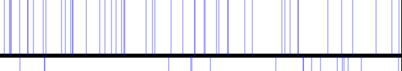
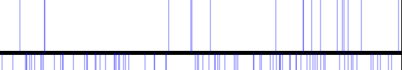
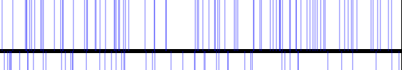
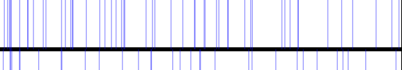

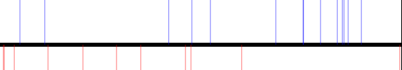
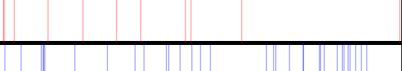


The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=25$

Signal Transduction R-HSA-162582



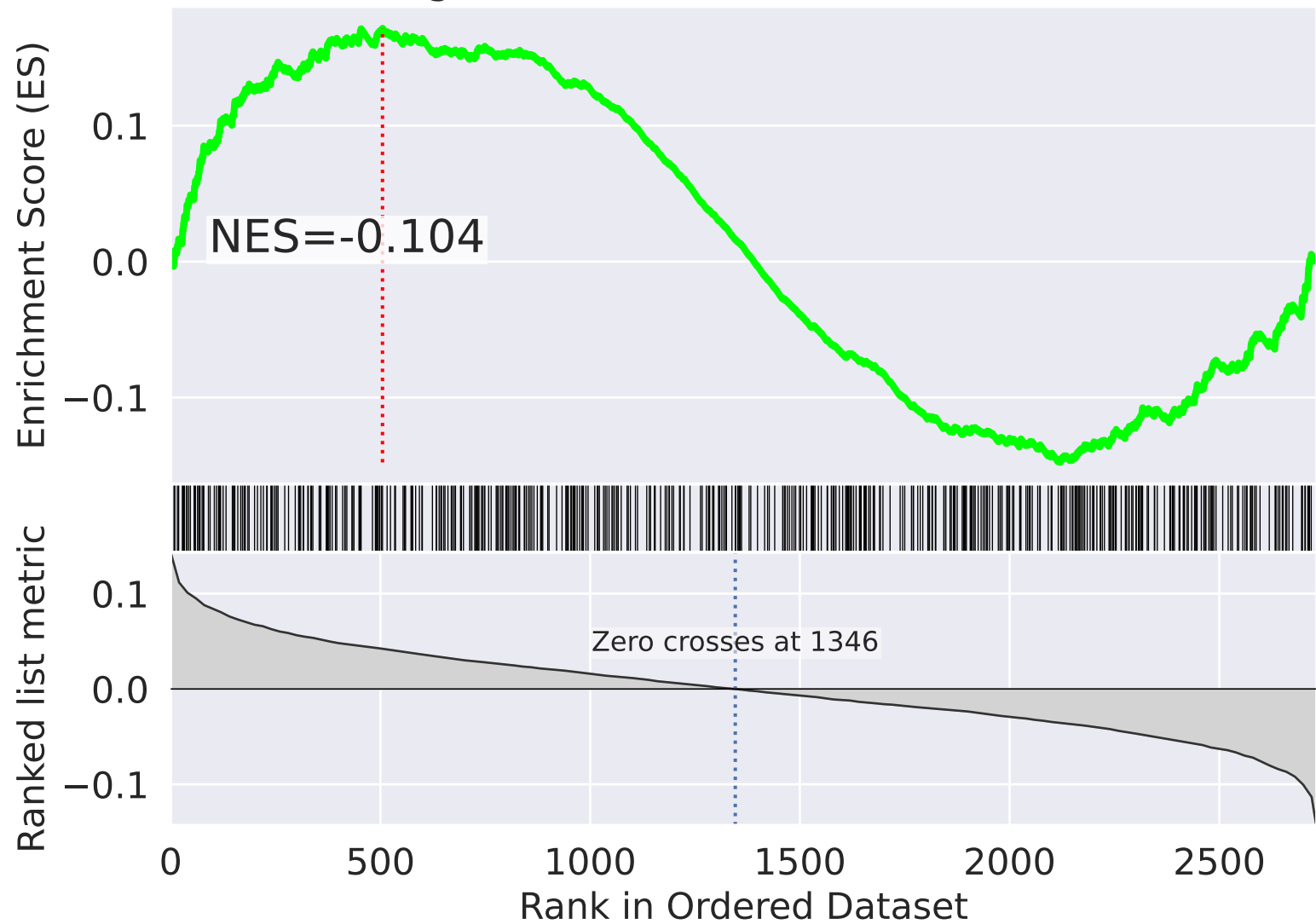
Signal Transduction R-HSA-162582



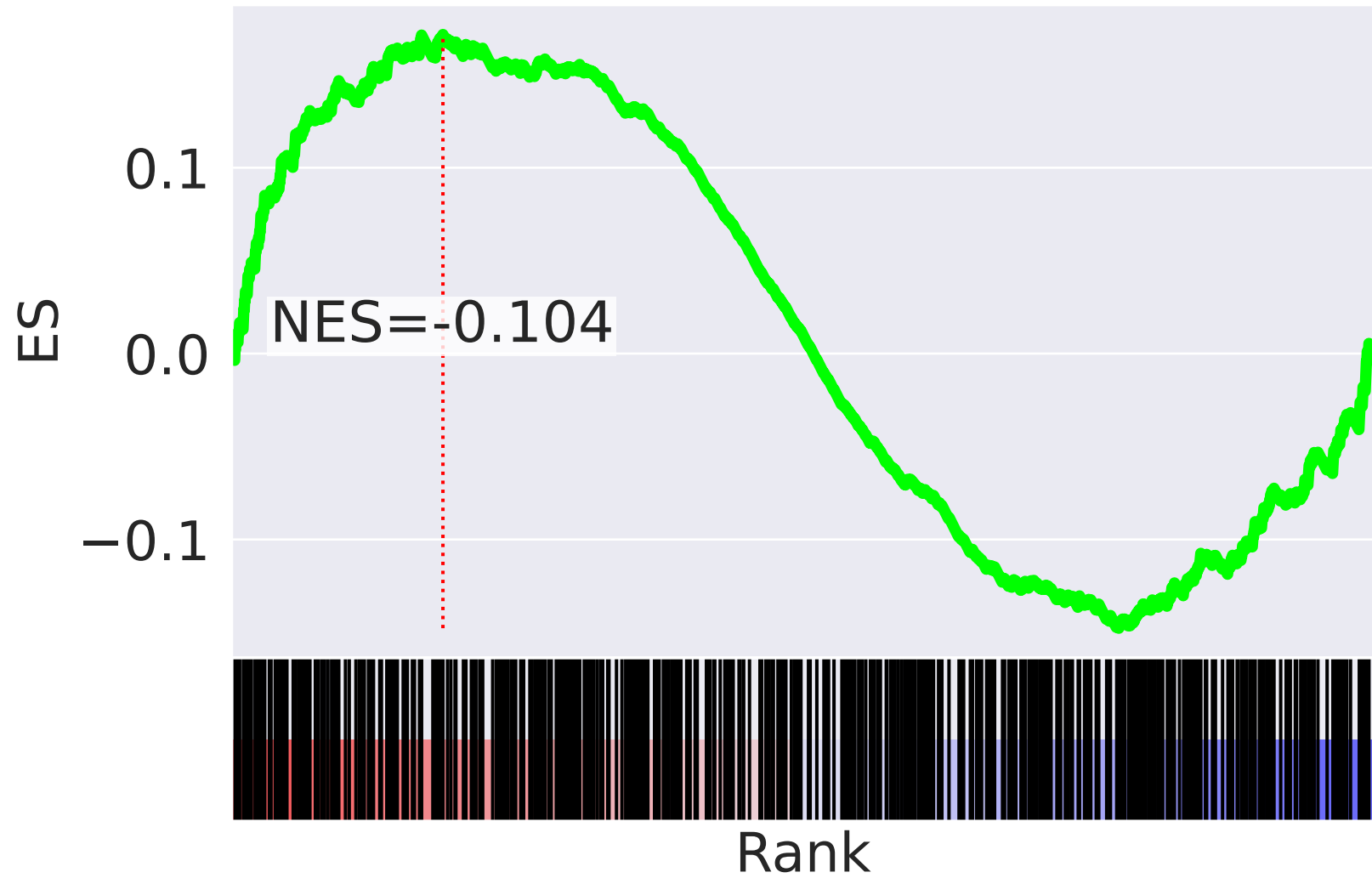
NES		SET
-5.048		Signaling By Receptor Tyrosine Kinases R-HSA-9006934
-4.540		Complex I Biogenesis R-HSA-6799198
-4.004		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.721		Respiratory Electron Transport R-HSA-611105
3.688		Metabolism Of Nucleotides R-HSA-15869
3.614		Metabolism Of Vitamins And Cofactors R-HSA-196854
-3.581		PPARA Activates Gene Expression R-HSA-1989781
-3.550		Costimulation By CD28 Family R-HSA-388841
-3.546		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.509		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206
-3.488		Signaling By Insulin Receptor R-HSA-74752
-3.484		CD28 Co-Stimulation R-HSA-389356
3.459		Nucleotide Biosynthesis R-HSA-8956320
-3.299		VEGFA-VEGFR2 Pathway R-HSA-4420097
-3.292		Insulin Receptor Signaling Cascade R-HSA-74751

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



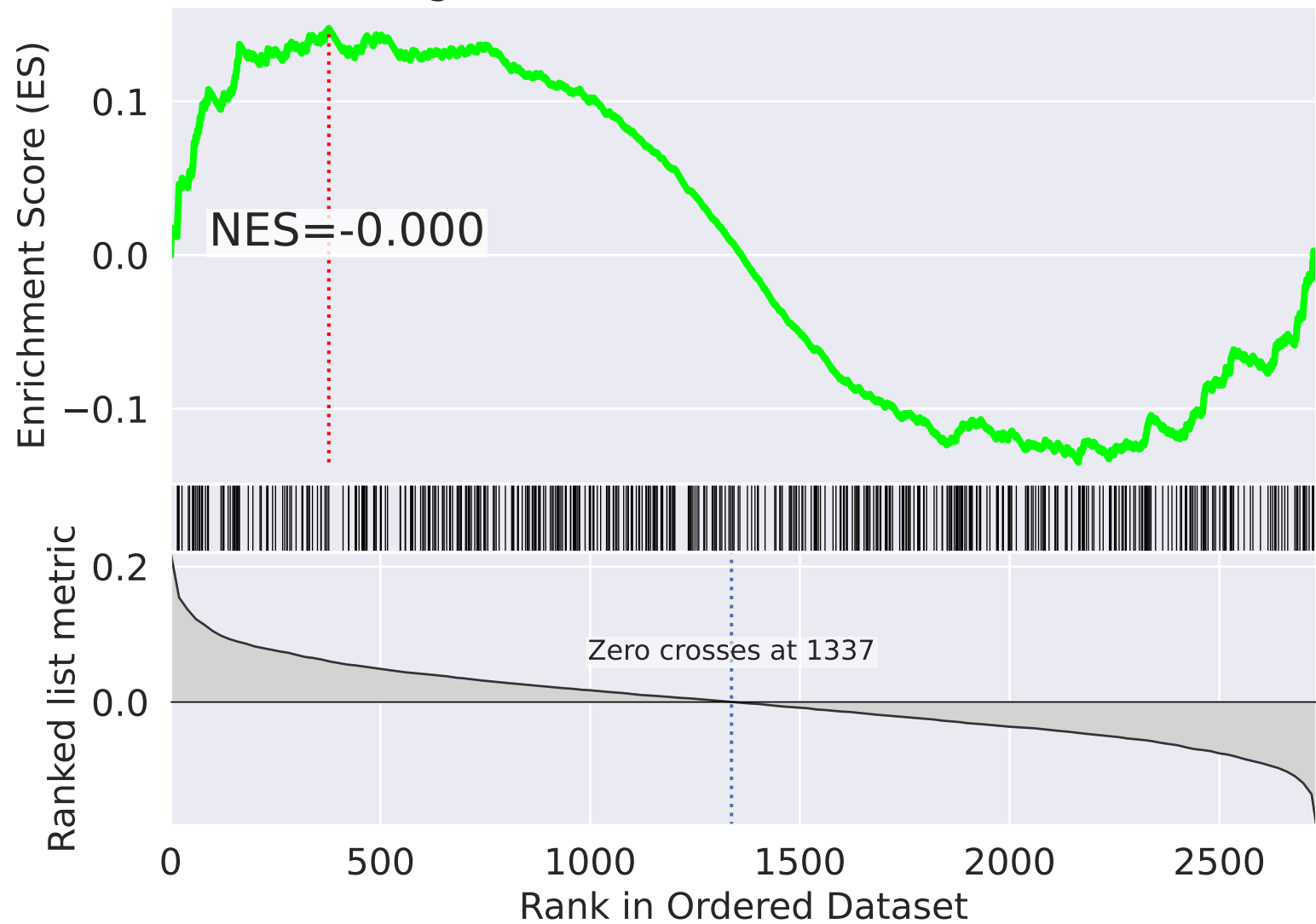
Signal Transduction R-HSA-162582



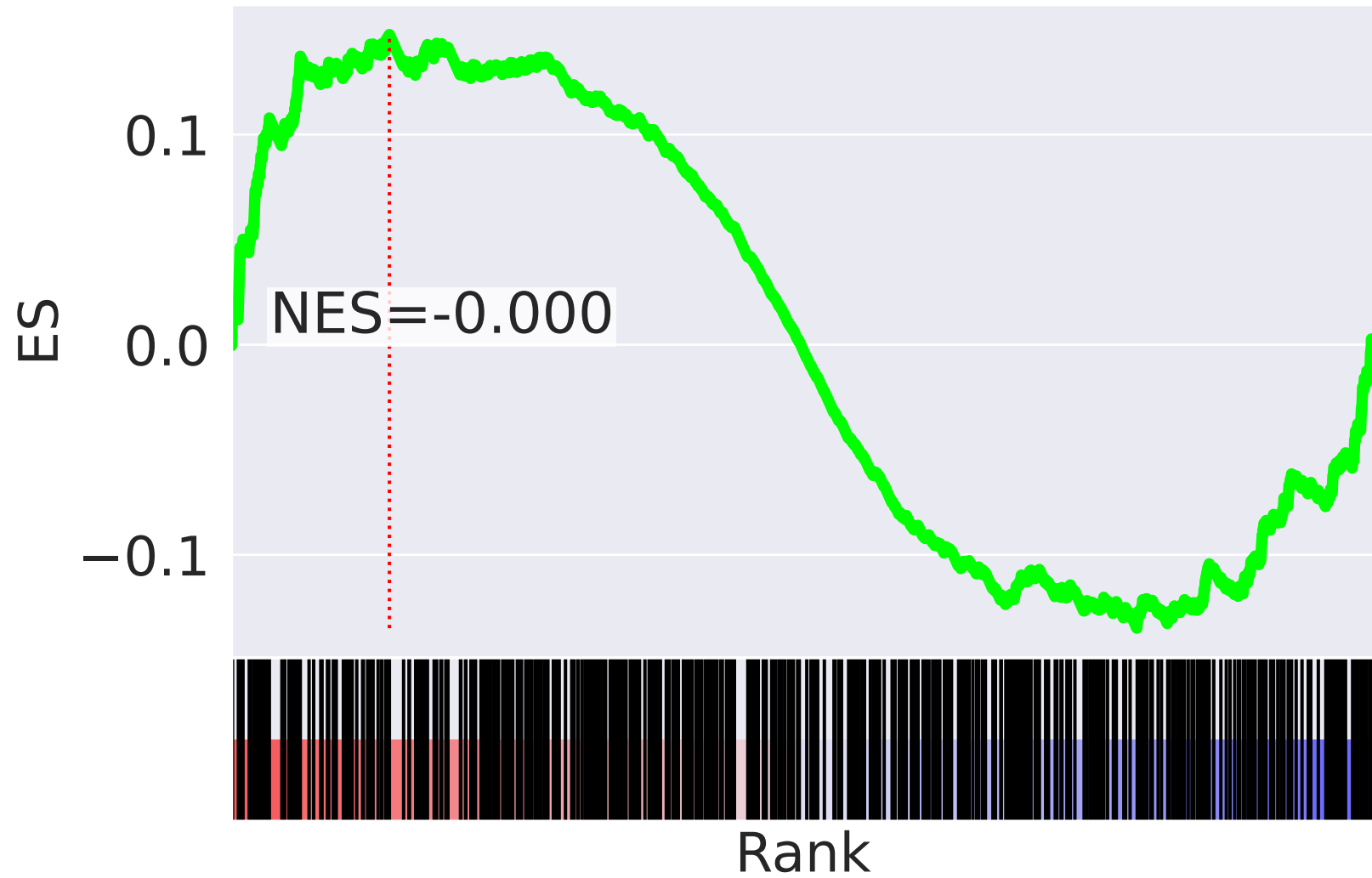
NES		SET
3.158		Processing Of Intronless Pre-mRNAs R-HSA-77595
-2.919		Extension Of Telomeres R-HSA-180786
2.898		Transcriptional Regulation By RUNX1 R-HSA-8878171
2.746		Processing Of Capped Intronless Pre-mRNA R-HSA-75067
2.743		RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
2.741		mRNA 3-End Processing R-HSA-72187
2.725		SHC1 Events In ERBB2 Signaling R-HSA-1250196
-2.663		EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
-2.663		Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
2.657		RNA Polymerase II Transcription Termination R-HSA-73856
2.617		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
2.595		Sulfur Amino Acid Metabolism R-HSA-1614635
2.571		Transcriptional Regulation By E2F6 R-HSA-8953750
-2.562		Cellular Response To Heat Stress R-HSA-3371556
-2.530		Translesion Synthesis By POLH R-HSA-110320


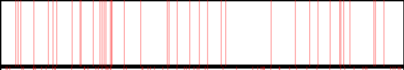
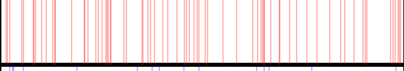
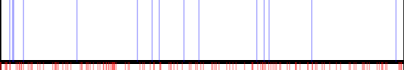
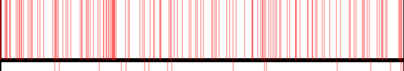
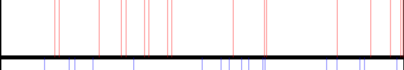

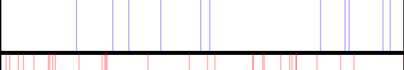
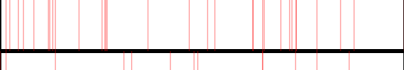
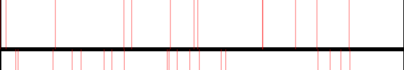
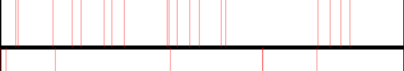
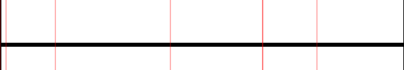
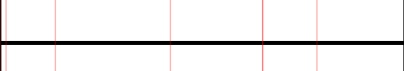
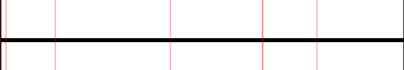

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=27$

Signal Transduction R-HSA-162582



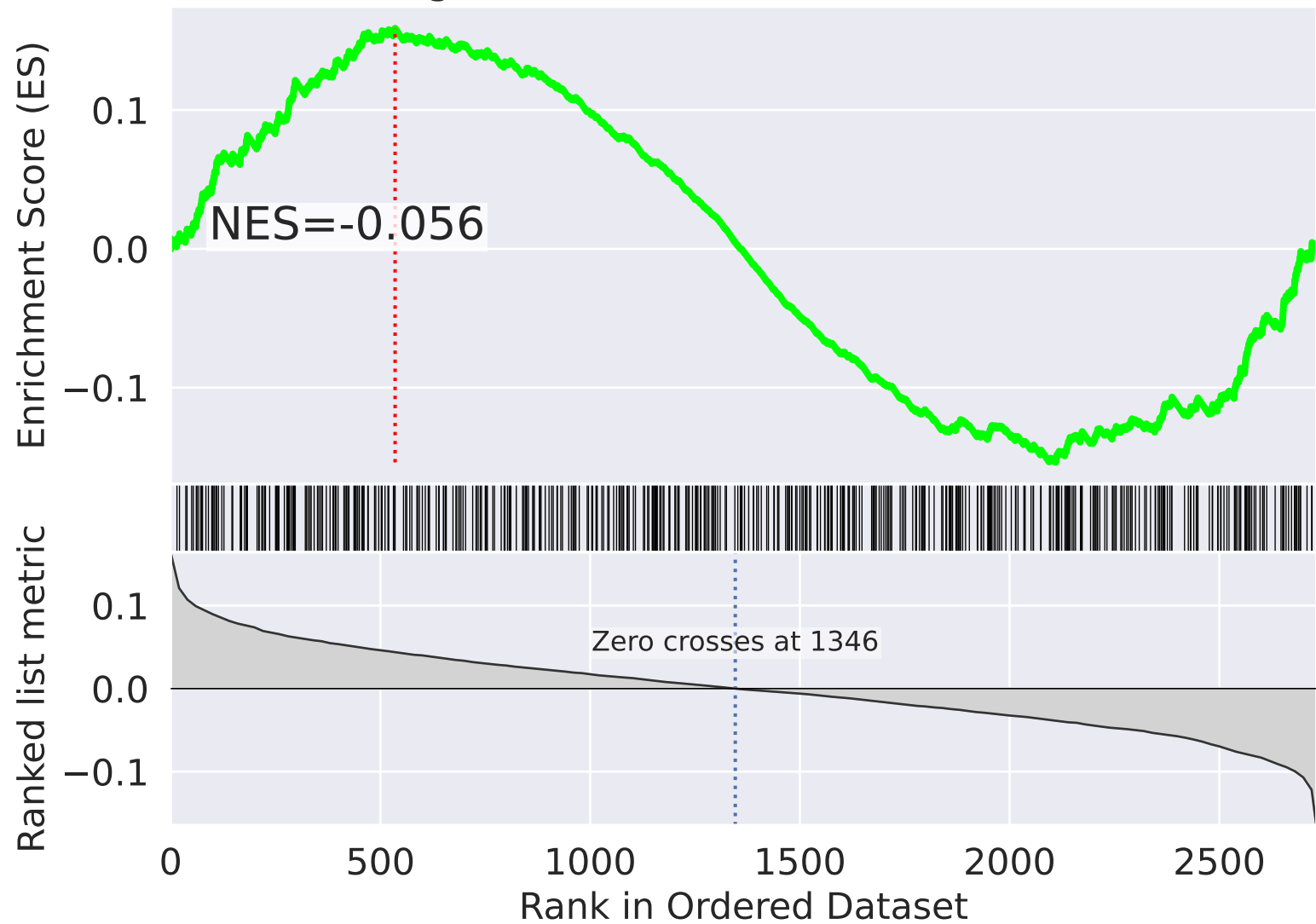
Signal Transduction R-HSA-162582



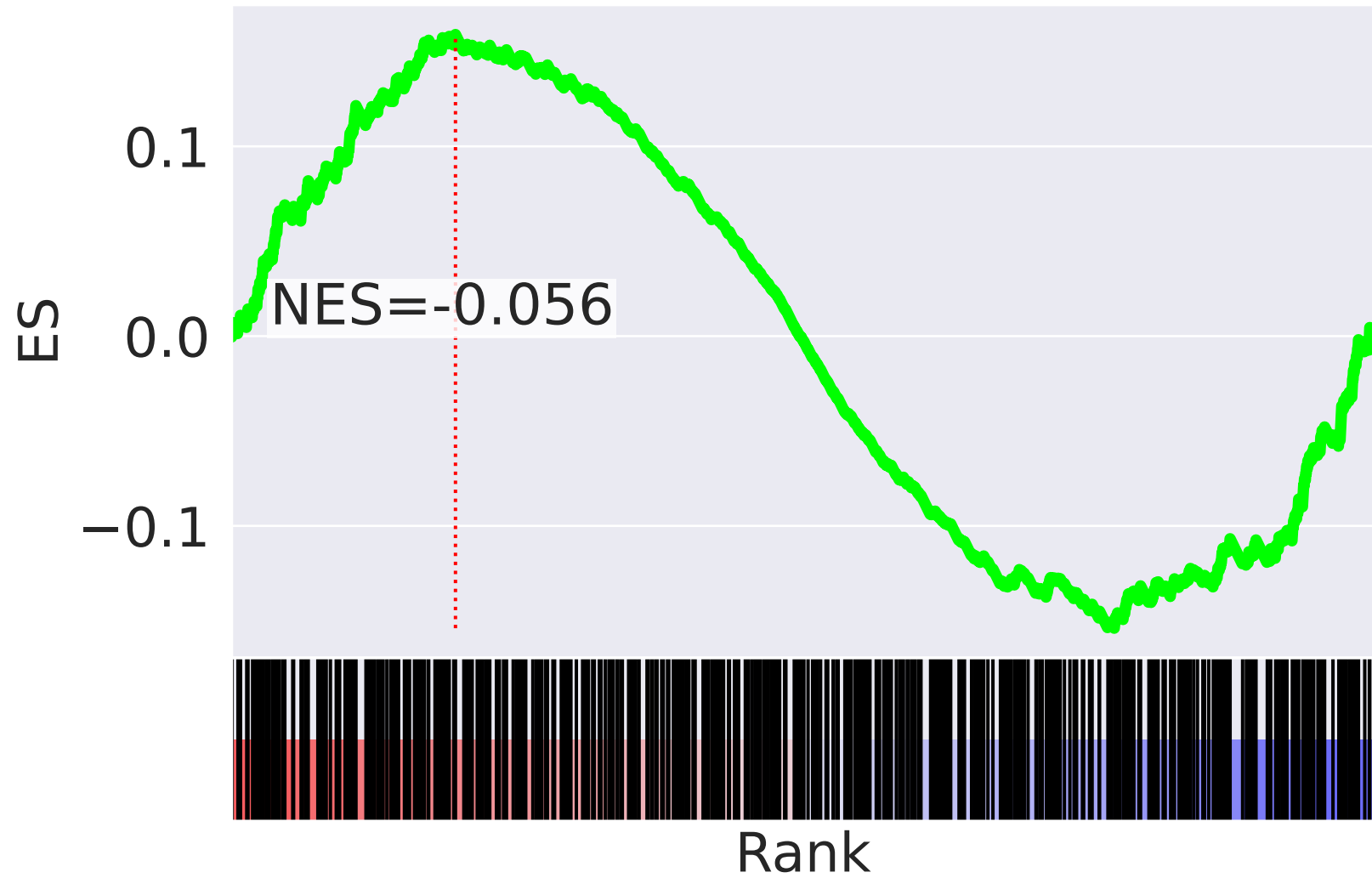
NES		SET
3.394		Fanconi Anemia Pathway R-HSA-6783310
3.110		Mitochondrial Biogenesis R-HSA-1592230
3.005		Signaling By Nuclear Receptors R-HSA-9006931
-2.987		RNA Polymerase III Transcription Initiation From Type 3 Promoter R-HSA-76071
2.878		DNA Repair R-HSA-73894
2.861		Translocation Of SLC2A4 (GLUT4) To Plasma Membrane R-HSA-1445148
-2.859		Endosomal Sorting Complex Required For Transport (ESCRT) R-HSA-917729
-2.856		SUMOylation Of Transcription Factors R-HSA-3232118
2.838		Activation Of HOX Genes During Differentiation R-HSA-5619507
2.789		Meiotic Synapsis R-HSA-1221632
2.652		Cristae Formation R-HSA-8949613
2.602		Cleavage Of Damaged Purine R-HSA-110331
2.602		Base-Excision Repair, AP Site Formation R-HSA-73929
2.602		Packaging Of Telomere Ends R-HSA-171306
2.602		Cleavage Of Damaged Pyrimidine R-HSA-110329

