

Table S1. Clinical parameters of TCGA COAD cohort

Variables	Patients (n=438)	MST(days)	HR(85%CI)	Log-rank P
Gender				0.545
Female	204	NA	1	
Male	234	2475	1.131(0.759-1.686)	
Age (years)§				0.112
<65	168	NA	1	
≥65	268	2475	1.420(0.919-2.194)	
Tumor stage £				<0.0001
I	73	NA	1	
II	167	2821	2.240(0.781-6.421)	
III	126	NA	4.068(1.434-11.538)	
IV	61	858	11.291(3.980-32.026)	
Tumor stage				<0.0001
I+II	240	3042	1	
III+IV	187	1711	3.097(2.009-4.772)	
STXBP5AS1				0.035
Low expression	219	2821	1	
High expression	219	2532	0.648(0.431-0.973)	

Notes: §Information of age was unavailable in 2 patients; £Information of tumor stage was unavailable in 11 patients.

Table S2. Co-expressed proteins encoding genes list of STXBP5-AS1 in COAD tumor tissues (the correlation coefficient ranked top20 up-regulated genes and down-regulated genes).

ID	ID	R	P Value
STXBP5-AS1	BIN1	-0.302	0.009133
STXBP5-AS1	PSMC4	-0.29	0.01205
STXBP5-AS1	VAV2	-0.286	0.013191
STXBP5-AS1	GNPDA1	-0.285	0.013491
STXBP5-AS1	POLDIP2	-0.281	0.014752
STXBP5-AS1	RUVBL1	-0.276	0.016472
STXBP5-AS1	AIFM2	-0.275	0.016837
STXBP5-AS1	SAE1	-0.274	0.017209
STXBP5-AS1	SLC25A39	-0.273	0.017588
STXBP5-AS1	LRRC20	-0.27	0.018768
STXBP5-AS1	COPRS	-0.269	0.019177
STXBP5-AS1	TPD52L2	-0.266	0.02045
STXBP5-AS1	BCL2L12	-0.266	0.02045
STXBP5-AS1	C10orf35	-0.264	0.021339
STXBP5-AS1	SMYD5	-0.259	0.023711
STXBP5-AS1	ATIC	-0.257	0.024722
STXBP5-AS1	CCT7	-0.256	0.025241
STXBP5-AS1	CHCHD6	-0.256	0.025241
STXBP5-AS1	IFITM3	-0.255	0.02577
STXBP5-AS1	GRINA	-0.255	0.02577
STXBP5-AS1	TMEM210	0.542	3.05E-05
STXBP5-AS1	RAP1GAP	0.546	2.65E-05
STXBP5-AS1	CCDC60	0.552	2.14E-05
STXBP5-AS1	GNE	0.552	2.14E-05
STXBP5-AS1	TCN1	0.562	1.49E-05
STXBP5-AS1	STXBP5	0.563	1.44E-05
STXBP5-AS1	FAM174B	0.57	1.11E-05
STXBP5-AS1	ARFGEF3	0.577	8.56E-06
STXBP5-AS1	CAPN9	0.577	8.56E-06
STXBP5-AS1	NEURL1	0.578	8.25E-06
STXBP5-AS1	LRRIQ4	0.584	6.58E-06
STXBP5-AS1	HEPACAM2	0.584	6.58E-06
STXBP5-AS1	ADAM2	0.585	6.34E-06
STXBP5-AS1	PLD1	0.609	2.51E-06
STXBP5-AS1	RHBDL3	0.614	2.06E-06
STXBP5-AS1	ANO7	0.636	8.47E-07
STXBP5-AS1	B3GNT6	0.653	4.18E-07
STXBP5-AS1	SMIM14	0.66	3.10E-07
STXBP5-AS1	GALNT8	0.668	2.20E-07
STXBP5-AS1	REP15	0.691	8.06E-08

Table S3. Function enrichment results of STXBP5-AS1 co-expressed genes.

Category	Term	Count	PValue
KEGG_PATHWAY	hsa00512:Mucin type O-Glycan biosynthesis	10	1.17E-06
KEGG_PATHWAY	hsa04141:Protein processing in endoplasmic reticulum	18	1.69E-04
KEGG_PATHWAY	hsa05014:Amyotrophic lateral sclerosis (ALS)	7	0.010082
KEGG_PATHWAY	hsa04922:Glucagon signaling pathway	10	0.011098
KEGG_PATHWAY	hsa04024:cAMP signaling pathway	15	0.015622
KEGG_PATHWAY	hsa04144:Endocytosis	17	0.017592
KEGG_PATHWAY	hsa04924:Renin secretion	7	0.030995
KEGG_PATHWAY	hsa04022:cGMP-PKG signaling pathway	12	0.033195
KEGG_PATHWAY	hsa05031:Amphetamine addiction	7	0.035347
GOTERM_CC_DIRECT	GO:0000139~Golgi membrane	57	6.72E-10
GOTERM_CC_DIRECT	GO:0016020~membrane	136	3.05E-08
GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	66	2.43E-07
GOTERM_MF_DIRECT	GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity	8	7.56E-06
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	37	6.09E-05
GOTERM_MF_DIRECT	GO:0005515~protein binding	399	7.91E-05
GOTERM_CC_DIRECT	GO:0005829~cytosol	166	2.81E-04
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	40	4.92E-04
GOTERM_BP_DIRECT	GO:0016266~O-glycan processing	10	5.27E-04
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	51	0.001341
GOTERM_BP_DIRECT	GO:0006486~protein glycosylation	13	0.001641
GOTERM_MF_DIRECT	GO:0005524~ATP binding	83	0.00175
GOTERM_BP_DIRECT	GO:0006047~UDP-N-acetylglucosamine metabolic process	4	0.001887
GOTERM_CC_DIRECT	GO:0070382~exocytic vesicle	5	0.002188
GOTERM_BP_DIRECT	GO:0051056~regulation of small GTPase mediated signal transduction	14	0.002429
GOTERM_MF_DIRECT	GO:0005085~guanyl-nucleotide exchange factor activity	13	0.002602
GOTERM_MF_DIRECT	GO:0017137~Rab GTPase binding	14	0.002676
GOTERM_MF_DIRECT	GO:0004571~mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	4	0.003027
GOTERM_MF_DIRECT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	10	0.003428
GOTERM_BP_DIRECT	GO:0030193~regulation of blood coagulation	5	0.003759
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	23	0.003909
GOTERM_BP_DIRECT	GO:0035023~regulation of Rho protein signal transduction	10	0.004481
GOTERM_MF_DIRECT	GO:0030246~carbohydrate binding	17	0.005274
GOTERM_BP_DIRECT	GO:0006895~Golgi to endosome transport	5	0.005751
GOTERM_BP_DIRECT	GO:0035265~organ growth	4	0.005922

GOTERM_CC_DIRECT	GO:0005737~cytoplasm	234	0.006491
GOTERM_CC_DIRECT	GO:0042589~zymogen granule membrane	4	0.007626
GOTERM_CC_DIRECT	GO:0030667~secretory granule membrane	5	0.007976
GOTERM_BP_DIRECT	GO:0045921~positive regulation of exocytosis	5	0.008344
GOTERM_BP_DIRECT	GO:0051402~neuron apoptotic process	6	0.008857
GOTERM_BP_DIRECT	GO:0034976~response to endoplasmic reticulum stress	9	0.009159
GOTERM_BP_DIRECT	GO:0048208~COPII vesicle coating	8	0.0098
GOTERM_BP_DIRECT	GO:0007399~nervous system development	21	0.009877
GOTERM_BP_DIRECT	GO:0045332~phospholipid translocation	5	0.009887
GOTERM_MF_DIRECT	GO:0005351~sugar:proton symporter activity	4	0.010556
GOTERM_BP_DIRECT	GO:0006888~ER to Golgi vesicle-mediated transport	14	0.010705
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	34	0.011141
GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	48	0.011974
GOTERM_BP_DIRECT	GO:0006886~intracellular protein transport	18	0.012332
GOTERM_BP_DIRECT	GO:0043087~regulation of GTPase activity	8	0.013679
GOTERM_CC_DIRECT	GO:0005811~lipid particle	8	0.013868
GOTERM_MF_DIRECT	GO:0030742~GTP-dependent protein binding	5	0.01402
GOTERM_MF_DIRECT	GO:0016740~transferase activity	10	0.014209
GOTERM_BP_DIRECT	GO:0045053~protein retention in Golgi apparatus	3	0.014293
GOTERM_MF_DIRECT	GO:0030618~transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity	3	0.014605
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	15	0.014847
GOTERM_BP_DIRECT	GO:0007257~activation of JUN kinase activity	6	0.015956
GOTERM_MF_DIRECT	GO:0005096~GTPase activator activity	20	0.016462
GOTERM_BP_DIRECT	GO:0060527~prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	3	0.020885
GOTERM_BP_DIRECT	GO:1903799~negative regulation of production of miRNAs involved in gene silencing by miRNA	3	0.020885
GOTERM_BP_DIRECT	GO:0060348~bone development	6	0.023801
GOTERM_BP_DIRECT	GO:0009791~post-embryonic development	8	0.024522
GOTERM_CC_DIRECT	GO:0030173~integral component of Golgi membrane	7	0.024596
GOTERM_BP_DIRECT	GO:0007030~Golgi organization	8	0.0262
GOTERM_MF_DIRECT	GO:0046332~SMAD binding	6	0.027218
GOTERM_MF_DIRECT	GO:0005544~calcium-dependent phospholipid binding	7	0.027286
GOTERM_CC_DIRECT	GO:0014069~postsynaptic density	14	0.027686
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	24	0.027891
GOTERM_MF_DIRECT	GO:0019902~phosphatase binding	6	0.032398
GOTERM_CC_DIRECT	GO:0043195~terminal bouton	7	0.032852

GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	7	0.034681
GOTERM_CC_DIRECT	GO:0030054~cell junction	27	0.034955
GOTERM_BP_DIRECT	GO:0009306~protein secretion	5	0.035723
GOTERM_CC_DIRECT	GO:0071141~SMAD protein complex	3	0.036118
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	15	0.03637
GOTERM_BP_DIRECT	GO:0050767~regulation of neurogenesis	4	0.036781
GOTERM_BP_DIRECT	GO:0060314~regulation of ryanodine-sensitive calcium-release channel activity	4	0.036781
GOTERM_BP_DIRECT	GO:0006623~protein targeting to vacuole	3	0.037001
GOTERM_BP_DIRECT	GO:0051963~regulation of synapse assembly	3	0.037001
GOTERM_BP_DIRECT	GO:0072659~protein localization to plasma membrane	7	0.037108
GOTERM_MF_DIRECT	GO:0043023~ribosomal large subunit binding	3	0.037774
GOTERM_BP_DIRECT	GO:0070059~intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	5	0.039429
GOTERM_BP_DIRECT	GO:0002931~response to ischemia	5	0.039429
GOTERM_CC_DIRECT	GO:0016529~sarcoplasmic reticulum	5	0.041637
GOTERM_BP_DIRECT	GO:0006491~N-glycan processing	4	0.042042
GOTERM_CC_DIRECT	GO:0016023~cytoplasmic, membrane-bounded vesicle	11	0.042886
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	39	0.045884
GOTERM_BP_DIRECT	GO:0032330~regulation of chondrocyte differentiation	3	0.046353
GOTERM_MF_DIRECT	GO:0047144~2-acylglycerol-3-phosphate O-acyltransferase activity	3	0.047308
GOTERM_MF_DIRECT	GO:0030145~manganese ion binding	6	0.047887

Table S4. Survival analysis results of STXBP5-AS1 co-expressed genes in COAD (Only gene list with P<0.05 is shown).

ID	P	HR	Low 95%CI	High 95%CI
EVI5	0.002106	0.502696	0.324275	0.779286
ABCA5	0.002836	0.523879	0.342671	0.800911
CCNJL	0.005046	0.548641	0.360626	0.834678
ZBTB7C	0.005864	0.551929	0.361638	0.842349
LRBA	0.007459	0.560966	0.367303	0.856738
FAM167A	0.007667	0.563147	0.369243	0.858877
LPCAT2	0.00824	0.560875	0.365231	0.86132
COTL1	0.00898	1.747004	1.149586	2.654887
BMPR1B	0.009567	1.74226	1.144804	2.65152
GALNT7	0.009695	0.56936	0.37156	0.872459
USP53	0.010274	0.577029	0.379165	0.878147
APAF1	0.010884	0.574624	0.375129	0.880211
PSME3	0.011093	0.583492	0.385016	0.88428
KIAA0319L	0.011404	0.582529	0.383281	0.885356
RALGPS2	0.011436	0.584981	0.386086	0.886337
SHC2	0.012012	1.70986	1.125071	2.598609
AFF1	0.012454	0.588305	0.388063	0.891873
CLCA1	0.013016	0.581445	0.379008	0.892009
B3GNT6	0.013865	0.586306	0.383209	0.897041
DSG2	0.014211	0.592215	0.389589	0.900228
EDEM3	0.01608	0.601405	0.397516	0.90987
TYSND1	0.017058	1.662661	1.094924	2.524779
GIF	0.01848	0.603991	0.397062	0.918762
TPD52L1	0.02326	1.627088	1.068575	2.477519
CD81	0.024003	1.611978	1.06487	2.44018
REP15	0.029968	0.62727	0.411677	0.955768
GCC2	0.030666	0.631947	0.416808	0.958133
CCDC62	0.031351	0.632782	0.41715	0.959876
MFSD6	0.032487	0.631068	0.413839	0.962323
DENND1B	0.035033	0.641474	0.42452	0.969306
SLC35B3	0.035618	0.639652	0.421636	0.970399
ADGRL3	0.036186	0.640228	0.42183	0.971699
KIAA1147	0.038056	0.641952	0.422291	0.975873
SCAMP1	0.038236	0.646226	0.427611	0.976608
NFS1	0.038725	0.645601	0.426362	0.977576
PCSK1	0.038742	0.645176	0.425799	0.977578
CHD9	0.04042	0.645762	0.425046	0.981089
SEC24A	0.041295	0.648329	0.427586	0.983031
C10orf35	0.041553	1.539204	1.016645	2.330361
TSPAN13	0.042475	1.53412	1.014634	2.319579
STXBP5	0.047552	0.652801	0.428116	0.995407
CREB3L1	0.047625	1.524007	1.00442	2.312377

Table S5. GSEA analysis between low- and high-STXBP5-AS1 phenotype using the c2 reference gene set.

