Autism

Table 1: The 40 highest-scoring gene sets ranked by TEMPO score for the ASD data set.

Rank	Gene Set	Score	p-value	FDR
1	regulation of cell migration involved in sprouting angiogenesis	3.82	0.01	0.11
2	secretion by cell	2.27	0.00	0.07
3	secretion	2.26	0.00	0.07
4	cell migration involved in sprouting angiogenesis	2.06	0.03	0.18
5	myeloid leukocyte activation	2.01	0.00	0.07
6	positive regulation of sequence-specific DNA binding transcription factor activity	1.93	0.00	0.07
7	positive regulation of NF-kappaB transcription factor activity	1.89	0.00	0.07
8	phospholipid metabolic process	1.87	0.00	0.07
9	inflammatory response	1.87	0.00	0.07
10	central nervous system neuron differentiation	1.86	0.00	0.07
11	positive regulation of endothelial cell proliferation	1.86	0.00	0.07
12	regulation of cell growth	1.82	0.00	0.07
13	formation of primary germ layer	1.82	0.00	0.07
14	phosphatidylinositol biosynthetic process	1.82	0.00	0.07
15	phosphatidylinositol metabolic process	1.80	0.00	0.07
16	regulation of growth	1.77	0.00	0.07
17	myeloid dendritic cell activation	1.77	0.00	0.07
18	positive regulation of growth	1.76	0.00	0.07
19	glycerophospholipid metabolic process	1.74	0.00	0.07
20	facial nerve development	1.72	0.01	0.12
21	facial nerve morphogenesis	1.72	0.01	0.10
22	nuclear division	1.72	0.00	0.07
23	alcohol metabolic process	1.72	0.00	0.07
24	regulation of sequence-specific DNA binding transcription factor activity	1.72	0.00	0.07
25	membrane fusion	1.71	0.00	0.07
26	morphogenesis of an epithelial bud	1.70	0.00	0.07
27	middle ear morphogenesis	1.69	0.00	0.07
28	actomyosin structure organization	1.69	0.00	0.07
29	organophosphate biosynthetic process	1.67	0.00	0.07
30	transition metal ion homeostasis	1.67	0.00	0.07
31	tissue homeostasis	1.65	0.00	0.07
32	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	1.65	0.00	0.08
33	negative regulation of neurotransmitter uptake	1.65	0.00	0.07
34	regulation of serotonin uptake	1.65	0.00	0.07
35	negative regulation of serotonin uptake	1.65	0.00	0.07
36	positive regulation of gene expression	1.62	0.00	0.07
37	sulfur compound catabolic process	1.60	0.00	0.07
38	platelet degranulation	1.59	0.00	0.08
39	regulation of nucleobase-containing compound metabolic process	1.59	0.00	0.08
40	androgen metabolic process	1.57	0.00	0.07

Table 2: The 40 highest-scoring upregulated gene sets returned by GSEA in ASD

Rank	Gene Set	NES	p-value	FDR
1	dorsal/ventral axis specification	-1.91	0.00	1.00
2	primary alcohol metabolic process	-1.89	0.00	1.00
3	regulation of chondrocyte differentiation	-1.89	0.00	0.78
4	positive regulation of chondrocyte differentiation	-1.88	0.00	0.67
5	positive regulation of camp biosynthetic process	-1.87	0.00	0.65
6	positive regulation of cyclic nucleotide biosynthetic process	-1.86	0.00	0.56
7	positive regulation of adenylate cyclase activity	-1.86	0.00	0.49
8	organ induction	-1.84	0.00	0.61
9	regulation of carbohydrate biosynthetic process	-1.84	0.00	0.54
10	positive regulation of smoothened signaling pathway	-1.81	0.00	0.67
11	positive regulation of lyase activity	-1.81	0.00	0.61
12	negative regulation of microtubule polymerization	-1.81	0.00	0.60
13	somatic motor neuron differentiation	-1.80	0.00	0.58
14	positive regulation of nucleotide biosynthetic process	-1.80	0.00	0.57
15	positive regulation of purine nucleotide biosynthetic process	-1.80	0.00	0.53
16	modulation by host of viral release from host cell	-1.79	0.00	0.51
17	positive regulation by host of viral release from host cell	-1.79	0.00	0.48
18	phototransduction	-1.79	0.00	0.47
19	negative regulation of t cell apoptotic process	-1.79	0.00	0.46
20	activation of adenylate cyclase activity	-1.79	0.00	0.44
21	negative regulation of platelet-derived growth factor receptor signaling pathway	-1.78	0.01	0.45
22	phototransduction, visible light	-1.77	0.00	0.47
23	notochord development	-1.77	0.01	0.46
24	apical junction assembly	-1.77	0.00	0.45
25	triglyceride catabolic process	-1.76	0.01	0.47
26	developmental induction	-1.76	0.00	0.48
27	regulation of cartilage development	-1.76	0.00	0.48
28	detection of light stimulus	-1.74	0.00	0.54
29	spinal cord development	-1.73	0.00	0.58
30	acid secretion	-1.73	0.00	0.56
31	digestion	-1.73	0.00	0.55
32	positive regulation of protein kinase a signaling	-1.73	0.00	0.55
33	lateral mesoderm development	-1.73	0.01	0.53
34	neutral lipid catabolic process	-1.73	0.01	0.53
35	acylglycerol catabolic process	-1.73	0.01	0.51
36	cyclic nucleotide metabolic process	-1.72	0.01	0.53
37	positive regulation of camp metabolic process	-1.71	0.00	0.58
38	detection of visible light	-1.71	0.00	0.57
39	negative regulation of vascular permeability	-1.71	0.01	0.57
40	aspartate transport	-1.71	0.01	0.56

