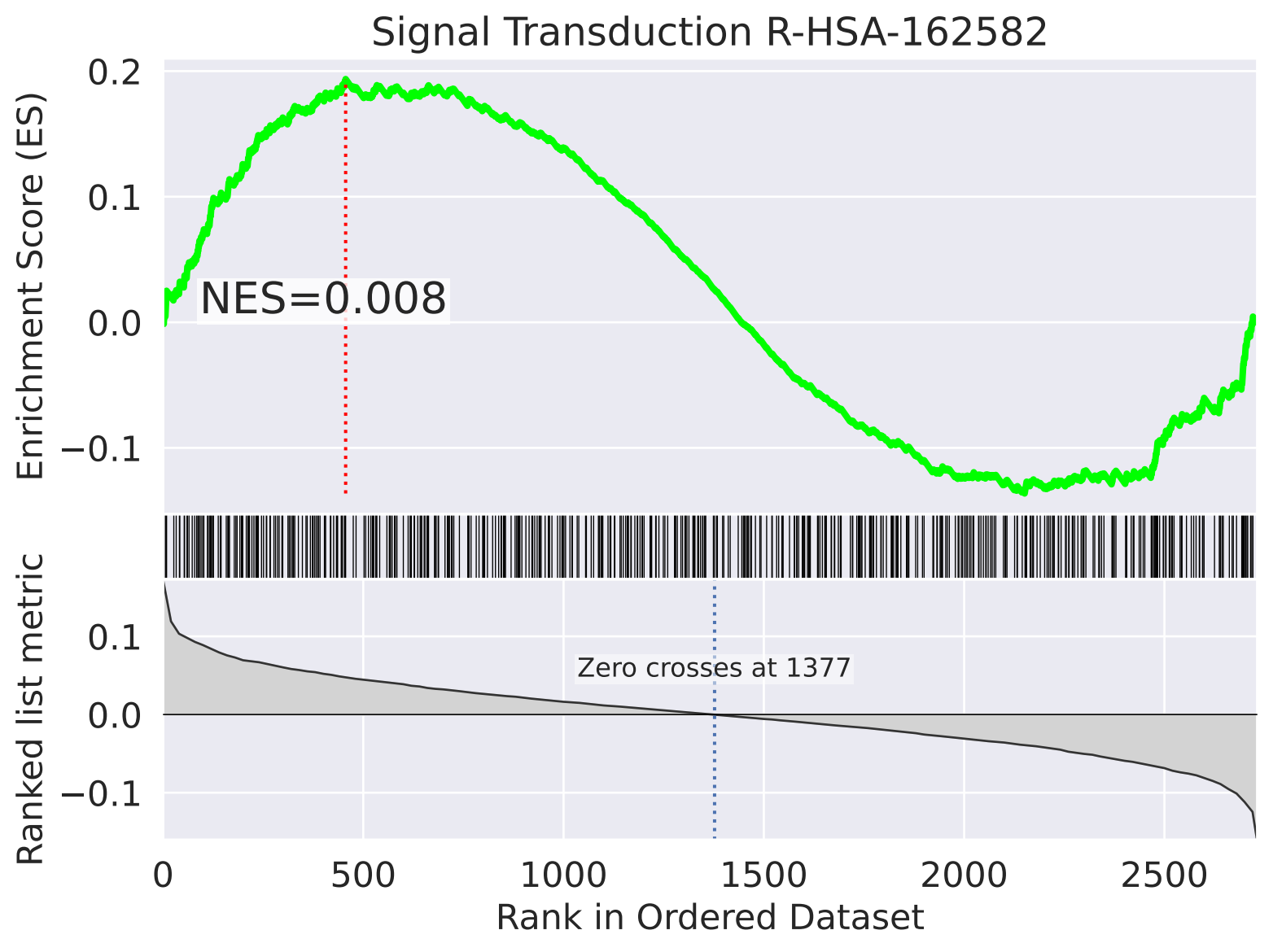
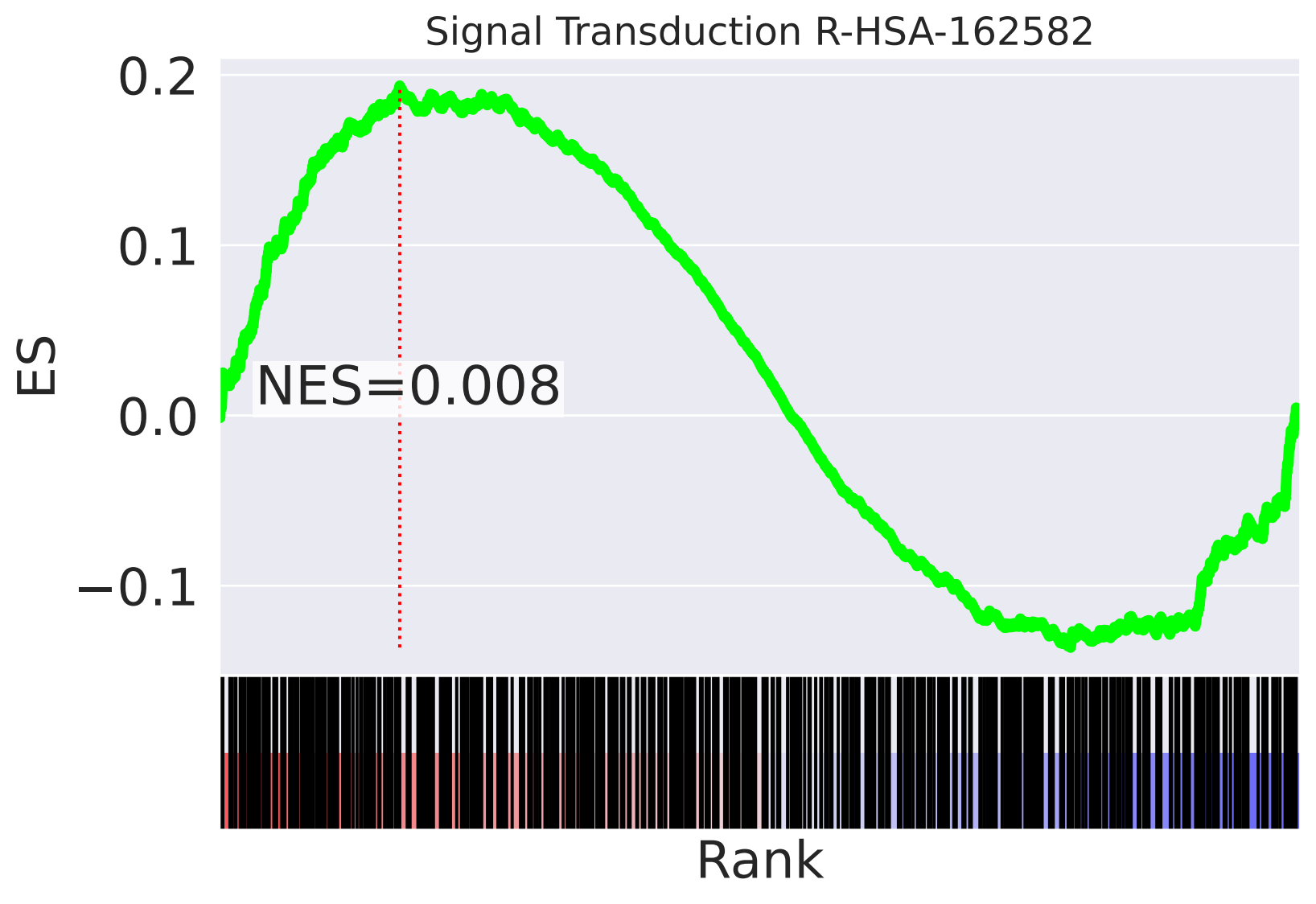
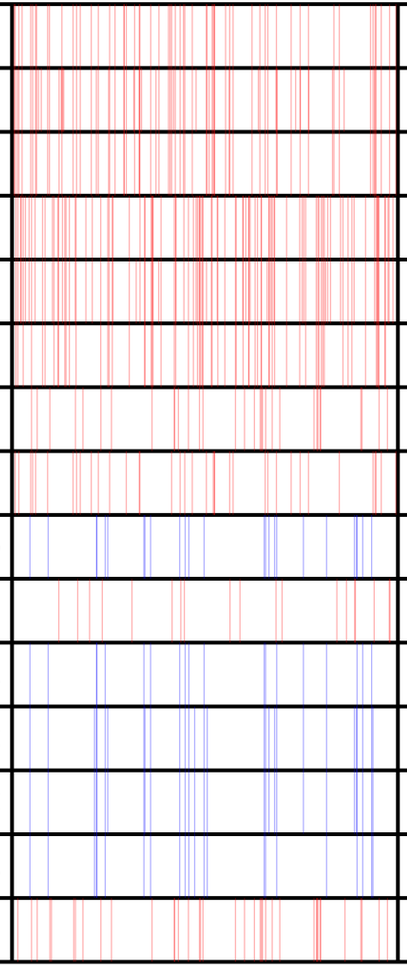
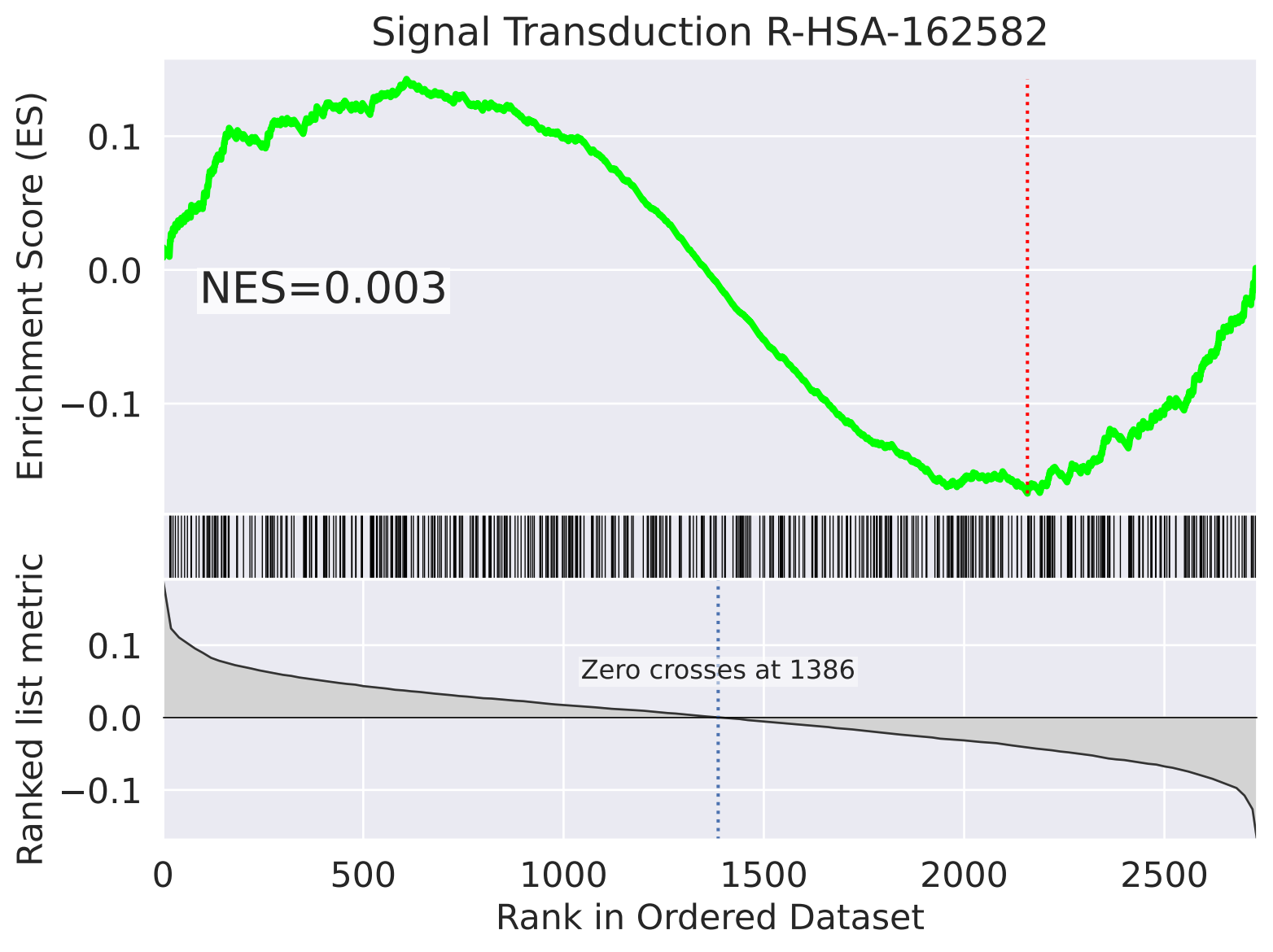
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=1

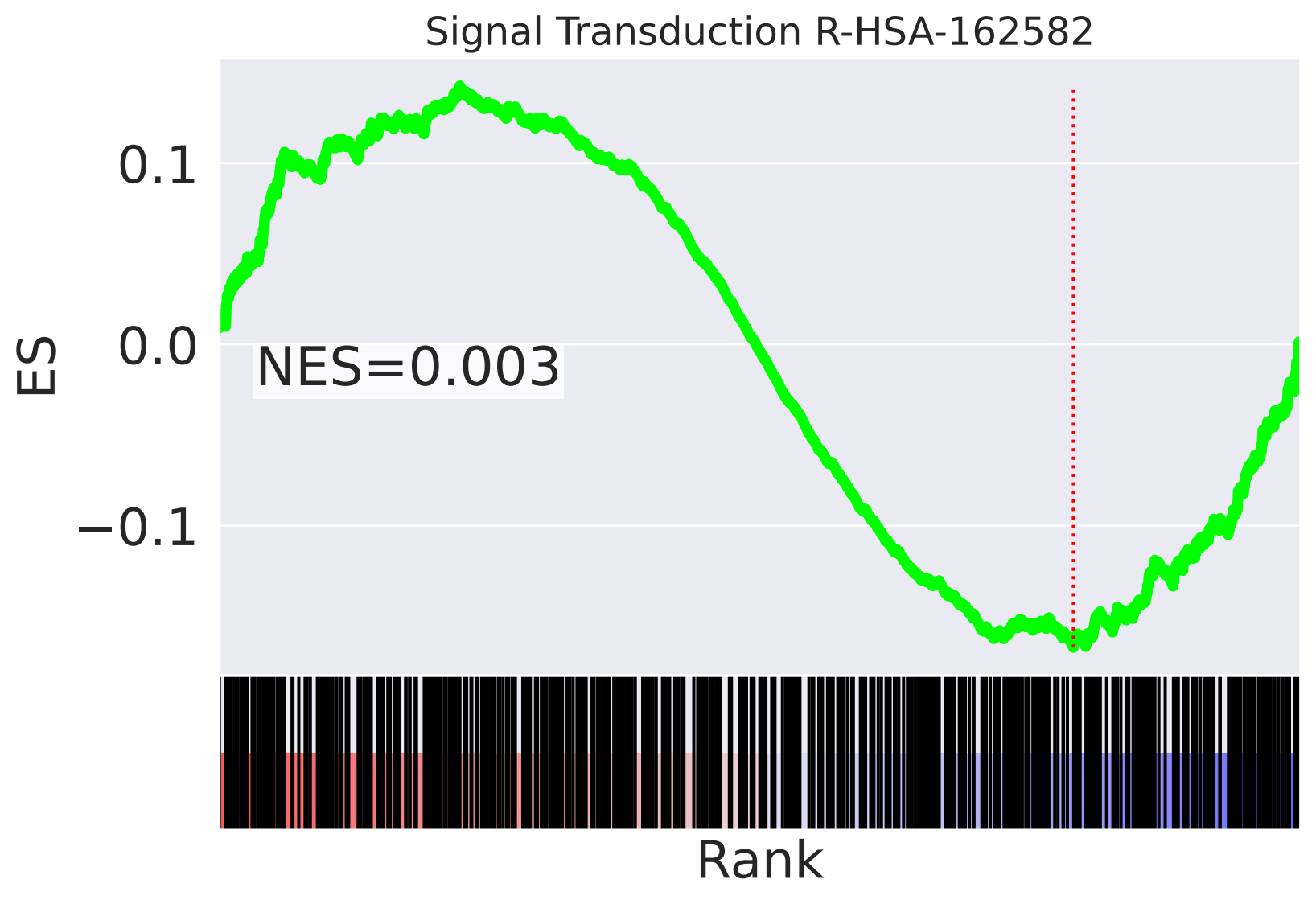

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=0.008
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1377
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

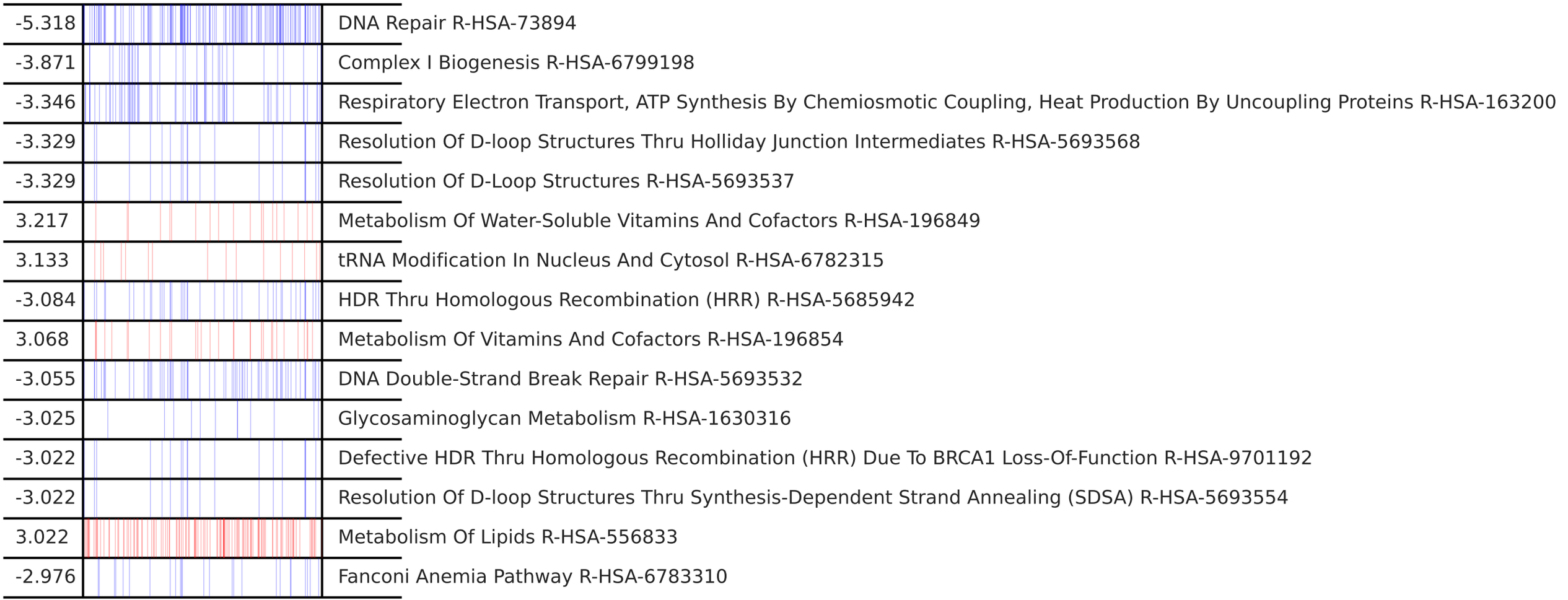

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=0.008
Rank

NES		SET
4.635		Respiratory Electron Transport R-HSA-611105
4.506		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.163		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.111		PIP3 Activates AKT Signaling R-HSA-1257604
4.025		Intracellular Signaling By Second Messengers R-HSA-9006925
3.884		PTEN Regulation R-HSA-6807070
3.855		Amino Acids Regulate mTORC1 R-HSA-9639288
3.851		Complex I Biogenesis R-HSA-6799198
-3.685		RNA Polymerase I Transcription Initiation R-HSA-73762
3.588		Retrograde Transport At Trans-Golgi-Network R-HSA-6811440
-3.581		RNA Polymerase I Transcription Termination R-HSA-73863
-3.552		RNA Polymerase I Transcription R-HSA-73864
-3.552		RNA Polymerase I Promoter Clearance R-HSA-73854
-3.541		RNA Polymerase I Promoter Escape R-HSA-73772
3.523		Cellular Response To Starvation R-HSA-9711097

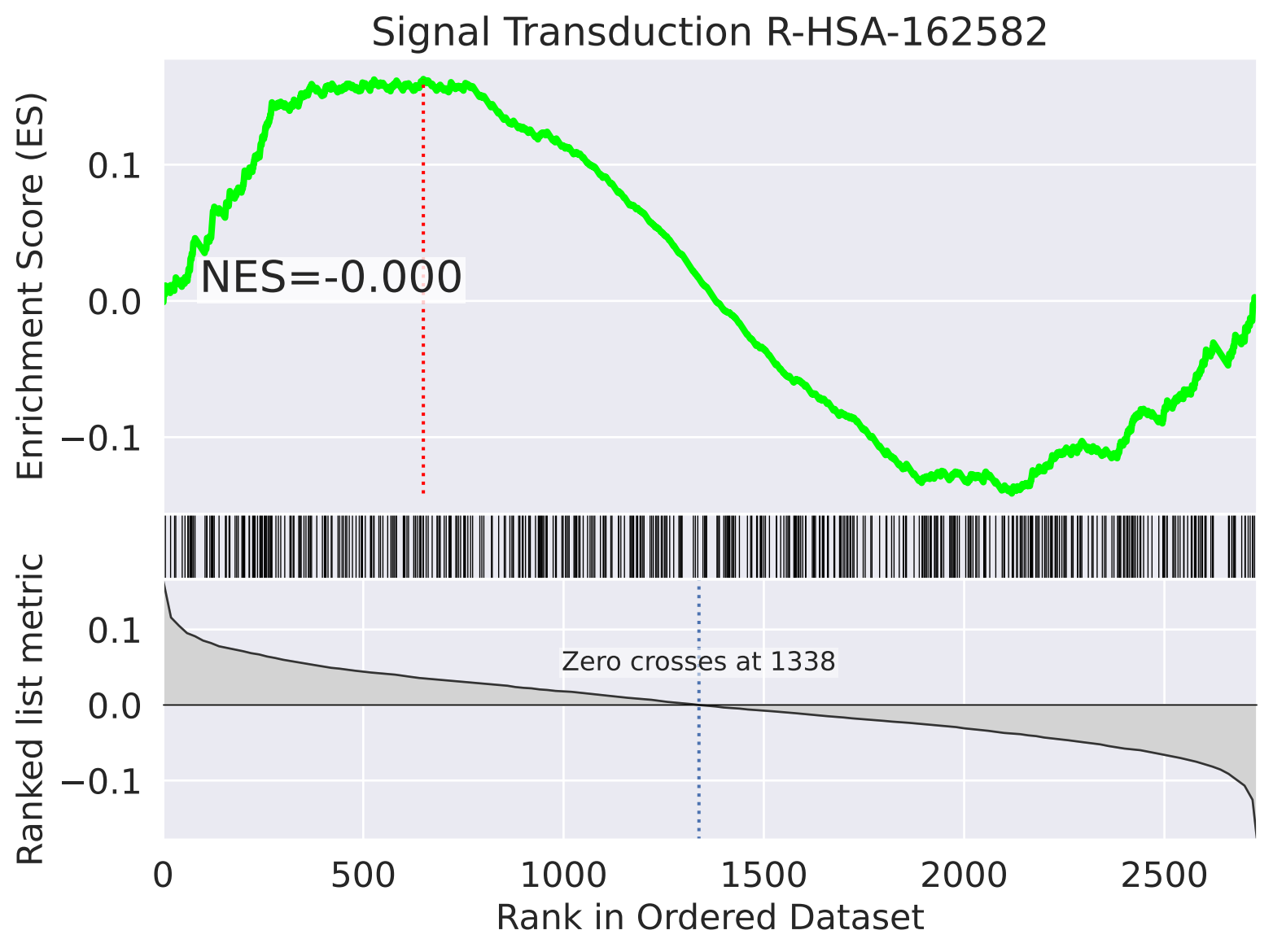
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=2

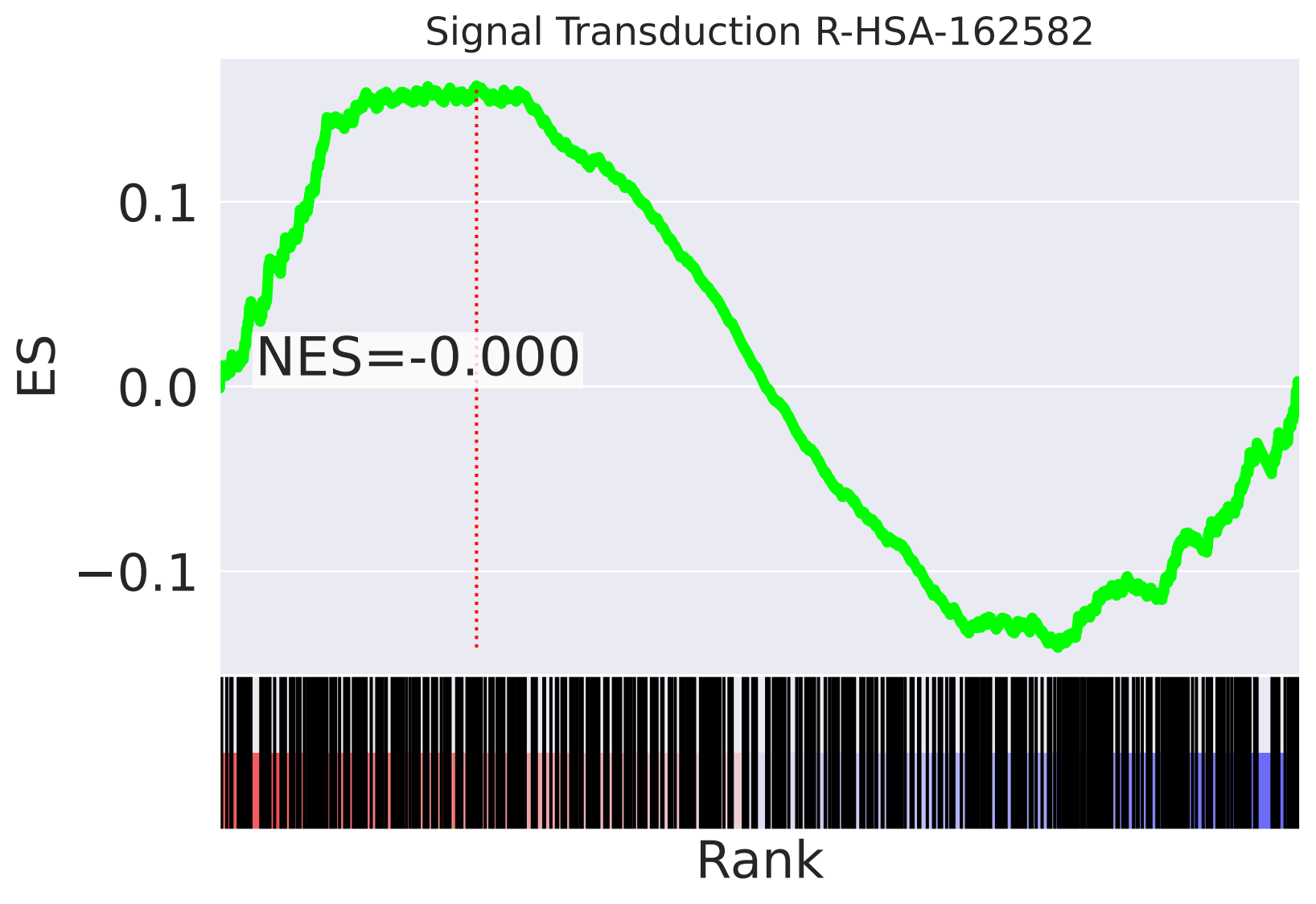

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=0.003
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1386
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

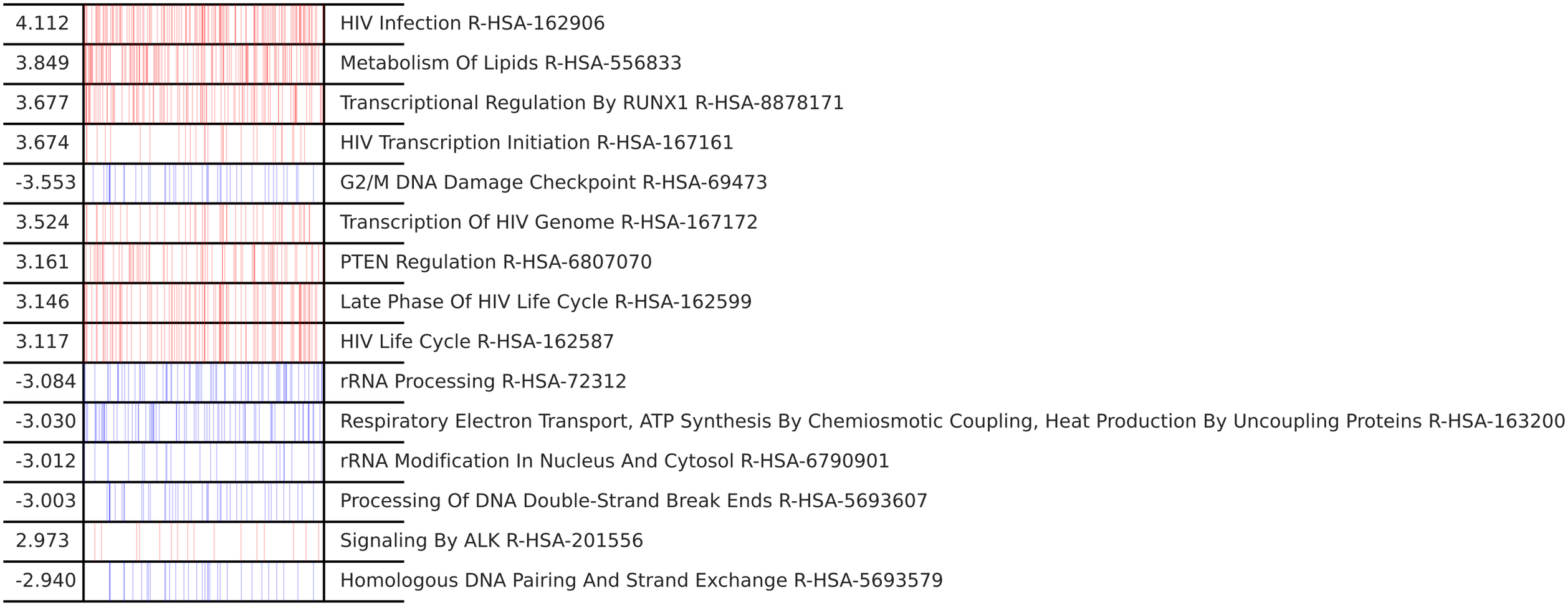

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=0.003
Rank


NES
SET
-5.318
DNA Repair R-HSA-73894
-3.871
Complex I Biogenesis R-HSA-6799198
-3.346
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.329
Resolution Of D-loop Structures Thru Holliday Junction Intermediates R-HSA-5693568
-3.329
Resolution Of D-Loop Structures R-HSA-5693537
3.217
Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.133
tRNA Modification In Nucleus And Cytosol R-HSA-6782315
-3.084
HDR Thru Homologous Recombination (HRR) R-HSA-5685942
3.068
Metabolism Of Vitamins And Cofactors R-HSA-196854
-3.055
DNA Double-Strand Break Repair R-HSA-5693532
-3.025
Glycosaminoglycan Metabolism R-HSA-1630316
-3.022
Defective HDR Thru Homologous Recombination (HRR) Due To BRCA1 Loss-Of-Function R-HSA-9701192
-3.022
Resolution Of D-loop Structures Thru Synthesis-Dependent Strand Annealing (SDSA) R-HSA-5693554
3.022
Metabolism Of Lipids R-HSA-556833
-2.976
Fanconi Anemia Pathway R-HSA-6783310

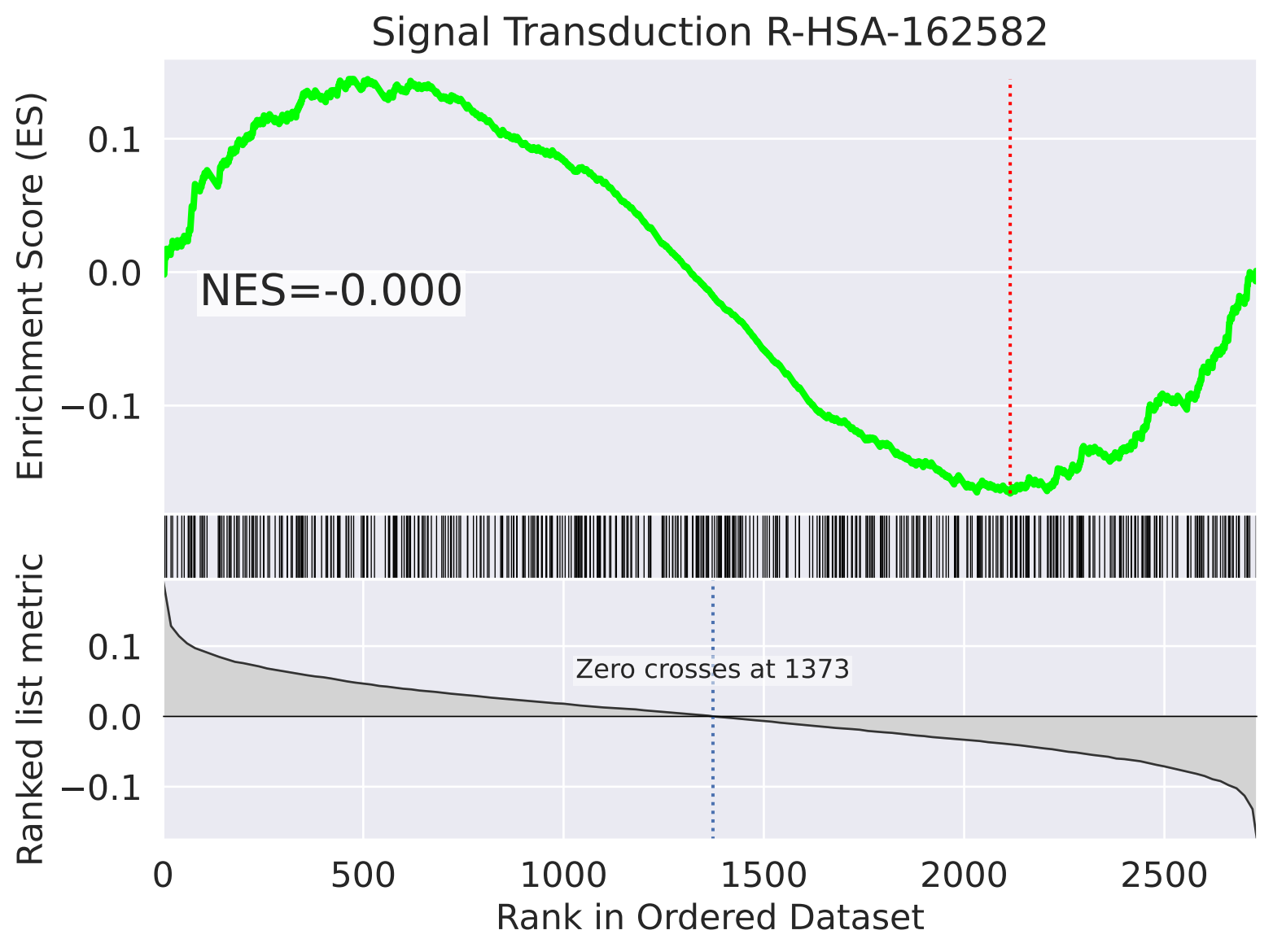
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=3

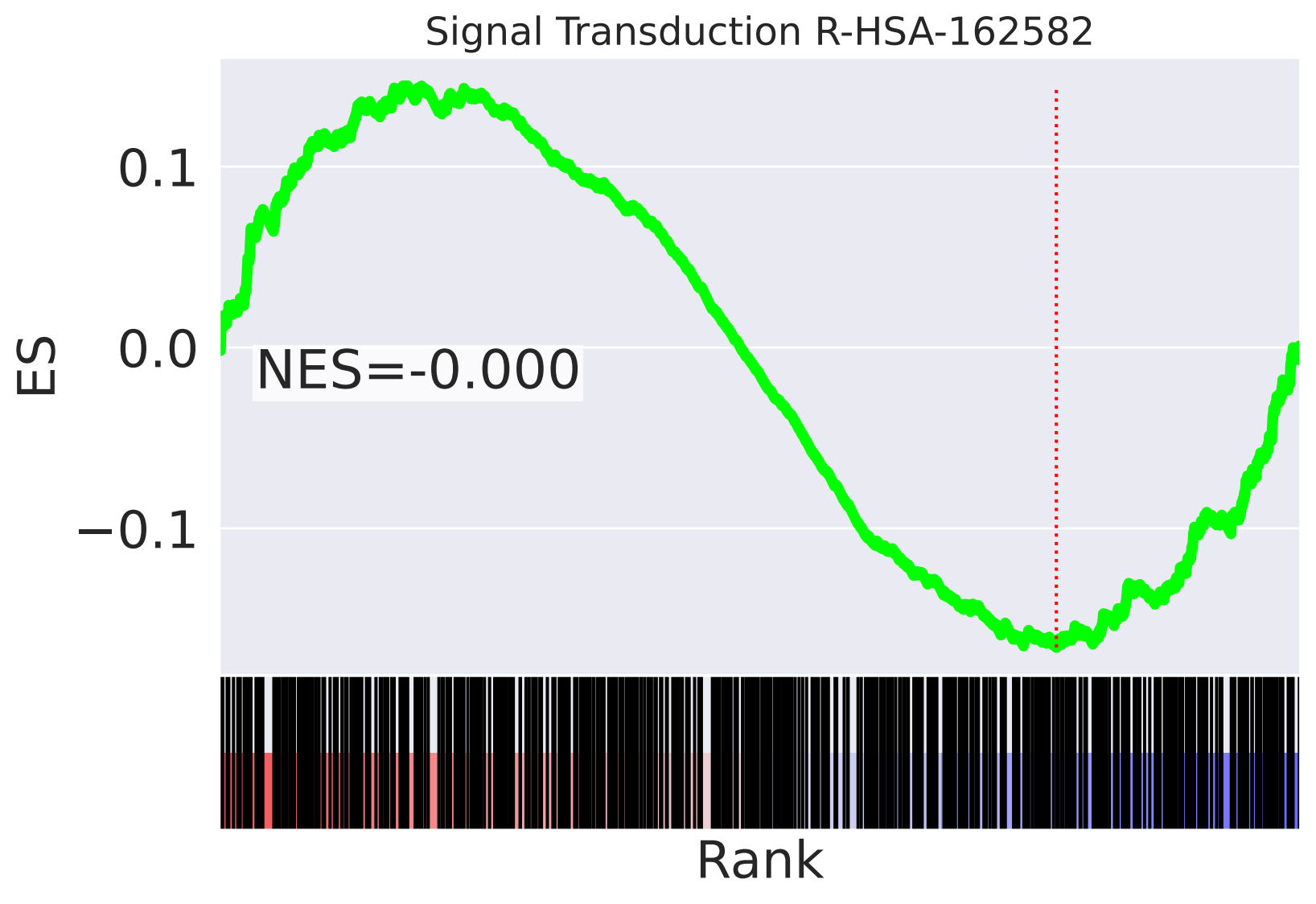

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1338
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

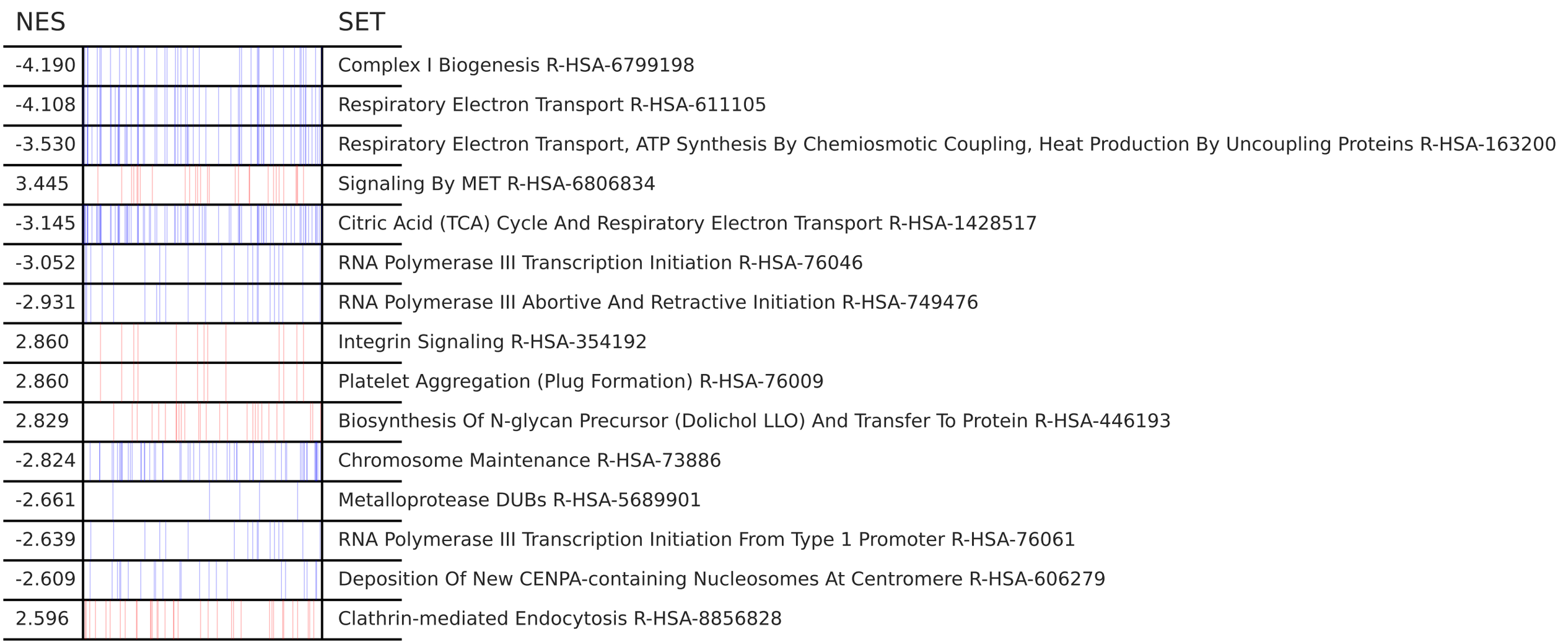

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
4.112
HIV Infection R-HSA-162906
3.849
Metabolism Of Lipids R-HSA-556833
3.677
Transcriptional Regulation By RUNX1 R-HSA-8878171
3.674
HIV Transcription Initiation R-HSA-167161
-3.553
G2/M DNA Damage Checkpoint R-HSA-69473
3.524
Transcription Of HIV Genome R-HSA-167172
3.161
PTEN Regulation R-HSA-6807070
3.146
Late Phase Of HIV Life Cycle R-HSA-162599
3.117
HIV Life Cycle R-HSA-162587
-3.084
rRNA Processing R-HSA-72312
-3.030
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-3.012
rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-3.003
Processing Of DNA Double-Strand Break Ends R-HSA-5693607
2.973
Signaling By ALK R-HSA-201556
-2.940
Homologous DNA Pairing And Strand Exchange R-HSA-5693579

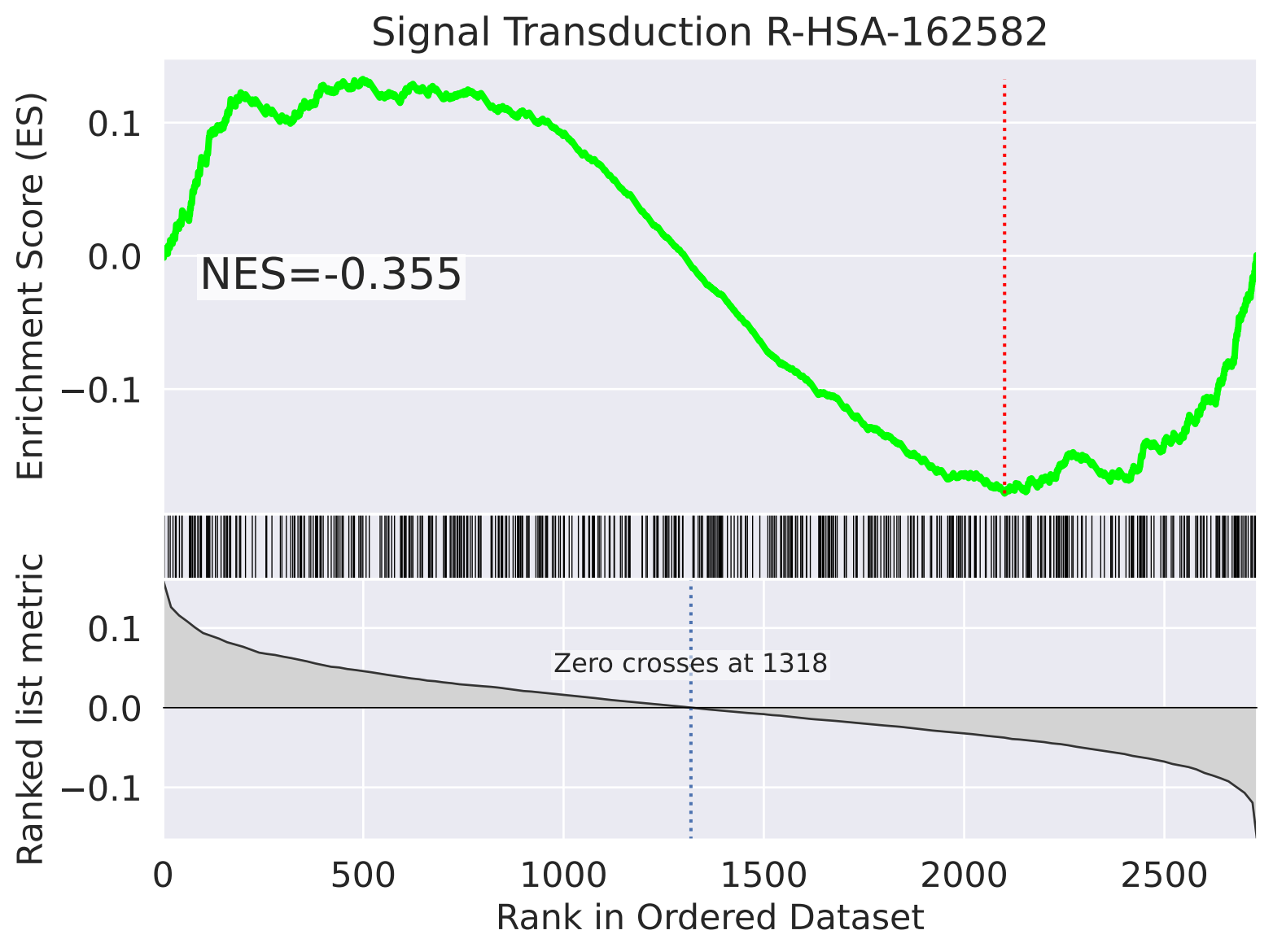
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=4

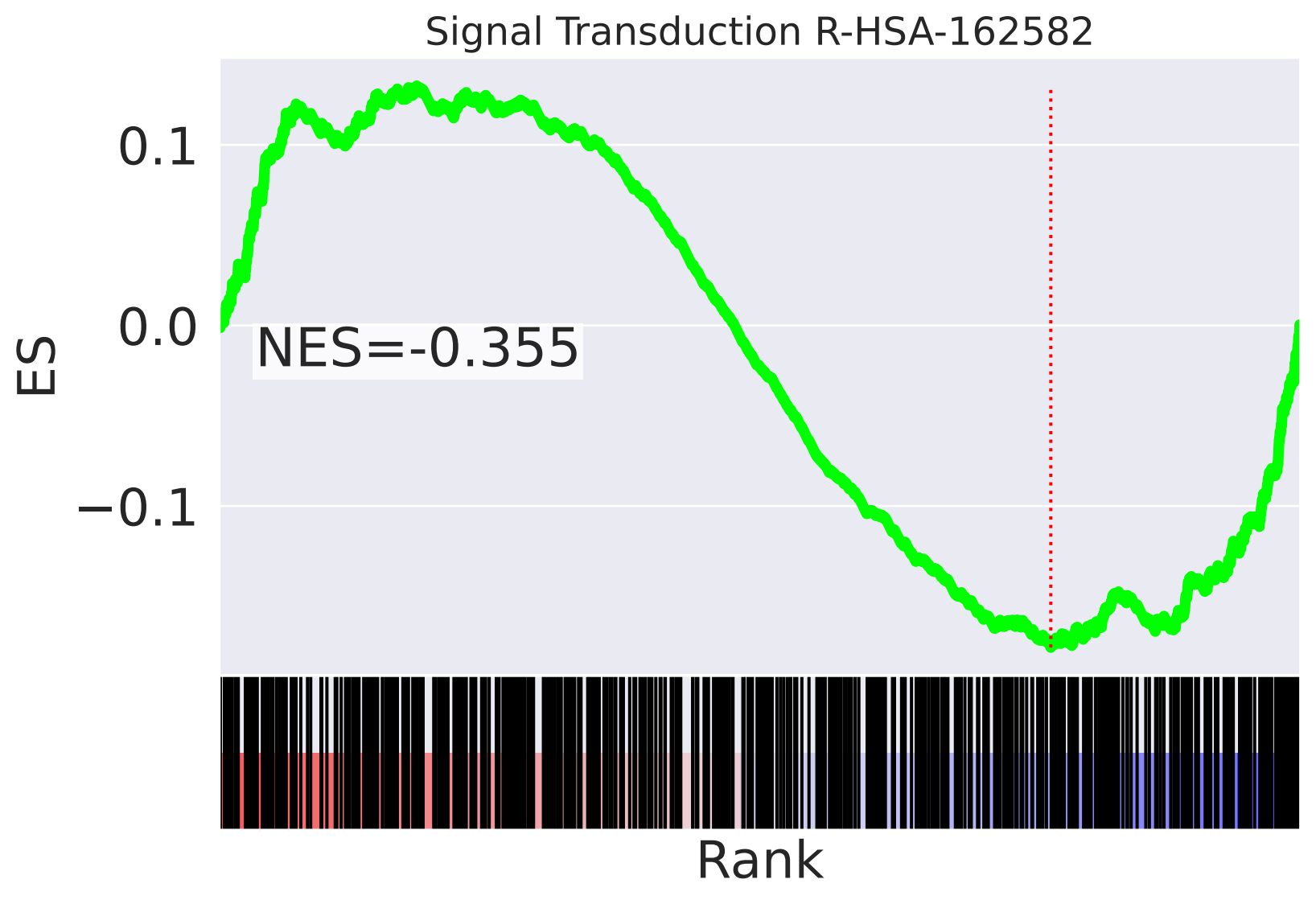

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1373
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

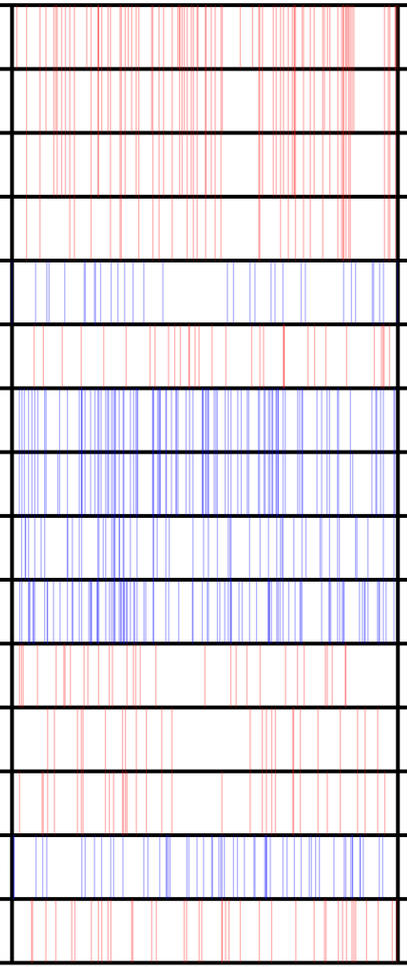

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-4.190
Complex I Biogenesis R-HSA-6799198
-4.108
Respiratory Electron Transport R-HSA-611105
-3.530
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.445
Signaling By MET R-HSA-6806834
-3.145
Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.052
RNA Polymerase III Transcription Initiation R-HSA-76046
-2.931
RNA Polymerase III Abortive And Retractive Initiation R-HSA-749476
2.860
Integrin Signaling R-HSA-354192
2.860
Platelet Aggregation (Plug Formation) R-HSA-76009
2.829
Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
-2.824
Chromosome Maintenance R-HSA-73886
-2.661
Metalloprotease DUBs R-HSA-5689901
-2.639
RNA Polymerase III Transcription Initiation From Type 1 Promoter R-HSA-76061
-2.609
Deposition Of New CENPA-containing Nucleosomes At Centromere R-HSA-606279
2.596
Clathrin-mediated Endocytosis R-HSA-8856828

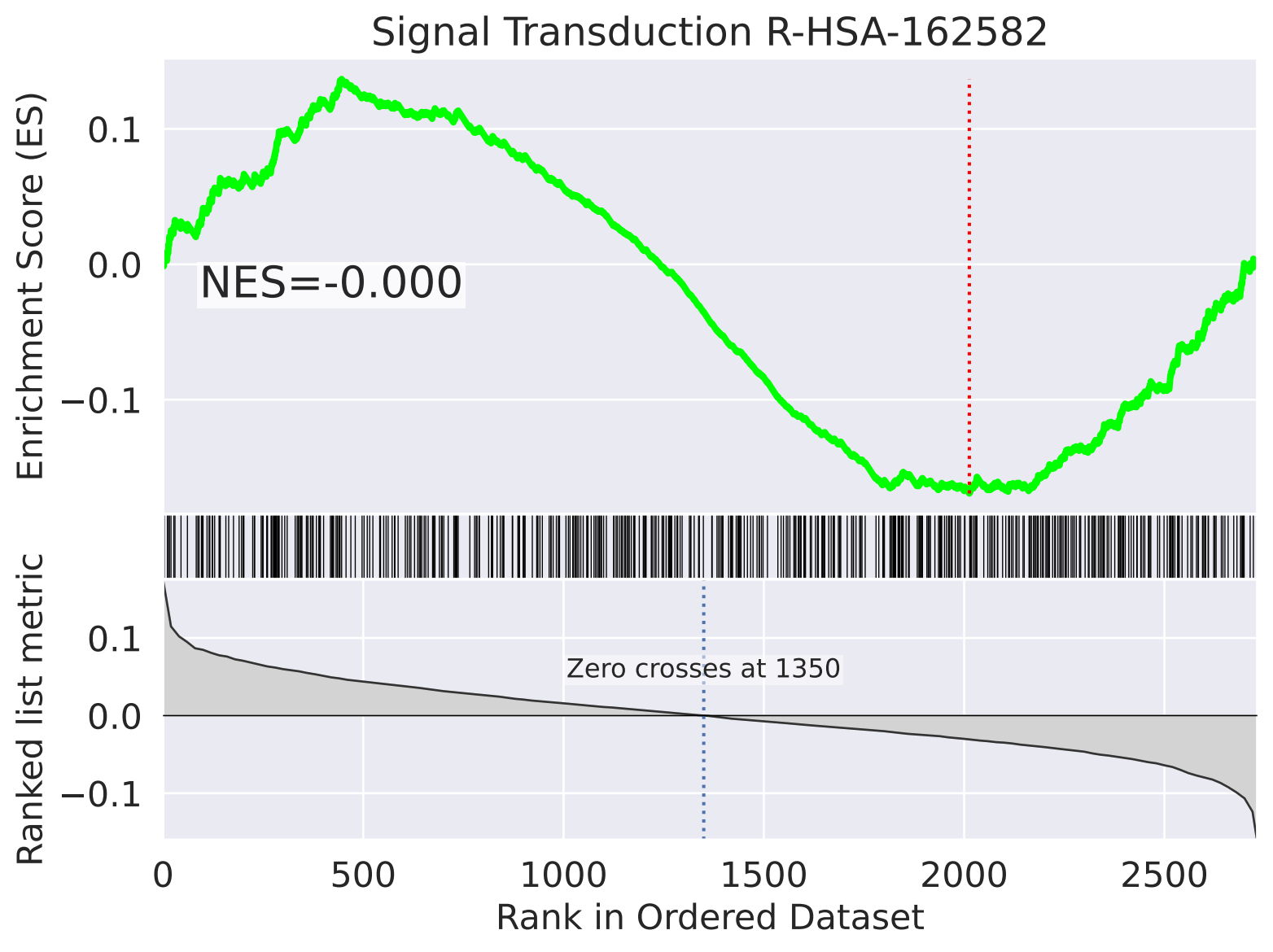
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=5

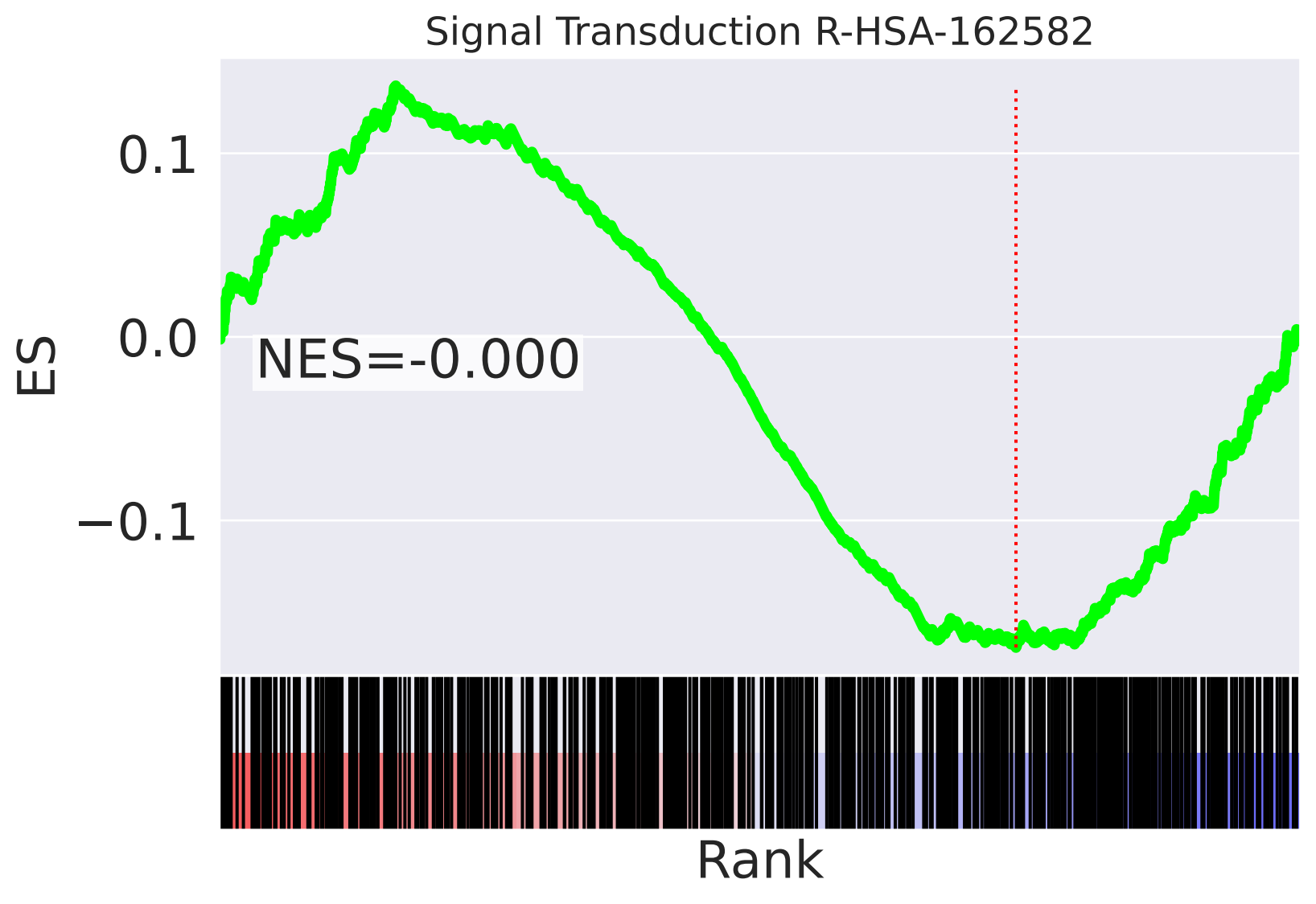

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.355
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1318
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

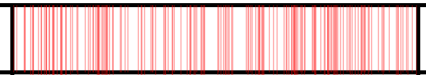
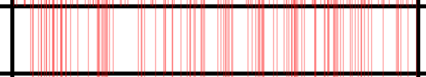
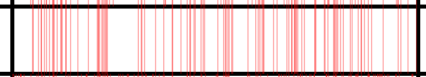
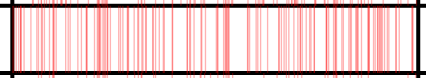
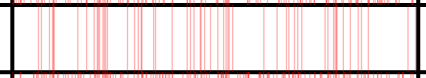
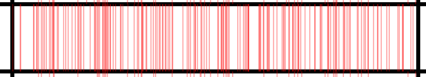
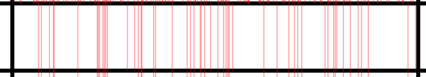
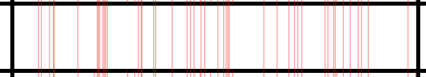
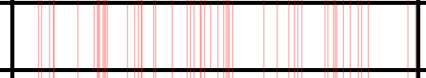
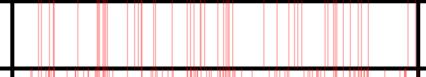
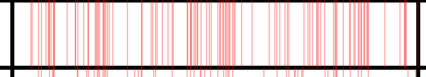
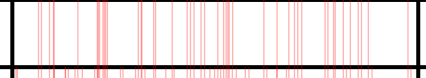

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.355
Rank

NES		SET
6.196		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.168		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.764		Respiratory Electron Transport R-HSA-611105
5.242		Complex I Biogenesis R-HSA-6799198
-3.770		Deadenylation-dependent mRNA Decay R-HSA-429914
3.503		tRNA Aminoacylation R-HSA-379724
-3.440		G2/M Transition R-HSA-69275
-3.407		Mitotic G2-G2/M Phases R-HSA-453274
-3.151		Signaling By ROBO Receptors R-HSA-376176
-3.141		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
3.122		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.116		Diseases Of Glycosylation R-HSA-3781865
3.078		Diseases Of Metabolism R-HSA-5668914
-3.066		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.057		Mitochondrial Biogenesis R-HSA-1592230

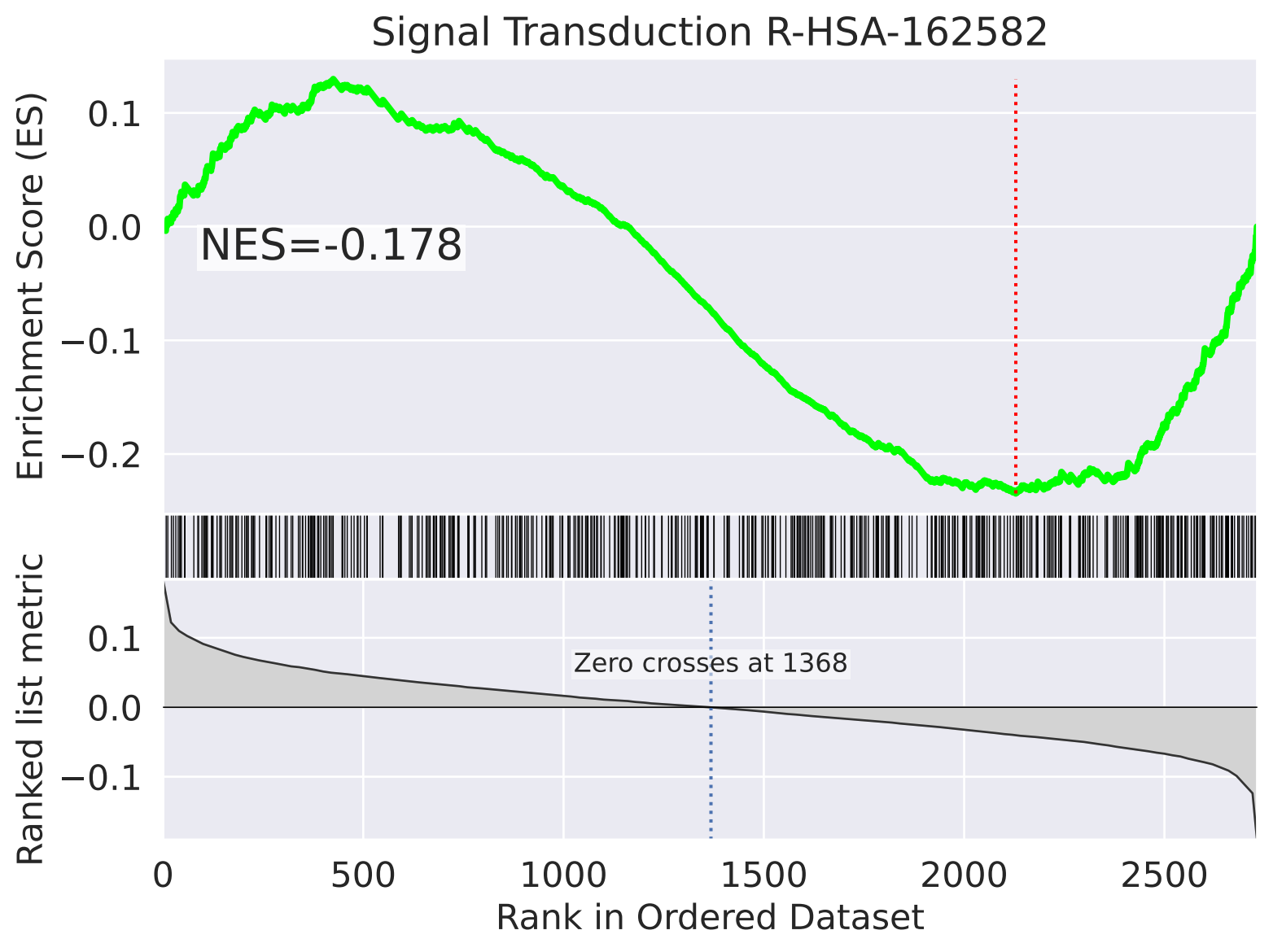
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=6

