Table S1 The biological functions of ITGB1-DT involved in STAD

Name	Size	NES	NOM P
Branched chain amino acid metabolic process	23	−2.2078602	0
Acetyl COA biosynthetic process from pyruvate	15	−2.174683	0
Acetyl COA biosynthetic process	22	−2.168471	0.002020202
Tetrapyrrole biosynthetic process	28	−2.1118453	0
RNA interference	17	−2.059235	0
DNA modification	118	−2.0516224	0
Mitochondrial transmembrane transport	109	−2.0409687	0.001984127
Aerobic respiration	86	−2.03962	0
Negative regulation of ATP metabolic process	28	−2.0383108	0
Histone h3 k4 methylation	53	−2.031951	0.00407332
Regulation of torc1 signaling	39	−2.0257764	0.004016064
Thioester biosynthetic process	53	−2.003325	0.002020202
Positive regulation of calcium mediated signaling	30	−2.002058	0
Negative regulation of defense response to virus	24	−1.9982717	0.001988072
Production of small RNA involved in gene silencing by RNA	56	−1.978467	0
Peptidyl lysine methylation	122	−1.973523	0.006198347
S adenosylmethionine metabolic process	15	−1.9695961	0.002074689
Negative regulation of mRNA metabolic process	88	−1.9687572	0.004158004
Regulation of histone h3 k4 methylation	28	−1.9610854	0.00621118
Negative regulation of interleukin 12 production	17	−1.9605496	0.002004008
Demethylation	72	−1.9578949	0.00203252
Response to glucagon	37	−1.9578651	0.002053388
Sister chromatid cohesion	62	−1.9547826	0.014799154
Porphyrin containing compound metabolic process	40	−1.9515313	0
Base excision repair	39	−1.9510381	0.016985139
Regulation of glial cell proliferation	32	−1.9501851	0
Nucleoside bisphosphate biosynthetic process	67	−1.9493454	0.004132231
Methionine metabolic process	16	−1.9488856	0
Histone methylation	130	−1.944727	0.006198347
Positive regulation by host of viral transcription	16	−1.944065	0.002012072
ATP metabolic process	312	−1.9348953	0.003976143
Torc1 signaling	47	−1.9343549	0.006060606
Photoperiodism	33	−1.9336711	0.003952569
Mitochondrial genome maintenance	21	−1.9316409	0.008316008
Regulation of RNA splicing	144	−1.9288024	0.006302521
Purine containing compound biosynthetic process	206	−1.9287037	0
Covalent chromatin modification	460	−1.9284416	0.006160164
Chromosome condensation	46	−1.9262824	0.010570824
DNA methylation or demethylation	96	−1.9223852	0.002070393
Regulation of sister chromatid cohesion	22	−1.9217824	0.01026694

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Regulation of monocyte differentiation	21	−1.9208174	0.002123142
Transcription by RNA polymerase iii	47	−1.914049	0.016260162
Regulation of mitochondrial membrane potential	71	−1.913926	0
Cell proliferation in hindbrain	17	−1.9110901	0
Fatty acid beta oxidation	75	−1.9075215	0.002053388
Regulation of cell cycle arrest	107	−1.9072556	0.004264392
Pre miRNA processing	15	−1.9017186	0.004024145
Energy derivation by oxidation of organic compounds	277	−1.9013313	0.003868472
Ribose phosphate biosynthetic process	194	−1.9006807	0
Protein demethylation	33	−1.8994819	0.00212766
NcRNA transcription	108	−1.8972708	0.016460905
Positive regulation of interleukin 10 production	38	−1.8947318	0.008163265
Ubiquinone metabolic process	18	−1.8921487	0.014198783
Mitochondrial transport	270	−1.8905923	0.00408998
N glycan processing	19	−1.8898333	0.00811359
Chromatin remodeling	207	−1.8895345	0.012269938
Negative regulation of histone methylation	21	−1.8887904	0.00621118
Positive regulation of RNA splicing	37	−1.8883421	0.012422361
Regulation of transcription by RNA polymerase iii	23	−1.8883001	0.004166667
Intrinsic apoptotic signaling pathway by p53 class mediator	74	−1.8862685	0.004166667
Glycoprotein catabolic process	27	−1.8858399	0.002012072
Regulation of protein export from nucleus	32	−1.8853811	0.006060606
Regulation of transcription involved in g1 s transition of mitotic cell cycle	35	−1.8853064	0.008316008
Cellular response to alkaloid	32	−1.8829983	0.003992016
Oocyte differentiation	47	−1.8826027	0.002066116
Response to oxygen radical	27	−1.8807331	0.007889546
Tricarboxylic acid cycle	34	−1.8801855	0.008438818
Protein methylation	168	−1.8778002	0.006289308
RNA destabilization	36	−1.8762772	0.010593221
Heme metabolic process	33	−1.8757842	0.008403362
Regulation of mRNA splicing via spliceosome	100	−1.8755081	0.014403292
Regulation of alternative mRNA splicing via spliceosome	57	−1.8749291	0.018518519
Mitotic sister chromatid cohesion	27	−1.8738884	0.017167382
Response to misfolded protein	24	−1.8720517	0.00204499
Regulation of t helper 17 type immune response	21	−1.8718263	0.008130081
Mirna metabolic process	29	−1.8711772	0.008130081
Glial cell proliferation	47	−1.8706264	0.002188184
Energy homeostasis	35	−1.8702449	0.002109705
DNA conformation change	349	−1.8698416	0.014893618
Mitotic chromosome condensation	15	−1.8687869	0.004166667
Alpha amino acid biosynthetic process	67	−1.8684282	0.006122449