Table 3: The 40 highest-scoring gene sets returned by maSigPro+GSEA preranked in ASD

Rank	Gene Set	NES	p-value	FDR
1	glutaminyl-trnagln biosynthesis via transamidation	1.48	0.00	1.00
2	vitamin b6 metabolic process	1.47	0.00	1.00
3	regulation of cortisol secretion	1.47	0.00	0.83
4	positive regulation of cortisol secretion	1.47	0.00	0.64
5	positive regulation of glucocorticoid secretion	1.46	0.00	0.60
6	pyridoxal phosphate metabolic process	1.46	0.01	0.54
7	cell-cell signaling involved in cell fate commitment	1.45	0.01	0.67
8	pyridoxal phosphate biosynthetic process	1.44	0.01	0.73
9	negative regulation of cortisol biosynthetic process	1.42	0.01	1.00
10	histone h2b conserved c-terminal lysine ubiquitination	1.42	0.01	1.00
11	negative regulation of tooth mineralization	1.42	0.01	1.00
12	negative regulation of aldosterone metabolic process	1.42	0.01	0.96
13	negative regulation of glucocorticoid biosynthetic process	1.42	0.00	0.89
14	sequestering of triglyceride	1.42	0.00	0.84
15	negative regulation of aldosterone biosynthetic process	1.41	0.01	0.80
16	negative regulation of steroid hormone biosynthetic process	1.41	0.00	0.81
17	aldehyde biosynthetic process	1.41	0.00	0.80
18	histone h3-k4 demethylation	1.40	0.01	0.91
19	negative regulation of glucocorticoid metabolic process	1.40	0.01	0.87
20	oxygen transport	1.40	0.00	0.97
21	cytoplasmic pattern recognition receptor signaling pathway in response to virus	1.39	0.01	0.99
22	regulation of toll-like receptor 9 signaling pathway	1.39	0.01	1.00
23	regulation of glucocorticoid metabolic process	1.39	0.00	1.00
24	udp-galactose transport	1.38	0.00	1.00
25	nephric duct morphogenesis	1.38	0.00	1.00
26	fatty acid beta-oxidation using acyl-coa dehydrogenase	1.38	0.01	1.00
27	negative regulation of endothelial cell differentiation	1.37	0.02	1.00
28	regulation of low-density lipoprotein particle clearance	1.37	0.00	1.00
29	phospholipase c-activating g-protein coupled acetylcholine receptor signaling pathway	1.37	0.00	1.00
30	regulation of glucocorticoid biosynthetic process	1.37	0.01	1.00
31	regulation of cortisol biosynthetic process	1.37	0.00	1.00
32	positive regulation of chaperone-mediated protein complex assembly	1.37	0.02	1.00
33	negative regulation of epithelial cell differentiation involved in kidney development	1.37	0.00	1.00
34	negative regulation of histone h3-k36 methylation	1.36	0.01	1.00
35	negative regulation of nephron tubule epithelial cell differentiation	1.36	0.00	1.00
36	negative regulation of interleukin-2 secretion	1.36	0.01	1.00
37	negative regulation of hormone biosynthetic process	1.36	0.00	1.00
38	regulation of chaperone-mediated protein complex assembly	1.36	0.02	1.00
39	regulation of type iii interferon production	1.35	0.03	1.00
40	urinary tract smooth muscle contraction	1.35	0.02	1.00