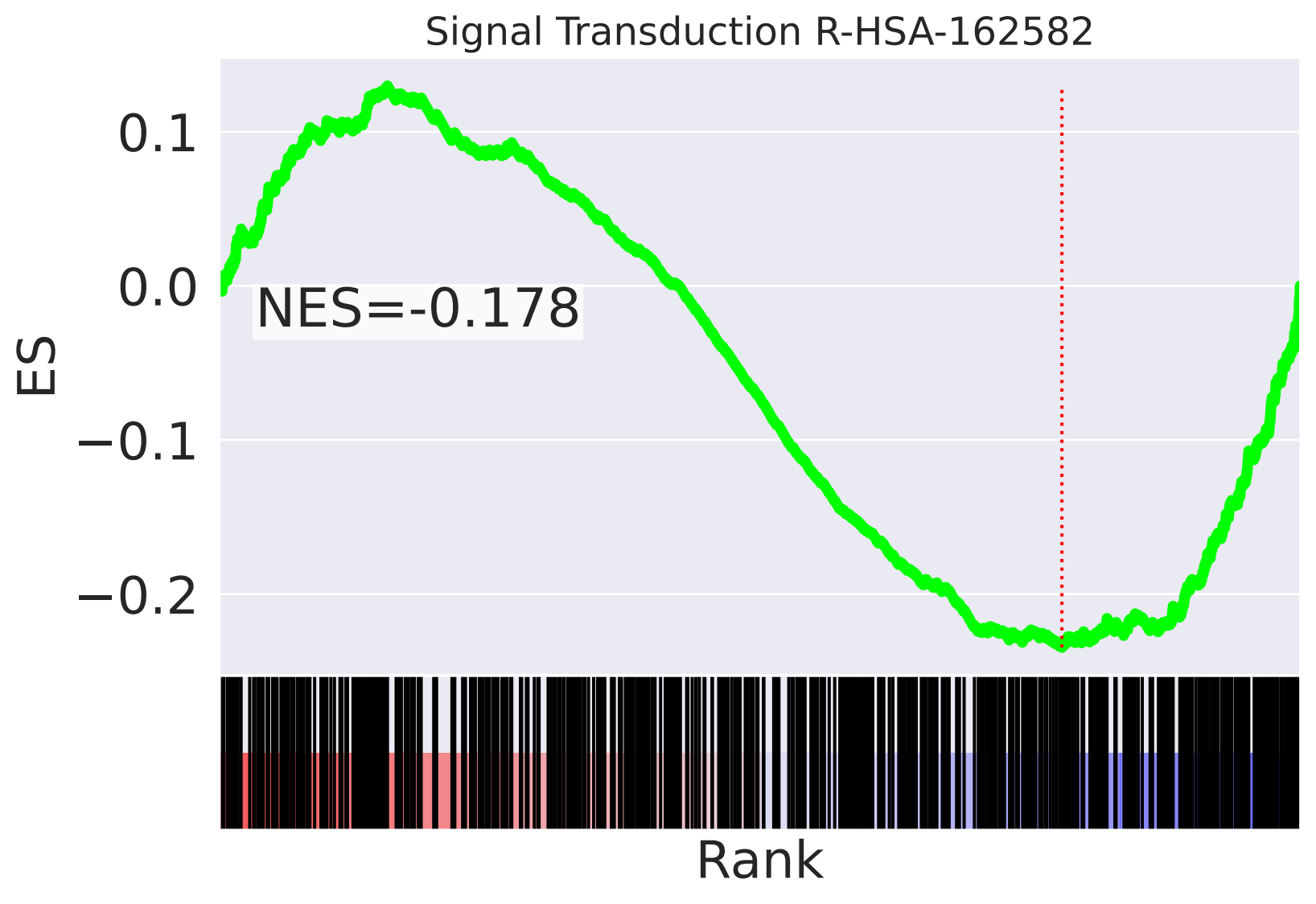

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1350
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

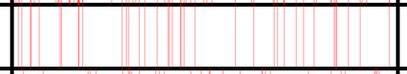
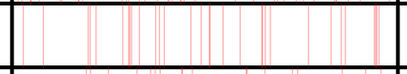
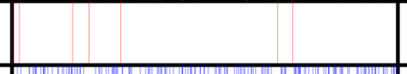
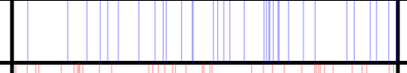
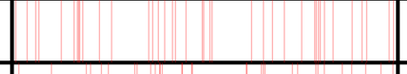
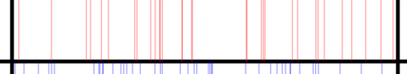
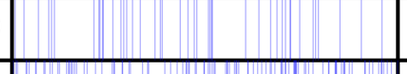
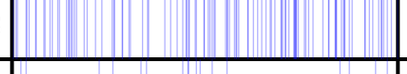
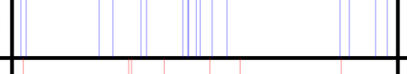
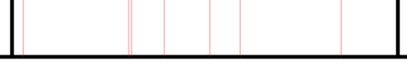

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.970		Adaptive Immune System R-HSA-1280218
5.881		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
5.494		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
5.494		HIV Infection R-HSA-162906
5.476		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
5.437		Cytokine Signaling In Immune System R-HSA-1280215
5.386		APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176409
5.367		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
5.353		Activation Of APC/C And APC/C:Cdc20 Mediated Degradation Of Mitotic Proteins R-HSA-176814
5.352		APC:Cdc20 Mediated Degradation Of Cell Cycle Proteins Before Cycle Checkpoint Satisfied R-HSA-179419
5.352		Cdc20:Phospho-APC/C Mediated Degradation Of Cyclin A R-HSA-174184
5.325		Deubiquitination R-HSA-5688426
5.310		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
5.298		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
5.282		DNA Replication Pre-Initiation R-HSA-69002

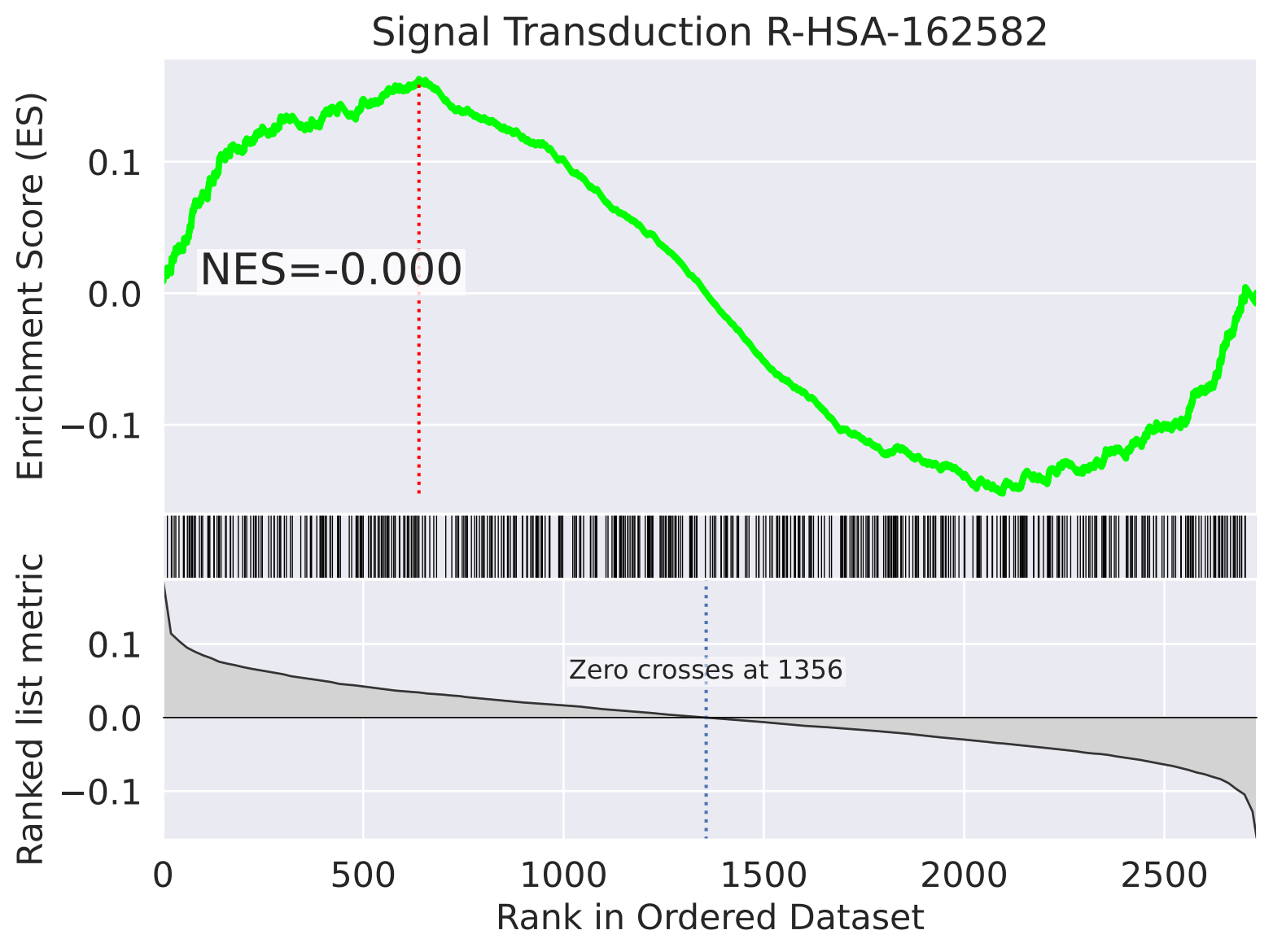
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=7

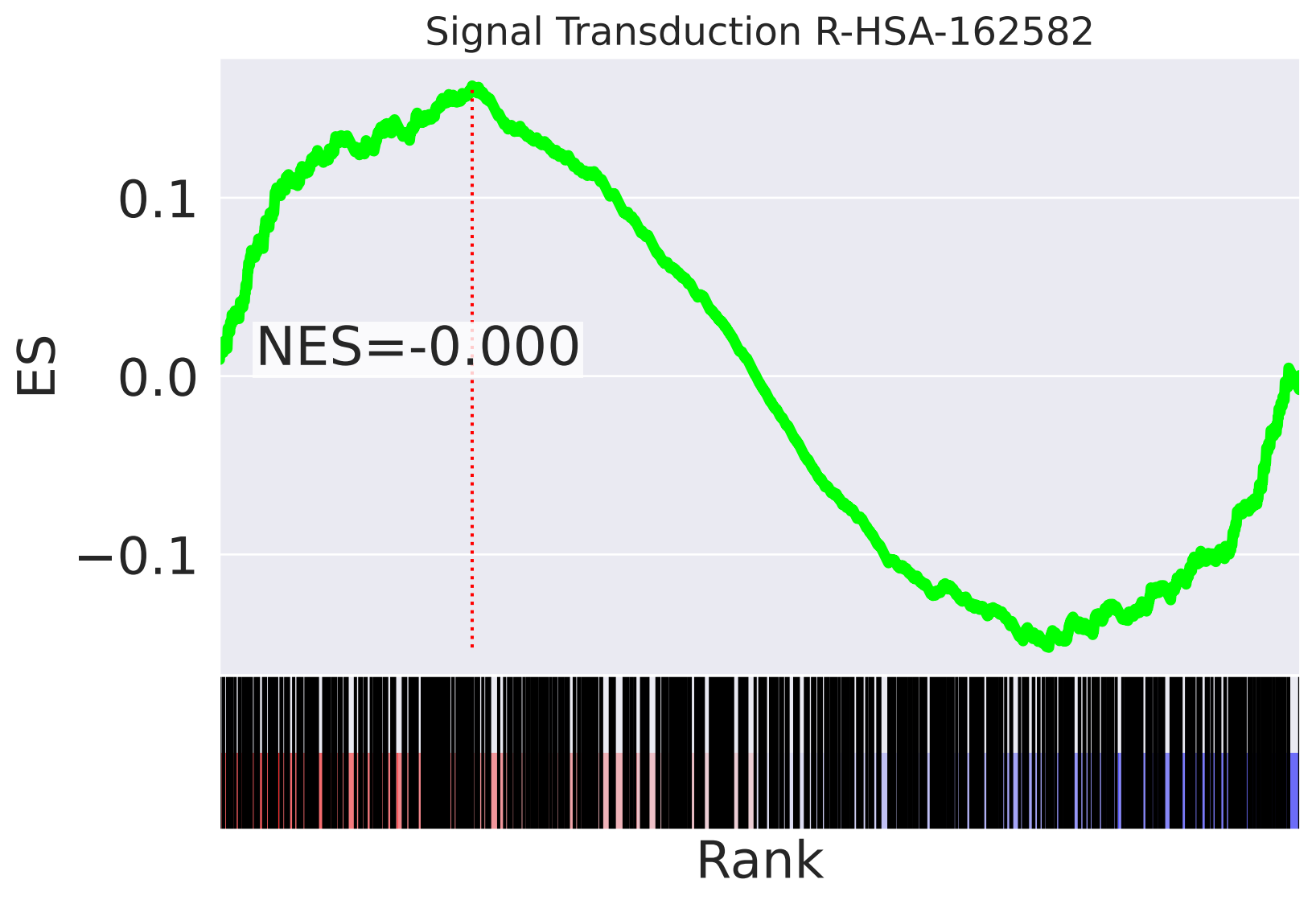

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
−0.2
NES=-0.178
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1368
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

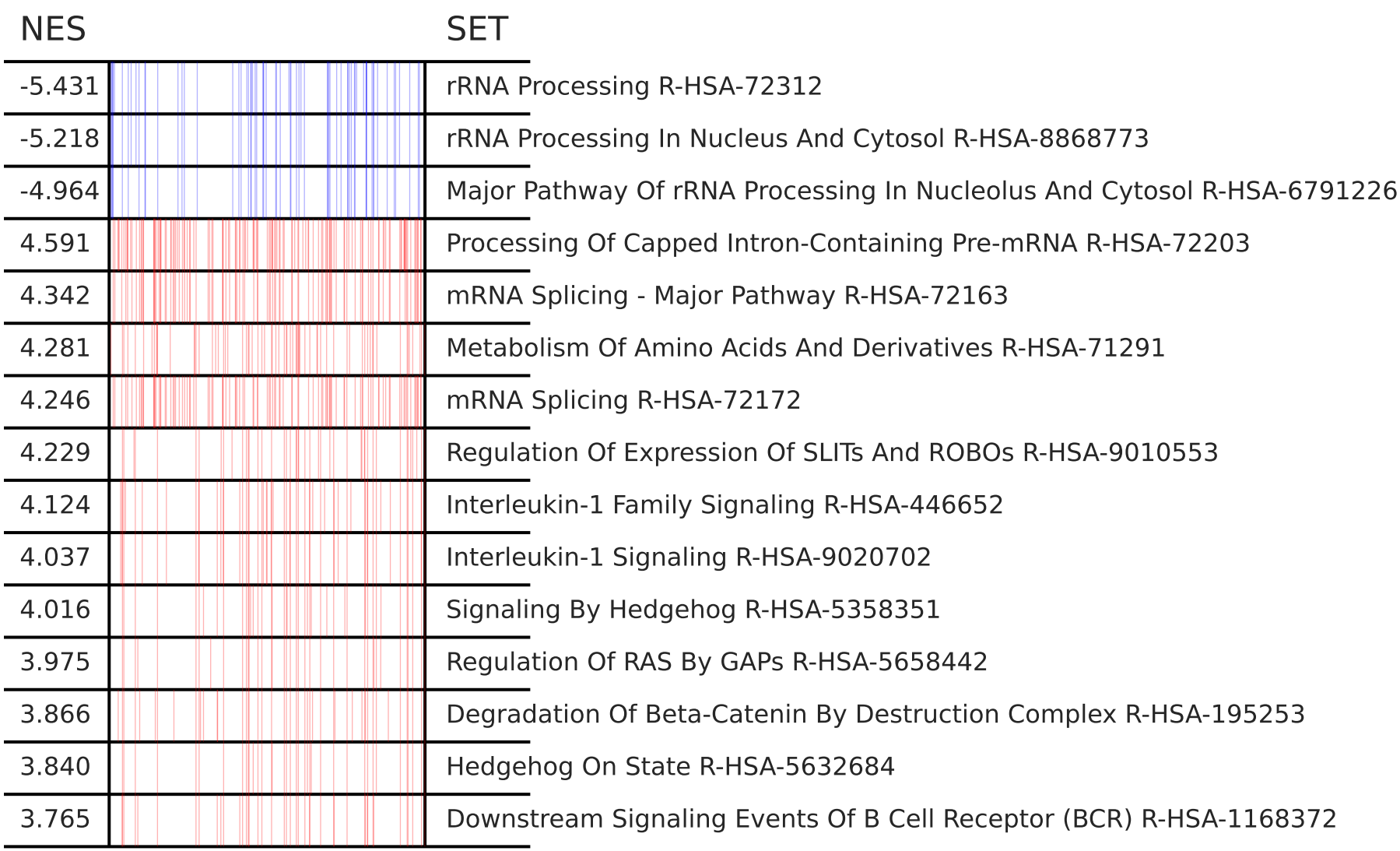

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
−0.2
ES
NES=-0.178
Rank

NES		SET
5.070		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
4.918		Respiratory Electron Transport R-HSA-611105
4.890		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
4.213		Complex I Biogenesis R-HSA-6799198
3.701		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.179		Mitochondrial tRNA Aminoacylation R-HSA-379726
3.042		rRNA Processing In Mitochondrion R-HSA-8868766
-3.019		Cell Cycle Checkpoints R-HSA-69620
-3.012		mRNA Splicing - Minor Pathway R-HSA-72165
3.000		TP53 Regulates Metabolic Genes R-HSA-5628897
2.954		tRNA Aminoacylation R-HSA-379724
-2.910		Cilium Assembly R-HSA-5617833
-2.838		S Phase R-HSA-69242
-2.820		Cyclin A/B1/B2 Associated Events During G2/M Transition R-HSA-69273
2.796		Metabolism Of Cofactors R-HSA-8978934

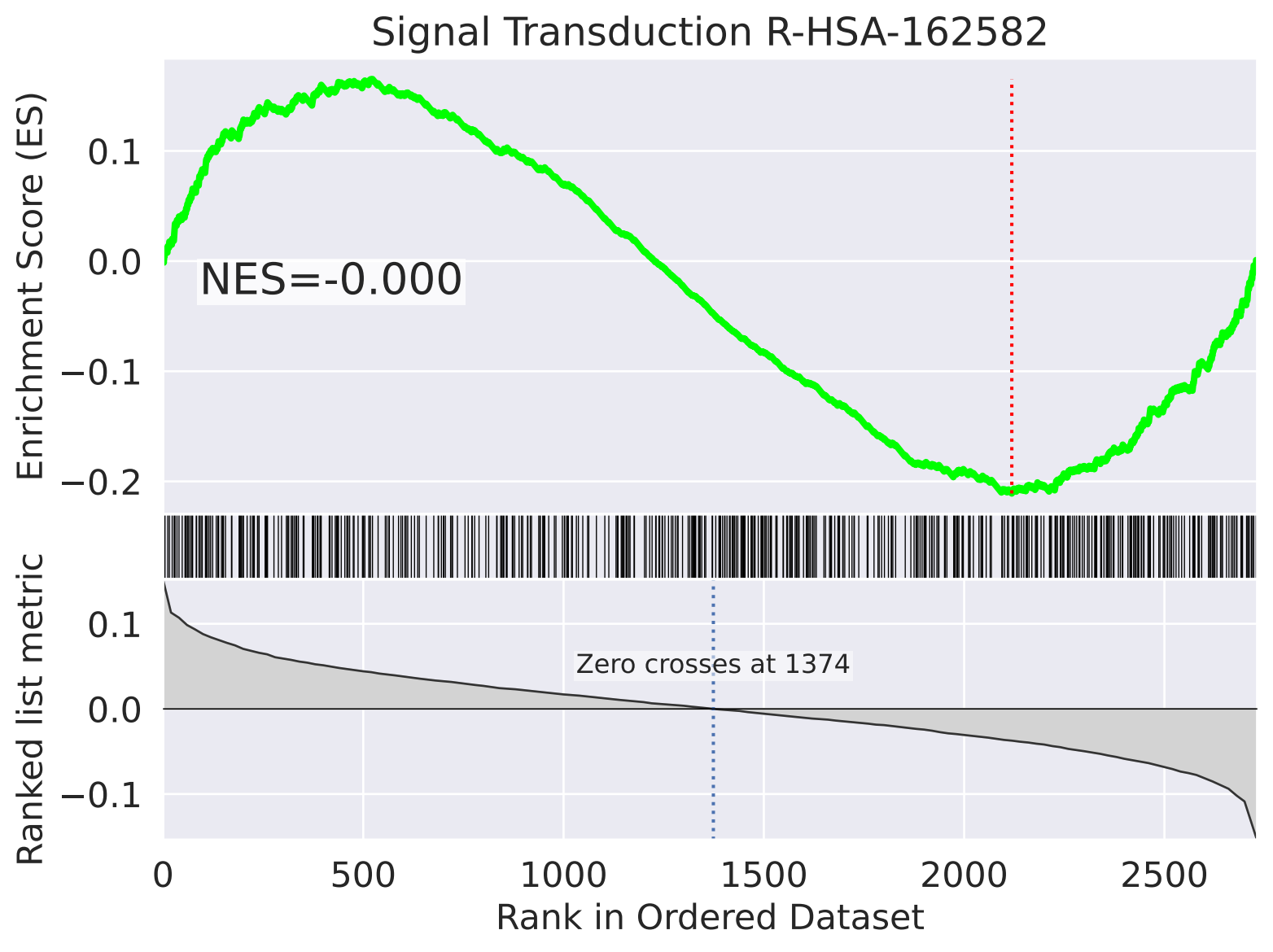
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=8

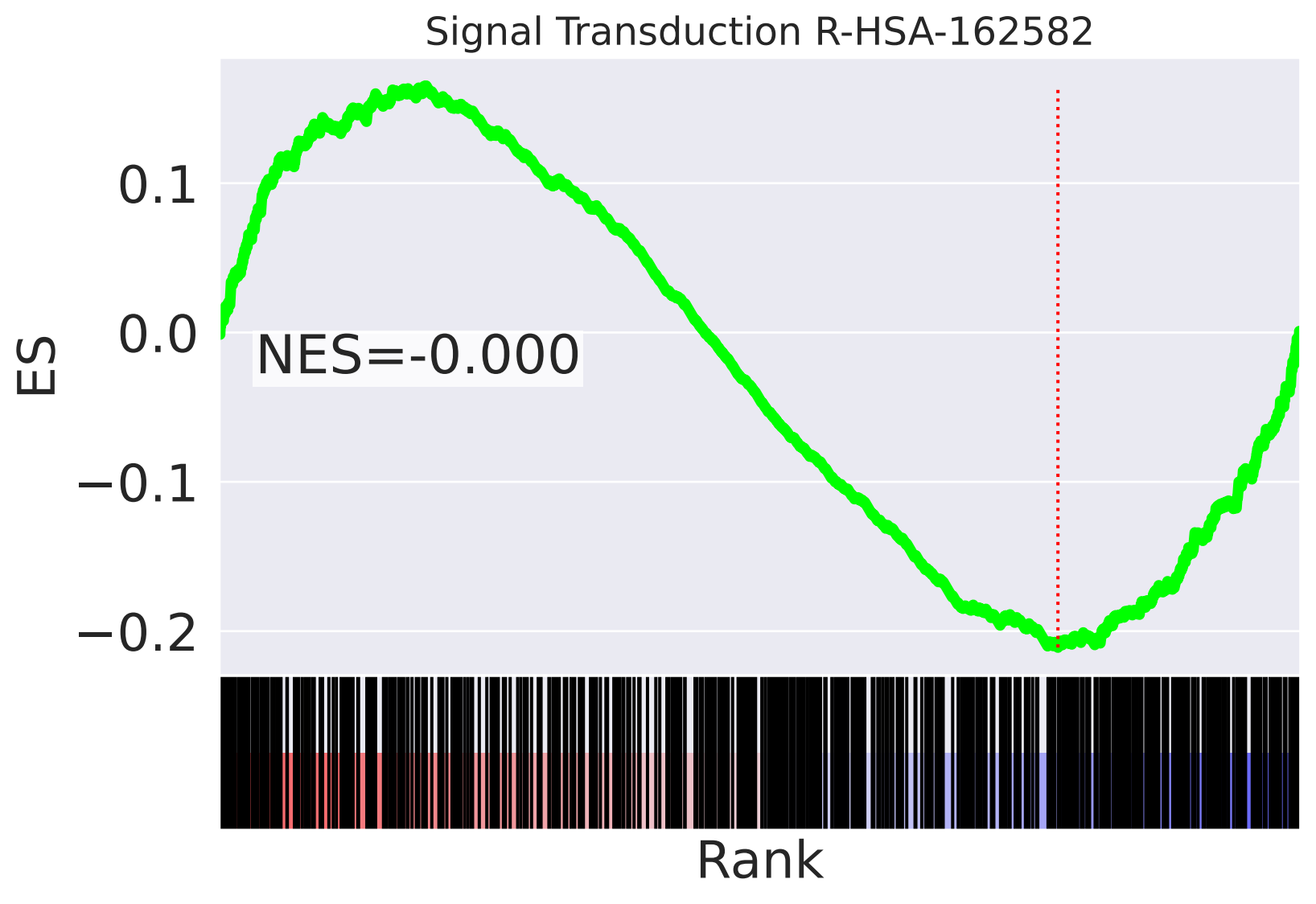

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1356
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

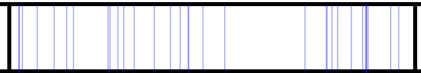
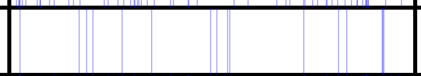
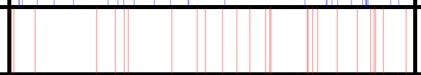
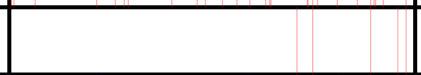
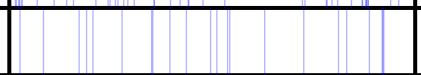
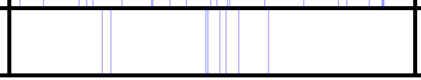

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-5.431
rRNA Processing R-HSA-72312
-5.218
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.964
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.591
Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.342
mRNA Splicing - Major Pathway R-HSA-72163
4.281
Metabolism Of Amino Acids And Derivatives R-HSA-71291
4.246
mRNA Splicing R-HSA-72172
4.229
Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
4.124
Interleukin-1 Family Signaling R-HSA-446652
4.037
Interleukin-1 Signaling R-HSA-9020702
4.016
Signaling By Hedgehog R-HSA-5358351
3.975
Regulation Of RAS By GAPs R-HSA-5658442
3.866
Degradation Of Beta-Catenin By Destruction Complex R-HSA-195253
3.840
Hedgehog On State R-HSA-5632684
3.765
Downstream Signaling Events Of B Cell Receptor (BCR) R-HSA-1168372

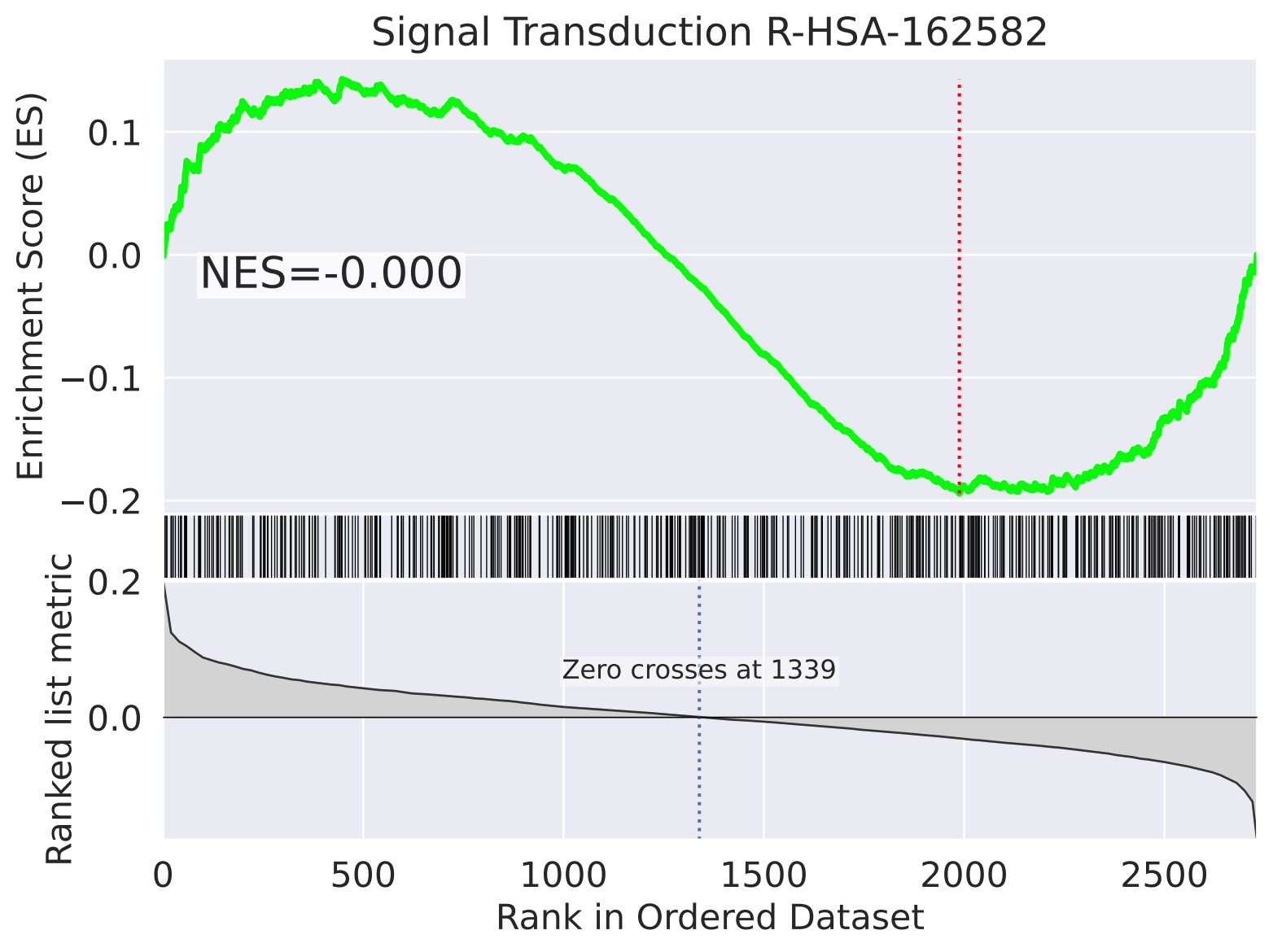
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=9

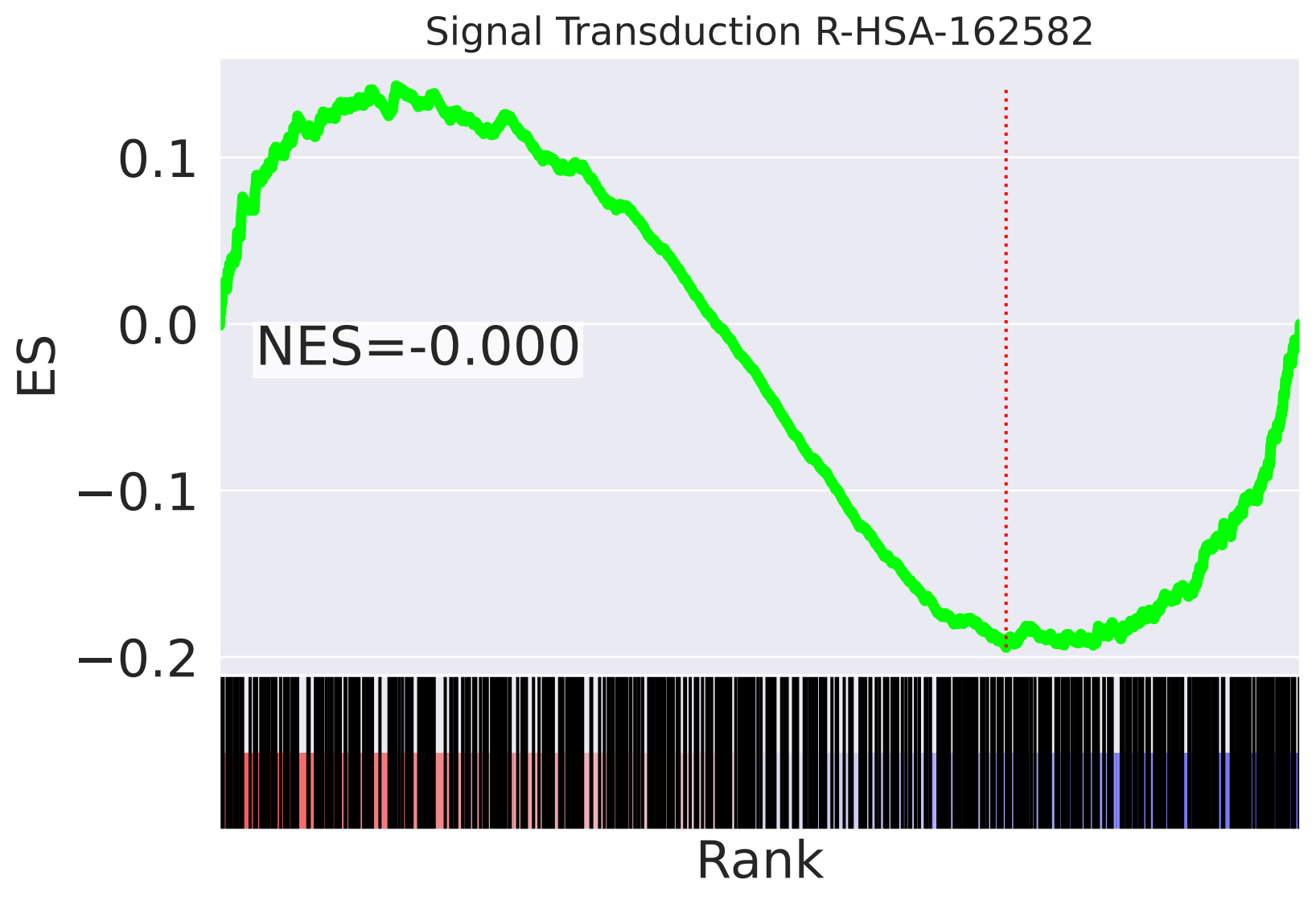

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
−0.2
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1374
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

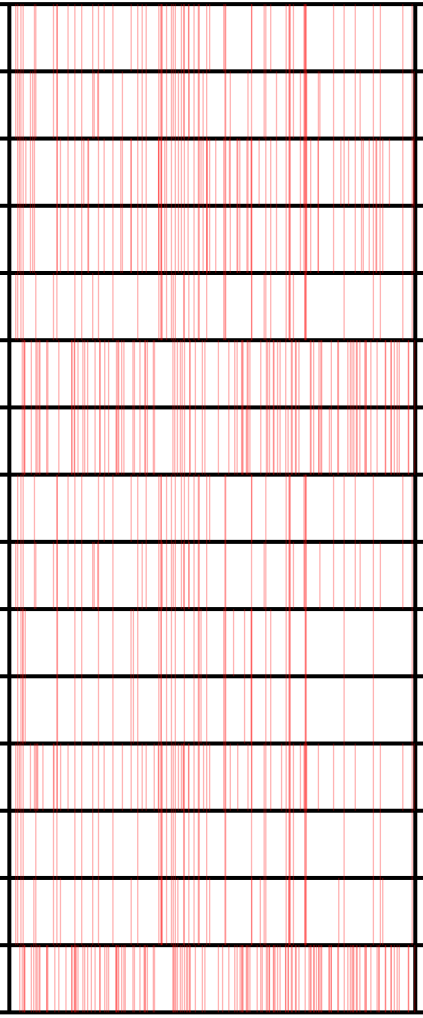

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
−0.2
ES
NES=-0.000
Rank

NES		SET
-3.290		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.290		Diseases Of DNA Repair R-HSA-9675135
-3.220		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.152		Cytosolic tRNA Aminoacylation R-HSA-379716
-2.912		HDR Thru Single Strand Annealing (SSA) R-HSA-5685938
-2.907		Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
-2.750		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
-2.718		RNA Polymerase III Transcription Initiation From Type 2 Promoter R-HSA-76066
-2.649		Impaired BRCA2 Binding To RAD51 R-HSA-9709570
2.590		TP53 Regulates Transcription Of Cell Cycle Genes R-HSA-6791312
2.562		PTK6 Regulates Cell Cycle R-HSA-8849470
-2.480		STAT5 Activation Downstream Of FLT3 ITD Mutants R-HSA-9702518
-2.471		HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-2.453		RNA Polymerase III Transcription Initiation R-HSA-76046
-2.444		Glyoxylate Metabolism And Glycine Degradation R-HSA-389661

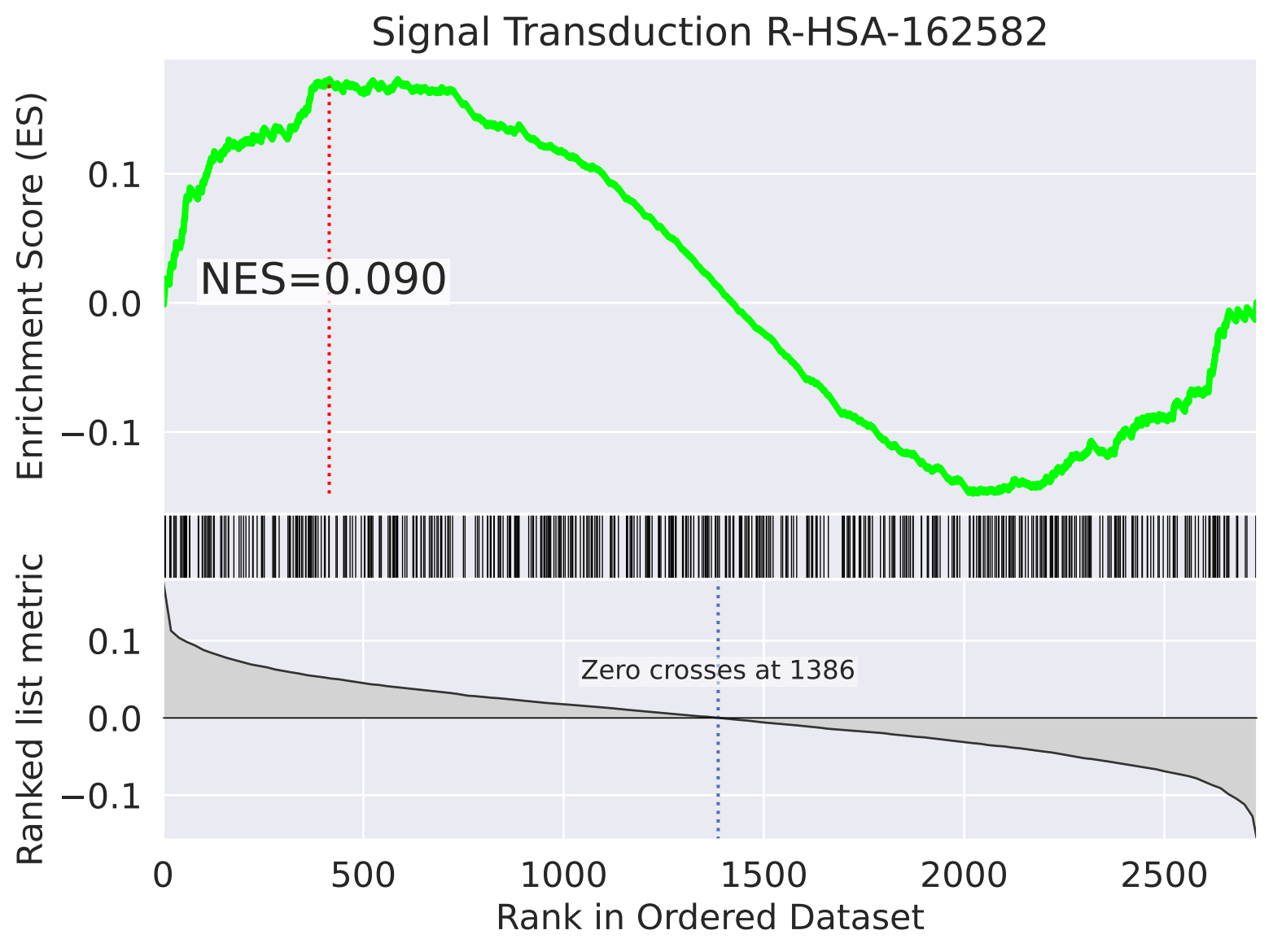
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=10

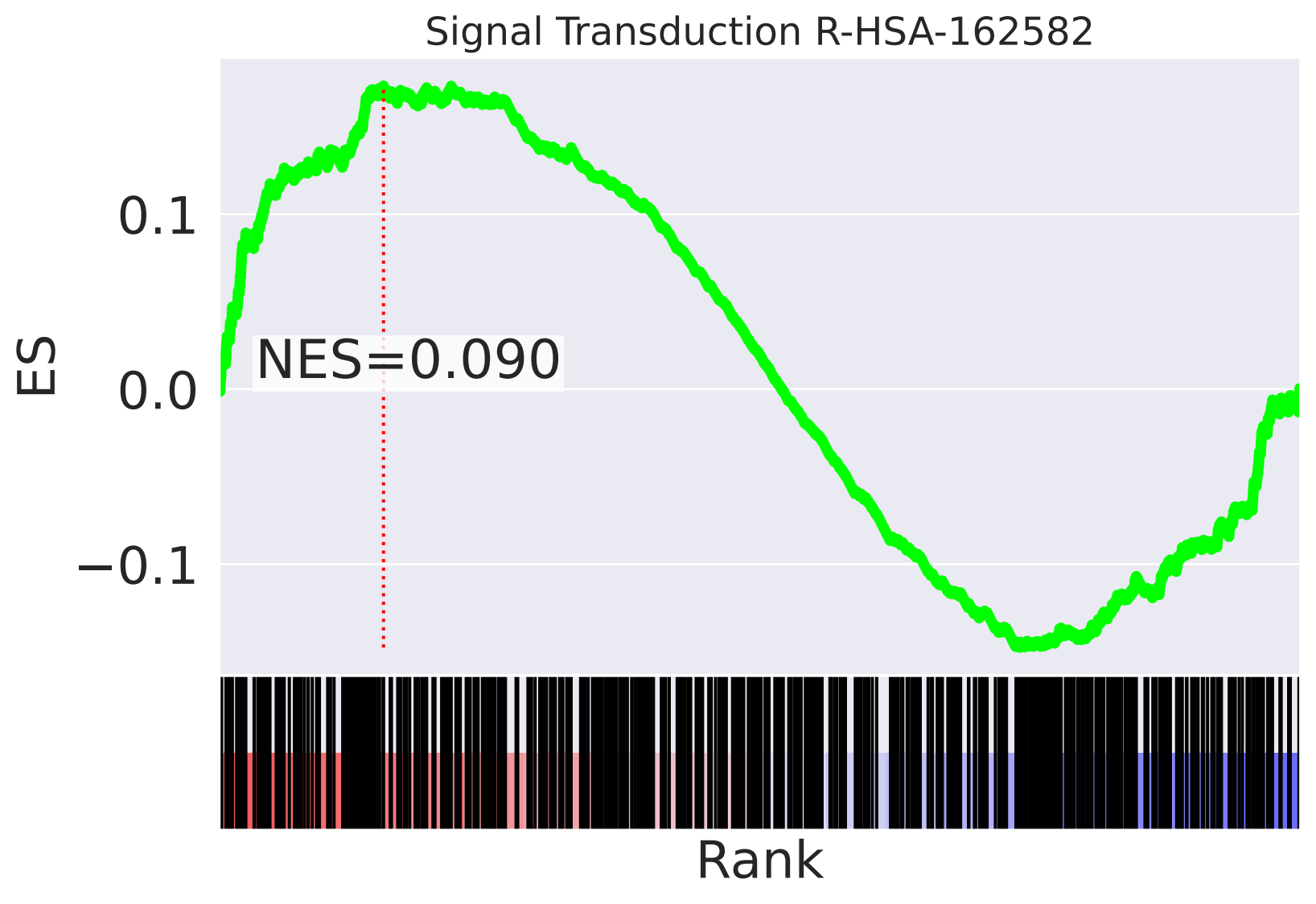

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
−0.2
NES=-0.000
Ranked list metric
0.2
0.0
Zero crosses at 1339
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

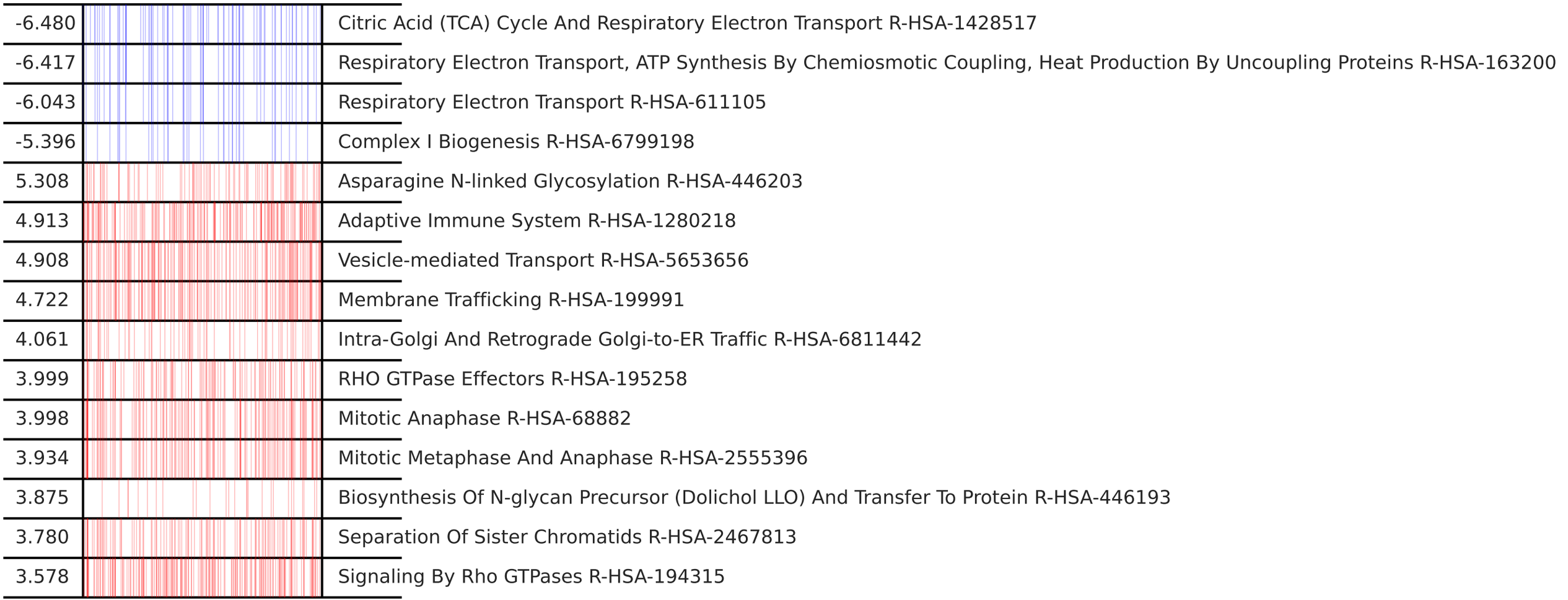

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
−0.2
ES
NES=-0.000
Rank

NES		SET
5.665		Switching Of Origins To A Post-Replicative State R-HSA-69052
5.431		DNA Replication Pre-Initiation R-HSA-69002
5.382		Mitotic G1 Phase And G1/S Transition R-HSA-453279
5.369		G1/S Transition R-HSA-69206
5.301		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
5.236		mRNA Splicing - Major Pathway R-HSA-72163
5.177		mRNA Splicing R-HSA-72172
5.134		Orc1 Removal From Chromatin R-HSA-68949
5.064		Assembly Of Pre-Replicative Complex R-HSA-68867
5.037		G1/S DNA Damage Checkpoints R-HSA-69615
5.019		p53-Dependent G1 DNA Damage Response R-HSA-69563
5.014		Synthesis Of DNA R-HSA-69239
5.004		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
4.982		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
4.982		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203

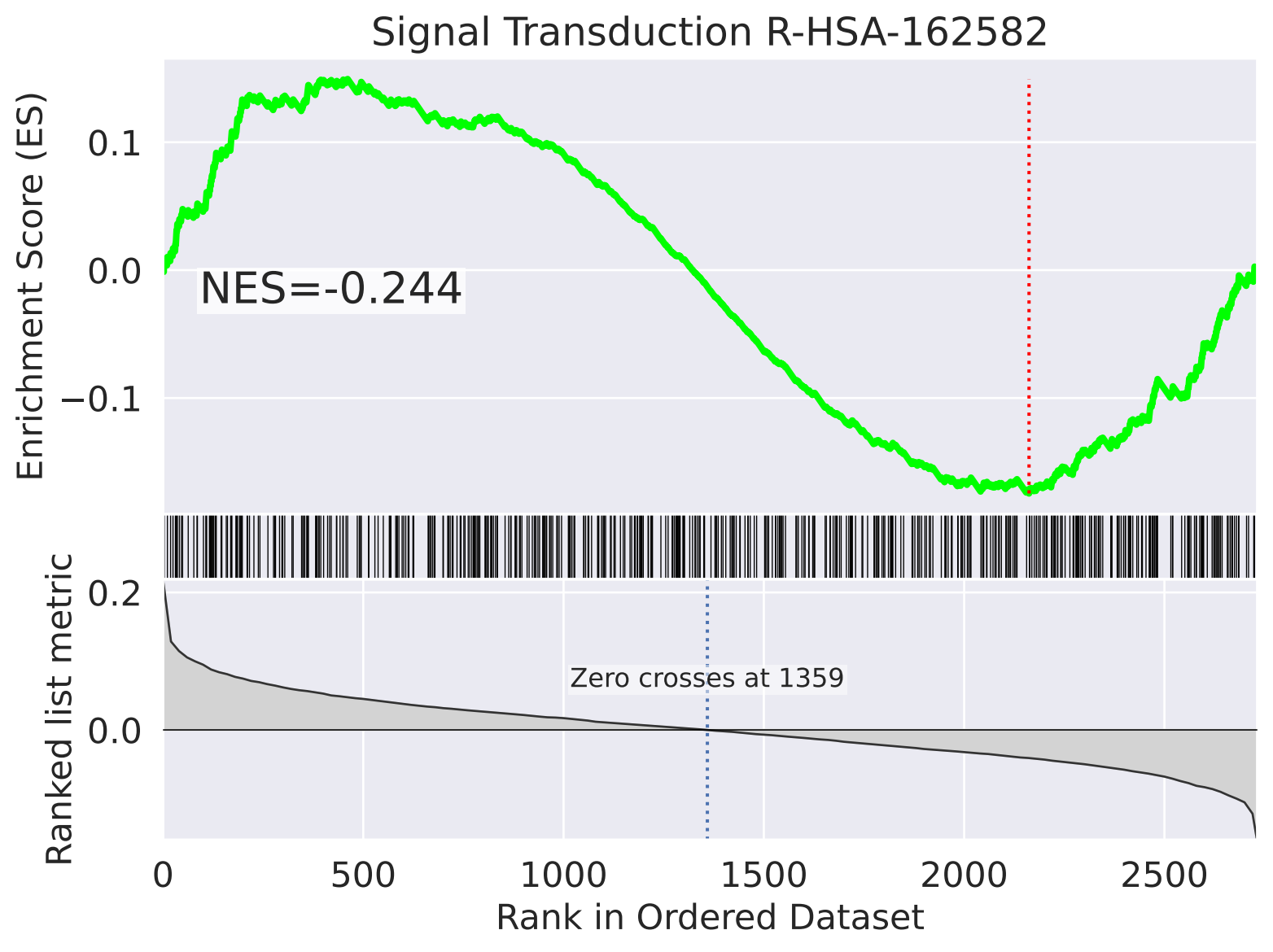
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=11

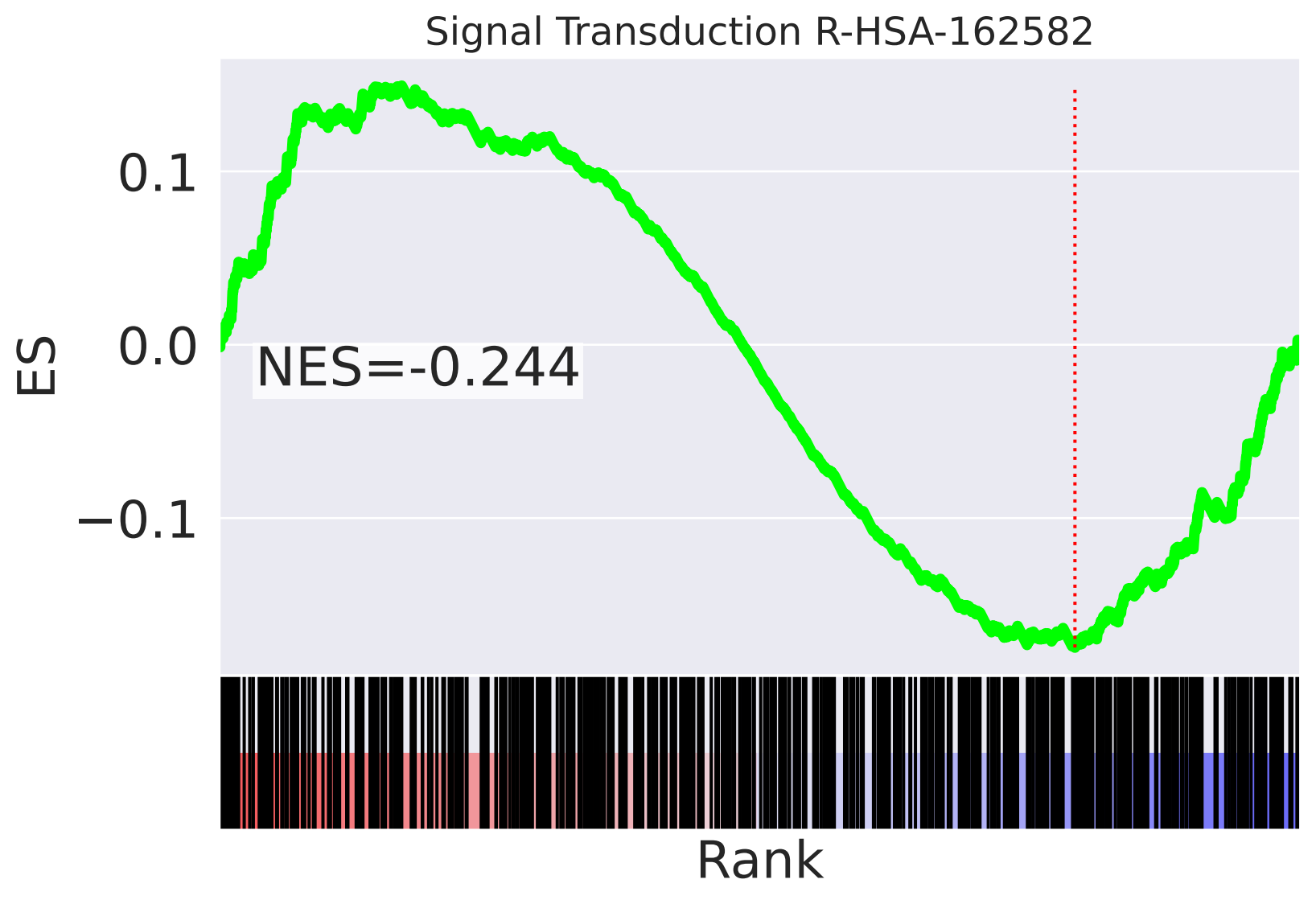

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=0.090
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1386
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

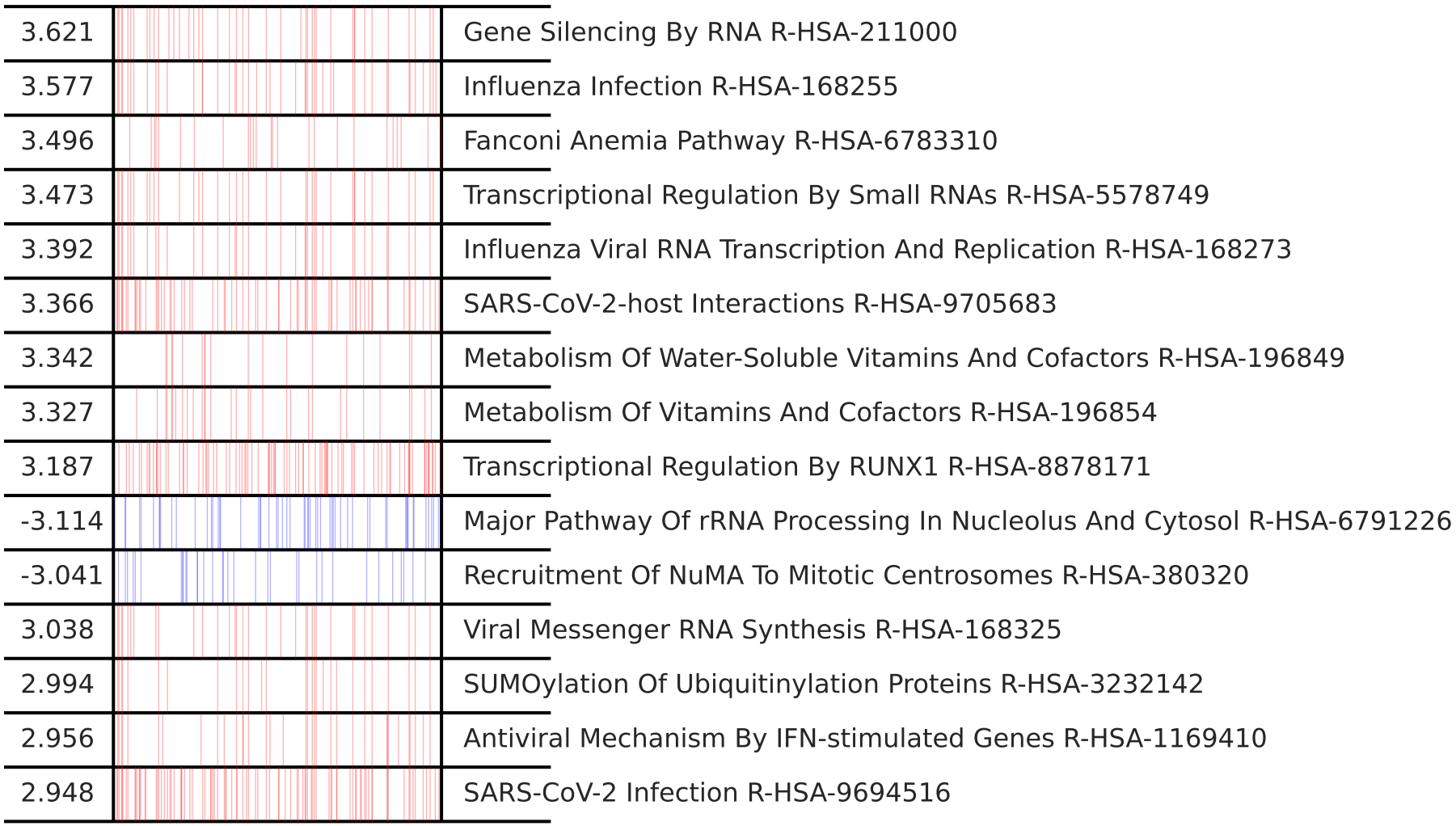

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=0.090
Rank


NES
SET
-6.480
Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-6.417
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-6.043
Respiratory Electron Transport R-HSA-611105
-5.396
Complex I Biogenesis R-HSA-6799198
5.308
Asparagine N-linked Glycosylation R-HSA-446203
4.913
Adaptive Immune System R-HSA-1280218
4.908
Vesicle-mediated Transport R-HSA-5653656
4.722
Membrane Trafficking R-HSA-199991
4.061
Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
3.999
RHO GTPase Effectors R-HSA-195258
3.998
Mitotic Anaphase R-HSA-68882
3.934
Mitotic Metaphase And Anaphase R-HSA-2555396
3.875
Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
3.780
Separation Of Sister Chromatids R-HSA-2467813
3.578
Signaling By Rho GTPases R-HSA-194315

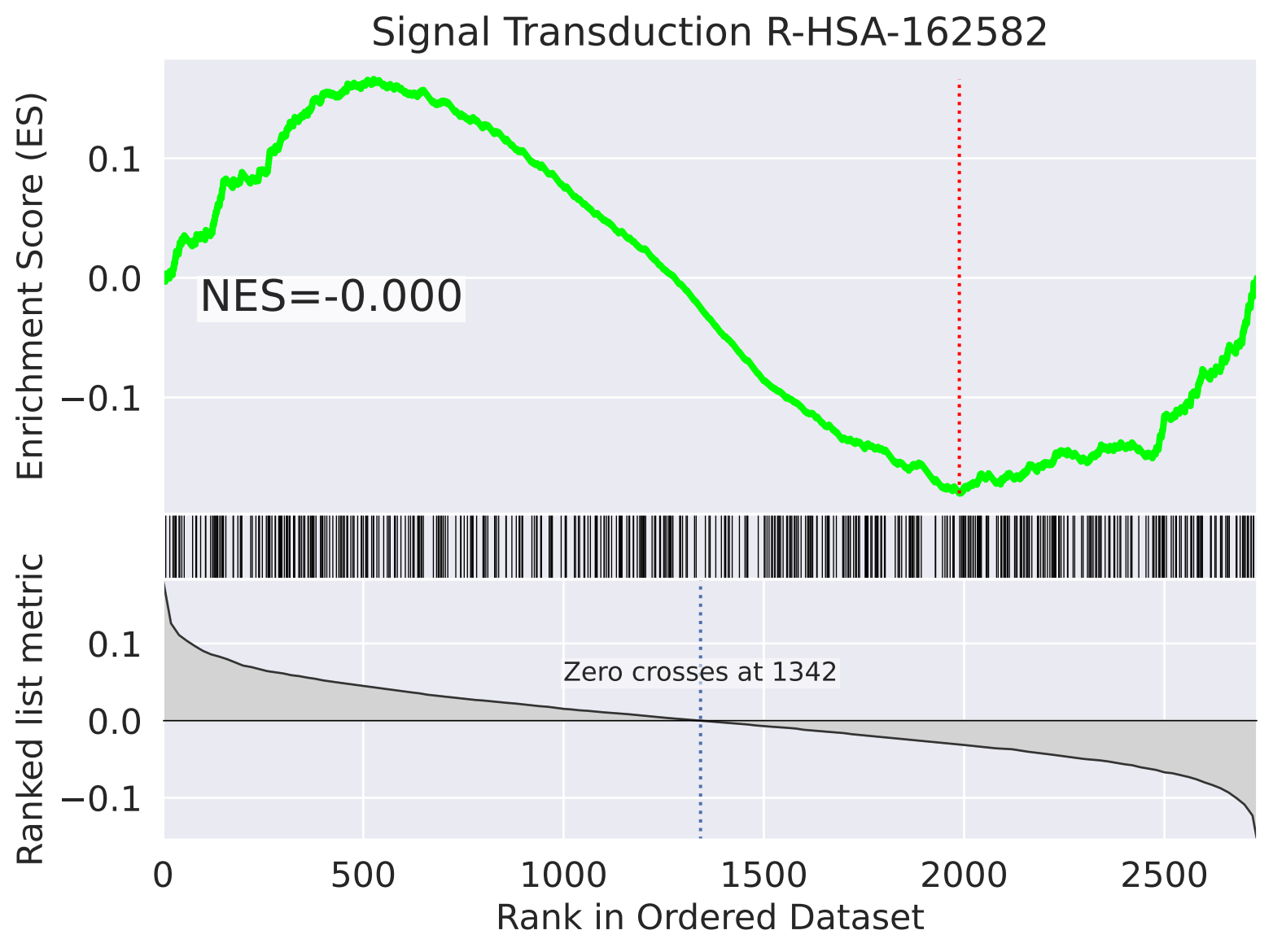
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=12