NAME	S	ES	NE	NO	FD
	I		S	M	R
	Z			p-va	q-v
	E			l	al
HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP	6	0.5	1.8	0.00	0.1
	6	445	064	824	279
		16	34	7	82
NADERI_BREAST_CANCER_PROGNOSIS_UP	5	0.5	1.8	0.01	0.1
	0	785	075	632	285
		6	27	7	77
REACTOME_MRNA_CAPPING	2	0.6	1.8	0.00	0.1
	9	140	183	207	285
		67	18	9	98
REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS	6	0.5	1.8	0.01	0.1
	3	859	089	875	288
		12	23		02
REACTOME_STABILIZATION_OF_P53	5	0.6	1.7	0.02	0.1
	5	366	947	286	296
		58	82	9	98
REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS	6	0.6	1.8	0.01	0.1
	6	104	094	476	300
		56	1	8	37
REACTOME_DNA_REPLICATION_PRE_INITIATION	8	0.6	1.8	0.01	0.1
	4	545	188	257	300
		6	06	9	39
REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL	1	0.6	1.8	0.01	0.1
	8	381	233	836	301
	9	16	47	7	8
KEGG_HOMOLOGOUS_RECOMBINATION	2	0.6	1.7	0.01	0.1
	8	352	931	171	302
		65	06	9	11
REACTOME_HEDGEHOG_OFF_STATE	1	0.4	1.8	0.01	0.1
	1	634	197	434	307
	1	66	78	4	46
BASAKI_YBX1_TARGETS_UP	2	0.5	1.8	0.02	0.1
	8	103	145	5	310
	0	87	45		95
KIM_ALL_DISORDERS_DURATION_CORR_DN	1	0.5	1.8	0.02	0.1
	4	843	242	028	310
	0	49	87	4	98
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	6	0.6	1.7	0.01	0.1
	0	741	948	244	312
		15	4	8	55

MATTIOLI_MGUS_VS_PCL	9	0.4	1.8	0.00	0.1
	9	999	113	833	312
		03	82	3	85
REACTOME_DEGRADATION_OF_DVL	5	0.6	1.8	0.01	0.1
	6	425	206	242	316
		23	39	2	3
SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	4	0.6	1.7	0.00	0.1
	6	033	973	806	316
		48	94	5	58
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION	5	0.5	1.8	0.00	0.1
	7	280	095	404	317
		03	63		68
REACTOME_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTRY_AND_IN_EARLY_MITOSIS	5	0.6	1.7	0.01	0.1
	4	641	984	659	321
		46	14	8	34
REACTOME_DNA_REPLICATION	1	0.6	1.8	0.00	0.1
	2	209	123	833	321
	6	89	21	3	63
GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN	3	0.5	1.8	0.01	0.1
	1	836	250	571	321
	6	81	82	7	68
REACTOME_DEGRADATION_OF_AXIN	5	0.6	1.7	0.02	0.1
	4	268	951	249	326
		05	06	5	11
GRADE_COLON_AND_RECTAL_CANCER_UP	2	0.5	1.7	0.01	0.1
	8	131	896	239	326
	7	53	22	7	52
VECCHI_GASTRIC_CANCER_EARLY_UP	4	0.4	1.7	0.02	0.1
	1	985	448	183	328
	5	89	65	4	66
REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	6	0.5	1.7	0.01	0.1
	9	134	455	212	331
		52	86	1	99
LEE_METASTASIS_AND_RNA_PROCESSING_UP	1	0.7	1.7	0.00	0.1
	6	204	989	200	333
		57	51	4	61
RHODES_UNDIFFERENTIATED_CANCER	6	0.6	1.8	0.01	0.1
	8	567	001	452	336
		43	6	3	64
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	7	0.6	1.7	0.01	0.1
	0	525	873	476	337
		67	42	8	59
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	8	0.6	1.7	0.02	0.1
	5	144	637	096	338
		74	75	4	95
WALLACE_JAK2_TARGETS_UP	2	0.6	1.7	0.01	0.1

	2	518	469	814	339
		37	17	5	31
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PROMOTER	2	0.6	1.8	0.00	0.1
	8	006	253	614	340
		92	47	8	2
TOMIDA_METASTASIS_UP	2	0.5	1.7	0.01	0.1
	6	863	456	467	342
		37	54	5	5
REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS	1	0.6	1.7	0.03	0.1
	6	028	646	125	343
	9	62	23		74
PRAMOONJAGO_SOX4_TARGETS_DN	4	0.5	1.7	0.01	0.1
	7	589	472	670	347
		16	31	1	35
REACTOME_BUTYRATE_RESPONSE_FACTOR_1_BRF1_BINDS_AND_DESTABILIZES_MRNA	1	0.6	1.7	0.01	0.1
	7	223	480	024	349
		65	39	6	32
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES	6	0.5	1.7	0.01	0.1
	1	139	651	609	349
		14	77	7	57
SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC	1	0.5	1.8	0.00	0.1
	0	295	259	613	354
	5	27	73	5	99
REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	3	0.6	1.7	0.00	0.1
	8	105	548	612	356
		48	83	2	23
REACTOME_INFLUENZA_INFECTION	1	0.5	1.7	0.04	0.1
	5	772	483	8	357
	4	74	81		32
REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER	8	0.5	1.7	0.01	0.1
	4	164	412	919	357
		99	44		84
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	2	0.6	1.7	0.01	0.1
	8	230	515	927	359
		41	72	2	39
REACTOME_ACTIVATION_OF_APC_C_AND_APC_C:CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	7	0.6	1.7	0.01	0.1
	5	368	654	910	36
		38	61	8	
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	2	0.5	1.7	0.01	0.1
	3	884	565	414	361
		16	92	1	37
REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRIC_CCT_IN_ACTIN_AND_TUBULIN_FOLDING	3	0.5	1.7	0.02	0.1
	3	993	502	132	362
		19	12	2	25
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	5	0.6	1.7	0.02	0.1
	3	642	585	484	362

		95	3	5	98
REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	5	0.6	1.7	0.02	0.1
	4	553	553	074	363
		12	3	7	22
REACTOME_DUAL_INCISION_IN_TC_NER	6	0.5	1.7	0.00	0.1
	5	385	662	630	363
		31	62	3	42
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	2	0.5	1.7	0.00	0.1
	8	755	672	618	364
		79	71	6	3
REACTOME_PCP_CE_PATHWAY	9	0.5	1.7	0.02	0.1
	1	143	838	306	364
		93	03	1	57
REACTOME_S_PHASE	1	0.5	1.7	0.02	0.1
	6	487	485	697	367
	0	15	63	1	05
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN	1	0.7	1.7	<0.0	0.1
	5	260	571	1	367
		57	24		61
KEGG_DNA_REPLICATION	3	0.6	1.7	0.01	0.1
	6	794	518	237	367
		46	63	1	99
REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	6	0.6	1.7	0.02	0.1
	1	106	524	725	373
		03	15	4	55
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	2	0.6	1.7	0.01	0.1
	6	454	587	565	373
		27	25	6	66
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13	1	0.5	1.7	0.02	0.1
	5	729	387	074	375
	9	35	45	7	01
KEGG_PYRIMIDINE_METABOLISM	9	0.5	1.8	0.00	0.1
	7	112	261	635	376
		8	73	6	89
REACTOME_REGULATION_OF_APOPTOSIS	5	0.6	1.7	0.02	0.1
	2	448	674	669	376
		1	17	4	96
CROONQUIST_NRAS_SIGNALING_DN	7	0.6	1.7	0.01	0.1
	0	864	747	652	378
		85	15	9	63
REACTOME_SIGNALING_BY_FGFR2_III_A_TM	1	0.5	1.7	0.00	0.1
	9	906	366	619	378
		4	76	8	85
REACTOME_CYCLIN_A:CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY	8	0.5	1.7	0.02	0.1
	5	775	811	531	379
		56	26	6	49

REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVIT	6	0.5	1.7	0.03	0.1
Y	8	393	318	636	379
		61	48	4	79
REACTOME_NUCLEOBASE_BIOSYNTHESIS	1	0.6	1.7	0.01	0.1
	5	903	300	818	379
		02	02	2	89
BHAT_ESR1_TARGETS_VIA_AKT1_UP	2	0.4	1.7	0.00	0.1
	7	519	592	402	380
	7	32	73	4	06
REACTOME_RNA_POLYMERASE_II_PRE_TRANSCRIPTION_EVEN	8	0.4	1.7	0.01	0.1
TS	0	851	308	4	381
		91	2		52
REACTOME_MITOTIC_G2_G2_M_PHASES	1	0.4	1.7	0.01	0.1
	9	642	369	070	385
	8	01	98	7	64
REACTOME_PIWI_INTERACTING_RNA_PIRNA_BIOGENESIS	2	0.5	1.7	0.00	0.1
	5	516	267	792	385
		92	41	1	68
BURTON_ADIPOGENESIS_PEAK_AT_16HR	4	0.6	1.7	0.02	0.1
	1	086	689	636	386
		18	2	9	87
REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	1	0.6	1.7	0.01	0.1
	8	416	256	234	386
		33	97	6	97
REACTOME_METABOLISM_OF_POLYAMINES	5	0.6	1.7	0.03	0.1
	8	186	185	118	387
		96	63	5	29
LU_EZH2_TARGETS_UP	2	0.5	1.7	0.01	0.1
	6	070	751	803	388
	5	21	55	6	68
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	3	0.4	1.7	0.02	0.1
	0	468	191	049	389
	4	79	97	2	39
CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	1	0.5	1.7	0.01	0.1
	3	134	675	871	389
	9	31	39	1	69
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3	9	0.4	1.7	0.01	0.1
	5	453	318	673	390
		82	66	6	08
LE_NEURONAL_DIFFERENTIATION_DN	1	0.6	1.7	0.01	0.1
	8	522	345	4	392
		63	4		68
ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP	4	0.5	1.7	0.02	0.1
	0	284	198	886	392
		29	29	6	9
REACTOME_TRANSLATION	2	0.5	1.7	0.04	0.1

	9	971	270	106	392
	1	85	15	8	93
SHEPARD_CRUSH_AND_BURN_MUTANT_UP	1	0.4	1.7	0.00	0.1
	9	348	279	829	393
	7	7	3	9	16
REACTOME_PTEN_REGULATION	1	0.4	1.7	0.01	0.1
	3	446	694	239	395
	6	86	9	7	08
REACTOME_HEDGEHOG_ON_STATE	8	0.4	1.7	0.01	0.1
	5	686	150	677	397
		85	57	1	63
WONG_EMBRYONIC_STEM_CELL_CORE	3	0.5	1.7	0.02	0.1
	2	705	756	714	397
	8	02	9		77
REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS	5	0.5	1.7	0.01	0.1
	7	720	321	417	397
		18	43		85
REACTOME_HIV_INFECTION	2	0.4	1.7	0.02	0.1
	2	660	200	132	400
	9	2	71	2	56
BASSO_B_LYMPHOCYTE_NETWORK	1	0.4	1.8	0.00	0.1
	4	869	261	642	400
	1	74	97	4	98
REACTOME_MITOTIC_G1_G1_S_PHASES	1	0.5	1.7	0.03	0.1
	4	379	208	601	401
	9	57	57	7	15
JAIN_NFKB_SIGNALING	7	0.4	1.7	<0.0	0.1
	2	678	766	1	402
		43	88		08
REACTOME_FGFR2_ALTERNATIVE_SPLICING	2	0.5	1.7	0.01	0.1
	7	716	163	214	403
		41	68	6	38
REACTOME_MITOCHONDRIAL_TRANSLATION	9	0.7	1.7	0.01	0.1
	4	001	136	960	403
		41	82	8	71
XU_CREBBP_TARGETS_UP	2	0.5	1.7	0.00	0.1
	1	423	125	809	406
		22	91	7	57
REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY	5	0.6	1.7	0.02	0.1
	5	241	697	282	407
		62	93	2	1
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	2	0.4	1.7	0.00	0.1
	0	015	150	847	407
	1	23	62	5	11
KEGG_PROTEASOME	4	0.6	1.7	0.03	0.1
	3	758	220	125	407