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



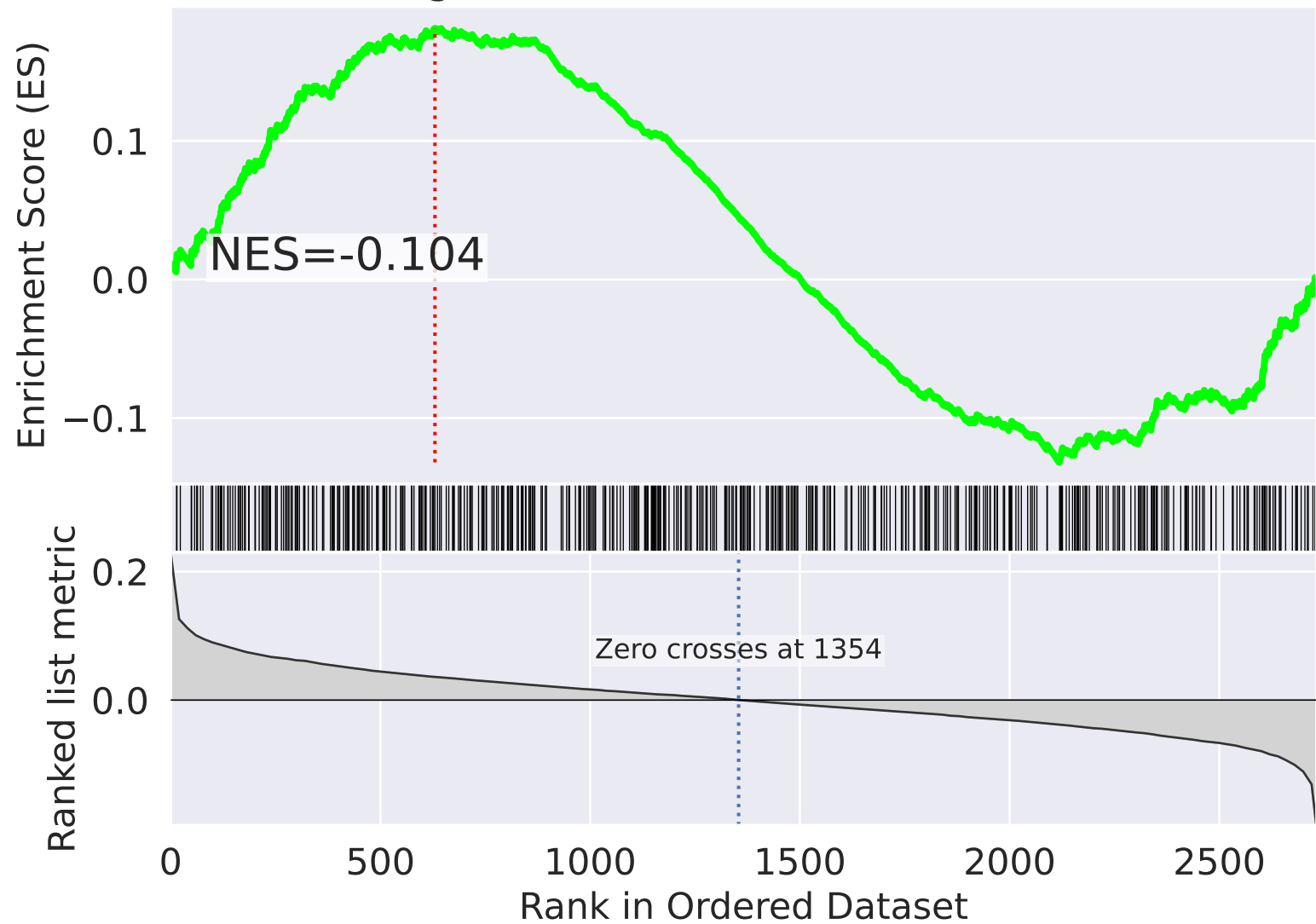
Signal Transduction R-HSA-162582



NES		SET
-3.923		Cell Cycle Checkpoints R-HSA-69620
-3.824		Mitotic G1 Phase And G1/S Transition R-HSA-453279
-3.708		Interleukin-1 Family Signaling R-HSA-446652
-3.701		Organelle Biogenesis And Maintenance R-HSA-1852241
-3.579		Complex I Biogenesis R-HSA-6799198
-3.500		Mitochondrial Biogenesis R-HSA-1592230
-3.493		Toll-like Receptor Cascades R-HSA-168898
-3.492		Synthesis Of DNA R-HSA-69239
-3.462		Toll Like Receptor 4 (TLR4) Cascade R-HSA-166016
3.381		Metabolism Of Nucleotides R-HSA-15869
-3.360		Death Receptor Signaling R-HSA-73887
-3.336		Toll Like Receptor 9 (TLR9) Cascade R-HSA-168138
-3.306		Interleukin-1 Signaling R-HSA-9020702
-3.279		Nucleotide-binding Domain, Leucine Rich Repeat Containing NLR Signaling Pathways R-HSA-168643
-3.227		G1/S Transition R-HSA-69206

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

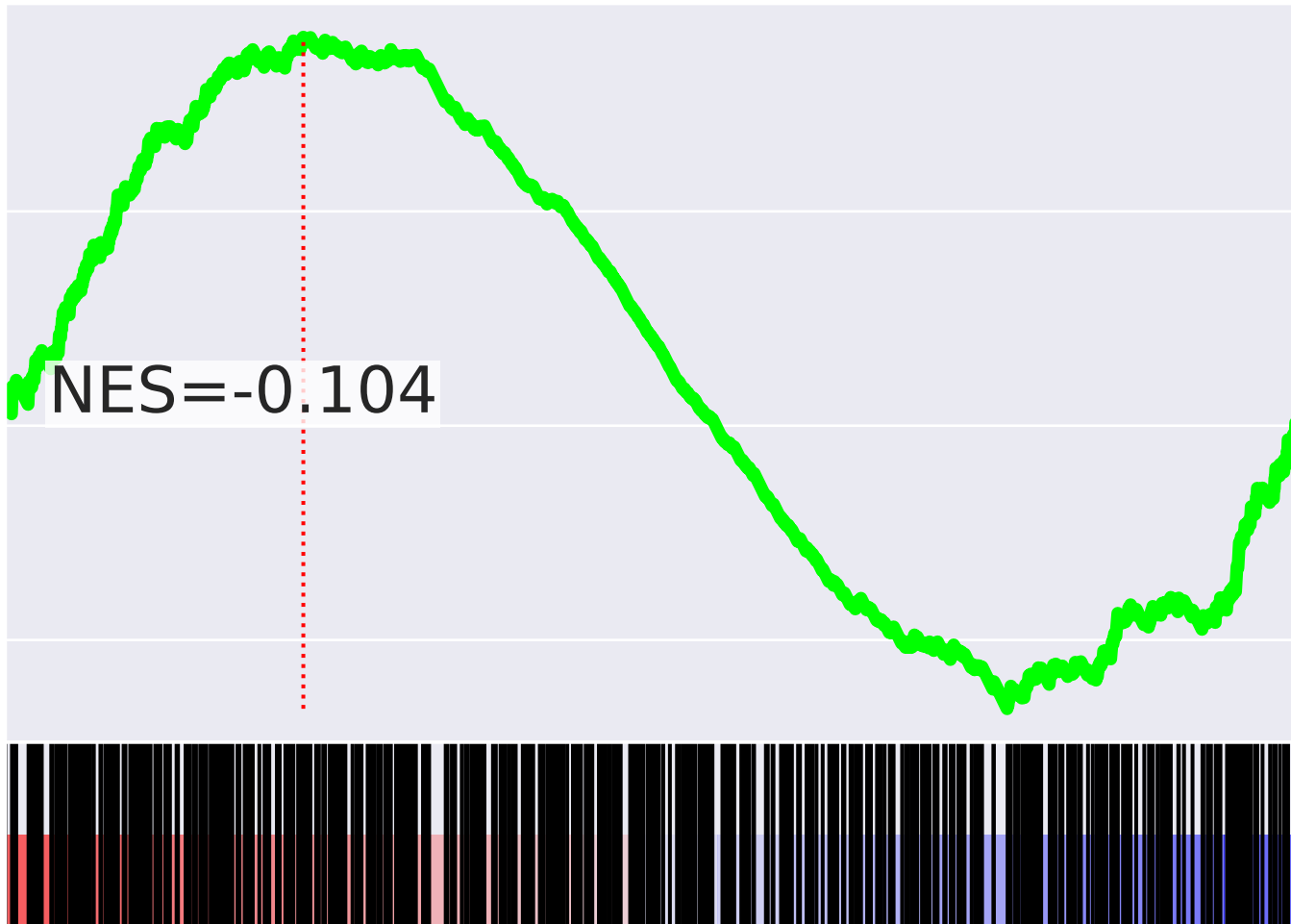
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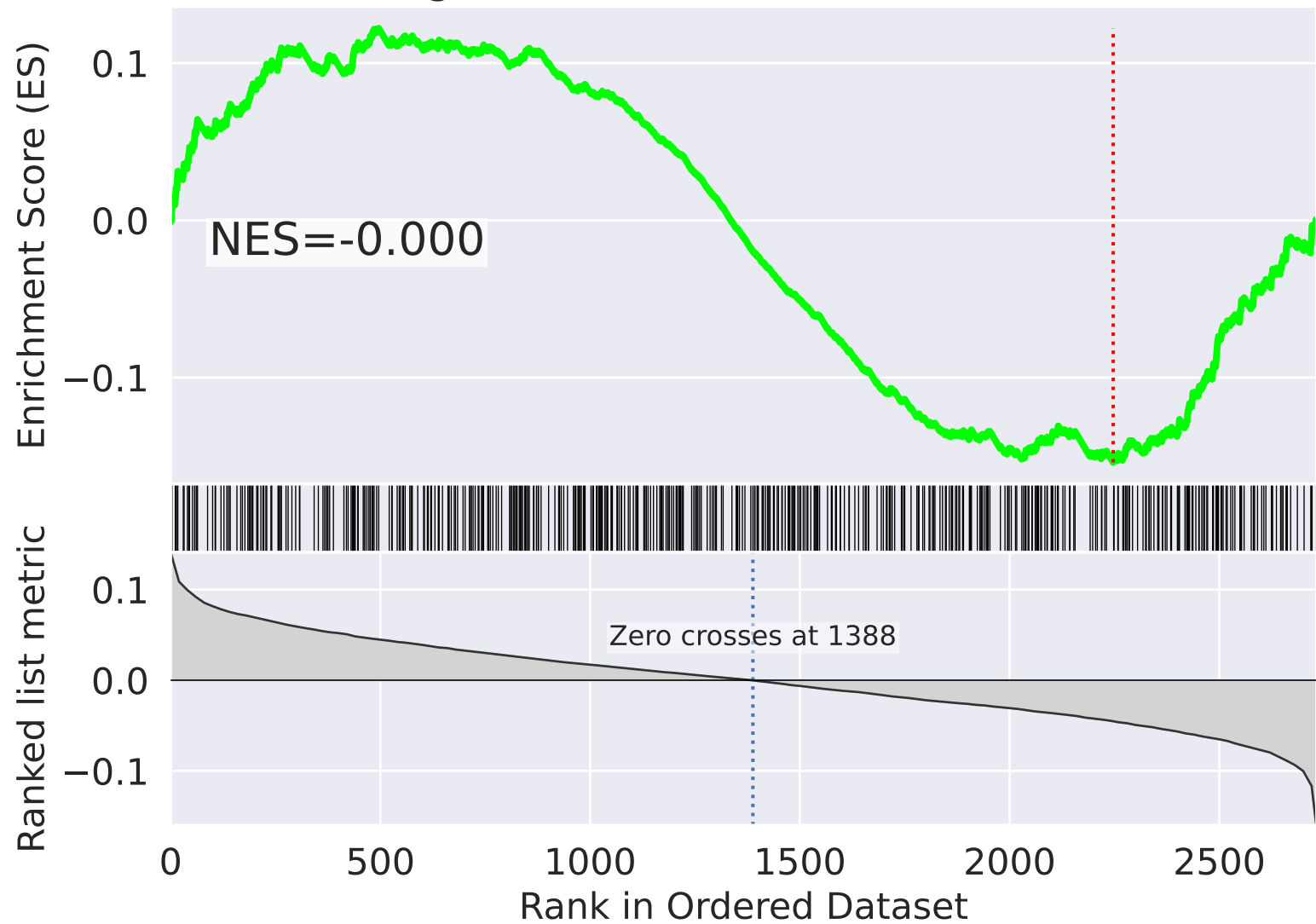
Rank



NES		SET
3.227		E3 Ubiquitin Ligases Ubiquitinate Target Proteins R-HSA-8866654
-3.214		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.211		Biological Oxidations R-HSA-211859
-3.010		Mitotic Metaphase And Anaphase R-HSA-2555396
2.963		Transcriptional Regulation By RUNX1 R-HSA-8878171
-2.929		Complex I Biogenesis R-HSA-6799198
-2.900		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
2.875		Signaling By ERBB2 R-HSA-1227986
2.835		Golgi Associated Vesicle Biogenesis R-HSA-432722
-2.824		rRNA Processing R-HSA-72312
-2.772		Resolution Of Sister Chromatid Cohesion R-HSA-2500257
2.746		Mitochondrial tRNA Aminoacylation R-HSA-379726
2.735		trans-Golgi Network Vesicle Budding R-HSA-199992
-2.735		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
2.725		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

ES

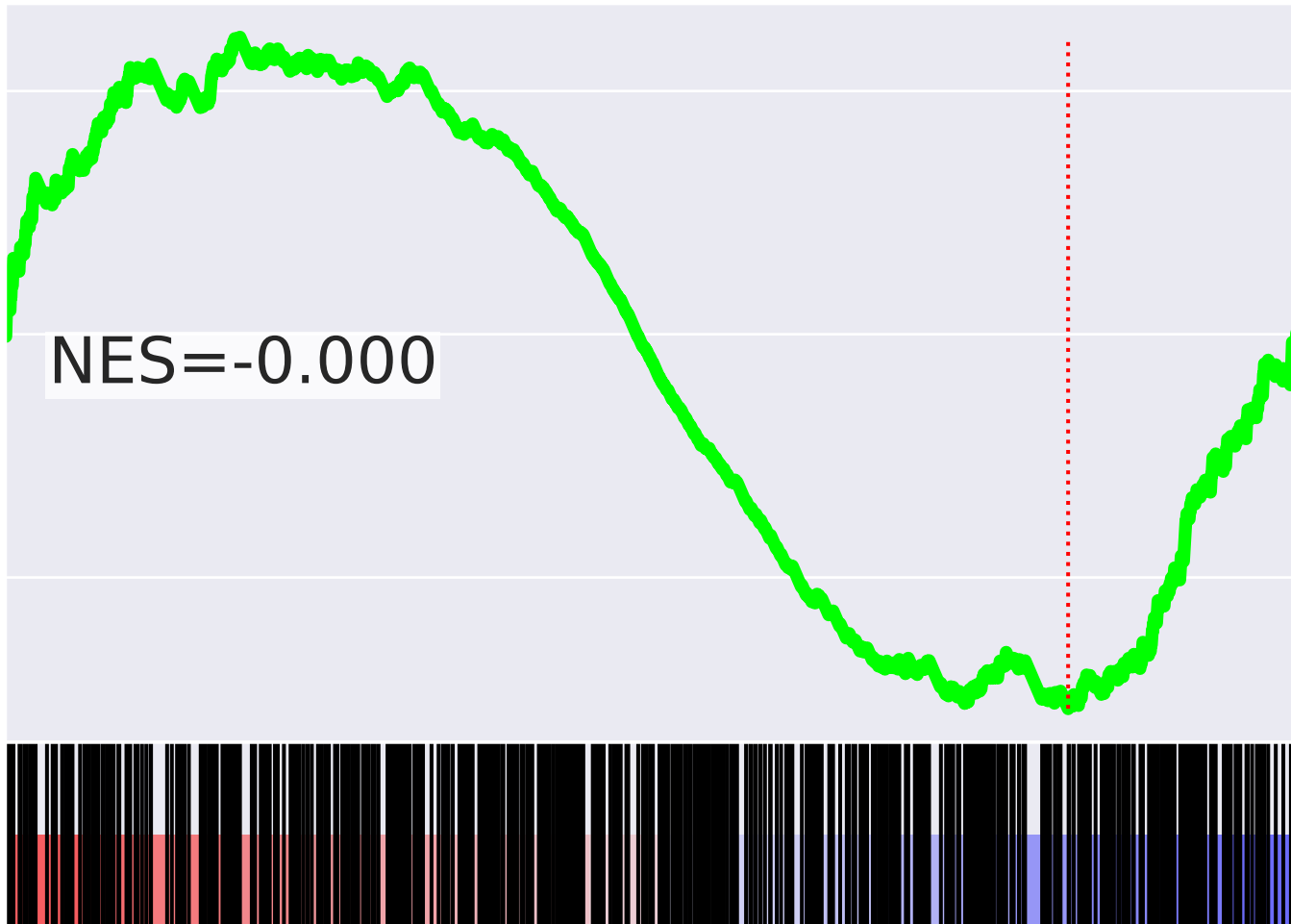
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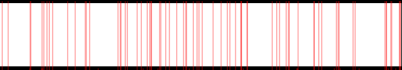
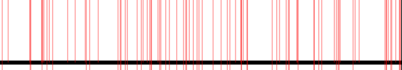
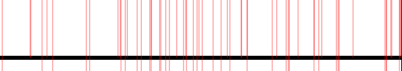
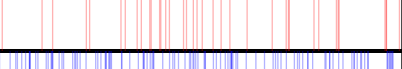
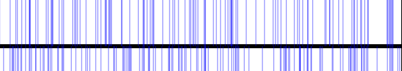
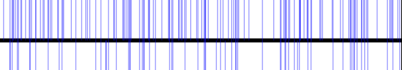

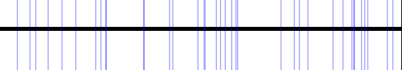
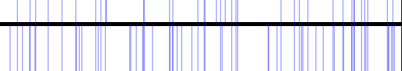
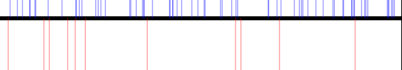
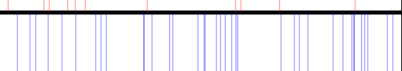

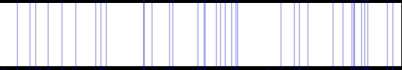
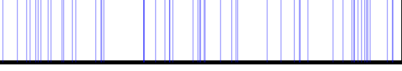

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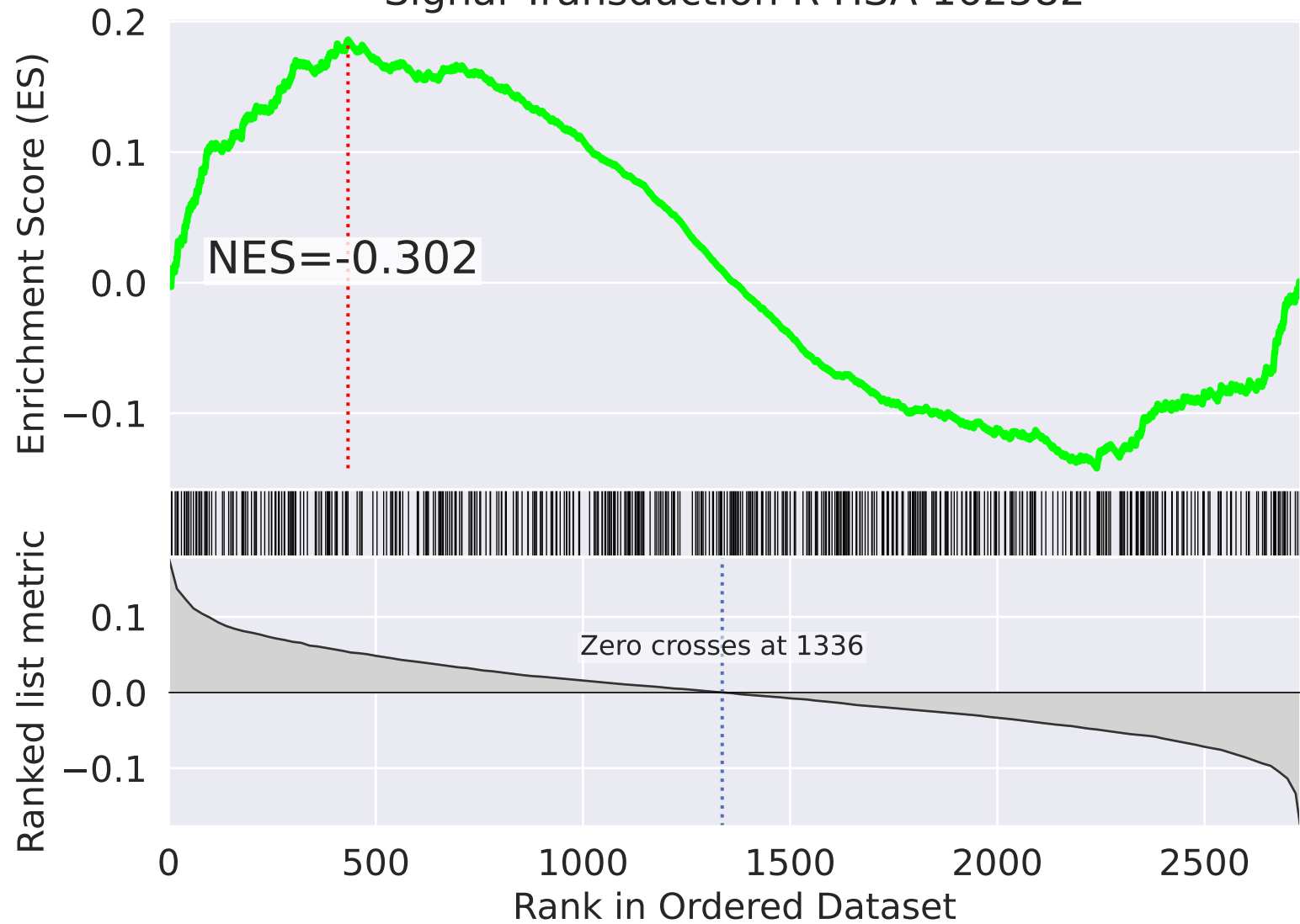
Rank



NES		SET
7.033		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.994		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.224		Respiratory Electron Transport R-HSA-611105
5.077		Complex I Biogenesis R-HSA-6799198
-3.986		Transport Of Small Molecules R-HSA-382551
-3.579		HIV Infection R-HSA-162906
-3.451		Disorders Of Transmembrane Transporters R-HSA-5619115
-3.442		Defective CFTR Causes Cystic Fibrosis R-HSA-5678895
-3.442		ABC Transporter Disorders R-HSA-5619084
-3.297		Metabolism Of Amino Acids And Derivatives R-HSA-71291
3.109		Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
-3.002		Hh Mutants Abrogate Ligand Secretion R-HSA-5387390
-3.002		Hh Mutants Are Degraded By ERAD R-HSA-5362768
-3.002		Hedgehog Ligand Biogenesis R-HSA-5358346
-2.965		Interleukin-1 Signaling R-HSA-9020702

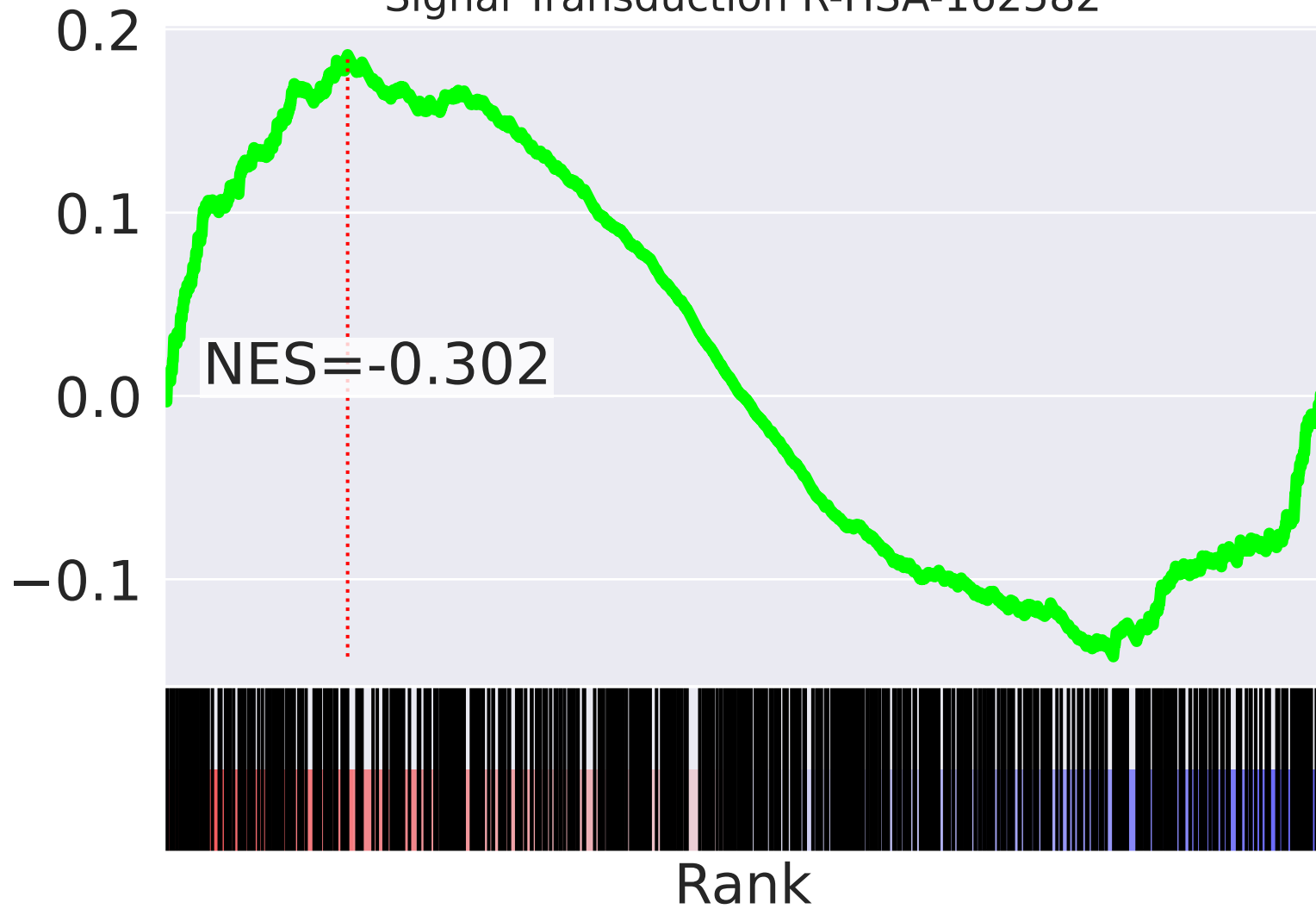
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=31$

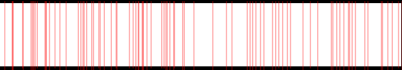
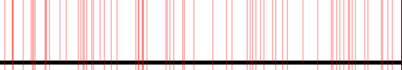
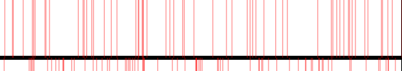
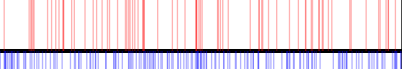
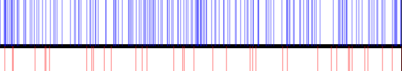
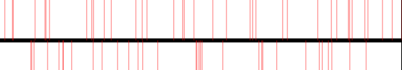

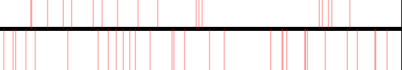
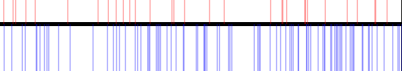
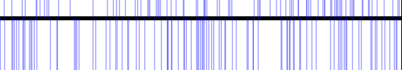
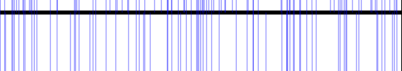
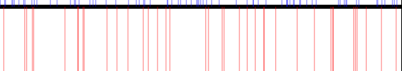
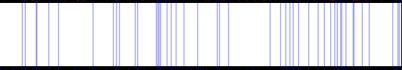
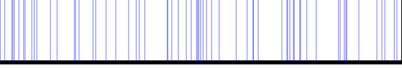