Huntingtons

Table 4: The 40 highest-scoring gene sets ranked by TEMPO score for the Huntington's Disease data set. Included significance values are for the score for all patients only

Rank	Gene Set	Overall Score	p-value	FDR	Sympomatic Score	Asymptomatic Score
1	negative regulation of DNA recombination	3.52	0.00	0.10	3.93	2.56
2	telomere maintenance via recombination	3.11	0.00	0.10	3.31	2.63
3	regulation of epidermal growth factor receptor signaling pathway	2.62	0.00	0.10	2.91	1.94
4	phototransduction	2.52	0.00	0.10	2.86	1.72
5	regulation of muscle organ development	2.49	0.00	0.10	2.89	1.54
6	regulation of striated muscle tissue development	2.46	0.00	0.10	2.80	1.64
7	regulation of muscle tissue development	2.46	0.00	0.10	2.80	1.64
8	regulation of ERBB signaling pathway	2.43	0.00	0.10	2.70	1.79
9	n. reg. of transcription from RNAP II promoter in response to stress	2.42	0.00	0.10	2.80	1.54
10	negative regulation of cation channel activity	2.34	0.01	0.10	2.55	1.84
11	regulation of anion transport	2.26	0.00	0.10	2.39	1.94
12	tumor necrosis factor-mediated signaling pathway	2.25	0.01	0.10	2.57	1.37
13	detection of visible light	2.21	0.00	0.10	2.53	1.45
14	regulation of sodium ion transmembrane transporter activity	2.16	0.00	0.10	2.52	1.30
15	negative regulation of protein acetylation	2.15	0.00	0.10	2.35	1.66
16	regulation of leukocyte degranulation	2.14	0.00	0.10	2.23	1.93
17	positive regulation of JUN kinase activity	2.14	0.00	0.10	2.45	1.42
18	mitotic recombination	2.14	0.00	0.10	2.23	1.76
19	regulation of phosphoprotein phosphatase activity	2.12	0.00	0.10	2.16	2.01
20	detection of light stimulus	2.10	0.00	0.10	2.40	1.40
21	regulation of blood vessel endothelial cell migration	2.08	0.00	0.10	2.12	1.97
22	cellular response to molecule of bacterial origin	2.03	0.00	0.10	2.20	1.27
23	negative regulation of peptidyl-lysine acetylation	2.03	0.00	0.10	2.25	1.52
24	cellular response to biotic stimulus	2.03	0.00	0.10	2.08	1.42
25	organophosphate catabolic process	2.02	0.00	0.10	2.24	1.51
26	reg. of transcription from RNAP II promoter in response to stress	2.02	0.01	0.10	2.29	1.37
27	intestinal absorption	2.02	0.00	0.10	2.30	1.35
28	regulation of centrosome cycle	1.98	0.01	0.10	2.01	1.91
29	regulation of peptidyl-lysine acetylation	1.98	0.00	0.10	2.17	1.51
30	digestion	1.95	0.01	0.10	2.25	1.24
31	DNA strand elongation	1.95	0.00	0.10	2.11	1.56
32	bile acid and bile salt transport	1.95	0.00	0.10	2.26	1.20
33	regulation of cholesterol metabolic process	1.94	0.00	0.10	2.12	1.51
34	regulation of transcription from RNA polymerase I promoter	1.89	0.01	0.10	2.10	1.42
35	regulation of nitric oxide biosynthetic process	1.89	0.00	0.10	1.90	1.88
36	protein heterooligomerization	1.89	0.00	0.10	2.36	1.74
37	positive regulation of transporter activity	1.88	0.01	0.10	2.19	1.14
38	regulation of alpha-beta T cell differentiation	1.87	0.01	0.10	2.06	1.41
39	cytochrome complex assembly	1.86	0.01	0.10	1.98	1.57
40	CD4-positive, alpha-beta T cell activation	1.85	0.00	0.10	2.09	1.28