		94	72		69
DANG_MYC_TARGETS_UP	1	0.5	1.7	0.01	0.1
	2	788	774	709	408
	8	6	39	4	14
REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX	8	0.5	1.7	0.03	0.1
	2	284	321	640	408
		56	64	3	59
REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	4	0.5	1.7	0.02	0.1
	4	639	209	066	409
		04	7	1	77
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	1	0.5	1.7	0.02	0.1
	3	060	223	754	413
	0	27	76	2	93
REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR_TC_NER	7	0.5	1.8	0.00	0.1
	8	559	270	212	416
		7	38	3	62
RAMASWAMY_METASTASIS_UP	6	0.4	1.7	0.01	0.1
	4	734	040	821	417
		43	96	9	29
REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	6	0.6	1.7	0.01	0.1
	0	502	701	910	418
		86	7	8	4
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	3	0.6	1.7	0.03	0.1
	7	331	045	984	421
		72	66	1	73
REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	1	0.6	1.6	0.01	0.1
	6	808	986	609	423
		6	56	7	87
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	4	0.6	1.6	0.02	0.1
	2	029	994	972	424
		63	28	4	
MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP	1	0.5	1.7	0.02	0.1
	0	022	101	464	424
	6	95	65	1	26
REACTOME_RRNA_PROCESSING	1	0.6	1.8	0.01	0.1
	9	332	283	836	425
	9	51	05	7	44
REACTOME_COMPLEX_I_BIOGENESIS	5	0.6	1.7	0.02	0.1
	5	770	000	674	425
		32	54	9	85
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	1	0.7	1.7	0.01	0.1
	8	341	048	980	427
		38	62	2	3
REACTOME_EXTENSION_OF_TELOMERES	3	0.6	1.7	0.01	0.1
	0	581	019	419	432
		21	92	9	62

REACTOME_HIV_LIFE_CYCLE	1	0.4	1.7	0.03	0.1
	4	576	002	666	432
	8	5	44		77
MOOTHA_VOXPPOS	7	0.6	1.7	0.02	0.1
	2	728	085	658	432
		25	52	5	83
ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP	8	0.5	1.8	0.00	0.1
	3	237	295	203	434
		99	46	3	54
BURTON_ADIPOGENESIS_5	1	0.5	1.7	0.03	0.1
	0	215	009	658	434
	9	11	23	5	89
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	1	0.6	1.7	0.04	0.1
	5	604	049	421	435
	1	37	51	1	19
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_DN	5	0.5	1.8	0.00	0.1
	4	809	312	801	438
		58	7	6	61
GROSS_HYPOXIA_VIA_HIF1A_UP	7	0.4	1.7	0.01	0.1
	3	700	051	252	442
		87	43	6	28
KEGG_BASE_EXCISION_REPAIR	3	0.5	1.7	0.02	0.1
	3	750	055	626	447
		79	47	3	17
WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP	1	0.5	1.6	0.02	0.1
	9	989	953	231	449
		86	11	2	35
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	6	0.6	1.8	0.01	0.1
	7	683	322	260	455
		84	13	5	07
ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN	2	0.5	1.7	0.02	0.1
	9	532	056	386	455
		74	4	1	64
IRITANI_MAD1_TARGETS_DN	4	0.6	1.8	0.00	0.1
	1	498	337	8	461
		44	82		66
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	8	0.5	1.8	0.01	0.1
	6	799	346	295	479
		04	02	9	91
REACTOME_HIV_ELONGATION_ARREST_AND_RECOVERY	3	0.6	1.8	0.00	0.1
	2	206	363	603	485
		01	93	6	41
REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME	5	0.5	1.6	0.03	0.1
	8	808	903	651	488
		44	2	1	88
REACTOME_SIGNALING_BY_NOTCH4	8	0.4	1.6	0.02	0.1

	2	866	908	375	490
		81	92	8	54
BILD_MYC_ONCOGENIC_SIGNATURE	1	0.5	2.0	<0.0	0.1
	9	087	816	1	495
	5	96	9		34
REACTOME_FORMATION_OF_HIV_ELONGATION_COMPLEX_IN_THE_ABSENCE_OF_HIV_TAT	4	0.5	1.8	0.00	0.1
	4	888	367	828	511
		14	2	2	57
PID_MYC_ACTIV_PATHWAY	7	0.5	1.8	0.01	0.1
	9	321	445	455	528
		98	31	3	41
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	7	0.6	1.8	0.00	0.1
	1	419	468	625	534
		71	7		14
NUTT_GBM_VS_AO_GLIOMA_DN	4	0.5	1.8	0.00	0.1
	4	487	372	400	535
		2	88	8	63
REACTOME_TRNA_PROCESSING	1	0.5	1.8	0.00	0.1
	0	832	410	410	545
	6	19	24	7	96
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	4	0.5	1.8	0.00	0.1
	1	494	385	609	548
		65	78	8	06
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	2	0.5	1.6	0.03	0.1
	6	721	820	080	548
		97	17	1	27
BENPORATH_MYC_TARGETS_WITH_EBOX	2	0.4	1.6	0.01	0.1
	2	009	832	057	551
	1	03	23	1	95
BARIS_THYROID_CANCER_UP	2	0.5	1.6	0.02	0.1
	4	571	820	096	556
		44	9	4	57
REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY	7	0.5	1.6	0.03	0.1
	2	239	834	347	558
		43	12	3	67
REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA	5	0.6	1.8	0.01	0.1
	4	821	469	263	570
		58		2	44
FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	4	0.7	1.9	<0.0	0.1
	8	333	946	1	570
		97	7		55
REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	4	0.6	1.8	0.00	0.1
	2	263	489	409	578
		34	13	8	15
REACTOME_REGULATION_OF_RAS_BY_GAPS	6	0.5	1.6	0.03	0.1
	7	216	787	797	578

		72	2	5	15
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNT	1	0.6	1.6	0.04	0.1
HESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTI	0	251	766	123	584
ON_BY_UNCOUPLING_PROTEINS	5	59	58	7	67
AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP	2	0.4	1.6	0.01	0.1
	8	266	772	574	586
	8	8	67	8	49
CHICAS_RB1_TARGETS_LOW_SERUM	8	0.4	1.6	0.02	0.1
	8	879	755	306	588
		87	07	1	93
REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AF	7	0.6	1.8	0.01	0.1
TER_G2_CHECKPOINT	7	162	530	271	590
		9	69	2	33
REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIV	8	0.6	1.8	0.00	0.1
E_STATE	9	386	501	626	598
		69	49	3	35
WHITEFORD_PEDIATRIC_CANCER_MARKERS	1	0.5	1.6	0.04	0.1
	1	829	733	573	605
	4	83	23	8	48
REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA	7	0.5	1.6	0.04	0.1
	4	291	685	228	606
		29	85	3	69
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	4	0.6	2.0	0.00	0.1
	9	252	041	205	607
		95	13	3	4
REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_	2	0.7	1.8	<0.0	0.1
IN_THE_ABSENCE_OF_TAT	3	033	685	1	610
		7	85		09
BAKKER_FOXO3_TARGETS_DN	1	0.3	1.6	0.00	0.1
	6	671	705	409	611
	4	42	23	8	88
REACTOME_TRISTETRAPROLIN_TTP_ZFP36_BINDS_AND_DESTA	1	0.6	1.6	0.03	0.1
BILIZES_MRNA	7	029	719	206	613
		95	49	4	1
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOU	4	0.6	1.6	0.04	0.1
S_ANTIGENS_ENDOSOMES	8	100	694	722	614
		7	34	8	89
REACTOME_ABC_TRANSPORTER_DISORDERS	7	0.5	1.6	0.03	0.1
	6	057	686	885	615
		53	23	5	02
KEGG_SPLICEOSOME	1	0.5	1.8	0.01	0.1
	2	799	538	446	620
	6	36	1	3	54
AMIT_SERUM_RESPONSE_480_MCF10A	3	0.5	1.6	0.01	0.1
	7	132	658	980	621
		72	11	2	82

BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP	2	0.3	1.6	0.00	0.1
	0	983	665	193	622
	7	81	47	1	09
ODONNELL_METASTASIS_DN	2	0.6	1.8	<0.0	0.1
	4	191	706	1	627
		63	34		48
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	1	0.4	1.6	0.02	0.1
	3	865	629	412	629
	8	14	42	3	09
PEART_HDAC_PROLIFERATION_CLUSTER_DN	7	0.5	1.8	0.00	0.1
	4	234	737	423	630
		28	1	7	78
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	6	0.5	1.6	0.03	0.1
	5	422	630	272	636
		68	78		7
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	2	0.5	1.8	0.00	0.1
	3	569	761	816	640
	7	2	7	3	74
REACTOME_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA	1	0.6	1.8	<0.0	0.1
	7	854	578	1	641
		76	47		02
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	9	0.6	1.6	0.04	0.1
	9	363	632	347	644
		56	09	8	09
MOREIRA_RESPONSE_TO_TSA_UP	2	0.6	1.8	0.00	0.1
	7	430	820	204	651
		63	99	9	35
PID_MYC_PATHWAY	2	0.5	1.8	0.00	0.1
	5	899	628	421	655
		72	39	1	75
SANSOM_APC_MYC_TARGETS	2	0.4	1.8	0.00	0.1
	3	650	541	407	660
	2	42	63	3	02
REACTOME_MICRORNA_MIRNA_BIOGENESIS	2	0.5	1.6	0.01	0.1
	4	506	583	596	660
		08	28	8	79
REACTOME_INFECTIOUS_DISEASE	3	0.4	1.6	0.03	0.1
	7	530	590	871	660
	5	9	08		96
REACTOME_DNA_STRAND_ELONGATION	3	0.6	1.6	0.03	0.1
	2	793	565	278	665
		5	32	7	12
SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	4	0.6	1.6	0.03	0.1
	4	183	567	991	671
		8	49	1	06
BURTON_ADIPOGENESIS_PEAK_AT_24HR	4	0.5	1.6	0.04	0.1

	4	914	530	480	673
		64	11	7	16
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	3	0.6	1.6	0.04	0.1
	6	642	541	356	676
		18	47	4	
KEGG_RNA_POLYMERASE	2	0.6	1.9	<0.0	0.1
	9	841	803	1	676
		37	55		48
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	4	0.4	1.8	0.00	0.1
	6	837	771	414	681
	8	79	96	1	21
SMID_BREAST_CANCER_LUMINAL_A_DN	1	0.7	1.8	0.00	0.1
	8	862	582	419	682
		12	64	3	84
REACTOME_APC_C:CDH1_MEDIATED_DEGRADATION_OF_CDC2	7	0.6	1.8	0.00	0.1
0_AND_OTHER_APC_C:CDH1_TARGETED_PROTEINS_IN_LATE_	1	693	835	418	683
MITOSIS_EARLY_G1		44	31	4	71
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2	1	0.4	1.6	0.03	0.1
	1	114	503	340	689
	7	5	51	3	41
BURTON_ADIPOGENESIS_4	4	0.5	1.6	0.02	0.1
	3	029	509	731	690
		9	56	1	04
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	4	0.4	1.6	0.03	0.1
	8	649	450	983	691
	4	02	29	2	75
ELVIDGE_HYPOXIA_DN	1	0.4	1.6	0.04	0.1
	4	431	456	184	693
	5	33	89	1	37
DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2	1	0.4	1.6	0.02	0.1
	1	162	469	310	694
	4	38	58	9	94
REACTOME_FGFR2_MUTANT_RECEPTOR_ACTIVATION	3	0.4	1.6	0.01	0.1
	1	969	489	006	696
		92	89		11
KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	8	0.4	1.6	0.01	0.1
	8	409	424	388	697
		48	39	9	23
MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_UP	2	0.5	1.6	0.03	0.1
	2	619	459	829	697
		36	68	8	57
SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	3	0.4	1.6	0.01	0.1
	9	777	428	195	701
		74	72	2	08
REACTOME_FANCONI_ANEMIA_PATHWAY	3	0.6	1.8	0.00	0.1
	9	112	898	205	703

		51	61	3	32
NAGY_TFTC_COMPONENTS_HUMAN	1	0.6	1.8	0.00	0.1
	9	549	857	407	705
		45	63	3	02
COLDREN_GEFITINIB_RESISTANCE_UP	8	0.4	1.6	0.01	0.1
	2	217	394	616	709
		4	15	2	87
REACTOME_MRNA_SPLICING	1	0.5	1.9	0.00	0.1
	8	824	231	811	732
	6	55	59	4	76
BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN	2	0.6	1.6	0.03	0.1
	0	199	342	092	740
		22	71	8	76
REACTOME_MTORC1_MEDIATED_SIGNALLING	2	0.5	1.6	0.03	0.1
	2	276	334	658	743
		3	59	5	47
REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER	3	0.6	2.0	<0.0	0.1
	8	398	108	1	744
		77	39		96
CUI_TCF21_TARGETS_2_UP	4	0.3	1.6	0.00	0.1
	0	759	310	613	749
	5	56	93	5	33
SONG_TARGETS_OF_IE86_CMV_PROTEIN	5	0.6	1.6	0.04	0.1
	5	099	315	842	750
		36	45	1	9
SCHUHMACHER_MYC_TARGETS_UP	7	0.6	1.9	<0.0	0.1
	9	721	688	1	756
		55	41		88
CHOW_RASSF1_TARGETS_DN	3	0.5	1.6	0.02	0.1
	0	216	294	966	760
		03	8	1	57
COLLER_MYC_TARGETS_UP	2	0.7	1.8	0.00	0.1
	4	244	901	211	771
		59	07		36
WELCSH_BRCA1_TARGETS_DN	1	0.6	2.0	<0.0	0.1
	3	202	260	1	772
	9	21	83		94
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	4	0.5	1.9	0.00	0.1
	7	929	159	801	780
		48	74	6	77
REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX	3	0.6	1.9	0.00	0.1
	3	543	108	209	781
		06	2	6	63
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	4	0.5	1.6	0.02	0.1
	7	147	259	459	788
		75	06		79