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

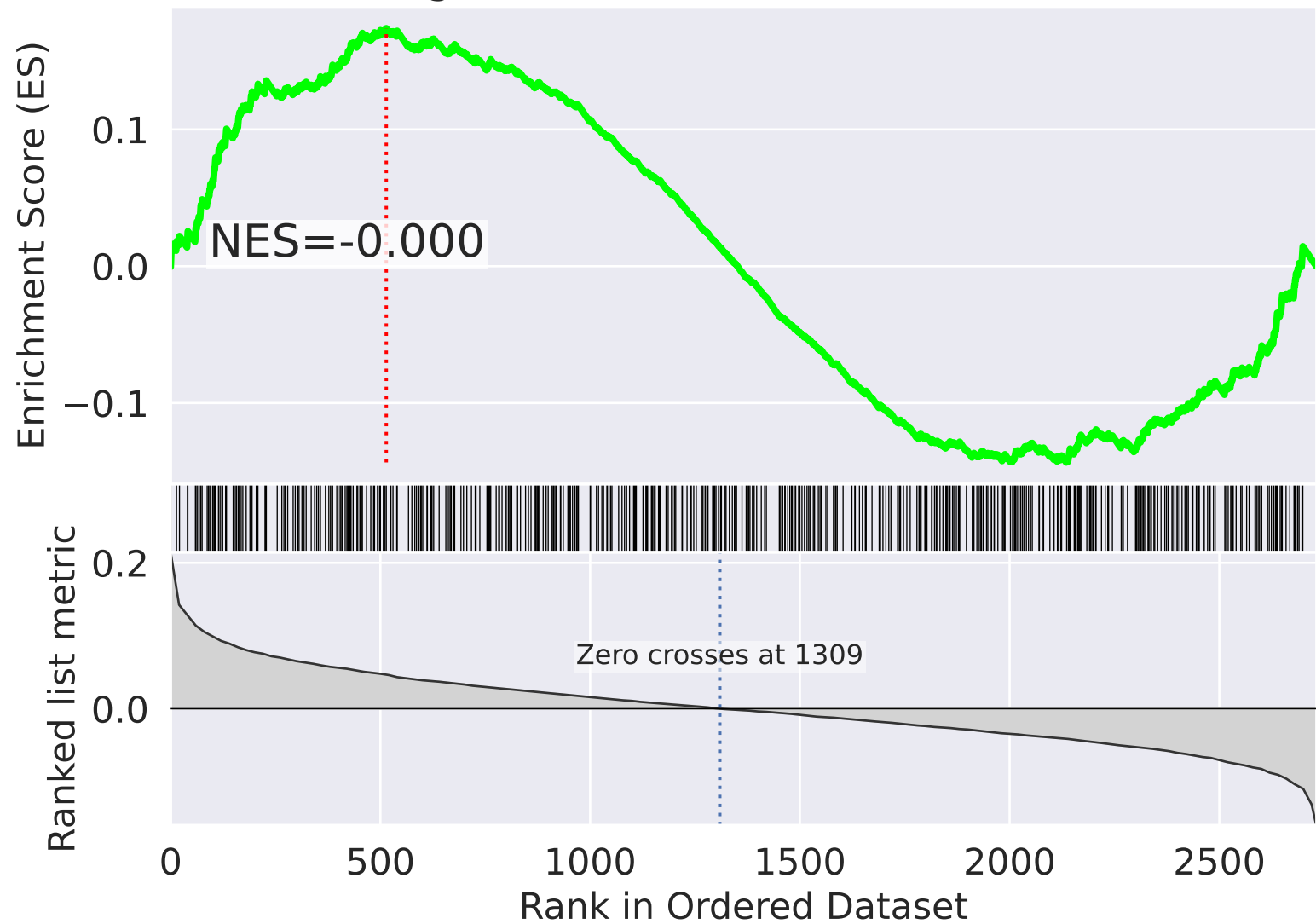
ES



NES		SET
6.566		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.079		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.782		Respiratory Electron Transport R-HSA-611105
4.644		Translation R-HSA-72766
-4.597		Cell Cycle Checkpoints R-HSA-69620
4.419		Complex I Biogenesis R-HSA-6799198
4.214		tRNA Aminoacylation R-HSA-379724
3.800		Mitochondrial tRNA Aminoacylation R-HSA-379726
3.640		Metabolism Of Vitamins And Cofactors R-HSA-196854
-3.486		Asparagine N-linked Glycosylation R-HSA-446203
-3.443		Mitotic Prometaphase R-HSA-68877
-3.366		Mitotic Spindle Checkpoint R-HSA-69618
3.336		TP53 Regulates Metabolic Genes R-HSA-5628897
-3.219		ER To Golgi Anterograde Transport R-HSA-199977
-3.134		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 $z=32$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES

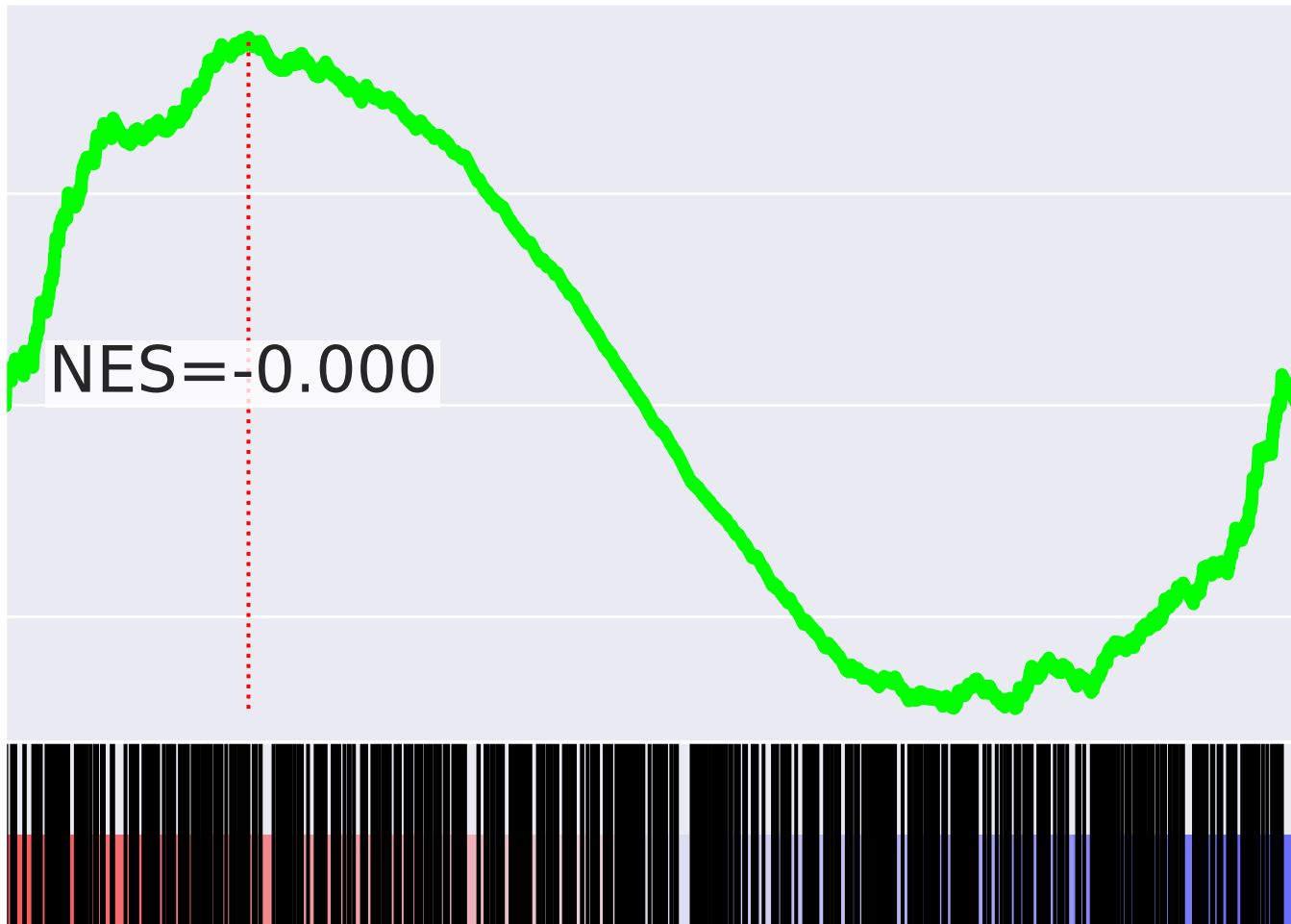
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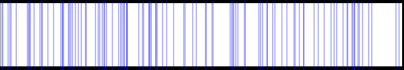
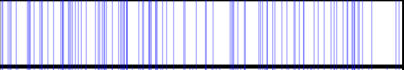
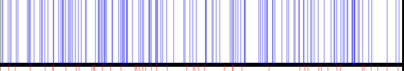
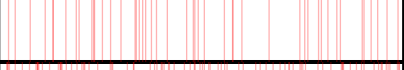
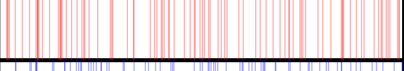
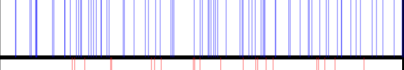
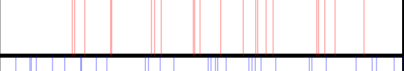
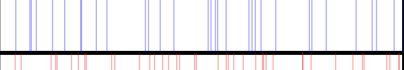
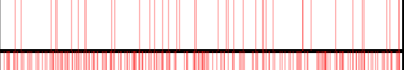
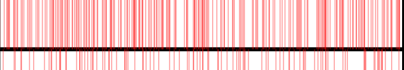
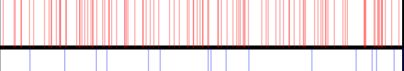
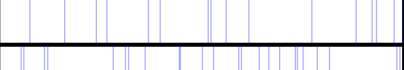
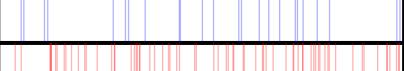
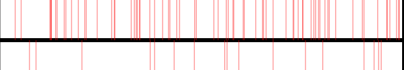

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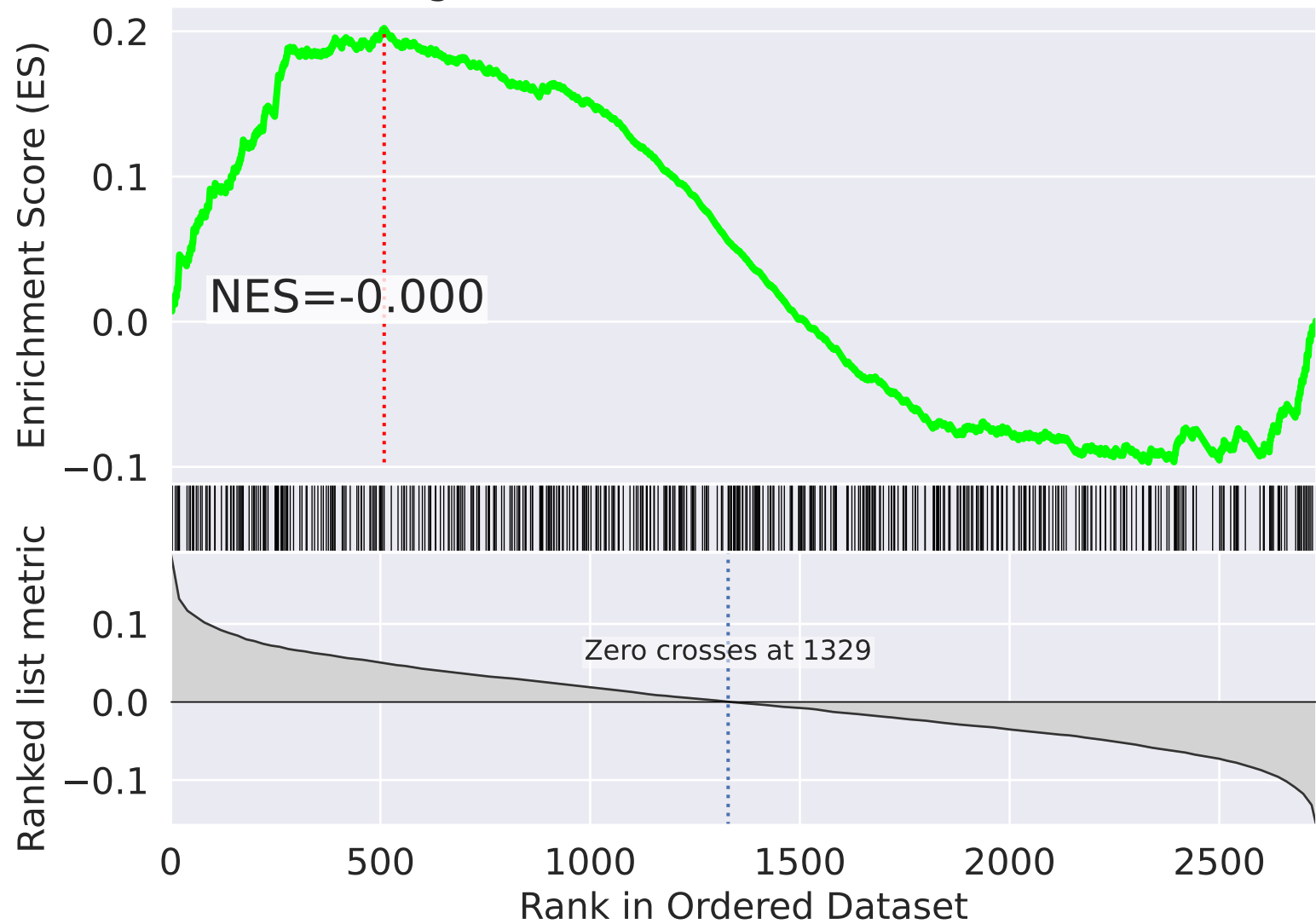
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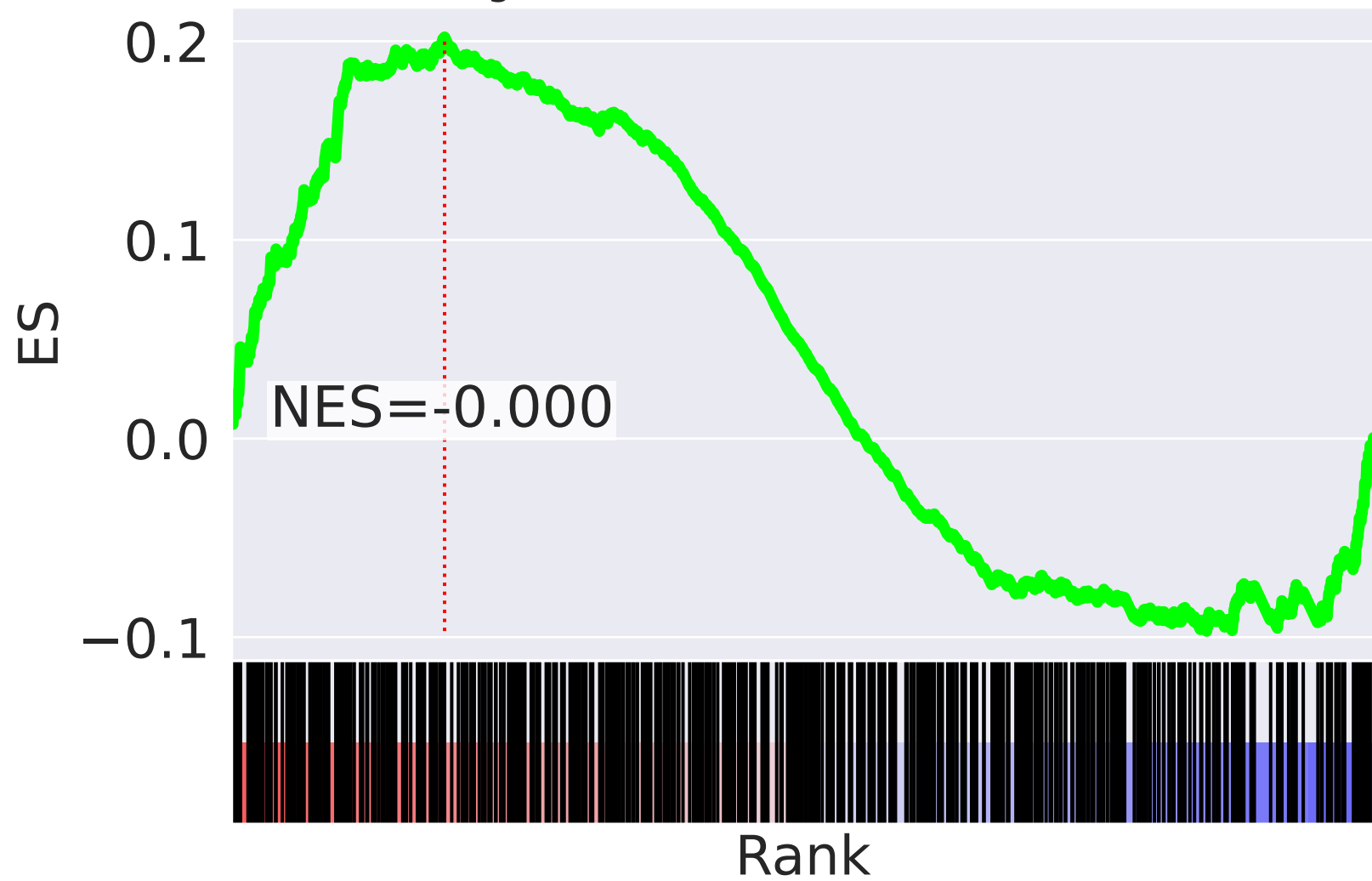
NES		SET
-4.260		mRNA Splicing R-HSA-72172
-4.141		mRNA Splicing - Major Pathway R-HSA-72163
-4.125		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.034		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
3.993		Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.859		Translation R-HSA-72766
3.745		Transcriptional Regulation Of Granulopoiesis R-HSA-9616222
-3.411		tRNA Aminoacylation R-HSA-379724
3.405		Estrogen-dependent Gene Expression R-HSA-9018519
3.388		Developmental Biology R-HSA-1266738
3.316		Chromatin Modifying Enzymes R-HSA-3247509
-3.274		Cytosolic tRNA Aminoacylation R-HSA-379716
-3.204		DNA Damage Recognition In GG-NER R-HSA-5696394
3.072		Signaling By Nuclear Receptors R-HSA-9006931
3.069		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 $z=33$

Signal Transduction R-HSA-162582



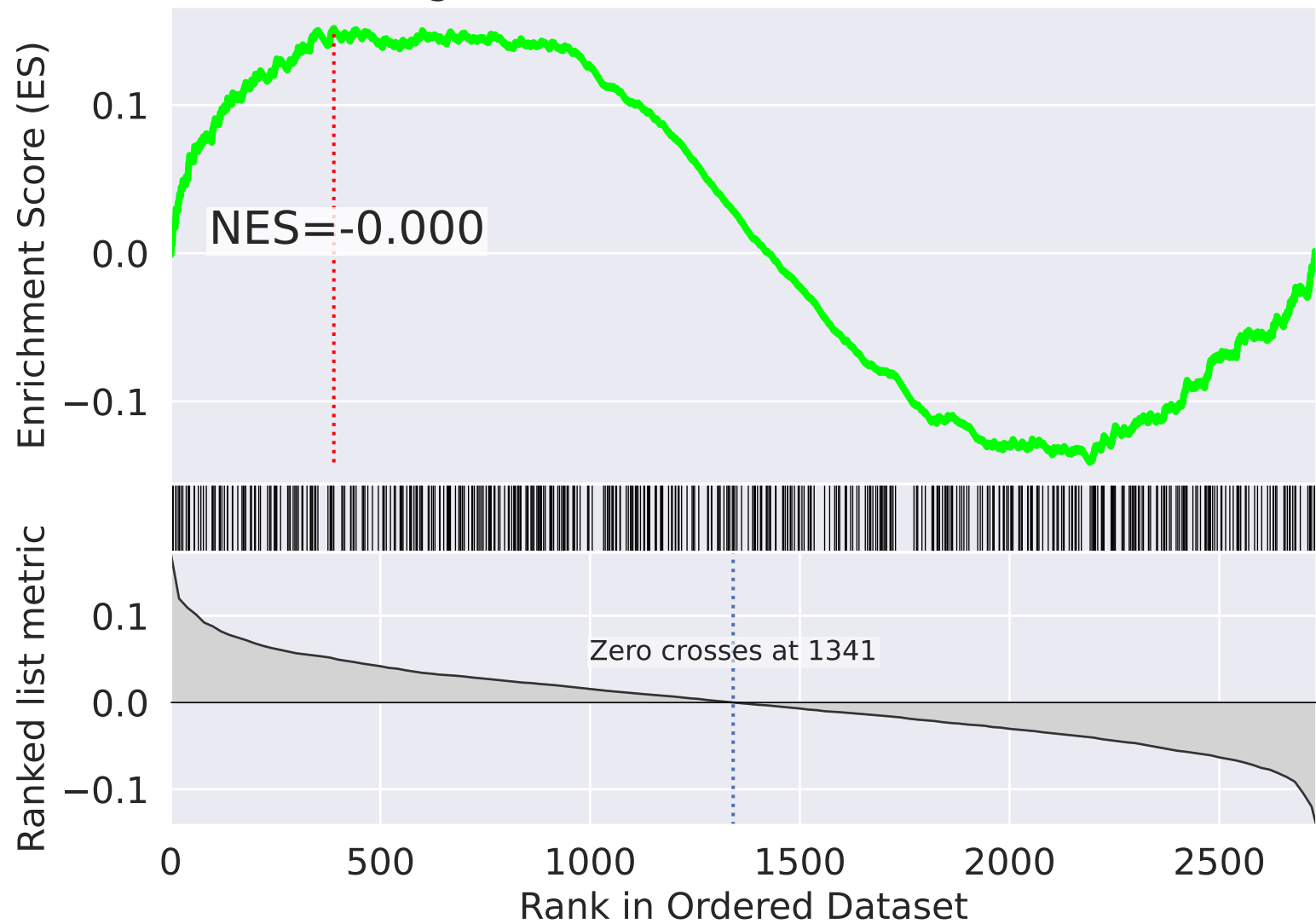
Signal Transduction R-HSA-162582



NES	SET
6.096	Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
5.993	mRNA Splicing - Major Pathway R-HSA-72163
5.956	mRNA Splicing R-HSA-72172
5.316	Mitotic Metaphase And Anaphase R-HSA-2555396
5.181	Mitotic Anaphase R-HSA-68882
5.061	M Phase R-HSA-68886
4.973	Neddylation R-HSA-8951664
4.920	HIV Infection R-HSA-162906
-4.863	Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.625	Separation Of Sister Chromatids R-HSA-2467813
4.516	Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
4.503	Host Interactions Of HIV Factors R-HSA-162909
4.490	Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
4.430	G2/M Transition R-HSA-69275
4.405	Oxygen-dependent Proline Hydroxylation Of Hypoxia-inducible Factor Alpha R-HSA-1234176