Table 5: The 40 highest-scoring gene sets returned by GSEA in Huntingtons

Rank	Gene Set	NES	p-value	FDR
1	regulation of symbiosis, encompassing mutualism through parasitism	-1.87	0.00	1.00
2	carnitine shuttle	-1.84	0.00	1.00
3	negative regulation of insulin receptor signaling pathway	-1.83	0.01	1.00
4	regulation of insulin receptor signaling pathway	-1.81	0.00	1.00
5	negative regulation of cellular response to insulin stimulus	-1.76	0.01	1.00
6	amino-acid betaine transport	-1.75	0.01	1.00
7	carnitine transport	-1.75	0.01	1.00
8	bone morphogenesis	-1.73	0.01	1.00
9	sarcomere organization	-1.73	0.01	1.00
10	endochondral ossification	-1.73	0.00	1.00
11	replacement ossification	-1.73	0.00	1.00
12	regulation of wound healing	-1.71	0.00	1.00
13	positive regulation of leukocyte chemotaxis	-1.71	0.02	1.00
14	actin-mediated cell contraction	-1.70	0.01	1.00
15	fatty acid transmembrane transport	-1.69	0.01	1.00
16	positive regulation of cell-substrate adhesion	-1.68	0.04	1.00
17	anterior/posterior axis specification	-1.68	0.01	1.00
18	regulation of blood pressure	-1.67	0.00	1.00
19	positive regulation of cell-matrix adhesion	-1.66	0.03	1.00
20	activation of mapkk activity	-1.65	0.02	1.00
21	positive regulation of endothelial cell proliferation	-1.65	0.01	1.00
22	phosphatidylglycerol biosynthetic process	-1.65	0.03	1.00
23	nucleoside bisphosphate metabolic process	-1.64	0.01	1.00
24	ribonucleoside bisphosphate metabolic process	-1.64	0.01	1.00
25	purine nucleoside bisphosphate metabolic process	-1.64	0.01	1.00
26	regulation of establishment or maintenance of cell polarity	-1.64	0.02	1.00
27	purine ribonucleoside bisphosphate metabolic process	-1.64	0.01	1.00
28	3'-phosphoadenosine 5'-phosphosulfate metabolic process	-1.64	0.01	1.00
29	copper ion transport	-1.64	0.03	1.00
30	bone development	-1.64	0.01	1.00
31	regulation of coagulation	-1.63	0.01	1.00
32	regulation of blood coagulation	-1.63	0.02	1.00
33	regulation of hemostasis	-1.63	0.02	1.00
34	n-acetylneuraminate metabolic process	-1.62	0.01	1.00
35	inflammatory response	-1.62	0.02	1.00
36	neutrophil activation	-1.62	0.04	1.00
37	endochondral bone morphogenesis	-1.61	0.02	1.00
38	regulated secretory pathway	-1.61	0.03	1.00
39	post-embryonic hemopoiesis	-1.61	0.00	1.00
40	trabecula formation	-1.61	0.02	1.00

Table 6: The 40 highest-scoring gene sets returned by maSigPro+GSEA preranked in Huntingtons

Rank	Gene Set	NES	p-value	FDR
1	steroid biosynthetic process	2.31	0.00	0.71
2	dna metabolic process	2.12	0.00	1.00
3	transcription-coupled nucleotide-excision repair	2.11	0.01	1.00
4	negative regulation of rna metabolic process	2.11	0.00	0.96
5	cellular response to reactive oxygen species	2.07	0.00	0.97
6	dna strand elongation involved in dna replication	2.05	0.00	1.00
7	negative regulation of nitrogen compound metabolic process	2.04	0.00	0.87
8	response to oxidative stress	2.04	0.00	0.77
9	cholesterol biosynthetic process	2.03	0.00	0.73
10	peroxisome fission	2.02	0.00	0.72
11	deoxyribose phosphate metabolic process	2.01	0.00	0.69
12	dna repair	2.01	0.00	0.65
13	cgmp metabolic process	2.01	0.00	0.61
14	sterol biosynthetic process	2.00	0.00	0.58
15	positive regulation of gtpase activity	2.00	0.01	0.54
16	regulation of dna-dependent transcription in response to stress	2.00	0.00	0.52
17	monocyte differentiation	1.98	0.00	0.56
18	regulation of histone h3-k4 methylation	1.98	0.00	0.53
19	negative regulation of transcription, dna-dependent	1.98	0.00	0.51
20	regulation of cytokine production involved in immune response	1.97	0.00	0.50
21	metabolic process	1.97	0.01	0.48
22	alcohol biosynthetic process	1.97	0.01	0.47
23	deoxyribonucleotide catabolic process	1.96	0.01	0.46
24	cholesterol metabolic process	1.96	0.01	0.45
25	regulation of nucleoside metabolic process	1.95	0.01	0.46
26	nucleotide-excision repair	1.94	0.01	0.47
27	negative regulation of immune effector process	1.94	0.01	0.45
28	regulation of transcription from rna polymerase ii promoter in response to stress	1.94	0.01	0.44
29	negative regulation of nucleobase-containing compound metabolic process	1.94	0.00	0.43
30	response to reactive oxygen species	1.93	0.01	0.43
31	deoxyribose phosphate catabolic process	1.93	0.00	0.42
32	protein k48-linked ubiquitination	1.93	0.01	0.41
33	regulation of ras protein signal transduction	1.93	0.01	0.40
34	sterol metabolic process	1.92	0.00	0.40
35	regulation of receptor activity	1.92	0.01	0.40
36	negative regulation of cellular macromolecule biosynthetic process	1.92	0.00	0.39
37	2'-deoxyribonucleotide metabolic process	1.92	0.01	0.38
38	regulation of production of molecular mediator of immune response	1.91	0.00	0.39
39	positive regulation of histone h3-k4 methylation	1.90	0.00	0.40
40	steroid metabolic process	1.90	0.01	0.39