PID_RB_1PATHWAY	6	0.4	1.6	0.02	0.1
	4	148	251	012	790
		97	28	1	19
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	5	0.6	2.0	<0.0	0.1
	2	973	434	1	797
		51	35		15
REACTOME_FORMATION_OF_TC_NER_PRE_INCISION_COMPLE X	5	0.6	1.9	0.00	0.1
	3	087	250	211	804
		14	28	9	06
LI_DCP2_BOUND_MRNA	8	0.6	1.8	0.00	0.1
	6	625	921	826	804
		8	45	4	13
REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CY TOSOL	5	0.6	1.9	0.00	0.1
	9	773	041	409	824
		77	73	8	26
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINAT ION	3	0.6	1.9	0.00	0.1
	1	447	291	195	839
		44	41	3	08
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	1	0.5	1.8	0.00	0.1
	1	392	936	208	860
	0	23	2	8	06
BIOCARTA_MCM_PATHWAY	1	0.6	1.6	0.03	0.1
	8	962	182	178	868
		5	99		88
DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP	5	0.5	1.6	0.03	0.1
	9	099	174	673	870
		61	59	5	47
ELVIDGE_HYPOXIA_BY_DMOG_DN	5	0.4	1.6	0.03	0.1
	9	569	160	048	879
		41	8	8	35
MANALO_HYPOXIA_DN	2	0.6	1.9	0.00	0.1
	8	445	543	205	886
	7	97	55	3	99
DANG_REGULATED_BY_MYC_UP	6	0.5	1.8	0.00	0.1
	7	679	966	213	899
		88	53	2	9
LIN_APC_TARGETS	7	0.5	1.6	0.04	0.1
	0	227	127	536	904
		9	83	1	24
ZHANG_RESPONSE_TO_CANTHARIDIN_DN	6	0.6	1.9	<0.0	0.1
	3	793	368	1	943
		5	68		29
SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	3	0.7	1.9	0.00	0.1
	1	387	293	407	975
		82	83	3	34
MELLMAN_TUT1_TARGETS_UP	2	0.5	1.6	0.02	0.2

	0	441	037	898	003
		35	32	6	26
ZAMORA_NOS2_TARGETS_UP	5	0.5	1.5	0.03	0.2
	0	036	998	640	029
		9	38	3	69
MUELLER_PLURINET	2	0.5	1.9	0.00	0.2
	9	704	404	417	029
	6	07	81	5	95
REACTOME_APC_C:CDC20_MEDIATED_DEGRADATION_OF_CYC LIN_B	2	0.6	1.5	0.03	0.2
	3	057	984	838	038
		99	92		35
KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN	4	0.4	1.5	0.02	0.2
	4	600	969	390	042
		96	24	4	56
WANG_RESPONSE_TO_BEXAROTENE_UP	3	0.4	1.5	0.03	0.2
	2	597	899	448	116
		54	32	3	16
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	1	0.3	1.5	0.02	0.2
	4	717	848	526	123
	1	7	02	3	24
REACTOME_DUAL_INCISION_IN_GG_NER	4	0.5	1.5	0.04	0.2
	1	191	850	651	137
		82	4	2	09
RIZ_ERYTHROID_DIFFERENTIATION_CCNE1	4	0.4	1.5	0.03	0.2
	3	520	748	621	168
		22	16	7	36
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	3	0.3	1.5	0.02	0.2
	5	668	651	822	206
	5	44	52	6	92
JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP	4	0.4	1.5	0.03	0.2
	8	375	673	420	210
		5	59	5	57
KEGG_PURINE_METABOLISM	1	0.3	1.5	0.02	0.2
	5	660	606	272	213
	1	41	12	7	06
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	5	0.4	1.5	0.04	0.2
	3	750	677	480	213
		84	83	7	48
MOOTHA_PGC	4	0.3	1.5	0.04	0.2
	1	997	622	564	214
	0	69	21	3	83
KYNG_RESPONSE_TO_H2O2_VIA_ERCC6	1	0.5	1.5	0.03	0.2
	7	692	680	232	218
		28	17	8	28
REACTOME_METABOLISM_OF_NUCLEOTIDES	9	0.4	1.5	0.03	0.2
	8	236	685	278	219

		64	75	7	14
KEGG_GLUTATHIONE_METABOLISM	4	0.4	1.5	0.04	0.2
	4	904	460	958	297
		81	34	7	44
DAIRKEE_CANCER_PRONE_RESPONSE_BPA	4	0.4	1.5	0.03	0.2
	9	441	469	711	299
		14	86	3	99
REACTOME_NEDDYLATION	2	0.3	1.5	0.04	0.2
	2	668	353	801	372
	7	37	74	7	34
SANSOM_APC_TARGETS_REQUIRE_MYC	2	0.5	2.0	<0.0	0.2
	1	760	955	1	387
	2	39	72		91

Table S6. GSEA analysis between low- and high-STXBP5-AS1 phenotype using the c5 reference gene set.

NAME	SI Z E	ES	NE S	NOM p-val	FDR q-val
GO_SNRNA_BINDING	38	0.68	2.19	<0.01	0.023
		847	184		358
		6	4		
GO_PYRIMIDINE_RIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	21	0.69	2.00	<0.01	0.145
		576	970		312
		6	5		
GO_MATURATION_OF_SSU_RRNA	44	0.68	1.94	<0.01	0.149
		011	556		607
		5	4		
GO_SM_LIKE_PROTEIN_FAMILY_COMPLEX	73	0.63	1.95	0.001	0.151
		835	103	912	183
		1	3		
GO_PROTEIN_TRANSMEMBRANE_IMPORT_INTO_INTRACELLULAR_ORGANELLE	34	0.66	1.92	<0.01	0.155
		870	499		307
		4	5		
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	34	0.71	1.97	<0.01	0.155
		772	119		886
		1	5		
GO_PRERIBOSOME	73	0.67	1.96	<0.01	0.157
		590	209		117
		8	4		
GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	31	0.73	1.95	<0.01	0.157
		894	451		632
		8	8		
GO_90S_PRERIBOSOME	30	0.69	1.93	0.001	0.158
		694	465	965	239
		9	6		
GO_RNA_POLYMERASE_ACTIVITY	43	0.66	2.05	<0.01	0.161
		966	993		371
			3		
GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_I_PROMOTER	35	0.64	1.92	<0.01	0.163
		326	619		581
		7	1		
GO_RRNA_METABOLIC_PROCESS	20	0.59	1.86	0.005	0.164
	0	971	456	837	423
		8	7		
GO_NCRNA_METABOLIC_PROCESS	43	0.54	1.86	0.005	0.165
	1	549	765	814	137
		1	2		
GO_NUCLEOLAR_PART	18	0.46	1.87	<0.01	0.165
	0	551	030		573

		5	5		
GO_PRECATALYTIC_SPLICEOSOME	44	0.66	1.86	0.007	0.165
		270	103	634	622
		8	4		
GO_TRNA_WOBBLE_URIDINE_MODIFICATION	15	0.72	1.83	0.003	0.169
		248	594	831	214
		3	4		
GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX	19	0.77	1.87	<0.01	0.170
		009	092		819
		5	6		
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	18	0.74	2.01	<0.01	0.171
		116	338		966
		4	7		
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	41	0.59	1.97	<0.01	0.173
		893	311		565
			7		
GO_NUCLEAR_EXOSOME_RNASE_COMPLEX	16	0.76	1.83	0.005	0.173
		924	599	952	594
		2	4		
GO_DNA_HELICASE_COMPLEX	15	0.69	1.85	<0.01	0.175
		698	333		711
		6	4		
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	0.67	1.87	0.003	0.175
		275	176	861	971
			1		
GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	77	0.52	1.83	0.007	0.176
		009	708	692	4
		7	1		
GO_MATURATION_OF_5_8S_RRNA	26	0.70	1.83	0.001	0.176
		884	941	946	827
		8	7		
GO_EXOSOME_RNASE_COMPLEX	25	0.70	1.98	<0.01	0.177
		588	328		575
		4	9		
GO_RIBOSOME_BIOGENESIS	27	0.59	1.87	0.007	0.179
		2	937	363	782
			5		164
GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	41	0.54	1.84	0.003	0.180
		234	016	906	649
		7	7		
GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I	62	0.55	1.84	0.001	0.181
		845	525	969	65
		7	8		
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	68	0.68	1.84	0.007	0.182
		146	189	722	396
		5	6		

GO_SMALL_SUBUNIT_PROCESSOME	37	0.66	1.84	0.005	0.185
		673	602	837	772
			7		
GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	22	0.77	1.82	0.001	0.185
		758	424	98	903
		5	1		
GO_TRANSCRIPTION_BY_RNA_POLYMERASE_III	54	0.52	1.87	0.004	0.186
		230	390		46
		3	7		
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	62	0.66	1.89	0.001	0.187
		526	461	898	113
		4	1		
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	42	0.53	1.81	0.019	0.189
	9	226	299	048	473
		1	5		
GO_RRNA_TRANSCRIPTION	30	0.62	1.90	0.004	0.191
		958	270	024	544
		6	1		
GO_RNA_POLYMERASE_III_ACTIVITY	15	0.71	1.81	<0.01	0.191
		623	884		709
		9	1		
GO_SNORNA_BINDING	24	0.73	1.89	<0.01	0.192
		457	728		475
		9	5		
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	80	0.64	1.81	0.017	0.192
		436	347	442	866
		2	9		
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	38	0.66	1.87	0.001	0.193
		205	461	957	256
		7	8		
GO_NCRNA_PROCESSING	35	0.55	1.88	0.005	0.195
	8	989	198	814	109
		1	7		
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	73	0.56	1.81	<0.01	0.196
		048	411		274
		7	3		
GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION	31	0.63	1.80	0.006	0.197
		517	671		055
		4	4		
GO_RNA_POLYMERASE_COMPLEX	10	0.49	1.77	0.007	0.197
	5	385	977	782	916
			2		
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA	21	0.71	1.77	0.005	0.198
		082	753	78	56
		4			
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	22	0.65	1.87	<0.01	0.198

		761	614		638
		2	6		
GO_RNA_MODIFICATION	15	0.50	1.78	0.008	0.198
	4	363	291	016	905
		2	3		
GO_ORGANELLAR_RIBOSOME	87	0.70	1.77	0.005	0.199
		987	528	682	611
		1	1		
GO_RNA_POLYMERASE_II_CORE_COMPLEX	15	0.68	1.79	0.011	0.200
		907	631	278	179
		9	8		
GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	26	0.67	1.78	0.009	0.200
		416	410	728	273
		4	3		
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	19	0.72	1.80	0.01	0.200
		150	028		524
		3	5		
GO_CAJAL_BODY	56	0.55	1.78	0.014	0.200
		035	020	344	572
		5	6		
GO_U2_TYPE_SPLICEOSOMAL_COMPLEX	81	0.57	1.78	0.021	0.202
		253	922	113	279
		7	8		
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	94	0.68	1.80	0.015	0.202
		189	138	656	737
		6			
GO_ANAPHASE_PROMOTING_COMPLEX	21	0.66	1.79	0.008	0.202
		464	716	016	871
		9	9		
GO_TRNA_PROCESSING	12	0.57	1.78	0.008	0.203
	5	596	450	065	279
		8	6		
GO_O_METHYLTRANSFERASE_ACTIVITY	24	0.62	1.88	0.003	0.203
		311	273	96	622
		2	4		
GO_PRERIBOSOME_LARGE_SUBUNIT_PRECURSOR	22	0.80	2.02	<0.01	0.204
		420	050		601
		8	7		
GO_TRNA_METABOLIC_PROCESS	17	0.56	1.78	0.023	0.205
	2	534	984	529	218
		6	4		
GO_PYRIMIDINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	16	0.66	1.78	0.001	0.206
		551	476	927	568
		9	1		
GO_CHAPERONE_COMPLEX	20	0.71	1.79	0.009	0.206
		538	113	597	827

		6	8		
GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	89	0.71	1.76	0.011	0.215
		157	505	278	302
		3	6		
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	45	0.51	1.75	0.007	0.221
		161	990	339	918
		2	8		
GO_MATURATION_OF_LSU_RRNA	20	0.72	1.75	0.009	0.221
		482	637	452	995
		3	1		
GO_BASE_EXCISION_REPAIR	41	0.54	1.70	0.030	0.223
		795	309	242	309
		3	5		
GO_TRANSLATIONAL_TERMINATION	10	0.67	1.75	0.022	0.223
	4	816	72	642	756
		1			
GO_ORGANELLE_INNER_MEMBRANE	48	0.52	1.75	0.015	0.224
	3	054	349	414	028
		2			
GO_CATALYTIC_ACTIVITY_ACTING_ON_RNA	33	0.45	1.70	0.021	0.224
	5	797	380	611	134
		2	8		
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	43	0.52	1.70	0.012	0.224
		422	472	939	864
		1	2		
GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	62	0.67	1.70	0.021	0.225
		669	566	154	371
		8			
GO_NUCLEOTIDE_EXCISION_REPAIR	10	0.49	1.74	0.015	0.225
	7	670	930	595	731
		9	6		
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	43	0.53	1.70	0.019	0.226
		956	651	084	
		8	6		
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	57	0.71	1.71	0.013	0.227
		855	116	619	215
		2	1		
GO_MITOCHONDRIAL_GENE_EXPRESSION	16	0.64	1.74	0.017	0.227
	0	643	995	682	704
		6	1		
GO_TRNA_WOBBLE_BASE_MODIFICATION	19	0.64	1.70	0.011	0.227
		305	952	788	823
		7	4		
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	10	0.43	1.70	0.012	0.228
	8	429	653	072	307
		9	5		

GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	81	0.47	1.71	0.026	0.228
		177	301	415	416
		5	7		
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	32	0.48	1.70	0.037	0.228
	0	082	762	255	761
		8	1		
GO_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	32	0.56	1.71	0.017	0.229
		270	522	274	011
		3	5		
GO_LARGE_RIBOSOMAL_SUBUNIT	11	0.67	1.71	0.028	0.229
	6	205	630	791	366
		1	7		
GO_RIBOSOME	22	0.60	1.71	0.039	0.229
	3	949	130	848	418
		2	2		
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	22	0.62	1.74	0.013	0.229
		077	571	462	837
			9		
GO_VIRAL_GENE_EXPRESSION	19	0.53	1.71	0.033	0.230
	0	983	325	01	478
		9	8		
GO_TELOMERASE_HOLOENZYME_COMPLEX	20	0.61	1.72	0.019	0.231
		898	493	685	387
		1	3		
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROMOTER	30	0.61	1.71	0.017	0.231
		401	650	822	624
		9	1		
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	10	0.48	1.74	0.021	0.232
	7	785	100	401	431
		2	6		
GO_TRNA_MODIFICATION	83	0.56	1.74	0.025	0.232
		575	251	743	72
		6	8		
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	98	0.52	1.73	0.021	0.233
		007	753	236	286
		5			
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	29	0.68	1.71	0.011	0.233
		309	687	364	487
		7	1		
GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	32	0.54	1.69	0.027	0.233
		576	247	613	563
		9	1		
GO_CATALYTIC_ACTIVITY_ACTING_ON_A_TRNA	11	0.54	1.72	0.027	0.233
	9	663	519	613	682
		5	8		
GO_MITOCHONDRIAL_TRANSLATION	13	0.65	1.73	0.023	0.234

	5	984	868	121	187
		6	6		
GO_DNA_REPLICATION_INITIATION	36	0.67	1.73	0.035	0.234
		779	380	928	501
		3	8		
GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS	22	0.70	1.69	0.025	0.234
		358	424	391	674
		6	4		
GO_TRANSLATIONAL_ELONGATION	13	0.59	1.69	0.037	0.234
	1	358	068	879	692
		5	4		
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	11	0.46	1.71	0.010	0.235
	5	901	735	04	294
		2	2		
GO_PEPTIDASE_COMPLEX	85	0.53	1.68	0.036	0.235
		378	908	122	378
		8	5		
GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	77	0.52	1.72	0.033	0.235
		269	576	138	602
		9	4		
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	21	0.68	1.69	0.019	0.235
		575	256	048	669
		8	4		
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	11	0.62	1.67	0.029	0.235
	0	031	750	47	727
		8	8		
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	35	0.58	1.67	0.035	0.235
		786	038	928	757
		1	5		
GO_RNA_SPLICING	40	0.46	1.71	0.029	0.235
	4	884	968	644	957
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	10	0.40	1.67	0.016	0.235
	9	787	130	981	98
		7	1		
GO_RRNA_MODIFICATION	33	0.58	1.66	0.031	0.236
		585	714	936	083
		8	9		
GO_NCRNA_3_END_PROCESSING	36	0.56	1.66	0.031	0.236
		547	514	311	299
			6		
GO_RNA_5_END_PROCESSING	21	0.66	1.66	0.031	0.236
		341	897	434	501
			8		
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	59	0.57	1.66	0.040	0.236
		488	596	936	582
		8	6		

GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY	16	0.69	1.67	0.021	0.236
		127	810	696	586
		8	9		
GO_RNA_POLYMERASE_III_COMPLEX	17	0.64	1.72	0.009	0.236
		665	681	766	676
		2	8		
GO_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	29	0.54	1.69	0.010	0.236
		257	438	309	72
		6	7		
GO_U1_SNRNP	18	0.68	1.66	0.019	0.237
		218	764	802	092
		5	7		
GO_REGULATION_OF_VIRAL_TRANSCRIPTION	64	0.45	1.67	0.010	0.237
		447	164	081	289
			5		
GO_SPLICEOSOMAL_COMPLEX	17	0.52	1.73	0.037	0.237
	0	820	399	698	383
		6	6		
GO_NCRNA_TRANSCRIPTION	10	0.46	1.68	0.029	0.237
	2	154	660	183	562
		3	5		
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	74	0.53	1.68	0.031	0.237
		383	077	373	708
		7	2		
GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	10	0.45	1.71	0.009	0.237
	7	969	741	416	982
		4			
GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_III	23	0.52	1.67	0.012	0.237
		626	846	048	999
		7	2		
GO_ENDOPEPTIDASE_COMPLEX	63	0.57	1.66	0.045	0.238
		576	33	977	143
		8			
GO_RNA_3_END_PROCESSING	13	0.48	1.71	0.029	0.238
	4	868	996	24	235
		4	2		
GO_INO80_TYPE_COMPLEX	24	0.55	1.67	0.020	0.238
		511	183	202	832
		1	7		
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	23	0.46	1.68	0.034	0.239
	9	849	118	286	006
		6	1		
GO_INTERCELLULAR_BRIDGE	56	0.44	1.72	0.001	0.239
		478	717	938	018
		2	5		
GO_SNRNA_PROCESSING	28	0.56	1.67	0.009	0.239

		659	469	69	211
		4	8		
GO_NEGATIVE_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	20	0.61	1.68	0.038	0.239
		039	230	536	358
			2		
GO_MITOCHONDRION_ORGANIZATION	48	0.41	1.68	0.013	0.239
	5	261	319	283	828
		4	8		
GO_PSEUDOURIDINE_SYNTHESIS	17	0.71	1.68	0.007	0.239
		207	434	828	841
		5	8		
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	23	0.62	1.72	0.023	0.239
	7	110	966	301	89
		9	1		
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	42	0.49	1.66	0.023	0.240
		643	033	576	094
		7	4		
GO_RIBOSOME_ASSEMBLY	59	0.63	1.72	0.021	0.240
		497	81	154	215
		7			
GO_ORGANELLE_ENVELOPE_LUMEN	85	0.50	1.67	0.026	0.240
		230	211	923	342
		2	4		
GO_RNA_CATABOLIC_PROCESS	37	0.43	1.67	0.028	0.241
	6	926	271	958	227
		3	5		
GO_PROTEIN_INSERTION_INTO_MEMBRANE	59	0.46	1.65	0.011	0.242
		683	735	538	197
		7	7		
GO_U2_SNRNP	19	0.65	1.65	0.028	0.242
		831	607	355	713
		4	1		
GO_REGULATION_OF_MITOCHONDRIAL_TRANSLATION	25	0.65	1.65	0.044	0.242
		143	491	146	896
		5			
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	98	0.40	1.65	0.003	0.243
		454	260	824	529
		6	4		
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA	75	0.50	1.65	0.044	0.243
		491	755	316	617
		4	5		
GO_OUTER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	16	0.62	1.65	0.031	0.243
		517	141	955	984
		8	9		

Table S7. DEG between high- and low-STXBP5-AS1 expression groups in COAD.

ID	logFC	PValue	FDR	ID	logFC	PValue	FDR
HIST1H1E	-5.609792	1.73E-73	3.03E-69	KRT6A	-1.812132	4.62E-10	1.71E-08
HIST1H1D	-5.438048	2.48E-68	2.18E-64	CBLN4	1.6715587	4.83E-10	1.78E-08
HIST1H1B	-5.887735	3.44E-67	2.01E-63	LCE3D	-2.557135	4.84E-10	1.78E-08
HIST1H4C	-6.048038	5.54E-65	2.43E-61	PAK5	2.4169058	5.18E-10	1.88E-08
HIST1H3B	-5.679372	3.35E-63	1.17E-59	FABP2	-1.083166	5.19E-10	1.88E-08
HIST1H4D	-5.477742	1.10E-61	3.22E-58	IL17C	1.2734573	5.39E-10	1.94E-08
HIST1H4E	-4.485252	3.09E-60	7.75E-57	CHRN2	1.383772	5.73E-10	2.06E-08
HIST1H2AI	-4.14767	4.05E-58	8.88E-55	CD70	1.0854033	5.94E-10	2.12E-08
HIST1H2BO	-4.6248	6.39E-56	1.24E-52	KRT81	1.1764014	6.00E-10	2.14E-08
HIST1H2AJ	-5.03882	1.35E-55	2.37E-52	HIST3H2BB	-1.01346	6.39E-10	2.25E-08
HIST1H2AD	-3.760225	9.04E-55	1.44E-51	PCDHGA8	-1.190256	7.36E-10	2.55E-08
HIST1H2AM	-3.81065	2.24E-53	3.27E-50	GIF	-1.332039	7.92E-10	2.72E-08
HIST1H3F	-4.808401	1.34E-50	1.81E-47	FGF8	1.2527451	8.18E-10	2.79E-08
PAEP	5.4060472	1.74E-50	2.18E-47	AC009163.2	-1.229019	8.26E-10	2.82E-08
HIST1H2BL	-3.756465	3.07E-50	3.59E-47	SLC4A10	-1.311499	9.17E-10	3.09E-08
HIST1H2BI	-5.795868	7.52E-49	8.23E-46	RETNLB	-1.358993	1.04E-09	3.45E-08
HIST1H2AH	-4.54805	4.92E-47	5.07E-44	JPH3	1.0115452	1.04E-09	3.45E-08
HIST1H3A	-4.222472	1.87E-46	1.82E-43	ADAM2	-1.930533	1.06E-09	3.51E-08
HIST1H2BF	-3.8599	6.27E-46	5.79E-43	TAS2R46	-1.561942	1.18E-09	3.87E-08
HIST1H3C	-4.424121	2.64E-44	2.31E-41	TRIM71	1.7211962	1.21E-09	3.93E-08
HIST1H3J	-3.906385	2.88E-44	2.40E-41	NPY1R	-1.121752	1.30E-09	4.19E-08
HIST2H2AC	-2.84128	8.01E-44	6.17E-41	ALDH1A2	-1.433192	1.34E-09	4.29E-08
HIST1H4B	-4.8358	8.09E-44	6.17E-41	EEF1A2	1.245248	1.60E-09	5.02E-08
HIST1H2AL	-4.186792	3.04E-43	2.22E-40	CDKL4	-1.097332	1.82E-09	5.58E-08
HIST2H2AB	-4.857422	3.34E-43	2.34E-40	RNF17	1.5188036	1.91E-09	5.81E-08
GPR83	3.1011893	9.82E-43	6.62E-40	PRLHR	-2.060906	2.08E-09	6.28E-08
HIST1H2BE	-3.790123	1.60E-42	1.01E-39	PRSS1	1.6241321	2.36E-09	6.95E-08
HIST1H2AB	-4.78184	1.62E-42	1.01E-39	KCNF1	1.0619567	2.50E-09	7.35E-08
HIST1H2BC	-2.675025	3.89E-40	2.35E-37	TBR1	1.6127779	2.52E-09	7.39E-08
HIST1H2BM	-4.7136	4.16E-38	2.43E-35	RIMS4	1.3862448	2.55E-09	7.43E-08
HIST1H2BG	-2.685197	7.51E-38	4.25E-35	DDIT4L	1.1306764	2.59E-09	7.47E-08
HIST2H2BF	-2.601902	2.90E-37	1.59E-34	BEST2	-1.350897	2.66E-09	7.63E-08
HIST1H3I	-4.158997	1.59E-35	8.46E-33	CTAG2	2.5860833	2.84E-09	8.10E-08
HIST1H4L	-5.438196	1.91E-34	9.87E-32	GP2	-1.96062	3.35E-09	9.38E-08
HIST1H2BB	-6.432312	3.78E-34	1.89E-31	SLC38A11	1.184307	3.36E-09	9.39E-08
HIST1H2BJ	-2.259606	4.84E-33	2.35E-30	ZMAT4	1.3585469	3.48E-09	9.61E-08
HIST1H2AG	-2.067482	6.50E-33	3.08E-30	DUSP9	1.1369299	3.52E-09	9.68E-08
HIST1H3G	-2.463551	1.54E-32	7.10E-30	SLIT1	1.0181144	3.57E-09	9.82E-08
HIST1H3D	-2.352117	1.78E-32	7.98E-30	CLPS	2.056425	3.75E-09	1.02E-07
ZNF460	-1.719692	1.62E-29	7.12E-27	CYP3A4	-1.265483	3.99E-09	1.07E-07
HIST1H4H	-2.333338	3.83E-29	1.64E-26	PLPPR3	1.2163644	4.26E-09	1.14E-07
REP15	-2.026697	6.44E-29	2.69E-26	FGF19	1.4561401	4.27E-09	1.14E-07
NNAT	-2.201727	7.88E-28	3.21E-25	TTC29	-2.282844	4.72E-09	1.24E-07
HIST1H2AE	-2.066772	1.02E-27	4.05E-25	SOHLH2	1.8638175	4.75E-09	1.25E-07