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

ES

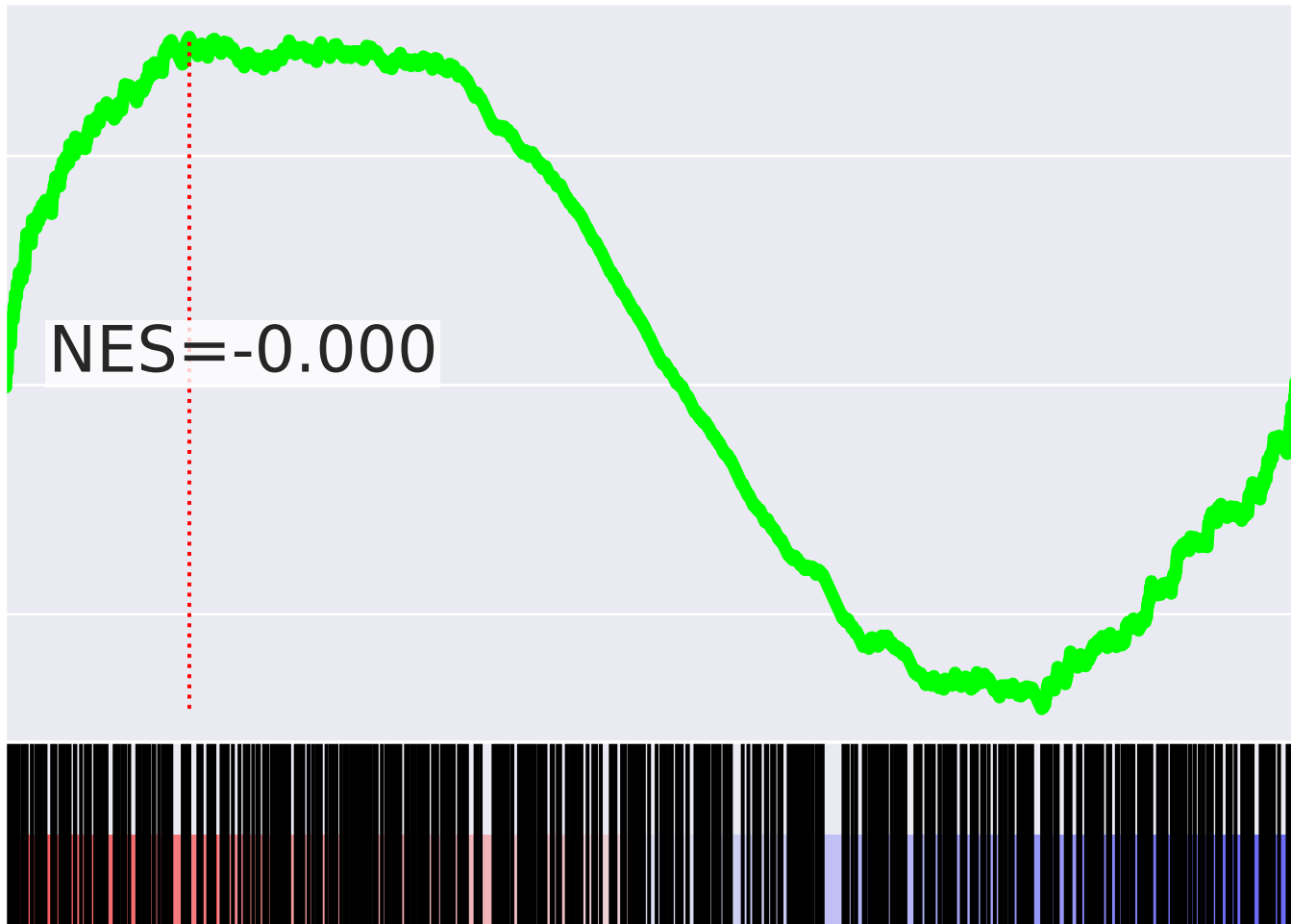
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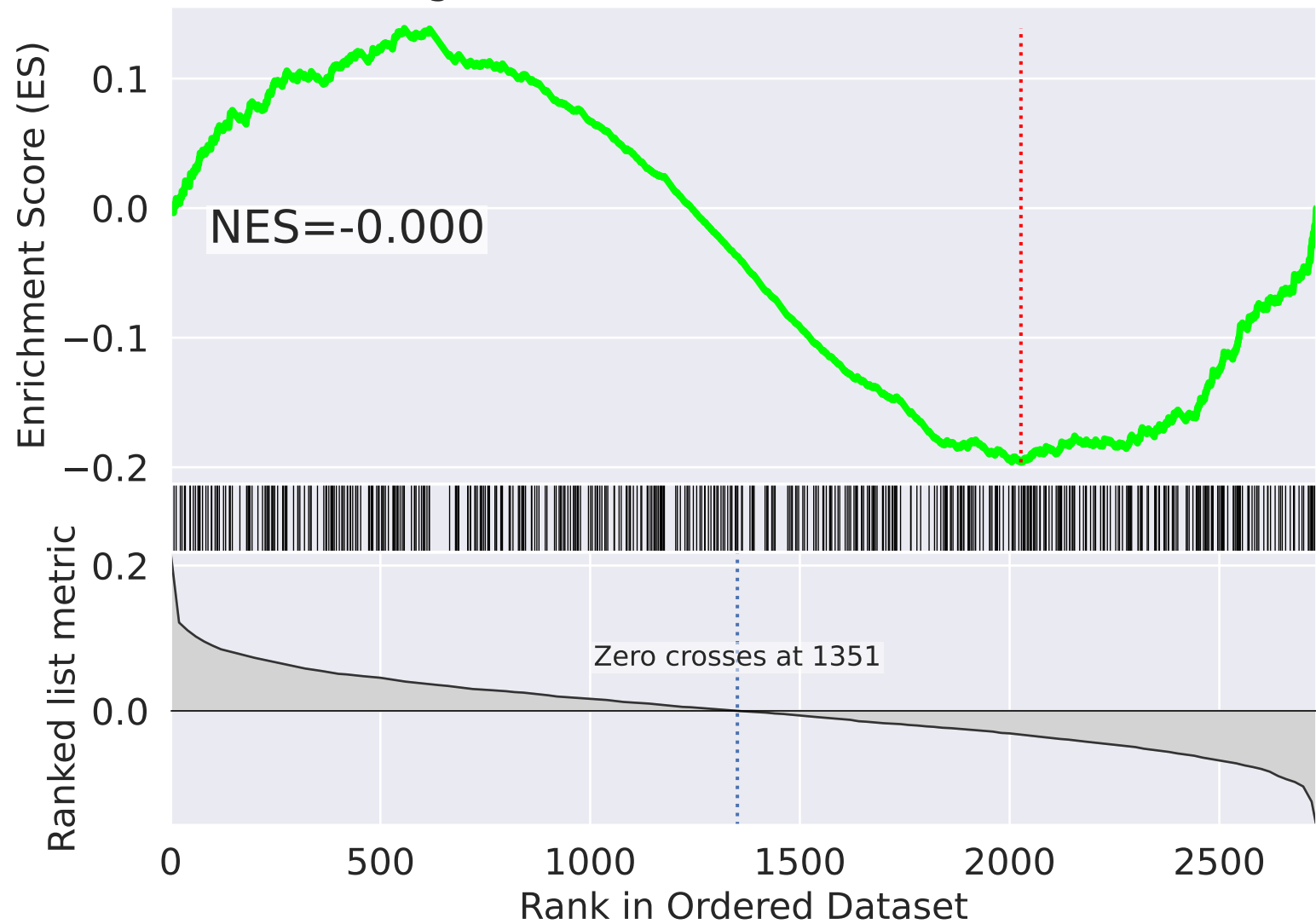
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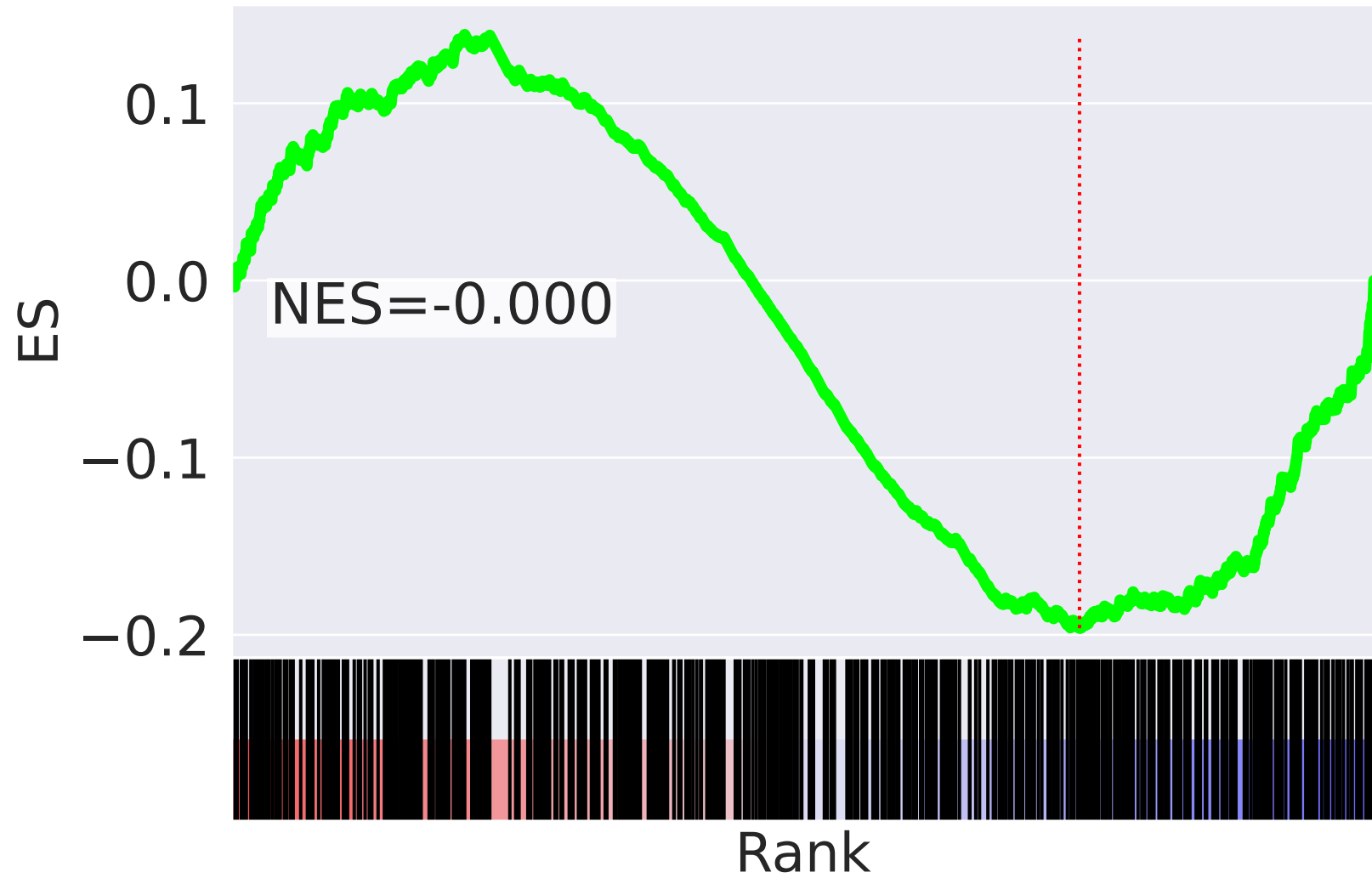
NES	SET
4.765	Mitotic Spindle Checkpoint R-HSA-69618
3.991	Separation Of Sister Chromatids R-HSA-2467813
3.958	Signaling By Rho GTPases R-HSA-194315
3.912	Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
3.912	EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
3.696	Signaling By Rho GTPases, Miro GTPases And RHOBTB3 R-HSA-9716542
3.602	Resolution Of Sister Chromatid Cohesion R-HSA-2500257
3.544	RHO GTPases Activate Formins R-HSA-5663220
3.375	Mitotic Anaphase R-HSA-68882
3.343	M Phase R-HSA-68886
3.314	Mitotic Metaphase And Anaphase R-HSA-2555396
3.159	HSP90 Chaperone Cycle For Steroid Hormone Receptors (SHR) In Presence Of Ligand R-HSA-3371497
3.137	Mitotic Prometaphase R-HSA-68877
2.976	Inactivation Of APC/C Via Direct Inhibition Of APC/C Complex R-HSA-141430
2.958	RHO GTPase Effectors R-HSA-195258

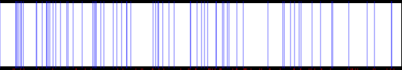
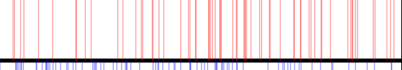
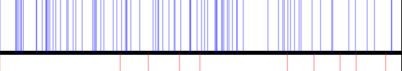
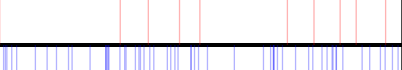
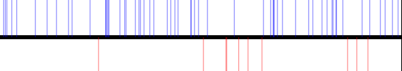
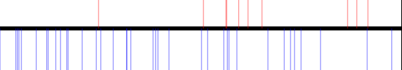
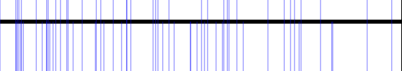

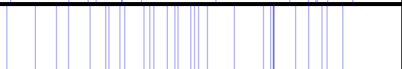

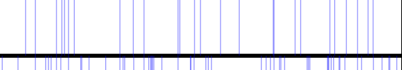
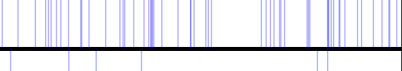
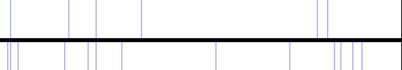
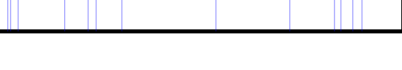

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=35$

Signal Transduction R-HSA-162582



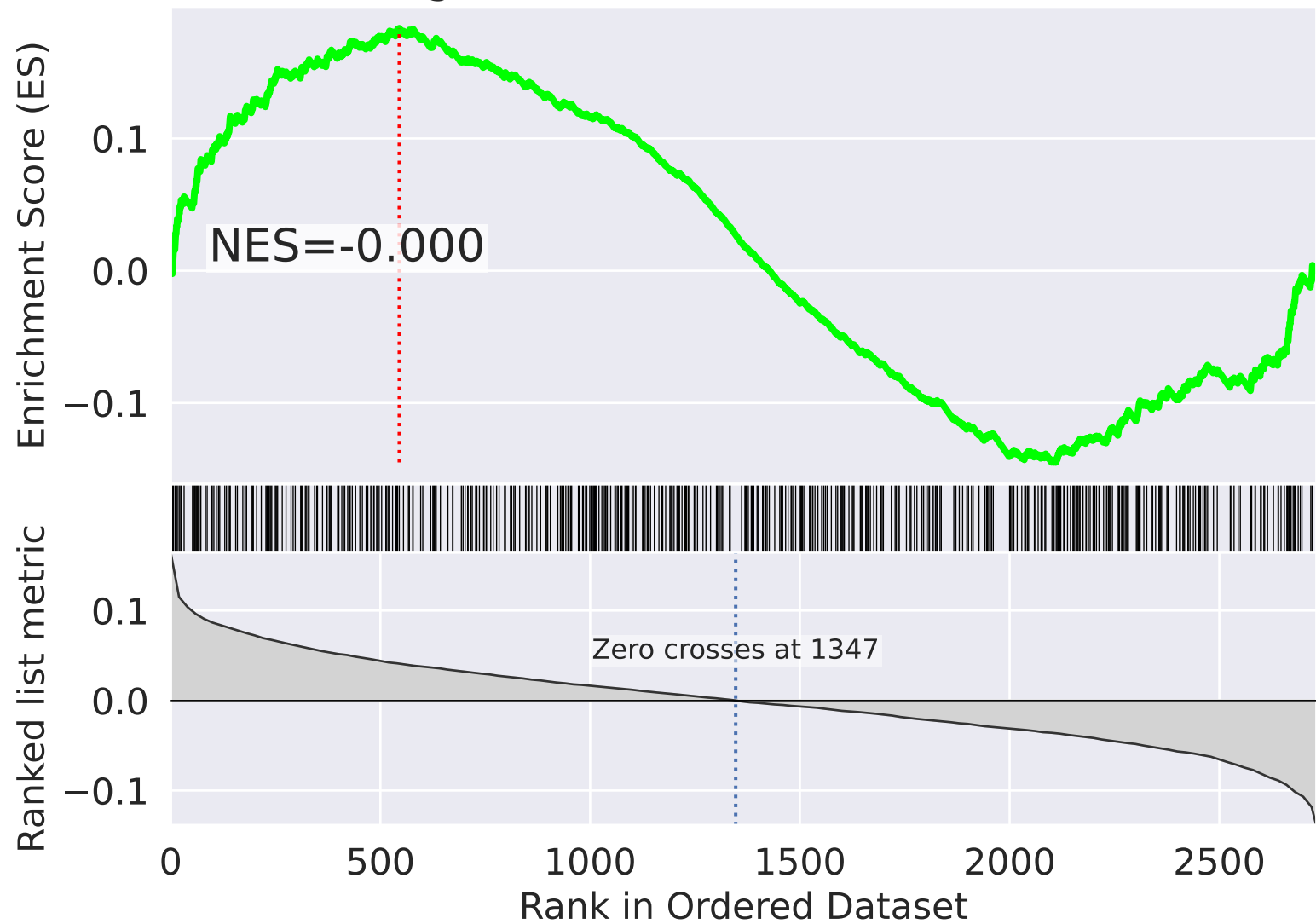
Signal Transduction R-HSA-162582



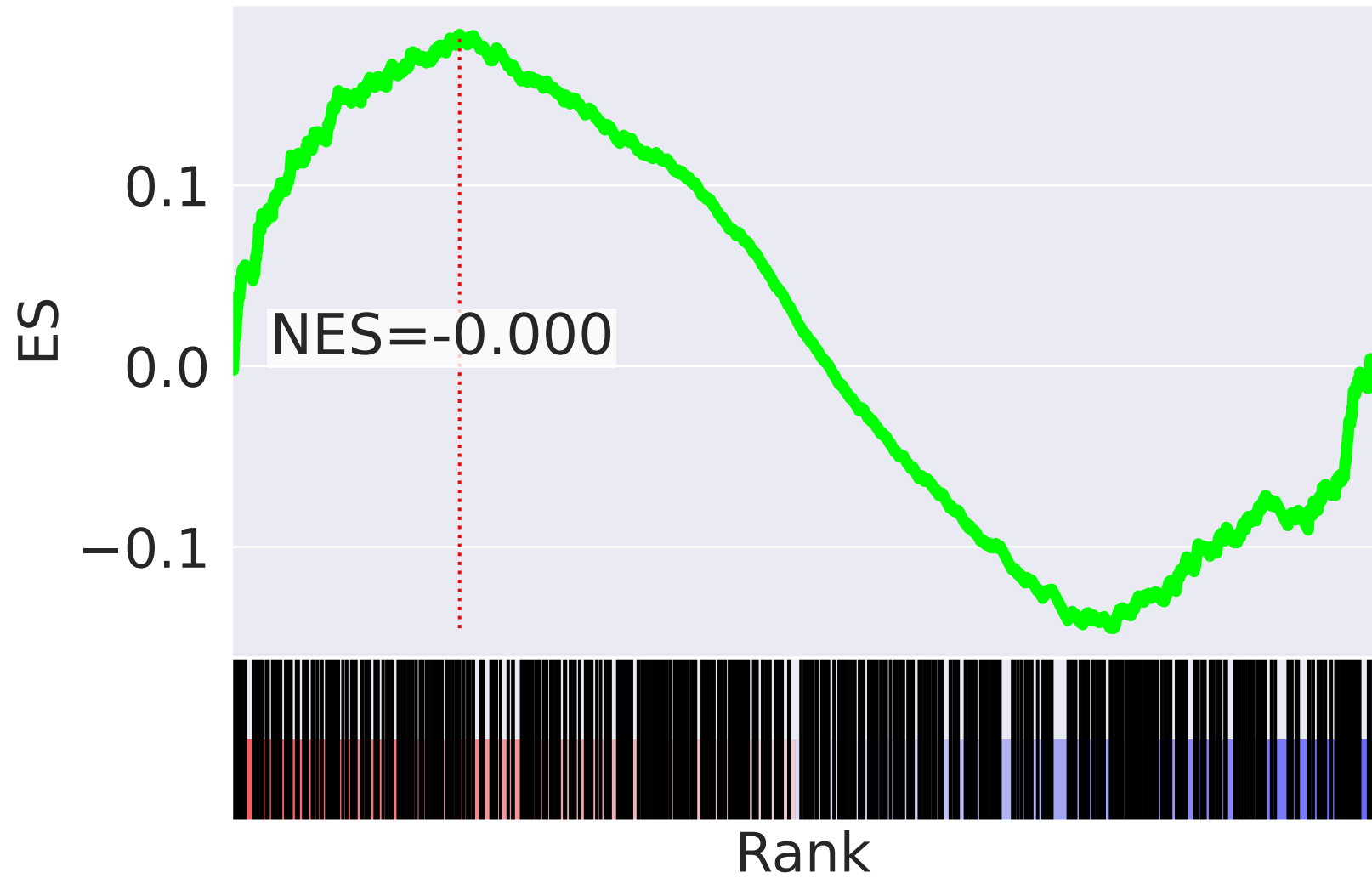
NES		SET
-4.297		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.663		Metabolism Of Amino Acids And Derivatives R-HSA-71291
-3.441		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.260		SUMOylation Of Transcription Cofactors R-HSA-3899300
-3.161		Chromosome Maintenance R-HSA-73886
3.071		Mitotic Telophase/Cytokinesis R-HSA-68884
-2.988		Complex I Biogenesis R-HSA-6799198
-2.919		Respiratory Electron Transport R-HSA-611105
-2.865		Signaling To ERKs R-HSA-187687
-2.806		Extension Of Telomeres R-HSA-180786
-2.785		Mitochondrial Iron-Sulfur Cluster Biogenesis R-HSA-1362409
-2.705		DNA Damage Bypass R-HSA-73893
-2.687		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
-2.671		Frs2-mediated Activation R-HSA-170968
-2.668		Downstream Signal Transduction R-HSA-186763

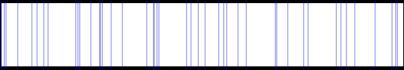
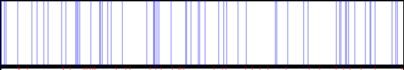
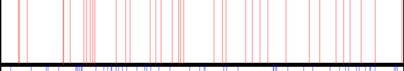
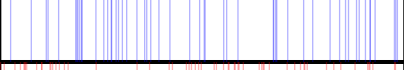
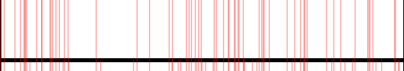
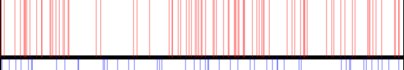
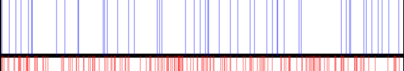
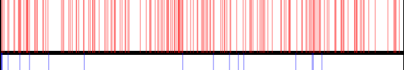
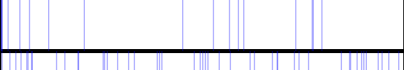
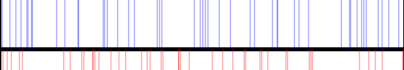
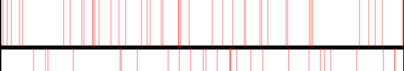
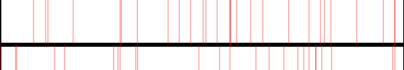

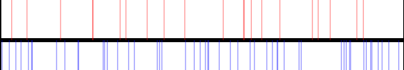

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=36$

Signal Transduction R-HSA-162582



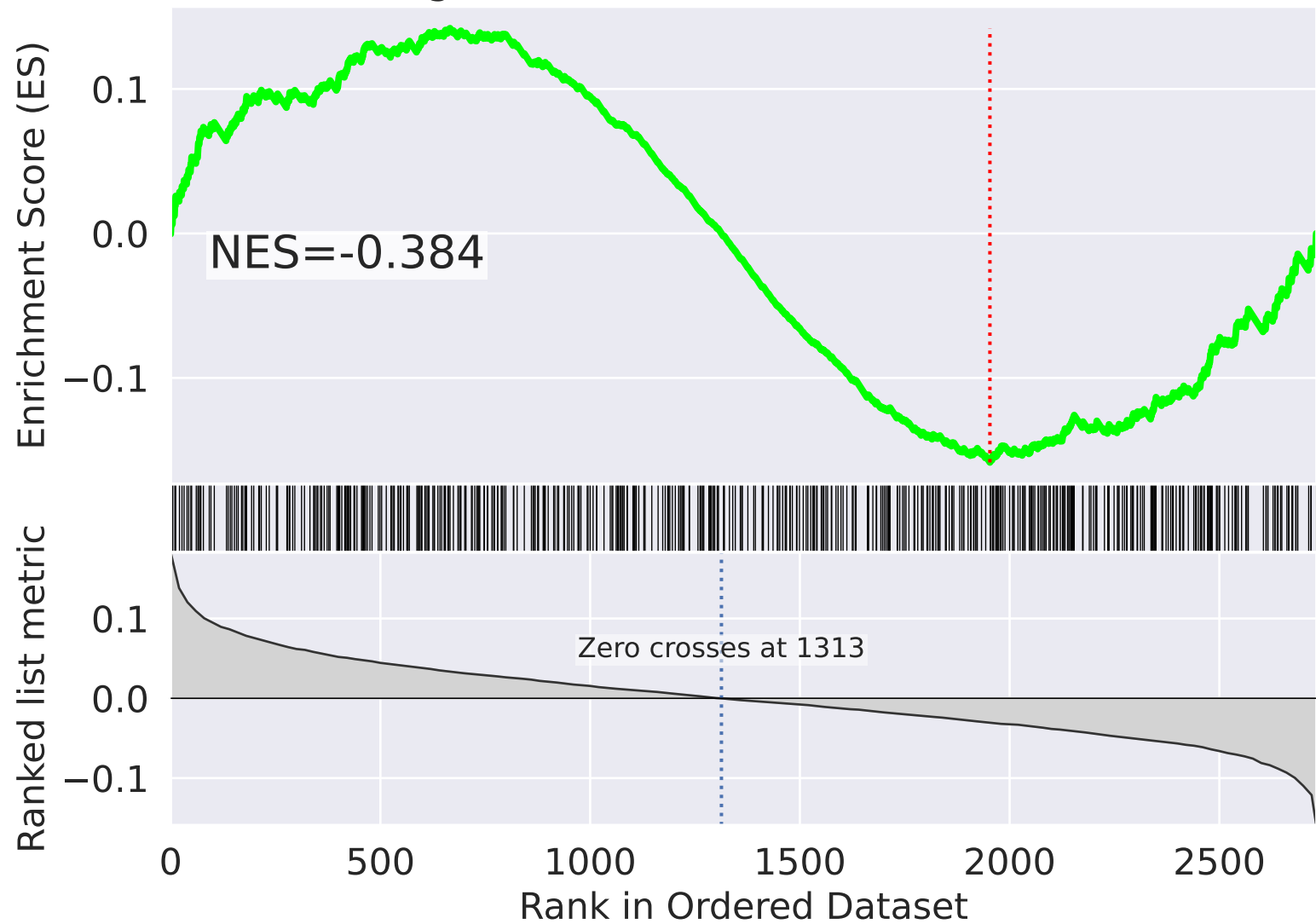
Signal Transduction R-HSA-162582



NES		SET
-3.385		Formation Of RNA Pol II Elongation Complex R-HSA-112382
-3.263		RNA Polymerase II Pre-transcription Events R-HSA-674695
2.916		Glucose Metabolism R-HSA-70326
-2.862		RNA Polymerase II Transcribes snRNA Genes R-HSA-6807505
2.794		Respiratory Electron Transport R-HSA-611105
2.729		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-2.718		PPARA Activates Gene Expression R-HSA-1989781
2.693		Cytokine Signaling In Immune System R-HSA-1280215
-2.675		Translocation Of SLC2A4 (GLUT4) To Plasma Membrane R-HSA-1445148
-2.673		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
2.665		Nuclear Envelope (NE) Reassembly R-HSA-2995410
2.662		Signaling By MET R-HSA-6806834
2.620		Cargo Recognition For Clathrin-Mediated Endocytosis R-HSA-8856825
2.605		Regulated Necrosis R-HSA-5218859
-2.577		Regulation Of Lipid Metabolism By PPARalpha R-HSA-400206

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

ES

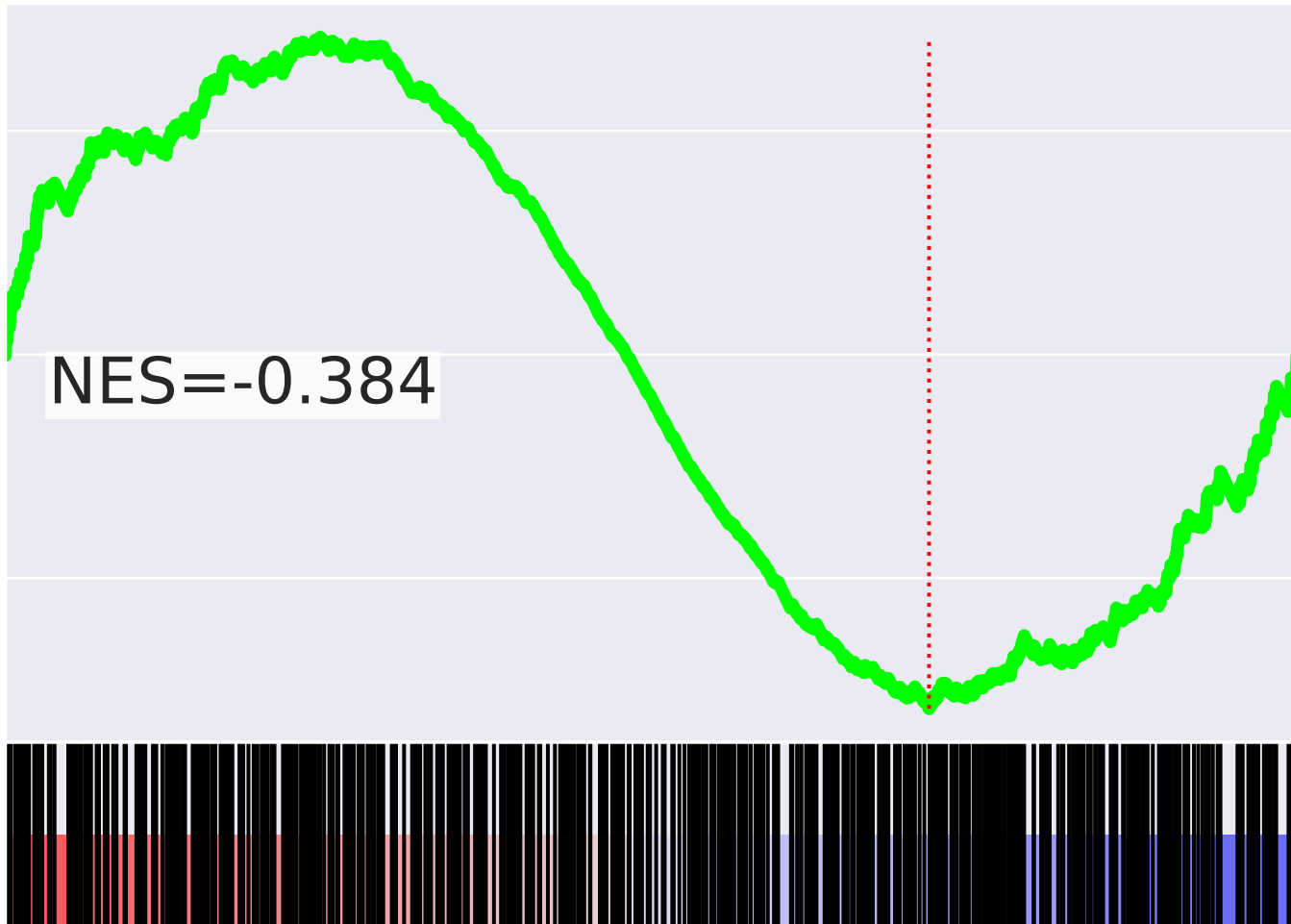
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0.0