Alzheimer's Disease

Table 7: The 40 highest-scoring gene sets ranked by TEMPO score for the Alzheimer's data set.

Rank	Gene Set	Score	p-value	FDR
1	peptidyl-tyrosine phosphorylation	2.739	0.002	0.006
2	peptidyl-tyrosine modification	2.739	0.002	0.006
3	phosphatidylcholine metabolic process	2.728	0.002	0.006
4	transcription elongation from RNA polymerase II promoter	2.597	0.002	0.006
5	ethanolamine-containing compound metabolic process	2.492	0.002	0.006
6	protein monoubiquitination	2.483	0.002	0.006
7	regulation of apoptotic signaling pathway	2.448	0.002	0.006
8	positive regulation of apoptotic signaling pathway	2.443	0.002	0.006
9	double-strand break repair via nonhomologous end joining	2.437	0.002	0.006
10	ammonium ion metabolic process	2.434	0.002	0.006
11	regulation of myeloid cell differentiation	2.430	0.002	0.006
12	positive regulation of transporter activity	2.427	0.002	0.006
13	central nervous system development	2.416	0.002	0.006
14	non-recombinational repair	2.406	0.002	0.006
15	cell cycle arrest	2.377	0.002	0.006
16	leukocyte cell-cell adhesion	2.373	0.002	0.006
17	alcohol metabolic process	2.368	0.002	0.006
18	cell proliferation	2.307	0.002	0.006
19	brain development	2.307	0.002	0.006
20	intrinsic apoptotic signaling pathway	2.299	0.002	0.006
21	apoptotic signaling pathway	2.291	0.002	0.006
22	peptidyl-lysine modification	2.271	0.002	0.006
23	nuclear import	2.271	0.002	0.006
24	negative regulation of cell proliferation	2.264	0.002	0.006
25	positive regulation of cell proliferation	2.259	0.002	0.006
26	T cell activation	2.258	0.002	0.006
27	T cell aggregation	2.258	0.002	0.006
28	regulation of leukocyte differentiation	2.249	0.002	0.006
29	head development	2.242	0.002	0.006
30	glycerophospholipid metabolic process	2.241	0.002	0.006
31	organic hydroxy compound metabolic process	2.235	0.002	0.006
32	positive regulation of mitochondrion organization	2.229	0.002	0.006
33	stress-activated protein kinase signaling cascade	2.215	0.002	0.006
34	stress-activated MAPK cascade	2.215	0.002	0.006
35	lymphocyte aggregation	2.213	0.002	0.006
36	immune response-activating cell surface receptor signaling pathway	2.197	0.002	0.006
37	regulation of hemopoiesis	2.188	0.002	0.006
38	cytokine production	2.179	0.002	0.006
39	regulation of intrinsic apoptotic signaling pathway	2.176	0.002	0.006
40	phospholipid metabolic process	2.167	0.002	0.006