COLEC10	-2.007024	2.37E-27	9.22E-25	TMEM249	1.0182247	4.78E-09	1.25E-07
HIST2H3D	-2.538414	3.14E-27	1.20E-24	ZPBP2	1.4614946	5.20E-09	1.33E-07
TFAP2B	4.9324	1.16E-26	4.34E-24	HCN4	1.2190824	5.24E-09	1.34E-07
LHX3	3.4401398	2.92E-26	1.07E-23	TRPM3	1.3254694	5.98E-09	1.50E-07
CHRNA4	3.7212652	4.13E-26	1.48E-23	GAL	1.0286609	6.20E-09	1.55E-07
GPR22	-2.385373	1.03E-25	3.55E-23	CTRC	1.0305868	6.49E-09	1.60E-07
HIST1H2BN	-1.581651	1.11E-25	3.75E-23	PHF21B	1.3754089	6.67E-09	1.64E-07
CLDN6	2.6151865	1.57E-25	5.17E-23	CLDN19	1.482786	6.86E-09	1.67E-07
PNMT	2.2610117	1.59E-25	5.17E-23	C19orf81	1.3266556	7.12E-09	1.73E-07
HIST1H2BH	-1.934131	1.66E-24	5.20E-22	DNASE1L3	-1.032325	7.32E-09	1.76E-07
HIST1H4A	-3.340588	2.02E-24	6.21E-22	MAEL	-1.418633	7.40E-09	1.78E-07
HIST4H4	-1.544525	3.77E-24	1.14E-21	GPR52	-1.554192	7.54E-09	1.81E-07
CALCB	3.9414688	1.80E-23	5.33E-21	PSG9	-2.634426	8.13E-09	1.94E-07
UGT2B4	-3.686344	1.82E-23	5.33E-21	CLDN8	-1.885228	9.01E-09	2.13E-07
CPA1	3.6696948	2.13E-23	6.11E-21	KIRREL2	1.0857926	9.07E-09	2.14E-07
ZBTB20	-1.331365	6.45E-23	1.82E-20	MROH2B	1.8297208	9.07E-09	2.14E-07
TCAP	1.5751864	9.26E-23	2.58E-20	AMER3	1.5845629	1.10E-08	2.52E-07
IGDCC3	2.7507925	1.05E-22	2.88E-20	TAS2R43	-1.382288	1.11E-08	2.54E-07
DCAF4L2	4.568086	1.48E-22	4.00E-20	FAM153A	-1.073024	1.49E-08	3.26E-07
CRCT1	-4.279701	2.93E-22	7.77E-20	C1QL4	1.1601898	1.56E-08	3.37E-07
HIST1H1C	-1.428279	8.81E-22	2.31E-19	DEFA6	-1.68007	1.57E-08	3.40E-07
TRPA1	-1.350696	9.51E-22	2.45E-19	CNTNAP4	1.700302	1.67E-08	3.56E-07
UGT3A1	3.6949494	9.66E-22	2.45E-19	LRRTM1	1.4596784	1.89E-08	3.97E-07
SYNGR4	-2.051495	1.44E-21	3.60E-19	CCDC190	-1.856342	1.93E-08	4.05E-07
SFTPC	4.635231	1.46E-21	3.60E-19	MYT1L	1.3585142	1.97E-08	4.10E-07
KCNQ2	2.632427	1.71E-21	4.17E-19	MMP13	-1.156005	1.97E-08	4.11E-07
FSIP2	-1.34768	1.92E-21	4.60E-19	C11orf21	1.0143236	2.06E-08	4.28E-07
HIST1H3H	-1.498006	2.13E-21	5.05E-19	C10orf113	-1.487899	2.13E-08	4.39E-07
CACNG6	2.9432425	2.74E-21	6.40E-19	LGALS14	1.7647053	2.25E-08	4.60E-07
LIPC	2.1783989	3.34E-21	7.71E-19	PCSK2	1.4591277	2.37E-08	4.83E-07
KRTAP4-6	3.6731871	5.67E-21	1.29E-18	CELF3	1.1027544	2.61E-08	5.27E-07
CLCA2	-2.57009	7.84E-21	1.76E-18	APOF	-1.491609	2.90E-08	5.77E-07
SELENOP	-1.184938	8.77E-21	1.93E-18	ITLN2	-1.633531	2.96E-08	5.85E-07
SLC16A7	-1.431203	8.81E-21	1.93E-18	UROC1	1.1232598	3.12E-08	6.11E-07
CXorf67	3.6258539	1.04E-20	2.25E-18	GPR15	-1.138453	3.24E-08	6.30E-07
HIST1H1A	-3.83254	1.59E-20	3.35E-18	KRT3	1.4234209	3.30E-08	6.40E-07
MYBPC3	-1.601179	1.66E-20	3.46E-18	GDF10	1.5681822	3.64E-08	6.97E-07
GPR50	3.2856688	1.87E-20	3.86E-18	RS1	1.1829526	3.66E-08	7.00E-07
AMBN	3.3534173	1.99E-20	4.06E-18	NTSR1	1.2325421	3.74E-08	7.12E-07
DPYSL5	2.3071154	2.15E-20	4.31E-18	CCKBR	1.630676	3.82E-08	7.24E-07
CLPSL1	3.4629815	2.16E-20	4.31E-18	FGF21	1.3169641	4.04E-08	7.60E-07
FCGBP	-1.826024	2.74E-20	5.40E-18	NTN3	1.0107566	4.24E-08	7.93E-07
GALP	3.6730518	3.97E-20	7.74E-18	CALB1	1.7198315	4.38E-08	8.14E-07
TAS2R30	-2.736361	5.14E-20	9.90E-18	SEMG2	1.9231293	4.64E-08	8.57E-07
BTBD18	-1.994763	5.78E-20	1.10E-17	BMP3	-1.105786	4.69E-08	8.63E-07
SOHLH1	3.5796366	8.12E-20	1.53E-17	IDO1	1.0517777	4.69E-08	8.63E-07

GALNTL6	-1.933532	1.09E-19	2.03E-17	OBP2A	1.2946658	4.76E-08	8.76E-07
CHRND	2.9554846	1.11E-19	2.05E-17	FAM216B	-1.038781	4.93E-08	9.03E-07
AIRE	2.3127612	1.33E-19	2.42E-17	SALL3	-2.469962	5.33E-08	9.65E-07
HIST1H4J	-1.66989	1.38E-19	2.50E-17	MAGEA10	2.1327507	5.36E-08	9.70E-07
CHGB	2.3815311	1.41E-19	2.52E-17	CELA3B	1.3429344	5.41E-08	9.78E-07
HRH3	3.0412941	1.94E-19	3.44E-17	KLK13	-1.290529	5.63E-08	1.01E-06
NEUROD4	3.6064562	2.07E-19	3.64E-17	ADGRA1	1.4171038	6.05E-08	1.08E-06
HIST1H4K	-1.787342	3.34E-19	5.80E-17	ATP6V0A4	1.2765261	6.34E-08	1.12E-06
FER1L6	-1.792425	5.30E-19	9.10E-17	RPRM	1.0351558	7.00E-08	1.22E-06
PRH2	-1.909778	5.98E-19	1.02E-16	AMY2A	1.6857865	7.03E-08	1.22E-06
CTRB2	2.6115442	1.28E-18	2.16E-16	CATSPER4	1.2242566	7.12E-08	1.23E-06
PNLIP	4.3309242	1.54E-18	2.57E-16	KRTAP1-1	1.5833409	7.72E-08	1.32E-06
WNT3A	1.9093129	1.87E-18	3.10E-16	AQP5	1.5785877	8.85E-08	1.49E-06
NXPE2	-1.383417	2.20E-18	3.61E-16	MEP1B	-1.00992	9.42E-08	1.56E-06
HEPACAM2	-1.781792	2.43E-18	3.94E-16	GABRP	1.2089313	9.53E-08	1.58E-06
CALCA	2.6355326	2.45E-18	3.94E-16	CHRNA9	-1.165317	1.28E-07	2.03E-06
SEZ6L	1.9910339	3.42E-18	5.41E-16	ZFR2	1.1164435	1.39E-07	2.18E-06
FOXR2	3.2552702	3.54E-18	5.53E-16	KLK6	1.1208537	1.42E-07	2.21E-06
CNBD2	1.3854824	3.77E-18	5.84E-16	KRT13	-1.327705	1.45E-07	2.24E-06
LRRTM2	-1.194066	3.89E-18	5.99E-16	DCT	1.4206236	1.47E-07	2.27E-06
POU5F2	-2.300261	3.99E-18	6.08E-16	ANXA8	-1.571167	1.62E-07	2.47E-06
CT45A1	3.9735267	4.24E-18	6.41E-16	UNC5D	-1.010811	1.69E-07	2.56E-06
HTR3C	-2.628374	5.32E-18	7.90E-16	RPRML	1.4929387	1.76E-07	2.65E-06
TUBA3C	3.0417264	6.73E-18	9.91E-16	CAMKV	1.1629299	1.76E-07	2.65E-06
ANO7	-1.241772	7.93E-18	1.16E-15	SULT1E1	1.3683322	1.90E-07	2.82E-06
KIF1A	1.9384169	1.07E-17	1.56E-15	NFE4	1.3070185	1.92E-07	2.84E-06
ADAD2	-2.24899	1.62E-17	2.33E-15	PRSS21	1.4879023	1.97E-07	2.90E-06
PPP1R17	3.0309667	1.78E-17	2.54E-15	FOXN4	1.2547342	2.05E-07	3.00E-06
NEUROD2	2.0425971	2.49E-17	3.49E-15	ZIC4	1.9091651	2.10E-07	3.05E-06
C16orf74	1.1924911	2.56E-17	3.57E-15	BBOX1	-1.030958	2.32E-07	3.33E-06
CHRNA2	2.5020757	3.63E-17	5.01E-15	FAM181B	-1.108728	2.36E-07	3.37E-06
NMRK2	3.1184518	3.66E-17	5.01E-15	CLEC2A	2.09194	2.46E-07	3.50E-06
KRT78	-3.076271	4.30E-17	5.85E-15	CES1	1.0343216	2.48E-07	3.52E-06
B3GNT6	-1.987156	4.48E-17	6.04E-15	IL17REL	-1.042948	2.90E-07	4.04E-06
LRRN3	-1.22144	5.39E-17	7.21E-15	PGC	1.1524551	2.96E-07	4.12E-06
SBK2	2.9255391	6.37E-17	8.46E-15	PRAME	1.1499546	2.97E-07	4.13E-06
ATP2B3	2.1469247	6.54E-17	8.62E-15	HIST2H3C	-1.197546	3.11E-07	4.29E-06
CTRB1	2.8400495	7.63E-17	9.90E-15	DPCR1	1.4130628	3.13E-07	4.31E-06
PTGER2	-1.078332	1.20E-16	1.55E-14	ERVW-1	-1.088463	3.18E-07	4.36E-06
KLHL32	-1.161251	1.28E-16	1.64E-14	KRT6C	-1.548101	3.30E-07	4.50E-06
UNCX	3.3110307	1.41E-16	1.79E-14	SAA2-SAA4	1.329412	3.76E-07	5.04E-06
CELA2A	2.3608436	1.47E-16	1.85E-14	CD200R1L	-1.259916	4.09E-07	5.42E-06
GRIP2	-1.202851	1.84E-16	2.31E-14	TF	1.0677624	4.15E-07	5.48E-06
SLC6A15	2.3014284	2.27E-16	2.82E-14	SH3GL3	1.3168084	4.21E-07	5.52E-06
NRAP	-1.695567	2.70E-16	3.31E-14	SAA2	1.0116294	4.33E-07	5.65E-06
RASD1	-1.241215	3.66E-16	4.45E-14	SCRT2	1.5906361	4.50E-07	5.83E-06