-0.1

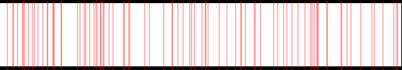
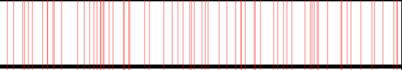
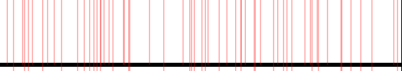
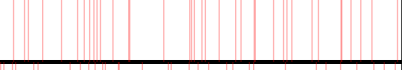
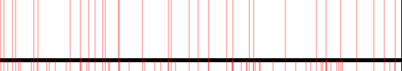
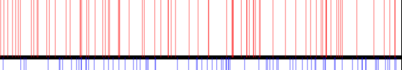
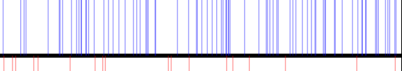
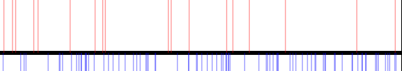
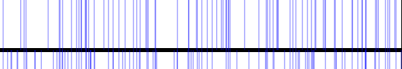
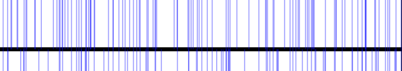
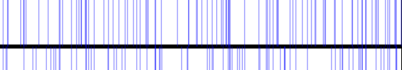
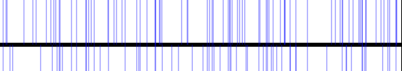
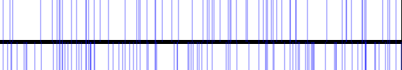
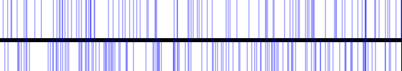

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Rank



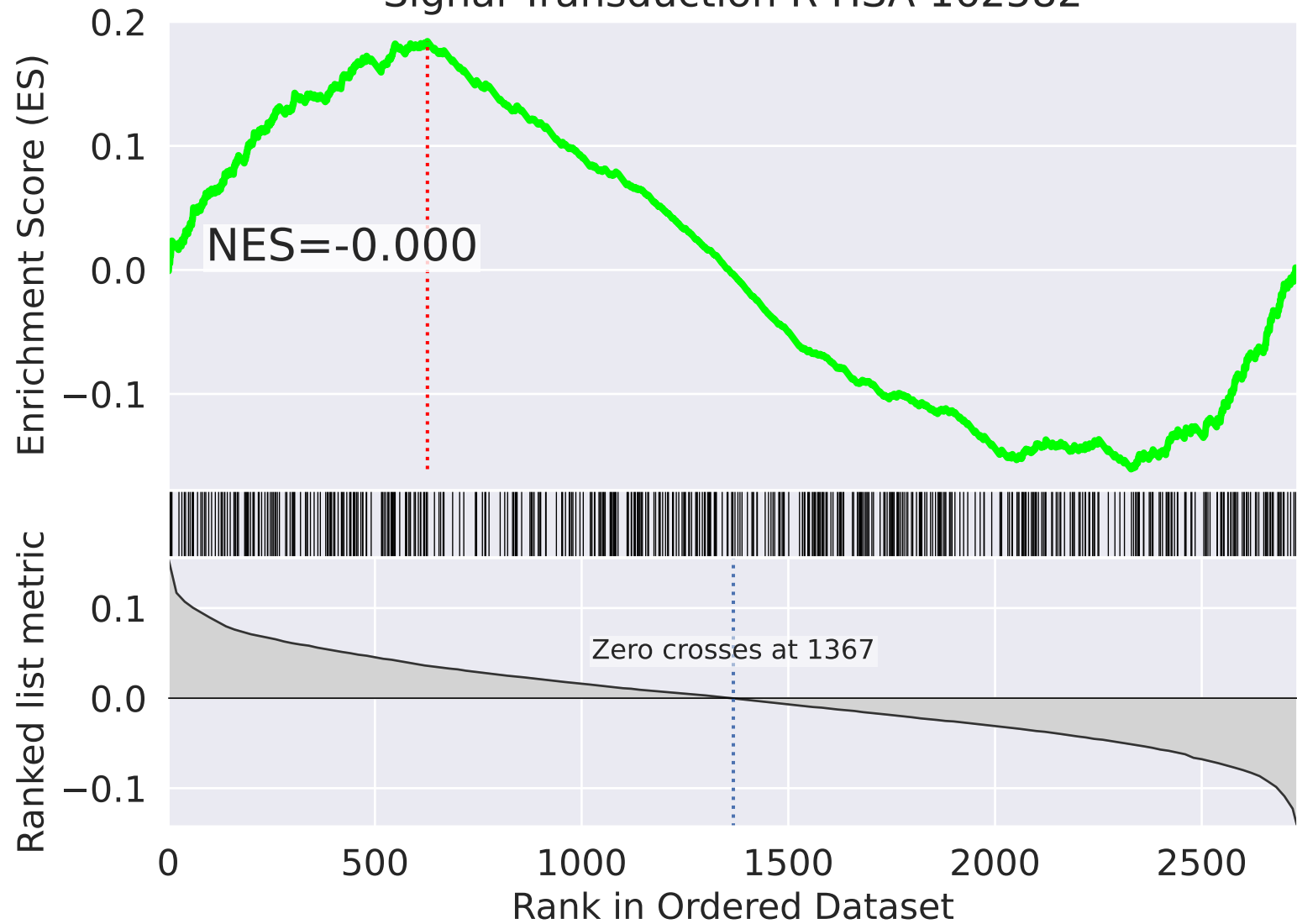
NES

SET

8.014		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
7.804		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.950		Respiratory Electron Transport R-HSA-611105
5.700		Complex I Biogenesis R-HSA-6799198
4.303		tRNA Aminoacylation R-HSA-379724
4.235		Translation R-HSA-72766
-3.963		RAF/MAP Kinase Cascade R-HSA-5673001
3.947		Mitochondrial tRNA Aminoacylation R-HSA-379726
-3.923		MAPK1/MAPK3 Signaling R-HSA-5684996
-3.880		Intracellular Signaling By Second Messengers R-HSA-9006925
-3.868		MAPK Family Signaling Cascades R-HSA-5683057
-3.866		Synthesis Of DNA R-HSA-69239
-3.851		Disorders Of Transmembrane Transporters R-HSA-5619115
-3.804		PIP3 Activates AKT Signaling R-HSA-1257604
-3.780		Signaling By Receptor Tyrosine Kinases R-HSA-9006934

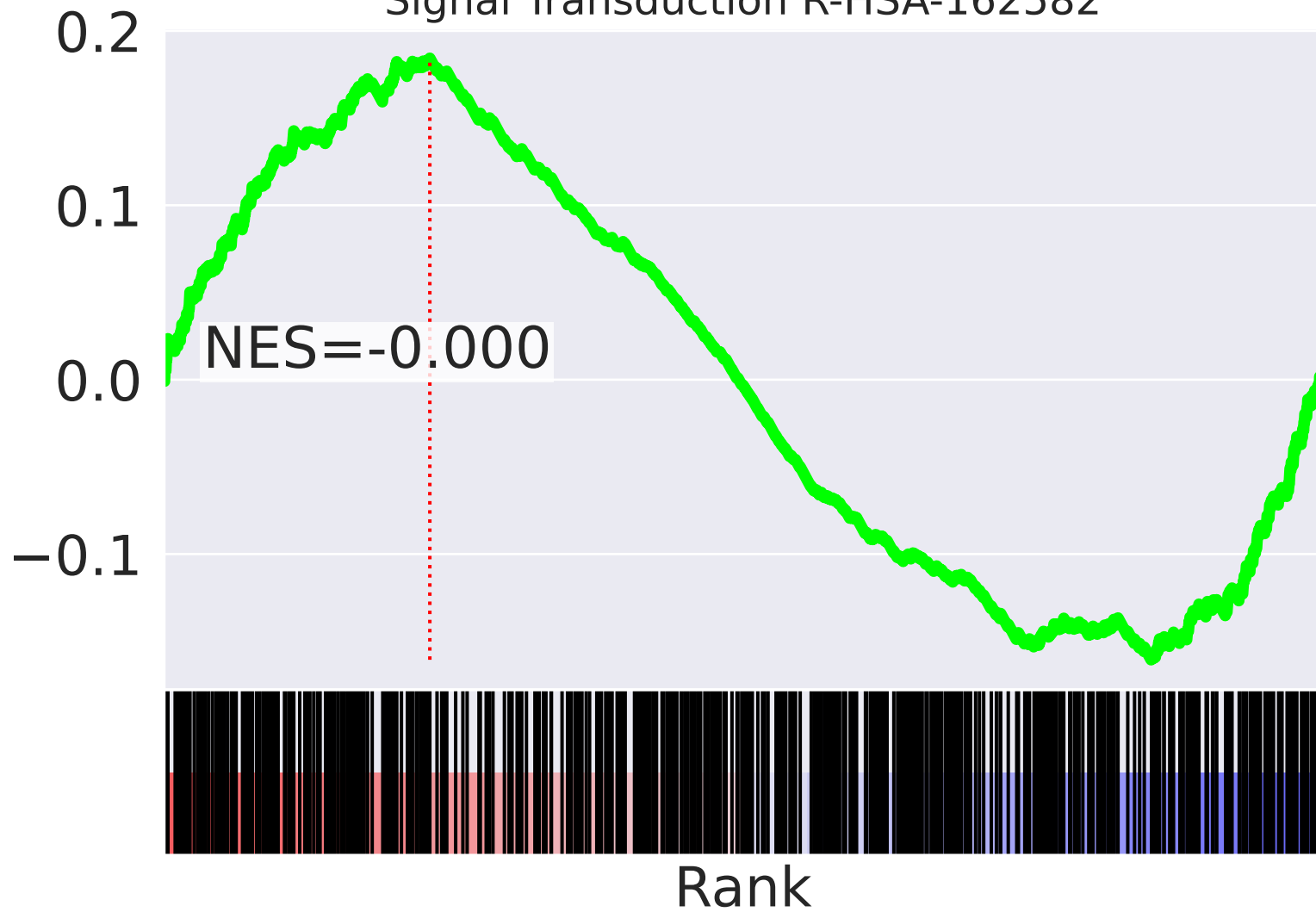
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=38$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

ES



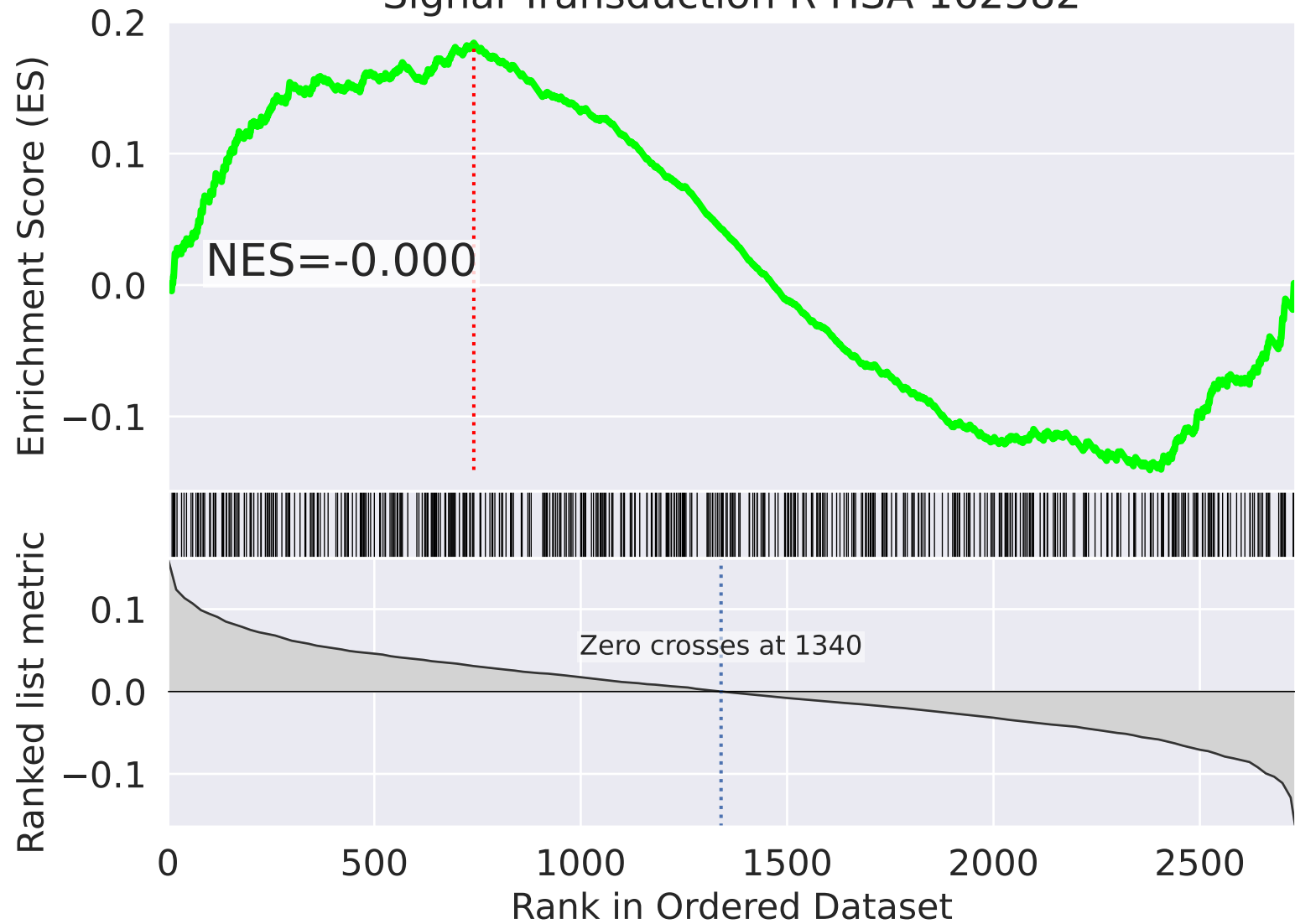
NES

SET

4.804		SARS-CoV Infections R-HSA-9679506
4.204		Host Interactions Of HIV Factors R-HSA-162909
3.875		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.836		SUMOylation R-HSA-2990846
3.805		ISG15 Antiviral Mechanism R-HSA-1169408
3.697		Antiviral Mechanism By IFN-stimulated Genes R-HSA-1169410
3.680		SUMO E3 Ligases SUMOylate Target Proteins R-HSA-3108232
3.572		Signaling By WNT R-HSA-195721
3.557		SARS-CoV-2-host Interactions R-HSA-9705683
3.545		Mitotic Prophase R-HSA-68875
3.541		Interferon Signaling R-HSA-913531
3.472		Glycolysis R-HSA-70171
3.393		SARS-CoV-2 Infection R-HSA-9694516
3.379		NS1 Mediated Effects On Host Pathways R-HSA-168276
3.348		Potential Therapeutics For SARS R-HSA-9679191

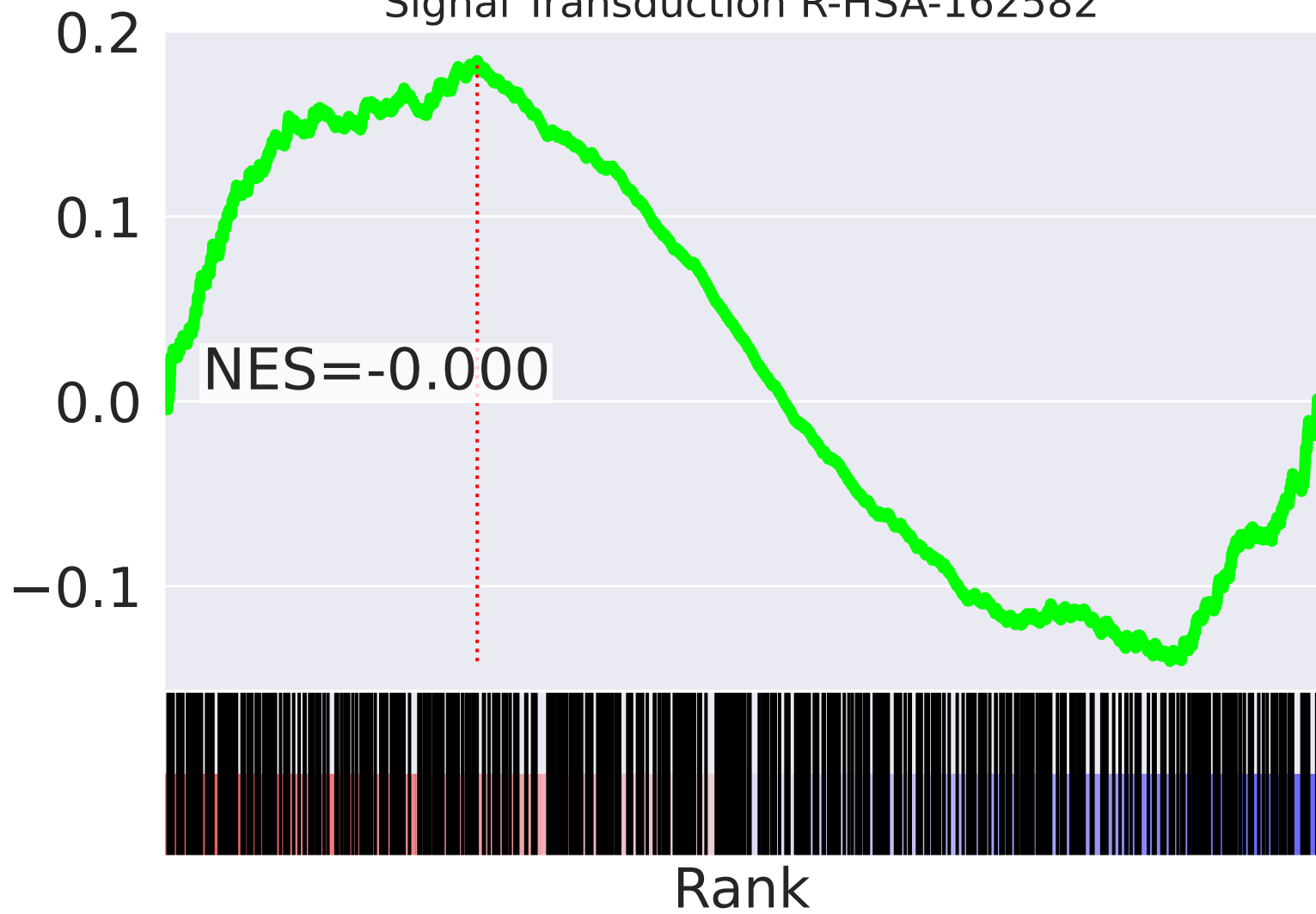
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=39$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

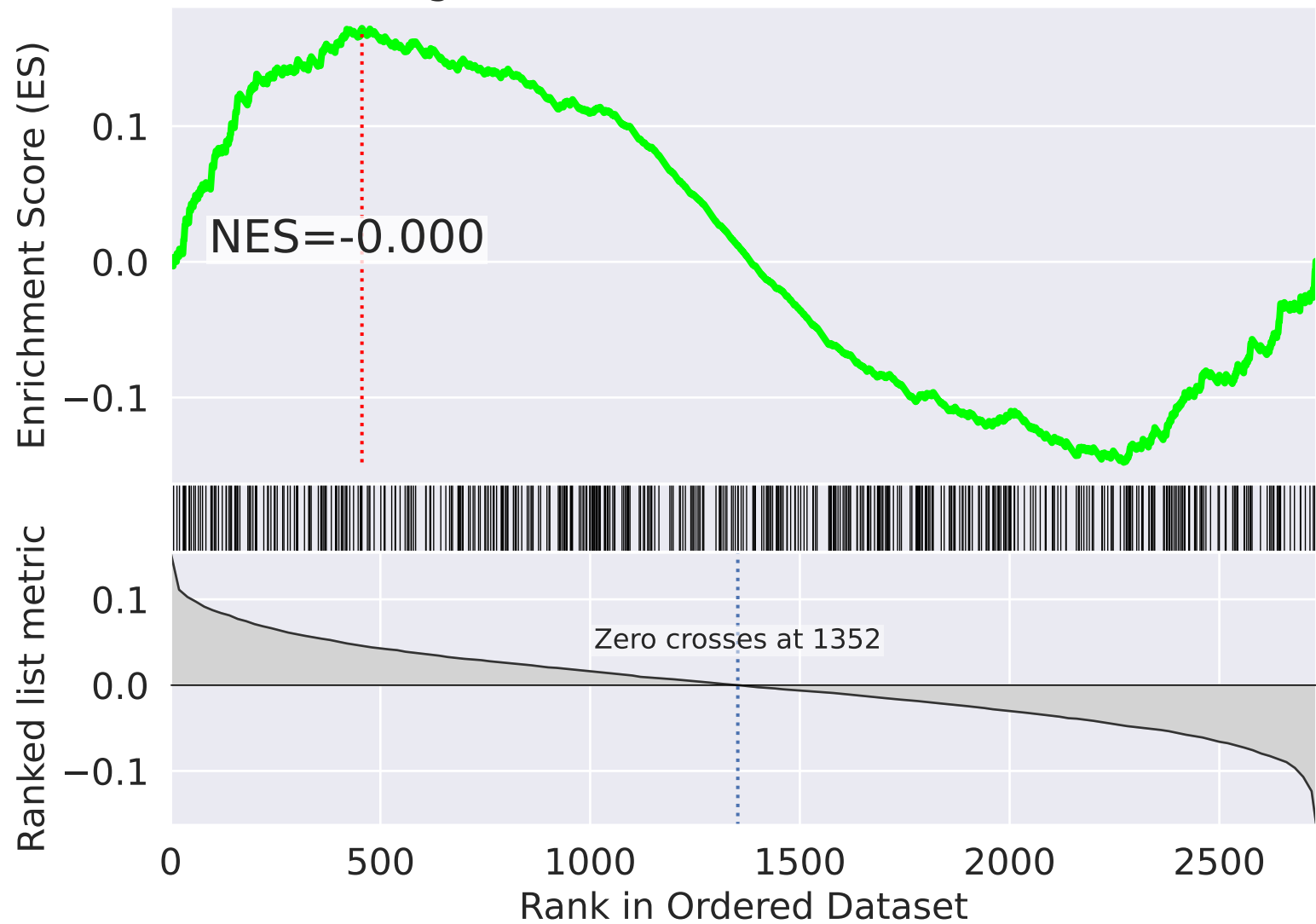
ES



NES	SET
5.308	Synthesis Of DNA R-HSA-69239
5.198	Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
5.166	APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
5.136	Switching Of Origins To A Post-Replicative State R-HSA-69052
5.037	CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
4.984	SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
4.902	DNA Replication R-HSA-69306
4.883	G2/M Transition R-HSA-69275
4.810	S Phase R-HSA-69242
4.794	DNA Replication Pre-Initiation R-HSA-69002
4.789	APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
4.771	APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176409
4.770	SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
4.764	Activation Of APC/C And APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176814
4.754	Mitotic G2-G2/M Phases R-HSA-453274

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

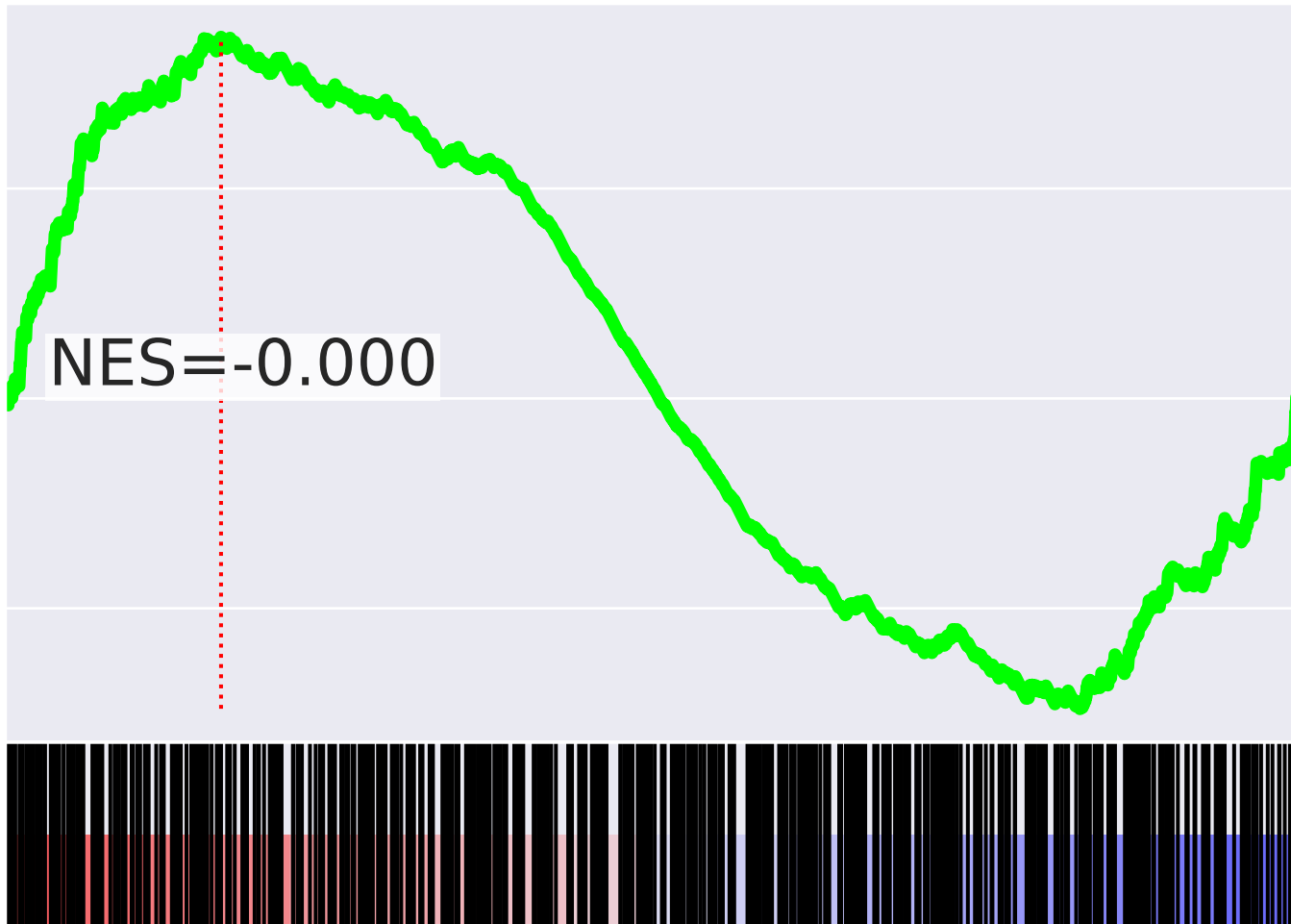
ES

NES=-0.000

-0.1


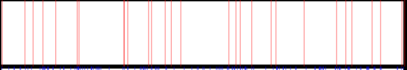
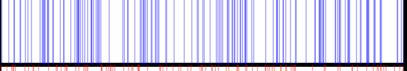
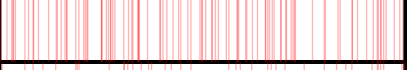
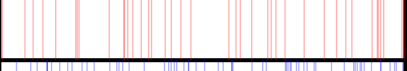
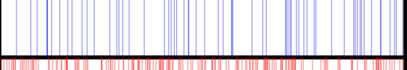
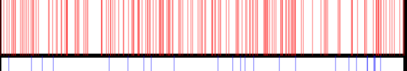
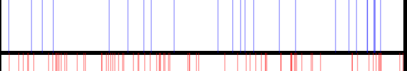
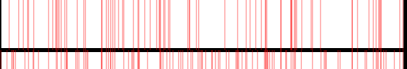
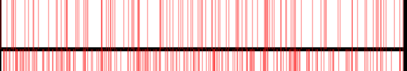
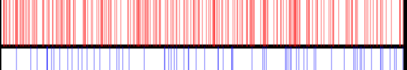
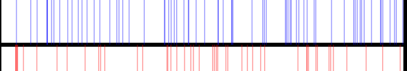
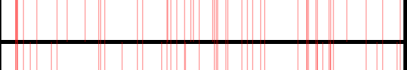
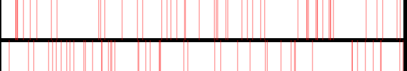