Table 8: The 40 highest-scoring gene sets returned by GSEA in Alzheimer's

Rank	Gene Set	NES	p-value	FDR
1	transepithelial transport	-2.064	0.000	0.025
2	neuron cell-cell adhesion	-1.929	0.000	0.135
3	inorganic anion transport	-1.921	0.000	0.106
4	cardiac ventricle morphogenesis	-1.916	0.000	0.087
5	neuron migration	-1.915	0.000	0.071
6	regulation of smad protein import into nucleus	-1.893	0.002	0.078
7	positive regulation of glycogen metabolic process	-1.885	0.000	0.076
8	chondroitin sulfate proteoglycan metabolic process	-1.881	0.000	0.071
9	cardiac muscle tissue morphogenesis	-1.869	0.000	0.077
10	mesenchyme morphogenesis	-1.864	0.000	0.075
11	chloride transport	-1.861	0.000	0.071
12	chondroitin sulfate metabolic process	-1.853	0.000	0.075
13	cyclic nucleotide metabolic process	-1.851	0.002	0.071
14	endocardial cushion formation	-1.851	0.000	0.066
15	mucopolysaccharide metabolic process	-1.847	0.000	0.065
16	positive regulation of glucose metabolic process	-1.843	0.000	0.065
17	muscle organ morphogenesis	-1.837	0.000	0.066
18	muscle tissue morphogenesis	-1.837	0.000	0.062
19	regulation of cholesterol storage	-1.833	0.000	0.062
20	regulation of glycogen metabolic process	-1.833	0.000	0.059
21	sodium-independent organic anion transport	-1.829	0.000	0.059
22	glycosaminoglycan metabolic process	-1.827	0.000	0.059
23	regulation of synapse assembly	-1.822	0.004	0.060
24	aminoglycan metabolic process	-1.817	0.000	0.063
25	positive regulation of glycogen biosynthetic process	-1.814	0.000	0.061
26	pulmonary valve development	-1.810	0.000	0.063
27	pulmonary valve morphogenesis	-1.810	0.000	0.061
28	chloride transmembrane transport	-1.808	0.000	0.060
29	cardioblast differentiation	-1.807	0.002	0.058
30	negative regulation of peptide hormone secretion	-1.799	0.000	0.061
31	inorganic anion transmembrane transport	-1.799	0.000	0.060
32	positive regulation of cardiac muscle tissue development	-1.797	0.000	0.059
33	glycosaminoglycan biosynthetic process	-1.795	0.000	0.059
34	positive regulation of lipid transport	-1.793	0.000	0.060
35	ventricular cardiac muscle tissue development	-1.785	0.000	0.065
36	blood vessel endothelial cell differentiation	-1.785	0.000	0.063
37	camp metabolic process	-1.784	0.006	0.062
38	excretion	-1.784	0.002	0.060
39	polyol transport	-1.783	0.000	0.060
40	aminoglycan biosynthetic process	-1.781	0.000	0.060

Table 9: The 40 highest-scoring gene sets returned by maSigPro+GSEA preranked in Alzheimer's

Rank	Gene Set	NES	p-value	FDR
1	equilibrioception	1.510	0.000	0.686
2	aortic valve morphogenesis	1.478	0.000	1.000
3	aortic valve development	1.469	0.001	0.976
4	alkaloid metabolic process	1.429	0.012	1.000
5	intracellular transport of viral protein in host cell	1.427	0.006	1.000
6	intracellular protein transport in other organism involved in symbiotic interaction	1.424	0.008	1.000
7	heterochromatin organization	1.421	0.001	1.000
8	symbiont intracellular protein transport in host	1.420	0.002	1.000
9	positive regulation of organic acid transport	1.419	0.005	1.000
10	atp synthesis coupled proton transport	1.418	0.000	1.000
11	energy coupled proton transport, down electrochemical gradient	1.417	0.000	1.000
12	mitochondrial atp synthesis coupled proton transport	1.415	0.000	0.986
13	wound healing, spreading of epidermal cells	1.409	0.008	1.000
14	regulation of axon extension involved in axon guidance	1.408	0.006	0.993
15	electron transport chain	1.407	0.000	0.951
16	oxygen homeostasis	1.406	0.007	0.911
17	positive regulation of icosanoid secretion	1.404	0.011	0.877
18	positive regulation of axon guidance	1.402	0.008	0.877
19	respiratory electron transport chain	1.402	0.000	0.833
20	camp-mediated signaling	1.401	0.000	0.793
21	spermatid nucleus differentiation	1.400	0.005	0.773
22	positive regulation of t cell differentiation in thymus	1.399	0.005	0.752
23	sperm chromatin condensation	1.398	0.012	0.732
24	negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	1.398	0.009	0.704
25	myelin assembly	1.397	0.009	0.694
26	positive regulation of transcription from rna polymerase ii promoter involved in heart development	1.395	0.015	0.696
27	cardiac chamber formation	1.395	0.010	0.672
28	heterochromatin assembly	1.394	0.005	0.658
29	positive regulation of axon extension involved in axon guidance	1.394	0.007	0.639
30	negative regulation of jun kinase activity	1.392	0.006	0.634
31	positive regulation of fatty acid transport	1.391	0.006	0.627
32	positive regulation of fibroblast apoptotic process	1.389	0.011	0.632
33	positive regulation of thymocyte aggregation	1.384	0.006	0.673
34	nls-bearing protein import into nucleus	1.383	0.000	0.664
35	camera-type eye photoreceptor cell differentiation	1.379	0.013	0.702
36	negative regulation of hydrogen peroxide-mediated programmed cell death	1.379	0.017	0.684
37	tissue regeneration	1.377	0.007	0.685
38	riboflavin metabolic process	1.366	0.015	0.806
39	translational elongation	1.366	0.000	0.786
40	regulation of rna export from nucleus	1.366	0.006	0.774

COPD

Table 10: The 40 highest-scoring gene sets ranked by TEMPO score for the COPD data set, using age.