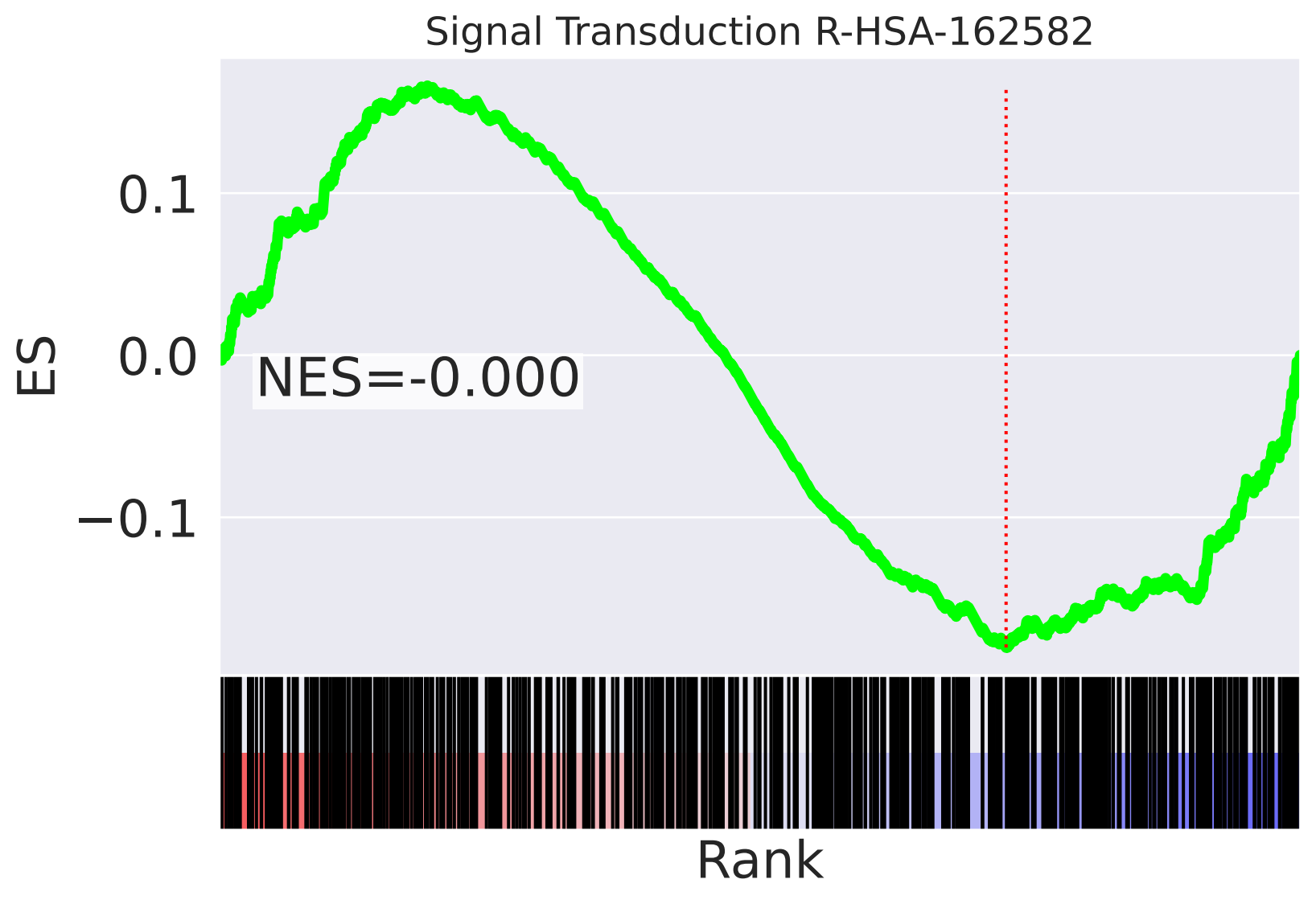

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.244
Ranked list metric
0.2
0.0
Zero crosses at 1359
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

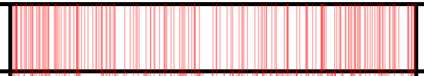
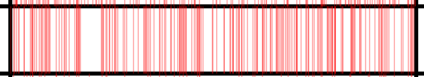
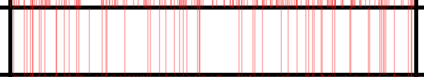
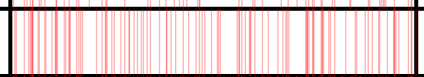
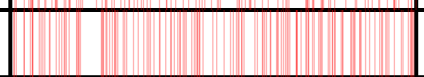
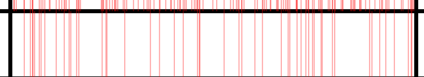
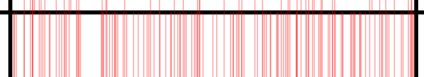
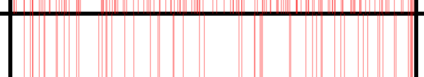
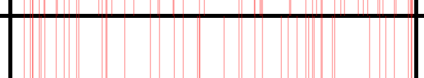
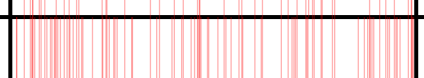
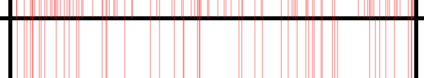
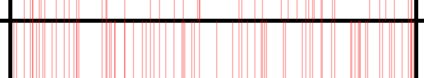
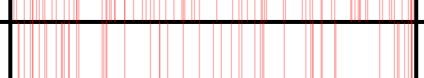
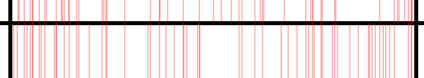

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.244
Rank


NES
SET
3.621
Gene Silencing By RNA R-HSA-211000
3.577
Influenza Infection R-HSA-168255
3.496
Fanconi Anemia Pathway R-HSA-6783310
3.473
Transcriptional Regulation By Small RNAs R-HSA-5578749
3.392
Influenza Viral RNA Transcription And Replication R-HSA-168273
3.366
SARS-CoV-2-host Interactions R-HSA-9705683
3.342
Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.327
Metabolism Of Vitamins And Cofactors R-HSA-196854
3.187
Transcriptional Regulation By RUNX1 R-HSA-8878171
-3.114
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.041
Recruitment Of NuMA To Mitotic Centrosomes R-HSA-380320
3.038
Viral Messenger RNA Synthesis R-HSA-168325
2.994
SUMOylation Of Ubiquitinylation Proteins R-HSA-3232142
2.956
Antiviral Mechanism By IFN-stimulated Genes R-HSA-1169410
2.948
SARS-CoV-2 Infection R-HSA-9694516

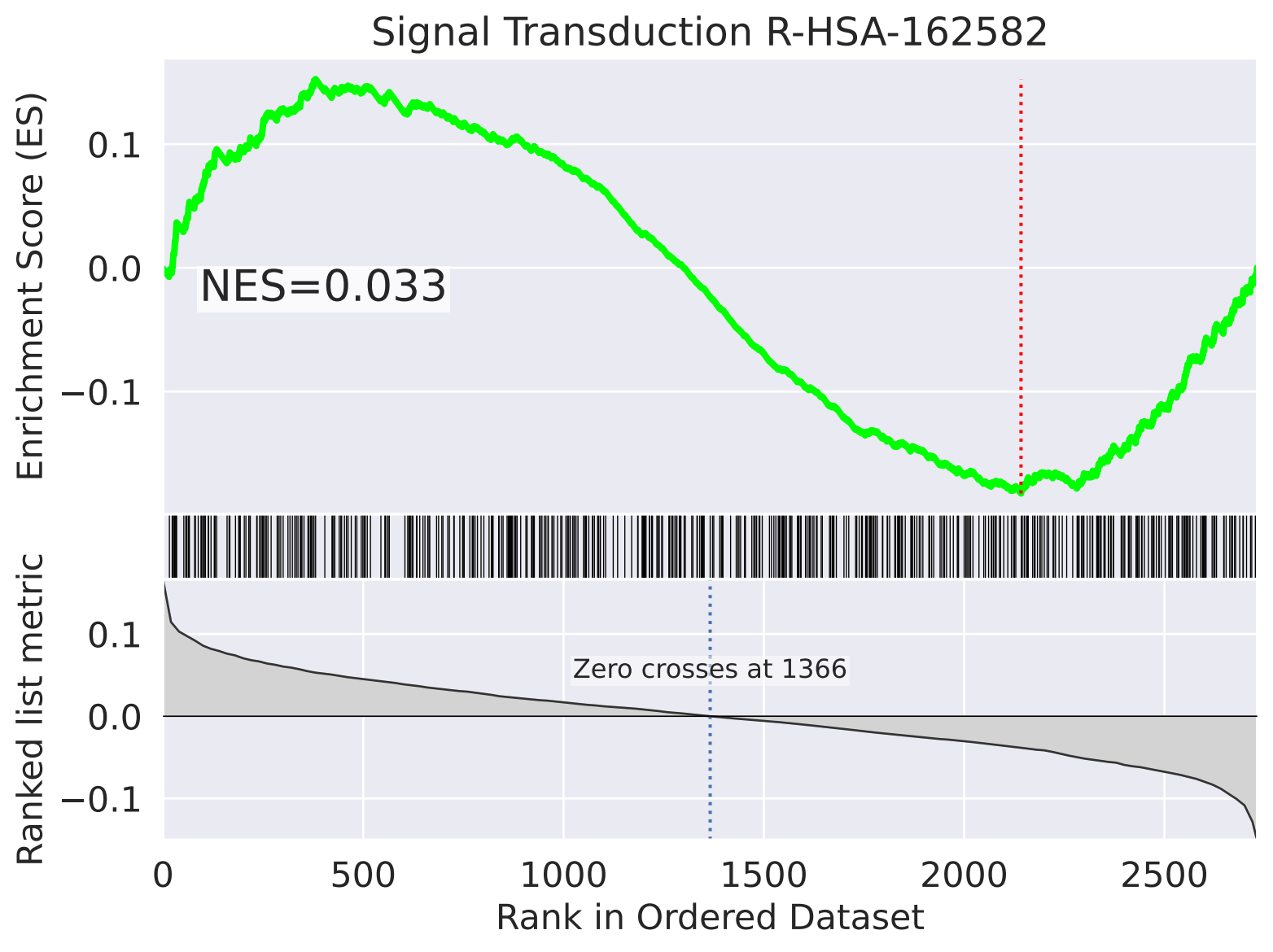
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=13

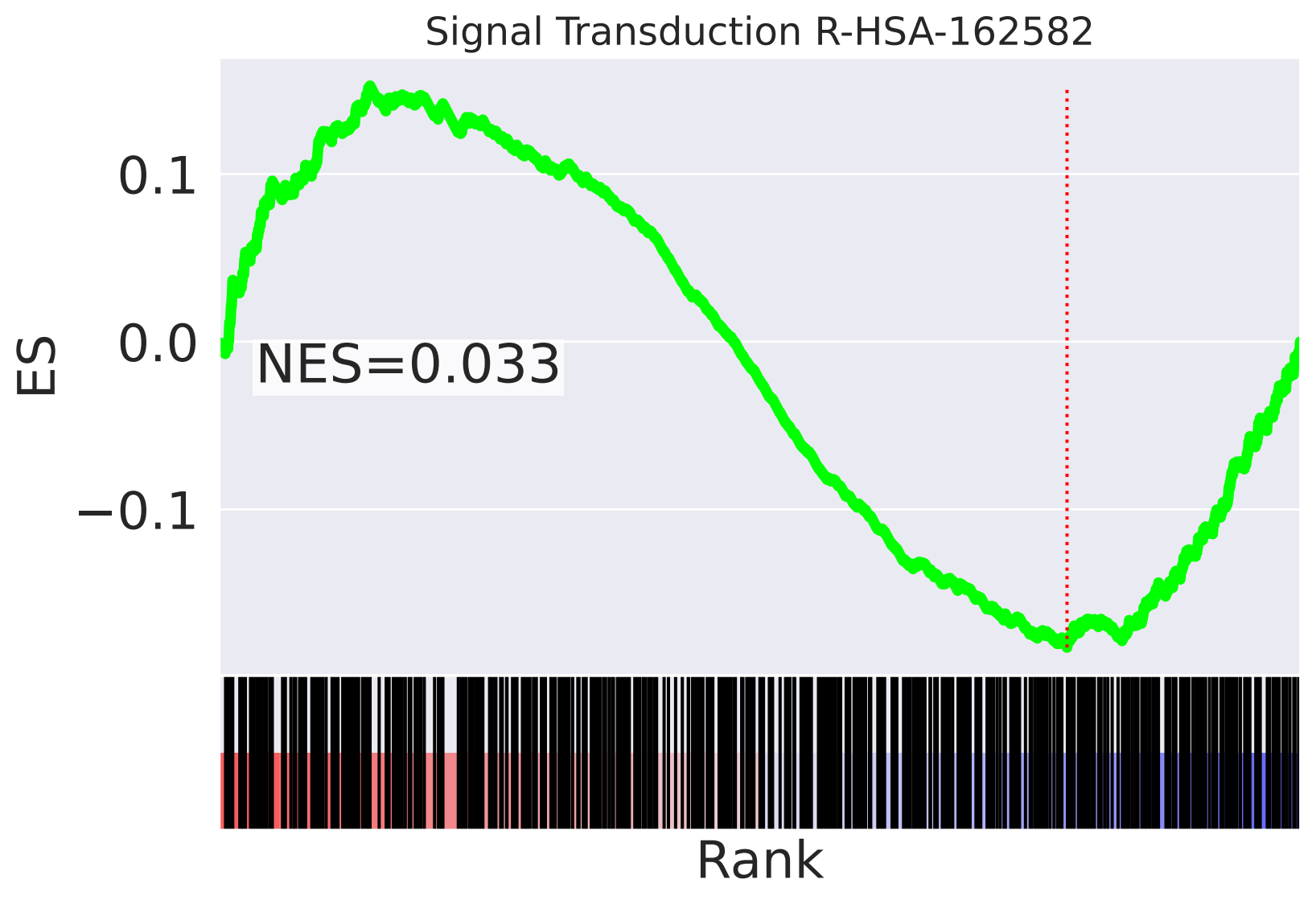

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1342
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

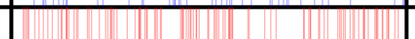

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.587		Cytokine Signaling In Immune System R-HSA-1280215
5.498		M Phase R-HSA-68886
5.445		Assembly Of Pre-Replicative Complex R-HSA-68867
5.412		Intracellular Signaling By Second Messengers R-HSA-9006925
5.367		Mitotic Anaphase R-HSA-68882
5.350		APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
5.345		Mitotic Metaphase And Anaphase R-HSA-2555396
5.324		Signaling By ROBO Receptors R-HSA-376176
5.315		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
5.308		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
5.302		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
5.286		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
5.251		Host Interactions Of HIV Factors R-HSA-162909
5.235		UCH Proteinases R-HSA-5689603
5.201		Switching Of Origins To A Post-Replicative State R-HSA-69052

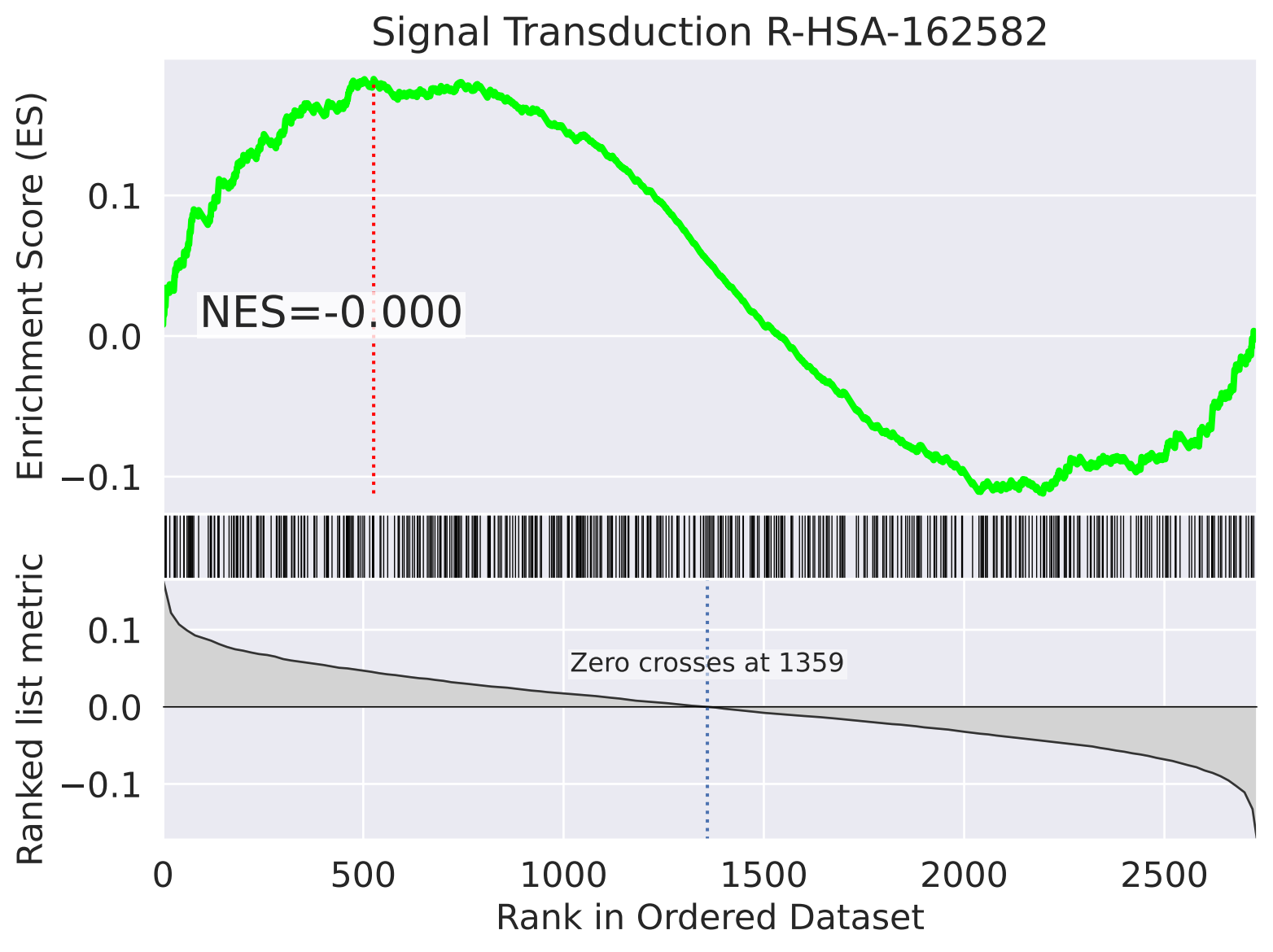
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=14

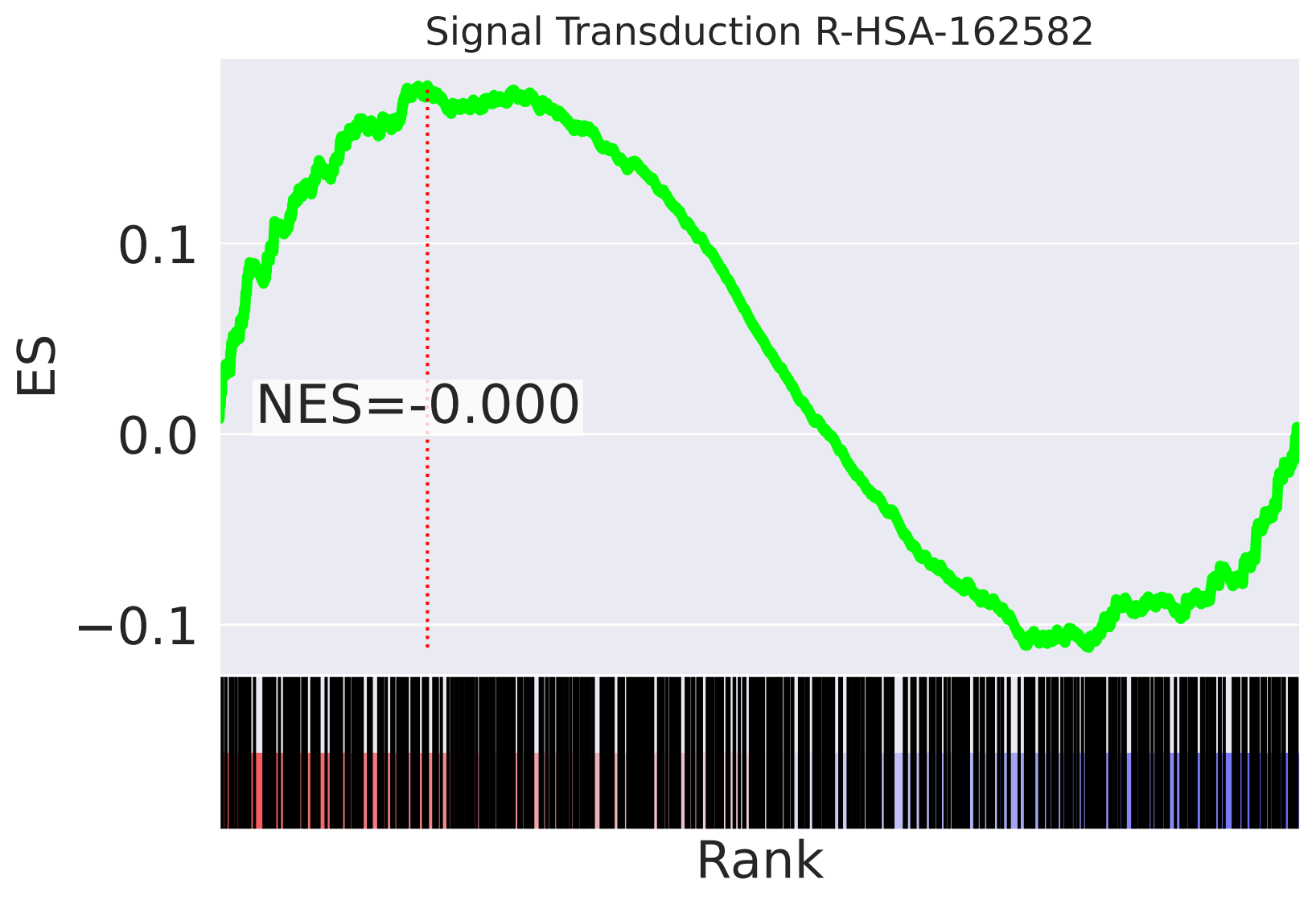

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=0.033
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1366
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

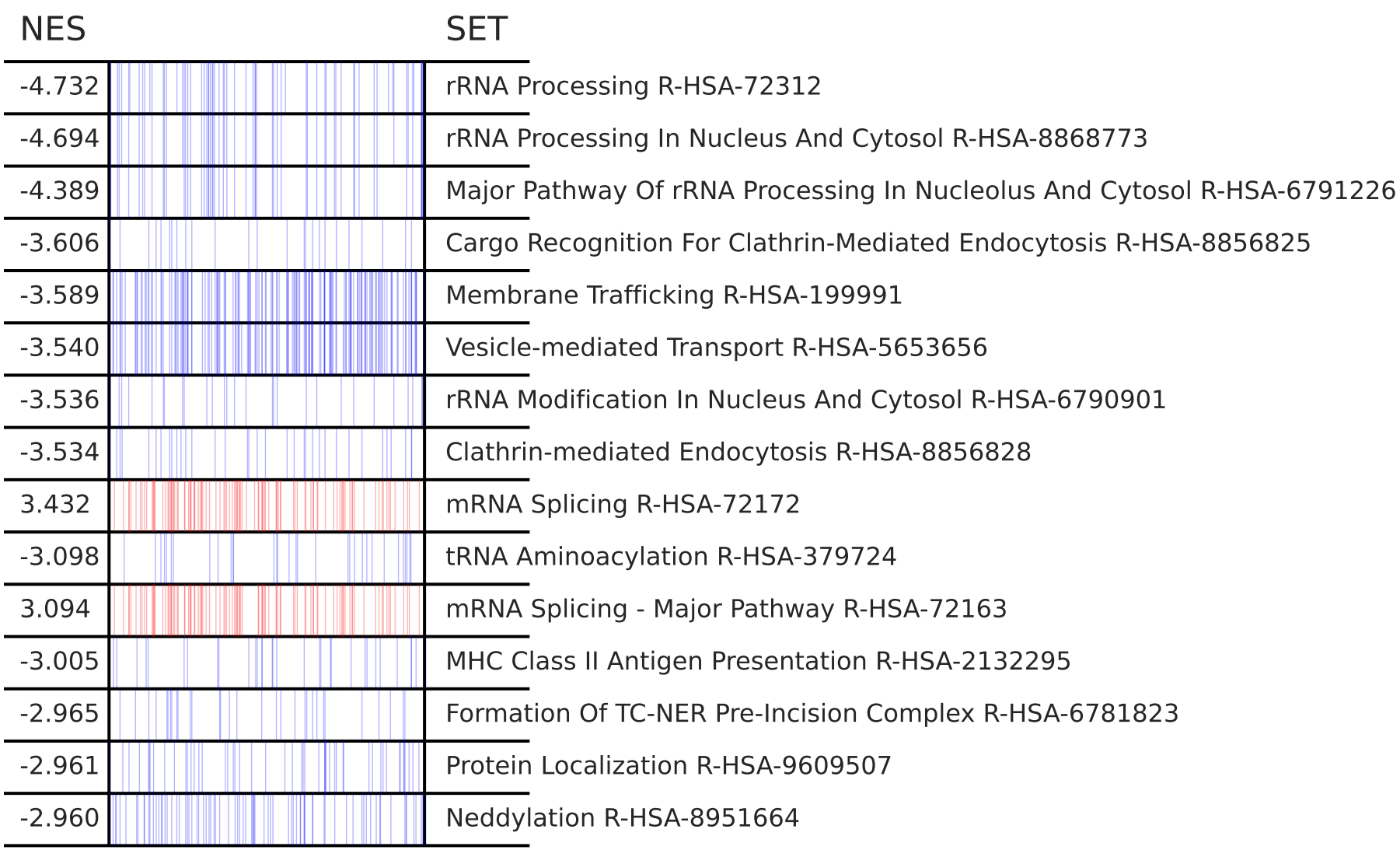

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=0.033
Rank

NES		SET
-4.925		rRNA Processing R-HSA-72312
-4.791		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-4.763		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.302		RNA Polymerase II Pre-transcription Events R-HSA-674695
3.592		HIV Transcription Initiation R-HSA-167161
3.463		mRNA Splicing - Minor Pathway R-HSA-72165
3.454		Transcription Of HIV Genome R-HSA-167172
-3.431		DNA Double Strand Break Response R-HSA-5693606
-3.419		Recruitment And ATM-mediated Phosphorylation Of Repair And Signal Proteins At DNA Double Strand Breaks R-HSA-5693565
-3.404		G2/M DNA Damage Checkpoint R-HSA-69473
3.331		mRNA Splicing R-HSA-72172
3.282		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-3.267		Nonhomologous End-Joining (NHEJ) R-HSA-5693571
3.215		Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.140		IRE1alpha Activates Chaperones R-HSA-381070

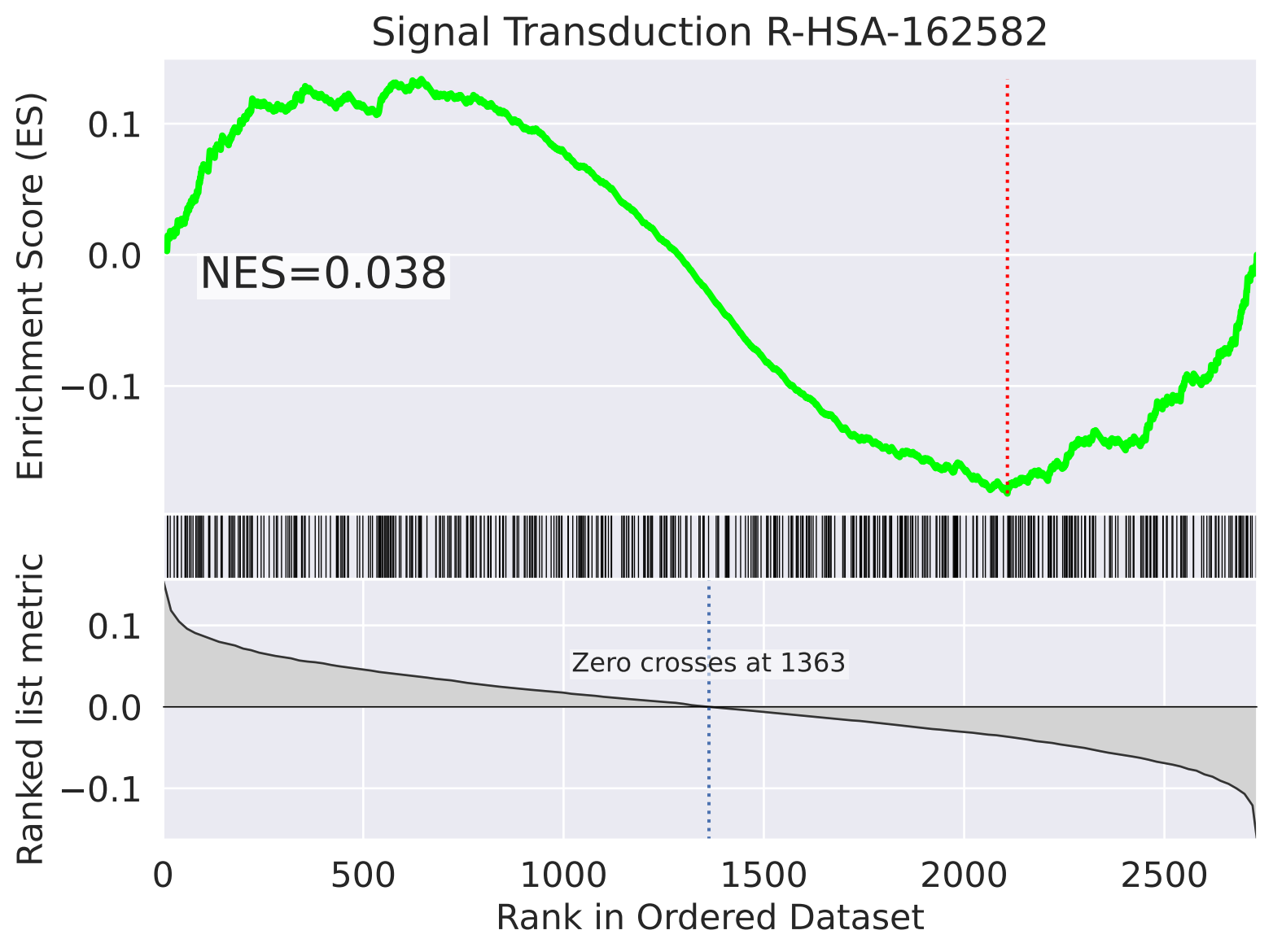
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=15

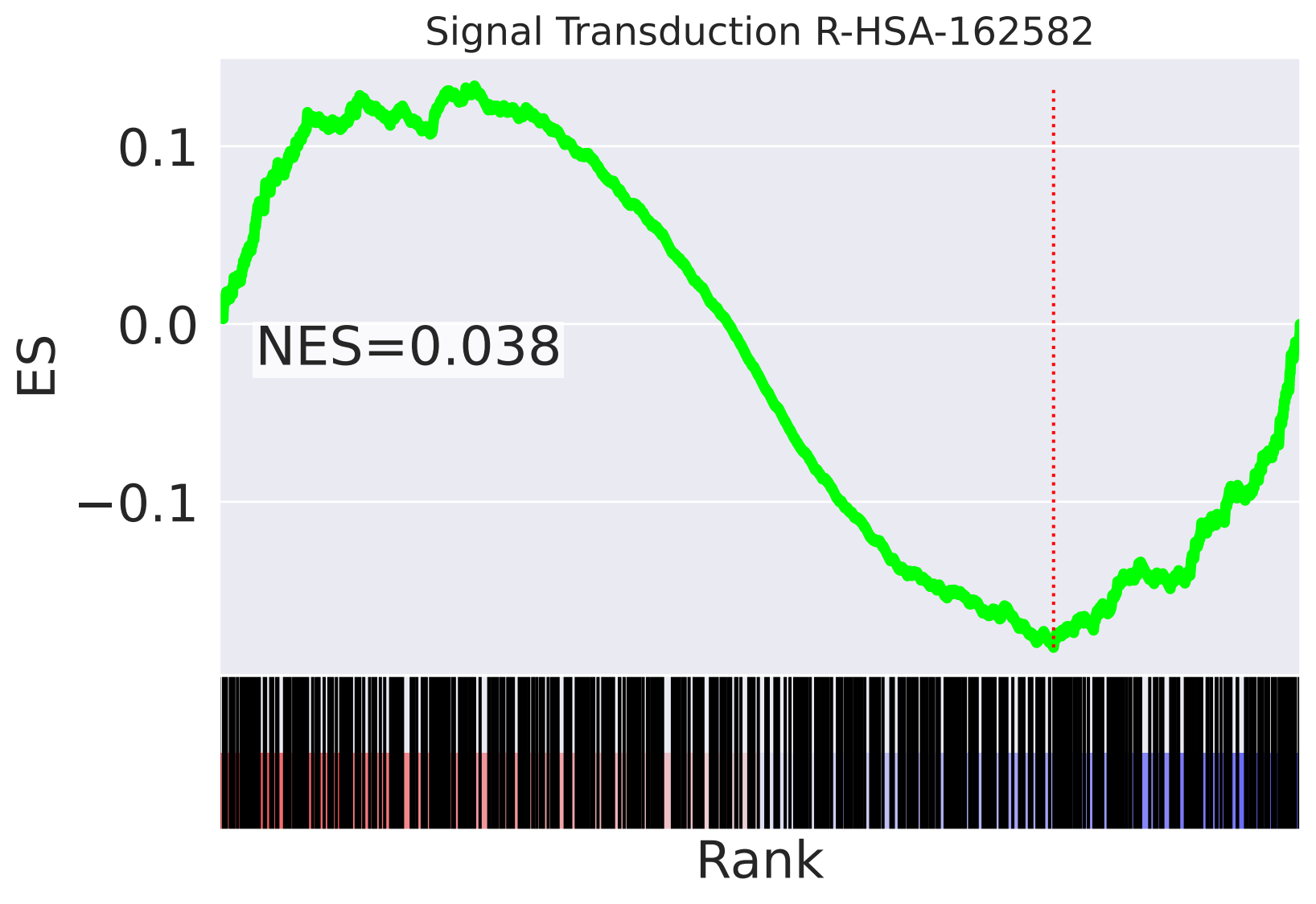

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1359
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

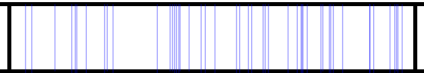
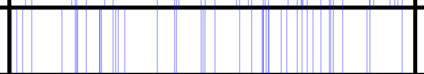
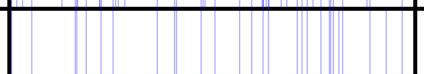
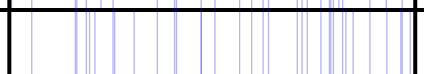
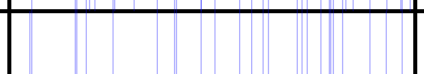
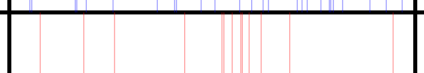
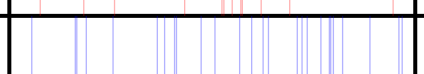
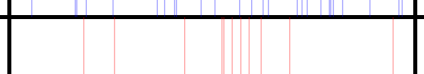
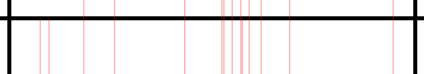
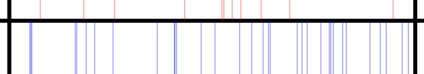
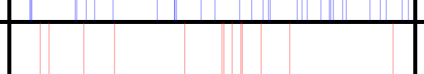
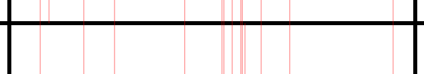

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-4.732
rRNA Processing R-HSA-72312
-4.694
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.389
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.606
Cargo Recognition For Clathrin-Mediated Endocytosis R-HSA-8856825
-3.589
Membrane Trafficking R-HSA-199991
-3.540
Vesicle-mediated Transport R-HSA-5653656
-3.536
rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-3.534
Clathrin-mediated Endocytosis R-HSA-8856828
3.432
mRNA Splicing R-HSA-72172
-3.098
tRNA Aminoacylation R-HSA-379724
3.094
mRNA Splicing - Major Pathway R-HSA-72163
-3.005
MHC Class II Antigen Presentation R-HSA-2132295
-2.965
Formation Of TC-NER Pre-Incision Complex R-HSA-6781823
-2.961
Protein Localization R-HSA-9609507
-2.960
Neddylation R-HSA-8951664

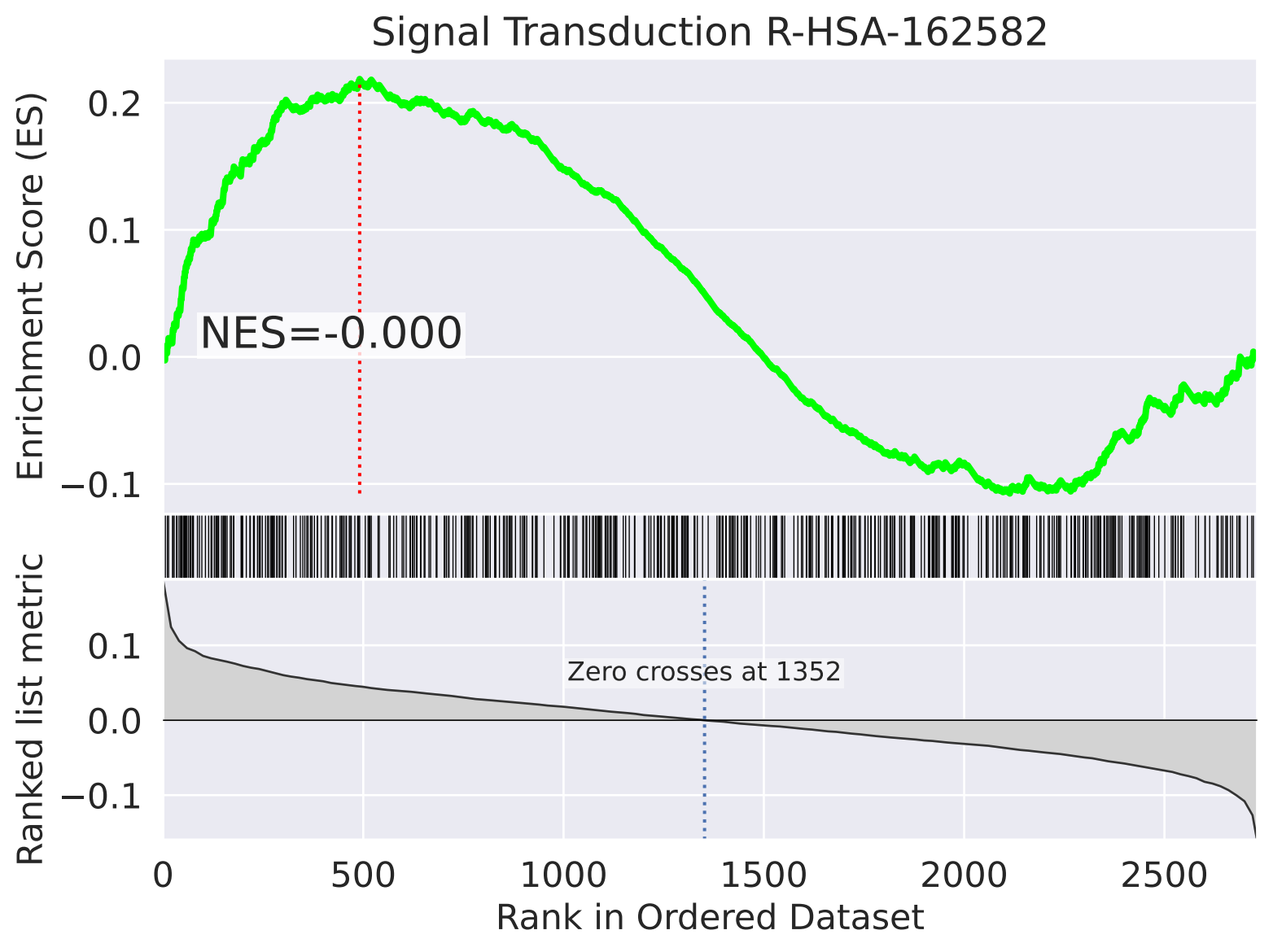
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=16

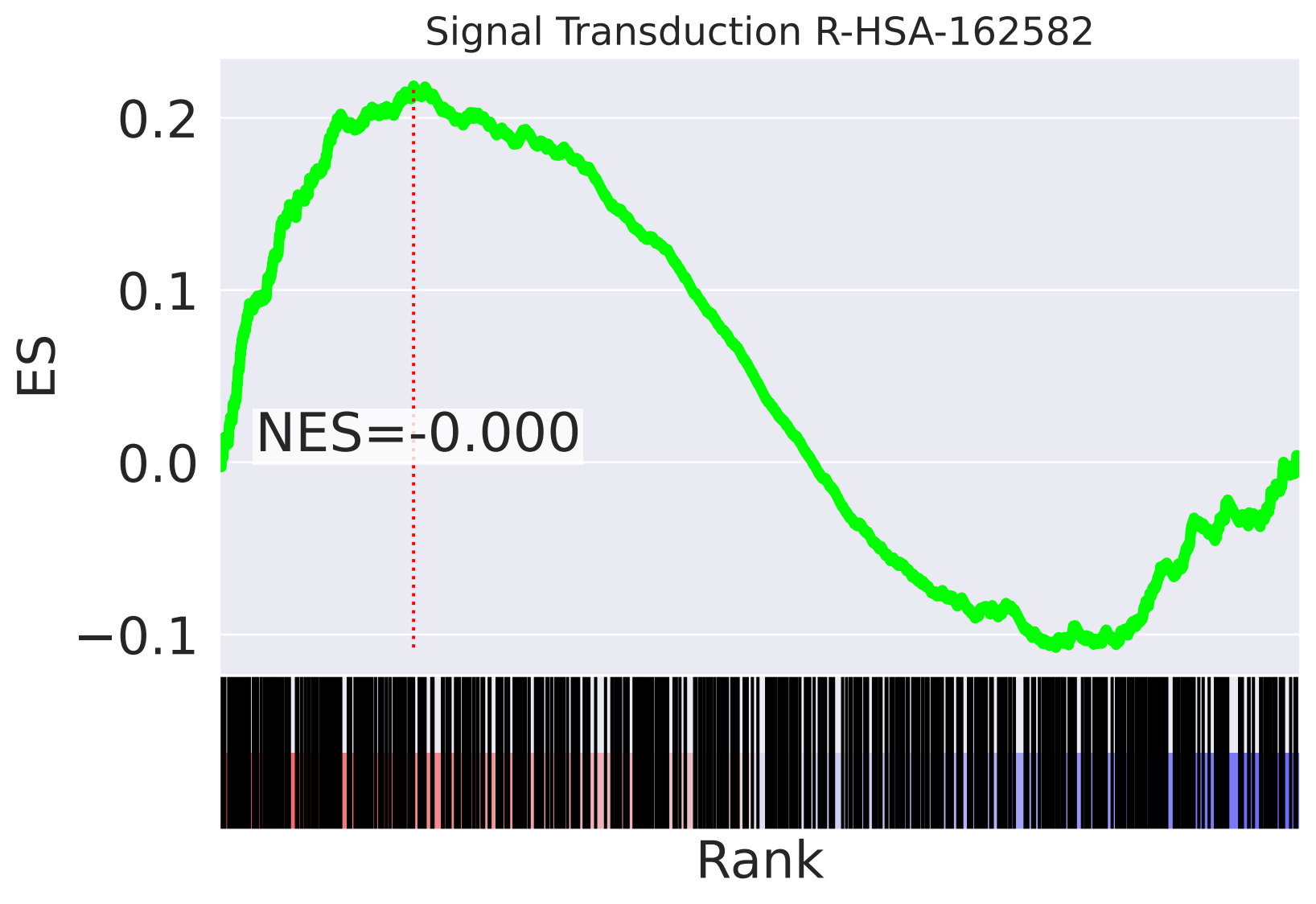

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=0.038
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1363
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

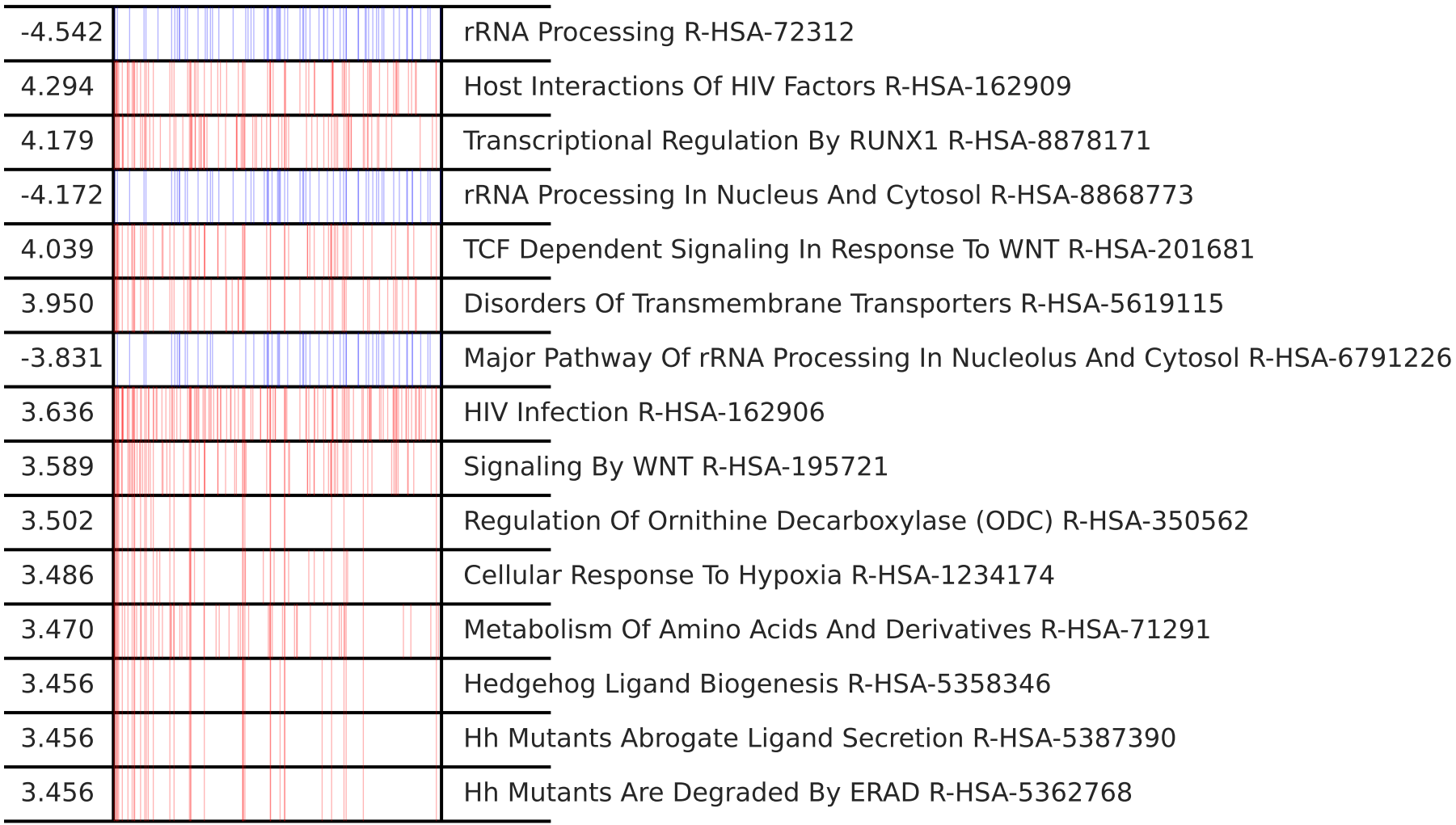

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=0.038
Rank

NES		SET
-4.169		Cellular Response To Heat Stress R-HSA-3371556
-4.084		Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
-3.580		HCMV Late Events R-HSA-9610379
-3.343		SUMOylation Of RNA Binding Proteins R-HSA-4570464
-3.233		Viral Messenger RNA Synthesis R-HSA-168325
-3.138		SUMOylation Of SUMOylation Proteins R-HSA-4085377
3.121		L13a-mediated Translational Silencing Of Ceruloplasmin Expression R-HSA-156827
3.060		Translation Initiation Complex Formation R-HSA-72649
-3.034		Nuclear Pore Complex (NPC) Disassembly R-HSA-3301854
3.016		Formation Of A Pool Of Free 40S Subunits R-HSA-72689
3.000		GTP Hydrolysis And Joining Of 60S Ribosomal Subunit R-HSA-72706
2.981		Formation Of Ternary Complex, And Subsequently, 43S Complex R-HSA-72695
-2.961		SUMOylation Of DNA Replication Proteins R-HSA-4615885
2.930		Ribosomal Scanning And Start Codon Recognition R-HSA-72702
2.898		mRNA Activation Upon Binding Of Cap-Binding Complex And eIFs, Subsequent Binding To 43S R-HSA-72662

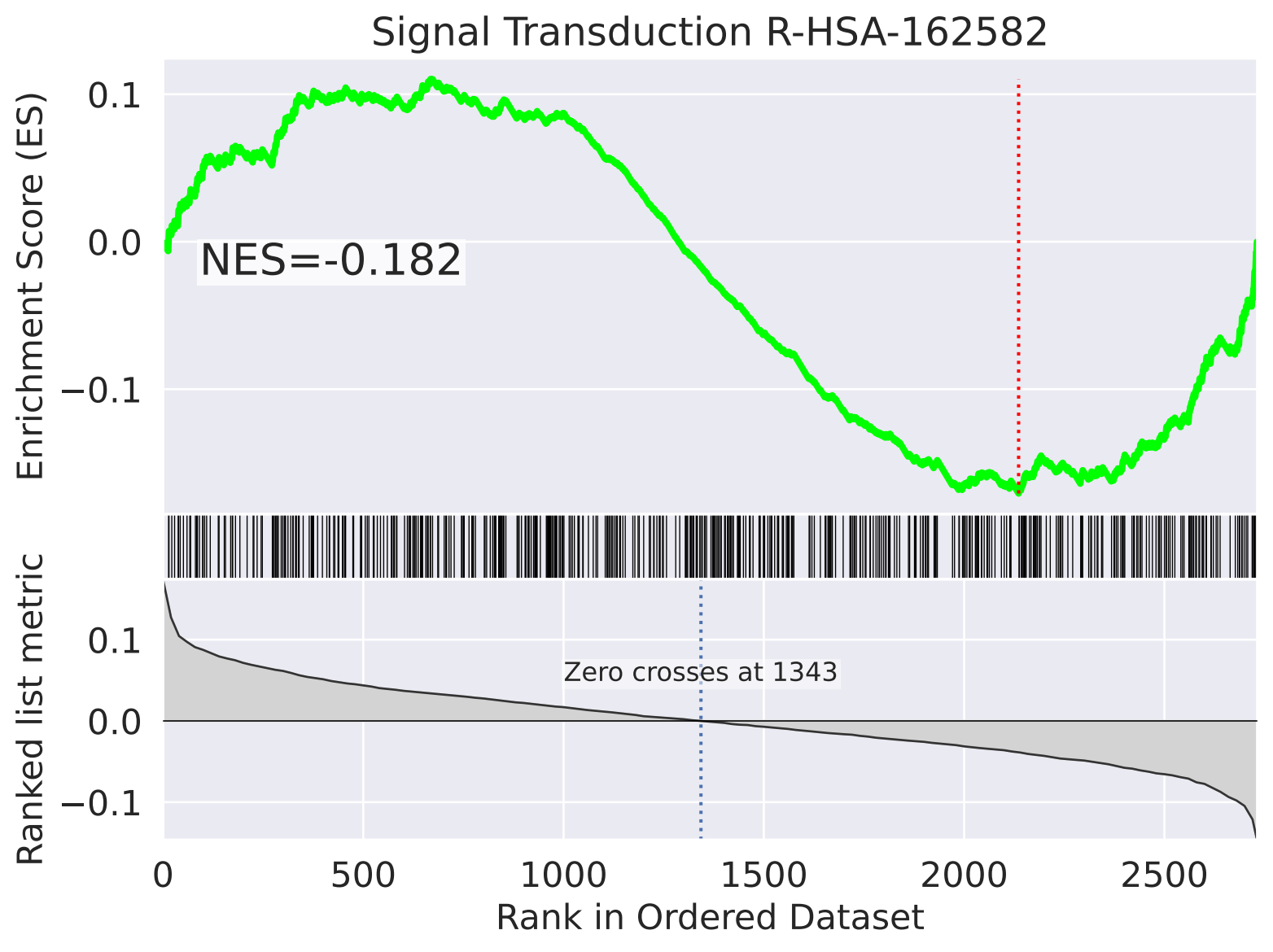
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=17

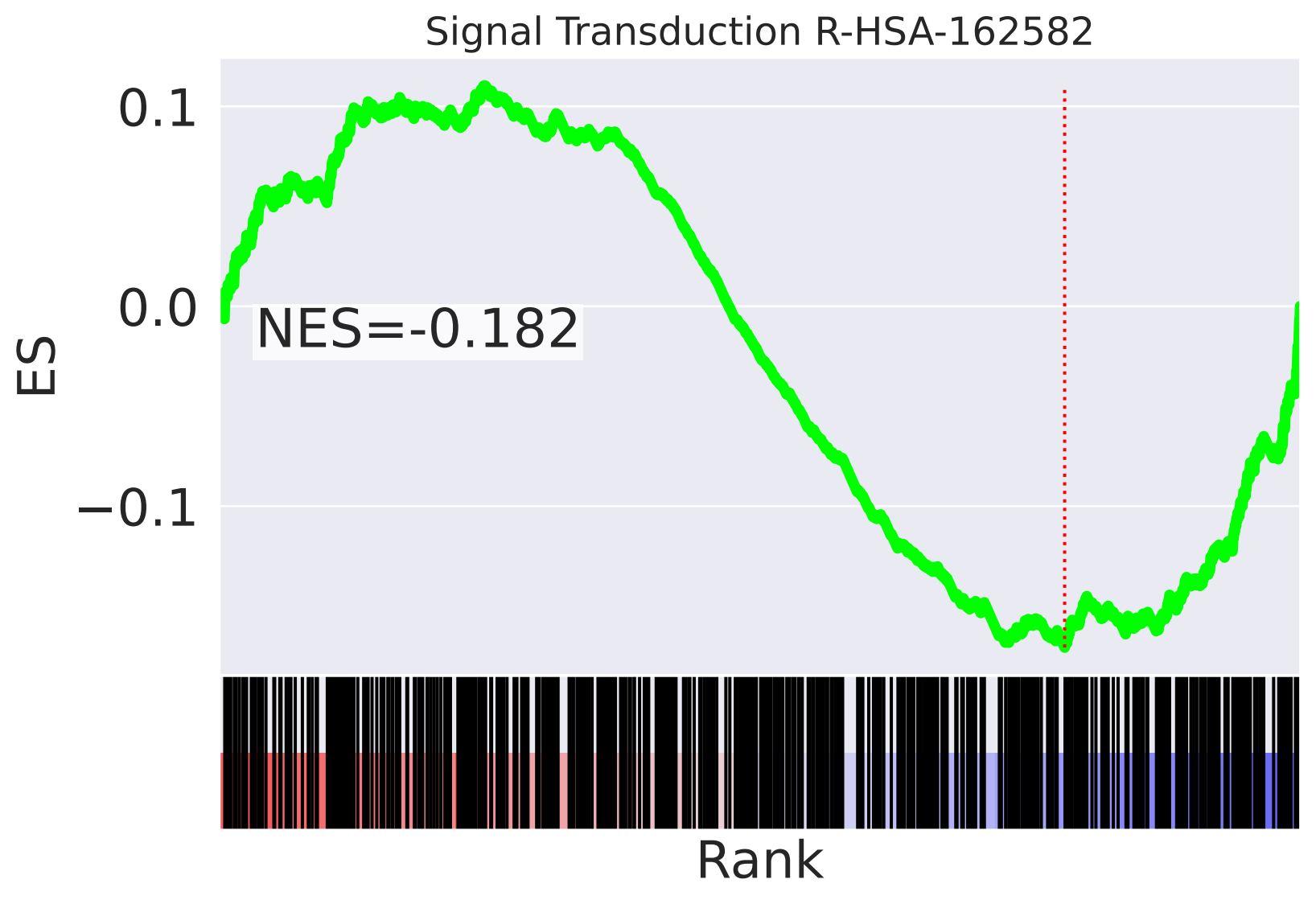

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1352
0
500
1000
1500
2000
2500
Rank in Ordered Dataset


Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-4.542
rRNA Processing R-HSA-72312
4.294
Host Interactions Of HIV Factors R-HSA-162909
4.179
Transcriptional Regulation By RUNX1 R-HSA-8878171
-4.172
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.039
TCF Dependent Signaling In Response To WNT R-HSA-201681
3.950
Disorders Of Transmembrane Transporters R-HSA-5619115
-3.831
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.636
HIV Infection R-HSA-162906
3.589
Signaling By WNT R-HSA-195721
3.502
Regulation Of Ornithine Decarboxylase (ODC) R-HSA-350562
3.486
Cellular Response To Hypoxia R-HSA-1234174
3.470
Metabolism Of Amino Acids And Derivatives R-HSA-71291
3.456
Hedgehog Ligand Biogenesis R-HSA-5358346
3.456
Hh Mutants Abrogate Ligand Secretion R-HSA-5387390
3.456
Hh Mutants Are Degraded By ERAD R-HSA-5362768

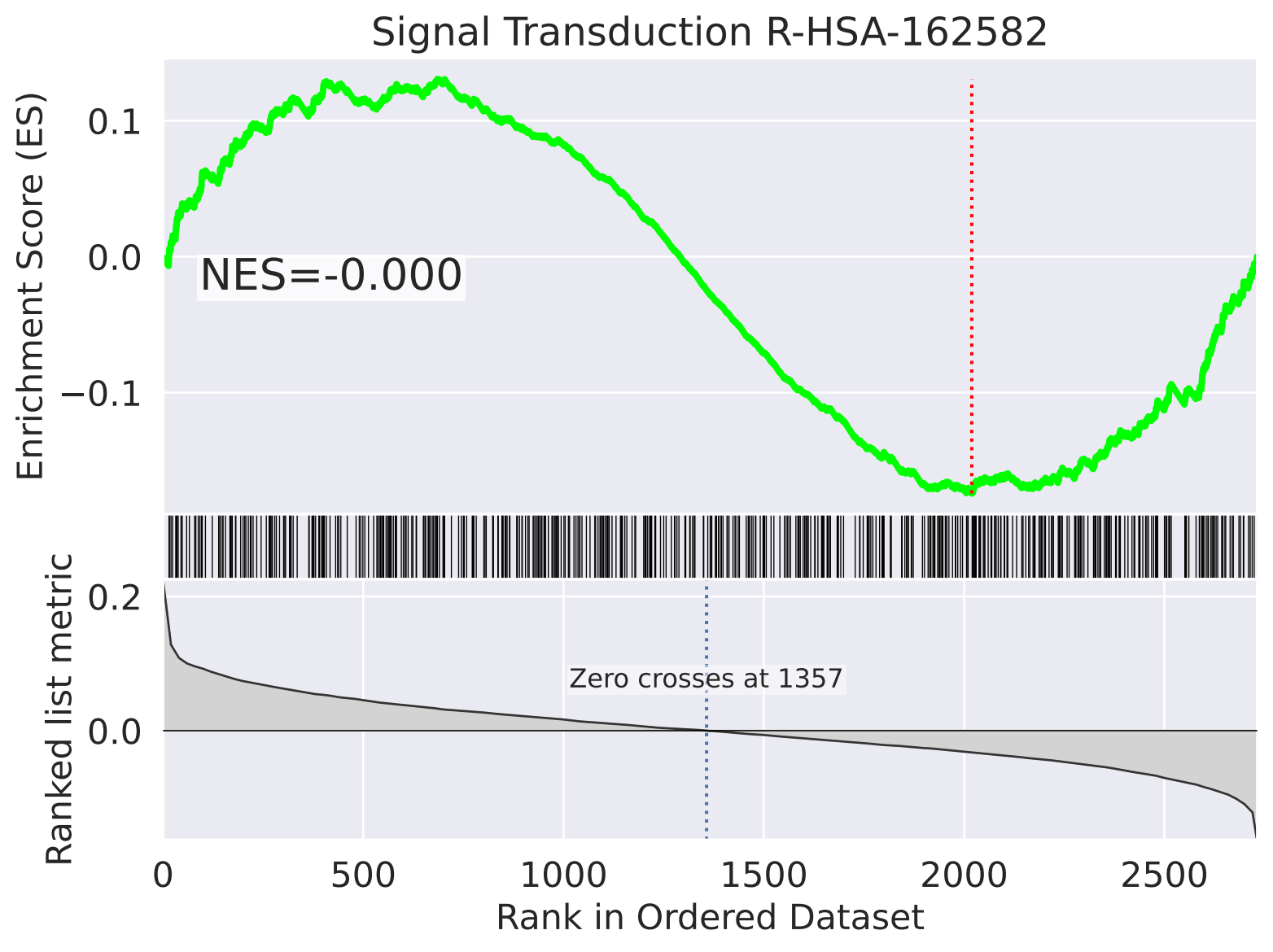
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=18

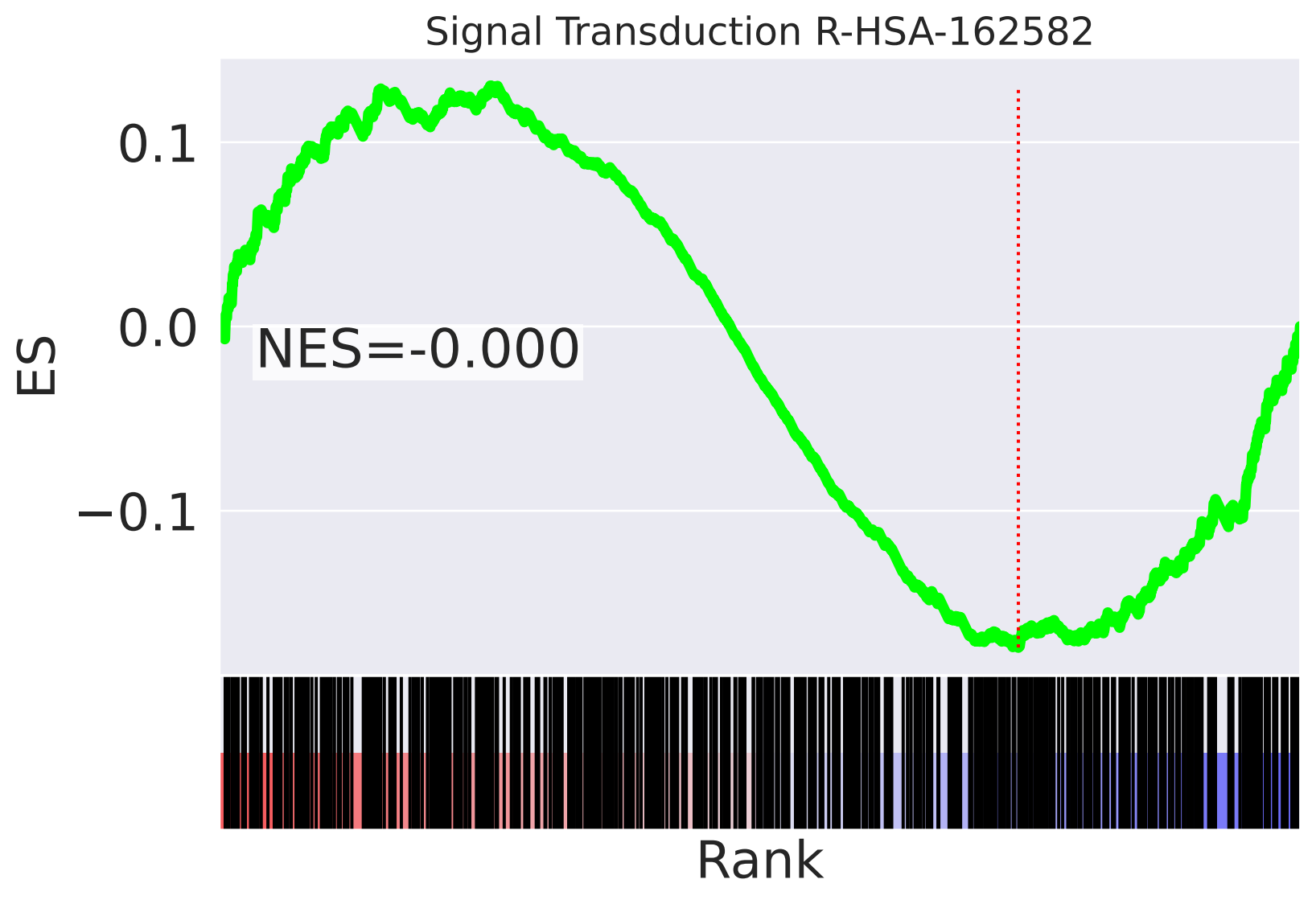

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.182
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1343
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