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
DNA packaging	237	−1.8667296	0.014227643
Protein localization to chromatin	29	−1.8655822	0.016260162
Protein k48 linked deubiquitination	35	−1.8638545	0.013916501
Histone h3 acetylation	60	−1.8629838	0.010141988
Positive regulation of cell cycle phase transition	105	−1.8611566	0.010373444
Folic acid containing compound metabolic process	27	−1.8605474	0.006329114
Stem cell proliferation	63	−1.8605392	0.010416667
Amino acid betaine metabolic process	17	−1.857552	0.003838772
Regulatory t cell differentiation	35	−1.8570753	0.013944224
Mitochondrial fusion	28	−1.8566906	0.008316008
Peptidyl lysine dimethylation	22	−1.8558216	0.012552301
Regulation of mRNA processing	139	−1.8545699	0.02258727
Regulation of autophagy of mitochondrion	31	−1.8527659	0.00203252
Protein targeting to mitochondrion	100	−1.8512914	0.008421052
Negative regulation of alcohol biosynthetic process	16	−1.8491862	0.008016032
Regulation of rig I signaling pathway	19	−1.8463405	0.015414258
Cell cycle g1 s phase transition	288	−1.8462751	0.01048218
Rig I signaling pathway	25	−1.8455057	0.012219959
Positive regulation of stem cell proliferation	22	−1.8453423	0.002087683
Positive regulation of mitotic cell cycle	116	−1.8440888	0.010330578
Regulation of ATP metabolic process	118	−1.8439859	0
Chromatin assembly or disassembly	218	−1.8435924	0.014227643
Microtubule nucleation	30	−1.84297	0.008016032
Regulation of circadian rhythm	118	−1.8429104	0.002114165
Cellular amino acid catabolic process	105	−1.8418019	0.002079002
Positive regulation of protein export from nucleus	20	−1.8406745	0.002020202
Protein localization to mitochondrion	146	−1.8399948	0.006224067
tRNA wobble base modification	21	−1.8388599	0.010548524
RNA phosphodiester bond hydrolysis endonucleolytic	78	−1.8371634	0.01863354
Negative regulation of mRNA processing	29	−1.8357357	0.023060797
Organic acid catabolic process	257	−1.8346181	0.002057613
Regulation of translational fidelity	20	−1.8323827	0.01875
RNA 3 end processing	153	−1.8311754	0.023404256
Response to ethanol	126	−1.8307611	0
Negative regulation of mRNA catabolic process	59	−1.8307191	0.01048218
Negative regulation of mRNA splicing via spliceosome	20	−1.8300965	0.01910828
mRNA 3 end processing	99	−1.8299795	0.025531914
G0 to g1 transition	46	−1.8291907	0.018255578
Pteridine containing compound metabolic process	33	−1.8273124	0.010548524
Cell cycle arrest	234	−1.8271204	0.0041841
Signal transduction by p53 class mediator	262	−1.8259721	0.023012552

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Regulation of gastrulation	17	−1.8259243	0.00422833
Protein localization to chromosome	91	−1.8258724	0.031578947
Alternative mRNA splicing via spliceosome	73	−1.825276	0.020746889
Histone h3 k36 methylation	15	−1.8249557	0.012738854
Beta catenin TCF complex assembly	31	−1.824728	0.016460905
Histone h3 k9 modification	45	−1.8239768	0.014553014
SnRNA transcription	75	−1.8224303	0.018518519
ATP dependent chromatin remodeling	89	−1.8211486	0.024340771
Entrainment of circadian clock	34	−1.8202766	0.018181818
Positive regulation of embryonic development	21	−1.8191936	0.00209205
RNA phosphodiester bond hydrolysis	154	−1.8175384	0.02258727
Regulation of histone methylation	61	−1.8173829	0.012526096
RNA phosphodiester bond hydrolysis exonucleolytic	43	−1.817286	0.022312373
Negative regulation of ATPase activity	18	−1.8161343	0.004008016
Positive regulation of mRNA catabolic process	52	−1.8158197	0.019027485
Positive regulation of transcription of notch receptor target	18	−1.8137099	0.019455252
Positive regulation of cell cycle arrest	81	−1.8136711	0.008510638
Corpus callosum development	15	−1.8136693	0.004158004
Methylation	353	−1.8117844	0.018828452
Positive regulation of torc1 signaling	17	−1.8107147	0.01443299
Positive regulation of b cell differentiation	15	−1.8101728	0.010121457
Nucleoside phosphate biosynthetic process	265	−1.8098713	0.002164502
Negative regulation of RNA splicing	25	−1.8064284	0.028571429
Kinetochore organization	22	−1.806186	0.029535865
rRNA transcription	32	−1.8059531	0.024793388
Negative regulation of chromosome organization	91	−1.8056563	0.037037037
Nuclear export	201	−1.8056129	0.027600849
Regulation of mRNA metabolic process	334	−1.8031839	0.026859503
Axis specification	82	−1.8026987	0.006224067
Small molecule catabolic process	429	−1.8018811	0.002016129
Negative regulation of RNA catabolic process	70	−1.8004179	0.014861995
Retrograde transport endosome to GOLGI	91	−1.8003691	0.012219959
Regulation of transcription by RNA polymerase I	33	−1.7991495	0.020491803
Cellular respiration	186	−1.7989057	0.03529412
Negative regulation of catabolic process	308	−1.7988442	0.00408998
Regulation of chromatin binding	23	−1.7987229	0.01048218
Fatty acid beta oxidation using acyl COA oxidase	15	−1.7961819	0.011560693
Regulation of hemopoiesis	411	−1.7958207	0.008230452
Monocyte differentiation	36	−1.7945495	0.015053763
Pyrimidine containing compound metabolic process	85	−1.7945249	0.006097561
Sister chromatid segregation	199	−1.7928562	0.04821803

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Inner mitochondrial membrane organization	55	−1.7911196	0.031936128
One carbon metabolic process	40	−1.790459	0.003944773
Pyruvate metabolic process	150	−1.7904296	0.014141414
Peptidyl lysine modification	389	−1.7893575	0.020746889
Cellular response to drug	63	−1.7887326	0.004219409
Regulation of generation of precursor metabolites and energy	160	−1.7866434	0.010245902
Negative regulation of mitochondrion organization	46	−1.7858384	0.004115226
Negative regulation of cell cycle g1 s phase transition	115	−1.7841921	0.00631579
mRNA export from nucleus	113	−1.7825959	0.031847134
Potassium ion export across plasma membrane	17	−1.7825466	0.012244898
Regulation of cellular amide metabolic process	478	−1.7825431	0.004140787
Maintenance of cell number	148	−1.7821255	0.0041841
Nuclear transport	343	−1.7819912	0.0186722
Chromatin disassembly	20	−1.7817075	0.024390243
Negative regulation of response to biotic stimulus	99	−1.7809945	0.02834008
Protein localization to chromosome centromeric region	25	−1.7801517	0.03909465
Histone deacetylation	77	−1.7793951	0.012474013
Negative regulation of alpha beta t cell differentiation	26	−1.7789695	0.00408998
Histone h3 k9 methylation	34	−1.7776991	0.014767933
Tetrahydrofolate metabolic process	19	−1.7755777	0.00845666
Regulation of ubiquitin protein transferase activity	53	−1.7751836	0.014314928
Mitochondrial membrane organization	139	−1.7741174	0.01446281
Regulation of triglyceride biosynthetic process	20	−1.7741044	0.010460251
Positive regulation of membrane permeability	65	−1.7739226	0.013752456
Membrane repolarization during ventricular cardiac muscle cell action potential	15	−1.7734907	0.008196721
Protein quality control for misfolded or incompletely synthesized proteins	28	−1.772703	0.010121457
DNA methylation	72	−1.7724217	0.010416667
DNA demethylation	28	−1.7705652	0.018108651
Regulation of oxidative phosphorylation	25	−1.7701945	0.009940358
Macromolecule methylation	300	−1.7663561	0.027777778
Lactate metabolic process	15	−1.7662627	0.004065041
Positive regulation of cell cycle process	299	−1.7662318	0.012295082
Regulation of histone deacetylation	28	−1.7659621	0.00814664
Nucleoside triphosphate metabolic process	108	−1.7655461	0.01629328
DNA dealkylation	34	−1.7654872	0.014256619
Protein acetylation	198	−1.7653732	0.016563147
Regulation of stress activated protein kinase signaling cascade	182	−1.7646856	0.006160164
Regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	17	−1.7641681	0.016877636
Regulation of amyloid beta clearance	17	−1.7639041	0.002016129
Acetyl COA metabolic process	38	−1.7632265	0.021645023