Rank	Gene Set	Score	p-value	FDR
1	alanine transport	305.977	0.002	0.019
2	positive regulation of interferon-gamma secretion	272.447	0.002	0.019
3	adult feeding behavior	221.133	0.002	0.019
4	positive regulation of phospholipid biosynthetic process	202.530	0.002	0.019
5	transcytosis	192.611	0.002	0.019
6	T-helper cell lineage commitment	183.348	0.002	0.019
7	T-helper 17 cell lineage commitment	183.348	0.002	0.019
8	nephric duct development	175.894	0.002	0.019
9	vascular smooth muscle cell development	174.913	0.002	0.019
10	regulation of interleukin-13 secretion	152.247	0.002	0.019
11	mRNA transcription from RNA polymerase II promoter	136.295	0.002	0.019
12	sperm chromatin condensation	132.503	0.002	0.019
13	opioid receptor signaling pathway	128.398	0.002	0.019
14	regulation of extracellular matrix organization	119.901	0.002	0.019
15	spermatid nucleus differentiation	113.009	0.002	0.019
16	epithelial tube branching involved in lung morphogenesis	108.991	0.002	0.019
17	RNA surveillance	106.868	0.002	0.019
18	purine nucleobase transport	98.518	0.002	0.019
19	monocyte chemotaxis	96.364	0.002	0.019
20	cell proliferation in forebrain	95.777	0.002	0.019
21	regulation of cell-cell adhesion mediated by cadherin	93.084	0.002	0.019
22	negative regulation of extracellular matrix organization	88.268	0.002	0.019
23	regulation of protein complex stability	86.933	0.002	0.019
24	regulation of oligodendrocyte differentiation	86.698	0.002	0.019
25	glutamine family amino acid metabolic process	83.558	0.002	0.019
26	sulfide oxidation	83.121	0.002	0.019
27	sulfide oxidation, using sulfide:quinone oxidoreductase	83.121	0.002	0.019
28	adrenal gland development	82.670	0.002	0.019
29	somatic stem cell division	80.102	0.002	0.019
30	pyrimidine-containing compound transmembrane transport	79.558	0.002	0.019
31	regulation of cardiac muscle cell membrane potential	79.468	0.002	0.019
32	negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	79.236	0.002	0.019
33	negative regulation of activin receptor signaling pathway	78.410	0.002	0.019
34	negative regulation of type 2 immune response	78.400	0.002	0.019
35	regulation of microvillus organization	77.182	0.002	0.019
36	regulation of microvillus assembly	77.182	0.002	0.019
37	glutamine transport	76.018	0.002	0.019
38	neuroblast proliferation	75.440	0.002	0.019
39	neutrophil homeostasis	74.654	0.002	0.019
40	sequestering of metal ion	73.463	0.004	0.029

Table 11: The 40 highest-scoring upregulated gene sets returned by GSEA in COPD.