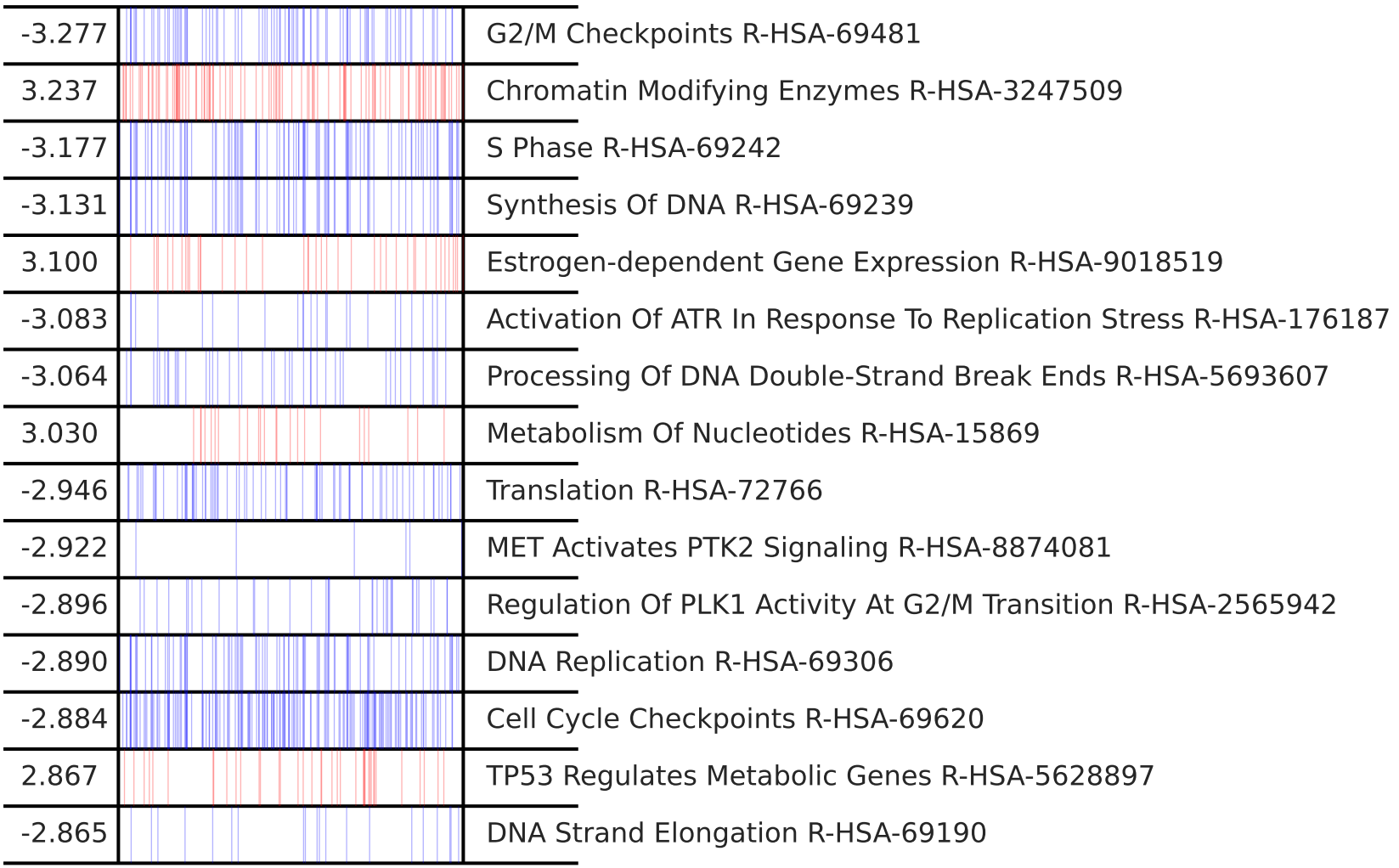

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.182
Rank

NES	SET
7.569	Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
7.499	Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.979	Respiratory Electron Transport R-HSA-611105
5.924	Complex I Biogenesis R-HSA-6799198
3.853	Mitochondrial Biogenesis R-HSA-1592230
3.686	TP53 Regulates Metabolic Genes R-HSA-5628897
-3.576	Fcgamma Receptor (FCGR) Dependent Phagocytosis R-HSA-2029480
-3.470	Regulation Of Actin Dynamics For Phagocytic Cup Formation R-HSA-2029482
3.395	Cytoprotection By HMOX1 R-HSA-9707564
-3.362	Signaling By MET R-HSA-6806834
-3.337	FCGR3A-mediated Phagocytosis R-HSA-9664422
-3.317	Signaling By Rho GTPases R-HSA-194315
-3.259	VEGFA-VEGFR2 Pathway R-HSA-4420097
-3.247	RAC2 GTPase Cycle R-HSA-9013404
-3.227	HATs Acetylate Histones R-HSA-3214847

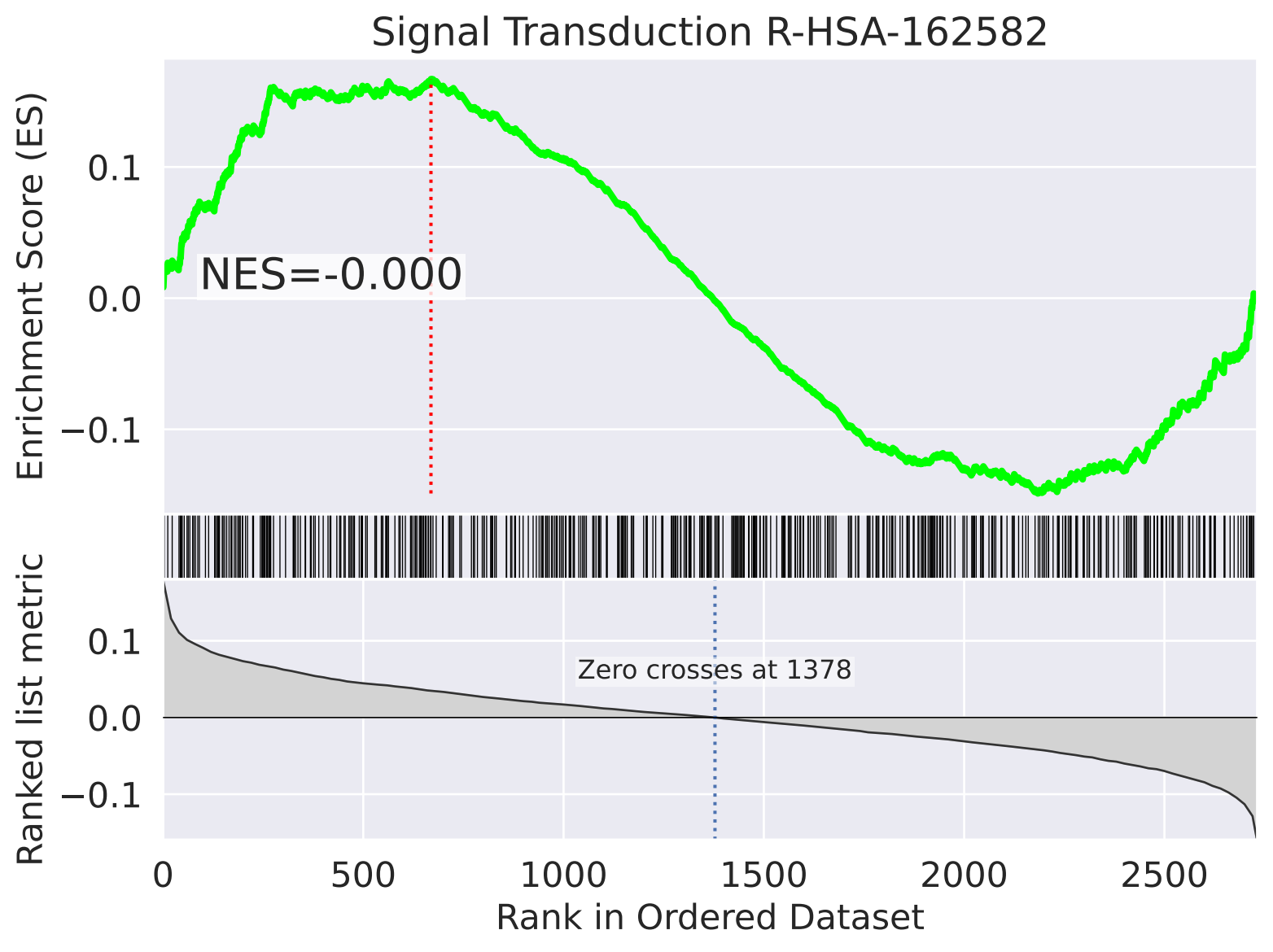
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=19

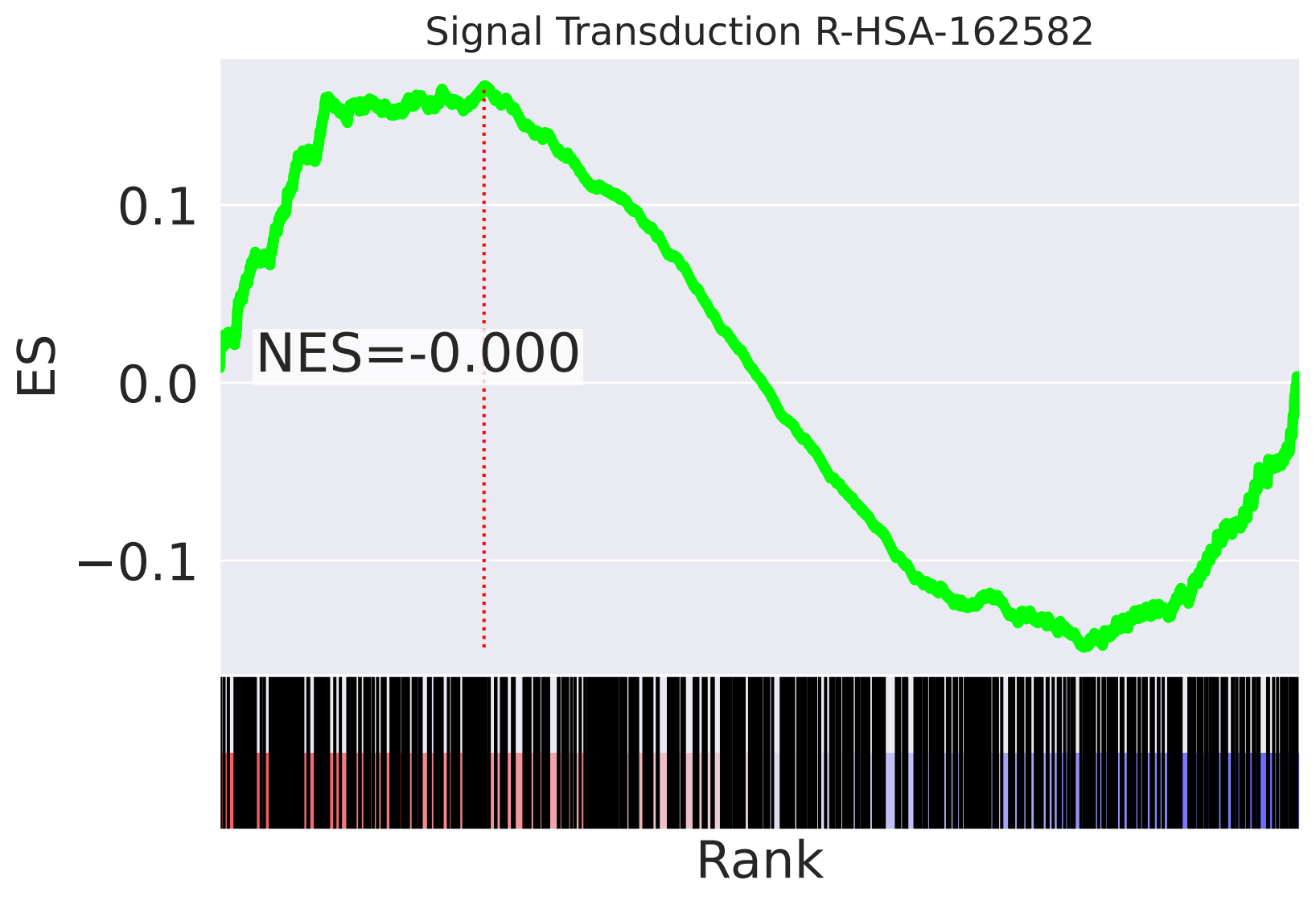

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.2
0.0
Zero crosses at 1357
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

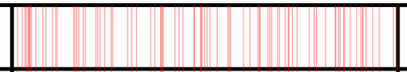
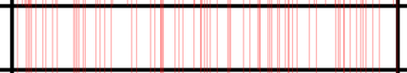
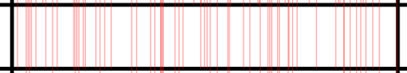
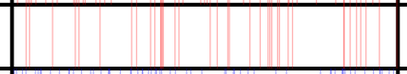
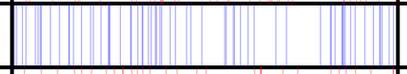
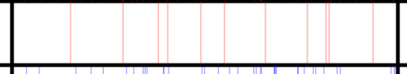
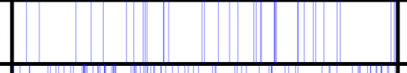
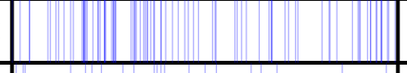
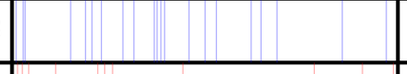
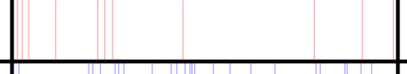
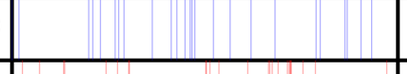
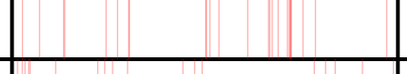
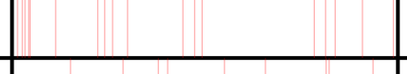
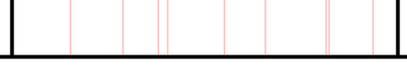

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-3.277
G2/M Checkpoints R-HSA-69481
3.237
Chromatin Modifying Enzymes R-HSA-3247509
-3.177
S Phase R-HSA-69242
-3.131
Synthesis Of DNA R-HSA-69239
3.100
Estrogen-dependent Gene Expression R-HSA-9018519
-3.083
Activation Of ATR In Response To Replication Stress R-HSA-176187
-3.064
Processing Of DNA Double-Strand Break Ends R-HSA-5693607
3.030
Metabolism Of Nucleotides R-HSA-15869
-2.946
Translation R-HSA-72766
-2.922
MET Activates PTK2 Signaling R-HSA-8874081
-2.896
Regulation Of PLK1 Activity At G2/M Transition R-HSA-2565942
-2.890
DNA Replication R-HSA-69306
-2.884
Cell Cycle Checkpoints R-HSA-69620
2.867
TP53 Regulates Metabolic Genes R-HSA-5628897
-2.865
DNA Strand Elongation R-HSA-69190

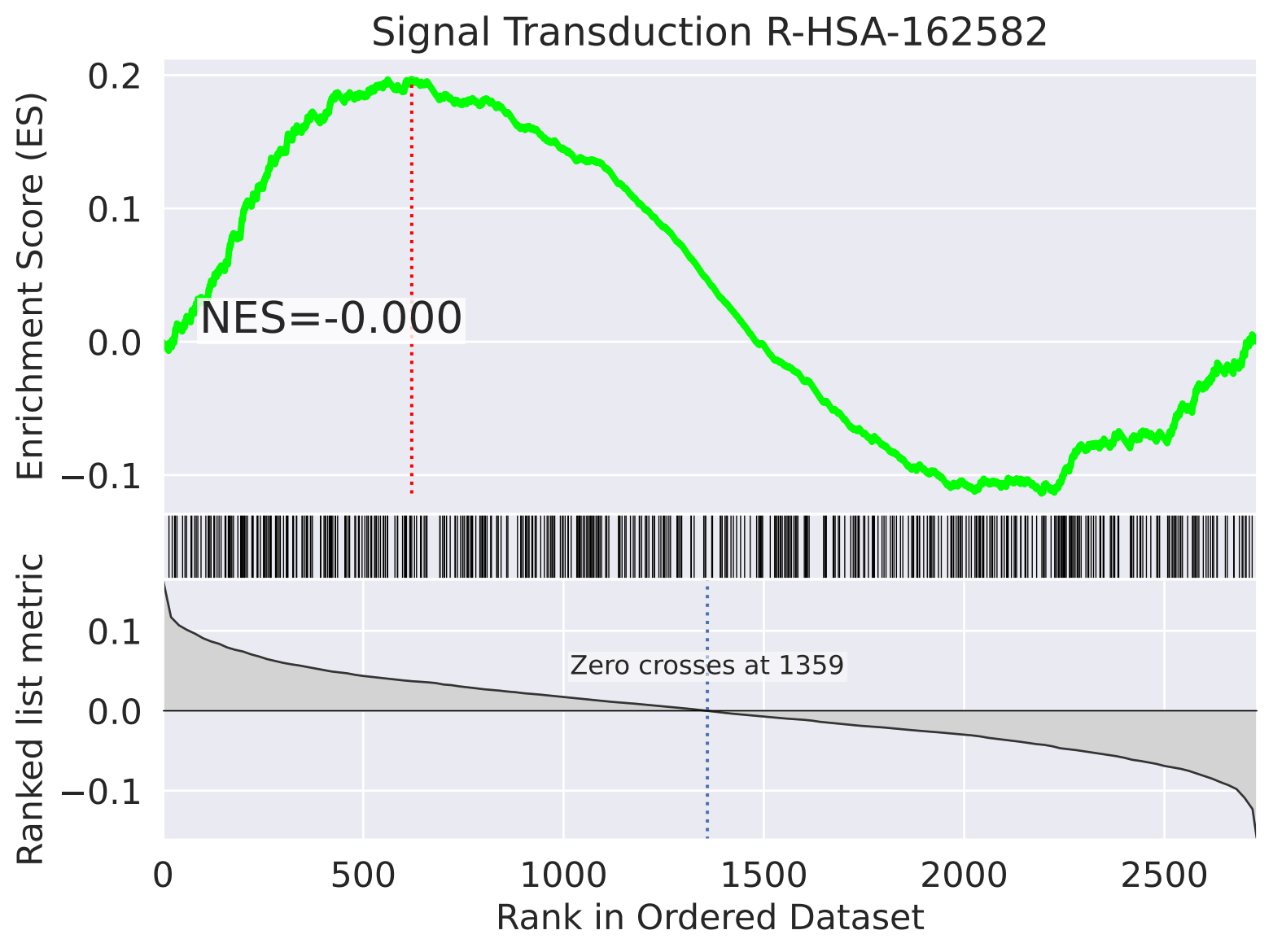
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=20

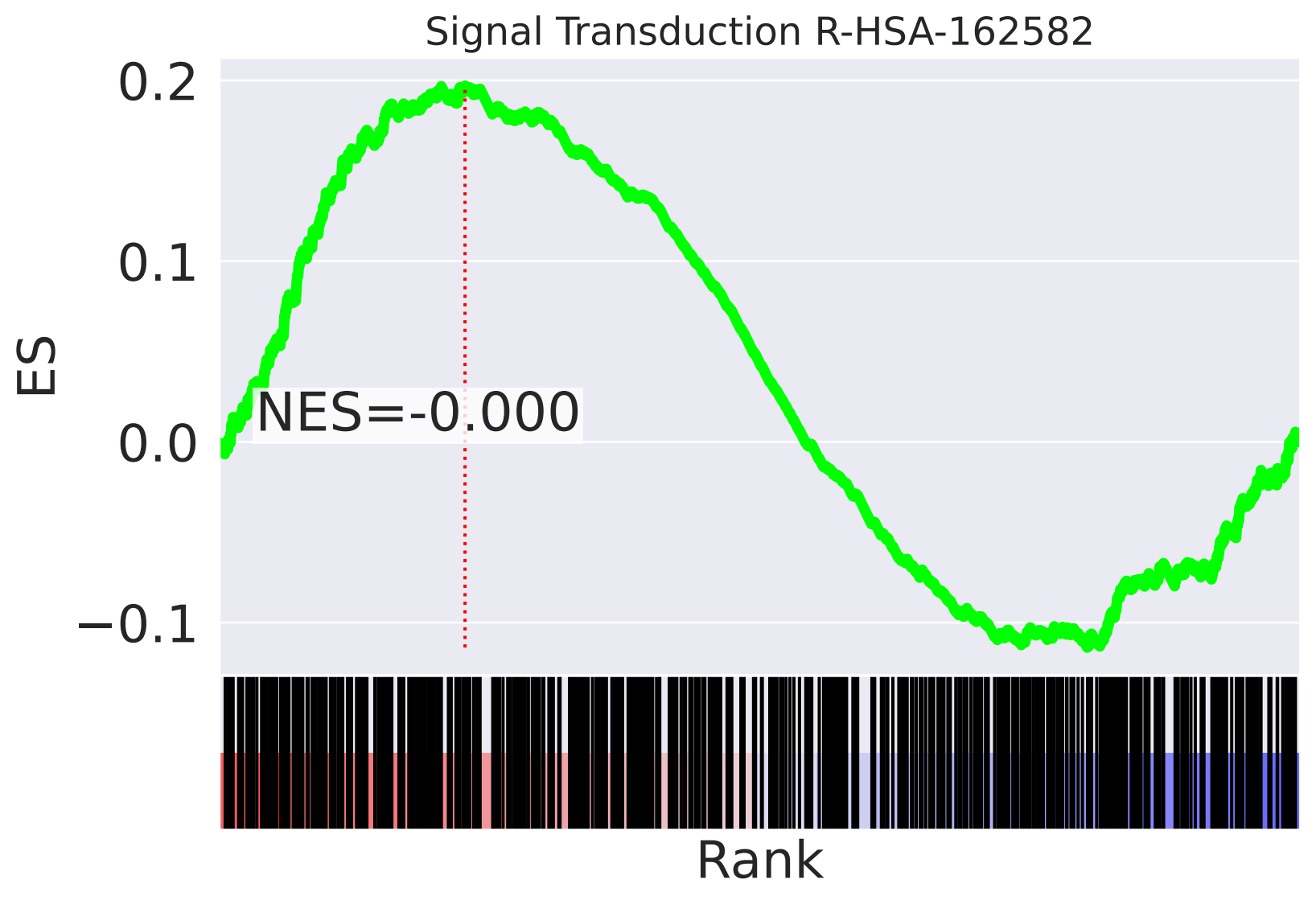

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1378
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

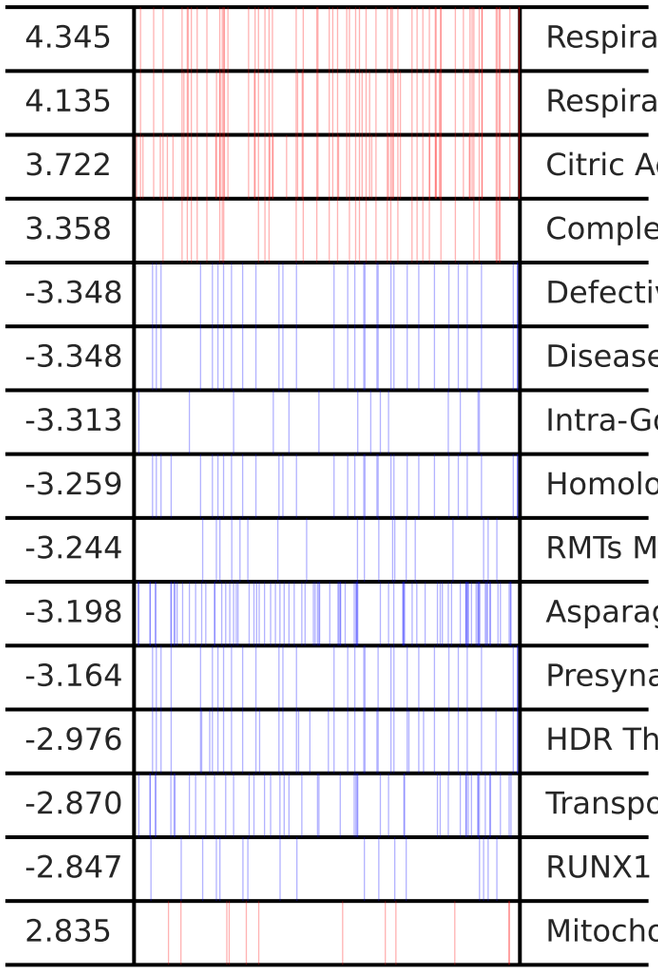

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.919		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.712		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.551		Respiratory Electron Transport R-HSA-611105
4.558		Complex I Biogenesis R-HSA-6799198
-3.296		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.219		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.136		Nucleotide Biosynthesis R-HSA-8956320
-3.043		Factors Involved In Megakaryocyte Development And Platelet Production R-HSA-983231
-2.952		Neutrophil Degranulation R-HSA-6798695
-2.928		COPII-mediated Vesicle Transport R-HSA-204005
2.926		Citric Acid Cycle (TCA Cycle) R-HSA-71403
-2.869		Diseases Of Glycosylation R-HSA-3781865
2.865		Fanconi Anemia Pathway R-HSA-6783310
2.843		Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
2.823		Purine Ribonucleoside Monophosphate Biosynthesis R-HSA-73817

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

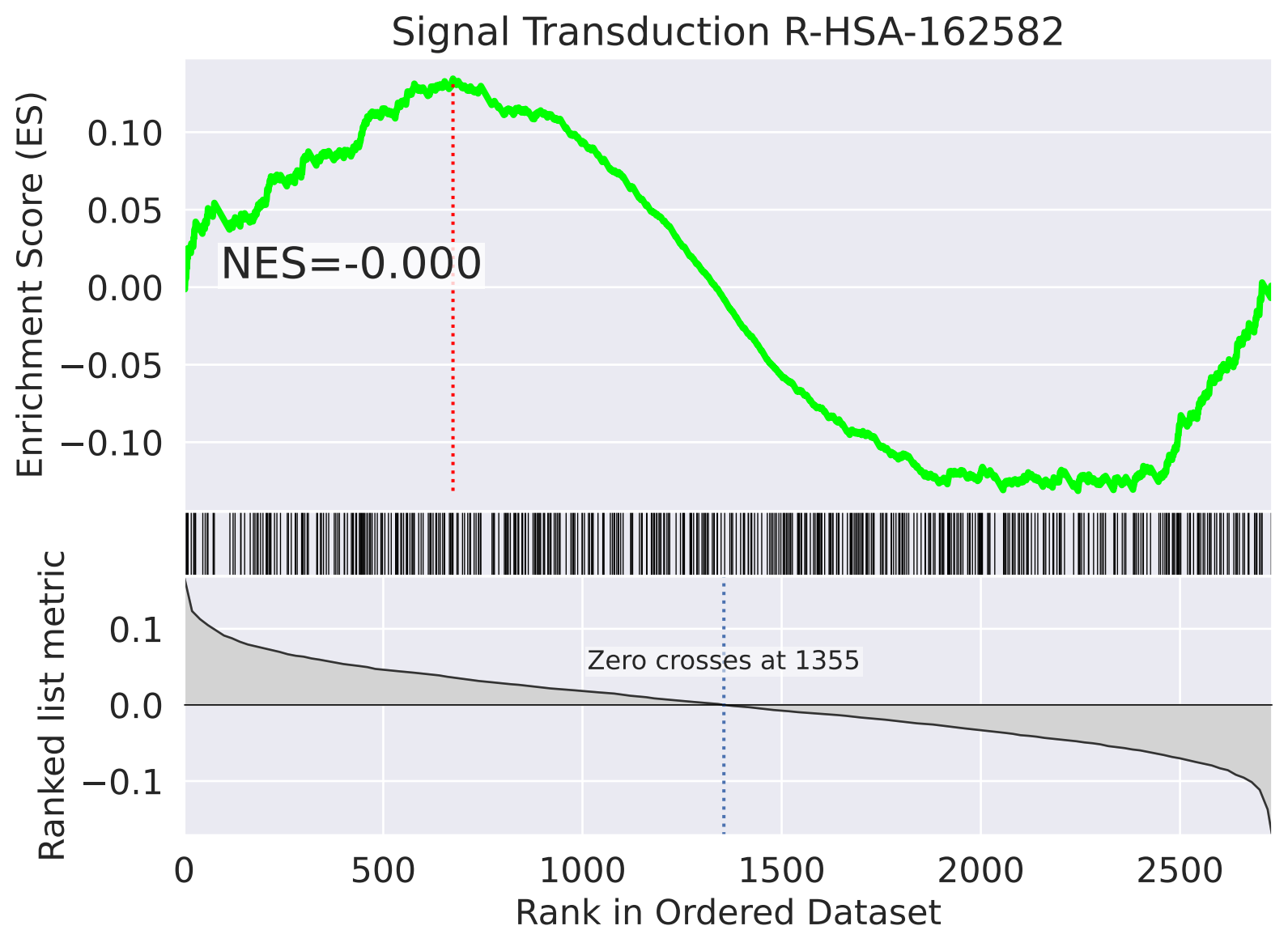

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1359
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

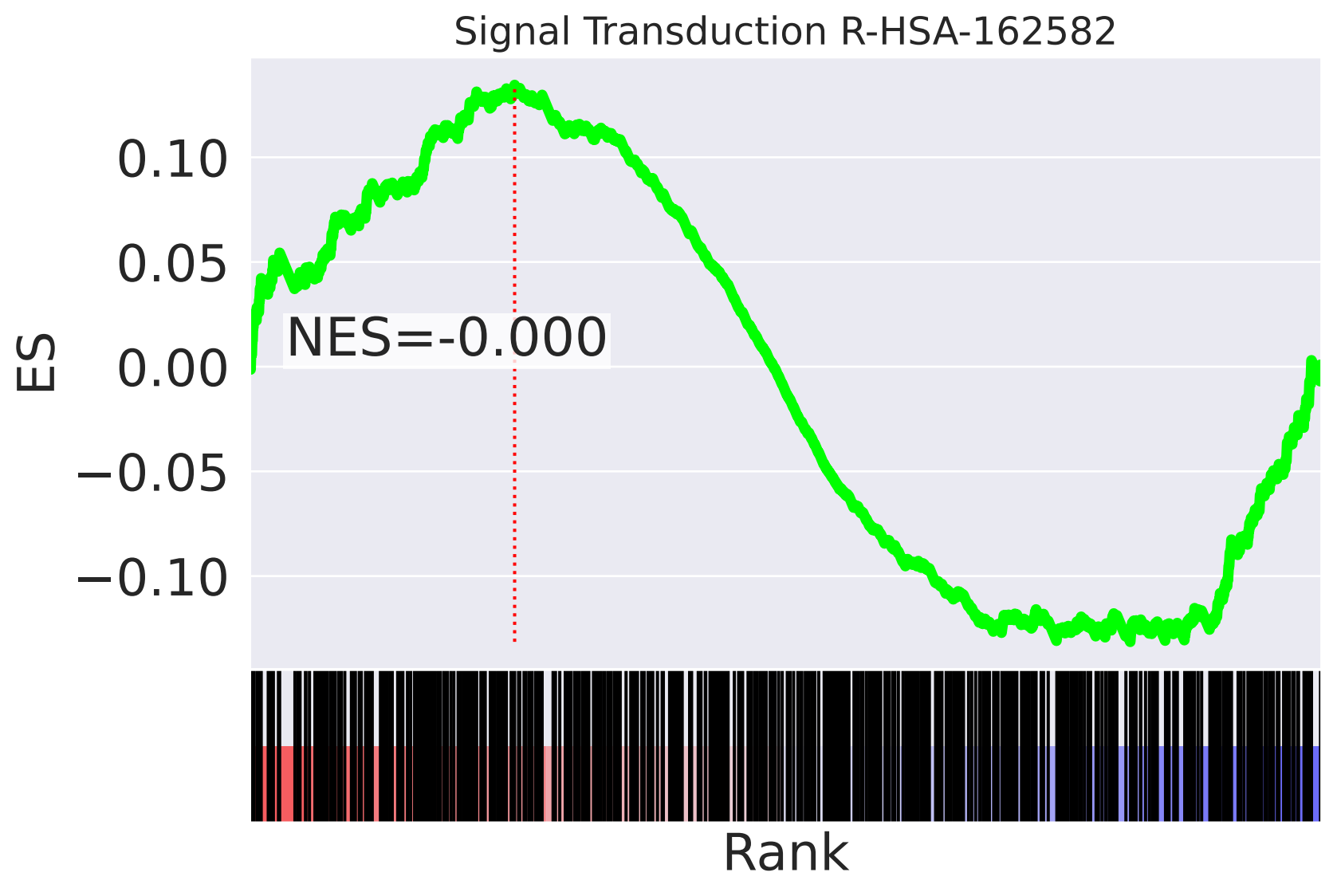

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank

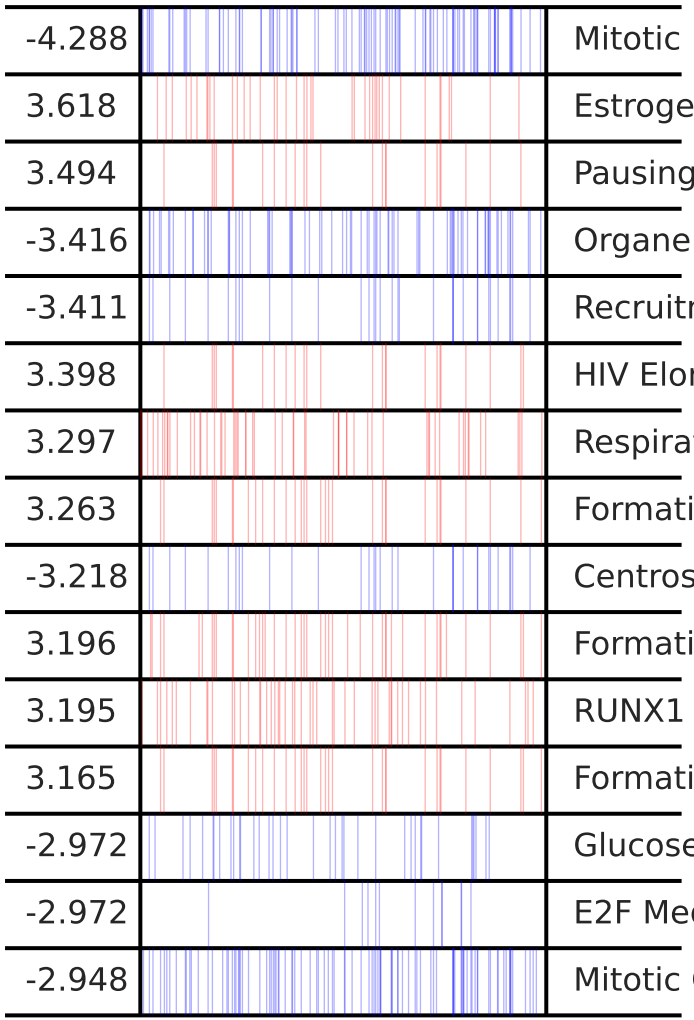


NES	SET
4.345	Respiratory Electron Transport R-HSA-611105
4.135	Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.722	Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
3.358	Complex I Biogenesis R-HSA-6799198
-3.348	Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.348	Diseases Of DNA Repair R-HSA-9675135
-3.313	Intra-Golgi Traffic R-HSA-6811438
-3.259	Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.244	RMTs Methylate Histone Arginines R-HSA-3214858
-3.198	Asparagine N-linked Glycosylation R-HSA-446203
-3.164	Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
-2.976	HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-2.870	Transport To Golgi And Subsequent Modification R-HSA-948021
-2.847	RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
2.835	Mitochondrial Iron-Sulfur Cluster Biogenesis R-HSA-1362409

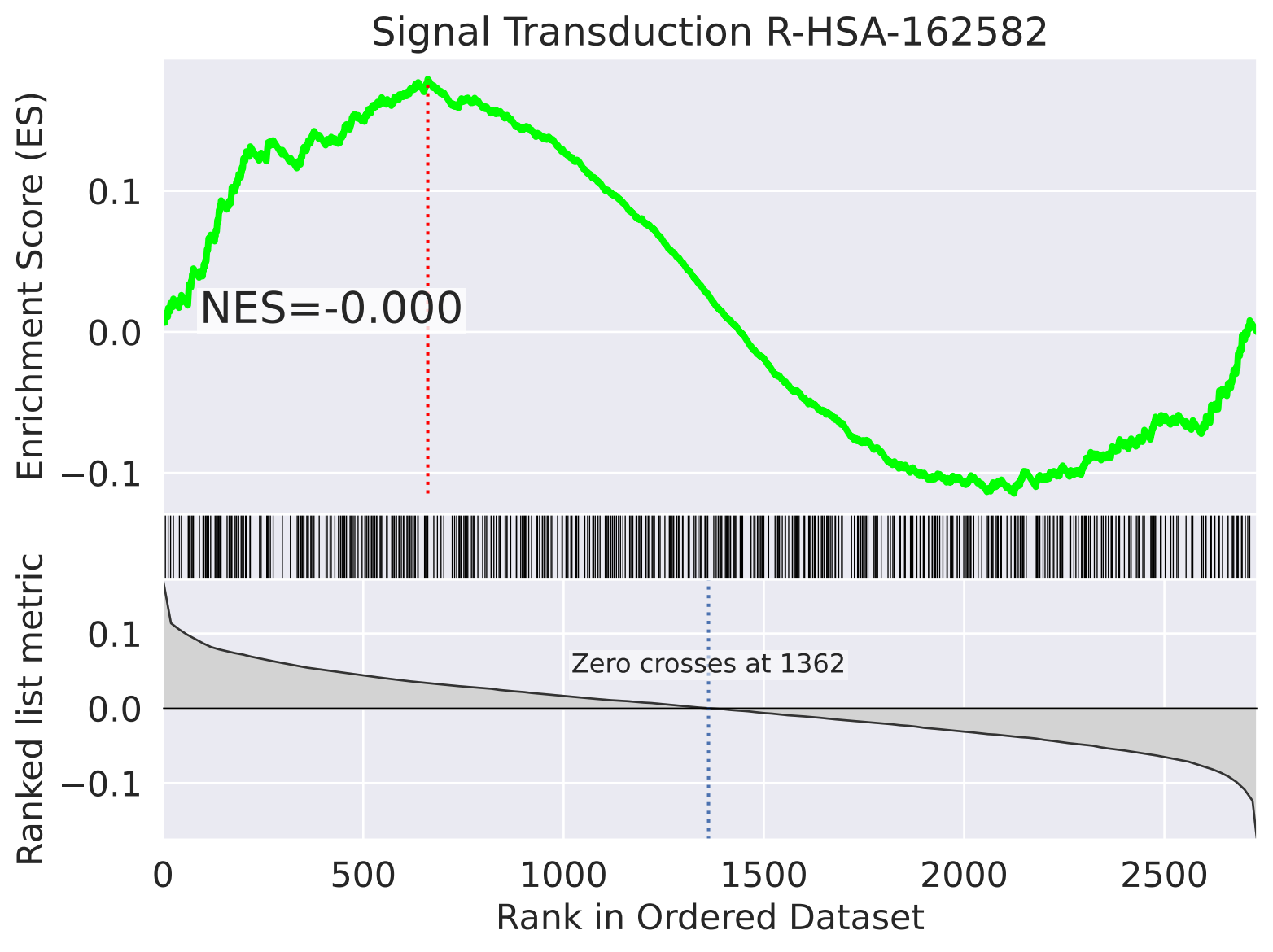
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=22

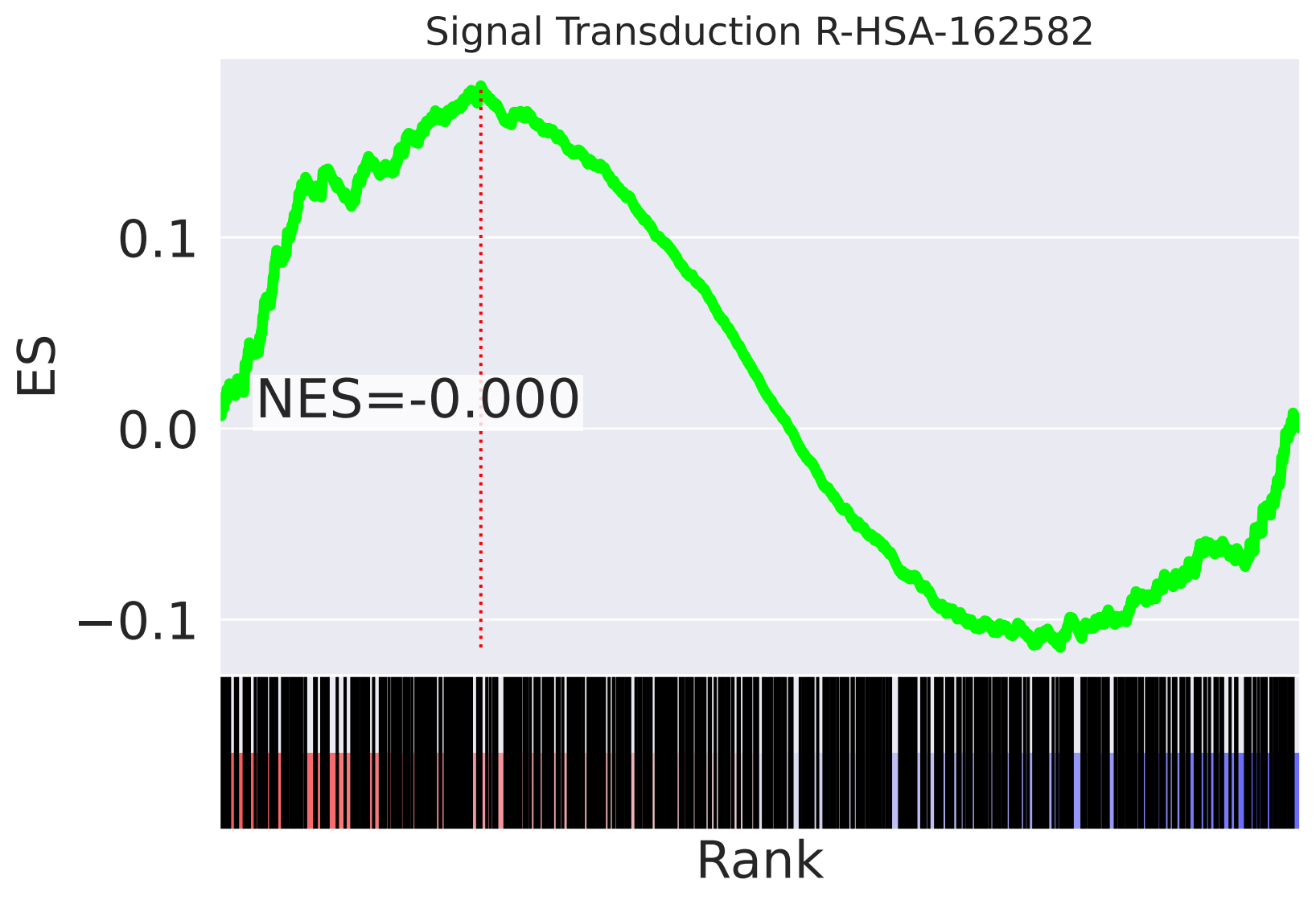

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.10
0.05
0.00
−0.05
−0.10
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1355
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

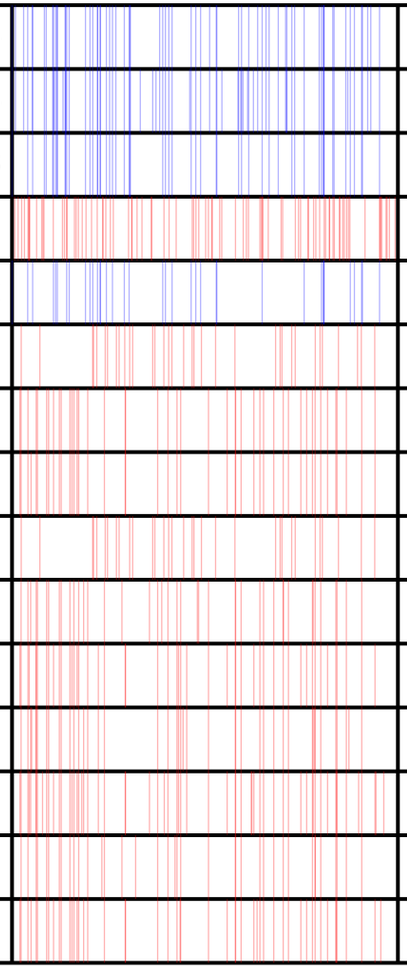

Signal Transduction R-HSA-162582
0.10
0.05
0.00
−0.05
−0.10
ES
NES=-0.000
Rank


NES
SET
-4.288
Mitotic Prometaphase R-HSA-68877
3.618
Estrogen-dependent Gene Expression R-HSA-9018519
3.494
Pausing And Recovery Of Tat-mediated HIV Elongation R-HSA-167238
-3.416
Organelle Biogenesis And Maintenance R-HSA-1852241
-3.411
Recruitment Of NuMA To Mitotic Centrosomes R-HSA-380320
3.398
HIV Elongation Arrest And Recovery R-HSA-167287
3.297
Respiratory Electron Transport R-HSA-611105
3.263
Formation Of HIV-1 Elongation Complex Containing HIV-1 Tat R-HSA-167200
-3.218
Centrosome Maturation R-HSA-380287
3.196
Formation Of RNA Pol II Elongation Complex R-HSA-112382
3.195
RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
3.165
Formation Of HIV Elongation Complex In Absence Of HIV Tat R-HSA-167152
-2.972
Glucose Metabolism R-HSA-70326
-2.972
E2F Mediated Regulation Of DNA Replication R-HSA-113510
-2.948
Mitotic G2-G2/M Phases R-HSA-453274

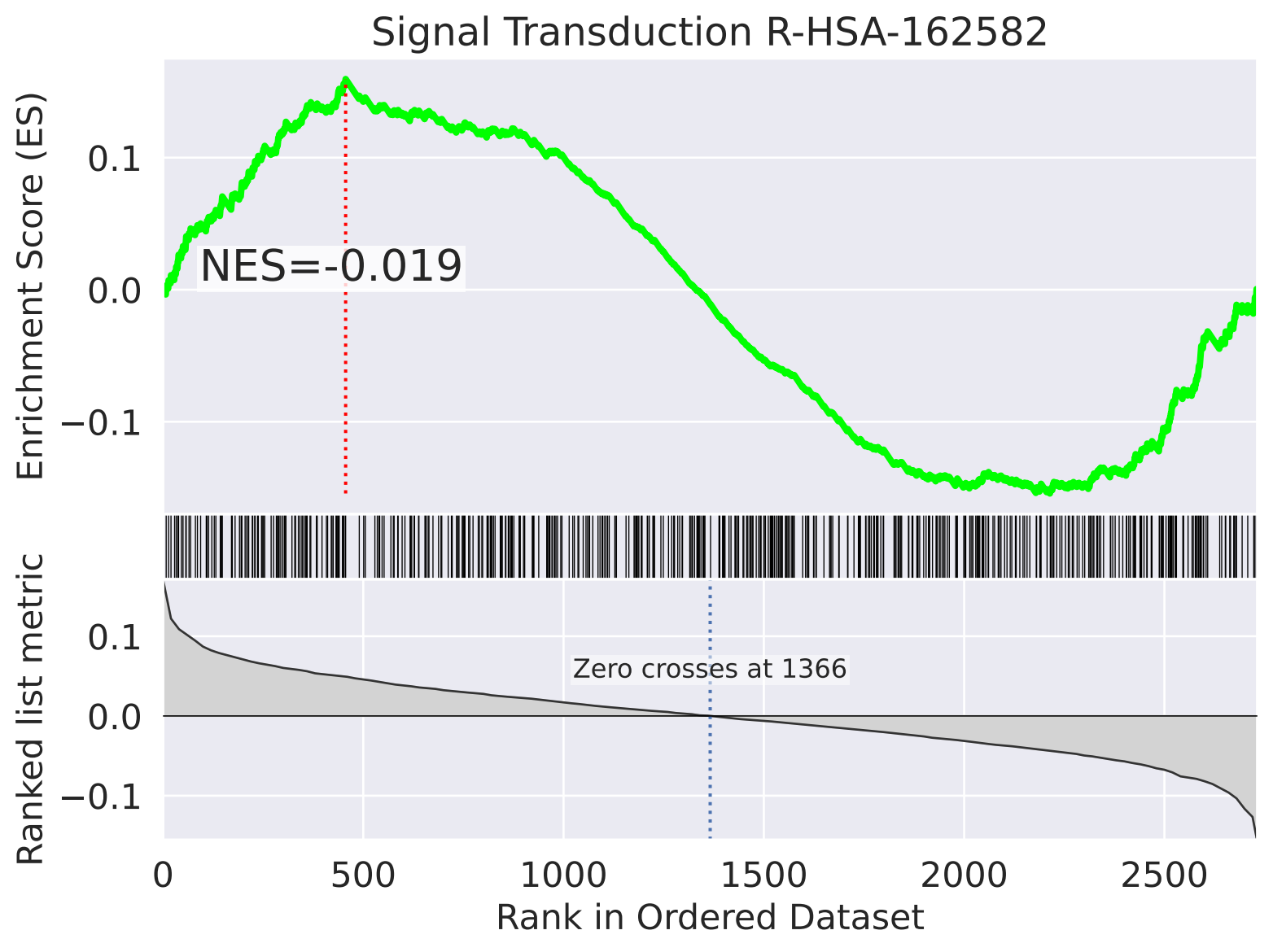
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=23

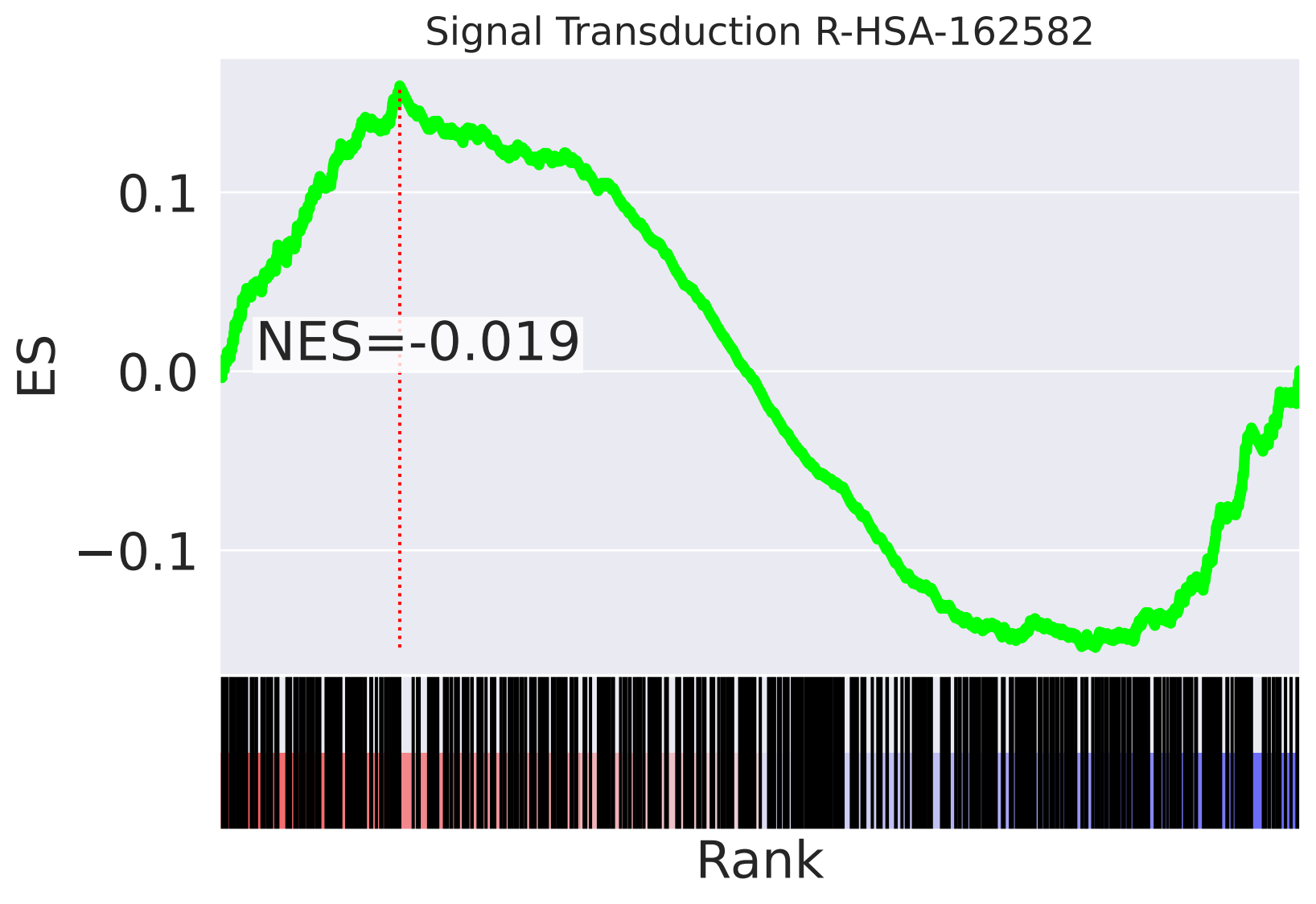

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1362
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

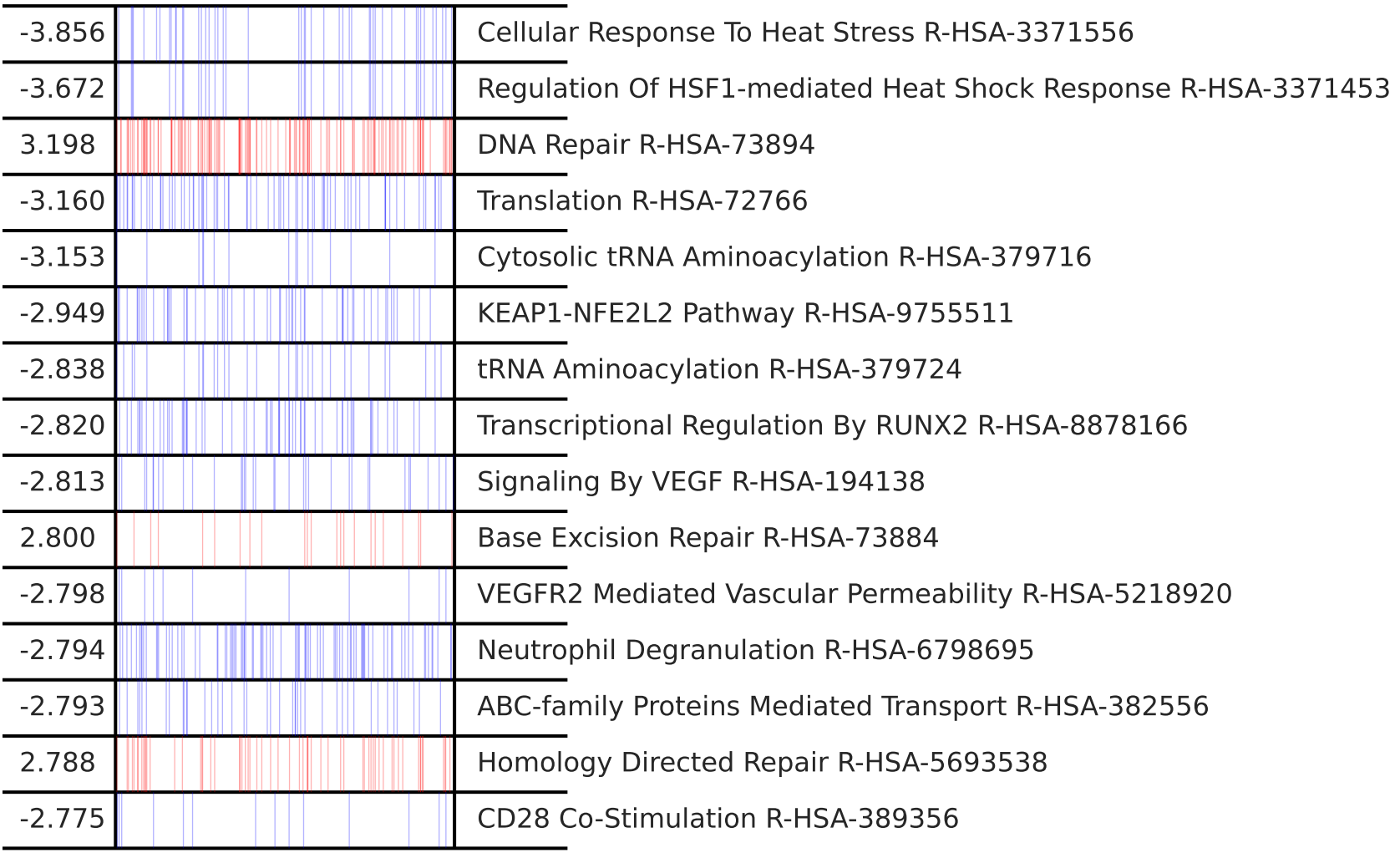

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
-5.164		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-5.054		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-4.853		Respiratory Electron Transport R-HSA-611105
4.258		Asparagine N-linked Glycosylation R-HSA-446203
-3.842		Complex I Biogenesis R-HSA-6799198
3.768		Signaling By VEGF R-HSA-194138
3.663		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
3.642		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
3.614		VEGFA-VEGFR2 Pathway R-HSA-4420097
3.580		Regulation Of RUNX2 Expression And Activity R-HSA-8939902
3.532		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
3.511		SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
3.445		Switching Of Origins To A Post-Replicative State R-HSA-69052
3.438		Regulation Of RUNX3 Expression And Activity R-HSA-8941858
3.437		APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178

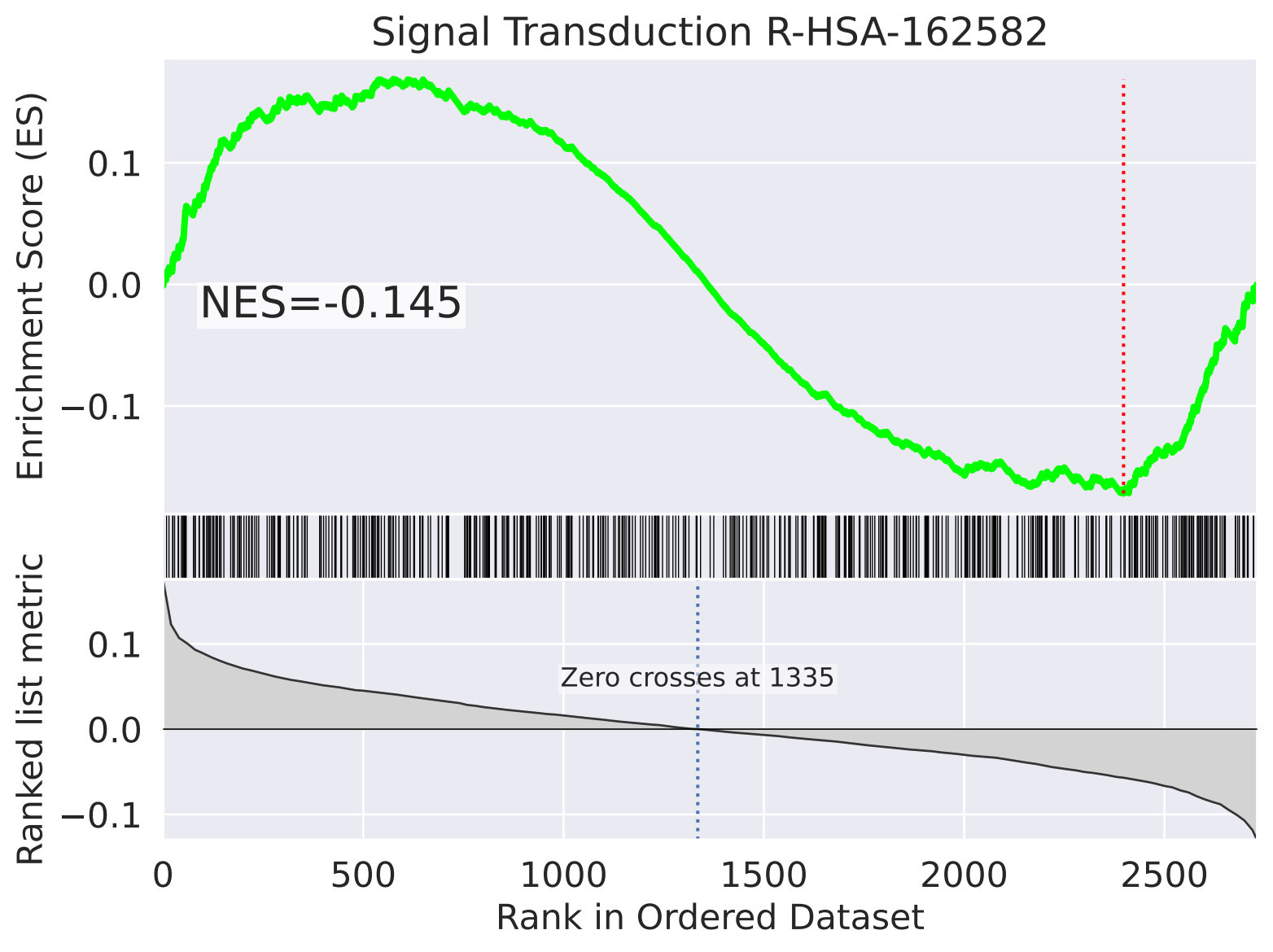
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=24