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Rank



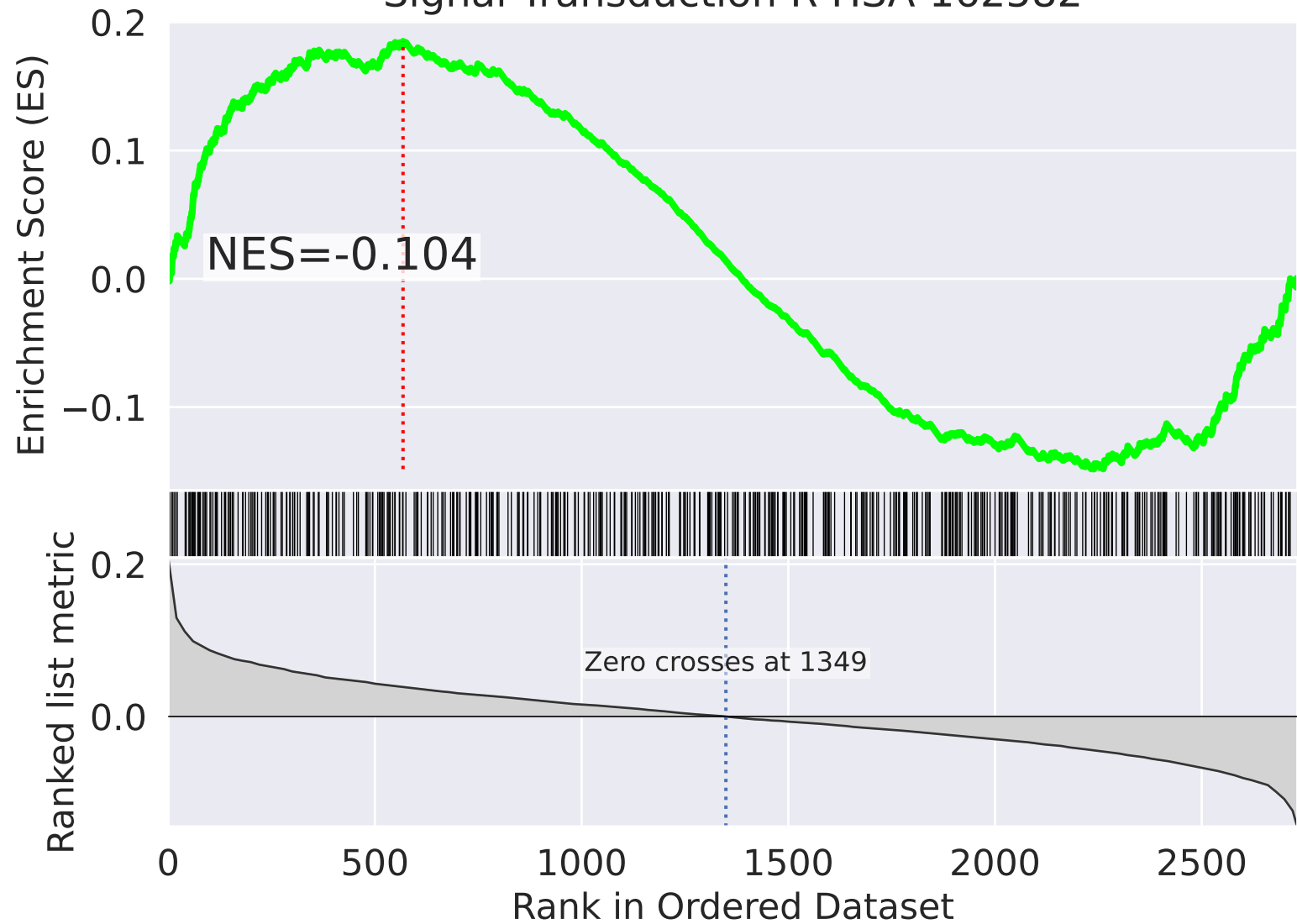
NES

SET

4.294		Metabolism Of Lipids R-HSA-556833
4.199		E3 Ubiquitin Ligases Ubiquitinate Target Proteins R-HSA-8866654
-4.183		DNA Repair R-HSA-73894
4.158		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
4.118		Protein Ubiquitination R-HSA-8852135
-4.083		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.051		Adaptive Immune System R-HSA-1280218
-3.967		Fanconi Anemia Pathway R-HSA-6783310
3.926		Host Interactions Of HIV Factors R-HSA-162909
3.918		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
3.816		Developmental Biology R-HSA-1266738
-3.741		rRNA Processing R-HSA-72312
3.693		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
3.680		PPARA Activates Gene Expression R-HSA-1989781
3.564		Beta-catenin Independent WNT Signaling R-HSA-3858494

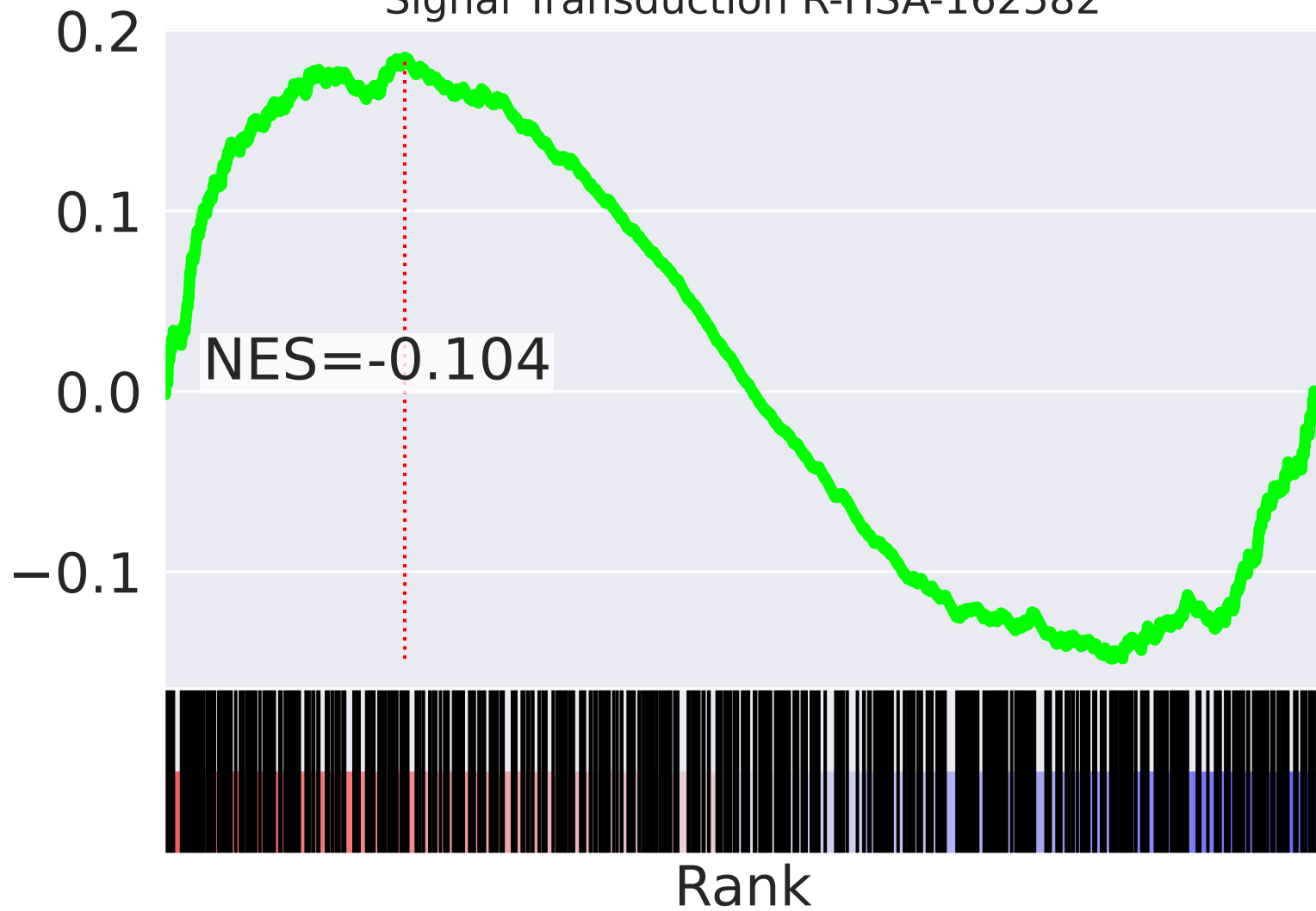
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=41$

Signal Transduction R-HSA-162582

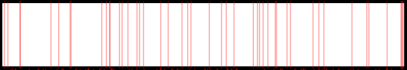
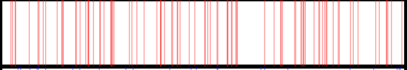
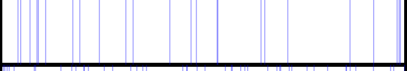
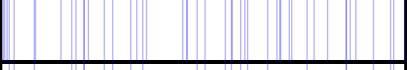
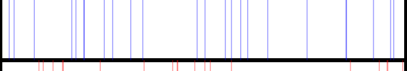
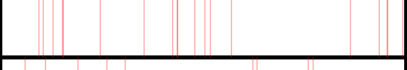
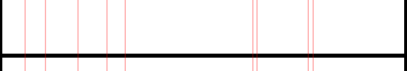
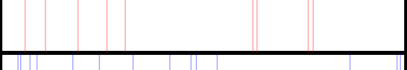
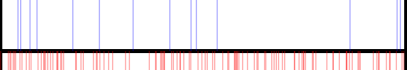
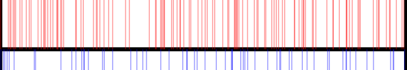
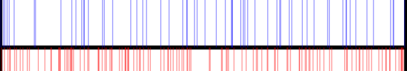
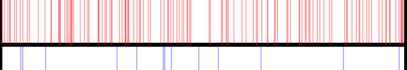

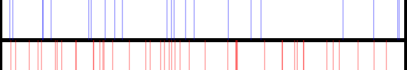
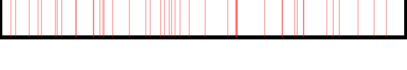


Signal Transduction R-HSA-162582

ES

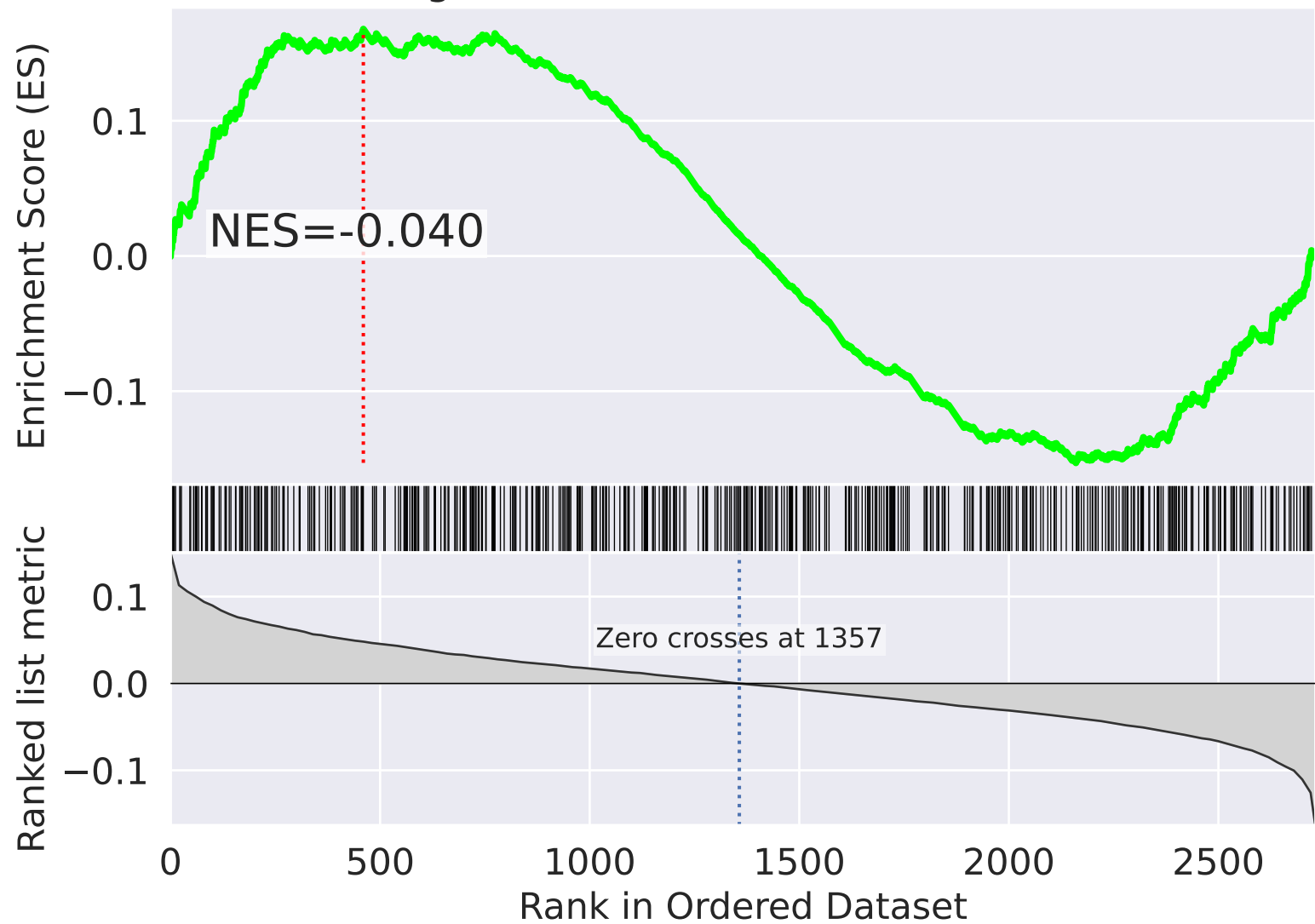


Rank

NES		SET
3.508		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
3.483		Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.432		Cell-Cell Communication R-HSA-1500931
-3.258		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
-3.240		DNA Damage Recognition In GG-NER R-HSA-5696394
3.214		RMTs Methylate Histone Arginines R-HSA-3214858
3.201		Metabolism Of Porphyrins R-HSA-189445
3.201		Heme Biosynthesis R-HSA-189451
-3.018		Cell Junction Organization R-HSA-446728
2.991		Transport Of Small Molecules R-HSA-382551
-2.764		Nucleotide Excision Repair R-HSA-5696398
2.747		Metabolism Of Lipids R-HSA-556833
-2.659		MET Promotes Cell Motility R-HSA-8875878
-2.657		Regulation Of Actin Dynamics For Phagocytic Cup Formation R-HSA-2029482
2.646		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 $z=42$

Signal Transduction R-HSA-162582



Signal Transduction R-HSA-162582

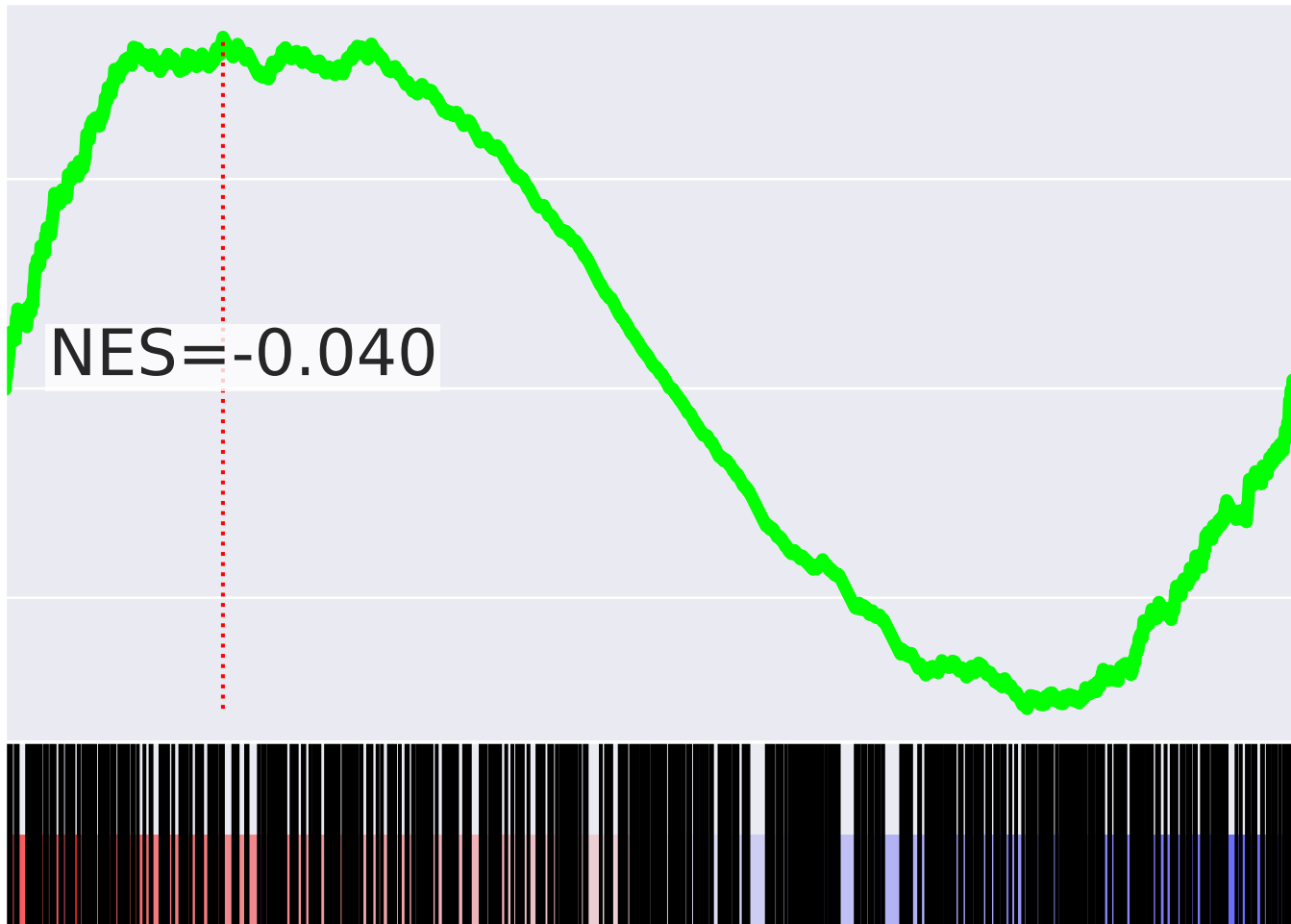
ES

NES=-0.040

-0.1

0.1

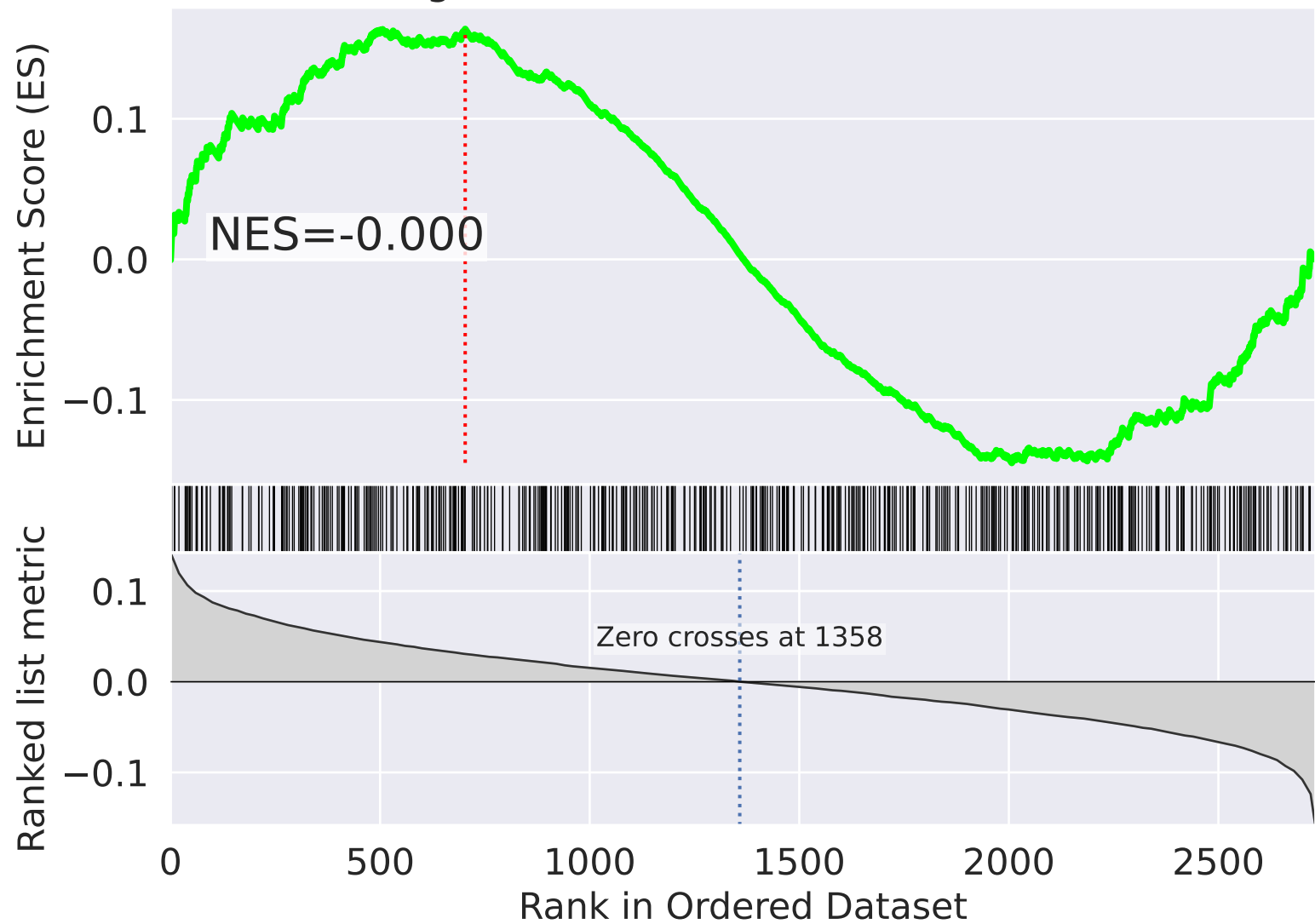
Rank



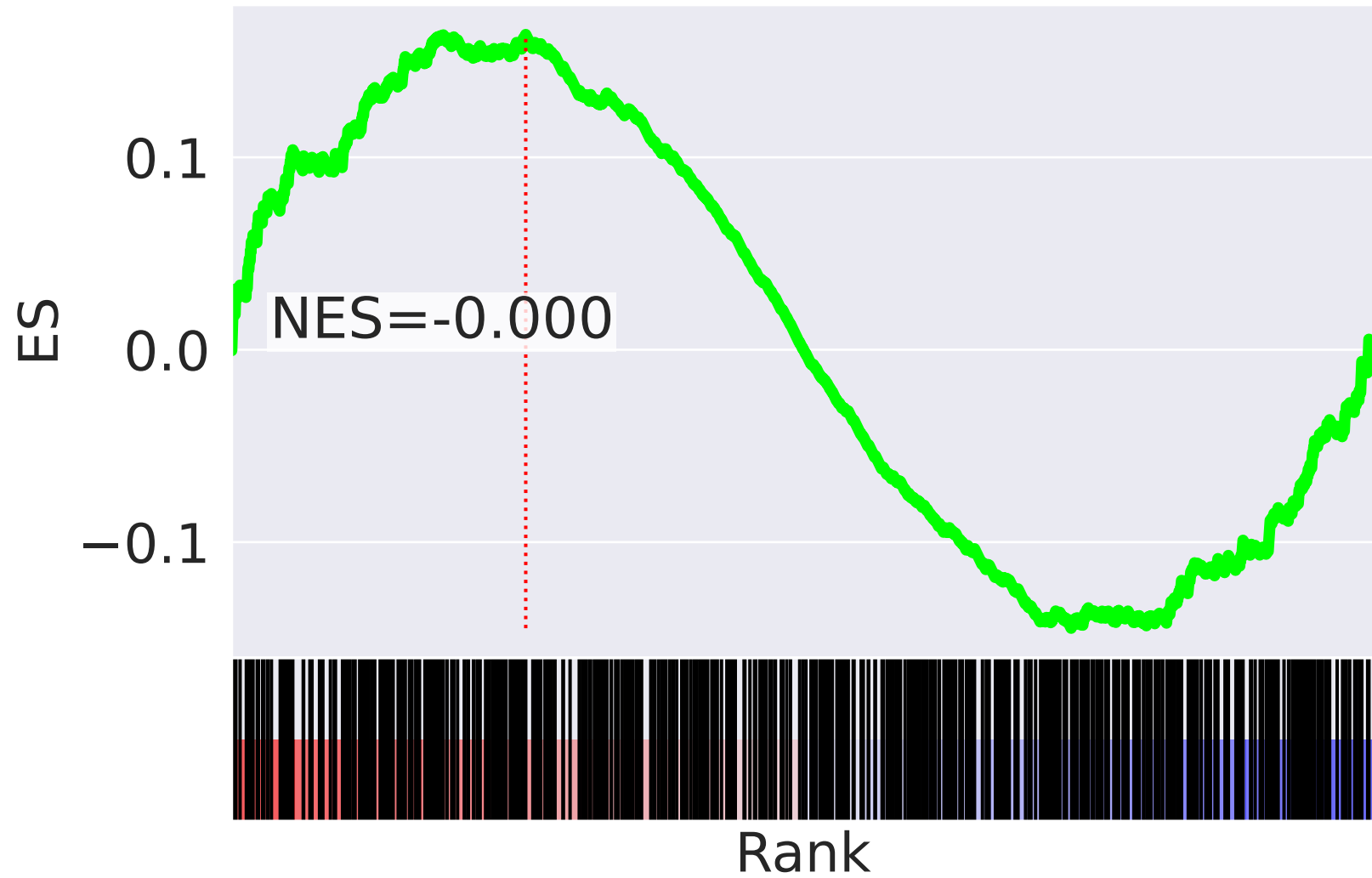
NES	SET
-4.473	Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
-4.104	Cell Cycle Checkpoints R-HSA-69620
-3.919	Postmitotic Nuclear Pore Complex (NPC) Reformation R-HSA-9615933
-3.846	Unattached Kinetochores Signal Amplification Via A MAD2 Inhibitory Signal R-HSA-141444
-3.846	EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025
-3.825	Resolution Of Sister Chromatid Cohesion R-HSA-2500257
-3.798	Mitotic Spindle Checkpoint R-HSA-69618
-3.745	SUMOylation Of SUMOylation Proteins R-HSA-4085377
-3.690	Rev-mediated Nuclear Export Of HIV RNA R-HSA-165054
-3.677	Metabolism Of Non-Coding RNA R-HSA-194441
-3.656	Interactions Of Rev With Host Cellular Proteins R-HSA-177243
-3.656	Nuclear Pore Complex (NPC) Disassembly R-HSA-3301854
-3.641	SUMOylation Of DNA Replication Proteins R-HSA-4615885
-3.631	RHO GTPases Activate Formins R-HSA-5663220
-3.597	RHO GTPase Effectors R-HSA-195258

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

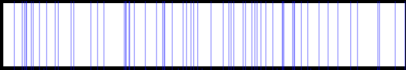
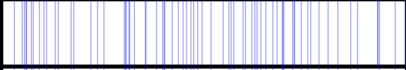
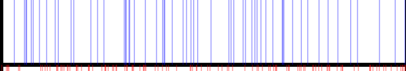
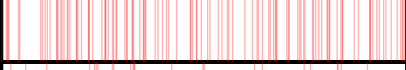
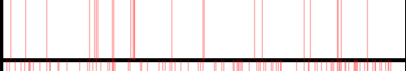
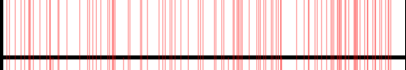
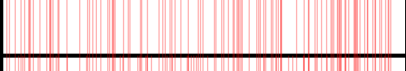

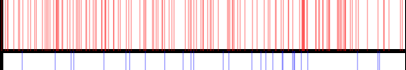
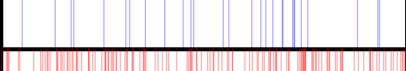
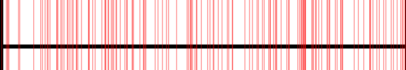
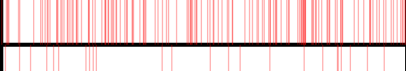

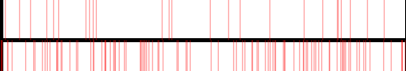
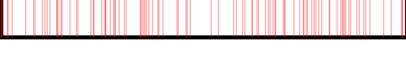