Rank	Gene Set	NES	p-value	FDR
1	peptidyl-proline hydroxylation	-1.917	0.002	1.000
2	positive regulation of nuclease activity	-1.838	0.002	1.000
3	regulation of isotype switching	-1.834	0.000	1.000
4	peptidyl-serine autophosphorylation	-1.827	0.000	1.000
5	oocyte differentiation	-1.812	0.004	1.000
6	sulfide oxidation	-1.761	0.002	1.000
7	sulfide oxidation, using sulfide:quinone oxidoreductase	-1.761	0.002	1.000
8	regulation of mitophagy	-1.750	0.000	1.000
9	macromolecule depalmitoylation	-1.746	0.002	1.000
10	iron-sulfur cluster assembly	-1.745	0.000	1.000
11	metallo-sulfur cluster assembly	-1.745	0.000	1.000
12	protein hydroxylation	-1.732	0.000	1.000
13	regulation of torc1 signaling	-1.729	0.006	1.000
14	response to misfolded protein	-1.716	0.004	1.000
15	negative regulation of macroautophagy	-1.711	0.002	1.000
16	mitochondrial atp synthesis coupled proton transport	-1.704	0.046	1.000
17	positive regulation of ruffle assembly	-1.697	0.018	1.000
18	oocyte development	-1.696	0.010	1.000
19	positive regulation of isotype switching	-1.695	0.008	1.000
20	activation of signaling protein activity involved in unfolded protein response	-1.686	0.011	1.000
21	nucleosome disassembly	-1.685	0.002	1.000
22	chromatin disassembly	-1.685	0.002	1.000
23	protein-dna complex disassembly	-1.685	0.002	1.000
24	positive regulation of erad pathway	-1.680	0.000	1.000
25	energy coupled proton transport, down electrochemical gradient	-1.679	0.048	1.000
26	atp synthesis coupled proton transport	-1.679	0.048	1.000
27	base-excision repair, ap site formation	-1.677	0.011	1.000
28	peptidyl-diphthamide metabolic process	-1.676	0.011	1.000
29	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	-1.676	0.011	1.000
30	positive regulation of neurotransmitter secretion	-1.672	0.004	1.000
31	mitochondrial respiratory chain complex assembly	-1.670	0.037	1.000
32	positive regulation of anoikis	-1.669	0.006	1.000
33	establishment of protein localization to mitochondrion	-1.668	0.034	1.000
34	regulation of autophagosome maturation	-1.663	0.004	1.000
35	protein localization to mitochondrion	-1.661	0.026	1.000
36	regulation of immunoglobulin production	-1.657	0.012	1.000
37	histone h4-k12 acetylation	-1.648	0.002	1.000
38	calcineurin-nfat signaling cascade	-1.643	0.011	1.000
39	regulation of nuclease activity	-1.643	0.006	1.000
40	heme biosynthetic process	-1.639	0.015	1.000

Table 12: The 40 highest-scoring upregulated gene sets returned by maSigPro+GSEA preranked in COPD using age as the time variable.

Rank	Gene Set	NES	p-value	FDR
1	ectodermal placode development	2.104	0.000	0.091
2	ectodermal placode morphogenesis	2.102	0.000	0.047
3	ectodermal placode formation	2.077	0.000	0.049
4	response to amino acid	1.988	0.000	0.117
5	peptidyl-methionine modification	1.966	0.001	0.124
6	positive regulation of er-associated ubiquitin-dependent protein catabolic process	1.934	0.000	0.147
7	ubiquinone biosynthetic process	1.933	0.000	0.130
8	base-excision repair, ap site formation	1.930	0.000	0.117
9	positive regulation of intracellular estrogen receptor signaling pathway	1.922	0.001	0.112
10	cellular response to amino acid stimulus	1.917	0.000	0.109
11	spliceosomal tri-snrnp complex assembly	1.914	0.000	0.103
12	protein monoubiquitination	1.906	0.000	0.105
13	histone ubiquitination	1.903	0.000	0.099
14	quinone biosynthetic process	1.891	0.000	0.106
15	ubiquinone metabolic process	1.887	0.000	0.104
16	short-chain fatty acid catabolic process	1.883	0.001	0.101
17	jun phosphorylation	1.881	0.002	0.099
18	acetyl-coa biosynthetic process from pyruvate	1.871	0.000	0.105
19	regulation of establishment of protein localization to telomere	1.869	0.003	0.102
20	trna threonylcarbamoyladenosine metabolic process	1.864	0.001	0.101
21	mitochondrial rna modification	1.862	0.002	0.100
22	intermediate filament organization	1.861	0.001	0.096
23	regulation of establishment of protein localization to chromosome	1.852	0.001	0.103
24	histone monoubiquitination	1.849	0.000	0.102
25	smad protein complex assembly	1.843	0.000	0.104
26	regulation of autophagosome maturation	1.840	0.001	0.104
27	spliceosomal snrnp assembly	1.839	0.000	0.101
28	mitochondrial rna processing	1.839	0.000	0.098
29	mitochondrial trna modification	1.836	0.002	0.097
30	depyrimidination	1.832	0.000	0.098
31	positive regulation of protein localization to cajal body	1.819	0.000	0.108
32	regulation of mrna 3'-end processing	1.816	0.000	0.108
33	regulation of low-density lipoprotein particle clearance	1.812	0.003	0.109
34	regulation of protein localization to cajal body	1.808	0.001	0.111
35	pyrimidine-containing compound transmembrane transport	1.797	0.001	0.121
36	mitochondrion morphogenesis	1.797	0.000	0.118
37	nucleobase-containing small molecule catabolic process	1.797	0.002	0.115
38	primary mirna processing	1.795	0.001	0.114
39	membrane depolarization during sa node cell action potential	1.792	0.009	0.115
40	viral release from host cell	1.791	0.000	0.114