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Regulation of JNK cascade	128	−1.7628106	0.008213553
Alpha amino acid catabolic process	87	−1.7627513	0.010183299
Mitotic nuclear division	296	−1.7620248	0.039337475
Regulation of cyclin dependent protein kinase activity	102	−1.7617135	0.024242423
Positive regulation of membrane potential	16	−1.7615687	0.008163265
Interleukin 12 production	59	−1.7597991	0.014373717
Interstrand cross link repair	57	−1.7582799	0.04
Negative regulation of stress activated protein kinase signaling cascade	47	−1.7581	0.012
N terminal protein amino acid acetylation	17	−1.7577665	0.01984127
Ribonucleoside triphosphate metabolic process	86	−1.7569556	0.016260162
Negative regulation of double strand break repair via homologous recombination	19	−1.7558566	0.023157895
Regulation of cell cycle g1 s phase transition	185	−1.7548633	0.006479482
Cristae formation	35	−1.7545353	0.043564357
Regulation of myeloid cell differentiation	255	−1.752755	0.004040404
Protein DNA complex subunit organization	277	−1.7524734	0.034
Cellular response to oxygen radical	23	−1.7522489	0.011627907
Regulation of intrinsic apoptotic signaling pathway by p53 class mediator	27	−1.7511067	0.016427105
Nucleotide transmembrane transport	16	−1.7510549	0.01632653
Positive regulation of mRNA metabolic process	84	−1.7505876	0.029473685
Regulation of DNA templated transcription elongation	51	−1.7496481	0.02244898
Regulation of stem cell proliferation	40	−1.7488687	0.006451613
Positive regulation of nucleocytoplasmic transport	61	−1.7488668	0.012121212
Regulation of histone modification	141	−1.7483774	0.0186722
Aspartate family amino acid metabolic process	50	−1.7481909	0.014403292
Circadian rhythm	212	−1.7476658	0.008510638
Kinetochore assembly	17	−1.7475177	0.033126295
Organelle disassembly	107	−1.7475057	0.0256917
Negative regulation of cellular catabolic process	251	−1.7450036	0.006147541
Vitamin transmembrane transport	17	−1.7447909	0.014989293
Cellular response to reactive oxygen species	152	−1.7446262	0.002145923
Phosphatidylinositol dephosphorylation	31	−1.744128	0.020449897
Regulation of t helper cell differentiation	38	−1.7436757	0.030612245
Regulation of leukocyte differentiation	277	−1.7421626	0.020746889
Negative regulation of cyclin dependent protein kinase activity	31	−1.7414011	0.020876827
Nucleosome organization	180	−1.7413962	0.030364372
Mitotic g1 s transition checkpoint	63	−1.7410647	0.029106028
Folic acid metabolic process	20	−1.7390722	0.02783726
T cell homeostasis	36	−1.7390503	0.024439918
Glycine metabolic process	19	−1.7387707	0.014112903
Positive regulation of glial cell proliferation	18	−1.7384058	0.014141414
Regulation of viral induced cytoplasmic pattern recognition receptor signaling pathway	23	−1.7375942	0.026717557

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Anterior posterior pattern specification	203	−1.7367613	0.008064516
Positive regulation of double strand break repair via nonhomologous end joining	16	−1.7366357	0.021141648
Sulfur amino acid metabolic process	37	−1.7358297	0.018367346
Purine containing compound metabolic process	457	−1.7348683	0.002083333
Deoxyribonucleotide metabolic process	40	−1.7348192	0.0256917
ATP synthesis coupled proton transport	27	−1.7347252	0.04263566
Negative regulation of response to DNA damage stimulus	82	−1.7342983	0.012820513
Positive regulation of p38mapk cascade	29	−1.734029	0.013043478
Regulation of response to reactive oxygen species	30	−1.7337806	0.012295082
Nucleotide transport	32	−1.7325768	0.00408998
Mitotic DNA replication	16	−1.7324624	0.03846154
Negative regulation of cellular amide metabolic process	218	−1.7323724	0.006276151
DNA geometric change	114	−1.7321285	0.045548655
T cell differentiation	245	−1.7320486	0.026915114
N terminal protein amino acid modification	29	−1.7312031	0.024242423
Platelet morphogenesis	21	−1.7300982	0.01417004
Negative regulation of cell cycle process	346	−1.729946	0.030991735
mRNA transport	151	−1.729908	0.035940804
Smooth muscle cell apoptotic process	27	−1.7298537	0.012195122
Histone h4 acetylation	67	−1.72967	0.026639344
Alpha beta t cell differentiation	106	−1.7296126	0.030612245
I kappa B phosphorylation	20	−1.7295784	0.01923077
Nuclear transcribed mRNA catabolic process deadenylation dependent decay	77	−1.7293934	0.028806584
Response to sterol depletion	17	−1.7288775	0.034979425
Histone h2a monoubiquitination	17	−1.7285534	0.023762377
P38mapk cascade	48	−1.7271767	0.014861995
Phospholipid dephosphorylation	45	−1.7263874	0.014583333
Brain morphogenesis	35	−1.7261211	0.008179959
Response to antibiotic	43	−1.7261002	0.01443299
T helper 17 type immune response	32	−1.7260537	0.016701462
Fatty acid catabolic process	106	−1.725936	0.02020202
Regulation of defense response to virus	69	−1.725737	0.028225806
Regulation of spindle checkpoint	15	−1.7256966	0.02742616
Lipid oxidation	110	−1.7246264	0.014112903
Lytic vacuole organization	70	−1.7237483	0.016563147
Regulation of alpha beta t cell differentiation	66	−1.7232727	0.036093418
Positive regulation of cell cycle	391	−1.7229004	0.012320329
Cellular amino acid biosynthetic process	77	−1.7224926	0.010683761
Negative regulation of response to cytokine stimulus	78	−1.7217823	0.002079002
Fructose metabolic process	15	−1.7217777	0.025316456
Ketone biosynthetic process	42	−1.7216209	0.00204918