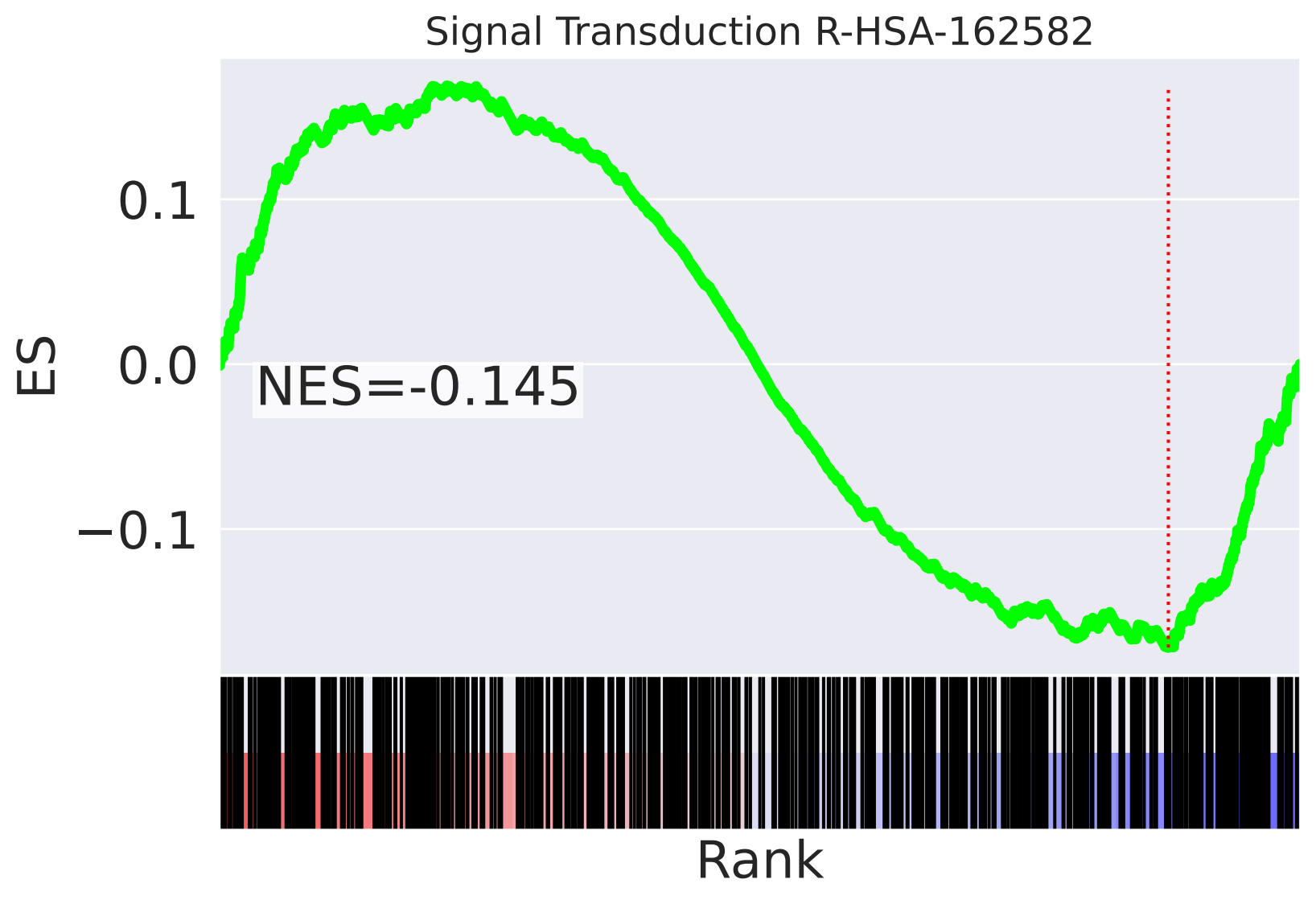

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.019
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1366
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

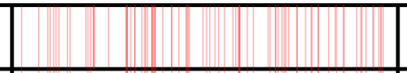
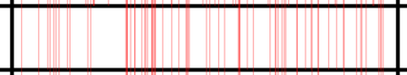
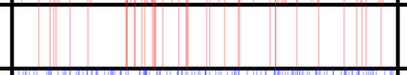
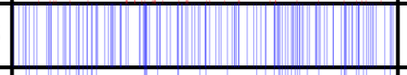
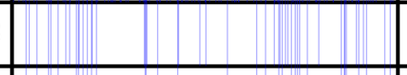
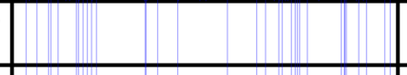
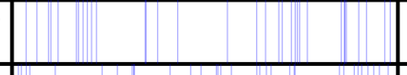
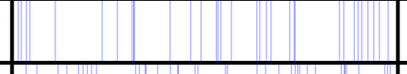
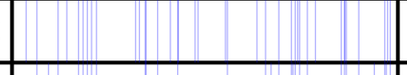
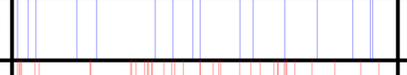
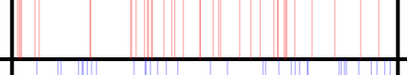
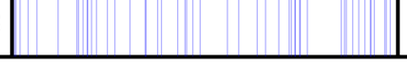

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.019
Rank


NES
SET
-3.856
Cellular Response To Heat Stress R-HSA-3371556
-3.672
Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
3.198
DNA Repair R-HSA-73894
-3.160
Translation R-HSA-72766
-3.153
Cytosolic tRNA Aminoacylation R-HSA-379716
-2.949
KEAP1-NFE2L2 Pathway R-HSA-9755511
-2.838
tRNA Aminoacylation R-HSA-379724
-2.820
Transcriptional Regulation By RUNX2 R-HSA-8878166
-2.813
Signaling By VEGF R-HSA-194138
2.800
Base Excision Repair R-HSA-73884
-2.798
VEGFR2 Mediated Vascular Permeability R-HSA-5218920
-2.794
Neutrophil Degranulation R-HSA-6798695
-2.793
ABC-family Proteins Mediated Transport R-HSA-382556
2.788
Homology Directed Repair R-HSA-5693538
-2.775
CD28 Co-Stimulation R-HSA-389356

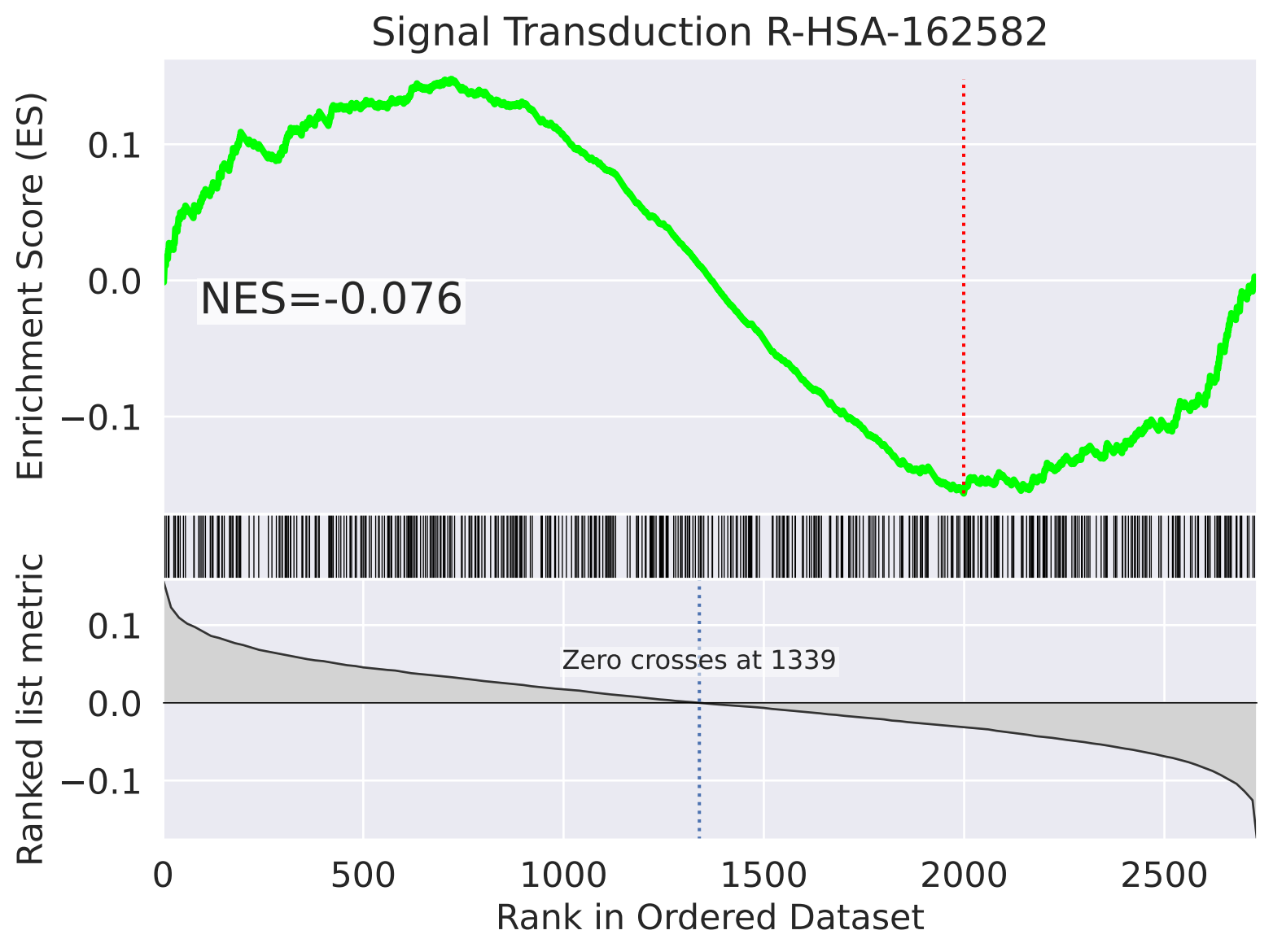
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=25

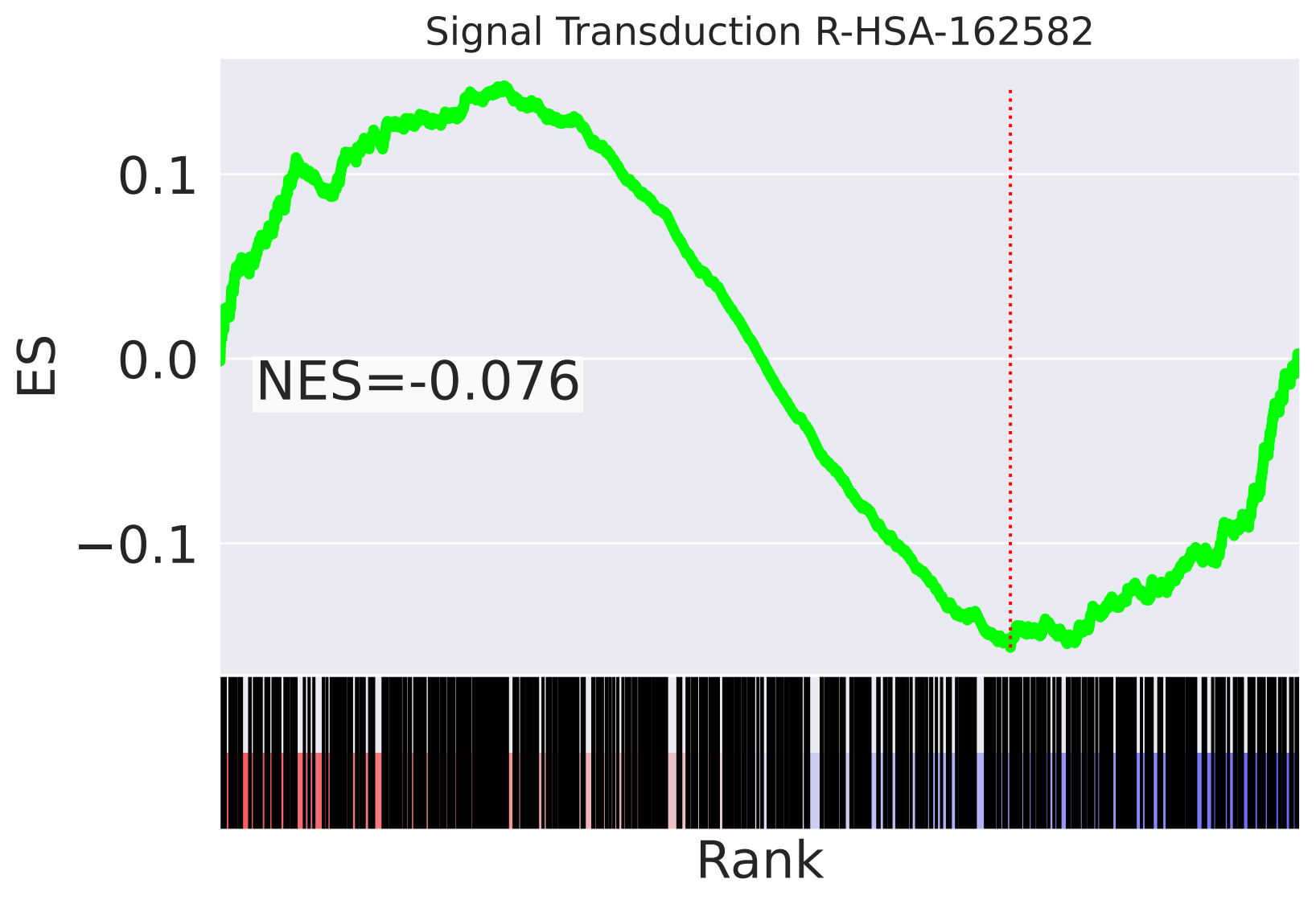

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.145
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1335
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

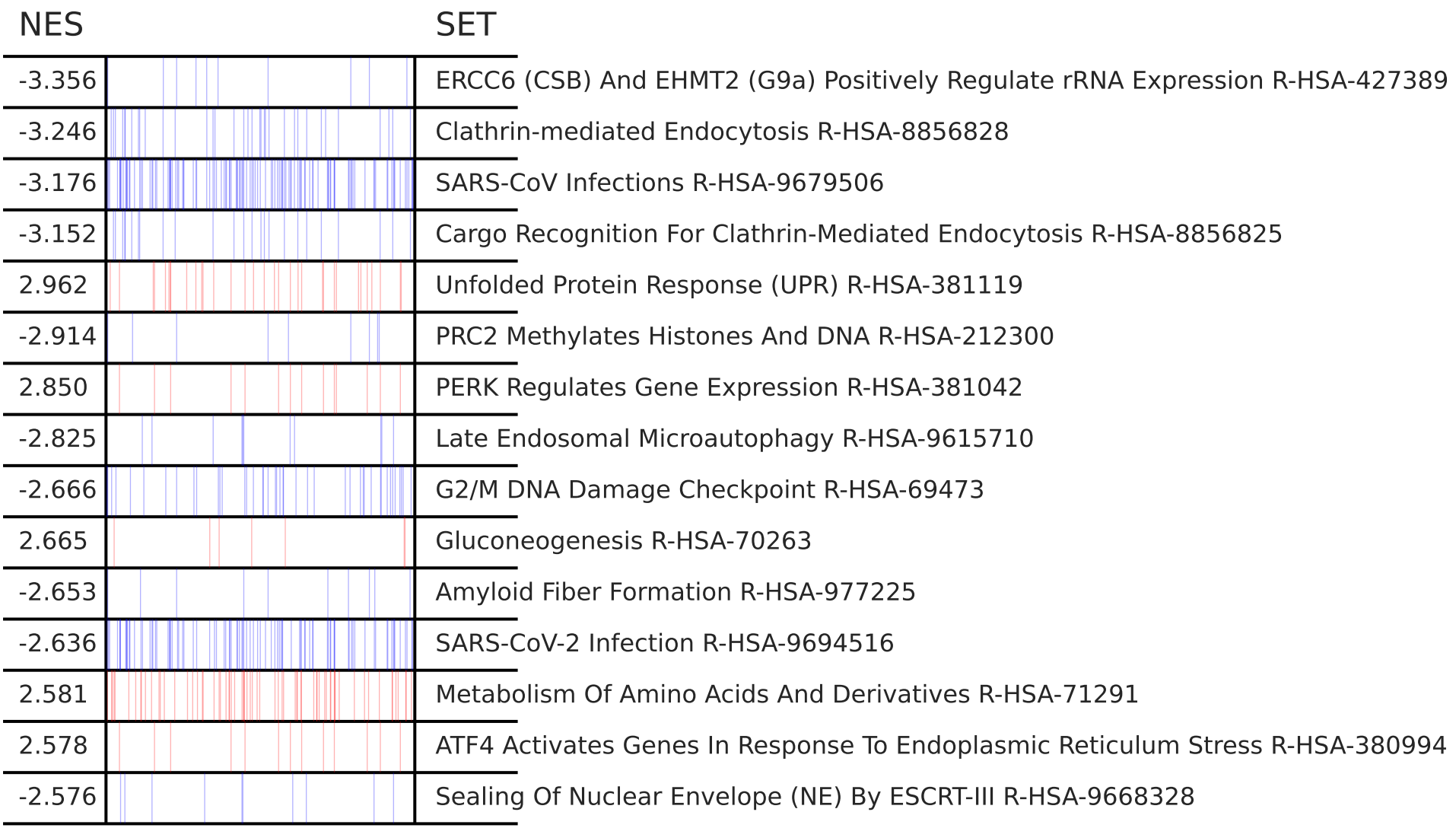

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.145
Rank

NES		SET
6.863		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.848		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.680		Respiratory Electron Transport R-HSA-611105
5.813		Complex I Biogenesis R-HSA-6799198
-3.633		Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-3.498		Transport Of Mature Transcript To Cytoplasm R-HSA-72202
-3.497		Transport Of Mature mRNA Derived From An Intronless Transcript R-HSA-159231
-3.497		Transport Of Mature mRNAs Derived From Intronless Transcripts R-HSA-159234
-3.248		Metabolism Of Steroids R-HSA-8957322
-3.182		Metabolism Of Non-Coding RNA R-HSA-194441
-3.150		NS1 Mediated Effects On Host Pathways R-HSA-168276
-3.140		TAK1-dependent IKK And NF-kappa-B Activation R-HSA-445989
3.132		TP53 Regulates Metabolic Genes R-HSA-5628897
-3.027		Nuclear Envelope Breakdown R-HSA-2980766
-3.018		SARS-CoV-2 Activates/Modulates Innate And Adaptive Immune Responses R-HSA-9705671

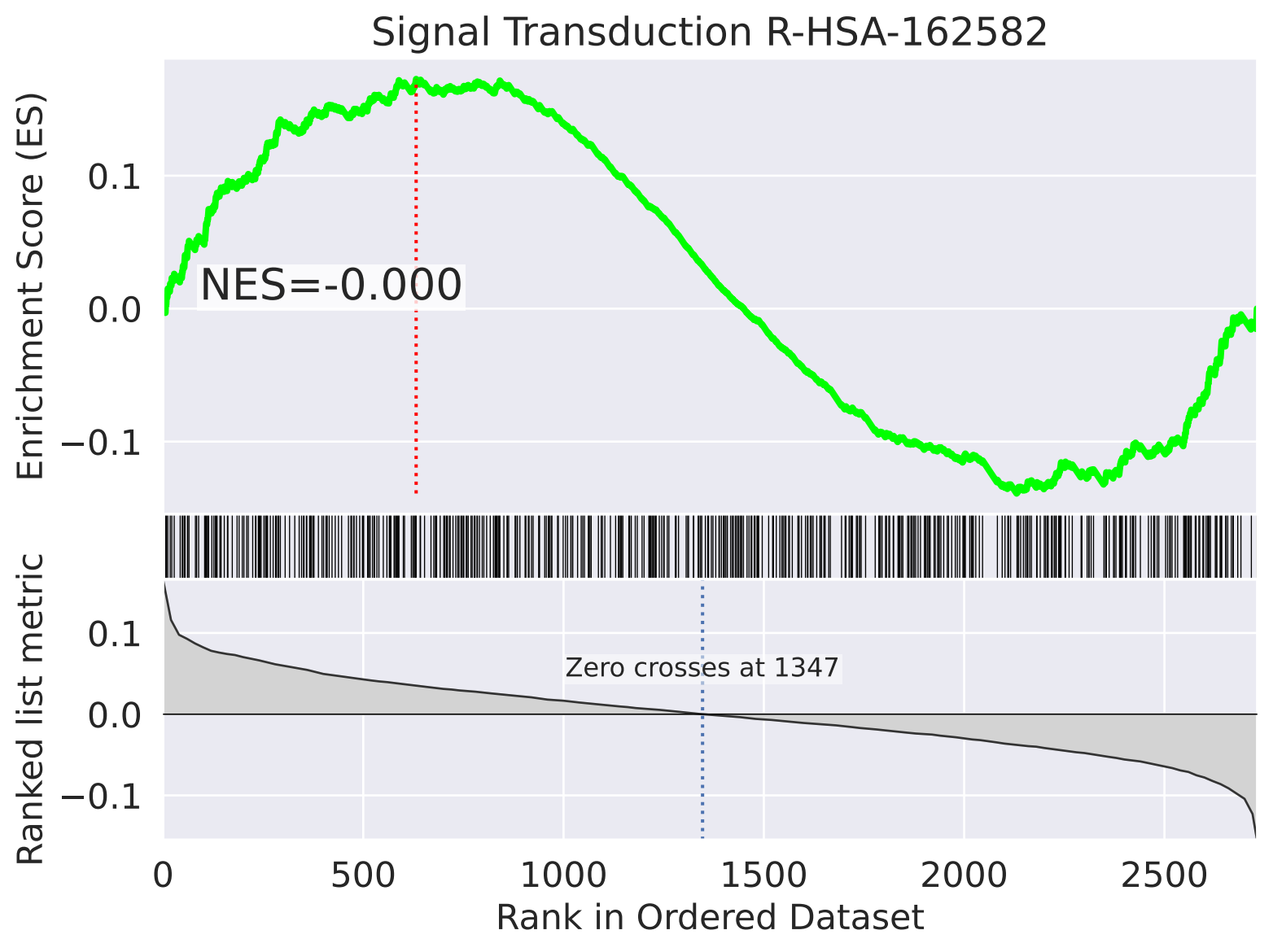
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=26

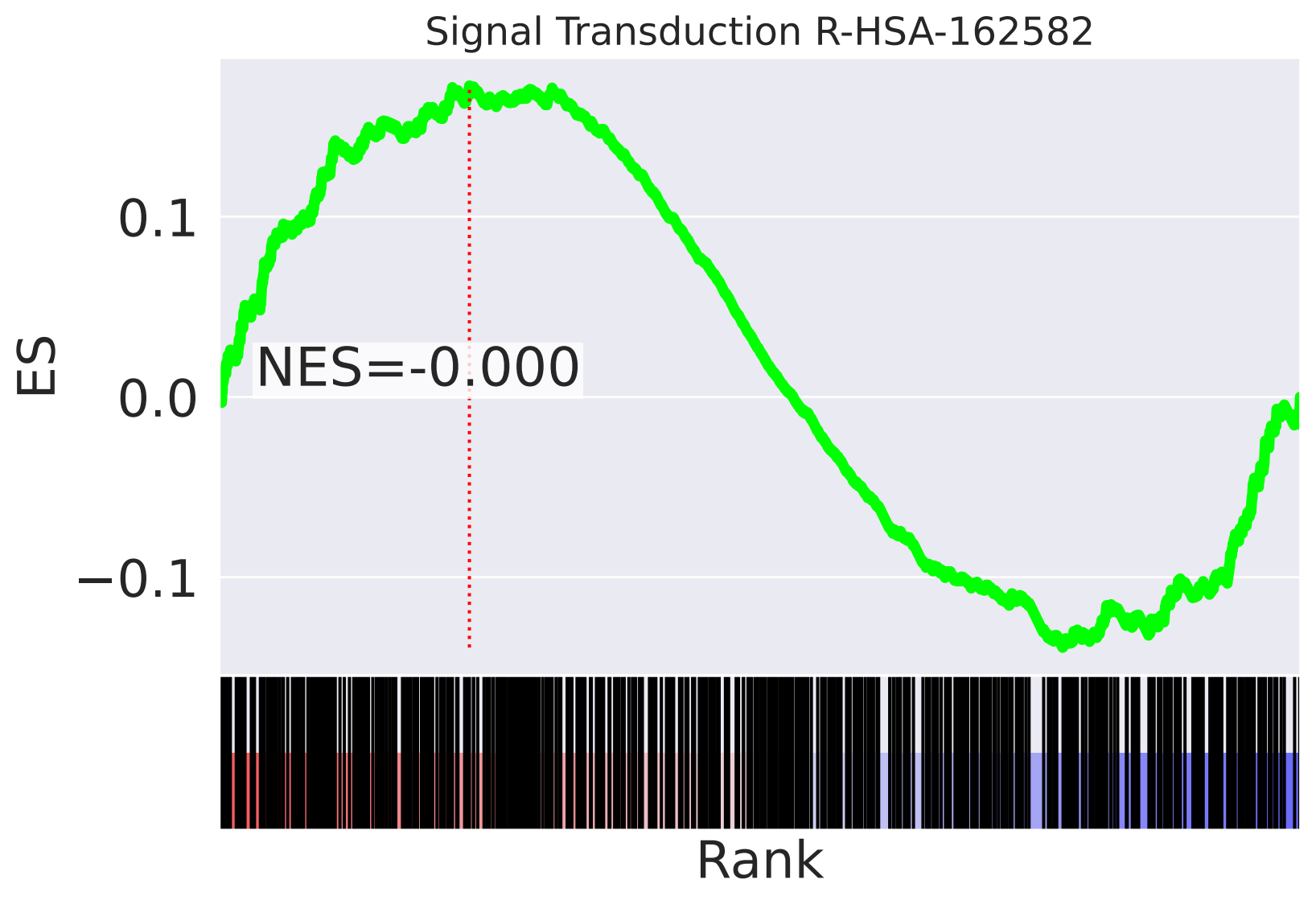

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.076
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1339
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

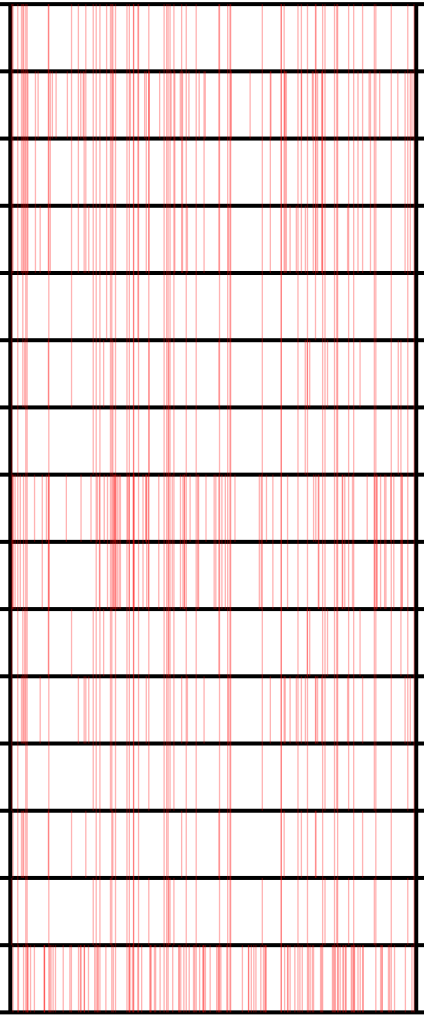

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.076
Rank


NES
SET
-3.356
ERCC6 (CSB) And EHMT2 (G9a) Positively Regulate rRNA Expression R-HSA-427389
-3.246
Clathrin-mediated Endocytosis R-HSA-8856828
-3.176
SARS-CoV Infections R-HSA-9679506
-3.152
Cargo Recognition For Clathrin-Mediated Endocytosis R-HSA-8856825
2.962
Unfolded Protein Response (UPR) R-HSA-381119
-2.914
PRC2 Methylates Histones And DNA R-HSA-212300
2.850
PERK Regulates Gene Expression R-HSA-381042
-2.825
Late Endosomal Microautophagy R-HSA-9615710
-2.666
G2/M DNA Damage Checkpoint R-HSA-69473
2.665
Gluconeogenesis R-HSA-70263
-2.653
Amyloid Fiber Formation R-HSA-977225
-2.636
SARS-CoV-2 Infection R-HSA-9694516
2.581
Metabolism Of Amino Acids And Derivatives R-HSA-71291
2.578
ATF4 Activates Genes In Response To Endoplasmic Reticulum Stress R-HSA-380994
-2.576
Sealing Of Nuclear Envelope (NE) By ESCRT-III R-HSA-9668328

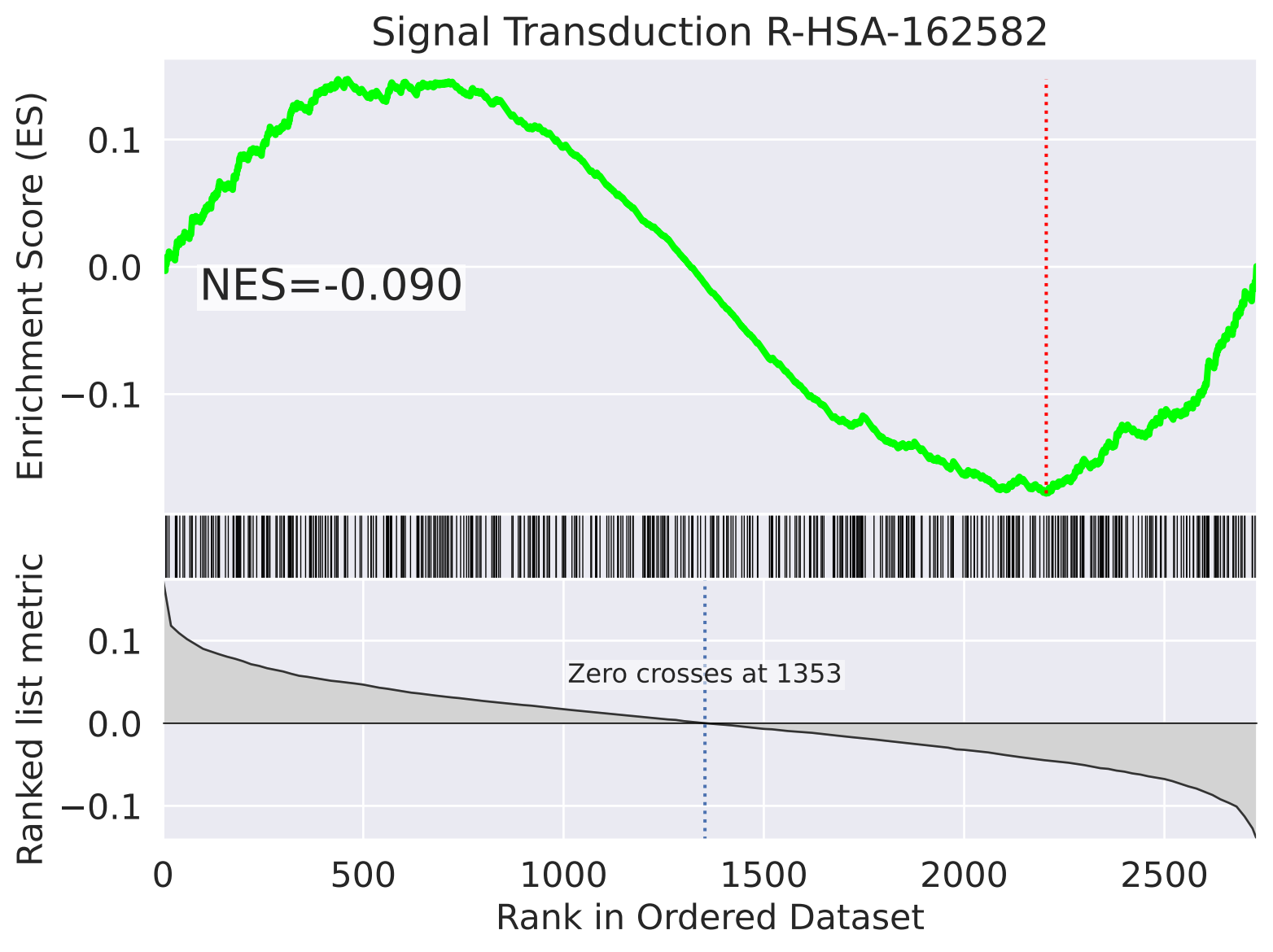
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=27

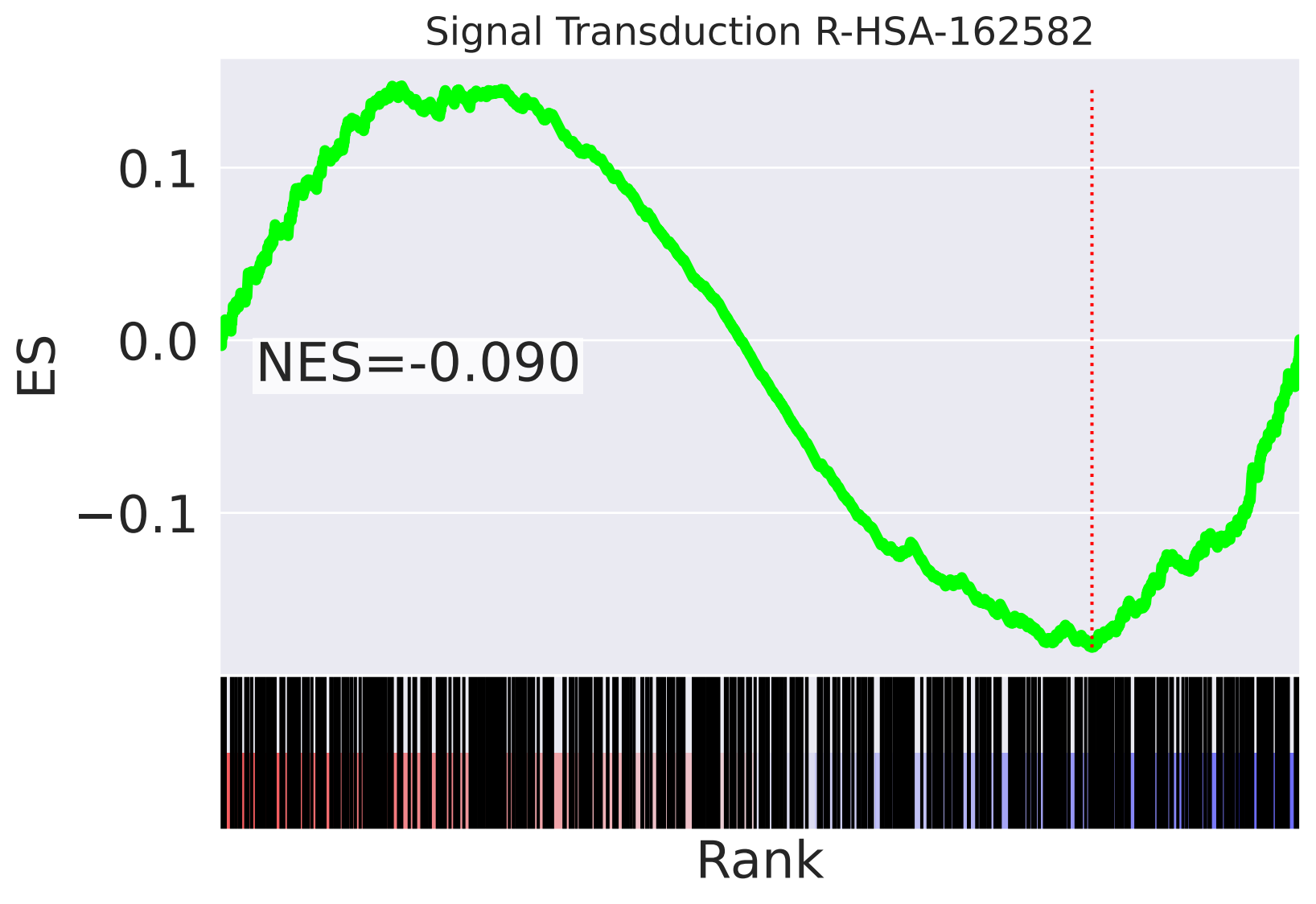

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1347
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

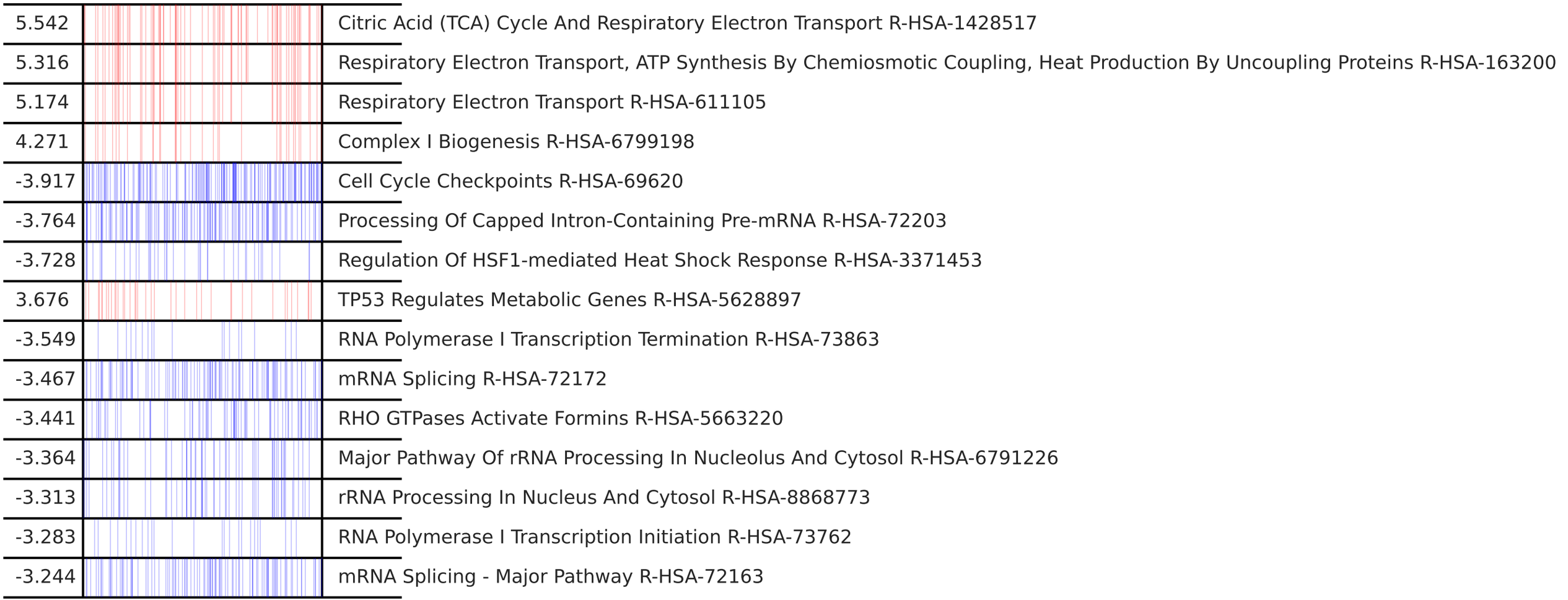

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.162		Switching Of Origins To A Post-Replicative State R-HSA-69052
4.934		S Phase R-HSA-69242
4.861		Synthesis Of DNA R-HSA-69239
4.777		DNA Replication R-HSA-69306
4.759		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
4.734		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
4.630		APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
4.383		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
4.316		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
4.300		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
4.278		DNA Replication Pre-Initiation R-HSA-69002
4.272		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
4.260		Orc1 Removal From Chromatin R-HSA-68949
4.130		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
4.101		HIV Infection R-HSA-162906

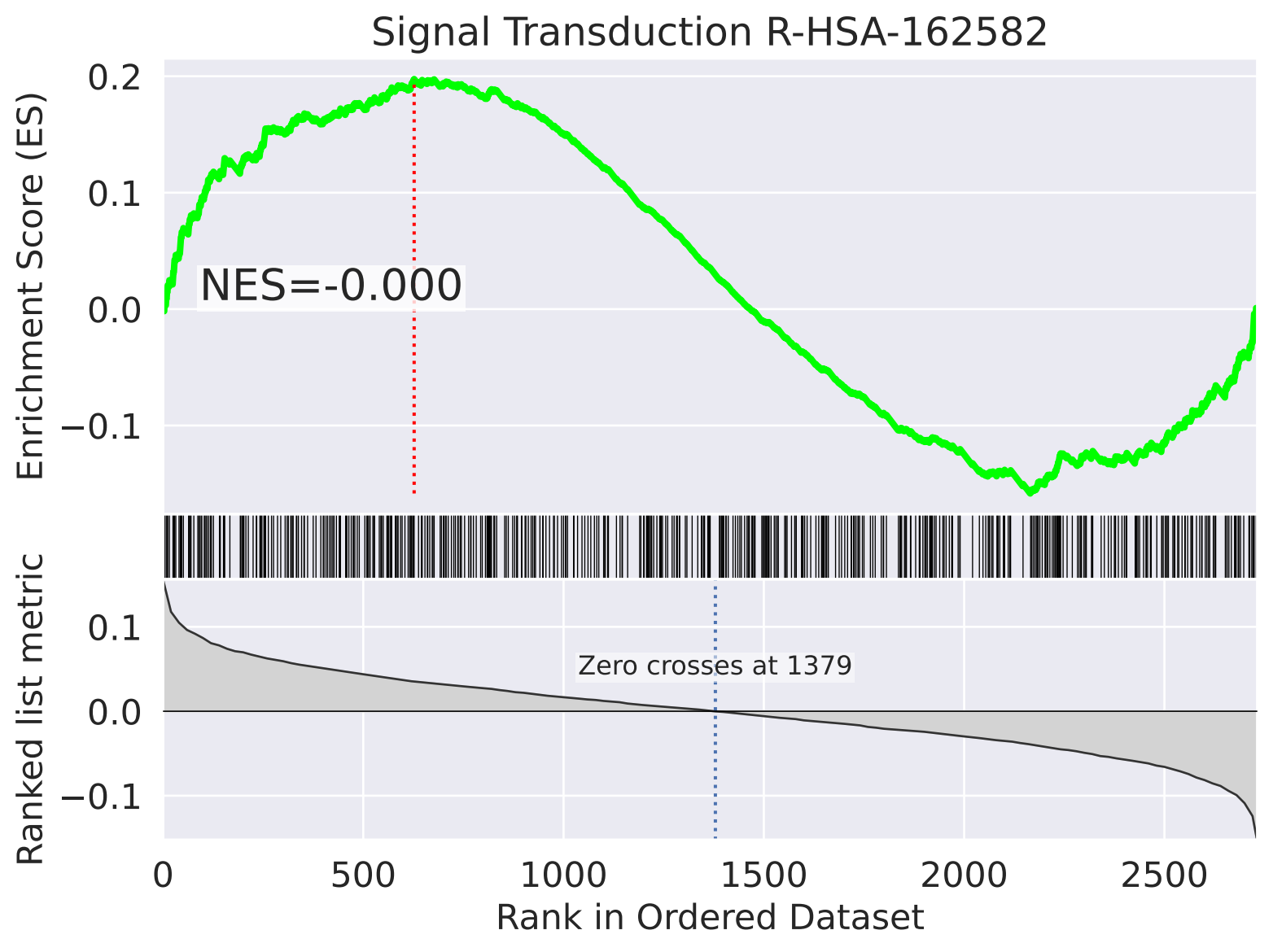
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=28

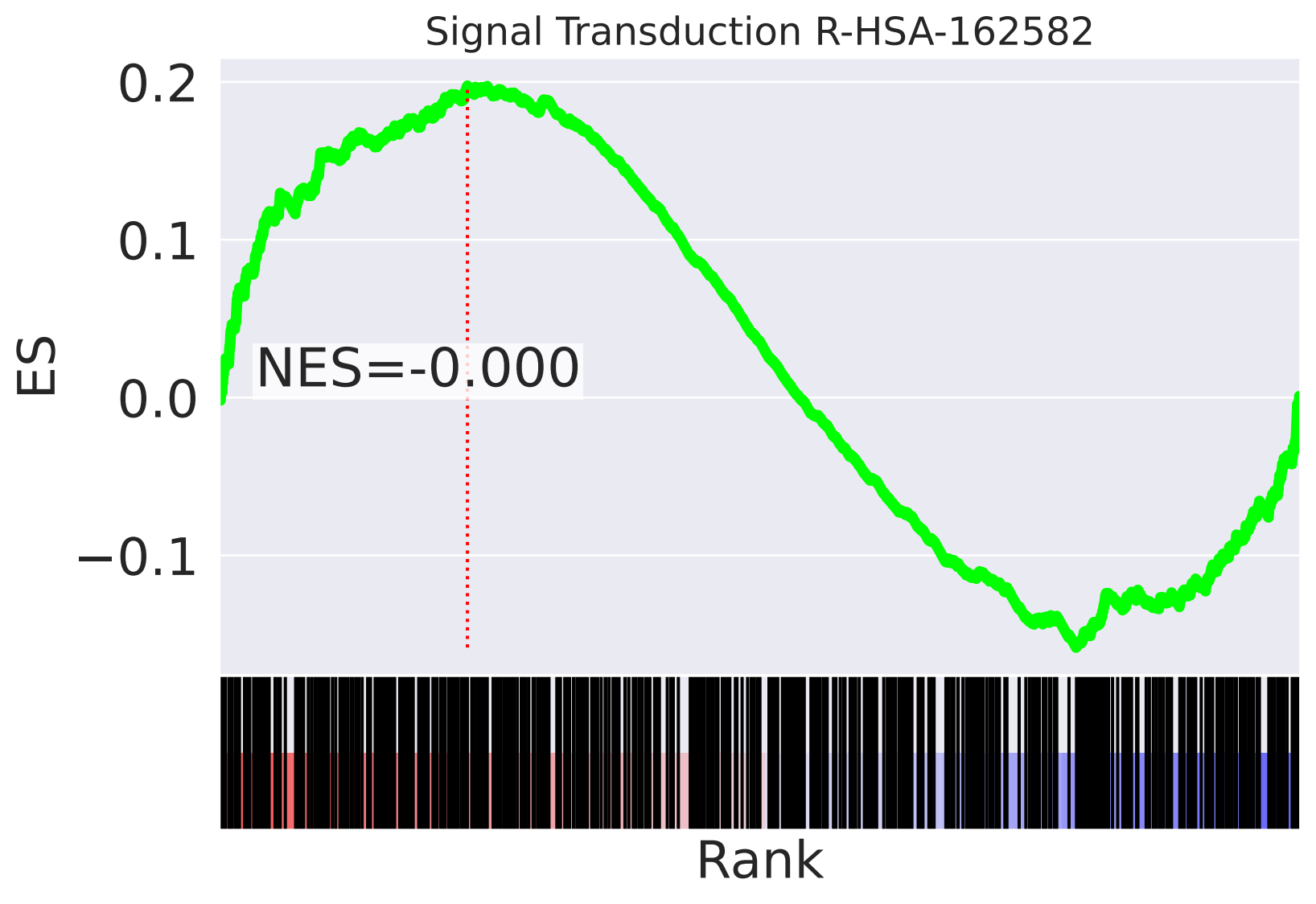

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.090
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1353
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

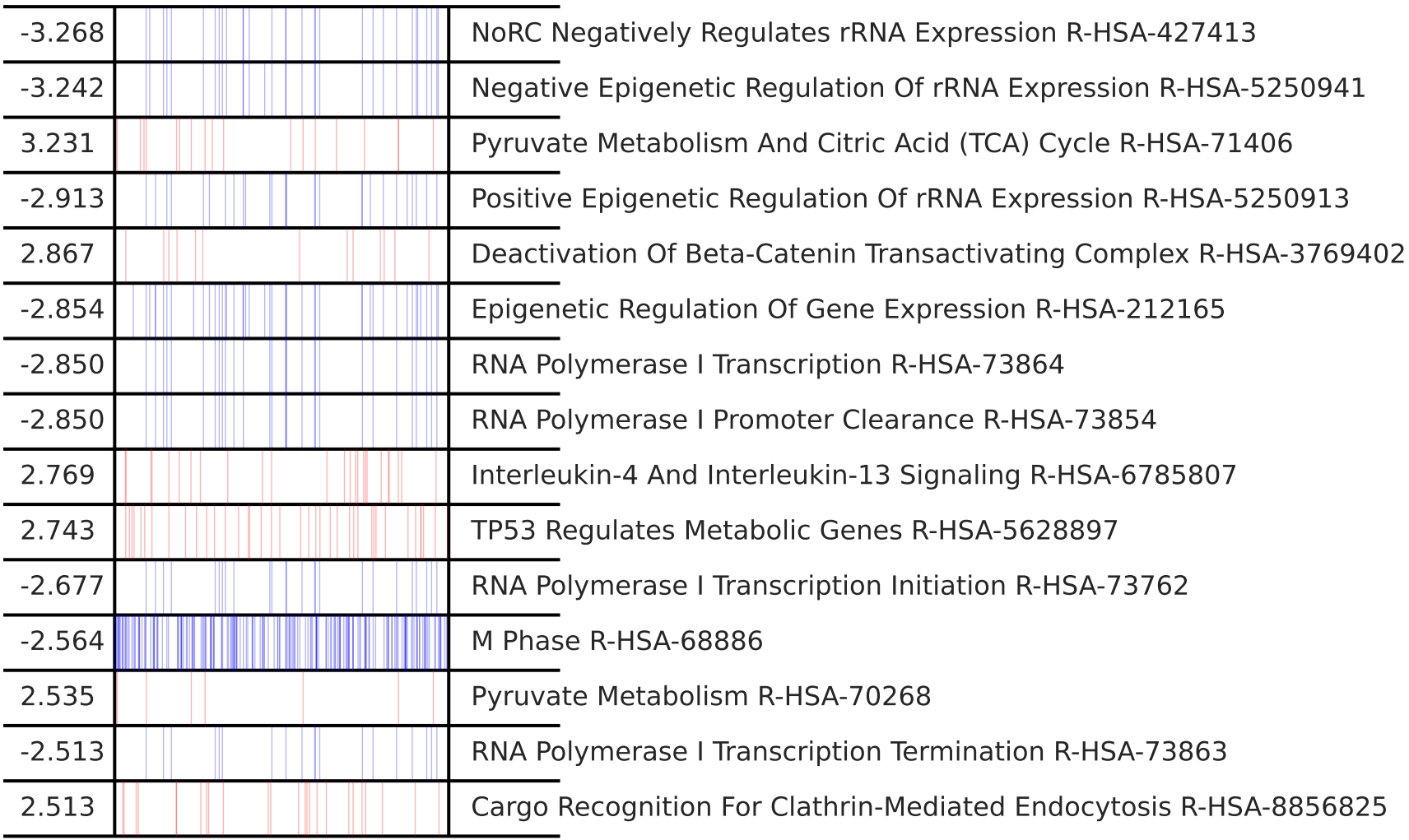

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.090
Rank


NES
SET
5.542
Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.316
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.174
Respiratory Electron Transport R-HSA-611105
4.271
Complex I Biogenesis R-HSA-6799198
-3.917
Cell Cycle Checkpoints R-HSA-69620
-3.764
Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
-3.728
Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
3.676
TP53 Regulates Metabolic Genes R-HSA-5628897
-3.549
RNA Polymerase I Transcription Termination R-HSA-73863
-3.467
mRNA Splicing R-HSA-72172
-3.441
RHO GTPases Activate Formins R-HSA-5663220
-3.364
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.313
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.283
RNA Polymerase I Transcription Initiation R-HSA-73762
-3.244
mRNA Splicing - Major Pathway R-HSA-72163

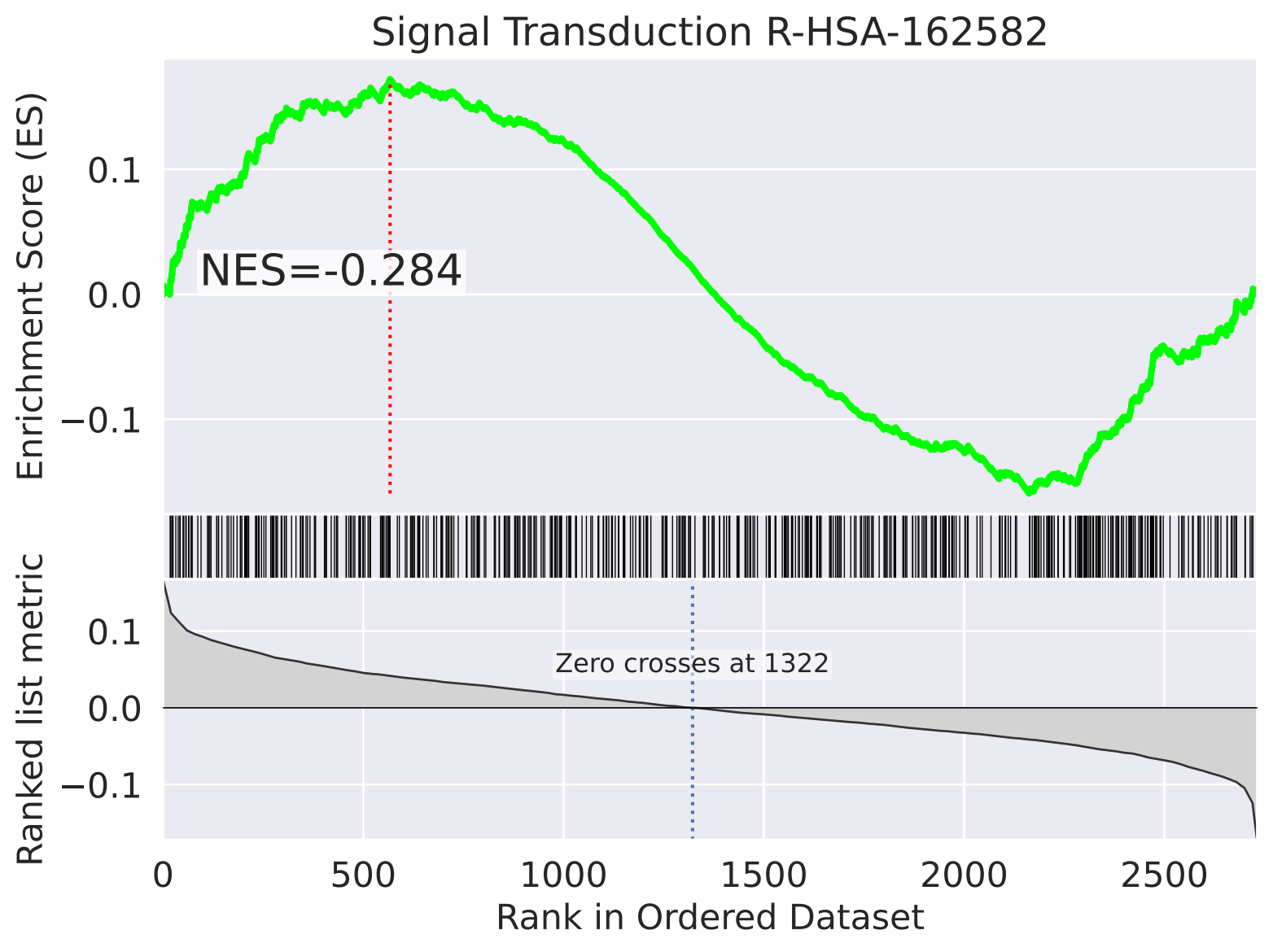
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=29

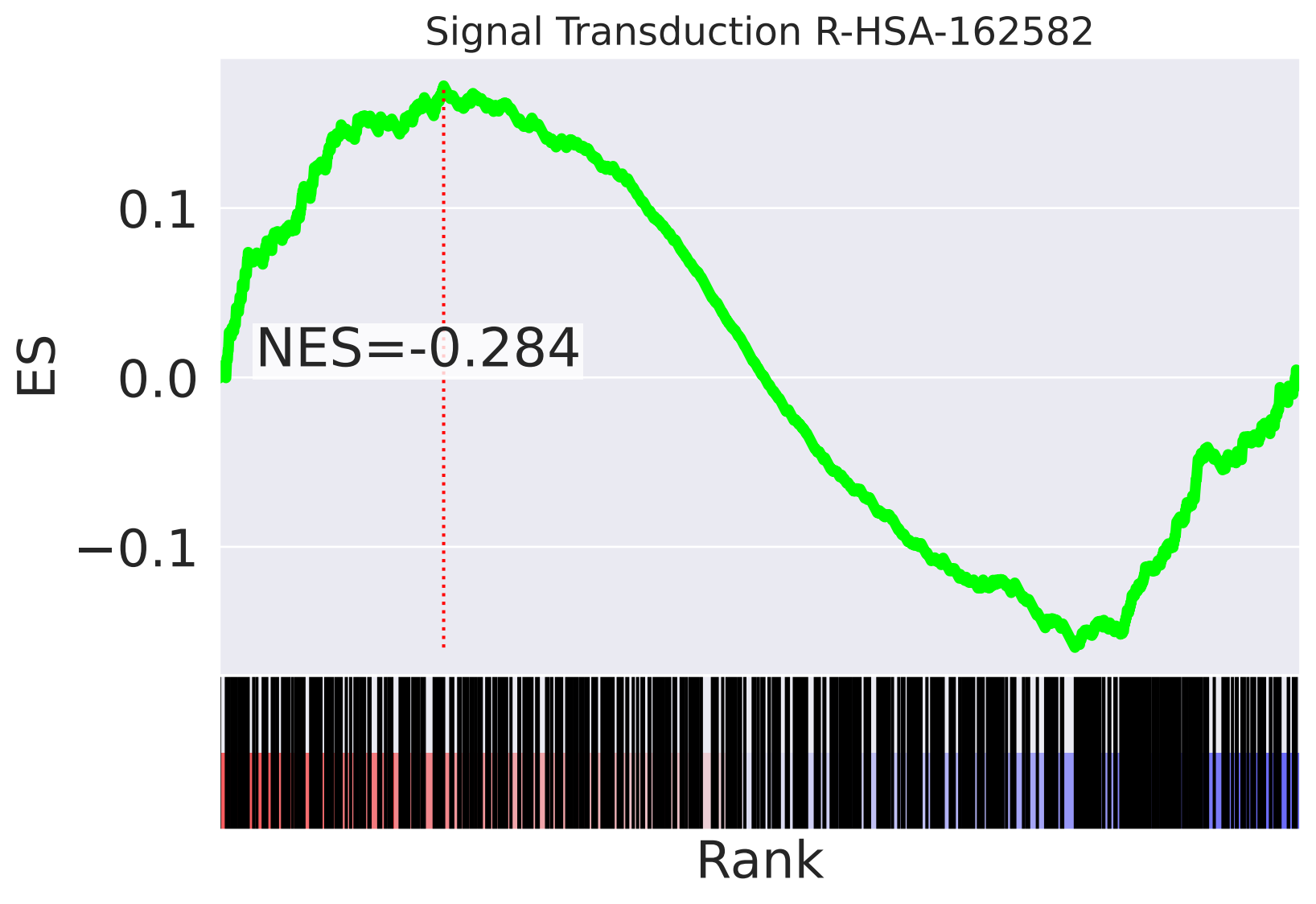

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1379
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

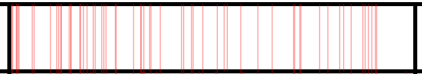
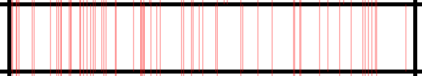
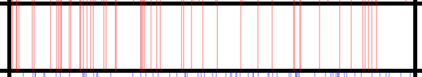
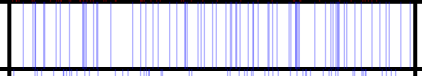
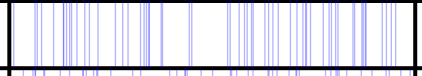
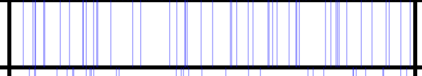
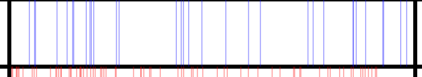
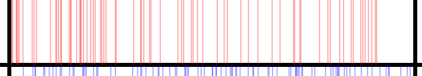
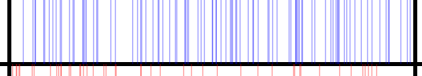
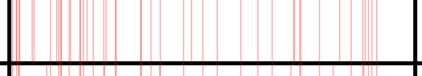
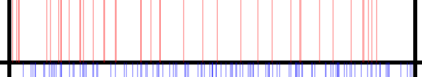
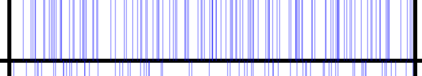
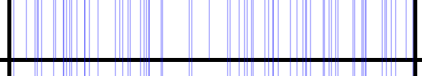
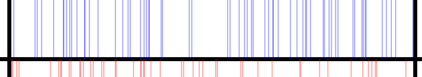
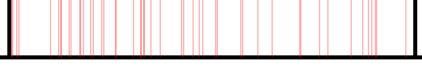

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-3.268
NoRC Negatively Regulates rRNA Expression R-HSA-427413
-3.242
Negative Epigenetic Regulation Of rRNA Expression R-HSA-5250941
3.231
Pyruvate Metabolism And Citric Acid (TCA) Cycle R-HSA-71406
-2.913
Positive Epigenetic Regulation Of rRNA Expression R-HSA-5250913
2.867
Deactivation Of Beta-Catenin Transactivating Complex R-HSA-3769402
-2.854
Epigenetic Regulation Of Gene Expression R-HSA-212165
-2.850
RNA Polymerase I Transcription R-HSA-73864
-2.850
RNA Polymerase I Promoter Clearance R-HSA-73854
2.769
Interleukin-4 And Interleukin-13 Signaling R-HSA-6785807
2.743
TP53 Regulates Metabolic Genes R-HSA-5628897
-2.677
RNA Polymerase I Transcription Initiation R-HSA-73762
-2.564
M Phase R-HSA-68886
2.535
Pyruvate Metabolism R-HSA-70268
-2.513
RNA Polymerase I Transcription Termination R-HSA-73863
2.513
Cargo Recognition For Clathrin-Mediated Endocytosis R-HSA-8856825

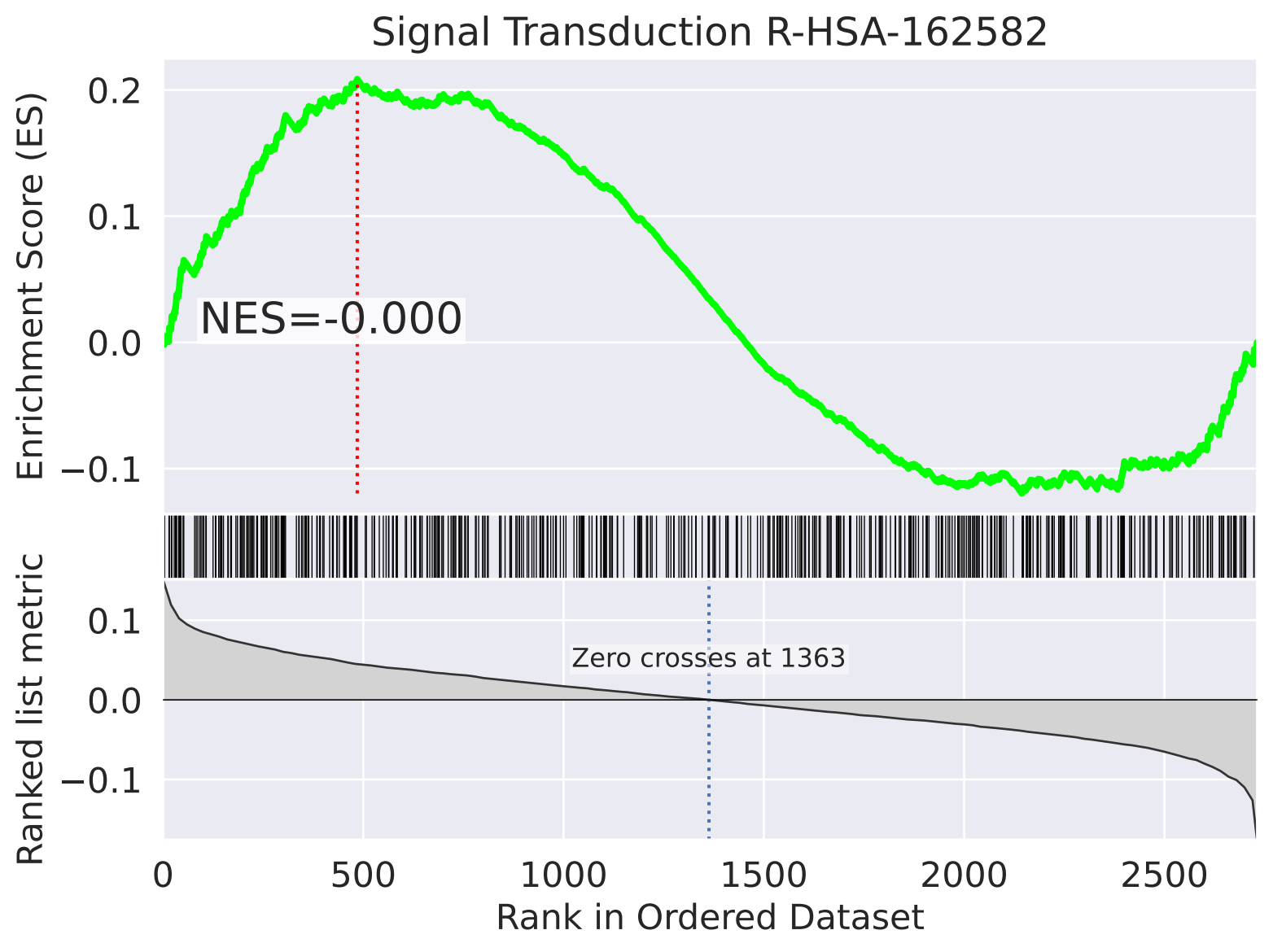
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=30