Signal Transduction R-HSA-162582



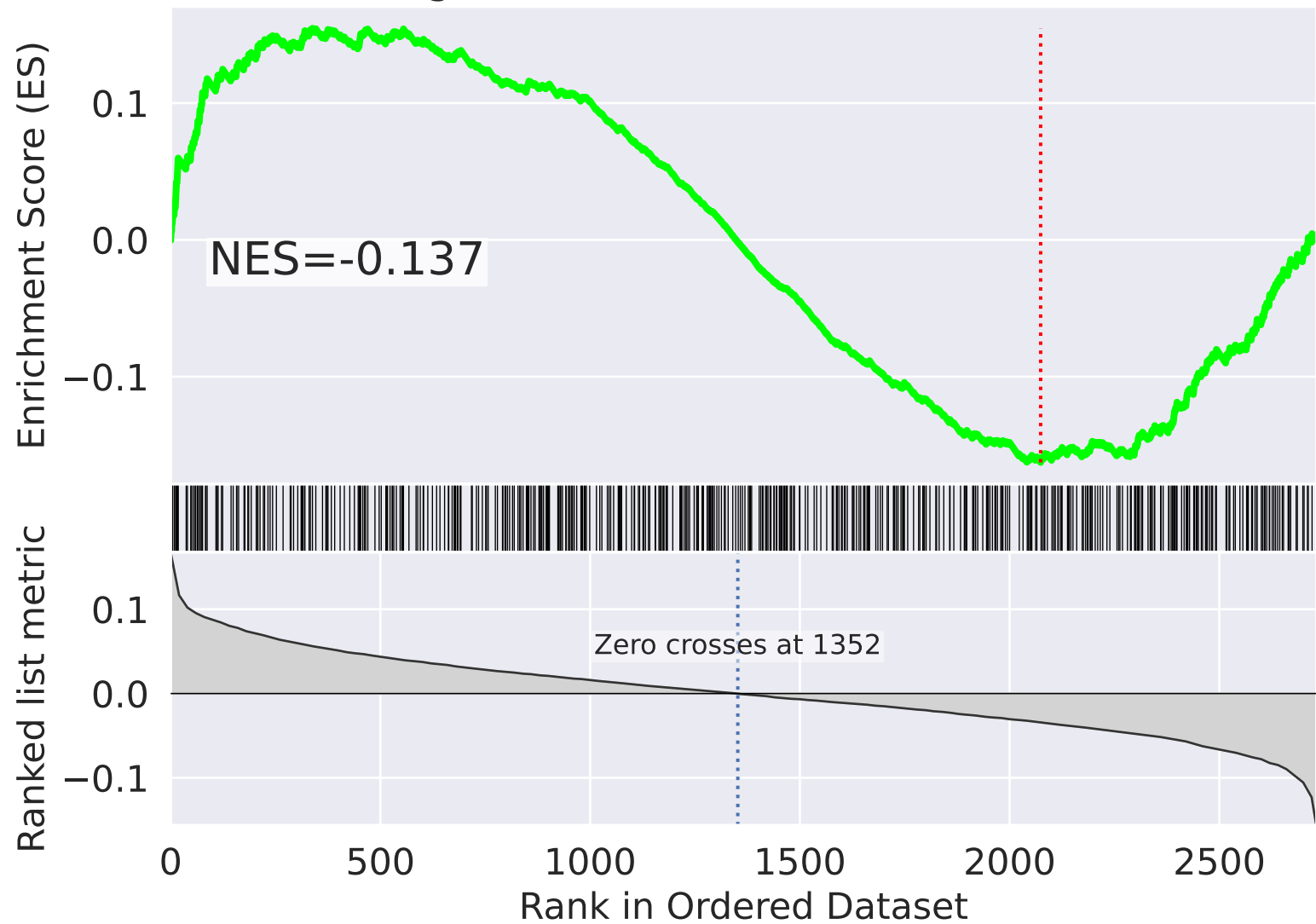
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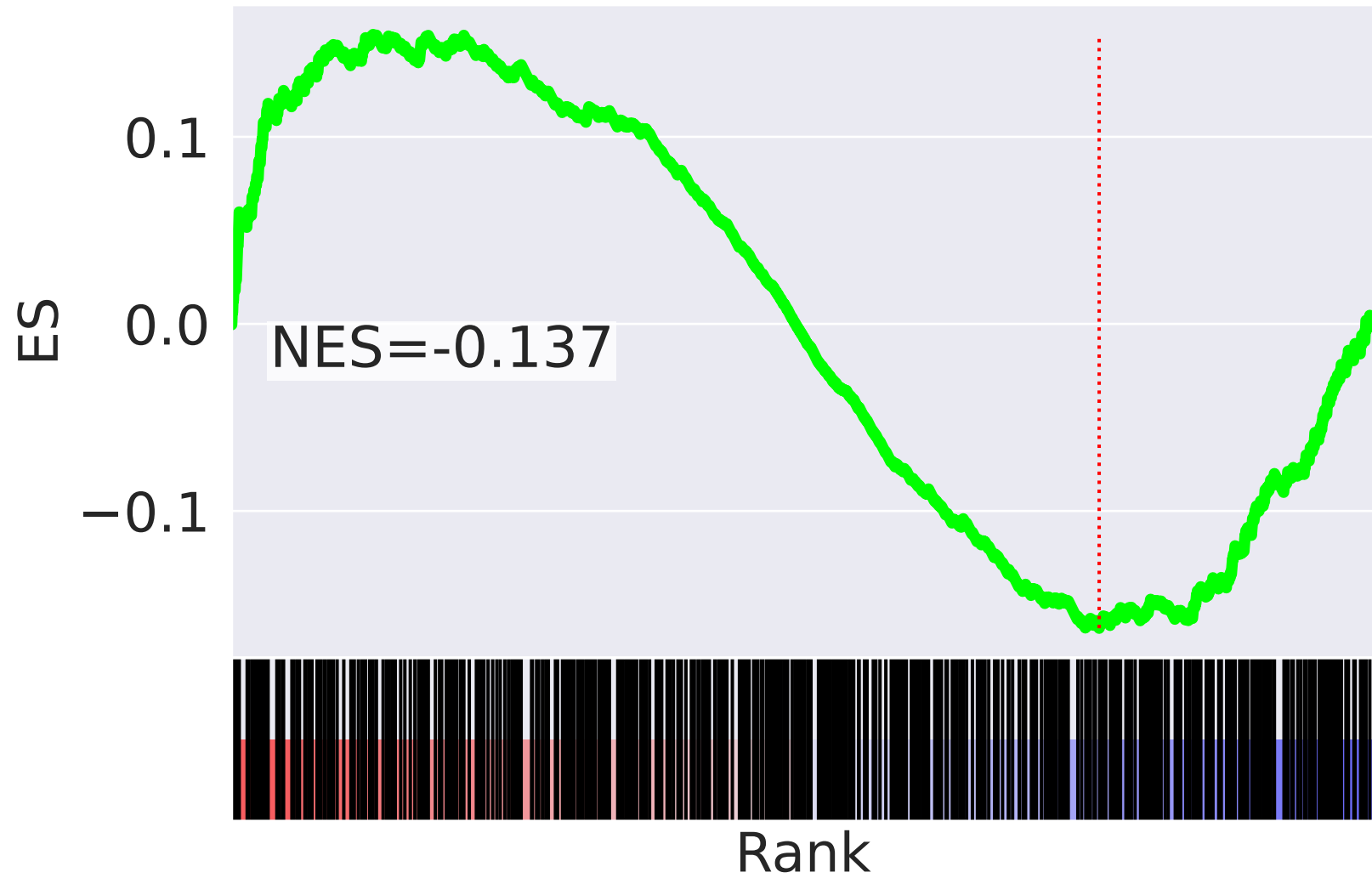
-5.625		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-5.489		rRNA Processing R-HSA-72312
-5.074		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.223		Separation Of Sister Chromatids R-HSA-2467813
4.060		Signaling By FGFR In Disease R-HSA-1226099
3.850		mRNA Splicing - Major Pathway R-HSA-72163
3.761		mRNA Splicing R-HSA-72172
3.757		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
3.719		HIV Infection R-HSA-162906
-3.621		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
3.620		Mitotic Anaphase R-HSA-68882
3.578		Mitotic Metaphase And Anaphase R-HSA-2555396
3.547		Pausing And Recovery Of Tat-mediated HIV Elongation R-HSA-167238
3.514		HIV Elongation Arrest And Recovery R-HSA-167287
3.510		Mitotic G2-G2/M Phases R-HSA-453274

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



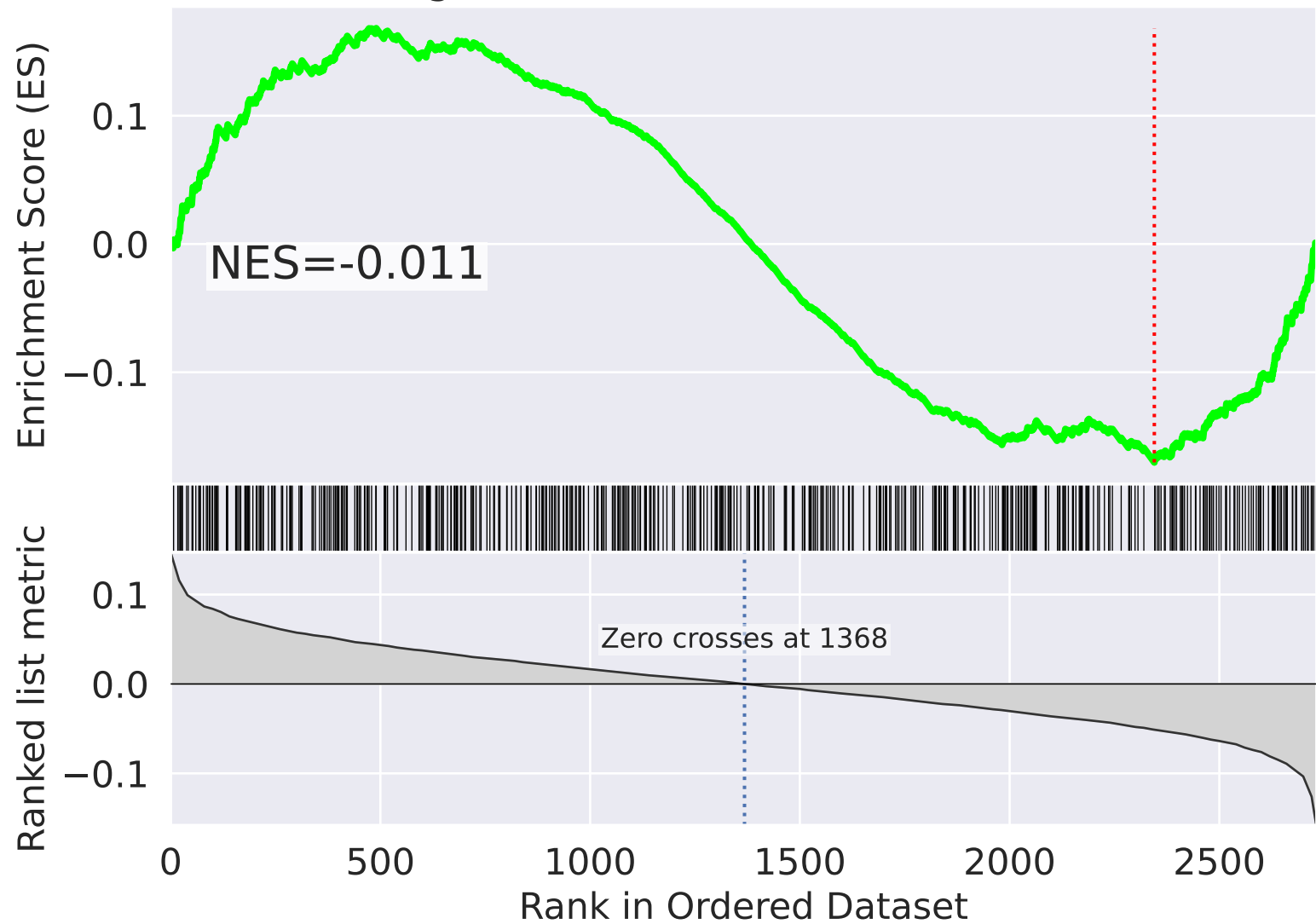
Signal Transduction R-HSA-162582



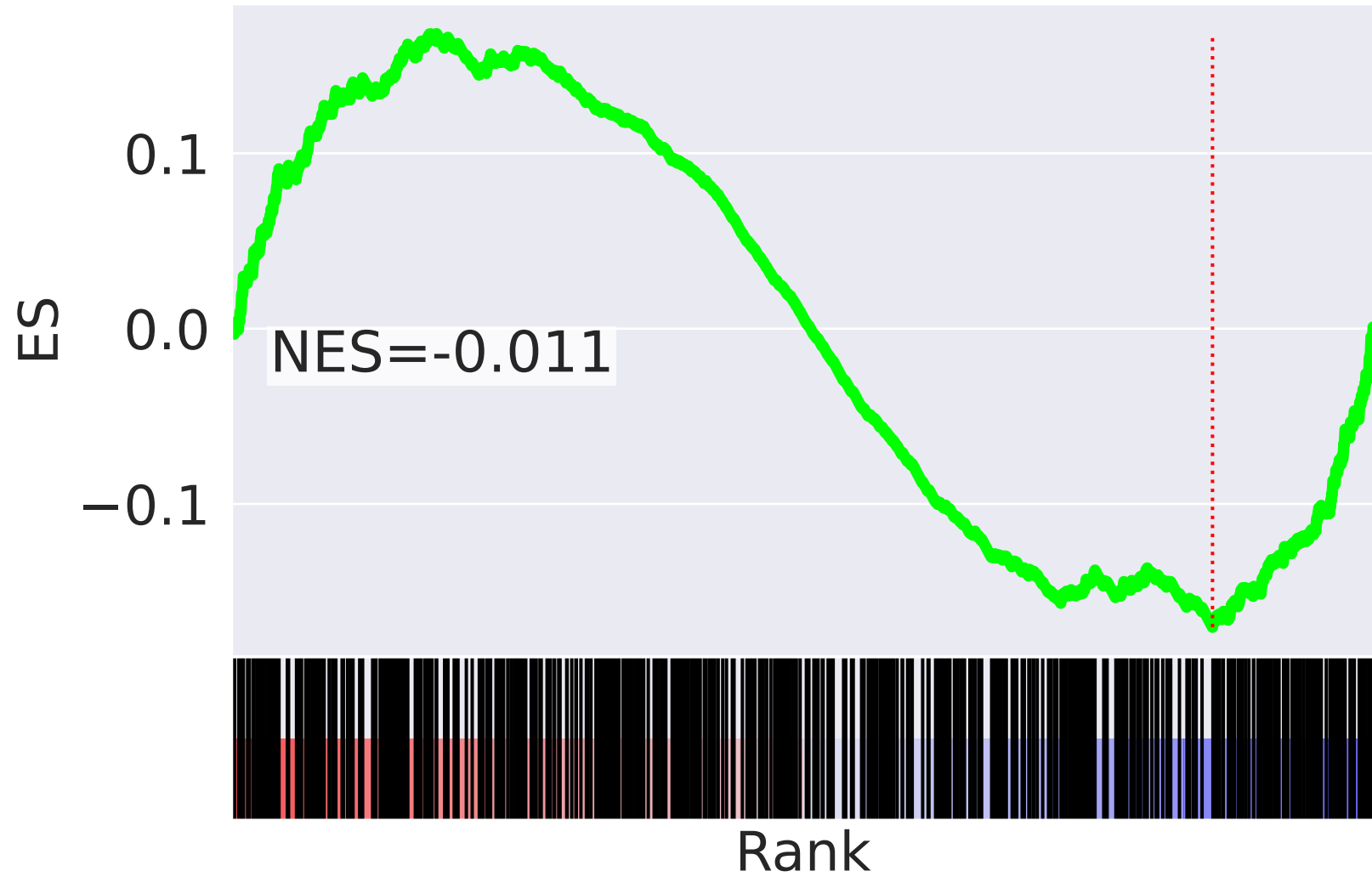
NES		SET
5.904		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.723		Respiratory Electron Transport R-HSA-611105
5.488		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.733		Complex I Biogenesis R-HSA-6799198
4.304		Translation R-HSA-72766
3.687		Mitochondrial tRNA Aminoacylation R-HSA-379726
-3.322		SUMO E3 Ligases SUMOylate Target Proteins R-HSA-3108232
3.308		tRNA Aminoacylation R-HSA-379724
-3.256		COPI-dependent Golgi-to-ER Retrograde Traffic R-HSA-6811434
-3.133		Mitotic Metaphase And Anaphase R-HSA-2555396
-2.971		SUMOylation R-HSA-2990846
-2.956		Mitotic Anaphase R-HSA-68882
-2.944		M Phase R-HSA-68886
-2.878		Mitotic Prophase R-HSA-68875
-2.876		Nuclear Envelope Breakdown R-HSA-2980766

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


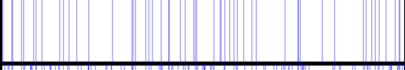
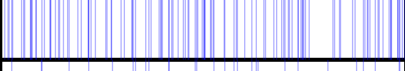
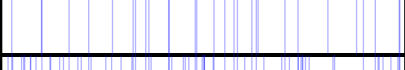
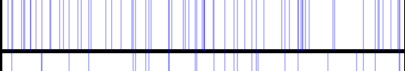

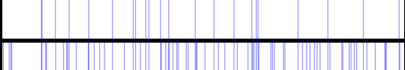
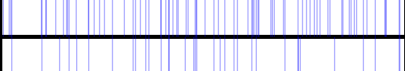
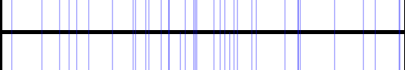
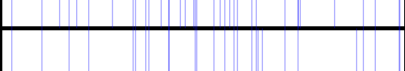



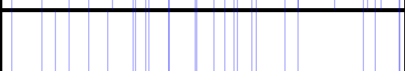



Signal Transduction R-HSA-162582



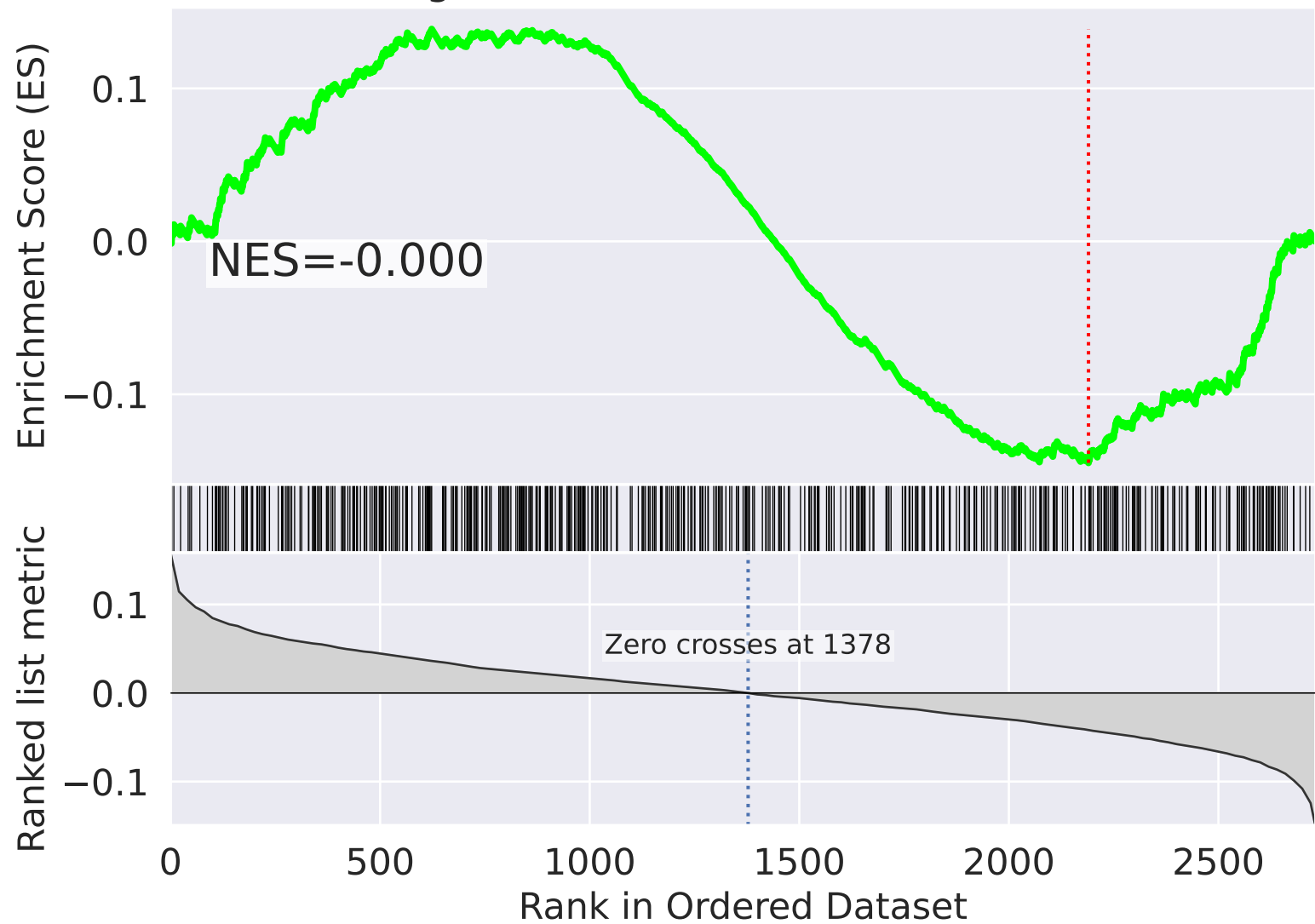
NES

SET

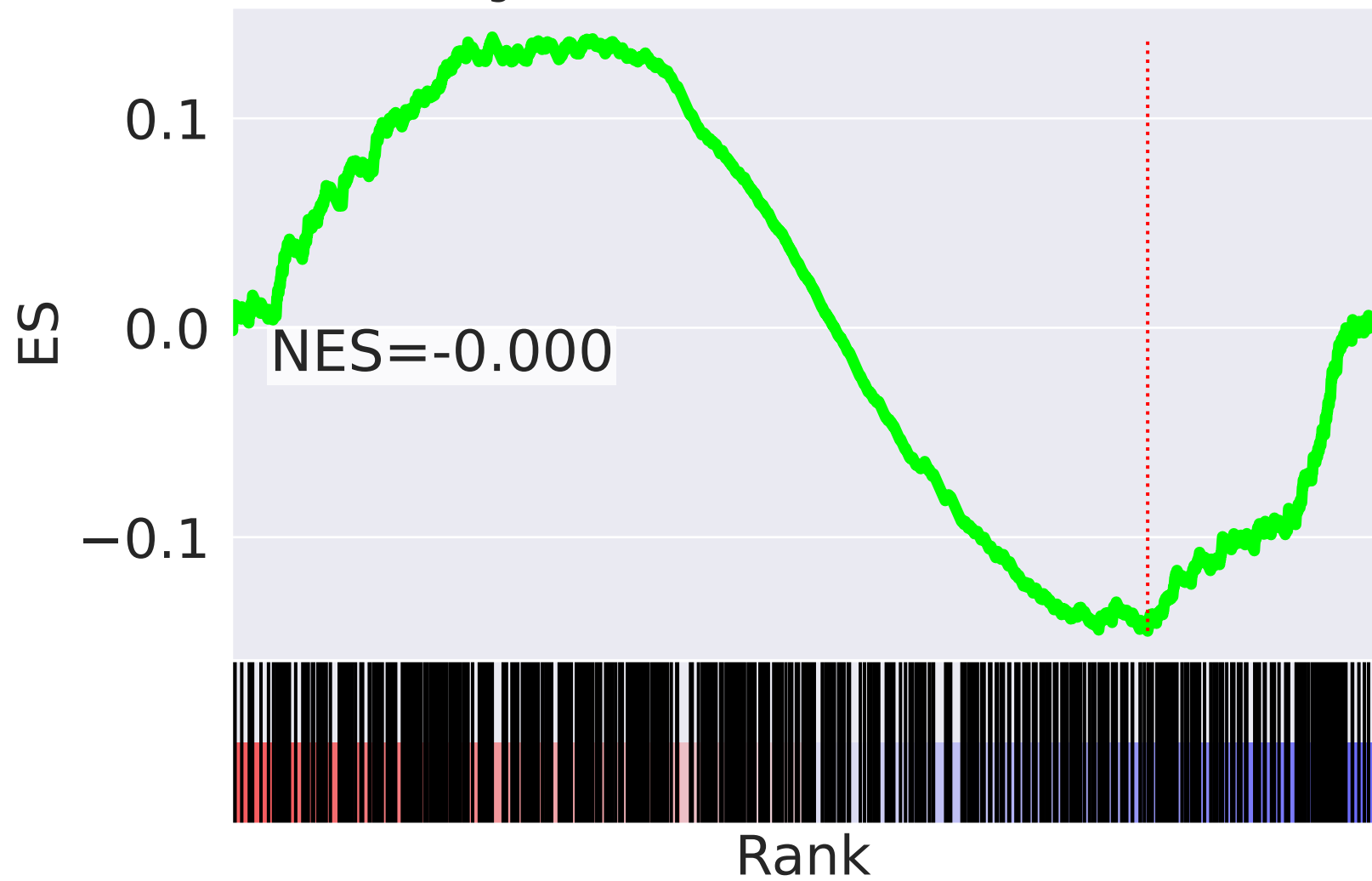
-3.852		SARS-CoV-2 Infection R-HSA-9694516
-3.787		Interferon Signaling R-HSA-913531
-3.716		SARS-CoV Infections R-HSA-9679506
-3.646		Interactions Of Rev With Host Cellular Proteins R-HSA-177243
-3.595		SARS-CoV-2-host Interactions R-HSA-9705683
-3.589		Rev-mediated Nuclear Export Of HIV RNA R-HSA-165054
-3.480		Postmitotic Nuclear Pore Complex (NPC) Reformation R-HSA-9615933
-3.413		Host Interactions Of HIV Factors R-HSA-162909
-3.371		ISG15 Antiviral Mechanism R-HSA-1169408
-3.304		Antiviral Mechanism By IFN-stimulated Genes R-HSA-1169410
-3.278		Export Of Viral Ribonucleoproteins From Nucleus R-HSA-168274
-3.278		NEP/NS2 Interacts With Cellular Export Machinery R-HSA-168333
-3.172		Nuclear Pore Complex (NPC) Disassembly R-HSA-3301854
-3.158		NS1 Mediated Effects On Host Pathways R-HSA-168276
-3.139		SUMOylation Of SUMOylation Proteins R-HSA-4085377

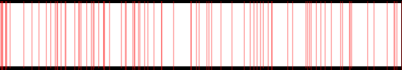
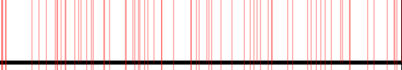
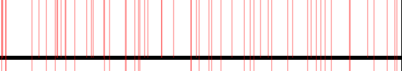
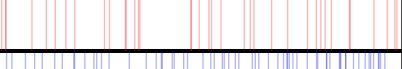
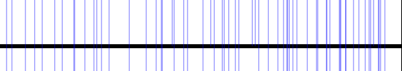
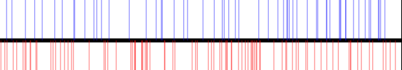
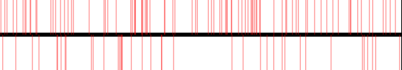

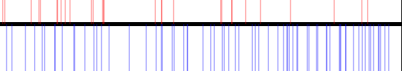
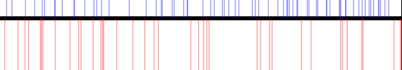
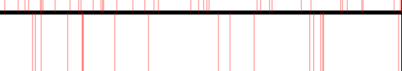
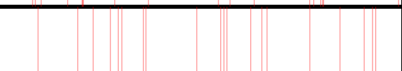