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Regulation of lymphocyte differentiation	174	−1.7212352	0.031578947
Lymphocyte homeostasis	57	−1.720615	0.026369167
Positive regulation of transcription from RNA polymerase ii promoter involved in cellular response to chemical stimulus	22	−1.7201304	0.010080645
Regulation of cd4 positive alpha beta t cell differentiation	50	−1.7195232	0.031185031
Regulation of mitochondrion organization	150	−1.7193552	0.014198783
Regulation of mRNA catabolic process	210	−1.7193383	0.035343036
Mitochondrial RNA processing	17	−1.7190748	0.037037037
Establishment of protein localization to mitochondrial membrane	53	−1.7186408	0.035196688
Regulation of protein modification by small protein conjugation or removal	236	−1.718544	0.01443299
Regulation of erythrocyte differentiation	47	−1.7176392	0.008438818
Regulation of DNA dependent DNA replication	47	−1.7173141	0.043841336
Regulation of chromosome organization	273	−1.7167584	0.040339705
Positive regulation of transcription by RNA polymerase I	23	−1.7166249	0.032323234
Positive regulation of protein modification by small protein conjugation or removal	136	−1.7160873	0.012396694
Regulation of nucleocytoplasmic transport	103	−1.7155322	0.018442623
Sex differentiation	262	−1.7153898	0
Response to interleukin 4	35	−1.7153695	0.025052192
Maturation of 5 8s rRNa from tricistronic rRNA transcript SSU rRNA 5 8s rRNA LSU rRNA	24	−1.7151608	0.037117902
Cellular response to glucose starvation	48	−1.7145221	0.0125
Regulation of double strand break repair via nonhomologous end joining	28	−1.7140701	0.026970955
Spindle organization	180	−1.7139362	0.037656903
DNA biosynthetic process	189	−1.7130541	0.03526971
Negative regulation of establishment of protein localization	123	−1.7116401	0.002222222
SnRNA processing	36	−1.7114629	0.03187251
Regulation of t cell differentiation	145	−1.7112755	0.041666668
Regulation of cell cycle checkpoint	31	−1.7103324	0.042372882
Protein localization to kinetochore	19	−1.7101021	0.044265594
Coenzyme a metabolic process	15	−1.7100279	0.014314928
Regulation of signal transduction by p53 class mediator	176	−1.7094628	0.04329897
RNA export from nucleus	142	−1.7093208	0.048625793
Nucleus localization	24	−1.7089349	0.02952756
Cleavage involved in rRNA processing	27	−1.7080226	0.038793102
Negative regulation of histone modification	45	−1.7074249	0.03006012
Polyol biosynthetic process	63	−1.7071784	0.004115226
Peptidyl lysine trimethylation	45	−1.7064384	0.029411765
RNA surveillance	15	−1.7062725	0.04233871
Positive regulation of DNA repair	74	−1.7062644	0.03966597
Protein DNA complex disassembly	20	−1.7062584	0.03448276
Lamellipodium morphogenesis	16	−1.7059451	0.015021459
Negative regulation of steroid metabolic process	29	−1.7057827	0.010309278

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Negative regulation of chromatin organization	64	−1.7051816	0.026209677
Glandular epithelial cell differentiation	47	−1.7038997	0.01622718
Cellular protein containing complex localization	20	−1.7038378	0.016096579
Negative regulation of NF kappa B transcription factor activity	89	−1.7028363	0.01048218
Positive regulation of cold induced thermogenesis	97	−1.7023791	0.008350731
Cellular response to reactive nitrogen species	17	−1.7022474	0.018329939
Monocarboxylic acid catabolic process	131	−1.701967	0.019569471
Positive regulation of histone h3 k4 methylation	18	−1.7005963	0.031446543
DNA synthesis involved in DNA repair	53	−1.7004093	0.03869654
Neuronal stem cell population maintenance	19	−1.7003747	0.024340771
Autophagy of mitochondrion	75	−1.7002213	0.023904383
Determination of adult lifespan	18	−1.6998173	0.028
Negative regulation of cd4 positive alpha beta t cell differentiation	22	−1.6996623	0.016563147
Regulation of chromatin organization	185	−1.6975431	0.030737706
Midbrain development	86	−1.6966314	0.006185567
Negative regulation of autophagy	82	−1.6963545	0.022540983
Negative regulation of telomere maintenance via telomere lengthening	27	−1.6953162	0.045725647
RNA splicing via transesterification reactions	383	−1.6941546	0.04831933
Negative regulation of DNA repair	36	−1.6939075	0.03177966
Regulation of cell cycle phase transition	465	−1.6932869	0.034836065
Deoxyribose phosphate catabolic process	27	−1.6932411	0.01992032
Negative regulation of ubiquitin dependent protein catabolic process	48	−1.6932117	0.026970955
Negative regulation of DNA metabolic process	123	−1.6924828	0.028688524
Peptidyl lysine acetylation	167	−1.6921589	0.027083334
Viral translation	16	−1.6913936	0.03773585
Regulation of protein localization to nucleus	130	−1.6913649	0.020283977
Negative regulation of DNA templated transcription elongation	17	−1.6899132	0.02258727
Regulation of osteoclast differentiation	63	−1.6889768	0.024539877
Positive regulation of ubiquitin protein transferase activity	34	−1.6882794	0.025104603
Glucose catabolic process	36	−1.6881521	0.041015625
Alpha amino acid metabolic process	190	−1.6881027	0.014767933
Trophectodermal cell differentiation	16	−1.6877993	0.027083334
Segmentation	95	−1.6873643	0.012244898
Negative regulation of torc1 signaling	17	−1.6871945	0.026104419
Response to alkaloid	99	−1.6854899	0.008281574
Signal transduction in response to DNA damage	130	−1.6852825	0.027196653
Negative regulation of circadian rhythm	15	−1.6849613	0.031055901
DNA recombination	291	−1.684319	0.0392562
Lipid modification	269	−1.6842712	0.012244898
RNA polyadenylation	46	−1.6842015	0.03726708
Protein modification by small protein removal	300	−1.6826141	0.034274194

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Spleen development	33	−1.6814978	0.03773585
Regulation of cellular respiration	22	−1.6813924	0.024048096
Negative regulation of phagocytosis	22	−1.6807977	0.024096385
Homeostasis of number of cells	248	−1.680783	0.018036073
Segment specification	17	−1.6805649	0.022222223
Negative regulation of DNA binding transcription factor activity	173	−1.6803266	0.004255319
Cell redox homeostasis	43	−1.680184	0.025490196
Regulation of DNA methylation	25	−1.6801215	0.01898734
Intracellular estrogen receptor signaling pathway	57	−1.6801138	0.023012552
Glucose metabolic process	210	−1.67997	0.010416667
Regulation of nuclear division	134	−1.6799066	0.047817048
Prostate gland development	41	−1.6798882	0.023012552
Lipid phosphorylation	71	−1.6793735	0.024896266
Aspartate family amino acid catabolic process	23	−1.6776662	0.018442623
Glutamine family amino acid catabolic process	26	−1.6757892	0.01775148
Regulation of intracellular steroid hormone receptor signaling pathway	73	−1.6754711	0.020576132
Cellular amino acid metabolic process	330	−1.6751516	0.034343433
Positive regulation of stress activated protein kinase signaling cascade	118	−1.6749102	0.02079002
Mitochondrial outer membrane permeabilization	55	−1.6745584	0.031809144
Positive regulation of bmp signaling pathway	32	−1.6742024	0.024896266
Nucleolar large rRNA transcription by RNA polymerase I	17	−1.6738211	0.047817048
Regulation of carbohydrate catabolic process	90	−1.6732037	0.025104603
Protein acylation	240	−1.6729228	0.027027028
DNA damage response signal transduction by p53 class mediator	106	−1.6728481	0.031185031
Regulation of protein targeting to mitochondrion	44	−1.6720059	0.018255578
Intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	44	−1.6718805	0.024742268
Regulation of pattern recognition receptor signaling pathway	101	−1.6699996	0.023012552
Negative regulation of hemopoiesis	104	−1.6699163	0.016563147
Response to testosterone	41	−1.6687516	0.010593221
Cd4 positive alpha beta t cell differentiation	80	−1.6682638	0.03586498
Production of molecular mediator involved in inflammatory response	82	−1.6676905	0.020449897
Type I interferon production	128	−1.6673585	0.04008016
Myeloid cell homeostasis	144	−1.6668317	0.01629328
Negative regulation of t helper cell differentiation	18	−1.6664853	0.033932135
Response to UV	146	−1.6657906	0.018947368
Histone deubiquitination	23	−1.6656587	0.043933053
Cellular response to UV	88	−1.665559	0.03125
Regulation of response to oxidative stress	83	−1.6647305	0.0125
Negative regulation of macroautophagy	35	−1.6647038	0.043564357
Glutamine metabolic process	23	−1.6646936	0.049281314
Development of primary sexual characteristics	217	−1.6620845	0.001984127