GALNT8	-1.370788	3.94E-16	4.77E-14	ATCAY	1.0095636	4.63E-07	5.97E-06
PNLDC1	1.635281	4.42E-16	5.27E-14	USP26	-1.208427	4.65E-07	5.98E-06
CRP	-2.604514	5.51E-16	6.53E-14	TMIGD1	-1.357469	5.20E-07	6.58E-06
RGS13	-1.462195	6.22E-16	7.32E-14	GOLGA6L2	1.3520623	5.26E-07	6.63E-06
C1orf61	1.5836229	1.24E-15	1.42E-13	KLF14	1.053364	5.48E-07	6.87E-06
FABP3	1.3122274	1.30E-15	1.48E-13	CRHR1	1.4227638	5.71E-07	7.13E-06
CACNG7	2.1056592	1.31E-15	1.48E-13	HCAR1	1.0489068	5.78E-07	7.19E-06
OBP2B	2.3972607	1.64E-15	1.85E-13	SLC38A3	1.1008015	6.69E-07	8.16E-06
ABCA4	-1.515138	1.73E-15	1.92E-13	FOXL2	1.3721146	7.15E-07	8.64E-06
MYL3	1.6484107	2.35E-15	2.58E-13	LRRC14B	1.0284391	7.23E-07	8.71E-06
PRSS56	3.0794769	2.41E-15	2.62E-13	LCN6	-1.033465	8.21E-07	9.74E-06
SLC6A3	1.6352569	3.12E-15	3.38E-13	SSX5	1.9028616	8.42E-07	9.97E-06
F7	1.7727683	3.39E-15	3.65E-13	VSTM2A	-1.170211	9.86E-07	1.14E-05
LRP1B	2.0017729	3.87E-15	4.12E-13	S100G	-1.215211	1.15E-06	1.30E-05
AQP3	-1.243876	5.55E-15	5.86E-13	PYY	-1.218362	1.18E-06	1.33E-05
MSMB	-2.801676	6.56E-15	6.81E-13	DCHS2	1.0566934	1.23E-06	1.38E-05
ST6GALNAC1	-1.00385	6.57E-15	6.81E-13	KRTAP3-1	1.3440443	1.25E-06	1.40E-05
COL20A1	1.8096008	6.83E-15	7.04E-13	HYDIN	1.0003167	1.29E-06	1.43E-05
C16orf54	-1.097119	6.92E-15	7.09E-13	DLX3	1.1948495	1.31E-06	1.45E-05
HPR	-2.093661	7.51E-15	7.65E-13	LYPD2	1.570215	1.33E-06	1.46E-05
IFNK	-2.645259	8.75E-15	8.86E-13	ZSCAN10	1.0206213	1.42E-06	1.55E-05
COX8C	2.3314199	1.28E-14	1.27E-12	OTOP2	-1.411608	1.43E-06	1.55E-05
LMX1A	2.0590215	1.35E-14	1.34E-12	INHA	1.1093779	1.49E-06	1.60E-05
PPBP	2.7211255	1.87E-14	1.81E-12	SH3GL2	1.0860603	1.50E-06	1.61E-05
CBFA2T3	-1.232814	1.87E-14	1.81E-12	CNGA3	-1.160729	1.50E-06	1.61E-05
ALOX15B	-1.34711	1.91E-14	1.84E-12	OR1N2	-2.122451	1.51E-06	1.62E-05
FBXO2	1.3652382	2.00E-14	1.91E-12	CYP2W1	1.0473038	1.62E-06	1.70E-05
SEZ6	1.8076619	2.07E-14	1.97E-12	COL2A1	1.3105674	1.63E-06	1.71E-05
NEURL1	-1.214889	2.19E-14	2.07E-12	FTCD	1.0838418	1.71E-06	1.78E-05
SHISA7	1.7365255	2.24E-14	2.12E-12	PRB2	-1.279735	1.72E-06	1.79E-05
HIST1H4F	-3.418083	2.63E-14	2.46E-12	ZFP42	1.5266873	1.78E-06	1.84E-05
AKAIN1	2.1412708	3.30E-14	3.06E-12	NKX2-5	1.3882698	1.84E-06	1.89E-05
UTS2B	1.6061676	3.90E-14	3.56E-12	REG4	-1.181563	1.85E-06	1.91E-05
SLC38A8	2.0291611	4.39E-14	3.97E-12	MAGEC1	1.9262589	1.93E-06	1.97E-05
ARHGAP36	2.1583854	4.58E-14	4.09E-12	TYR	1.6209184	1.98E-06	2.01E-05
P2RY4	-1.44199	5.04E-14	4.48E-12	SLC7A14	1.1815676	2.11E-06	2.12E-05
RBM44	-1.013009	6.49E-14	5.71E-12	PCDHB8	-1.024812	2.31E-06	2.28E-05
SCG3	1.7096702	9.83E-14	8.53E-12	AP3B2	1.053461	2.31E-06	2.28E-05
TPSG1	-1.33046	1.02E-13	8.77E-12	INSL5	-1.515049	2.47E-06	2.41E-05
TCHH	1.5514011	1.16E-13	9.89E-12	CT45A10	2.0532015	2.48E-06	2.41E-05
CHST5	-1.346512	1.56E-13	1.32E-11	PRMT8	1.0860917	2.48E-06	2.42E-05
CHST8	1.7661954	1.86E-13	1.56E-11	B4GALNT2	-1.194658	2.52E-06	2.45E-05
CAPN9	-1.244766	2.01E-13	1.68E-11	SLC17A8	-1.183282	2.59E-06	2.50E-05
SFTPA1	2.8402856	2.18E-13	1.81E-11	SYT4	1.1869242	2.64E-06	2.55E-05
TAS2R13	-1.970174	2.49E-13	2.03E-11	TLX3	1.4774075	2.95E-06	2.80E-05
LINC00694	-1.186399	2.50E-13	2.03E-11	KCNE1B	-1.742779	3.08E-06	2.90E-05

SI	-1.642304	2.72E-13	2.19E-11	UGT2B17	-1.145653	3.19E-06	2.98E-05
KIF19	-1.474135	2.99E-13	2.38E-11	SEC14L4	1.1194448	3.23E-06	3.01E-05
DSG1	-1.081652	3.07E-13	2.44E-11	DMRT3	1.0032422	3.23E-06	3.01E-05
SPRR2B	-2.963448	3.10E-13	2.45E-11	REG3G	1.7782947	3.46E-06	3.18E-05
NAT8L	1.3652195	3.22E-13	2.53E-11	CDC20B	1.0937419	3.75E-06	3.40E-05
SERPINB13	-3.50036	3.31E-13	2.59E-11	OVCH1	-1.143234	3.92E-06	3.54E-05
CCDC83	-1.987447	3.59E-13	2.77E-11	RLBP1	1.0538574	4.70E-06	4.14E-05
GLYATL2	-1.521598	3.81E-13	2.93E-11	VSTM2B	1.497234	4.88E-06	4.28E-05
KCNJ13	-1.995785	4.94E-13	3.75E-11	SAA4	1.0528389	4.89E-06	4.29E-05
SLITRK1	2.1966833	5.27E-13	3.98E-11	SLC36A2	1.1487226	4.92E-06	4.30E-05
ATOH1	-1.351333	6.71E-13	5.00E-11	DLK1	1.6953771	5.06E-06	4.41E-05
TMPRSS11D	-2.144702	7.00E-13	5.20E-11	CPA2	1.0129871	5.18E-06	4.50E-05
SLC4A4	-1.272903	8.90E-13	6.47E-11	AHSG	1.3056197	5.29E-06	4.57E-05
FGF6	2.5815135	8.97E-13	6.50E-11	AQP4	1.2052366	5.50E-06	4.73E-05
FGL1	-2.400341	9.23E-13	6.63E-11	LKAAEAR1	1.2233895	5.51E-06	4.73E-05
BTN1A1	1.397147	9.26E-13	6.63E-11	BEST3	1.1062867	5.79E-06	4.93E-05
NR0B1	1.8765318	1.01E-12	7.13E-11	FZD10	1.0670724	6.33E-06	5.31E-05
TMEM61	-1.080952	1.14E-12	7.91E-11	GUCA2B	-1.134006	6.92E-06	5.74E-05
ALK	-1.825641	1.16E-12	8.06E-11	AFP	1.1502473	7.32E-06	6.02E-05
SLC8A3	-1.376045	1.23E-12	8.49E-11	CELA3A	1.2043448	7.45E-06	6.11E-05
MAGEB1	2.7578546	1.33E-12	9.11E-11	ACTL6B	1.1052772	7.52E-06	6.16E-05
IRGM	-2.019513	1.46E-12	9.91E-11	KRT4	1.2067244	7.58E-06	6.21E-05
ZDHHC22	1.9236601	1.54E-12	1.04E-10	SCGB3A2	-1.285184	8.06E-06	6.55E-05
PRSS48	-1.771238	1.59E-12	1.07E-10	KRTAP13-2	-1.479632	8.53E-06	6.86E-05
CYP1A1	-2.42666	1.93E-12	1.27E-10	SFTPB	1.2834915	9.11E-06	7.23E-05
VSIG1	-1.443703	2.07E-12	1.36E-10	SULT2A1	1.1996299	9.23E-06	7.31E-05
LUZP2	-1.108808	2.18E-12	1.42E-10	KRT5	-1.437554	9.31E-06	7.36E-05
GSTA1	-1.385475	2.28E-12	1.48E-10	SORCS3	1.1064193	9.54E-06	7.51E-05
DLX5	1.4425714	2.46E-12	1.58E-10	LIPF	1.6156862	1.21E-05	9.25E-05
FAM177B	-1.345795	2.54E-12	1.62E-10	PBOV1	-1.268291	1.36E-05	0.0001016
ZNF479	-3.394555	2.60E-12	1.66E-10	NOTUM	1.0501836	1.37E-05	0.0001019
CRNN	-2.84563	2.91E-12	1.83E-10	SLITRK6	-1.014594	1.38E-05	0.0001024
SAA1	1.4759248	3.29E-12	2.04E-10	HBZ	1.876635	1.48E-05	0.0001094
KRT31	2.3560733	4.23E-12	2.59E-10	RPTN	1.5522914	1.51E-05	0.0001109
ZNF578	-1.263417	6.75E-12	3.97E-10	LINC01314	1.0128324	1.53E-05	0.0001124
COL26A1	1.1852709	7.29E-12	4.24E-10	KLRG2	1.060652	1.55E-05	0.0001137
RHBDL3	-1.289823	8.15E-12	4.71E-10	TKTL1	1.464721	1.72E-05	0.0001239
RASL10B	1.0540383	8.28E-12	4.78E-10	ANKRD34C	1.2183323	1.72E-05	0.000124
TMEM213	1.7880091	8.87E-12	5.07E-10	ATP12A	-1.336882	1.77E-05	0.0001267
TAAR1	-2.817762	9.89E-12	5.61E-10	AC011473.4	-1.641567	1.83E-05	0.0001306
HTR3E	-1.611537	1.07E-11	6.03E-10	LRRC53	1.3376302	1.96E-05	0.0001382
KLK4	1.5065618	1.10E-11	6.18E-10	GFY	1.100956	1.97E-05	0.0001388
KRT37	1.8820649	1.10E-11	6.18E-10	GNAT3	-1.517338	2.05E-05	0.0001431
ITLN1	-1.700398	1.12E-11	6.28E-10	BHLHA9	1.1383672	2.07E-05	0.000144
C20orf204	1.1371742	1.18E-11	6.57E-10	SCGB1A1	-1.739115	2.23E-05	0.0001542
HSF5	1.6137511	1.31E-11	7.17E-10	IGFALS	-1.009595	2.42E-05	0.000165

CER1	2.0783045	1.34E-11	7.30E-10	MYBPHL	1.1142612	3.10E-05	0.000203
RHBG	1.2076119	1.38E-11	7.52E-10	GPHA2	1.0048822	3.12E-05	0.0002036
EPHB6	1.4238447	1.39E-11	7.57E-10	KRT32	1.250768	3.12E-05	0.0002036
IGF2	2.0018263	1.58E-11	8.55E-10	LITD1	-1.003548	3.15E-05	0.0002052
PAGE2	2.01334	1.77E-11	9.49E-10	TRPM1	1.0784805	3.27E-05	0.0002117
CRISP3	-2.553675	1.86E-11	9.95E-10	SPATA22	-1.081709	3.86E-05	0.0002425
SLC1A6	1.8222299	1.94E-11	1.03E-09	BRDT	1.0092331	4.10E-05	0.0002552
CLCA4	-1.759103	2.09E-11	1.10E-09	CA1	-1.095544	4.13E-05	0.0002569
SLC26A9	-1.89822	2.36E-11	1.24E-09	GCG	-1.365199	4.21E-05	0.0002609
TSPAN32	1.198575	2.50E-11	1.31E-09	CPN1	1.0770569	4.38E-05	0.0002699
TMCO2	-1.837882	2.52E-11	1.31E-09	GALNT13	-1.017826	4.40E-05	0.0002705
SPRR2E	-2.893625	3.64E-11	1.83E-09	MYOC	1.1785249	4.99E-05	0.0003002
PRODH2	2.1081067	3.96E-11	1.99E-09	XAGE2	1.6363979	5.08E-05	0.0003043
TPH1	-1.121172	4.00E-11	2.00E-09	MS4A12	-1.041735	6.05E-05	0.0003524
LYPD8	-1.255869	4.73E-11	2.35E-09	FAM25A	1.2068566	6.91E-05	0.0003919
CPLX2	1.3708984	4.86E-11	2.40E-09	PAX4	1.2211239	6.98E-05	0.0003958
CCDC60	-1.494497	5.00E-11	2.47E-09	DRD5	-1.210499	7.13E-05	0.0004033
EMX2	2.0804659	5.04E-11	2.48E-09	HSD3B2	-1.109224	7.54E-05	0.0004235
TMEM210	-1.619843	5.12E-11	2.51E-09	IVL	-1.521663	7.75E-05	0.000434
NCAN	1.6390064	5.66E-11	2.77E-09	SOAT2	1.0053323	8.79E-05	0.0004855
OGDHL	1.2791147	5.80E-11	2.82E-09	MAGEB17	1.0668633	9.38E-05	0.0005127
TP63	-1.288461	6.36E-11	3.07E-09	MUC15	-1.302314	9.47E-05	0.000516
CDH22	1.9058161	6.56E-11	3.15E-09	PRR9	1.4250586	0.0001108	0.0005905
CLCA1	-1.794184	6.62E-11	3.17E-09	HSPB3	1.0249806	0.0001234	0.0006434
SCGB2A1	-1.223694	6.68E-11	3.19E-09	PIP	-1.161274	0.0001277	0.0006615
VSIG2	-1.22858	7.10E-11	3.38E-09	PROK1	1.1172041	0.0001768	0.0008693
CHST13	1.0559363	7.12E-11	3.38E-09	BPIFB2	1.2936928	0.0001803	0.0008836
KRT14	-2.600927	7.86E-11	3.69E-09	LIN28A	1.2498911	0.0001821	0.0008916
PDYN	2.3990366	7.88E-11	3.69E-09	SERPINA9	-1.09358	0.0001918	0.0009308
PCDHA1	-1.888699	8.61E-11	3.98E-09	ZIC1	1.2704971	0.0002008	0.000968
ZG16	-1.709932	8.70E-11	4.01E-09	TCP11	-1.086815	0.0002144	0.001023
TMEM229A	2.1742857	8.76E-11	4.02E-09	SLC18A3	1.0048659	0.0002245	0.0010626
DGKB	-1.595286	8.83E-11	4.03E-09	KRT24	-1.367046	0.0002348	0.0011019
MUC21	1.9495458	9.00E-11	4.09E-09	DMRT1	1.1719634	0.0002852	0.0012999
KRT38	1.9695272	1.12E-10	5.01E-09	NDST4	1.0872445	0.0003276	0.0014613
TAS2R50	-1.649773	1.16E-10	5.14E-09	LIN28B	1.5407586	0.0003332	0.001483
GNG13	-1.36269	1.24E-10	5.46E-09	NKX6-3	1.3317919	0.0003625	0.0015848
IL36G	-1.31316	1.24E-10	5.46E-09	TRDN	-1.065055	0.0004016	0.0017268
RPE65	1.7464619	1.40E-10	6.09E-09	CCL25	1.1719039	0.0004243	0.0018047
IRX4	2.0885753	1.64E-10	7.07E-09	GC	-1.184243	0.000529	0.0021671
MIA	1.3723102	1.74E-10	7.41E-09	SLURP1	-1.017284	0.0005527	0.0022543
TCN1	-1.540012	1.79E-10	7.63E-09	APOB	1.0135529	0.0005925	0.0023872
SHISA3	-1.096602	1.88E-10	7.95E-09	PTF1A	1.1816283	0.0006012	0.0024161
IL1RAPL2	-2.270044	1.92E-10	8.09E-09	DEFA5	-1.094099	0.0008245	0.0031474
JCHAIN	-1.222295	2.02E-10	8.47E-09	KRT35	1.0278618	0.0008331	0.0031727
SLC7A10	1.6061239	2.07E-10	8.64E-09	GAD2	-1.409394	0.0008885	0.0033676