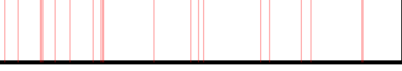

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=46$

Signal Transduction R-HSA-162582



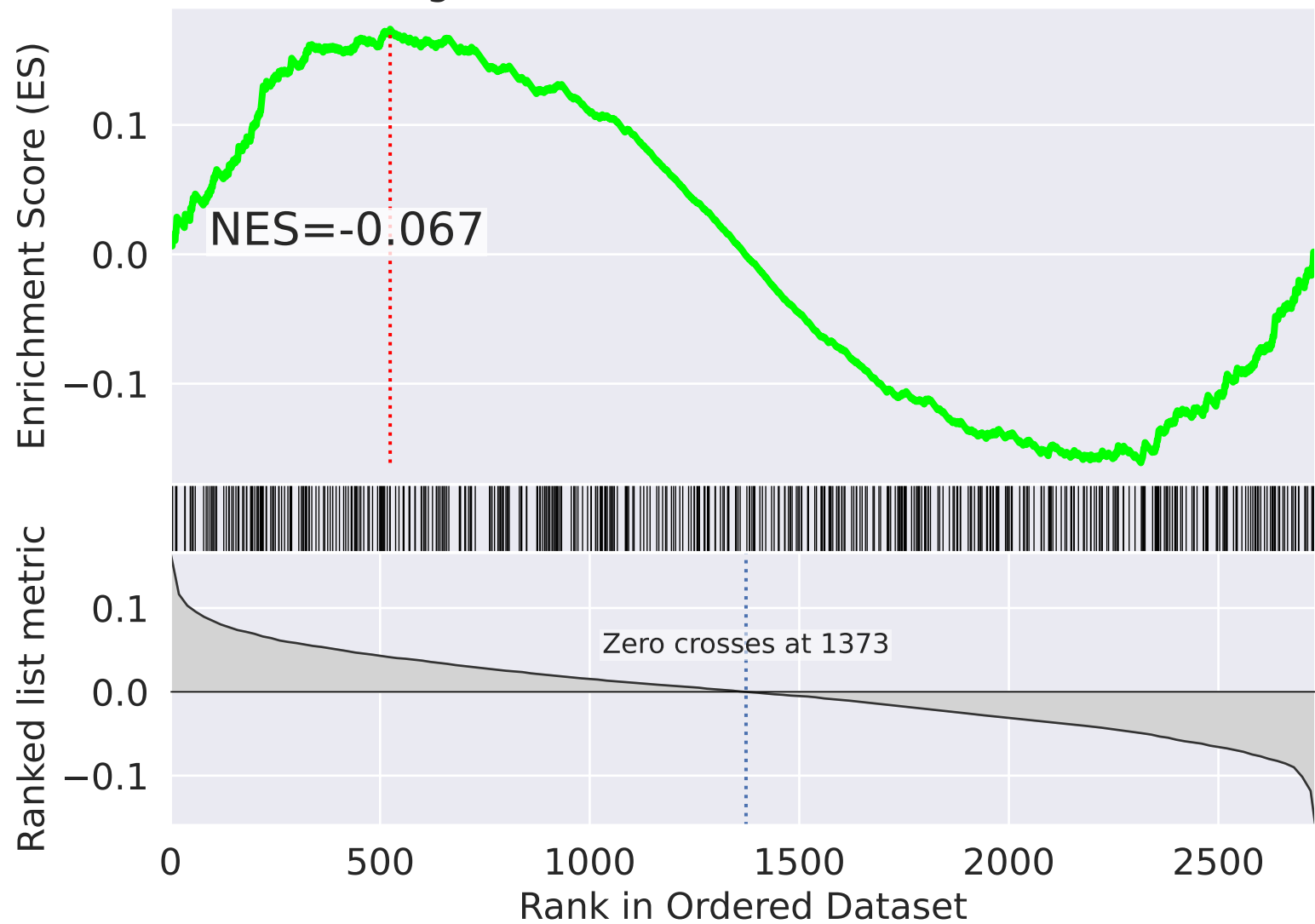
Signal Transduction R-HSA-162582



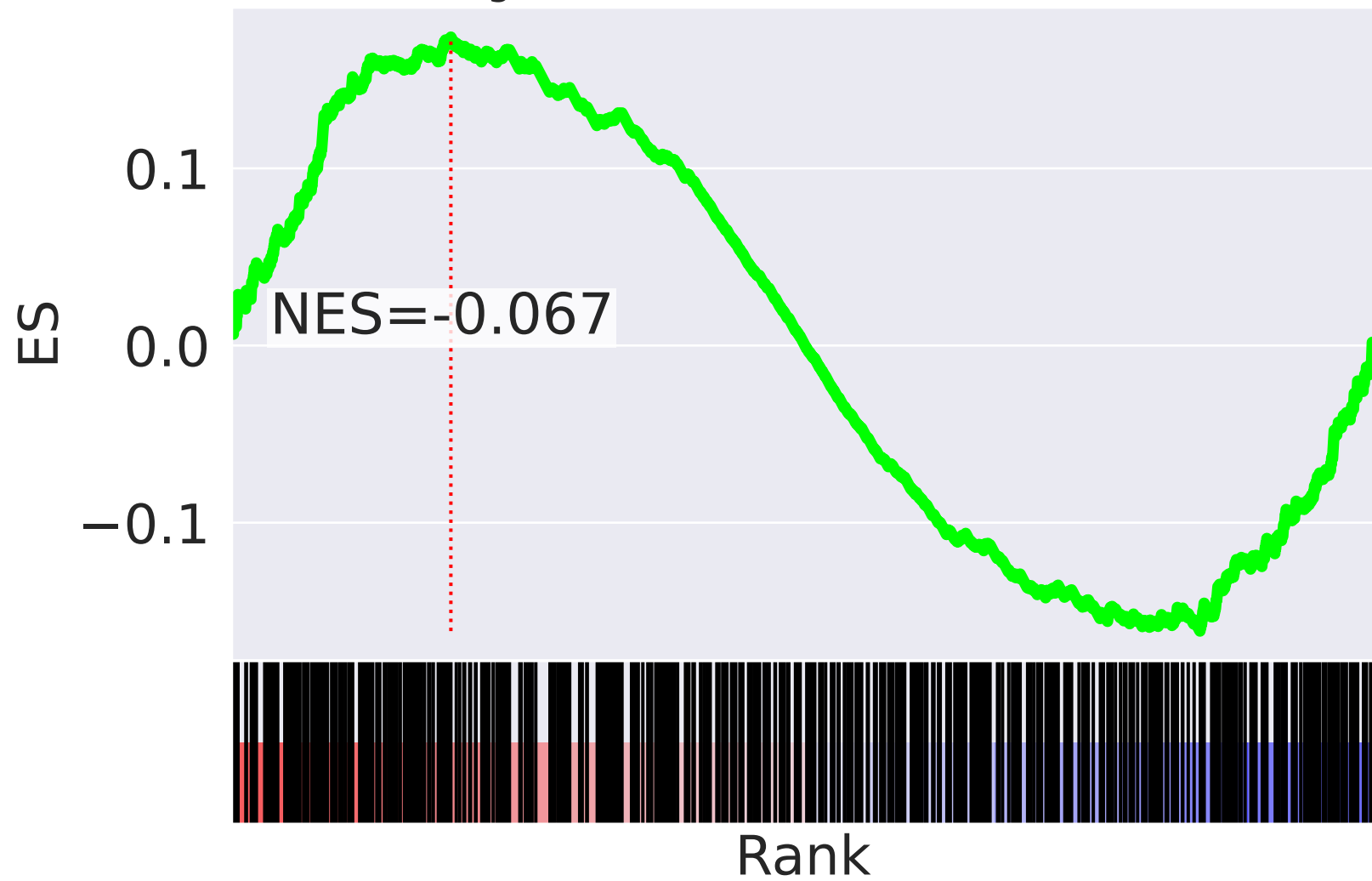
NES		SET
6.965		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.878		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.472		Respiratory Electron Transport R-HSA-611105
5.179		Complex I Biogenesis R-HSA-6799198
-4.141		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.923		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.407		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.399		TP53 Regulates Metabolic Genes R-HSA-5628897
3.343		Cytoprotection By HMOX1 R-HSA-9707564
-3.036		rRNA Processing R-HSA-72312
3.023		Mitochondrial Biogenesis R-HSA-1592230
2.965		Mitochondrial tRNA Aminoacylation R-HSA-379726
2.958		Intrinsic Pathway For Apoptosis R-HSA-109606
-2.936		DNA Damage Bypass R-HSA-73893
2.921		Transcriptional Activation Of Mitochondrial Biogenesis R-HSA-2151201

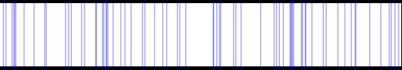
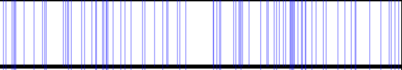
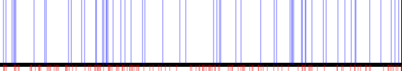
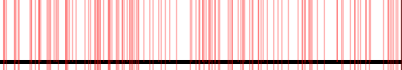
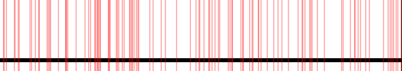
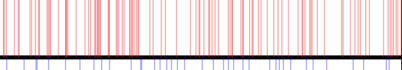
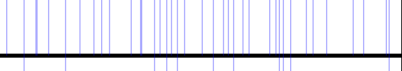
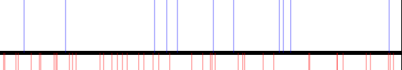
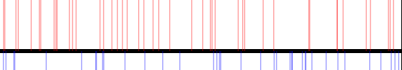
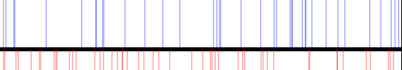
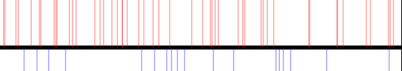
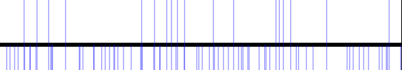
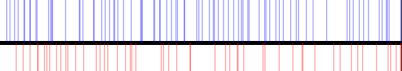
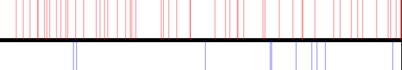

The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=47$

Signal Transduction R-HSA-162582



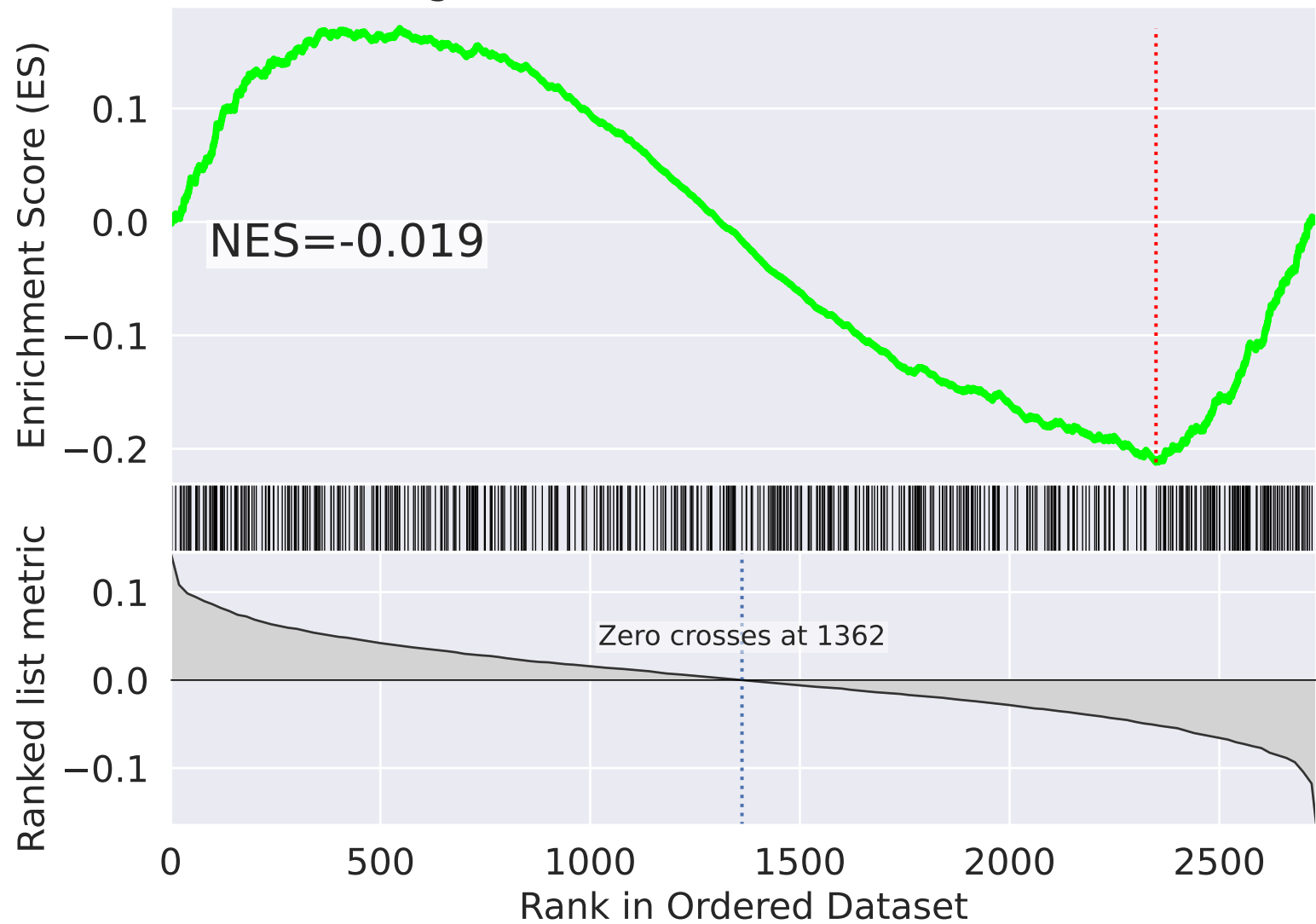
Signal Transduction R-HSA-162582



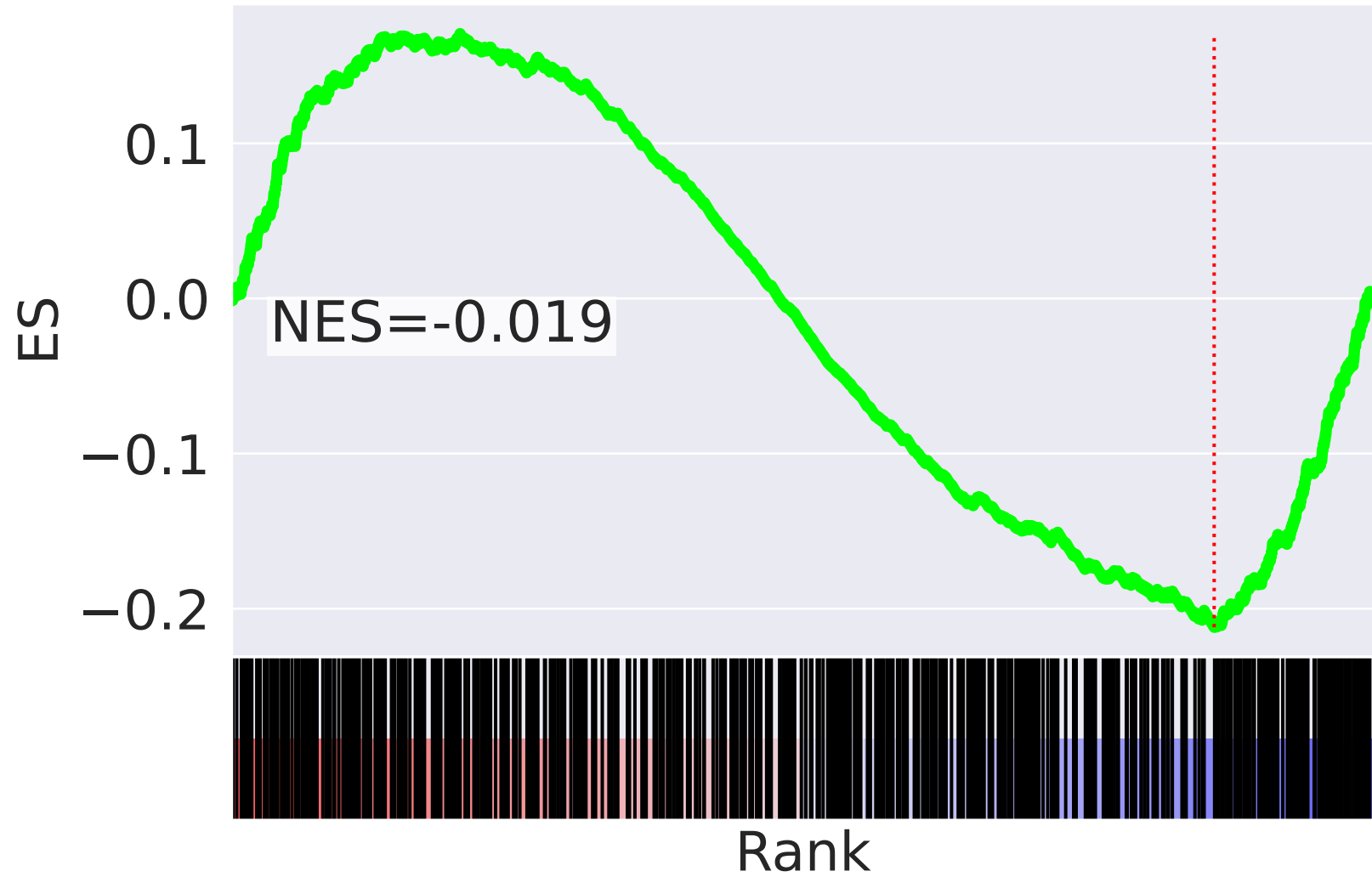
NES		SET
-5.088		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-4.541		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.793		Respiratory Electron Transport R-HSA-611105
3.501		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
3.397		mRNA Splicing R-HSA-72172
3.279		mRNA Splicing - Major Pathway R-HSA-72163
-3.055		Mitochondrial Biogenesis R-HSA-1592230
-2.937		Formation Of ATP By Chemiosmotic Coupling R-HSA-163210
2.867		Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
-2.819		Complex I Biogenesis R-HSA-6799198
2.794		Transport Of Mature Transcript To Cytoplasm R-HSA-72202
-2.768		Cristae Formation R-HSA-8949613
-2.646		Organelle Biogenesis And Maintenance R-HSA-1852241
2.645		RNA Polymerase II Transcribes snRNA Genes R-HSA-6807505
-2.623		Mitochondrial Translation R-HSA-5368287

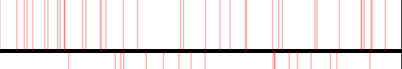
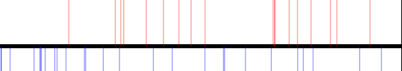

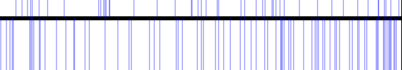
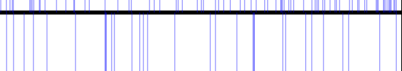
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension $z=48$

Signal Transduction R-HSA-162582



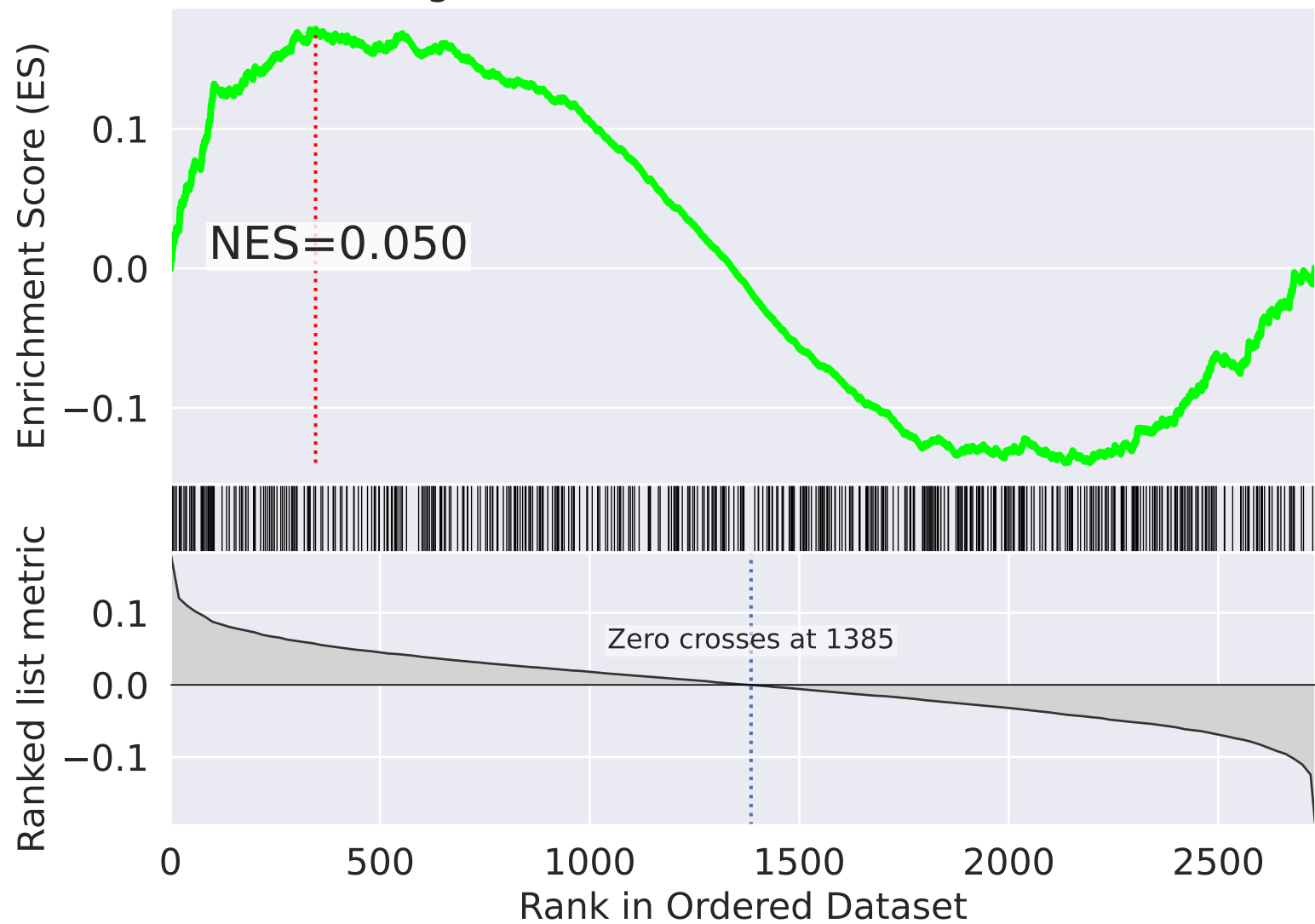
Signal Transduction R-HSA-162582



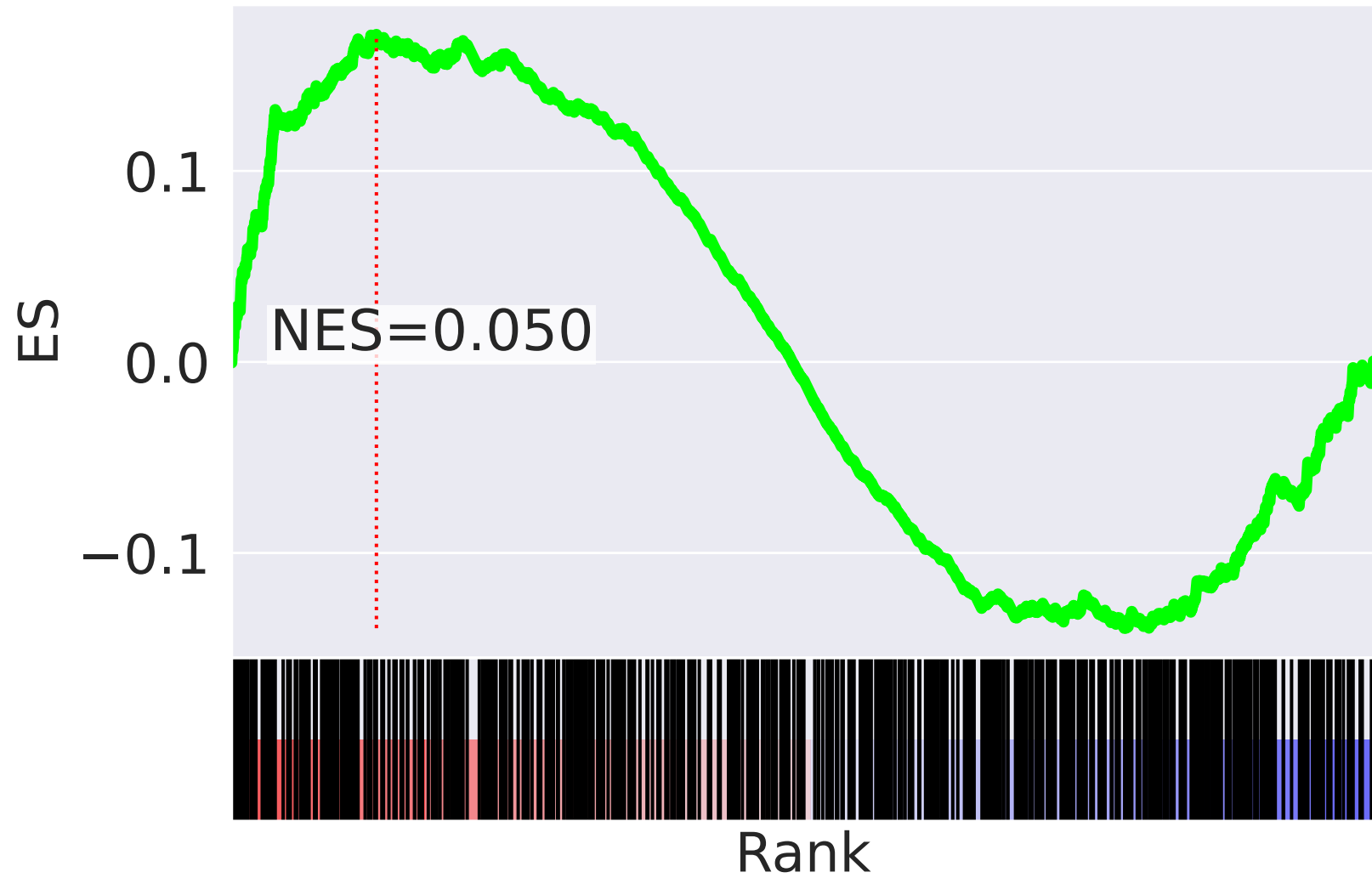
NES		SET
5.124		Respiratory Electron Transport R-HSA-611105
4.801		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.618		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.211		Complex I Biogenesis R-HSA-6799198
3.506		Mitochondrial tRNA Aminoacylation R-HSA-379726
-3.340		Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
-3.321		Signaling By NOTCH1 R-HSA-1980143
-3.315		Constitutive Signaling By NOTCH1 HD+PEST Domain Mutants R-HSA-2894862
-3.240		SMAD2/SMAD3:SMAD4 Heterotrimer Regulates Transcription R-HSA-2173796
-3.191		Transcriptional Regulation Of White Adipocyte Differentiation R-HSA-381340
-3.188		Signaling By NOTCH R-HSA-157118
-3.155		Formation Of TC-NER Pre-Incision Complex R-HSA-6781823
-3.124		PPARA Activates Gene Expression R-HSA-1989781
3.050		Base Excision Repair R-HSA-73884
3.020		Glycosaminoglycan Metabolism R-HSA-1630316

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



NES

SET

4.859		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
4.688		mRNA Splicing - Major Pathway R-HSA-72163
4.561		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
4.399		mRNA Splicing R-HSA-72172
4.139		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
3.988		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
3.952		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
3.839		Adaptive Immune System R-HSA-1280218
3.832		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
3.816		Cytokine Signaling In Immune System R-HSA-1280215
3.573		Vif-mediated Degradation Of APOBEC3G R-HSA-180585
3.552		SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113
3.522		ABC-family Proteins Mediated Transport R-HSA-382556
3.463		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
3.461		p53-Dependent G1 DNA Damage Response R-HSA-69563