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Negative regulation of cell cycle phase transition	257	−1.6618727	0.03966597
Nucleic acid phosphodiester bond hydrolysis	296	−1.661523	0.047817048
Mitotic DNA integrity checkpoint	105	−1.6610409	0.04489796
Negative regulation of alpha beta t cell activation	41	−1.6606497	0.026209677
Histone h3 k4 trimethylation	17	−1.6596062	0.033195022
Regulation of DNA repair	130	−1.6581519	0.048117153
Positive regulation of cellular amide metabolic process	163	−1.6574653	0.031185031
Positive regulation of tor signaling	42	−1.6568929	0.02258727
Positive regulation of translational initiation	30	−1.6565046	0.034764826
Potassium ion import across plasma membrane	47	−1.6561873	0.015810277
Protein sumoylation	81	−1.6560924	0.044624746
T cell differentiation involved in immune response	72	−1.655399	0.04158004
Negative regulation of intracellular protein transport	41	−1.6546173	0.020120725
Rhythmic process	294	−1.6545103	0.008583691
Protein localization to nucleus	275	−1.6542635	0.030425964
Aspartate family amino acid biosynthetic process	21	−1.6541734	0.041753653
Vitamin biosynthetic process	19	−1.6523294	0.020746889
Walking behavior	25	−1.6513389	0.027196653
Negative regulation of MAPK cascade	174	−1.6512583	0.008179959
Sulfur amino acid biosynthetic process	17	−1.6510024	0.025157232
Monosaccharide catabolic process	62	−1.6508496	0.027613413
Serine family amino acid biosynthetic process	21	−1.6494894	0.022267206
Positive regulation of double strand break repair	41	−1.6492496	0.048117153
Single stranded viral RNA replication via double stranded DNA intermediate	20	−1.6491617	0.041666668
Positive regulation of mitochondrion organization	83	−1.6484723	0.027777778
Negative regulation of activated t cell proliferation	15	−1.6478177	0.036608864
Negative regulation of JNK cascade	36	−1.6473446	0.027833002
Adaptive thermogenesis	153	−1.6471554	0.006302521
Midbrain dopaminergic neuron differentiation	16	−1.6453391	0.034979425
Cellular response to ATP	17	−1.6448852	0.018367346
Intrinsic apoptotic signaling pathway	280	−1.6440625	0.01443299
Positive regulation of mRNA splicing via spliceosome	23	−1.6440499	0.04517454
Negative regulation of organelle assembly	41	−1.6435958	0.018255578
Cytokine production involved in inflammatory response	63	−1.6435833	0.024844721
Homeostasis of number of cells within a tissue	26	−1.6435144	0.02244898
Erythrocyte homeostasis	120	−1.6425128	0.016260162
Somatic recombination of immunoglobulin gene segments	54	−1.6420319	0.044354837
Negative regulation of cell aging	27	−1.6403829	0.03258656
Tetrapyrrole metabolic process	62	−1.6392416	0.028629856
T cell lineage commitment	27	−1.6390072	0.045544554
Response to gamma radiation	53	−1.6383994	0.048681542

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Macromolecule deacylation	109	−1.6380738	0.020833334
Gastrulation with mouth forming second	23	−1.6380479	0.034274194
Tripartite regional subdivision	16	−1.6374621	0.020408163
Regulation of response to DNA damage stimulus	220	−1.637368	0.045548655
Modulation of process of other organism	123	−1.6369833	0.014141414
Negative regulation of posttranscriptional gene silencing	22	−1.636863	0.027833002
Pyrimidine containing compound catabolic process	40	−1.6368303	0.021825397
Regulation of establishment of protein localization to mitochondrion	72	−1.635895	0.028
Diol metabolic process	29	−1.6350031	0.023166023
Negative regulation of lymphocyte differentiation	54	−1.6343825	0.030737706
Cellular response to sterol depletion	15	−1.634275	0.047227927
Cytoplasmic pattern recognition receptor signaling pathway in response to virus	32	−1.6341653	0.044
Positive regulation of alpha beta T cell differentiation	48	−1.6340162	0.04631579
Epithelial cell fate commitment	15	−1.6337209	0.033932135
Cellular response to leptin stimulus	19	−1.6328557	0.03655914
Negative regulation of mitotic cell cycle	311	−1.6326127	0.042016808
Aging	296	−1.6322792	0.0041841
Protein import	194	−1.6317749	0.028571429
Positive regulation of hemopoiesis	153	−1.6310676	0.03368421
Response to ATP	31	−1.630752	0.014285714
Monosaccharide metabolic process	272	−1.6302173	0.012320329
Ribonucleoside triphosphate biosynthetic process	72	−1.6300616	0.048484847
Superoxide metabolic process	68	−1.6299493	0.043912176
Negative regulation of proteasomal ubiquitin dependent protein catabolic process	35	−1.629804	0.026639344
Positive regulation of myeloid cell differentiation	102	−1.6293753	0.014705882
Myeloid cell differentiation	415	−1.629221	0.026
Interleukin 10 production	61	−1.6284888	0.0373444
Nuclear transcribed mRNA poly a tail shortening	35	−1.6276671	0.045548655
Protein phosphopantetheinylation	331	−1.6276591	0.02053388
Regulation of skeletal muscle contraction	15	−1.6268514	0.033542976
Negative regulation of osteoclast differentiation	27	−1.6264398	0.044715445
Pyrimidine deoxyribonucleotide metabolic process	23	−1.6256508	0.043912176
Regulation of DNA metabolic process	349	−1.6253417	0.047916666
Protein polyubiquitination	337	−1.6238636	0.033797216
Beta catenin destruction complex disassembly	21	−1.6238517	0.034068137
Metencephalon development	101	−1.6232531	0.012345679
Protein autoprocessing	24	−1.6225023	0.018108651
Positive regulation of chromatin organization	100	−1.6223253	0.035416666
Response to alcohol	233	−1.6212864	0.002040816
Negative regulation of muscle cell differentiation	63	−1.6212797	0.023861172
Iron ion transmembrane transport	19	−1.6201888	0.040816326