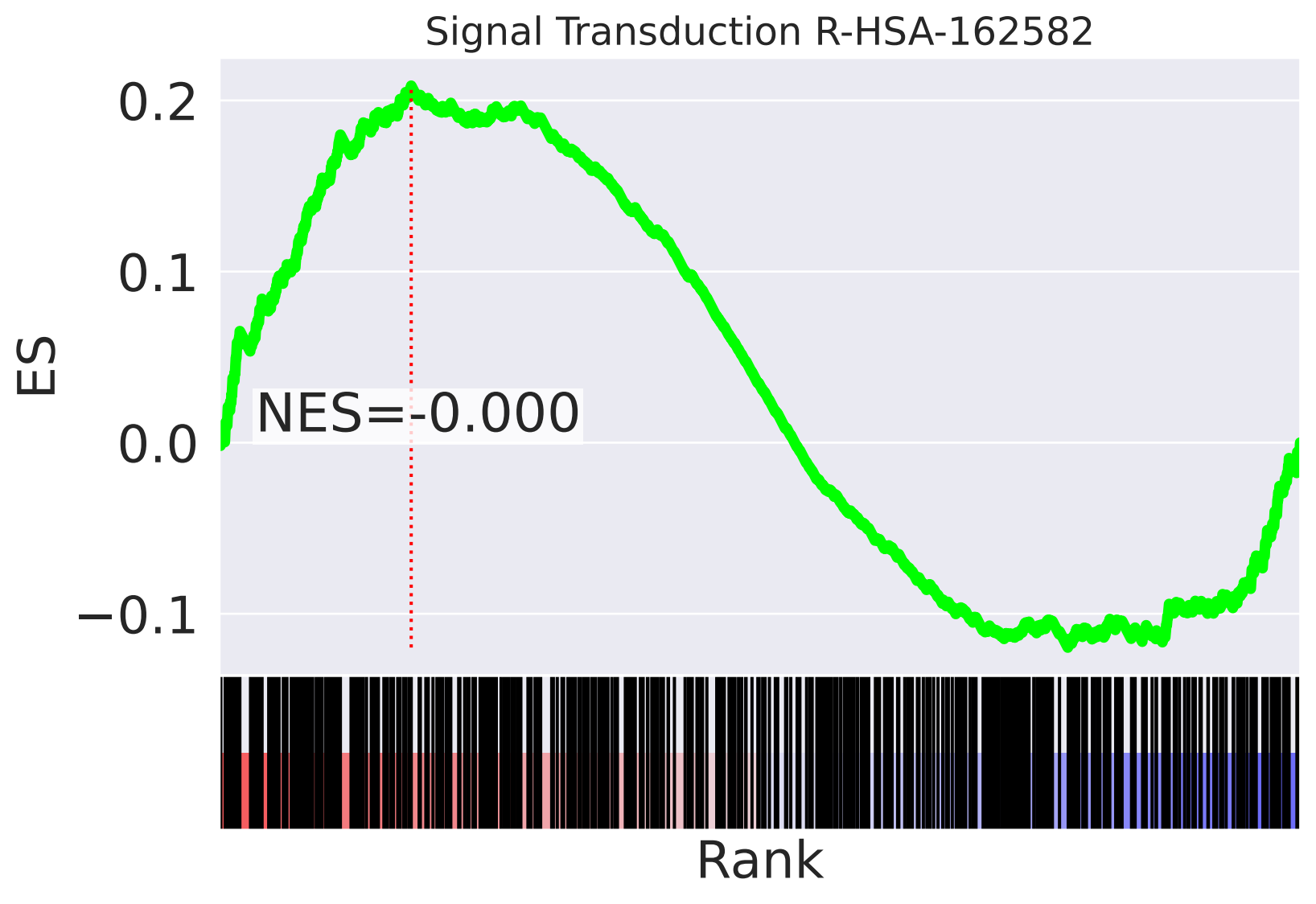

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.284
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1322
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

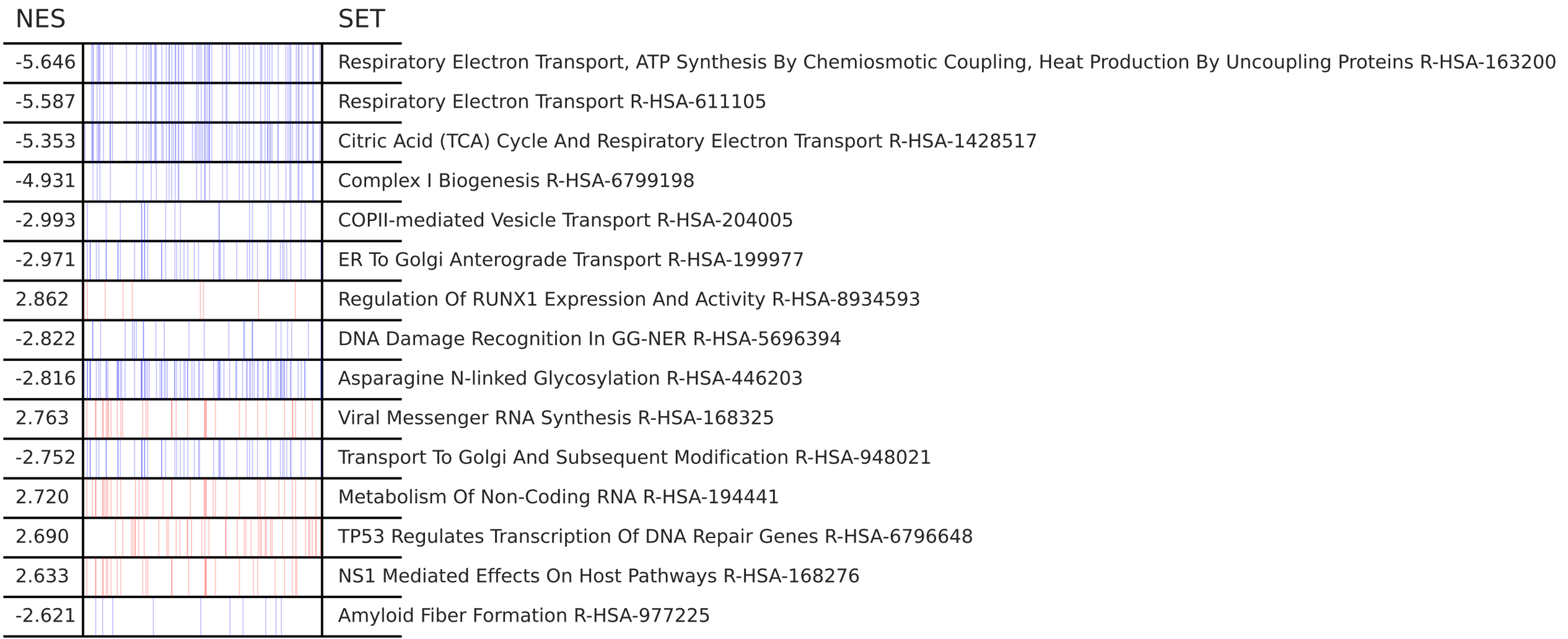

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.284
Rank

NES		SET
3.983		Assembly Of Pre-Replicative Complex R-HSA-68867
3.783		Switching Of Origins To A Post-Replicative State R-HSA-69052
3.716		CDK-mediated Phosphorylation And Removal Of Cdc6 R-HSA-69017
-3.694		SARS-CoV-2-host Interactions R-HSA-9705683
-3.664		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.658		SARS-CoV-2 Activates/Modulates Innate And Adaptive Immune Responses R-HSA-9705671
-3.656		Amino Acids Regulate mTORC1 R-HSA-9639288
3.595		DNA Replication Pre-Initiation R-HSA-69002
-3.570		SARS-CoV-2 Infection R-HSA-9694516
3.536		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
3.479		Regulation Of PTEN Stability And Activity R-HSA-8948751
-3.465		SARS-CoV Infections R-HSA-9679506
-3.421		rRNA Processing R-HSA-72312
-3.401		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
3.350		Orc1 Removal From Chromatin R-HSA-68949

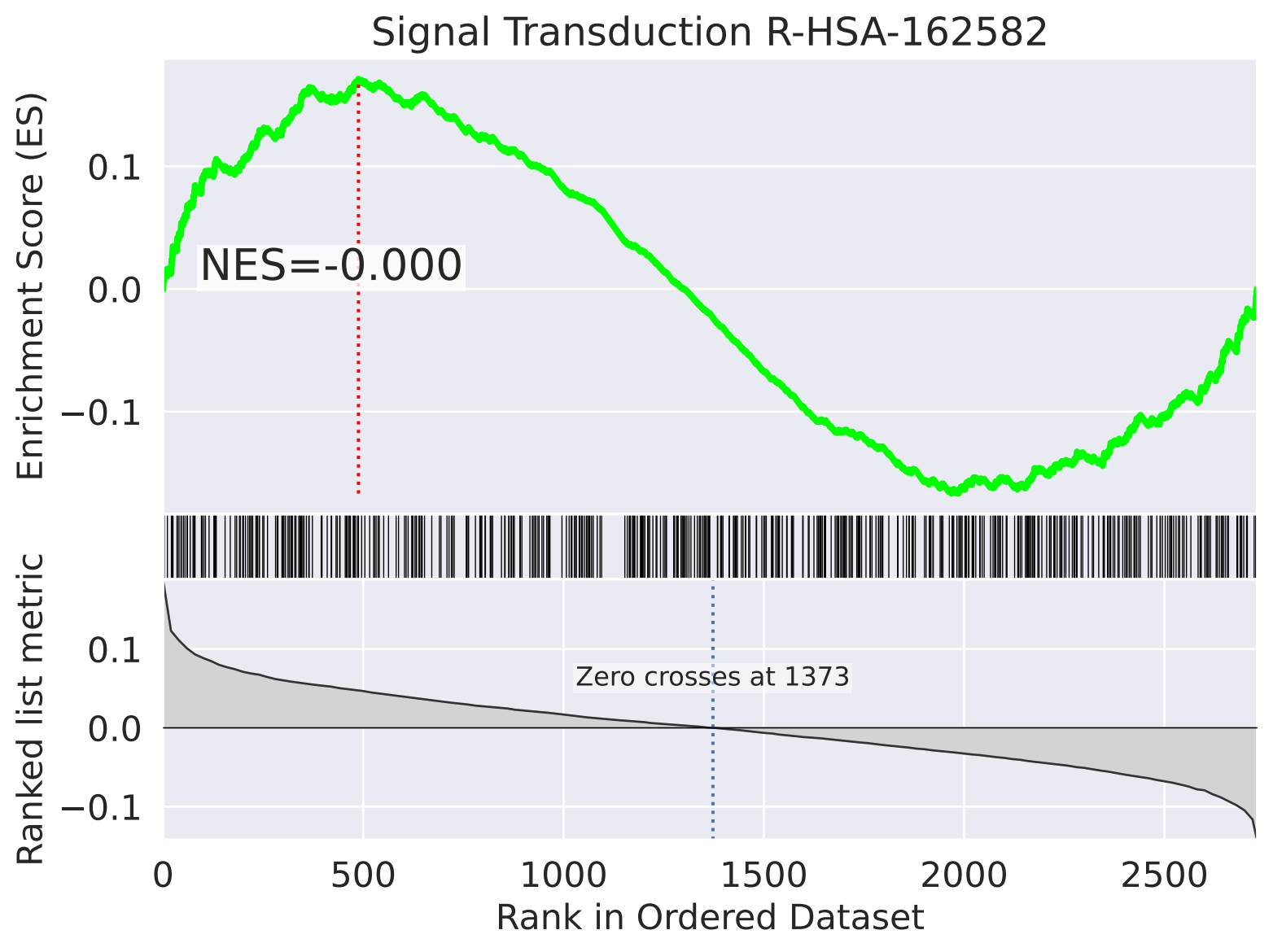
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=31

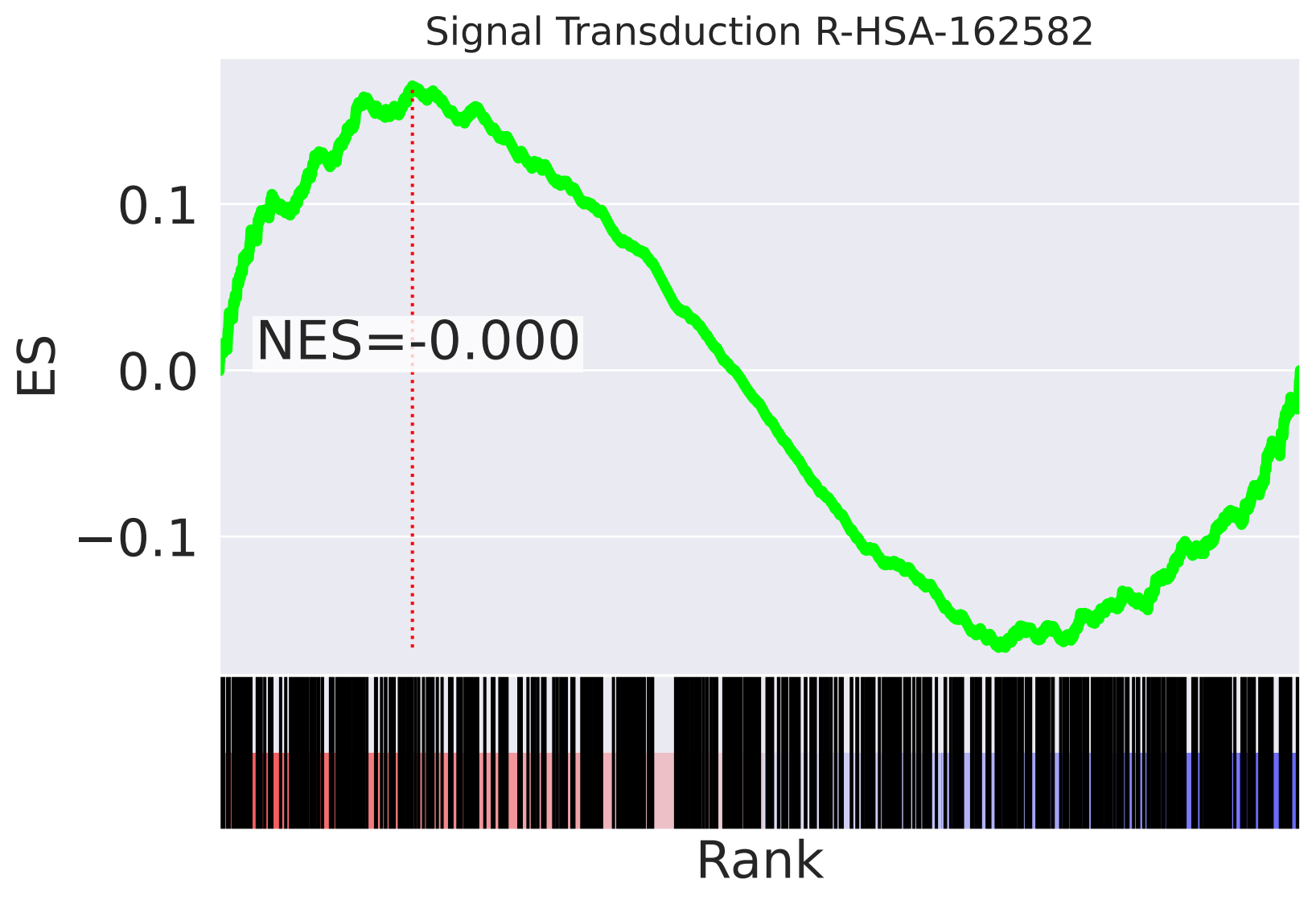

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1363
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

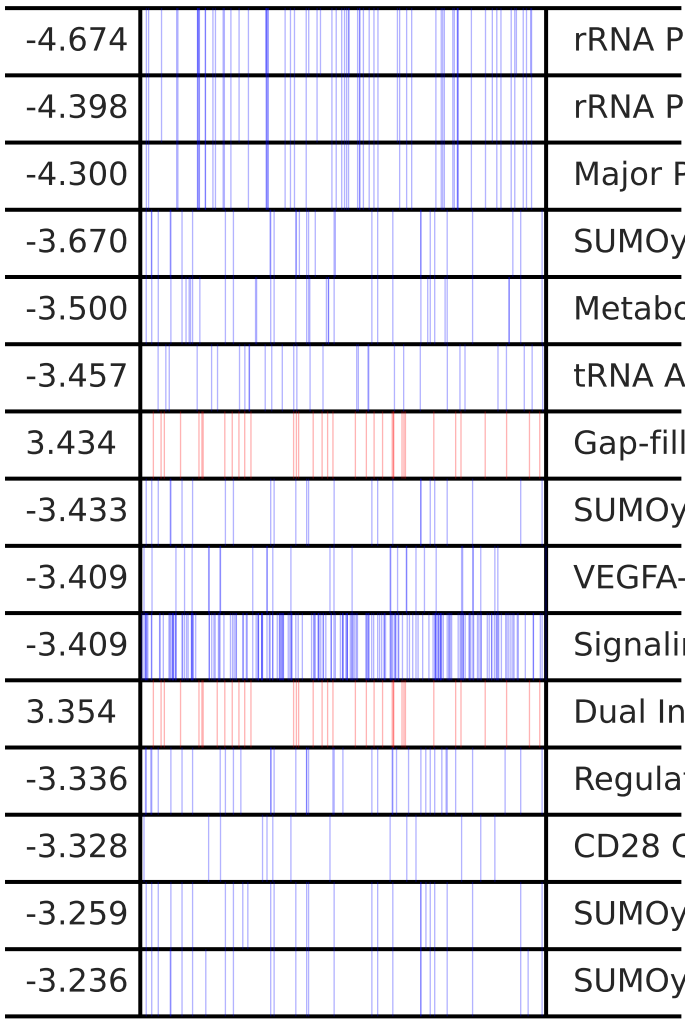

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-5.646
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-5.587
Respiratory Electron Transport R-HSA-611105
-5.353
Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-4.931
Complex I Biogenesis R-HSA-6799198
-2.993
COPII-mediated Vesicle Transport R-HSA-204005
-2.971
ER To Golgi Anterograde Transport R-HSA-199977
2.862
Regulation Of RUNX1 Expression And Activity R-HSA-8934593
-2.822
DNA Damage Recognition In GG-NER R-HSA-5696394
-2.816
Asparagine N-linked Glycosylation R-HSA-446203
2.763
Viral Messenger RNA Synthesis R-HSA-168325
-2.752
Transport To Golgi And Subsequent Modification R-HSA-948021
2.720
Metabolism Of Non-Coding RNA R-HSA-194441
2.690
TP53 Regulates Transcription Of DNA Repair Genes R-HSA-6796648
2.633
NS1 Mediated Effects On Host Pathways R-HSA-168276
-2.621
Amyloid Fiber Formation R-HSA-977225

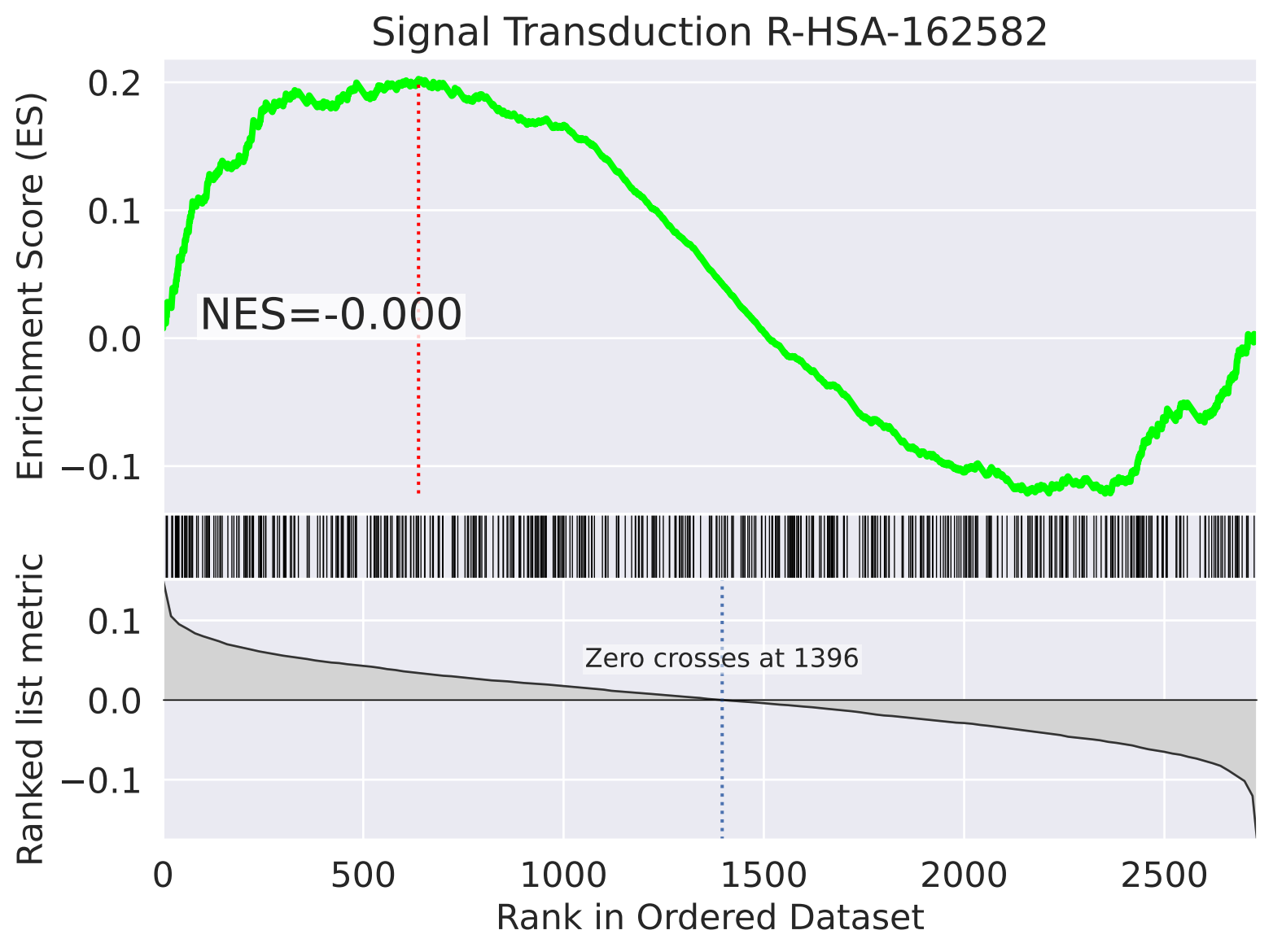
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=32

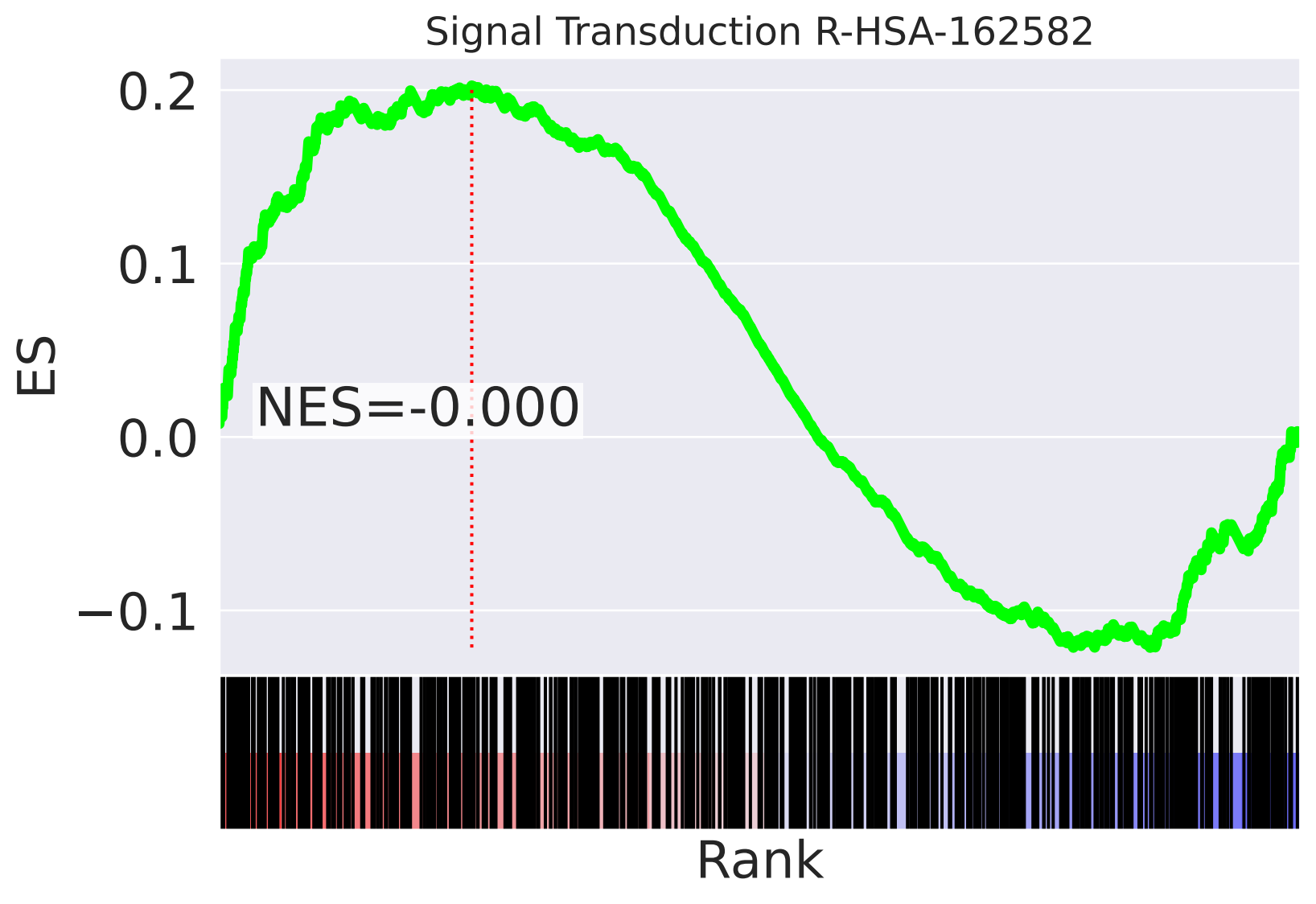

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1373
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

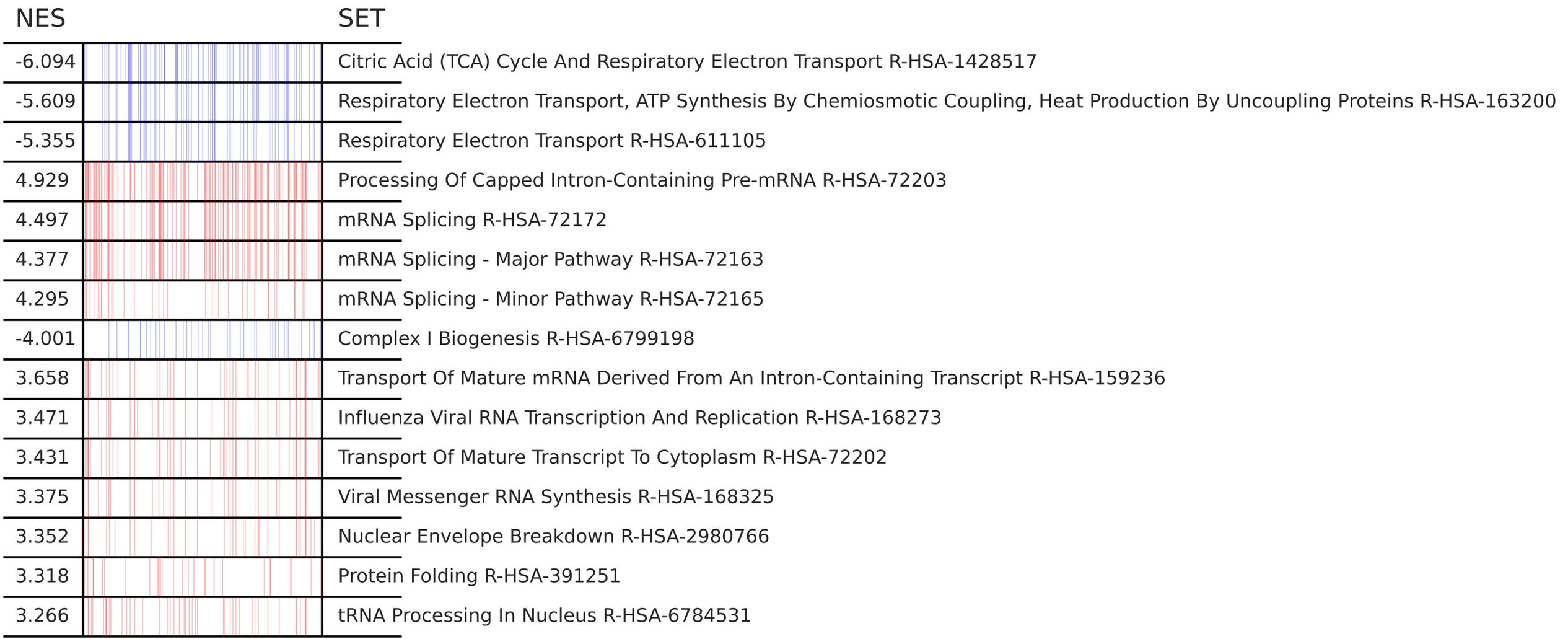

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-4.674
rRNA Processing R-HSA-72312
-4.398
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.300
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.670
SUMOylation Of DNA Replication Proteins R-HSA-4615885
-3.500
Metabolism Of Non-Coding RNA R-HSA-194441
-3.457
tRNA Aminoacylation R-HSA-379724
3.434
Gap-filling DNA Repair Synthesis And Ligation In TC-NER R-HSA-6782210
-3.433
SUMOylation Of SUMOylation Proteins R-HSA-4085377
-3.409
VEGFA-VEGFR2 Pathway R-HSA-4420097
-3.409
Signaling By Rho GTPases R-HSA-194315
3.354
Dual Incision In TC-NER R-HSA-6782135
-3.336
Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
-3.328
CD28 Co-Stimulation R-HSA-389356
-3.259
SUMOylation Of RNA Binding Proteins R-HSA-4570464
-3.236
SUMOylation Of Ubiquitinylation Proteins R-HSA-3232142

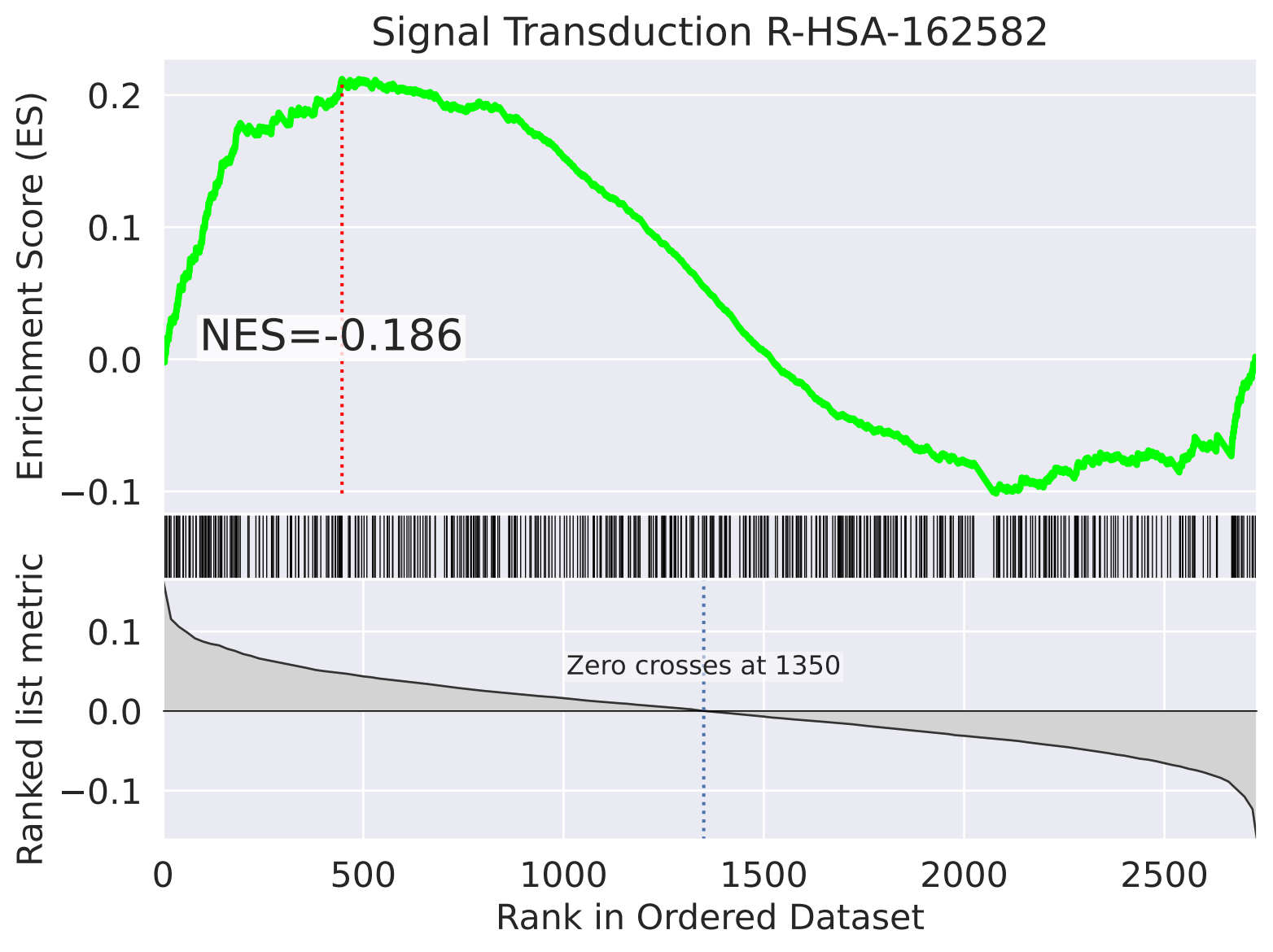
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=33

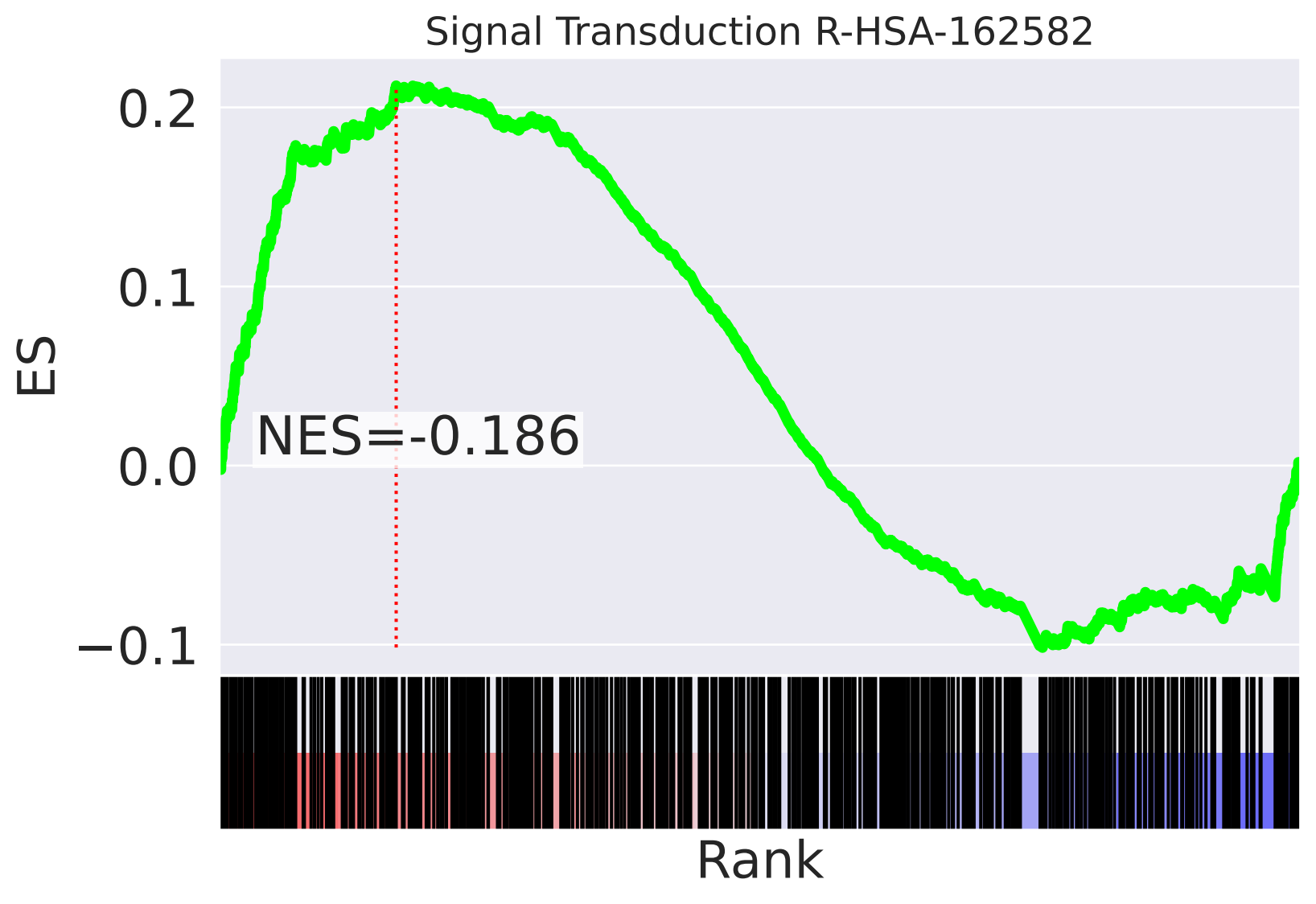

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1396
0
500
1000
1500
2000
2500
Rank in Ordered Dataset


Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-6.094
Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
-5.609
Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-5.355
Respiratory Electron Transport R-HSA-611105
4.929
Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.497
mRNA Splicing R-HSA-72172
4.377
mRNA Splicing - Major Pathway R-HSA-72163
4.295
mRNA Splicing - Minor Pathway R-HSA-72165
-4.001
Complex I Biogenesis R-HSA-6799198
3.658
Transport Of Mature mRNA Derived From An Intron-Containing Transcript R-HSA-159236
3.471
Influenza Viral RNA Transcription And Replication R-HSA-168273
3.431
Transport Of Mature Transcript To Cytoplasm R-HSA-72202
3.375
Viral Messenger RNA Synthesis R-HSA-168325
3.352
Nuclear Envelope Breakdown R-HSA-2980766
3.318
Protein Folding R-HSA-391251
3.266
tRNA Processing In Nucleus R-HSA-6784531

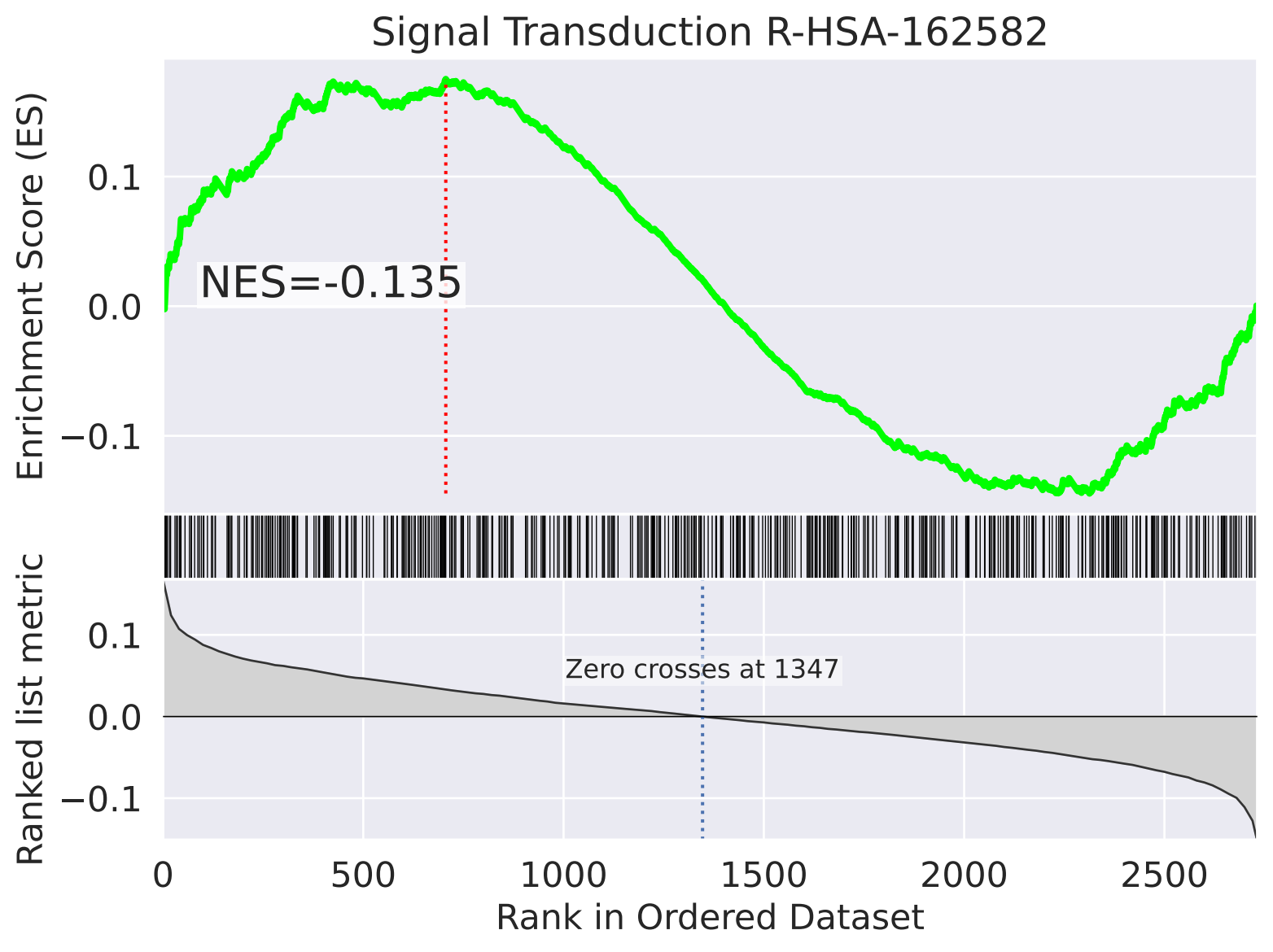
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=34

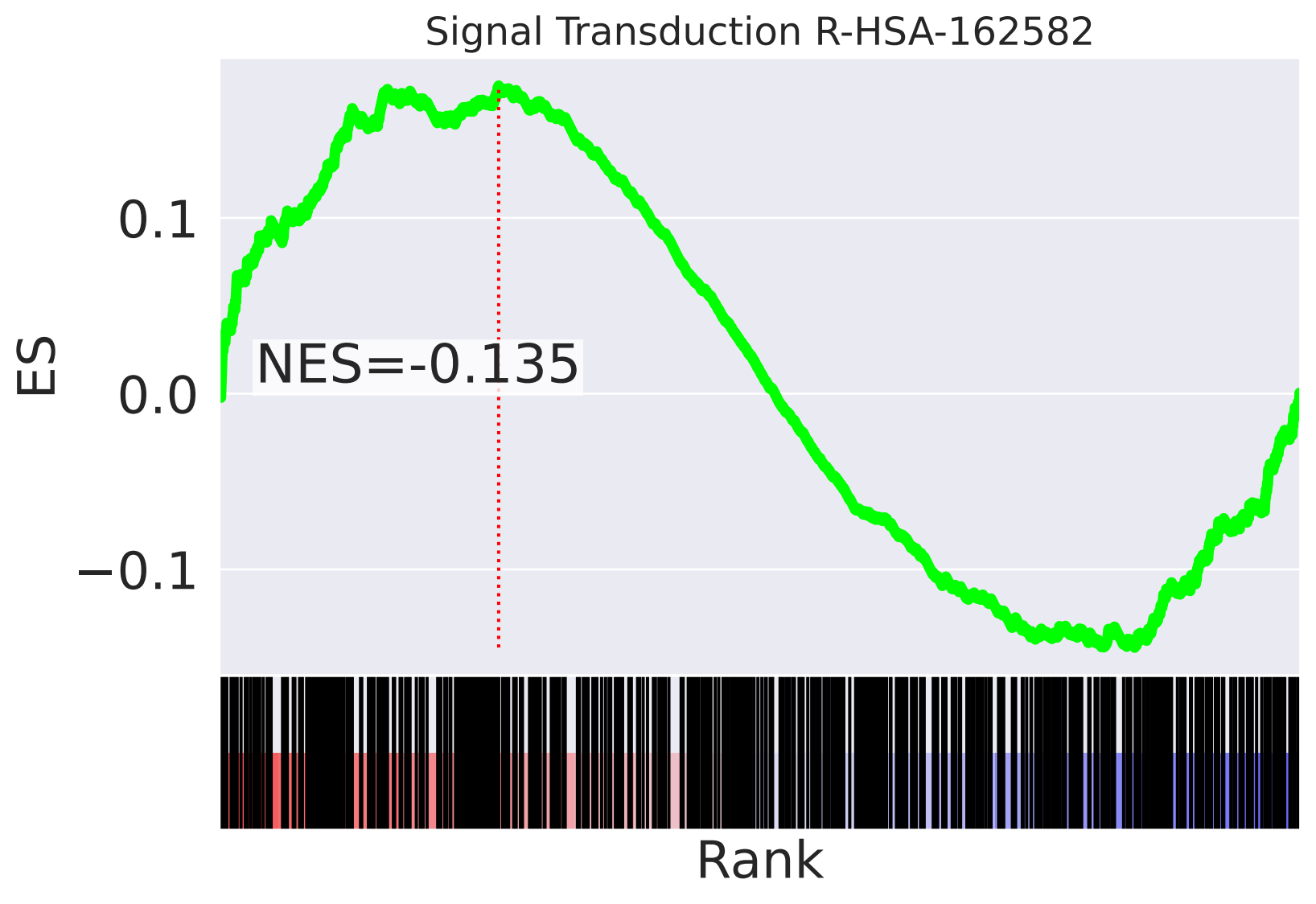

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.186
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1350
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

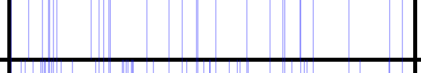
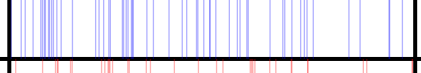
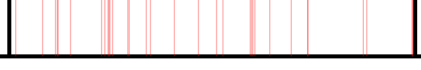

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.186
Rank

NES	SET
-3.872	Downstream Signaling Events Of B Cell Receptor (BCR) R-HSA-1168372
-3.852	Activation Of NF-kappaB In B Cells R-HSA-1169091
-3.775	Signaling By B Cell Receptor (BCR) R-HSA-983705
-3.748	Interleukin-1 Signaling R-HSA-9020702
-3.594	ABC-family Proteins Mediated Transport R-HSA-382556
-3.589	FCERI Mediated NF-kB Activation R-HSA-2871837
-3.559	Antigen processing-Cross Presentation R-HSA-1236975
-3.442	Downstream TCR Signaling R-HSA-202424
-3.382	Fc Epsilon Receptor (FCERI) Signaling R-HSA-2454202
-3.375	FBXL7 Down-Regulates AURKA During Mitotic Entry And In Early Mitosis R-HSA-8854050
-3.361	Ubiquitin-dependent Degradation Of Cyclin D R-HSA-75815
-3.329	CLEC7A (Dectin-1) Signaling R-HSA-5607764
-3.302	Interleukin-1 Family Signaling R-HSA-446652
-3.274	Vpu Mediated Degradation Of CD4 R-HSA-180534
-3.274	Signaling By Insulin Receptor R-HSA-74752

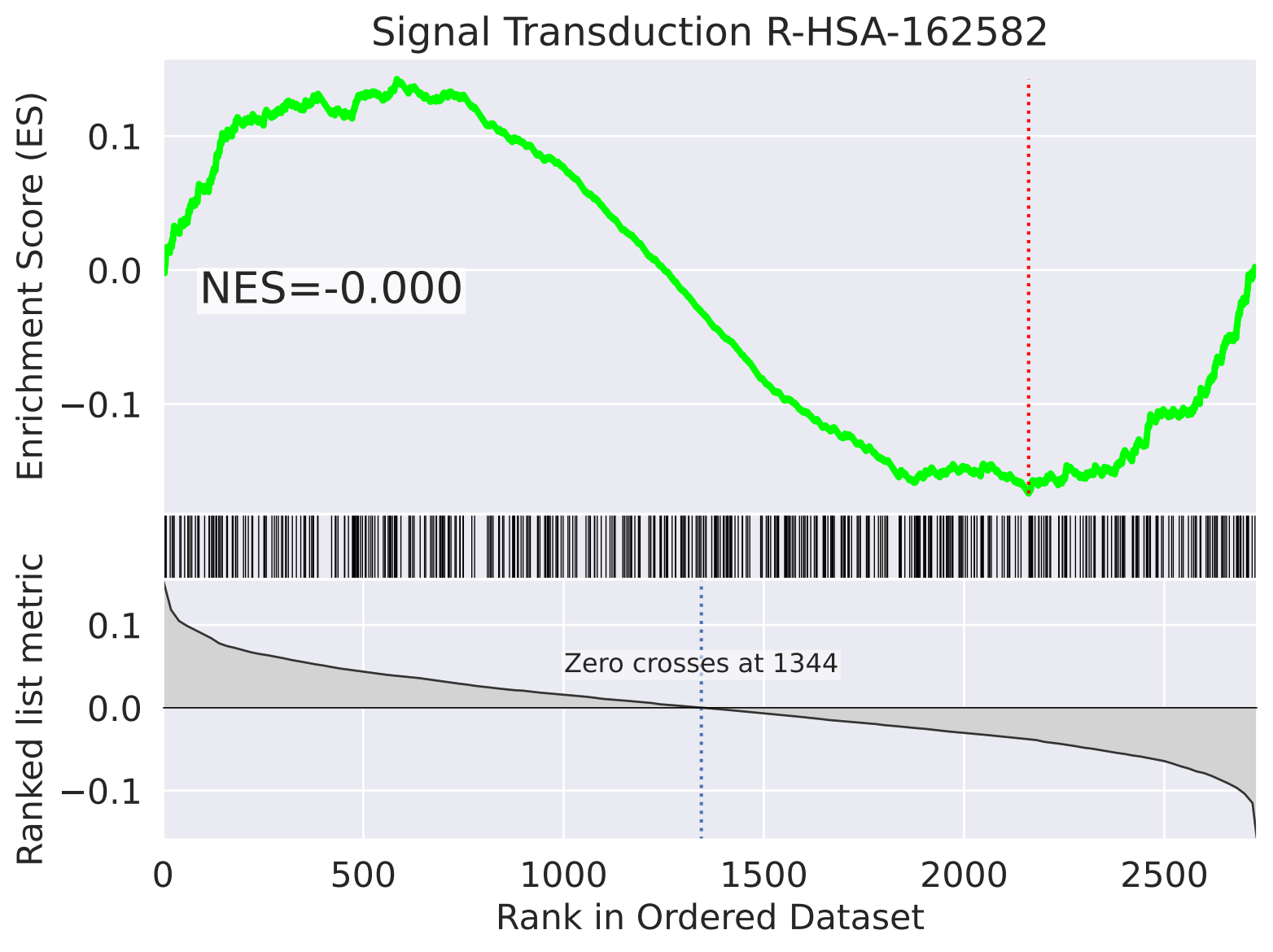
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=35

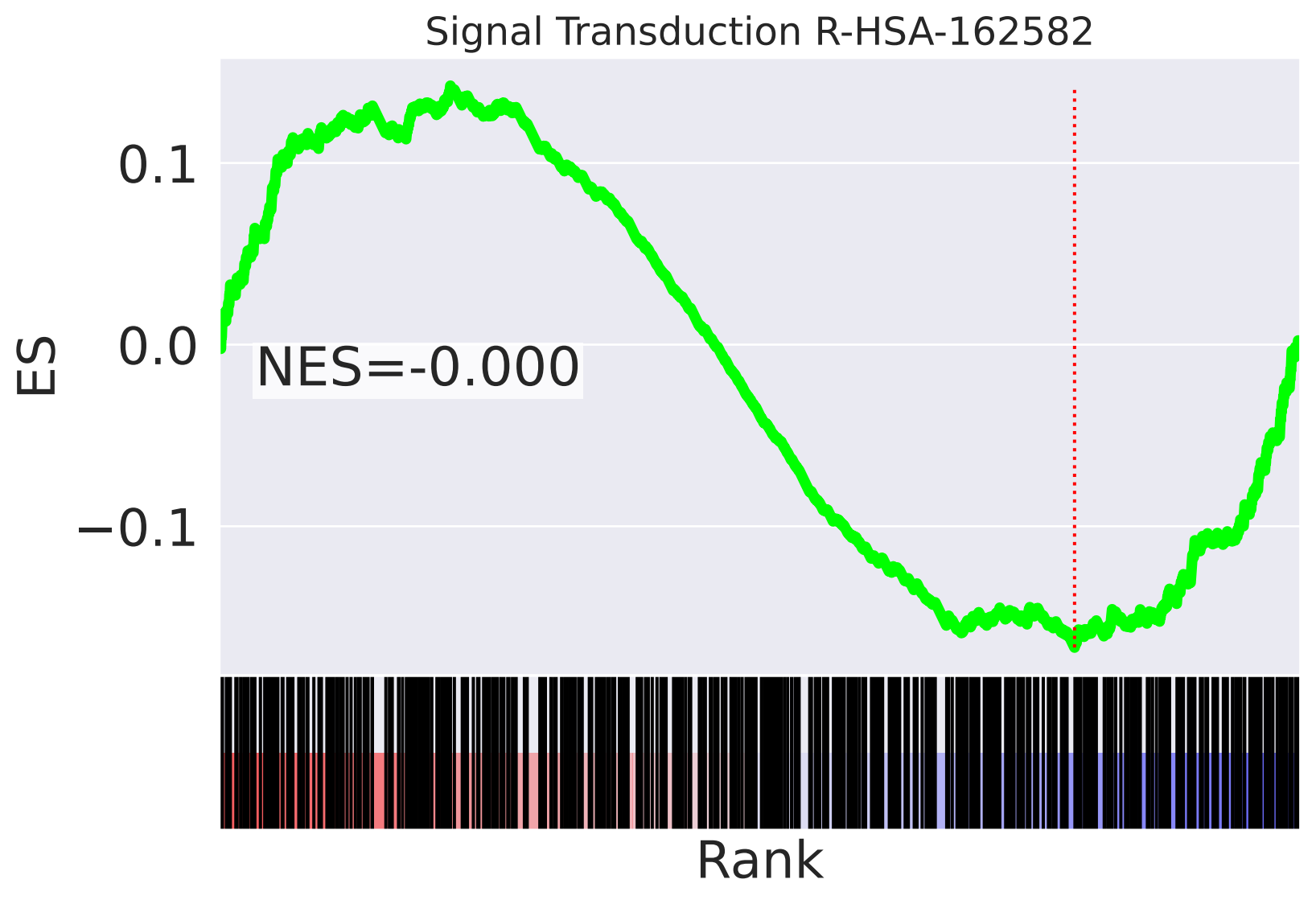

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.135
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1347
0
500
1000
1500
2000
2500
Rank in Ordered Dataset


Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.135
Rank

NES		SET
-4.010		G2/M DNA Damage Checkpoint R-HSA-69473
-3.611		Processing Of DNA Double-Strand Break Ends R-HSA-5693607
-3.547		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
-3.546		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.546		Diseases Of DNA Repair R-HSA-9675135
-3.372		Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange R-HSA-5693616
-3.354		HDR Thru Homologous Recombination (HRR) R-HSA-5685942
-3.306		HDR Thru Homologous Recombination (HRR) Or Single Strand Annealing (SSA) R-HSA-5693567
-3.225		Homology Directed Repair R-HSA-5693538
-3.219		DNA Double-Strand Break Repair R-HSA-5693532
-3.184		Impaired BRCA2 Binding To RAD51 R-HSA-9709570
-3.129		HDR Thru Single Strand Annealing (SSA) R-HSA-5685938
-3.043		Regulation Of TP53 Activity Thru Phosphorylation R-HSA-6804756
2.906		AUF1 (hnRNP D0) Binds And Destabilizes mRNA R-HSA-450408
2.876		Cross-presentation Of Soluble Exogenous Antigens (Endosomes) R-HSA-1236978

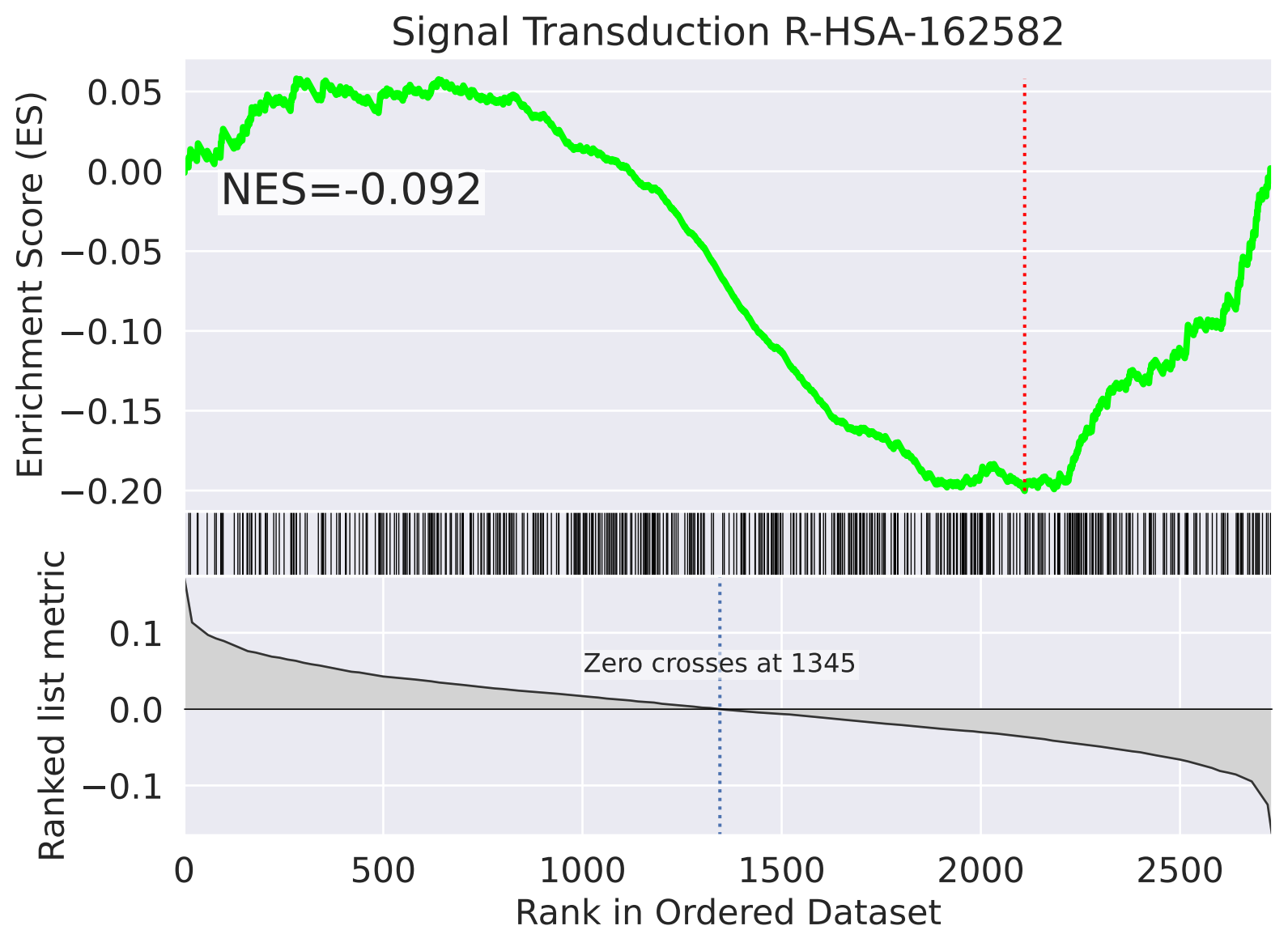
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=36

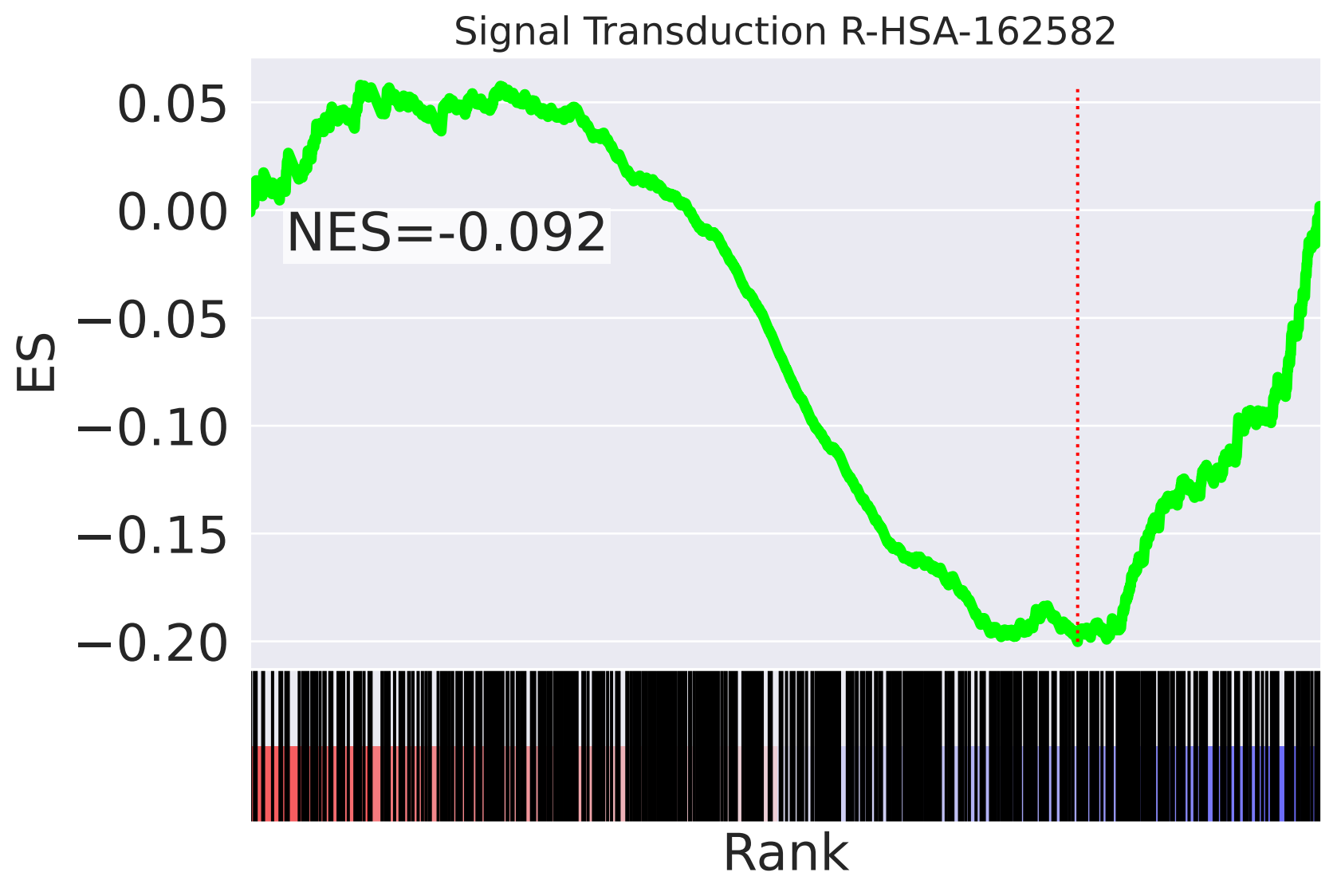

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1344
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

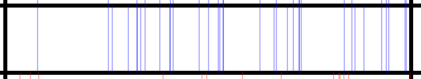
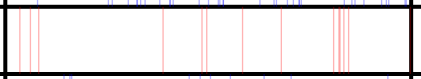
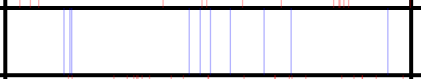
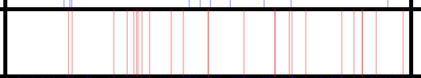
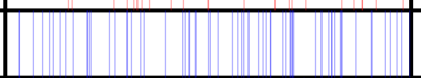
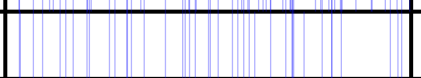
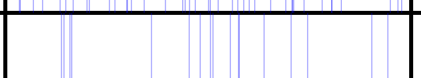
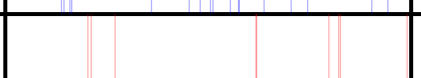
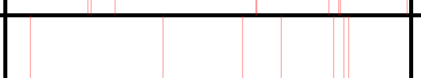
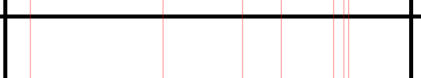
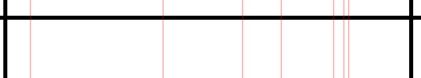
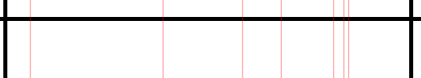
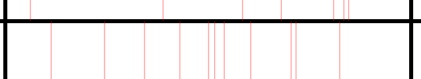