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Positive regulation of smooth muscle cell apoptotic process	16	−1.6198796	0.023554605
Regulation of phagocytosis	92	−1.6196482	0.037924152
Amine biosynthetic process	39	−1.6191268	0.014403292
Negative regulation of protein serine threonine kinase activity	137	−1.6186186	0.024948025
Endonucleolytic cleavage involved in rRNA processing	15	−1.61818	0.049250536
Positive regulation of notch signaling pathway	55	−1.6164119	0.03629032
Regulation of intracellular protein transport	245	−1.6156065	0.024539877
Immunoglobulin production involved in immunoglobulin mediated immune response	54	−1.6148481	0.042424243
Positive regulation of cell cycle g1 s phase transition	54	−1.6140438	0.027027028
Intracellular lipid transport	46	−1.6138853	0.022633744
Nucleoside triphosphate biosynthetic process	83	−1.6135577	0.039337475
Activation of protein kinase A activity	18	−1.6132474	0.027613413
Positive regulation of translation	133	−1.6126299	0.04411765
3 UTR mediated mRNA stabilization	24	−1.6124866	0.040983606
Negative regulation of organelle organization	339	−1.6096703	0.030674847
Response to reactive oxygen species	217	−1.609409	0.004255319
Regulation of nucleotide metabolic process	120	−1.6090721	0.016563147
Neural precursor cell proliferation	137	−1.6088848	0.01622718
ERAD pathway	101	−1.6086744	0.03742204
Hematopoietic stem cell proliferation	25	−1.6077869	0.048582997
Response to starvation	195	−1.6073282	0.018556701
Regionalization	326	−1.6072775	0.024640657
Negative regulation of translational initiation	19	−1.6064686	0.04761905
Mononuclear cell differentiation	409	−1.6063935	0.036809817
Androgen receptor signaling pathway	40	−1.6053817	0.03125
Mitochondrion localization	47	−1.6052072	0.031446543
Mitochondrial calcium ion homeostasis	26	−1.6050293	0.035639413
Apoptotic mitochondrial changes	114	−1.6045432	0.04606526
Protein localization to cytoskeleton	58	−1.6033881	0.046938777
Regulation of androgen receptor signaling pathway	25	−1.6031978	0.03526971
Proton transmembrane transport	157	−1.6024008	0.037254903
Multicellular organism growth	130	−1.6021006	0.02096436
Regulation of notch signaling pathway	106	−1.6016703	0.031809144
Positive regulation of calcineurin mediated signaling	15	−1.6013751	0.028680688
Positive regulation of g1 s transition of mitotic cell cycle	43	−1.6011177	0.029227557
Negative regulation of DNA biosynthetic process	39	−1.6009995	0.024242423
Negative regulation of protein acetylation	23	−1.6000491	0.045738045
Regulation of cytoplasmic translation	21	−1.5988313	0.040983606
Positive regulation of transmembrane receptor protein serine threonine kinase signaling pathway	104	−1.5985142	0.02892562
Negative regulation of GTPase activity	45	−1.5985053	0.030737706
Female sex differentiation	111	−1.5973519	0.014314928

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Positive regulation of osteoclast differentiation	27	−1.5968063	0.034623217
Cellular response to virus	66	−1.5955181	0.049689442
Peptidyl tyrosine dephosphorylation	103	−1.5933717	0.035123967
Negative regulation of muscle cell apoptotic process	40	−1.593262	0.040816326
Myelin maintenance	17	−1.5928352	0.028806584
Response to nerve growth factor	50	−1.5924956	0.03773585
Positive regulation of histone methylation	36	−1.5924687	0.046511628
Thioester metabolic process	105	−1.5915738	0.03420523
Lymphoid progenitor cell differentiation	21	−1.5907227	0.04048583
Genetic imprinting	25	−1.5902236	0.041749503
Negative regulation of toll like receptor signaling pathway	42	−1.5901978	0.04042553
Positive regulation of receptor internalization	25	−1.5901623	0.03941909
Somite development	84	−1.5894107	0.031128405
Embryonic axis specification	36	−1.5883812	0.028513238
Protein localization to microtubule organizing center	35	−1.5879331	0.04347826
Regulation of intrinsic apoptotic signaling pathway in response to DNA damage	37	−1.5873759	0.025263159
Metal ion export	47	−1.5843056	0.02952756
Negative regulation of response to reactive oxygen species	16	−1.5825096	0.035714287
Regulation of autophagy	326	−1.5824143	0.046277665
Carbohydrate catabolic process	197	−1.5823156	0.036144577
Response to arsenic containing substance	30	−1.5822371	0.045738045
NADP metabolic process	35	−1.5813199	0.044660196
Hindbrain development	139	−1.581005	0.018480493
Negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	30	−1.5807744	0.025316456
Hematopoietic progenitor cell differentiation	160	−1.5803748	0.04208417
Endocrine hormone secretion	45	−1.5790174	0.030612245
Meiotic chromosome separation	25	−1.5780205	0.041749503
Positive regulation of regulated secretory pathway	51	−1.577401	0.02008032
Anterior posterior axis specification	49	−1.5769607	0.026639344
Regulation of transcription elongation from RNA polymerase ii promoter	30	−1.5767645	0.046464648
Modulation by symbiont of host process	37	−1.5763813	0.032323234
Positive regulation of voltage gated potassium channel activity	15	−1.5763658	0.034836065
Cell aging	108	−1.5754569	0.033195022
CD8 positive alpha beta t cell activation	27	−1.5752507	0.046511628
Response to peptide hormone	434	−1.5712157	0.014644352
Metanephric mesenchyme development	15	−1.5708829	0.044025157
Negative regulation of release of cytochrome c from mitochondria	17	−1.5704823	0.038383838
Response to cadmium ion	61	−1.5692194	0.042424243
Intracellular steroid hormone receptor signaling pathway	113	−1.5688676	0.045833334
Regulation of oxidoreductase activity	107	−1.5686047	0.008080808
Negative regulation of fibroblast proliferation	31	−1.5684894	0.048625793

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Regulation of membrane permeability	84	−1.5671988	0.04347826
Response to oxidative stress	434	−1.5665556	0.004032258
Multicellular organismal movement	56	−1.5649332	0.02004008
Diol biosynthetic process	22	−1.5614227	0.046938777
Polyol metabolic process	129	−1.5605205	0.016842104
Response to purine containing compound	143	−1.5595783	0.01268499
Positive regulation of JNK cascade	84	−1.5592804	0.043659043
Nucleoside diphosphate metabolic process	156	−1.5579473	0.03877551
Response to nutrient	165	−1.556976	0.008385744
Cellular response to glucagon stimulus	26	−1.5569177	0.04742268
Response to interleukin 6	50	−1.5549229	0.046908315
Muscle cell apoptotic process	74	−1.5515076	0.035416666
Neuron fate commitment	59	−1.5508404	0.021598272
Regulation of receptor internalization	53	−1.5506214	0.03950104
Regulation of DNA binding transcription factor activity	438	−1.5504847	0.023109244
Protein tetramerization	83	−1.5490031	0.008179959
Maintenance of protein localization in organelle	42	−1.5483346	0.044
Intrinsic apoptotic signaling pathway in response to DNA damage	100	−1.5483096	0.04526749
Signal transduction in absence of ligand	66	−1.5478947	0.028282829
Ventricular cardiac muscle cell action potential	34	−1.5475842	0.049407113
Response to insulin	278	−1.5474361	0.027083334
Regulation of neural precursor cell proliferation	81	−1.5457006	0.02892562
Hippocampus development	73	−1.5456679	0.027833002
Regulation of tumor necrosis factor mediated signaling pathway	62	−1.5453833	0.044354837
Positive regulation of cellular response to transforming growth factor beta stimulus	28	−1.5453763	0.048117153
Sulfur compound metabolic process	374	−1.5448781	0.032258064
Steroid hormone mediated signaling pathway	134	−1.5447112	0.041666668
Response to monosaccharide	194	−1.5444921	0.010330578
Amyloid beta clearance	36	−1.5441899	0.045544554
Cell death in response to oxidative stress	80	−1.543623	0.042
Male sex differentiation	153	−1.5436226	0.016260162
Negative regulation of cytokine production involved in inflammatory response	33	−1.5429053	0.037623763
Cardiac muscle cell membrane repolarization	36	−1.5423841	0.045360826
Oxidative demethylation	19	−1.5423373	0.04715128
Response to leukemia inhibitory factor	80	−1.5420749	0.03164557
Cellular response to toxic substance	119	−1.5418657	0.034
Response to carbohydrate	219	−1.5406684	0.008547009
Regulation of intrinsic apoptotic signaling pathway	157	−1.5387132	0.020703934
Regulation of ubiquitin dependent protein catabolic process	160	−1.5385683	0.038854804
Nucleoside bisphosphate metabolic process	139	−1.5381739	0.046558704
Stress activated protein kinase signaling cascade	274	−1.5378847	0.047034767

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Cellular response to steroid hormone stimulus	201	−1.5373834	0.023554605
Cellular response to alcohol	89	−1.5366545	0.04117647
Negative regulation of response to oxidative stress	21	−1.5358887	0.044624746
Response to fibroblast growth factor	145	−1.5350378	0.028397566
Regulation of release of cytochrome c from mitochondria	44	−1.5347651	0.04684318
Cellular response to starvation	156	−1.5301088	0.041152265
Response to radiation	446	−1.529972	0.028282829
Regulation of intracellular transport	346	−1.5296175	0.045081966
Regulation of protein catabolic process	381	−1.5295329	0.03285421
Carbohydrate derivative catabolic process	197	−1.5283238	0.022
Columnar cuboidal epithelial cell differentiation	80	−1.5272627	0.039583333
Organism emergence from protective structure	22	−1.5259644	0.036144577
Mitochondrial depolarization	22	−1.5251387	0.041841004
Cell fate commitment	249	−1.5250818	0.017094018
Negative regulation of myeloid cell differentiation	92	−1.5235796	0.032128513
Regulation of ATP biosynthetic process	20	−1.5229788	0.045738045
Blastoderm segmentation	19	−1.522152	0.037113402
Negative regulation of intracellular transport	56	−1.5220208	0.04024145
Regulation of Wnt signaling pathway	362	−1.5205027	0.04048583
Response to light stimulus	318	−1.5191535	0.016260162
Protein o linked mannosylation	18	−1.5190501	0.046421662
Negative regulation of cysteine type endopeptidase activity	78	−1.5176477	0.04233871
Intrinsic apoptotic signaling pathway in response to oxidative stress	44	−1.5169054	0.04897959
Protein dephosphorylation	323	−1.5148258	0.032128513
Temperature homeostasis	171	−1.5127823	0.042016808
Sulfur compound biosynthetic process	190	−1.5117128	0.03285421
Fibroblast growth factor receptor signaling pathway	111	−1.5098379	0.040733196
Fatty acid derivative metabolic process	81	−1.5094826	0.041501977
Skeletal muscle cell differentiation	64	−1.5077516	0.033613447
Protein stabilization	190	−1.5073259	0.035051547
Negative regulation of interleukin 17 production	21	−1.5053355	0.042372882
Response to extracellular stimulus	476	−1.5042822	0.01863354
Negative regulation of peptide secretion	72	−1.5039394	0.034632035
Cellular response to light stimulus	133	−1.5024246	0.04821803
Canonical Wnt signaling pathway	330	−1.5018495	0.044444446
Cellular response to chemical stress	337	−1.4991809	0.033755273
Development of primary female sexual characteristics	97	−1.4986604	0.030425964
Negative regulation of phosphorylation	396	−1.4978212	0.041753653
Negative regulation of transferase activity	287	−1.4965155	0.034907598
Reproductive system development	408	−1.4961774	0.022088353
Potassium ion homeostasis	29	−1.4957451	0.042424243

Table S1 *(continued)*

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Table S1 *(continued)*

Name	Size	NES	NOM P
Multicellular organism aging	31	−1.4946206	0.036809817
Regulation of cellular protein catabolic process	250	−1.4933577	0.04453441
Regulation of apoptotic signaling pathway	344	−1.4912292	0.038306452
Cellular oxidant detoxification	99	−1.4907516	0.037475344
Cellular response to peptide hormone stimulus	324	−1.4871088	0.026915114
Fatty acid derivative biosynthetic process	61	−1.4868658	0.041666668
Detoxification	135	−1.4867979	0.04950495
Anatomical structure homeostasis	466	−1.4843942	0.036217302
Cellular response to peptide	389	−1.4824512	0.036885247
Reactive oxygen species metabolic process	277	−1.4813846	0.03245436
Regulation of meiotic cell cycle	46	−1.4759362	0.046184737
Regulation of reproductive process	157	−1.4755288	0.020366598
Regulation of cysteine type endopeptidase activity	227	−1.4747247	0.041749503
Hormone mediated signaling pathway	193	−1.4683001	0.031055901
Response to oxygen levels	379	−1.4682676	0.03420523
Negative regulation of neuron death	195	−1.4679656	0.03909465
Endocrine system development	122	−1.4679238	0.040983606
Response to organophosphorus	129	−1.4660169	0.03164557
Negative regulation of reproductive process	57	−1.4654235	0.036585364
Odontogenesis of dentin containing tooth	84	−1.4640496	0.04526749
Signal transduction involved in regulation of gene expression	17	−1.4621644	0.04621849
Positive regulation of oligodendrocyte differentiation	22	−1.4590212	0.045454547
Cellular response to oxygen levels	225	−1.4552218	0.046184737
Regulation of production of small RNA involved in gene silencing by RNA	26	−1.4507045	0.04918033
Negative regulation of neuron differentiation	63	−1.4465864	0.044989776
Neuron death	341	−1.4461293	0.045548655
Cellular response to inorganic substance	215	−1.4384733	0.04517454
Response to toxic substance	236	−1.4381549	0.044715445
Negative regulation of anion transport	208	−1.4282134	0.04121475
Response to steroid hormone	330	−1.420433	0.049586777
Response to drug	359	−1.4180926	0.031914894
Response to estradiol	125	−1.4070609	0.044871796

STAD, stomach adenocarcinoma; JNK, c-Jun NH2-terminal kinase.