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES	SET
6.163	mRNA Splicing R-HSA-72172
5.963	mRNA Splicing - Major Pathway R-HSA-72163
5.893	Processing Of Capped Intron-Containing Pre-mRNA R-HSA-72203
4.952	S Phase R-HSA-69242
4.639	Synthesis Of DNA R-HSA-69239
4.636	HIV Infection R-HSA-162906
4.457	DNA Replication R-HSA-69306
-4.375	rRNA Processing R-HSA-72312
4.097	Separation Of Sister Chromatids R-HSA-2467813
-4.066	rRNA Processing In Nucleus And Cytosol R-HSA-8868773
4.040	DNA Replication Pre-Initiation R-HSA-69002
4.037	Switching Of Origins To A Post-Replicative State R-HSA-69052
4.003	Signaling By NOTCH4 R-HSA-9013694
3.996	SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
3.979	SCF-beta-TrCP Mediated Degradation Of Emi1 R-HSA-174113

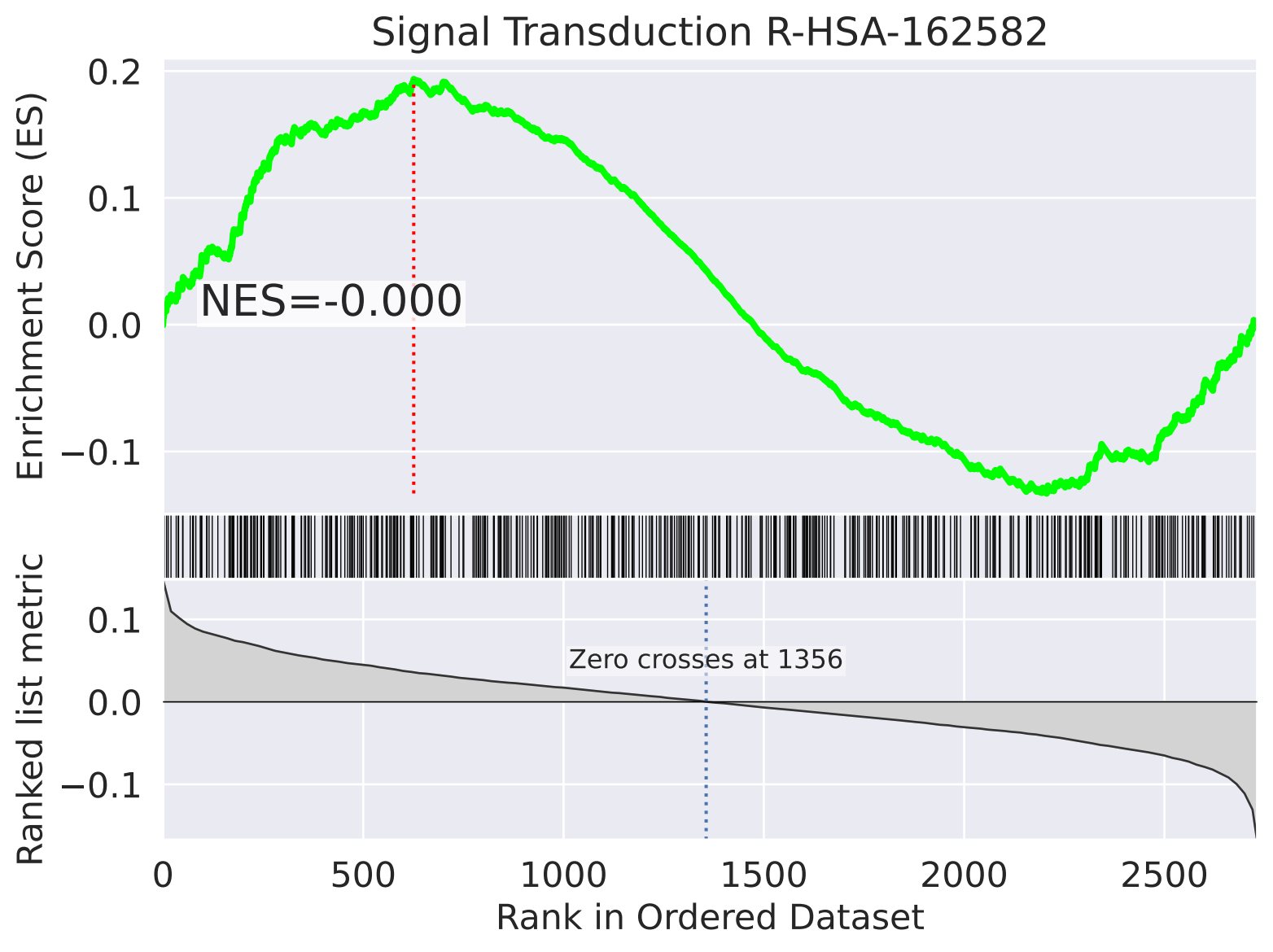
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=37

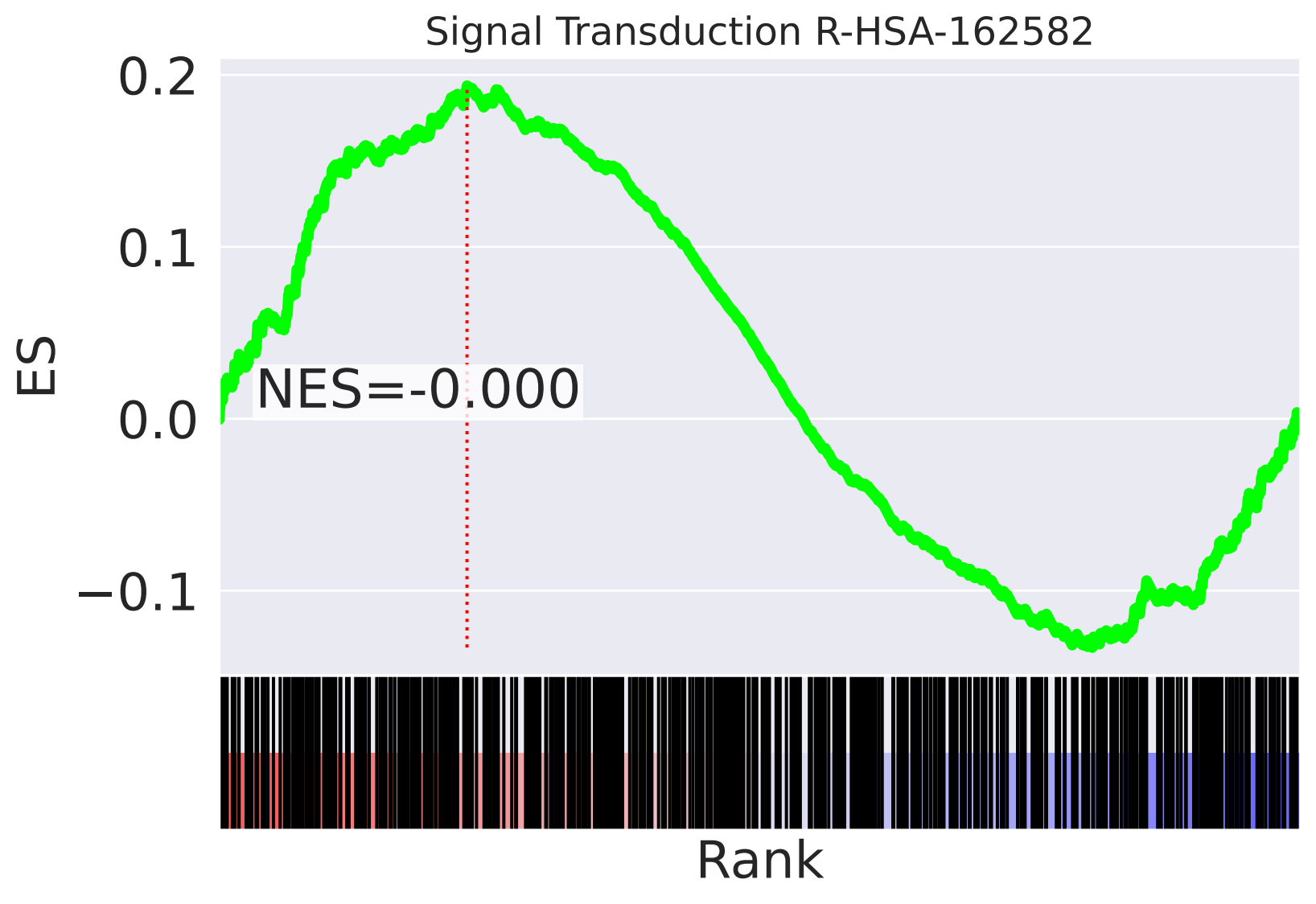

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.05
0.00
−0.05
−0.10
−0.15
−0.20
NES=-0.092
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1345
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

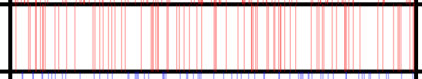
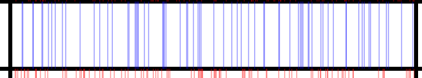
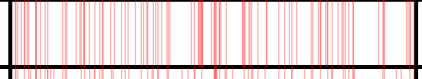
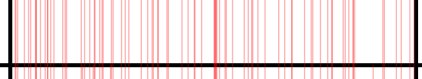
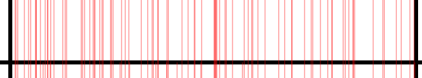
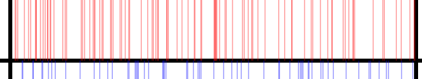
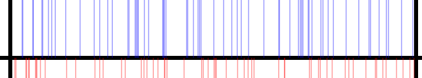
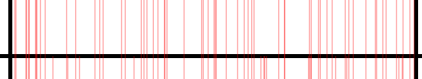
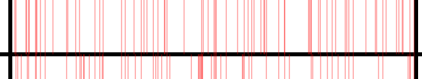
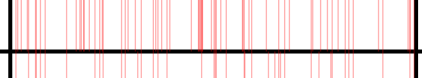
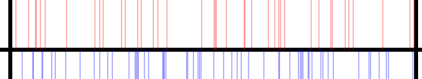
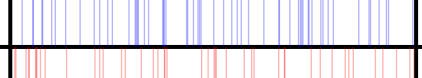
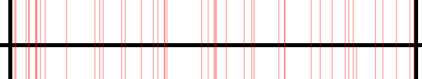
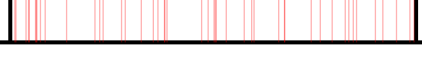

Signal Transduction R-HSA-162582
0.05
0.00
−0.05
−0.10
−0.15
−0.20
ES
NES=-0.092
Rank

NES		SET
-3.056		Transport Of Small Molecules R-HSA-382551
-2.955		Cargo Recognition For Clathrin-Mediated Endocytosis R-HSA-8856825
-2.949		Clathrin-mediated Endocytosis R-HSA-8856828
2.780		Inhibition Of DNA Recombination At Telomere R-HSA-9670095
-2.779		Fatty acyl-CoA Biosynthesis R-HSA-75105
2.767		Fanconi Anemia Pathway R-HSA-6783310
-2.714		Disorders Of Transmembrane Transporters R-HSA-5619115
-2.667		ABC-family Proteins Mediated Transport R-HSA-382556
-2.623		Fatty Acid Metabolism R-HSA-8978868
2.564		Basigin Interactions R-HSA-210991
2.501		Packaging Of Telomere Ends R-HSA-171306
2.501		Cleavage Of Damaged Pyrimidine R-HSA-110329
2.501		Base-Excision Repair, AP Site Formation R-HSA-73929
2.501		Cleavage Of Damaged Purine R-HSA-110331
2.484		Regulation Of Necroptotic Cell Death R-HSA-5675482

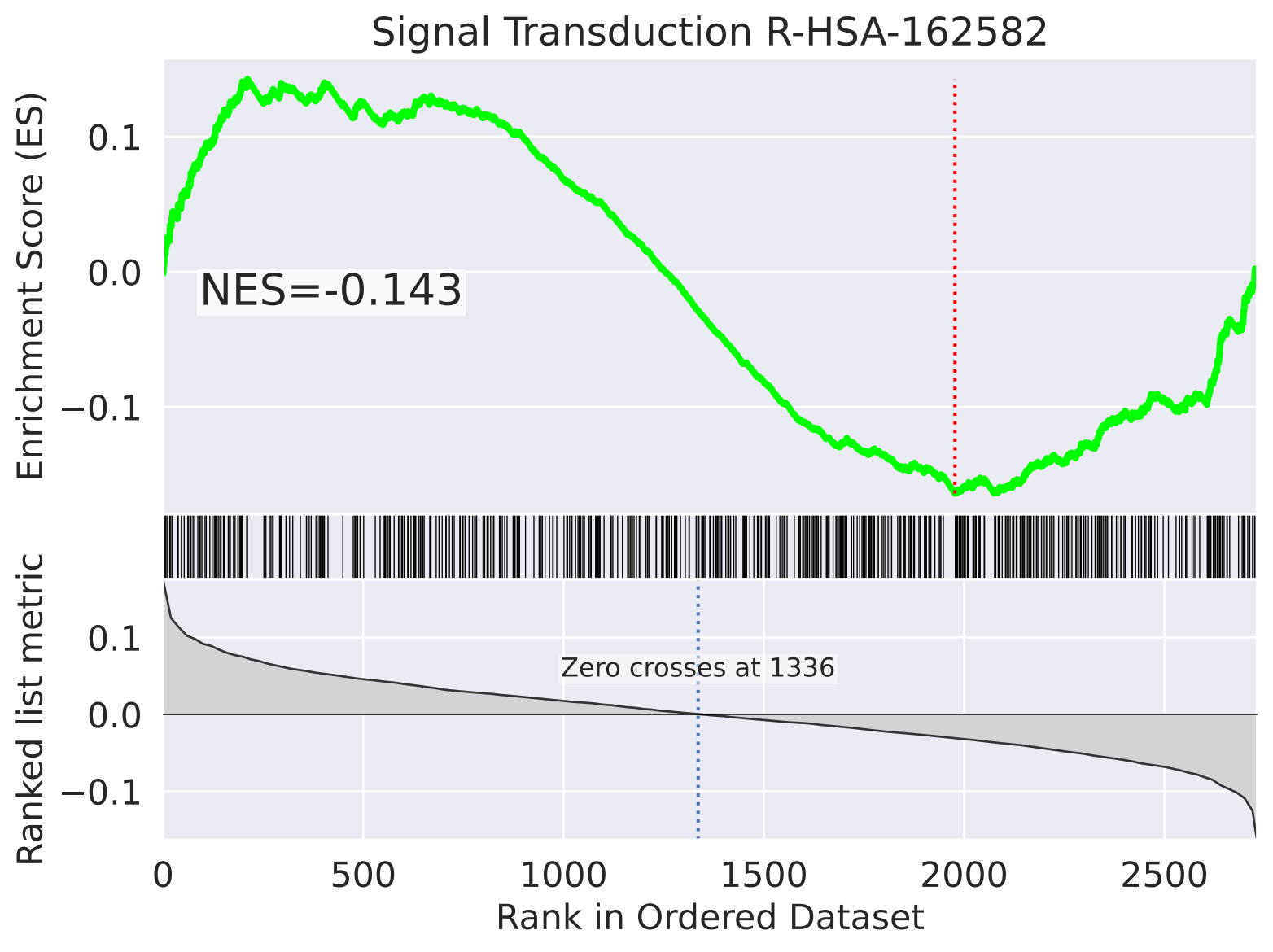
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=38

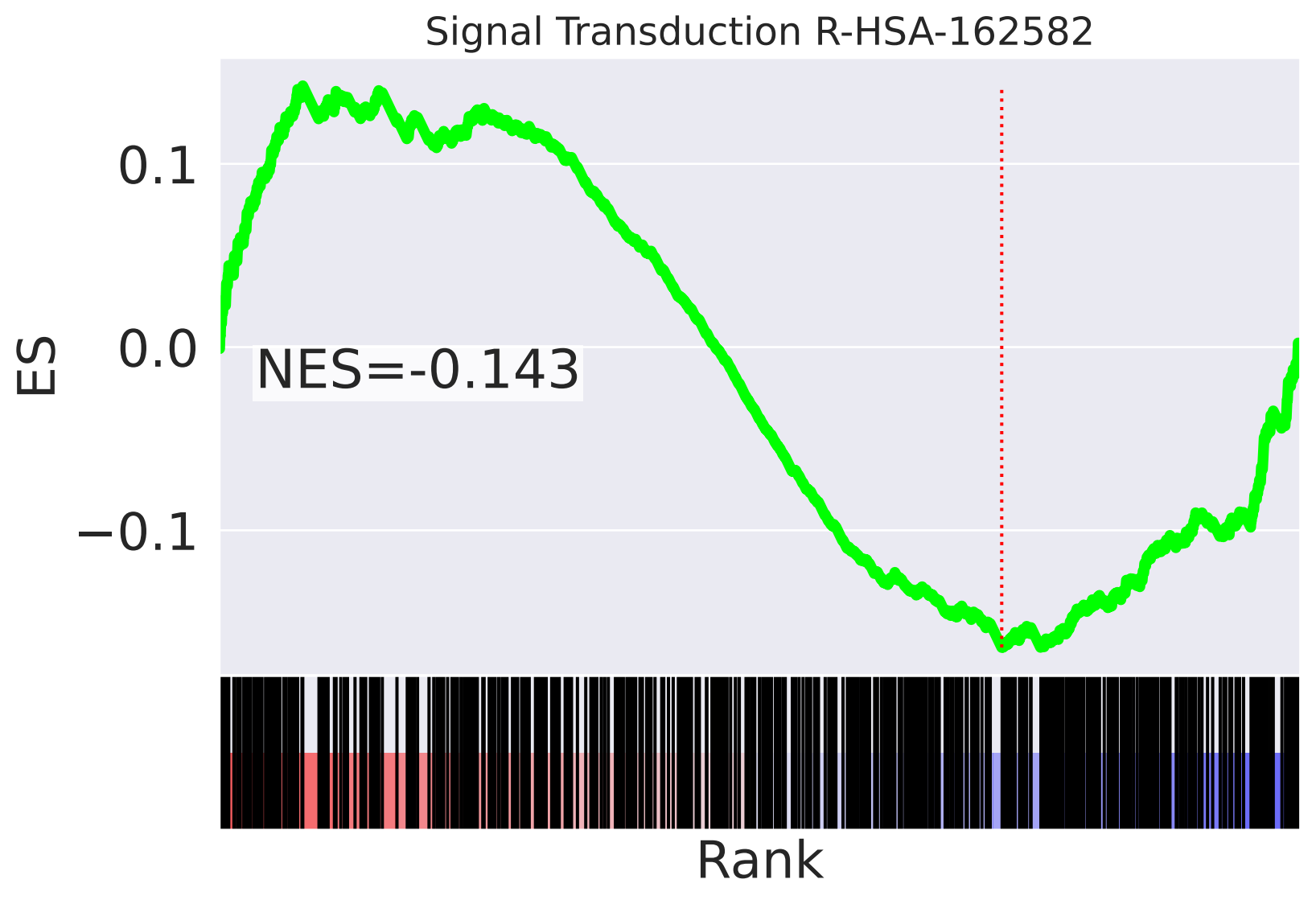

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1356
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

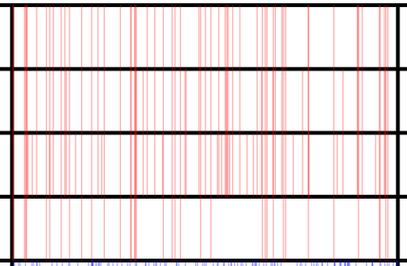

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.401		Intracellular Signaling By Second Messengers R-HSA-9006925
5.383		Host Interactions Of HIV Factors R-HSA-162909
-5.383		rRNA Processing R-HSA-72312
5.308		PIP3 Activates AKT Signaling R-HSA-1257604
5.253		RAF/MAP Kinase Cascade R-HSA-5673001
5.156		MAPK1/MAPK3 Signaling R-HSA-5684996
5.127		MAPK Family Signaling Cascades R-HSA-5683057
-5.124		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
5.048		Assembly Of Pre-Replicative Complex R-HSA-68867
5.040		DNA Replication Pre-Initiation R-HSA-69002
5.013		PTEN Regulation R-HSA-6807070
4.914		PCP/CE Pathway R-HSA-4086400
-4.860		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
4.857		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
4.849		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154

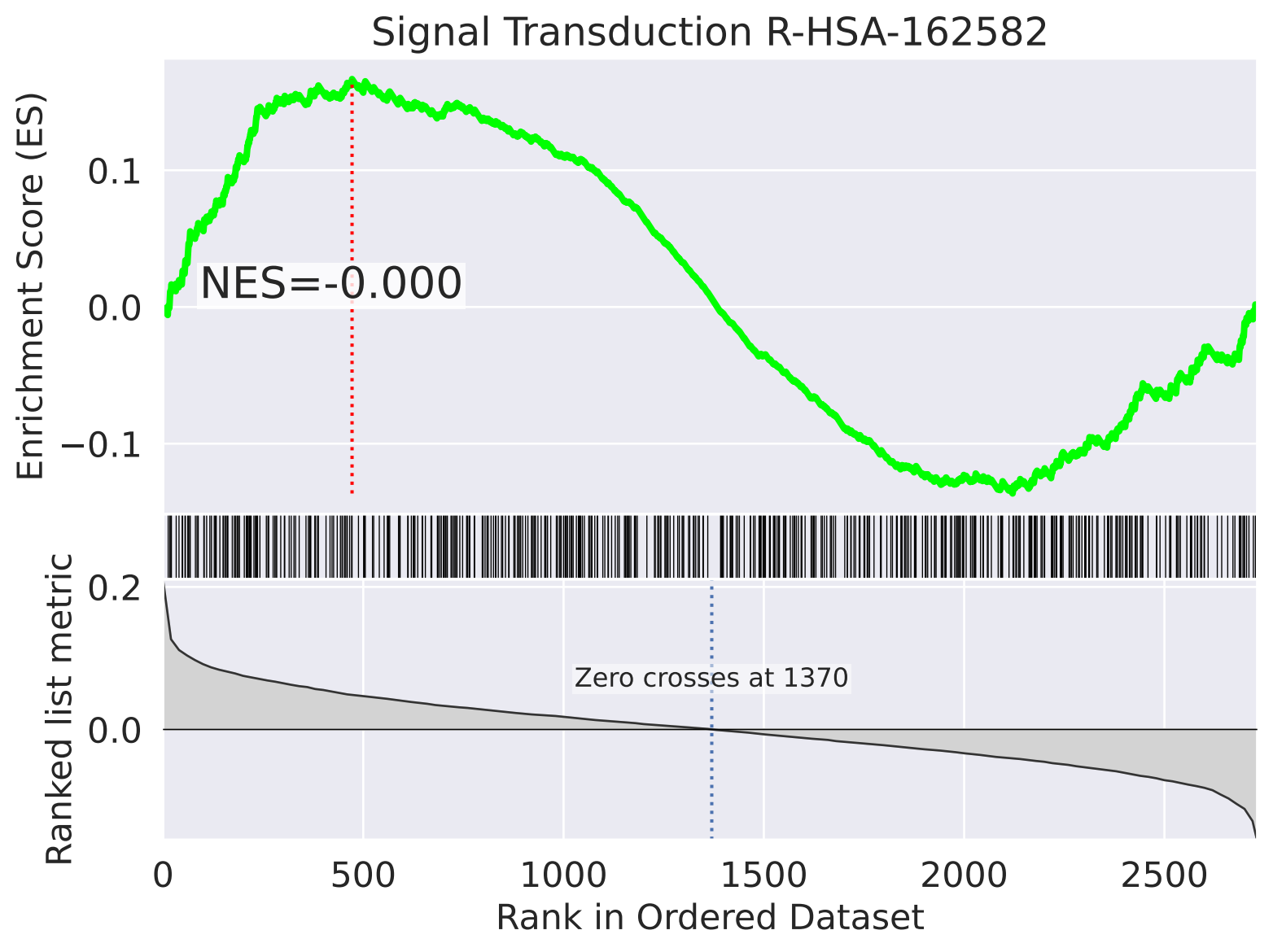
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=39

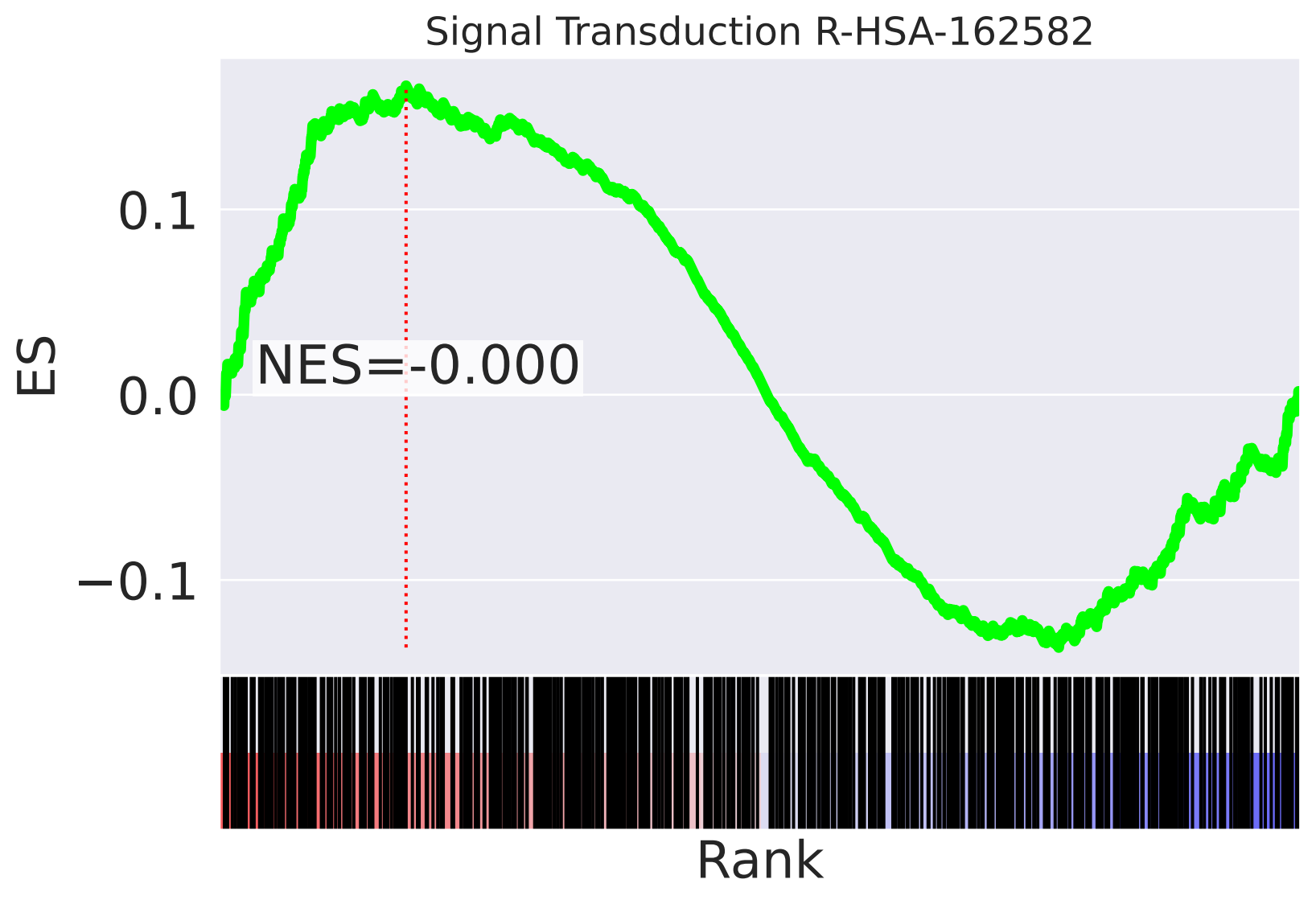

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.143
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1336
0
500
1000
1500
2000
2500
Rank in Ordered Dataset


Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.143
Rank

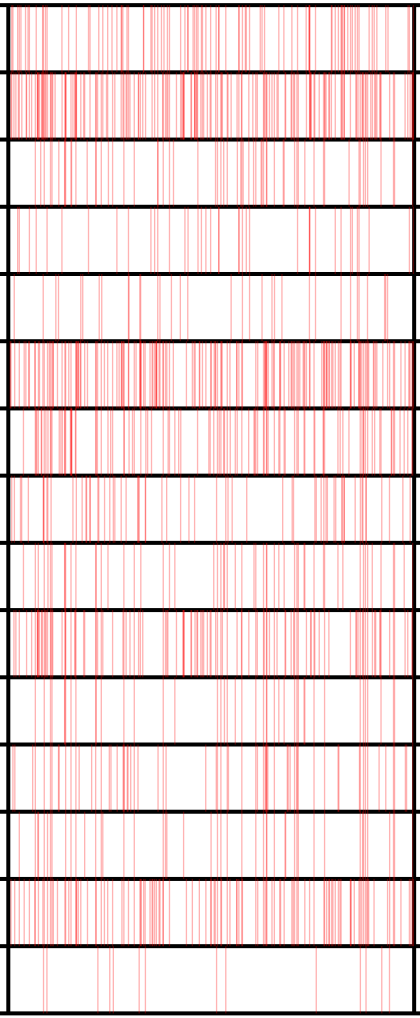
NES		SET
6.373		Respiratory Electron Transport R-HSA-611105
6.303		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
6.227		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
5.239		Complex I Biogenesis R-HSA-6799198
-4.372		Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
-3.922		Adaptive Immune System R-HSA-1280218
-3.768		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.633		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-3.590		Regulation Of APC/C Activators Between G1/S And Early Anaphase R-HSA-176408
-3.588		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
-3.473		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
3.441		RUNX1 Interacts With Co-Factors Whose Precise Effect On RUNX1 Targets Is Not Known R-HSA-8939243
-3.423		Antigen Processing: Ubiquitination And Proteasome Degradation R-HSA-983168
-3.408		APC:Cdc20 Mediated Degradation Of Cell Cycle Proteins Before Cycle Checkpoint Satisfied R-HSA-179419
-3.408		Cdc20:Phospho-APC/C Mediated Degradation Of Cyclin A R-HSA-174184

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

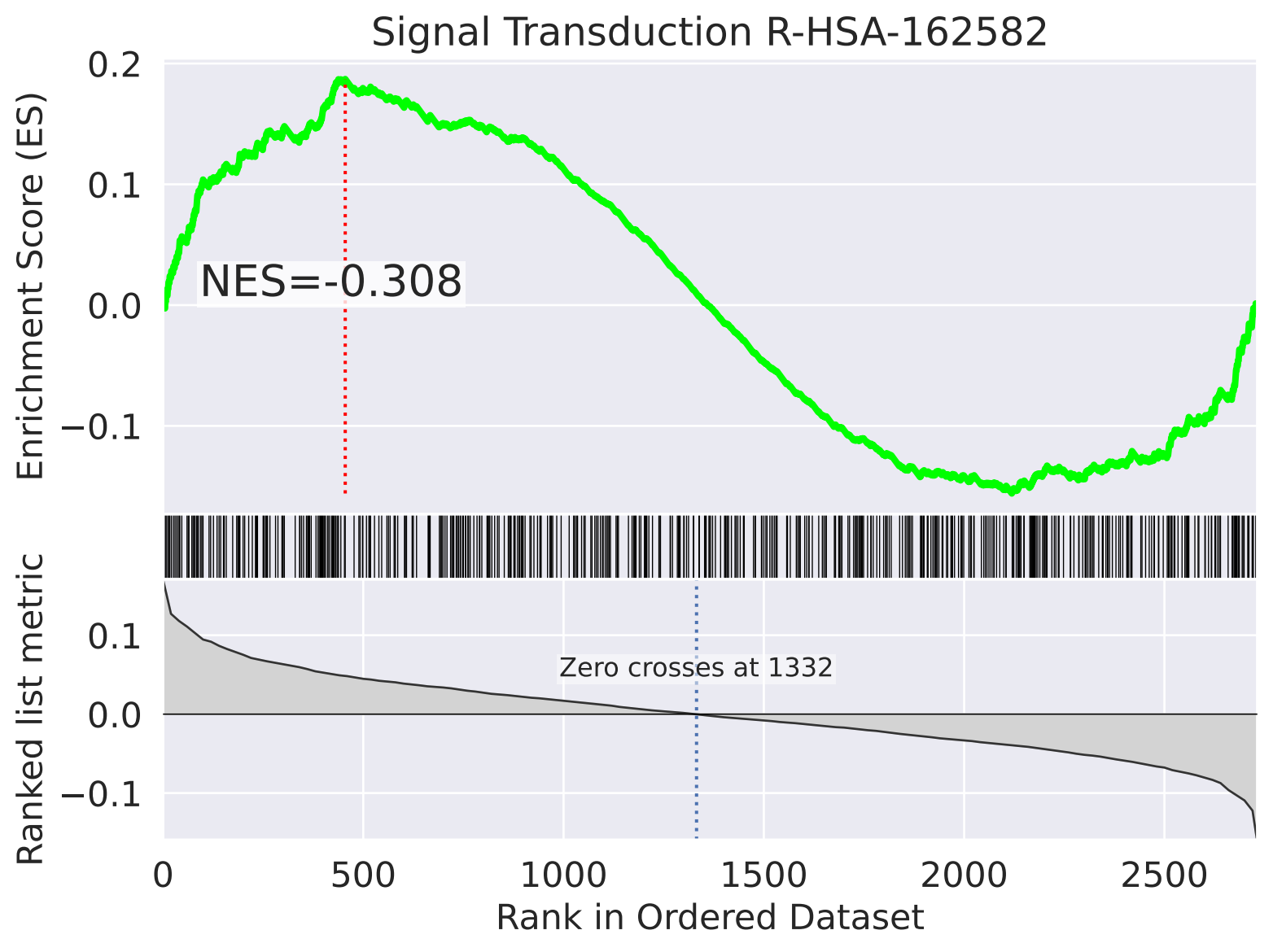

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
0.2
Ranked list metric
0.0
Zero crosses at 1370
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

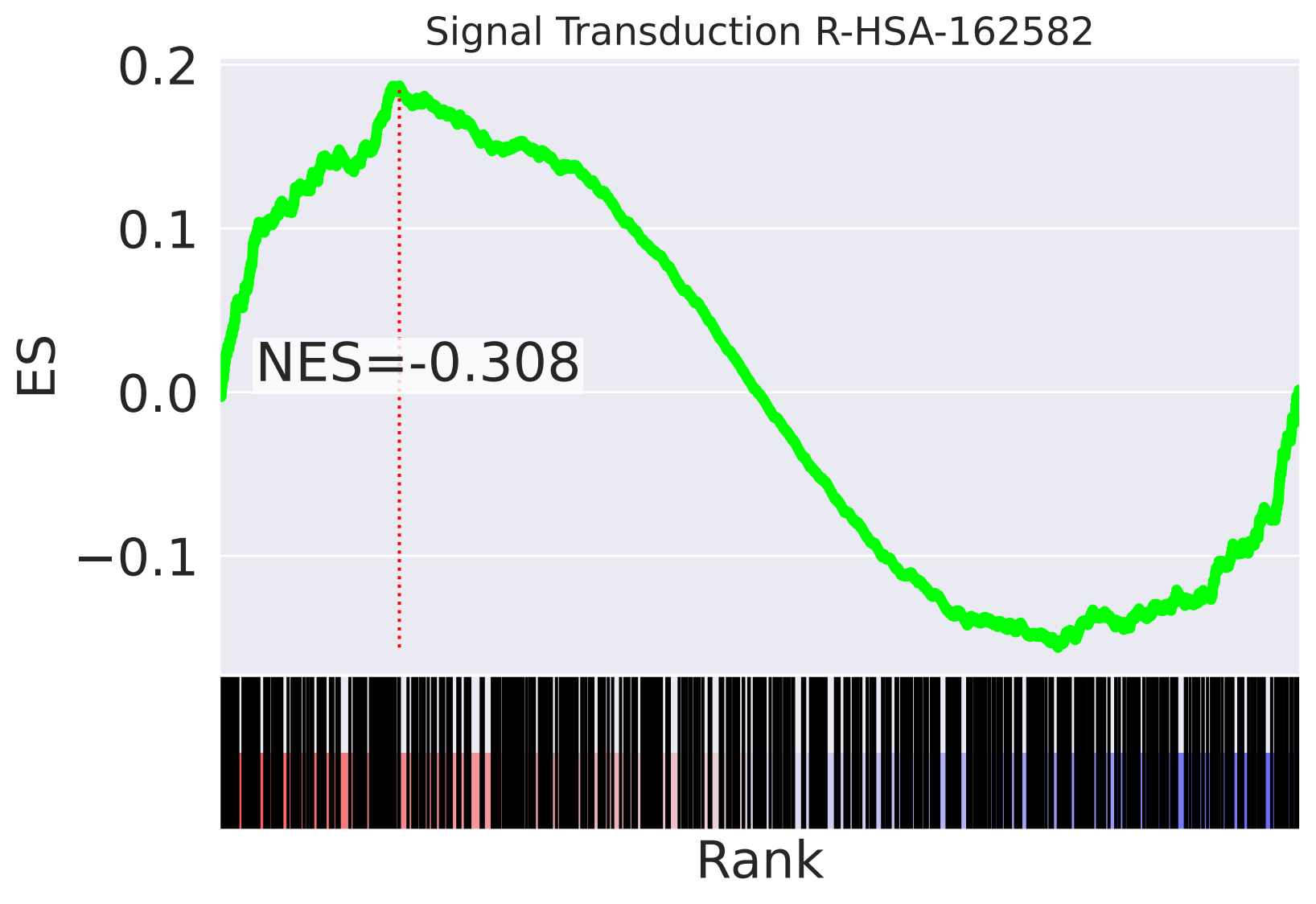

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

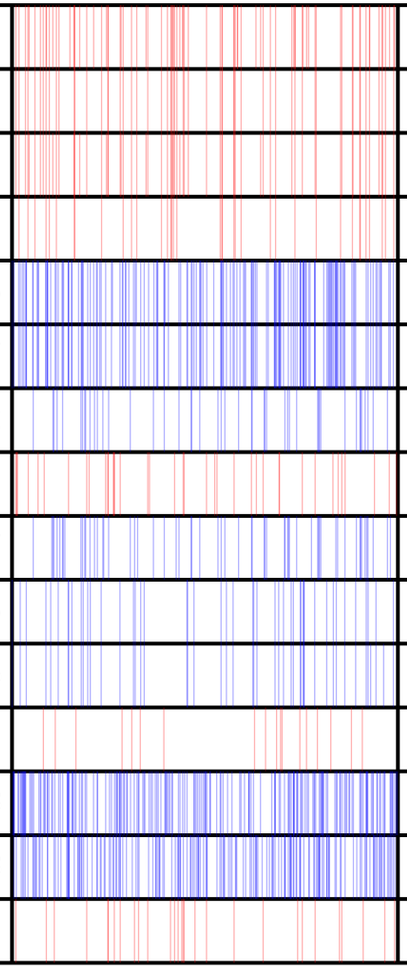
NES	SET
4.291	Hemostasis R-HSA-109582
4.221	Adaptive Immune System R-HSA-1280218
3.886	Transcriptional Regulation By RUNX2 R-HSA-8878166
3.789	Platelet Activation, Signaling And Aggregation R-HSA-76002
3.708	Leishmania Infection R-HSA-9658195
3.705	Cytokine Signaling In Immune System R-HSA-1280215
3.658	S Phase R-HSA-69242
3.635	Intra-Golgi And Retrograde Golgi-to-ER Traffic R-HSA-6811442
3.605	Cyclin A:Cdk2-associated Events At S Phase Entry R-HSA-69656
3.483	Class I MHC Mediated Antigen Processing And Presentation R-HSA-983169
3.461	SCF(Skp2)-mediated Degradation Of P27/P21 R-HSA-187577
3.458	Metabolism Of Amino Acids And Derivatives R-HSA-71291
3.430	Antigen processing-Cross Presentation R-HSA-1236975
3.429	Signaling By Interleukins R-HSA-449147
3.416	Intra-Golgi Traffic R-HSA-6811438



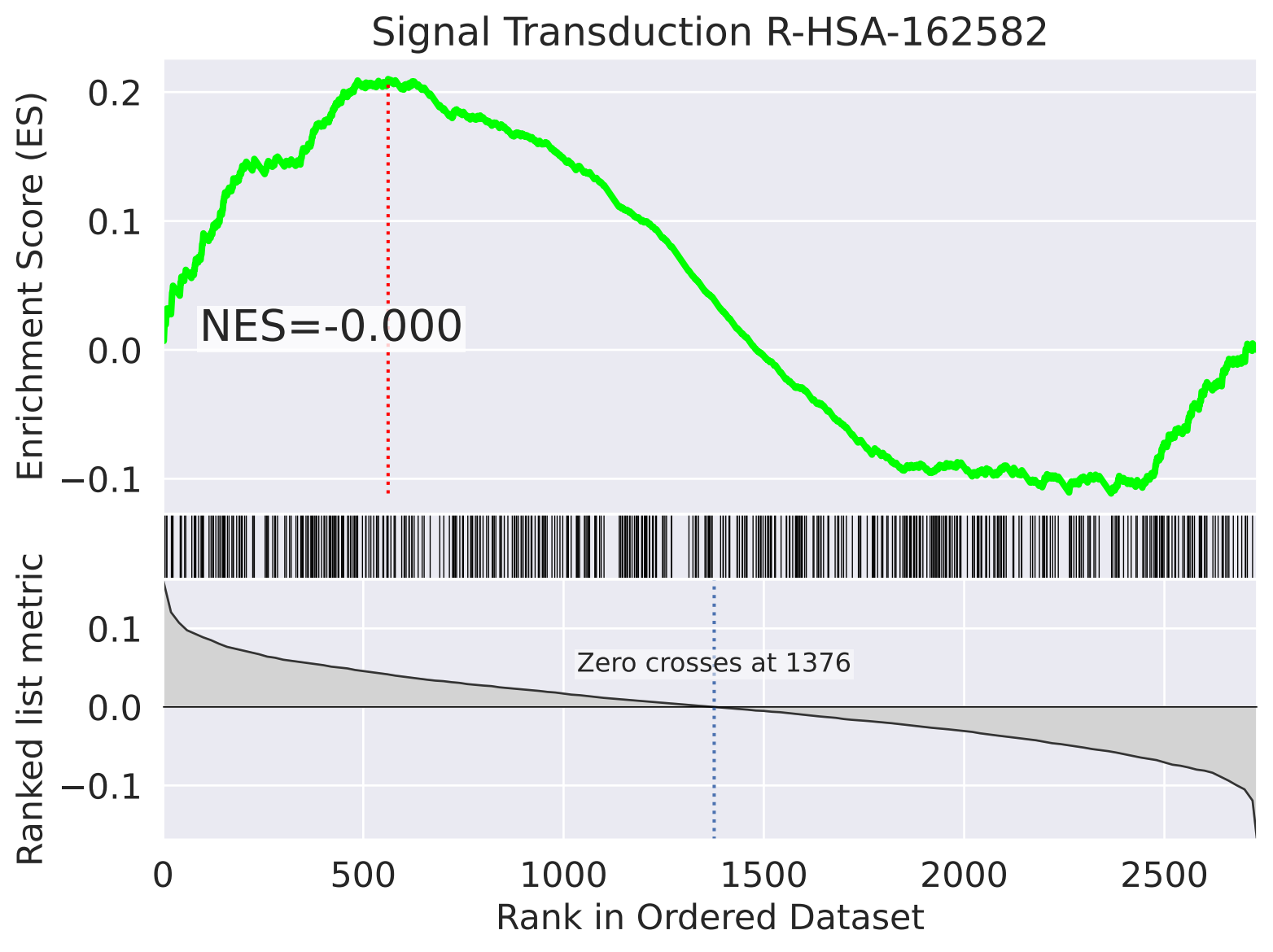
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=41

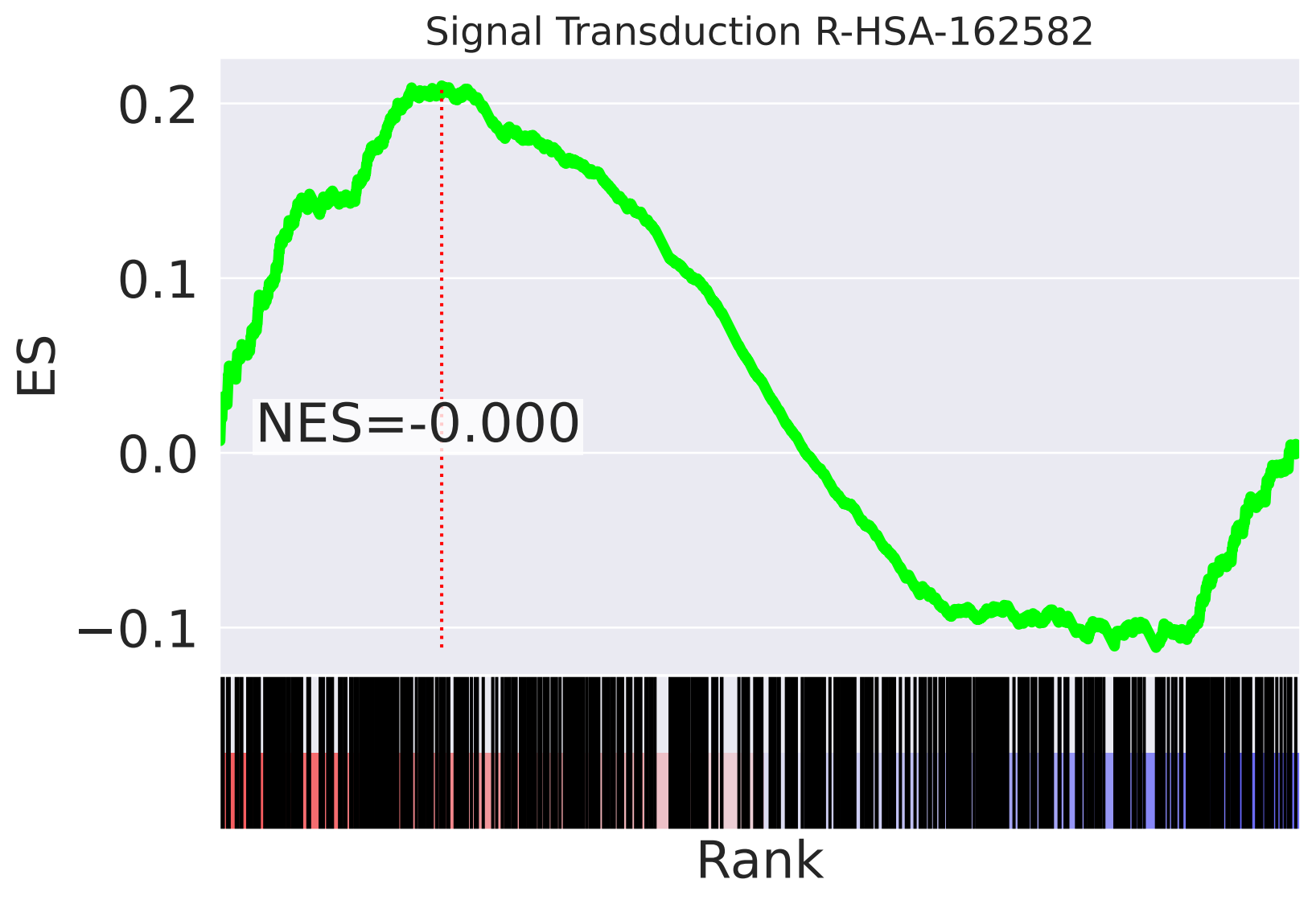

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.308
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1332
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

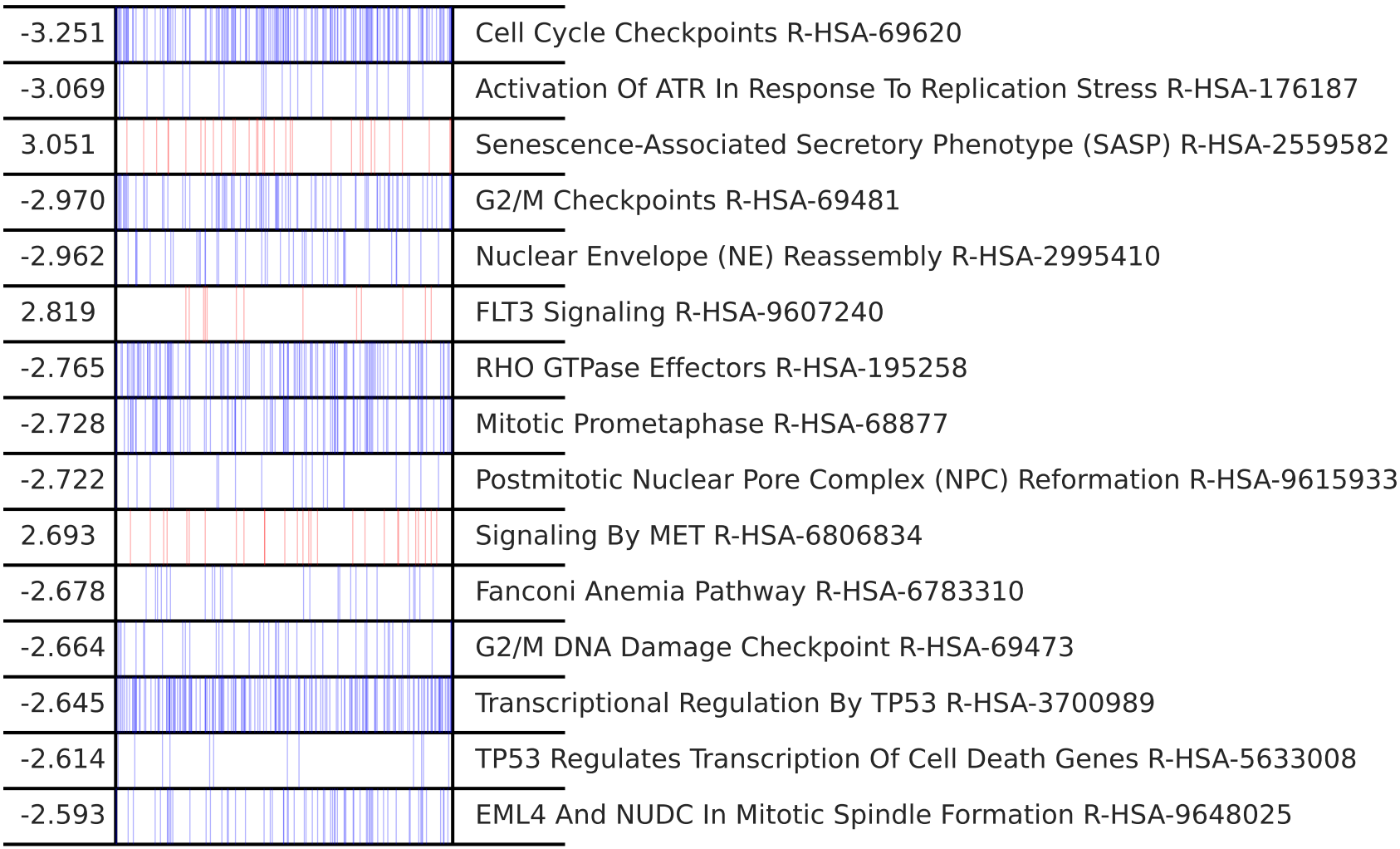

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.308
Rank

NES		SET
6.688		Citric Acid (TCA) Cycle And Respiratory Electron Transport R-HSA-1428517
6.466		Respiratory Electron Transport R-HSA-611105
6.282		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
5.210		Complex I Biogenesis R-HSA-6799198
-3.985		Vesicle-mediated Transport R-HSA-5653656
-3.897		Membrane Trafficking R-HSA-199991
-3.892		Global Genome Nucleotide Excision Repair (GG-NER) R-HSA-5696399
3.813		TP53 Regulates Metabolic Genes R-HSA-5628897
-3.807		Nucleotide Excision Repair R-HSA-5696398
-3.515		ER To Golgi Anterograde Transport R-HSA-199977
-3.486		Transport To Golgi And Subsequent Modification R-HSA-948021
3.445		Mitochondrial tRNA Aminoacylation R-HSA-379726
-3.348		Signaling By Rho GTPases, Miro GTPases And RHOBTB3 R-HSA-9716542
-3.328		Adaptive Immune System R-HSA-1280218
3.304		Cytoprotection By HMOX1 R-HSA-9707564

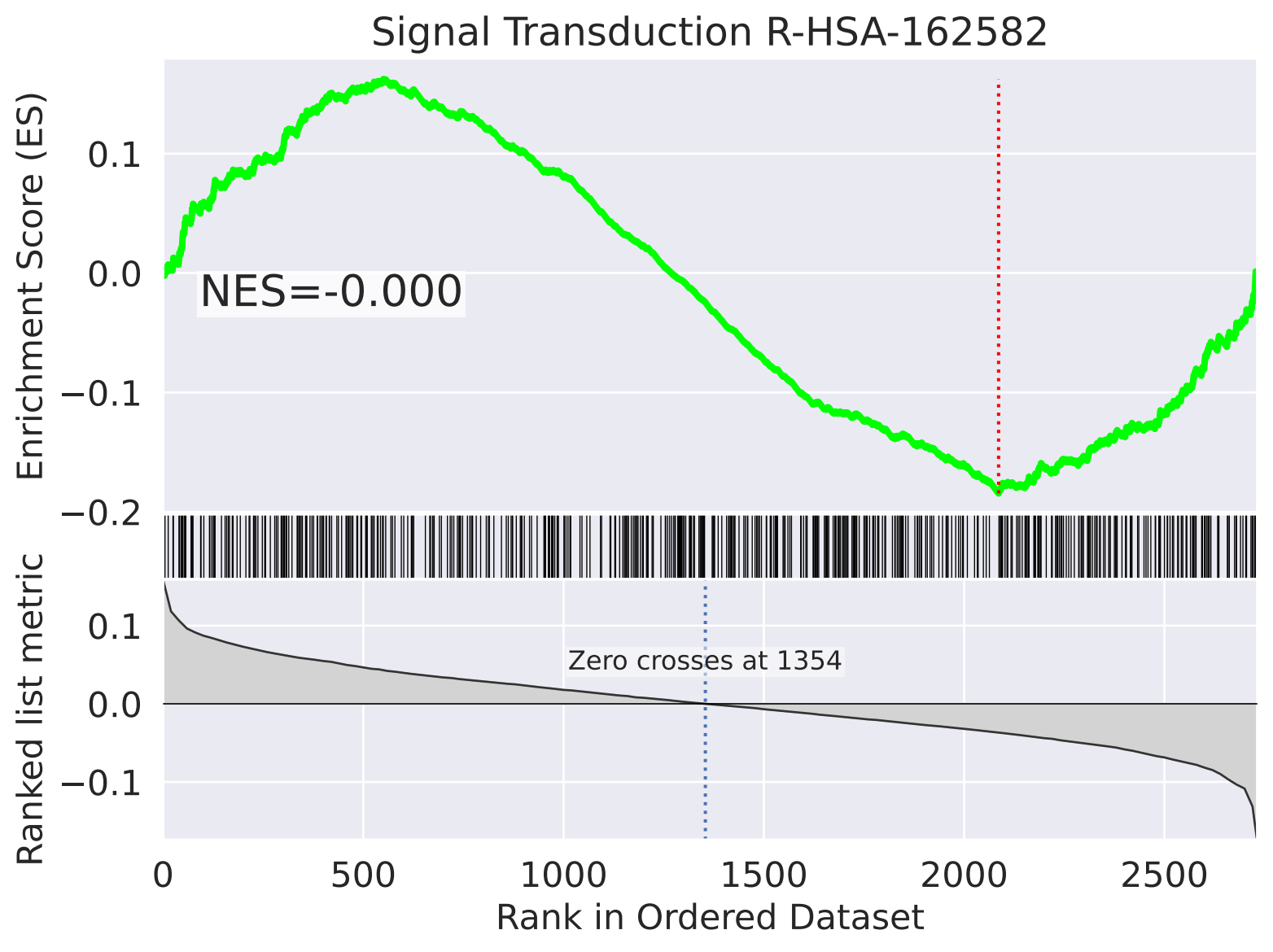
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=42

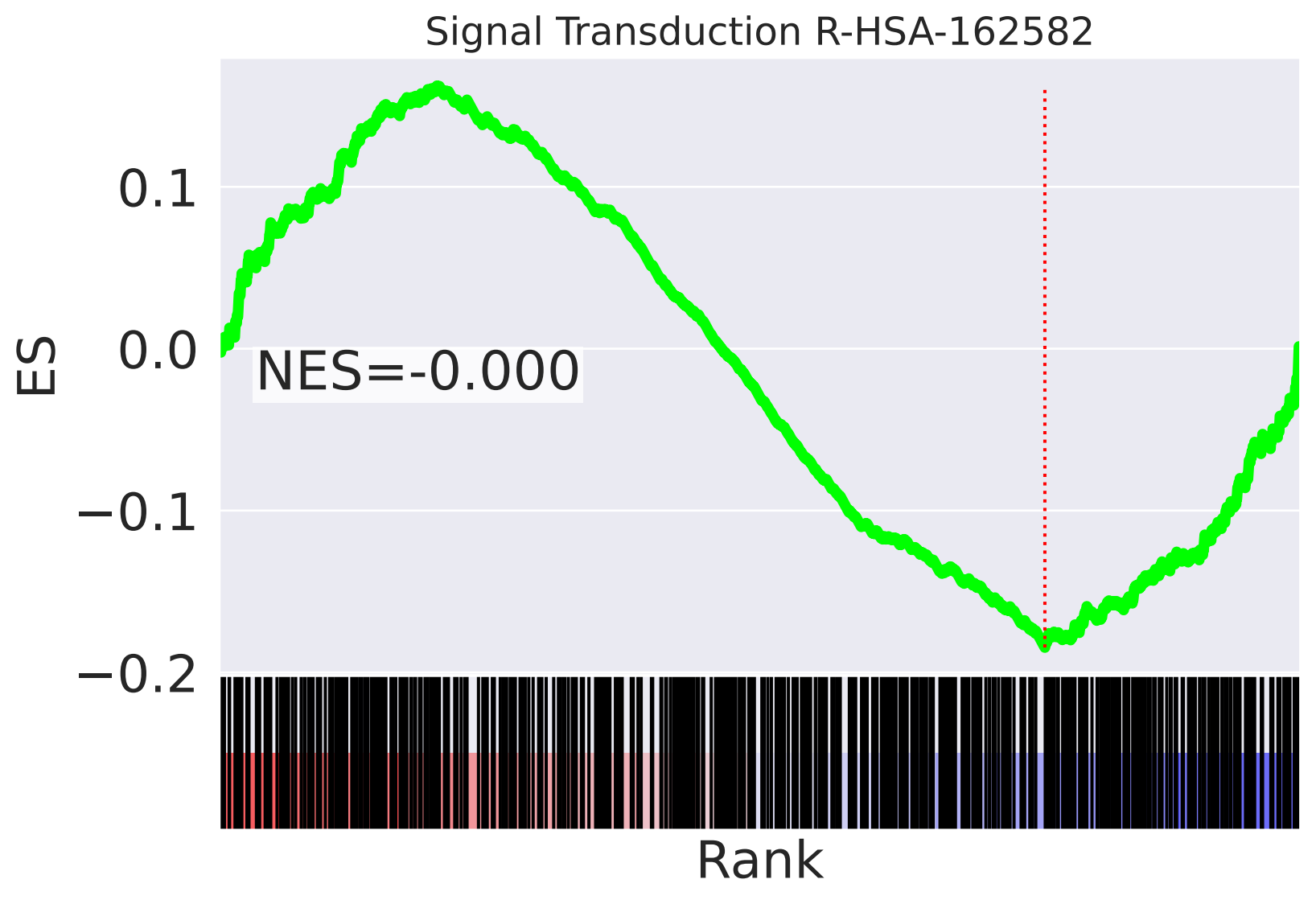

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1376
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

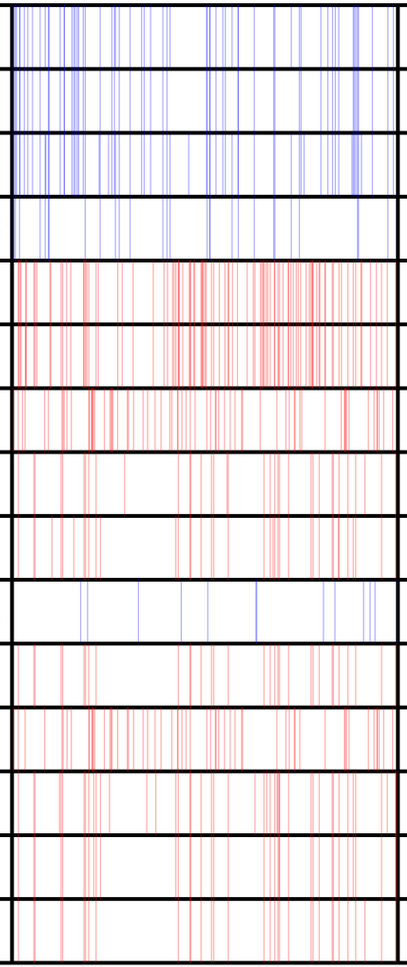

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-3.251
Cell Cycle Checkpoints R-HSA-69620
-3.069
Activation Of ATR In Response To Replication Stress R-HSA-176187
3.051
Senescence-Associated Secretory Phenotype (SASP) R-HSA-2559582
-2.970
G2/M Checkpoints R-HSA-69481
-2.962
Nuclear Envelope (NE) Reassembly R-HSA-2995410
2.819
FLT3 Signaling R-HSA-9607240
-2.765
RHO GTPase Effectors R-HSA-195258
-2.728
Mitotic Prometaphase R-HSA-68877
-2.722
Postmitotic Nuclear Pore Complex (NPC) Reformation R-HSA-9615933
2.693
Signaling By MET R-HSA-6806834
-2.678
Fanconi Anemia Pathway R-HSA-6783310
-2.664
G2/M DNA Damage Checkpoint R-HSA-69473
-2.645
Transcriptional Regulation By TP53 R-HSA-3700989
-2.614
TP53 Regulates Transcription Of Cell Death Genes R-HSA-5633008
-2.593
EML4 And NUDC In Mitotic Spindle Formation R-HSA-9648025

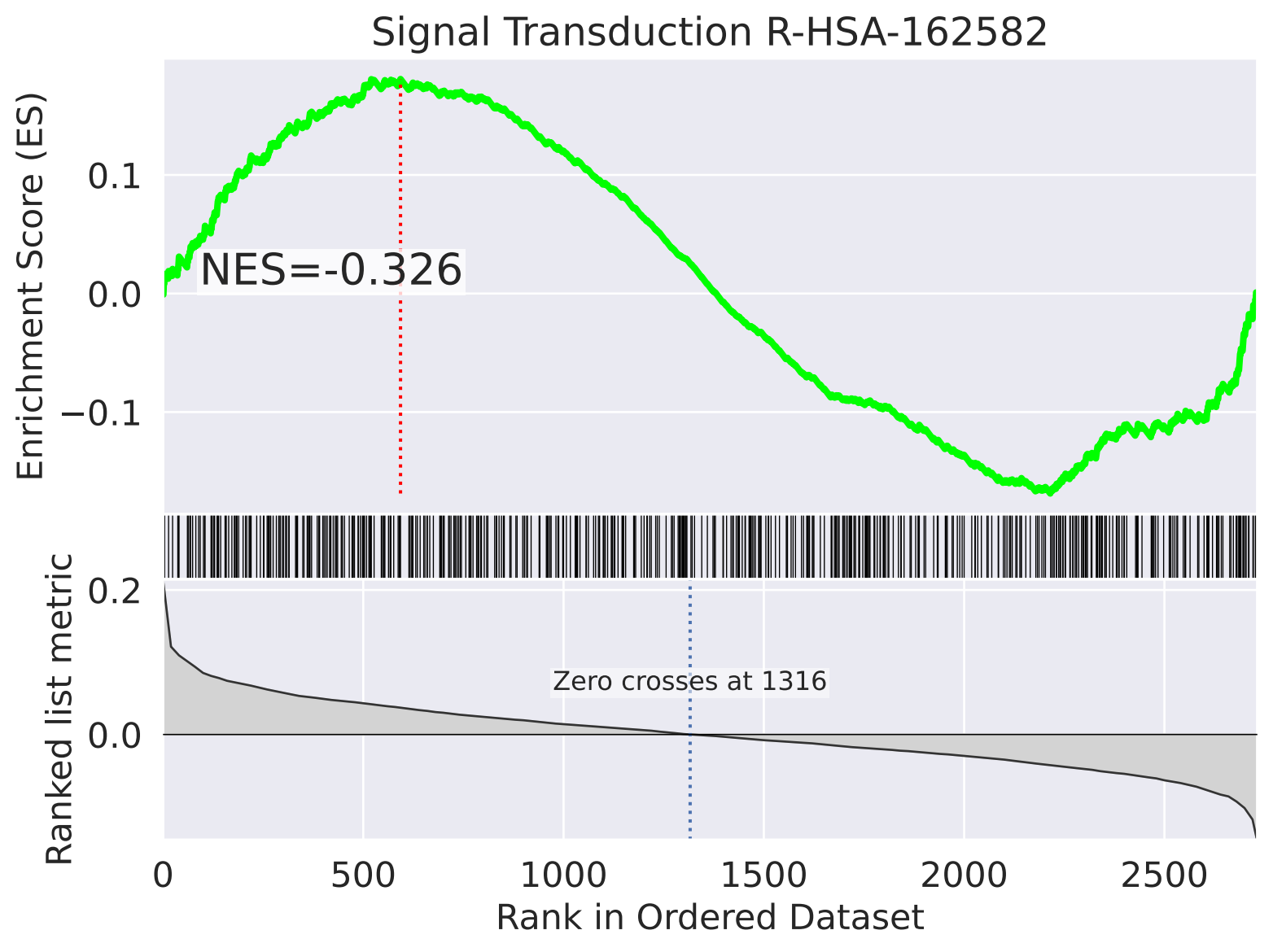
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=43