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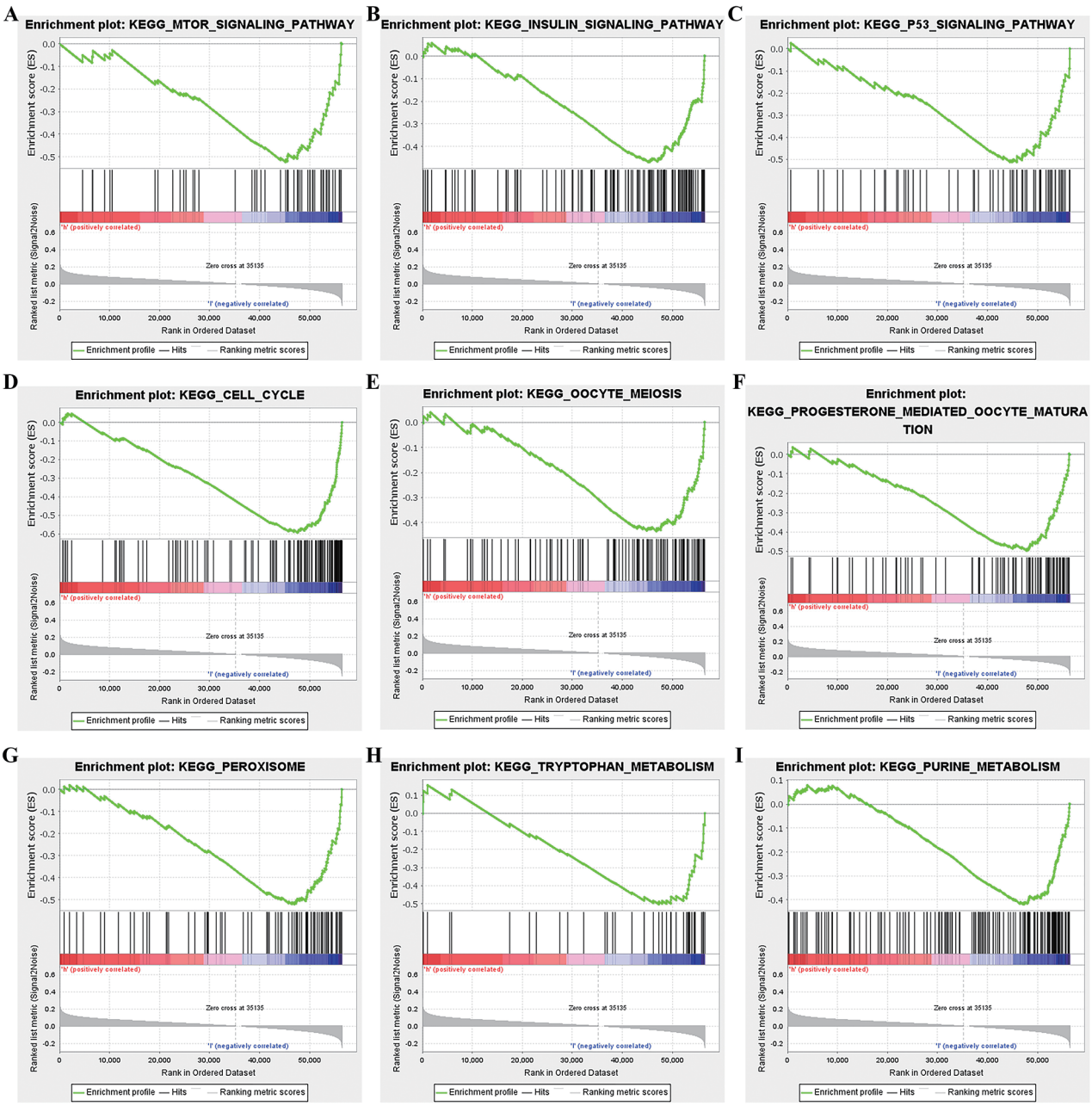

Figure S1 The signaling mechanisms of ITGB1-DT involved in STAD progression. STAD, stomach adenocarcinoma.

https://dx.doi.org/10.21037/jgo-22-233

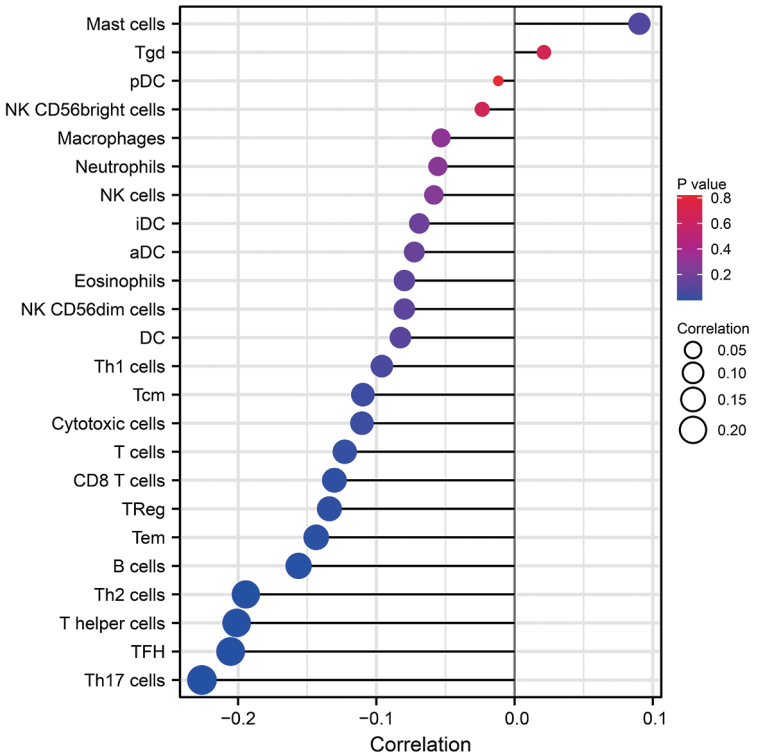

Figure S2 ITGB1-DT expression is correlated with immune infiltrated cells in STAD. STAD, stomach adenocarcinoma.

https://dx.doi.org/10.21037/jgo-22-233