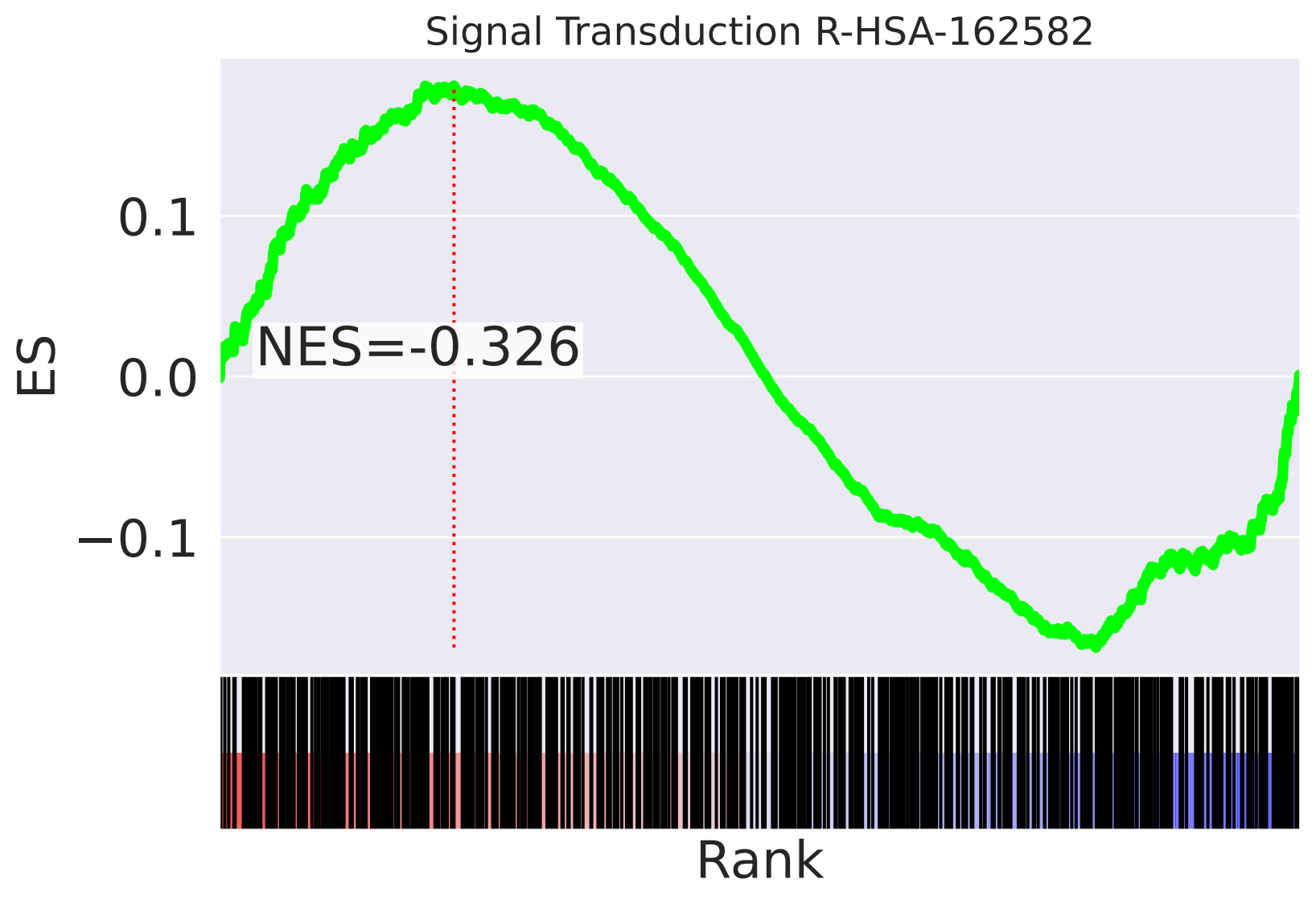

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
−0.2
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1354
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

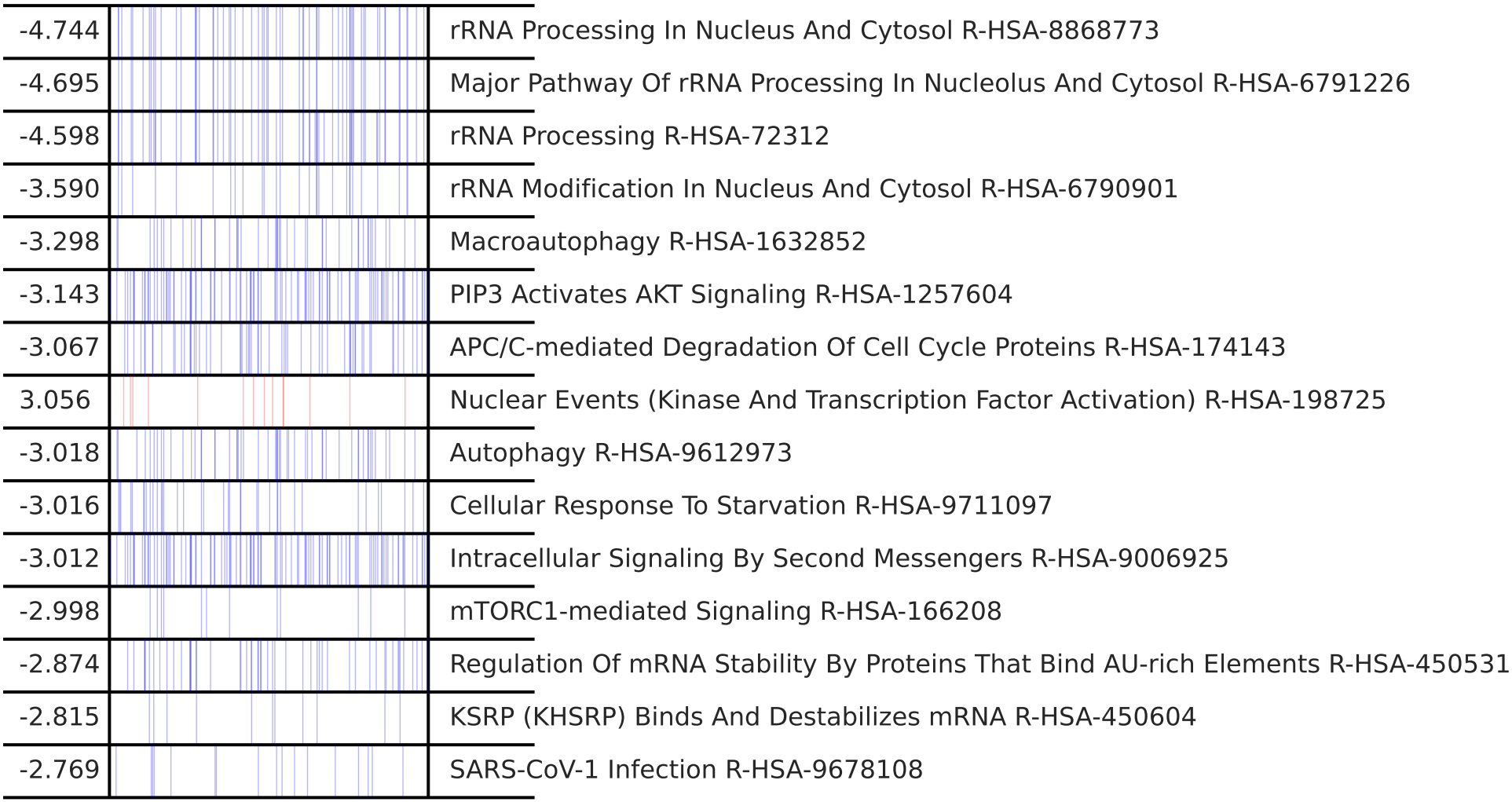

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
−0.2
ES
NES=-0.000
Rank

NES		SET
-6.390		rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-6.172		Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-6.104		rRNA Processing R-HSA-72312
-4.083		rRNA Modification In Nucleus And Cytosol R-HSA-6790901
3.984		G2/M Transition R-HSA-69275
3.930		Mitotic G2-G2/M Phases R-HSA-453274
3.367		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
3.219		Metabolism Of Polyamines R-HSA-351202
3.180		Regulation Of RAS By GAPs R-HSA-5658442
-3.171		MET Promotes Cell Motility R-HSA-8875878
3.139		Cross-presentation Of Soluble Exogenous Antigens (Endosomes) R-HSA-1236978
3.139		Respiratory Electron Transport R-HSA-611105
3.137		Signaling By Hedgehog R-HSA-5358351
3.130		Hedgehog On State R-HSA-5632684
3.128		Regulation Of Ornithine Decarboxylase (ODC) R-HSA-350562

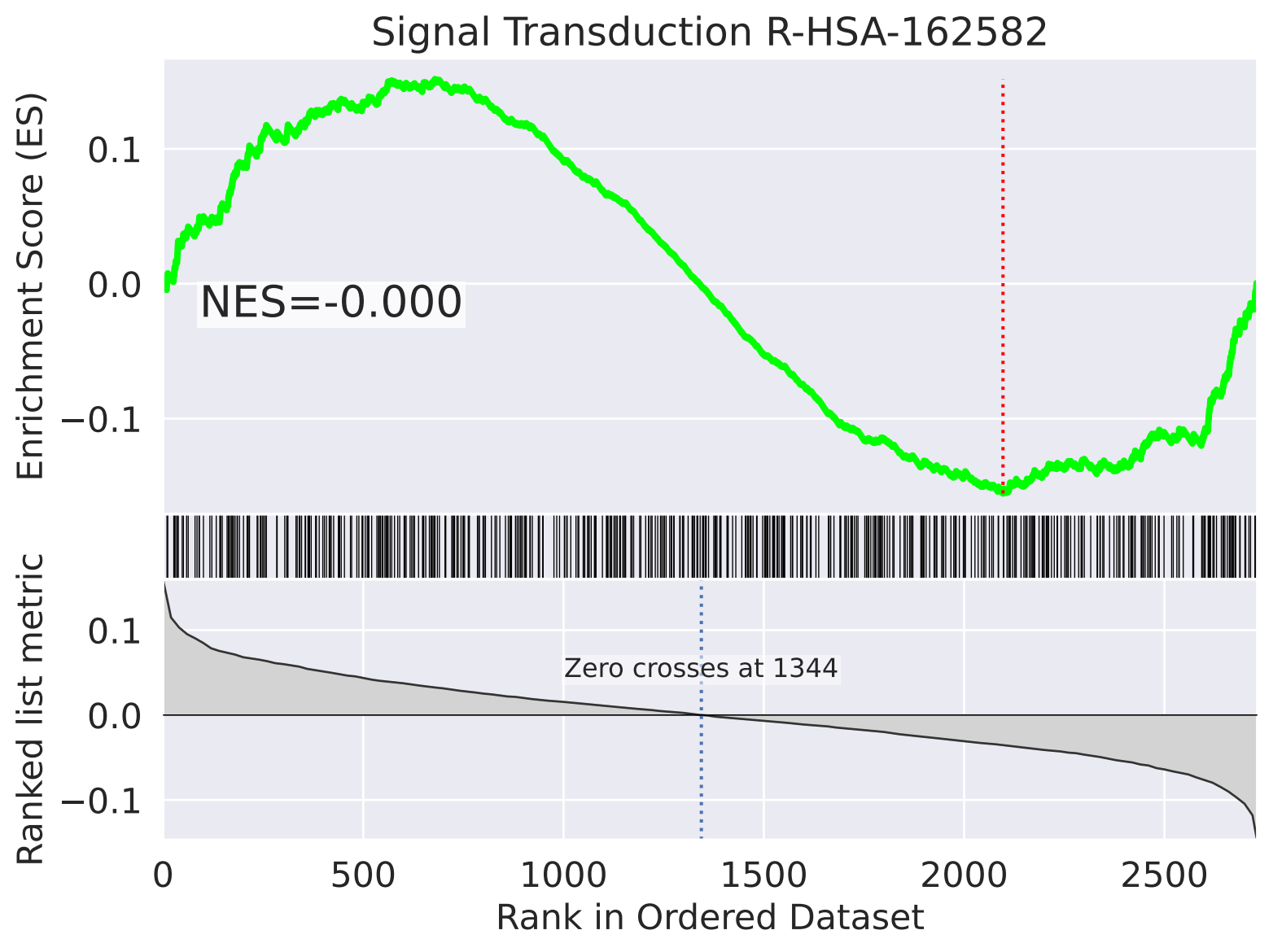
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=44

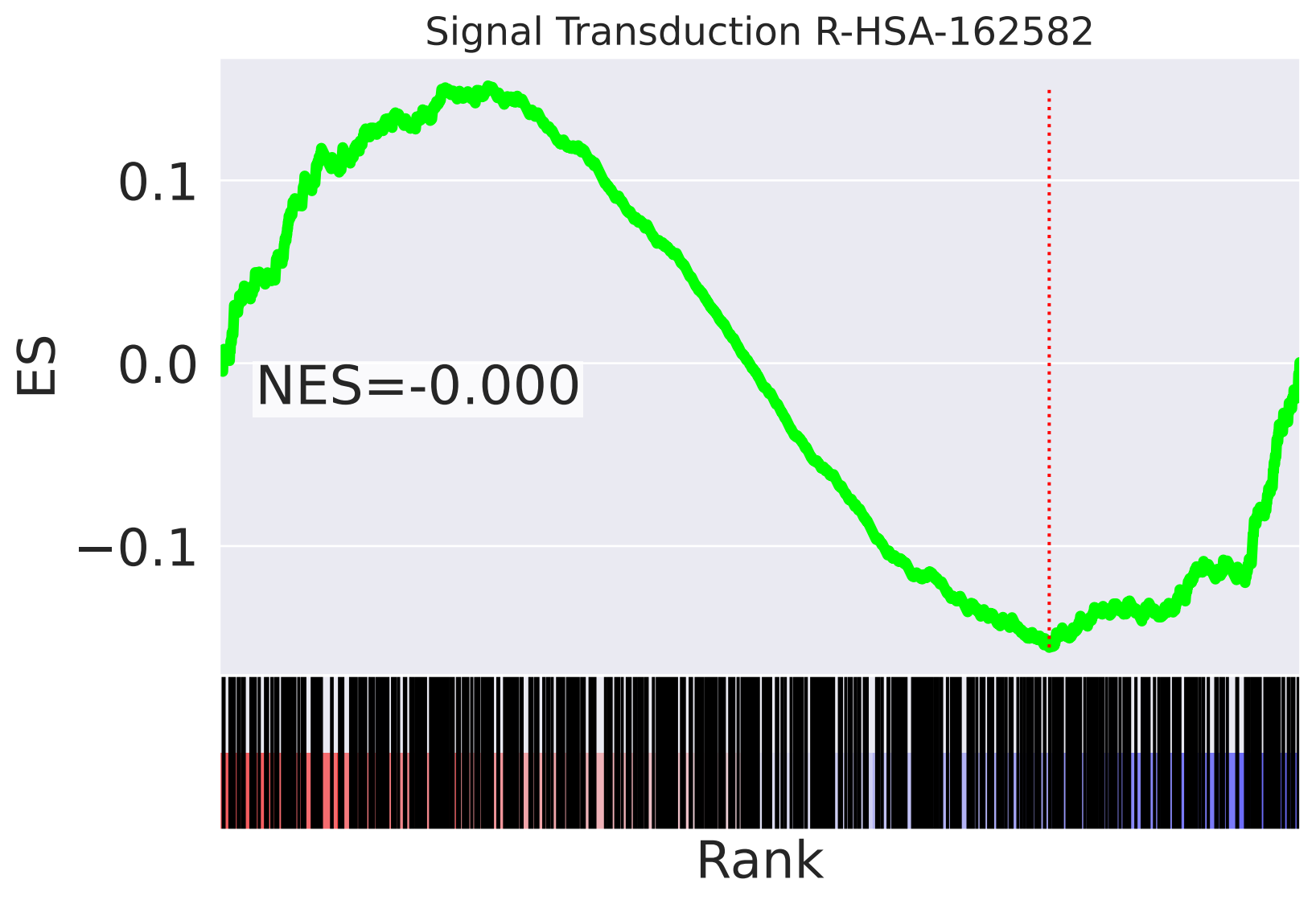

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.326
Ranked list metric
0.2
0.0
Zero crosses at 1316
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

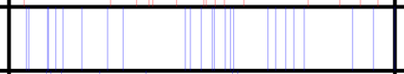
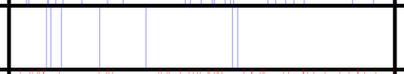
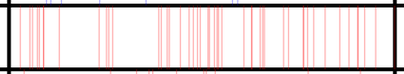
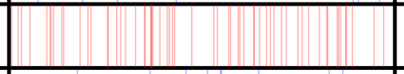
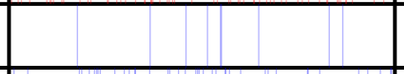
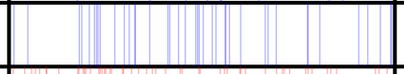
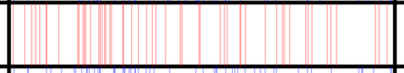
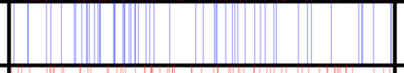
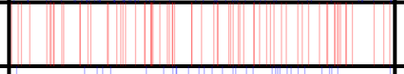
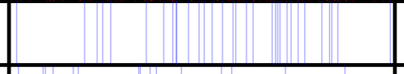

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.326
Rank


NES
SET
-4.744
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-4.695
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
-4.598
rRNA Processing R-HSA-72312
-3.590
rRNA Modification In Nucleus And Cytosol R-HSA-6790901
-3.298
Macroautophagy R-HSA-1632852
-3.143
PIP3 Activates AKT Signaling R-HSA-1257604
-3.067
APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
3.056
Nuclear Events (Kinase And Transcription Factor Activation) R-HSA-198725
-3.018
Autophagy R-HSA-9612973
-3.016
Cellular Response To Starvation R-HSA-9711097
-3.012
Intracellular Signaling By Second Messengers R-HSA-9006925
-2.998
mTORC1-mediated Signaling R-HSA-166208
-2.874
Regulation Of mRNA Stability By Proteins That Bind AU-rich Elements R-HSA-450531
-2.815
KSRP (KHSRP) Binds And Destabilizes mRNA R-HSA-450604
-2.769
SARS-CoV-1 Infection R-HSA-9678108

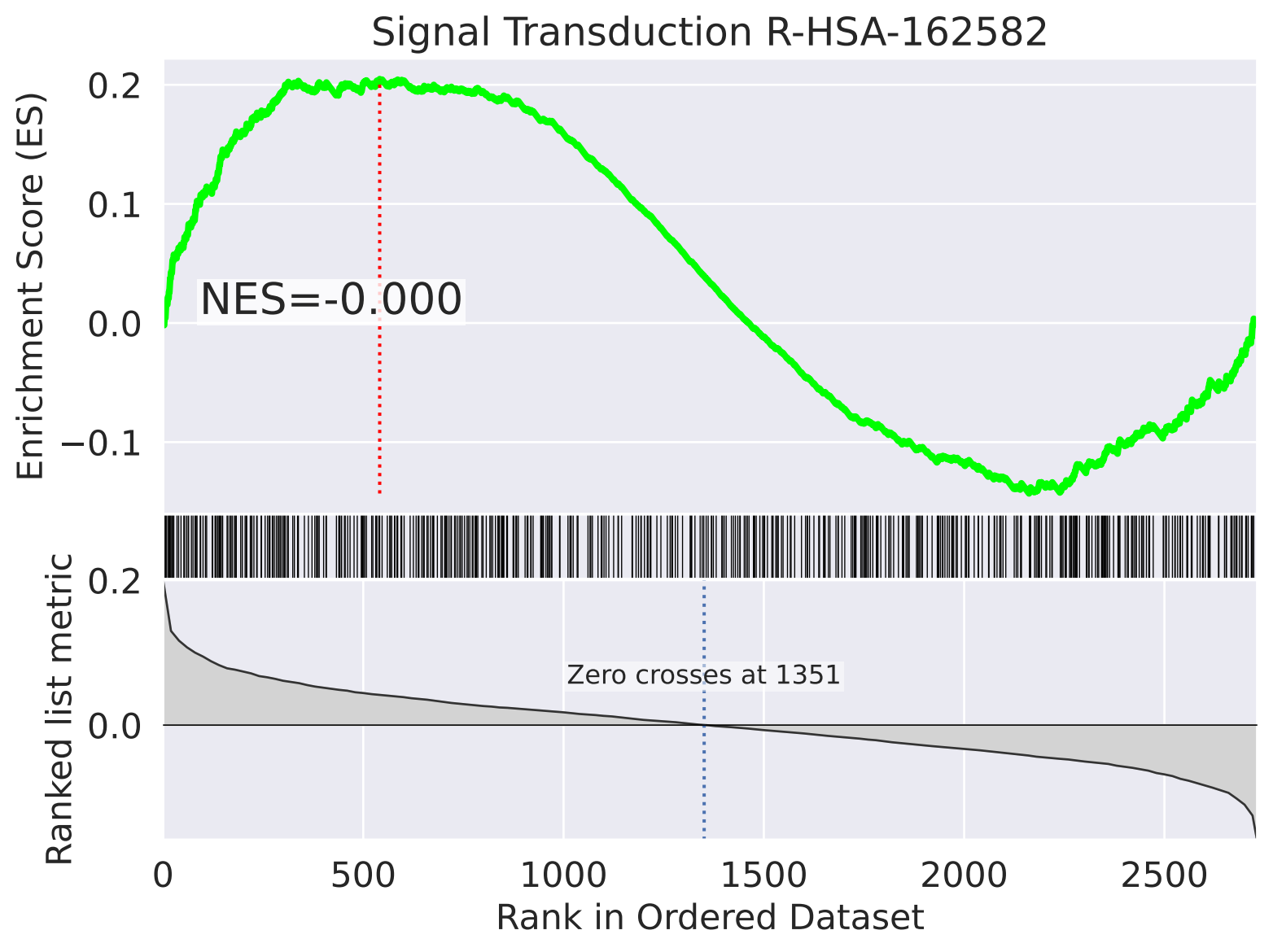
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=45

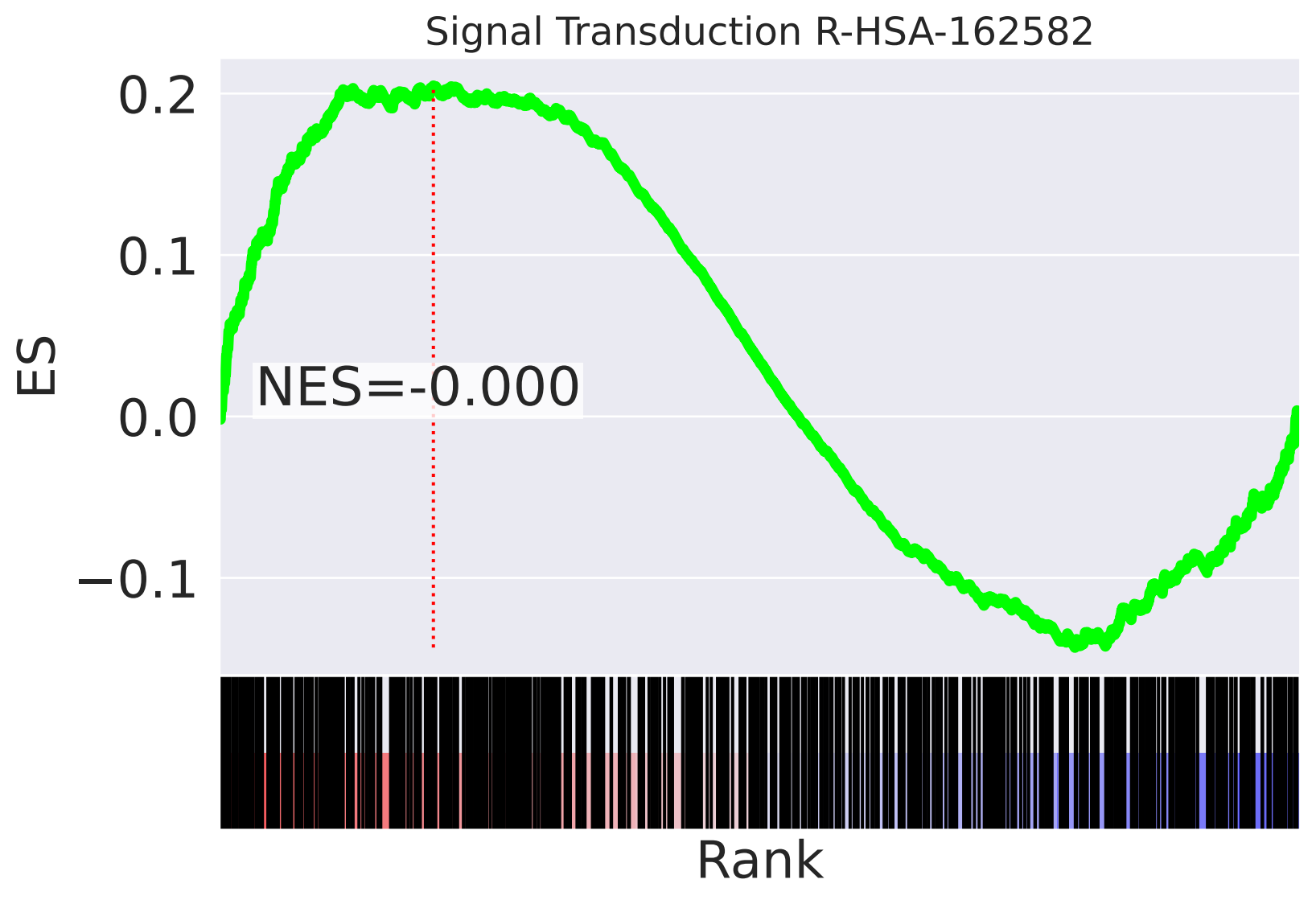

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1344
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

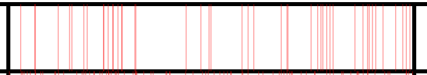
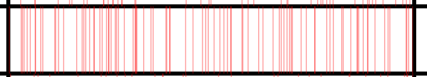
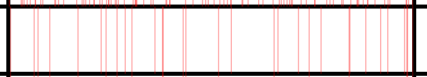
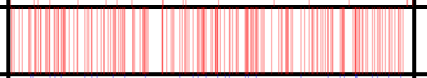
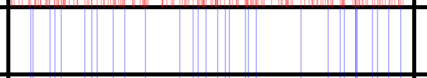
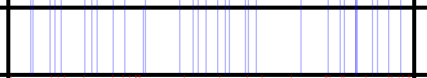
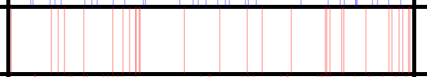
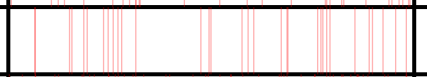
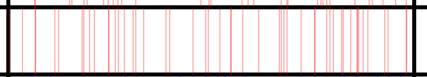
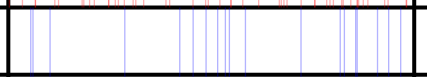
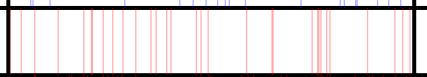
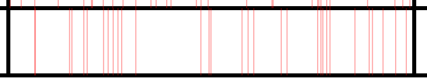

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
-2.866		Glycosaminoglycan Metabolism R-HSA-1630316
2.865		trans-Golgi Network Vesicle Budding R-HSA-199992
-2.762		Fanconi Anemia Pathway R-HSA-6783310
-2.672		Heparan Sulfate/Heparin (HS-GAG) Metabolism R-HSA-1638091
2.600		Antigen processing-Cross Presentation R-HSA-1236975
2.572		Golgi Associated Vesicle Biogenesis R-HSA-432722
-2.559		rRNA Processing In Mitochondrion R-HSA-8868766
2.553		Respiratory Electron Transport R-HSA-611105
-2.525		Polo-like Kinase Mediated Events R-HSA-156711
-2.520		Regulation Of HSF1-mediated Heat Shock Response R-HSA-3371453
2.519		RNA Polymerase II Transcribes snRNA Genes R-HSA-6807505
-2.515		Metabolism Of Carbohydrates R-HSA-71387
2.483		Respiratory Electron Transport, ATP Synthesis By Chemiosmotic Coupling, Heat Production By Uncoupling Proteins R-HSA-163200
-2.481		tRNA Aminoacylation R-HSA-379724
-2.456		Phosphorylation Of APC/C R-HSA-176412

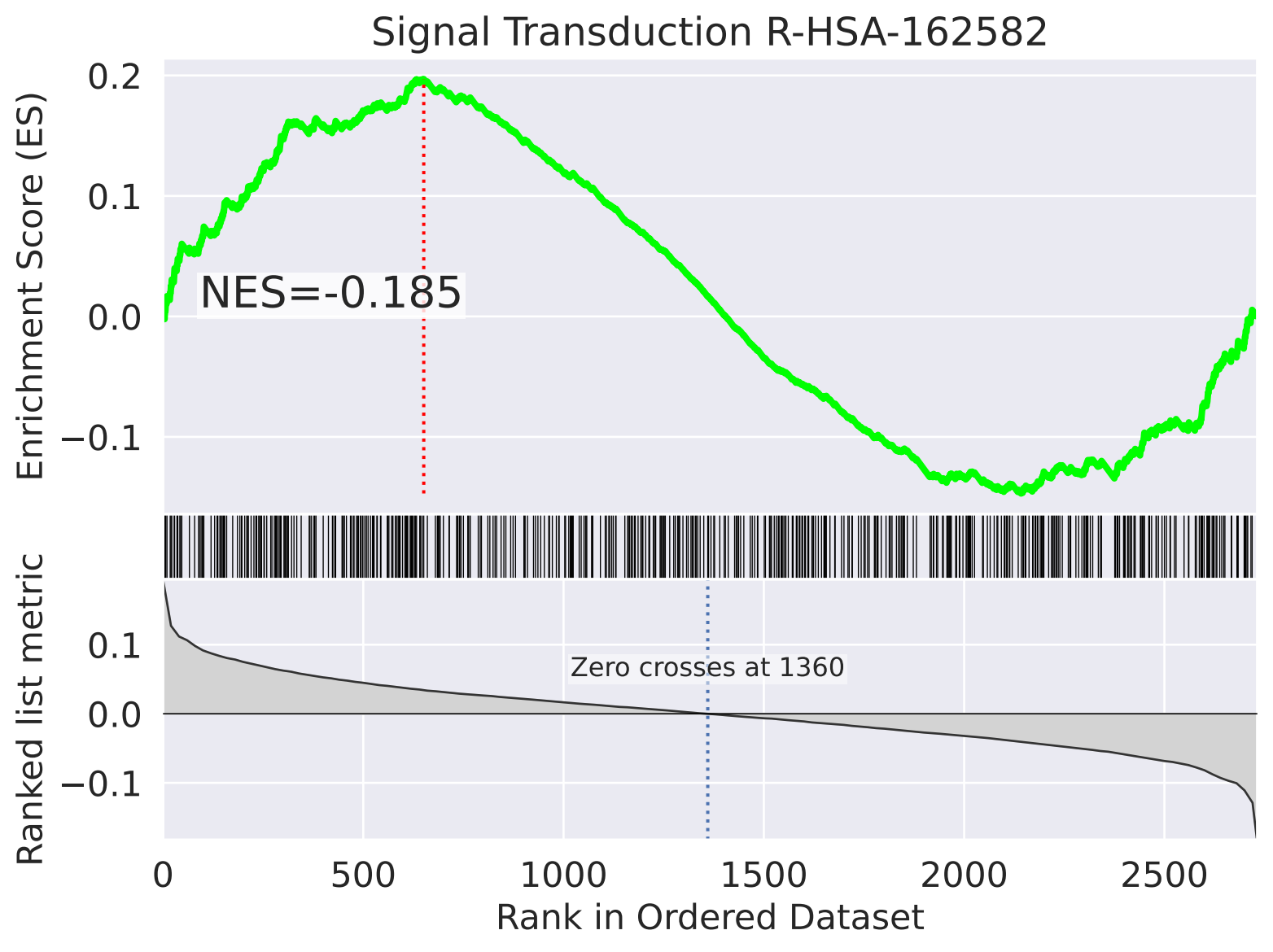
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=46

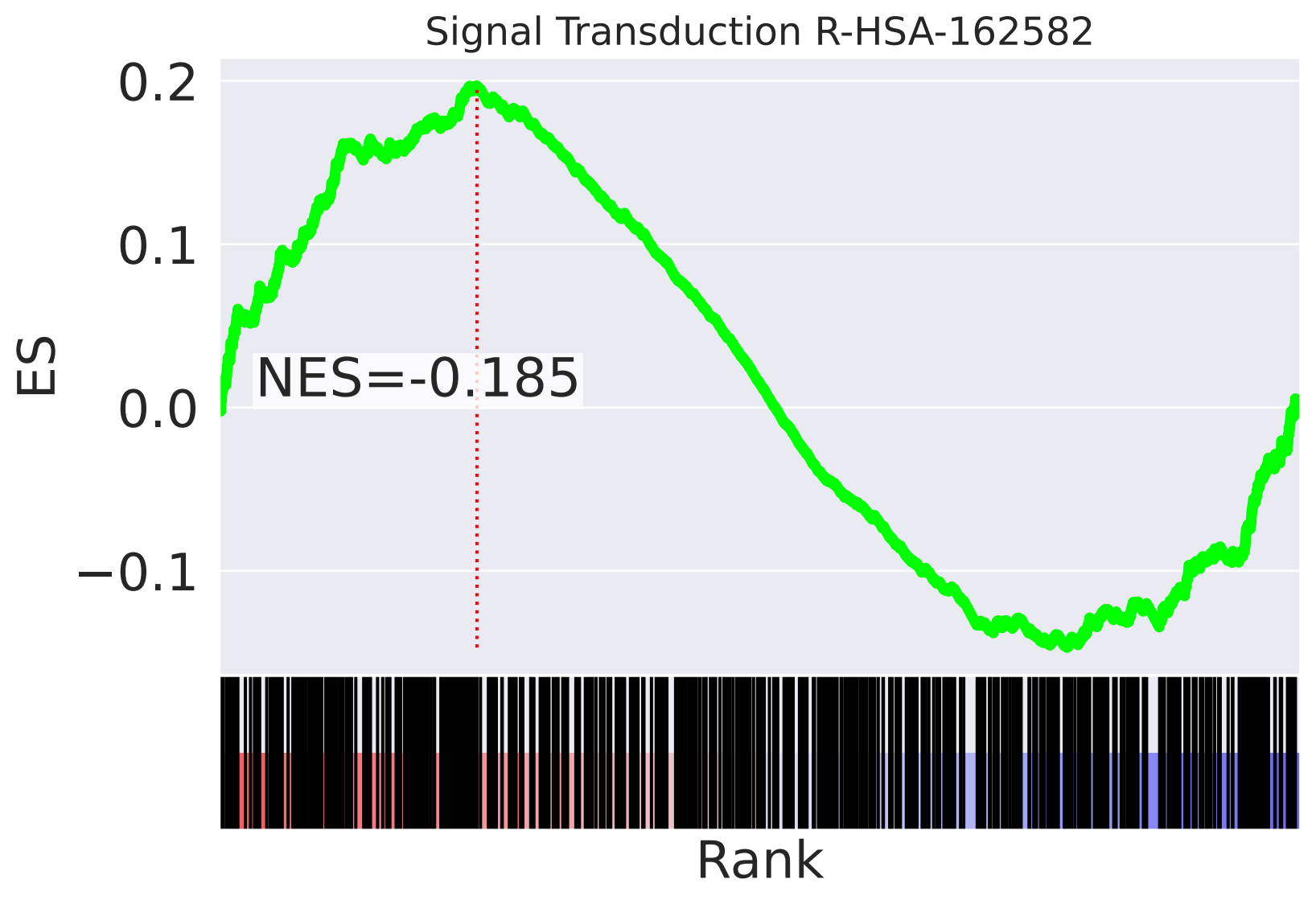

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.2
0.0
Zero crosses at 1351
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

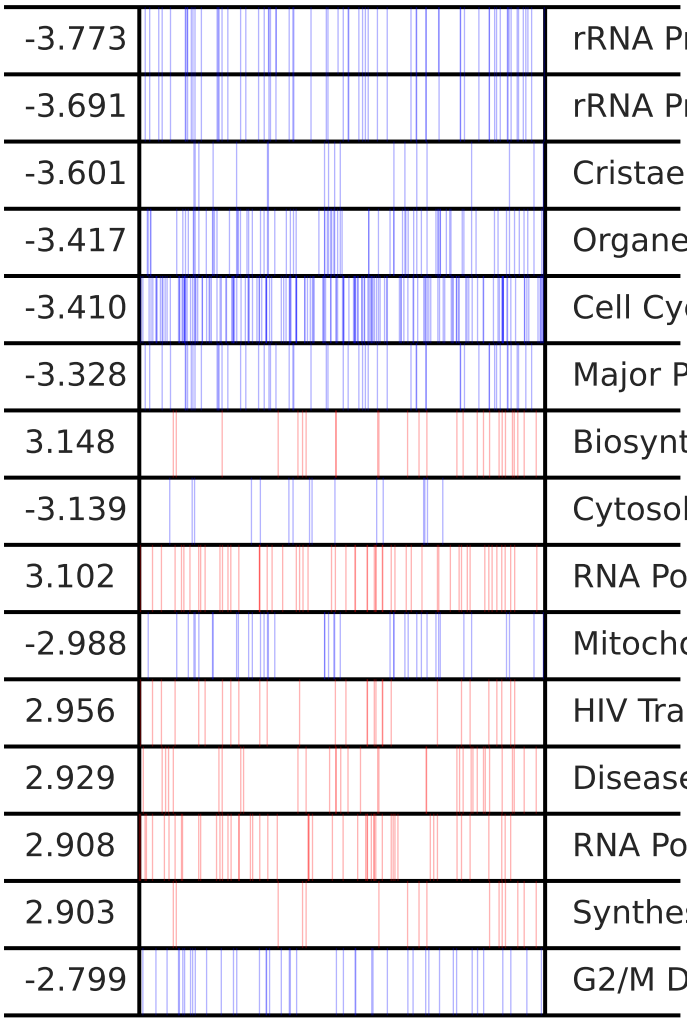

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
3.975		Epigenetic Regulation Of Gene Expression R-HSA-212165
3.521		Transcriptional Regulation By RUNX1 R-HSA-8878171
3.516		Metabolism Of Vitamins And Cofactors R-HSA-196854
3.357		Metabolism Of Water-Soluble Vitamins And Cofactors R-HSA-196849
3.338		Transcriptional Regulation By TP53 R-HSA-3700989
-3.262		Defective Homologous Recombination Repair (HRR) Due To BRCA2 Loss Of Function R-HSA-9701190
-3.262		Diseases Of DNA Repair R-HSA-9675135
-3.235		Homologous DNA Pairing And Strand Exchange R-HSA-5693579
3.181		Oxidative Stress Induced Senescence R-HSA-2559580
3.150		Negative Epigenetic Regulation Of rRNA Expression R-HSA-5250941
3.091		RUNX1 Regulates Transcription Of Genes Involved In Differentiation Of HSCs R-HSA-8939236
-3.080		Resolution Of D-loop Structures Thru Synthesis-Dependent Strand Annealing (SDSA) R-HSA-5693554
-3.080		Defective HDR Thru Homologous Recombination (HRR) Due To BRCA1 Loss-Of-Function R-HSA-9701192
3.065		Activation Of HOX Genes During Differentiation R-HSA-5619507
3.058		NoRC Negatively Regulates rRNA Expression R-HSA-427413

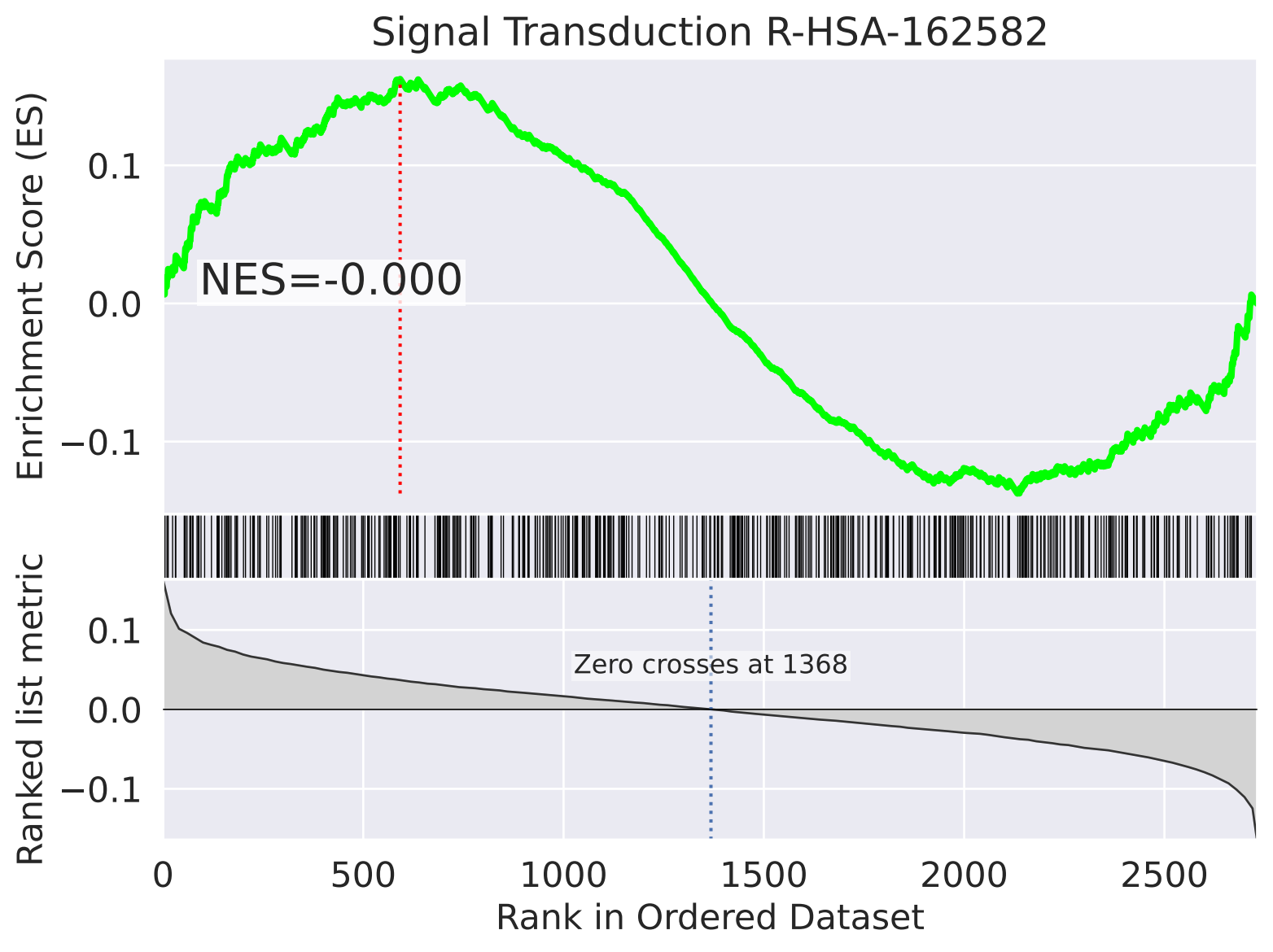
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=47

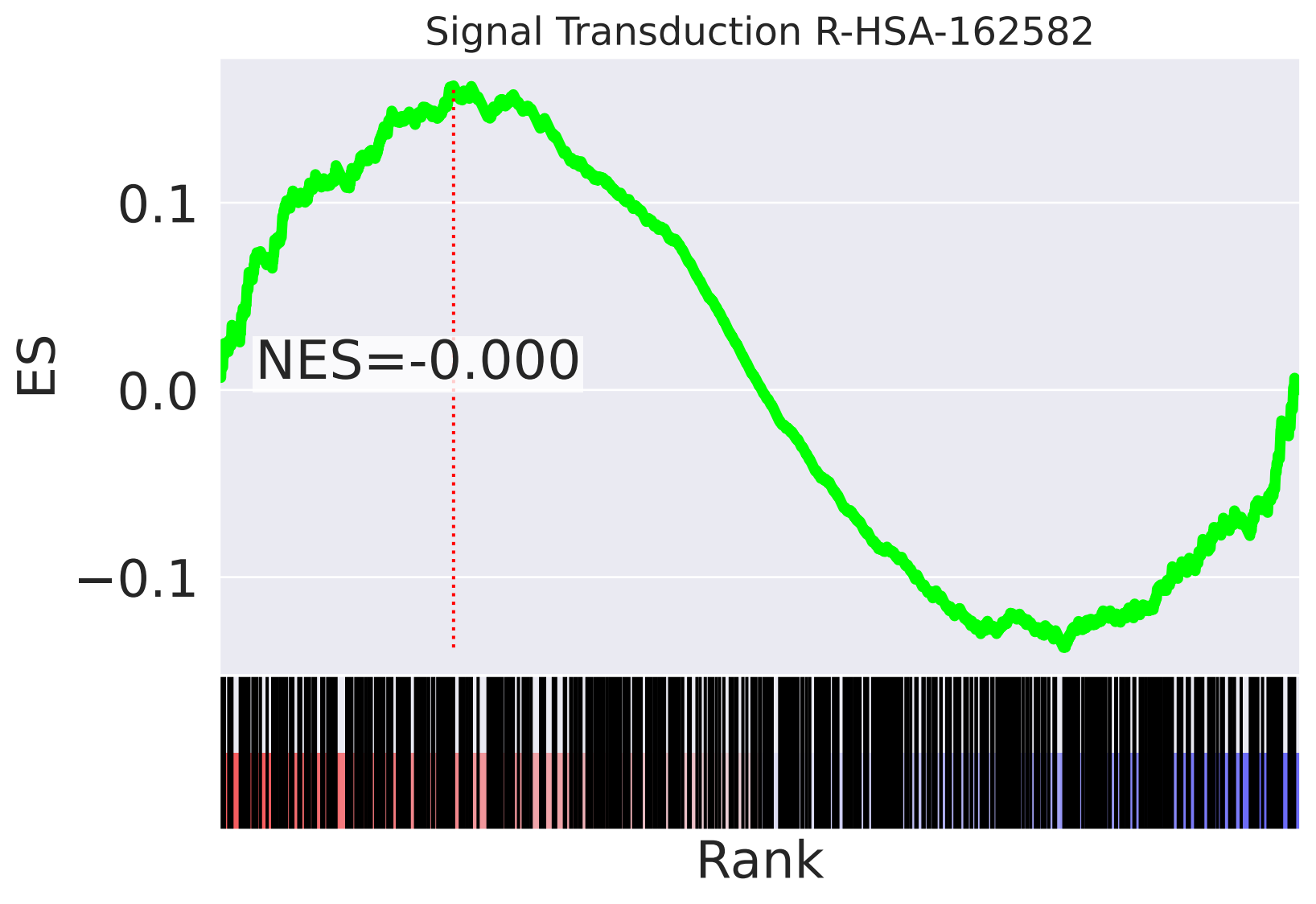

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.2
0.1
0.0
−0.1
NES=-0.185
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1360
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

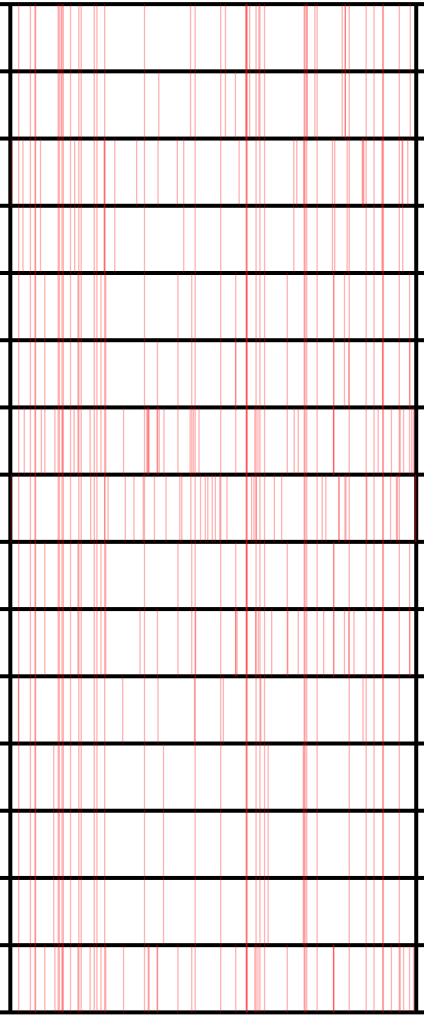

Signal Transduction R-HSA-162582
0.2
0.1
0.0
−0.1
ES
NES=-0.185
Rank


NES
SET
-3.773
rRNA Processing R-HSA-72312
-3.691
rRNA Processing In Nucleus And Cytosol R-HSA-8868773
-3.601
Cristae Formation R-HSA-8949613
-3.417
Organelle Biogenesis And Maintenance R-HSA-1852241
-3.410
Cell Cycle Checkpoints R-HSA-69620
-3.328
Major Pathway Of rRNA Processing In Nucleolus And Cytosol R-HSA-6791226
3.148
Biosynthesis Of N-glycan Precursor (Dolichol LLO) And Transfer To Protein R-HSA-446193
-3.139
Cytosolic tRNA Aminoacylation R-HSA-379716
3.102
RNA Polymerase II Pre-transcription Events R-HSA-674695
-2.988
Mitochondrial Biogenesis R-HSA-1592230
2.956
HIV Transcription Initiation R-HSA-167161
2.929
Diseases Of Metabolism R-HSA-5668914
2.908
RNA Polymerase II Transcribes snRNA Genes R-HSA-6807505
2.903
Synthesis Of Substrates In N-glycan Biosythesis R-HSA-446219
-2.799
G2/M DNA Damage Checkpoint R-HSA-69473

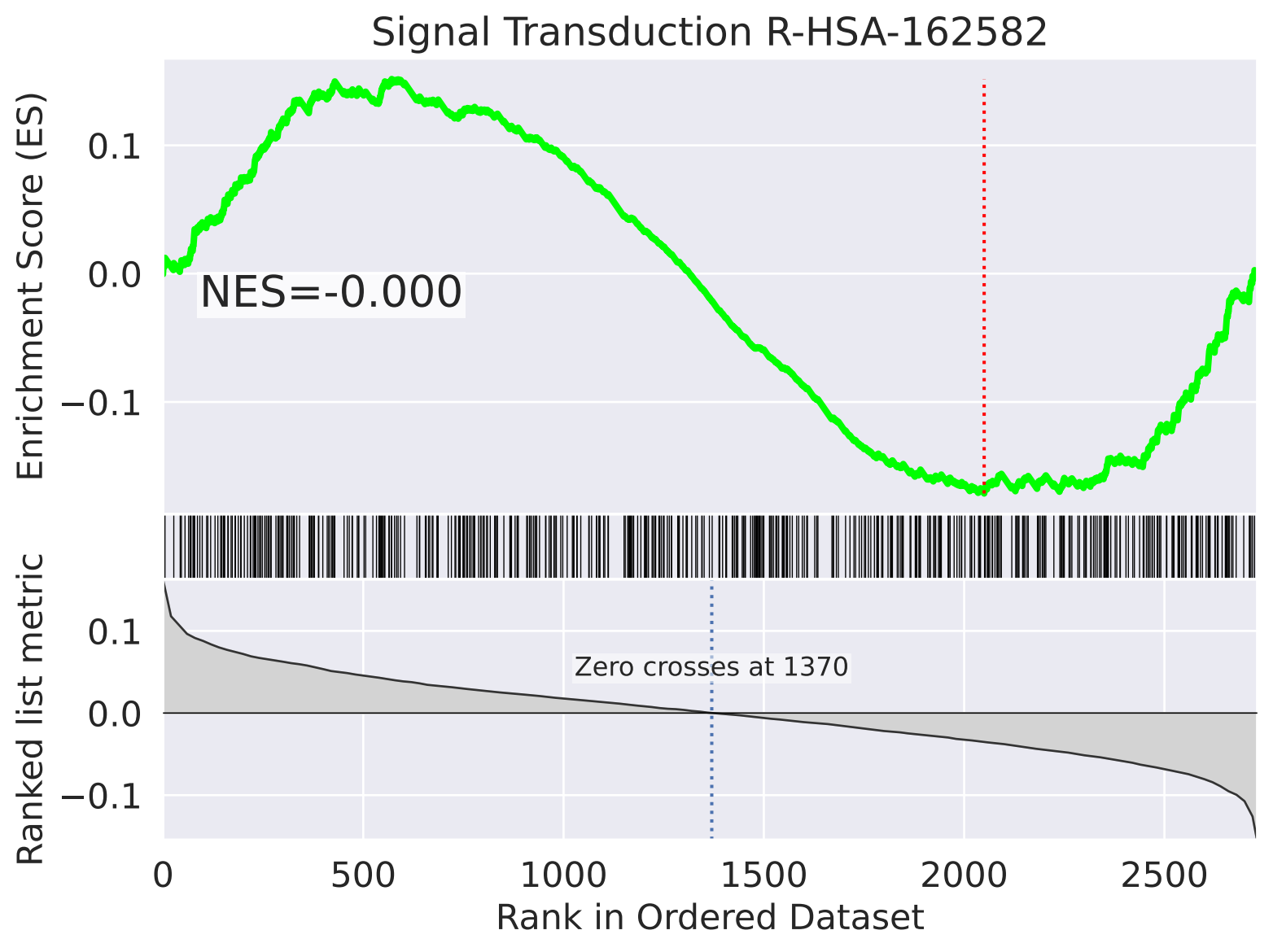
The three following figures visualize the negative control gene set enrichment analysis results for Signal Transduction R-HSA-162582 in the latent dimension z=48

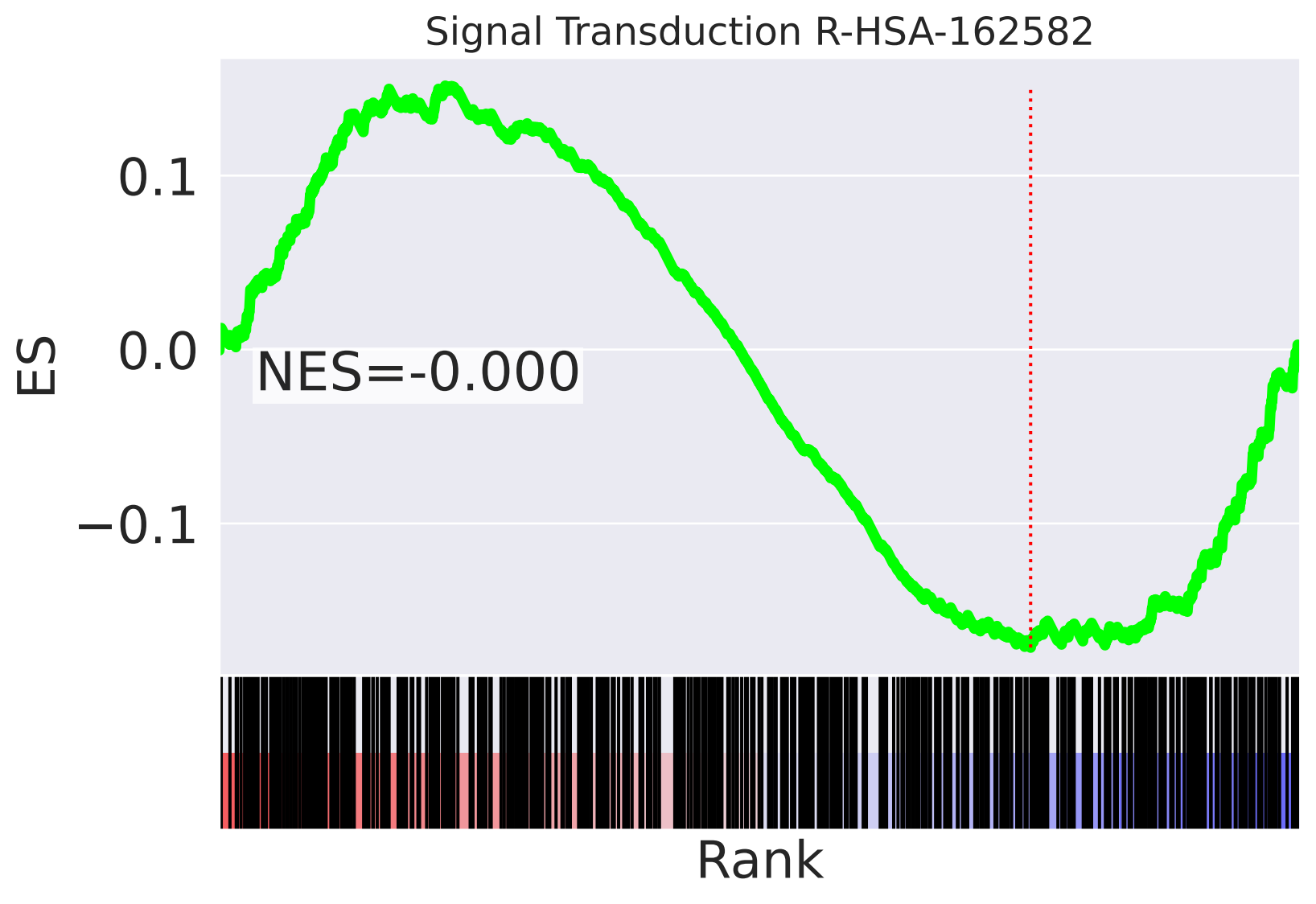

Signal Transduction R-HSA-162582
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1368
0
500
1000
1500
2000
2500
Rank in Ordered Dataset

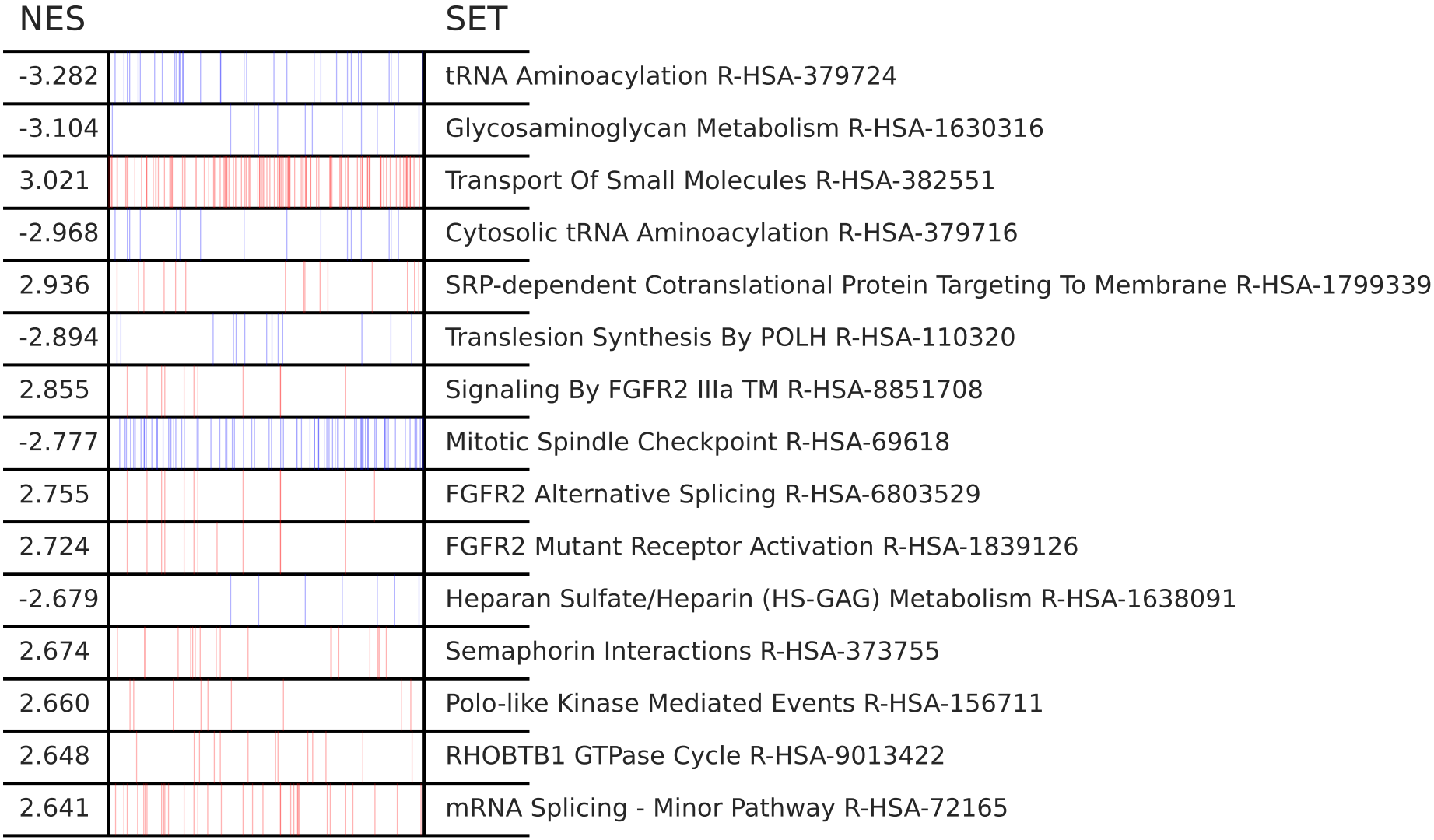

Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank

NES		SET
5.779		ER-Phagosome Pathway R-HSA-1236974
5.749		Antigen processing-Cross Presentation R-HSA-1236975
5.650		Signaling By ROBO Receptors R-HSA-376176
5.634		Regulation Of Expression Of SLITs And ROBOs R-HSA-9010553
5.584		APC/C:Cdc20 Mediated Degradation Of Securin R-HSA-174154
5.576		APC/C:Cdh1 Mediated Degradation Of Cdc20 And APC/C:Cdh1 Targets In Late Mitosis/Early G1 R-HSA-174178
5.573		DNA Replication Pre-Initiation R-HSA-69002
5.548		Metabolism Of Amino Acids And Derivatives R-HSA-71291
5.513		Autodegradation Of Cdh1 By Cdh1:APC/C R-HSA-174084
5.452		APC/C-mediated Degradation Of Cell Cycle Proteins R-HSA-174143
5.447		PCP/CE Pathway R-HSA-4086400
5.438		Hedgehog Ligand Biogenesis R-HSA-5358346
5.438		Hh Mutants Abrogate Ligand Secretion R-HSA-5387390
5.438		Hh Mutants Are Degraded By ERAD R-HSA-5362768
5.426		Assembly Of Pre-Replicative Complex R-HSA-68867

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
Enrichment Score (ES)
0.1
0.0
−0.1
NES=-0.000
Ranked list metric
0.1
0.0
−0.1
Zero crosses at 1370
0
500
1000
1500
2000
2500
Rank in Ordered Dataset


Signal Transduction R-HSA-162582
0.1
0.0
−0.1
ES
NES=-0.000
Rank


NES
SET
-3.282
tRNA Aminoacylation R-HSA-379724
-3.104
Glycosaminoglycan Metabolism R-HSA-1630316
3.021
Transport Of Small Molecules R-HSA-382551
-2.968
Cytosolic tRNA Aminoacylation R-HSA-379716
2.936
SRP-dependent Cotranslational Protein Targeting To Membrane R-HSA-1799339
-2.894
Translesion Synthesis By POLH R-HSA-110320
2.855
Signaling By FGFR2 IIIa TM R-HSA-8851708
-2.777
Mitotic Spindle Checkpoint R-HSA-69618
2.755
FGFR2 Alternative Splicing R-HSA-6803529
2.724
FGFR2 Mutant Receptor Activation R-HSA-1839126
-2.679
Heparan Sulfate/Heparin (HS-GAG) Metabolism R-HSA-1638091
2.674
Semaphorin Interactions R-HSA-373755
2.660
Polo-like Kinase Mediated Events R-HSA-156711
2.648
RHOBTB1 GTPase Cycle R-HSA-9013422
2.641
mRNA Splicing - Minor Pathway R-HSA-72165