MGAT5B	1.0360896	2.22E-10	9.15E-09	MT4	1.3200531	0.0010781	0.0039863
CDH12	2.2596061	2.58E-10	1.04E-08	NTS	-1.050255	0.0010913	0.0040299
NEUROD1	2.2463322	2.69E-10	1.07E-08	RHAG	1.2123393	0.0011909	0.0043392
CHRNA7	-1.244649	2.69E-10	1.07E-08	SAGE1	1.2292124	0.0013334	0.0047744
GLP1R	1.5805223	2.77E-10	1.09E-08	XKR7	1.0130495	0.0015198	0.0053272
POU3F2	1.2794791	2.84E-10	1.11E-08	BPIFB4	-1.098732	0.0016908	0.0058347
MLN	2.289581	2.86E-10	1.12E-08	HOXC13	1.0902752	0.0019278	0.0065342
NTRK3	1.177568	2.94E-10	1.14E-08	DAZ1	1.2895124	0.0031927	0.0099007
MMP8	1.6981865	3.32E-10	1.27E-08	SP9	1.0371283	0.0033135	0.0102245
PLSCR5	-2.674294	3.49E-10	1.33E-08	SSX1	-1.267772	0.0039466	0.0118523
CALML5	2.3122375	3.88E-10	1.47E-08	MAGEA9B	1.2028866	0.0047881	0.0139105
CTNNA2	1.7490958	3.95E-10	1.50E-08	HOXC12	1.0284406	0.0058428	0.0164484
COX7B2	2.4519109	4.03E-10	1.51E-08	CDH9	1.0418542	0.0063574	0.0176225
AC007040.2	1.1692465	4.03E-10	1.51E-08	HBE1	1.0580499	0.0066571	0.0183057
RGN	1.1409741	4.38E-10	1.63E-08	MAGEB2	-1.153926	0.0085544	0.0225164
IGF2BP1	1.6784141	4.39E-10	1.63E-08				

Table S8. Functional enrichment of DEG between high- and low-STXBP5-AS1 expression groups.

Category	Term	Count	%	P Value
KEGG_PATHWAY	hsa05322:Systemic lupus erythematosus	47	0.079195	3.79E-36
KEGG_PATHWAY	hsa05034:Alcoholism	51	0.085935	1.21E-34
KEGG_PATHWAY	hsa05203:Viral carcinogenesis	25	0.042125	3.33E-08
KEGG_PATHWAY	hsa04972:Pancreatic secretion	12	0.02022	1.83E-04
KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	21	0.035385	5.86E-04
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	10	0.01685	0.002013
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	13	0.021905	0.007588
KEGG_PATHWAY	hsa04742:Taste transduction	6	0.01011	0.014303
KEGG_PATHWAY	hsa00512:Mucin type O-Glycan biosynthesis	5	0.008425	0.016768
KEGG_PATHWAY	hsa04975:Fat digestion and absorption	5	0.008425	0.03593
KEGG_PATHWAY	hsa00140:Steroid hormone biosynthesis	6	0.01011	0.0384
KEGG_PATHWAY	hsa05033:Nicotine addiction	5	0.008425	0.038947
KEGG_PATHWAY	hsa05204:Chemical carcinogenesis	7	0.011795	0.043855
GOTERM_CC_DIRECT	GO:0000786~nucleosome	50	0.08425	7.71E-50
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	41	0.069085	5.25E-32
GOTERM_BP_DIRECT	GO:0032200~telomere organization	20	0.0337	7.36E-24
GOTERM_CC_DIRECT	GO:0005576~extracellular region	124	0.208941	2.32E-23
GOTERM_BP_DIRECT	GO:0000183~chromatin silencing at rDNA	22	0.03707	2.64E-23
GOTERM_CC_DIRECT	GO:0000788~nuclear nucleosome	23	0.038755	1.90E-22
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	60	0.1011	3.70E-22
GOTERM_BP_DIRECT	GO:0006335~DNA replication-dependent nucleosome assembly	20	0.0337	1.00E-21
GOTERM_BP_DIRECT	GO:0045814~negative regulation of gene expression, epigenetic	22	0.03707	9.57E-20
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	30	0.05055	2.88E-19
GOTERM_BP_DIRECT	GO:0051290~protein heterotetramerization	20	0.0337	9.70E-19
GOTERM_BP_DIRECT	GO:0045815~positive regulation of gene expression, epigenetic	22	0.03707	1.87E-17
GOTERM_CC_DIRECT	GO:0000228~nuclear chromosome	20	0.0337	3.19E-16
GOTERM_MF_DIRECT	GO:0042393~histone binding	25	0.042125	7.75E-14
GOTERM_CC_DIRECT	GO:0005615~extracellular space	92	0.15502	8.68E-14
GOTERM_BP_DIRECT	GO:0031047~gene silencing by RNA	23	0.038755	7.78E-13
GOTERM_BP_DIRECT	GO:0045653~negative regulation of megakaryocyte differentiation	11	0.018535	1.34E-11
GOTERM_BP_DIRECT	GO:0060968~regulation of gene silencing	9	0.015165	7.11E-11
GOTERM_BP_DIRECT	GO:0016233~telomere capping	11	0.018535	3.07E-10
GOTERM_BP_DIRECT	GO:0006336~DNA replication-independent nucleosome assembly	11	0.018535	1.32E-09

GOTERM_CC_DIRECT	GO:0000784~nuclear chromosome, telomeric region	21	0.035385	1.66E-09
GOTERM_BP_DIRECT	GO:0006352~DNA-templated transcription, initiation	11	0.018535	4.86E-08
GOTERM_BP_DIRECT	GO:0007586~digestion	13	0.021905	2.11E-07
GOTERM_BP_DIRECT	GO:0034080~CENP-A containing nucleosome assembly	11	0.018535	3.06E-07
GOTERM_BP_DIRECT	GO:1904837~beta-catenin-TCF complex assembly	11	0.018535	3.06E-07
GOTERM_BP_DIRECT	GO:0019731~antibacterial humoral response	11	0.018535	3.86E-07
GOTERM_MF_DIRECT	GO:0042166~acetylcholine binding	9	0.015165	4.48E-07
GOTERM_BP_DIRECT	GO:0006342~chromatin silencing	11	0.018535	4.83E-07
GOTERM_MF_DIRECT	GO:0031492~nucleosomal DNA binding	11	0.018535	5.84E-07
GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	24	0.04044	8.32E-07
GOTERM_MF_DIRECT	GO:0004889~acetylcholine-activated cation-selective channel activity	8	0.01348	2.61E-06
GOTERM_CC_DIRECT	GO:0005892~acetylcholine-gated channel complex	8	0.01348	4.41E-06
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	23	0.038755	5.06E-06
GOTERM_BP_DIRECT	GO:0007271~synaptic transmission, cholinergic	9	0.015165	8.57E-06
GOTERM_BP_DIRECT	GO:0006303~double-strand break repair via nonhomologous end joining	11	0.018535	1.21E-05
GOTERM_MF_DIRECT	GO:0005179~hormone activity	13	0.021905	1.62E-05
GOTERM_CC_DIRECT	GO:0005882~intermediate filament	14	0.02359	3.13E-05
GOTERM_MF_DIRECT	GO:0015464~acetylcholine receptor activity	7	0.011795	3.71E-05
GOTERM_MF_DIRECT	GO:0015276~ligand-gated ion channel activity	8	0.01348	6.43E-05
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	118	0.198831	6.97E-05
GOTERM_CC_DIRECT	GO:0045095~keratin filament	12	0.02022	1.89E-04
GOTERM_CC_DIRECT	GO:0000790~nuclear chromatin	17	0.028645	2.21E-04
GOTERM_BP_DIRECT	GO:0035881~amacrine cell differentiation	4	0.00674	2.31E-04
GOTERM_BP_DIRECT	GO:0009235~cobalamin metabolic process	6	0.01011	2.76E-04
GOTERM_CC_DIRECT	GO:0034774~secretory granule lumen	5	0.008425	3.17E-04
GOTERM_BP_DIRECT	GO:0006508~proteolysis	30	0.05055	3.18E-04
GOTERM_BP_DIRECT	GO:0035094~response to nicotine	7	0.011795	6.18E-04
GOTERM_BP_DIRECT	GO:0002227~innate immune response in mucosa	6	0.01011	6.54E-04
GOTERM_BP_DIRECT	GO:0007626~locomotory behavior	10	0.01685	7.11E-04
GOTERM_BP_DIRECT	GO:0007631~feeding behavior	7	0.011795	7.16E-04
GOTERM_BP_DIRECT	GO:0008544~epidermis development	10	0.01685	7.75E-04
GOTERM_BP_DIRECT	GO:0006953~acute-phase response	7	0.011795	8.26E-04
GOTERM_BP_DIRECT	GO:0006811~ion transport	12	0.02022	0.001159
GOTERM_BP_DIRECT	GO:0007612~learning	8	0.01348	0.001233

GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	20	0.0337	0.001454
GOTERM_MF_DIRECT	GO:0015171~amino acid transmembrane transporter activity	7	0.011795	0.002201
GOTERM_CC_DIRECT	GO:0001533~cornified envelope	7	0.011795	0.002296
GOTERM_MF_DIRECT	GO:0005230~extracellular ligand-gated ion channel activity	6	0.01011	0.002383
GOTERM_BP_DIRECT	GO:0010737~protein kinase A signaling	4	0.00674	0.002484
GOTERM_BP_DIRECT	GO:0098655~cation transmembrane transport	7	0.011795	0.002495
GOTERM_BP_DIRECT	GO:0007218~neuropeptide signaling pathway	10	0.01685	0.002622
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	14	0.02359	0.002761
GOTERM_BP_DIRECT	GO:0007585~respiratory gaseous exchange	6	0.01011	0.002767
GOTERM_BP_DIRECT	GO:0050830~defense response to Gram-positive bacterium	9	0.015165	0.003184
GOTERM_BP_DIRECT	GO:0010842~retina layer formation	5	0.008425	0.003349
GOTERM_CC_DIRECT	GO:0034364~high-density lipoprotein particle	5	0.008425	0.003696
GOTERM_MF_DIRECT	GO:0030246~carbohydrate binding	14	0.02359	0.004602
GOTERM_MF_DIRECT	GO:0001664~G-protein coupled receptor binding	7	0.011795	0.0049
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	60	0.1011	0.005193
GOTERM_MF_DIRECT	GO:0033038~bitter taste receptor activity	5	0.008425	0.005348
GOTERM_BP_DIRECT	GO:0001580~detection of chemical stimulus involved in sensory perception of bitter taste	6	0.01011	0.005678
GOTERM_BP_DIRECT	GO:0042391~regulation of membrane potential	8	0.01348	0.005936
GOTERM_CC_DIRECT	GO:0097440~apical dendrite	4	0.00674	0.005989
GOTERM_CC_DIRECT	GO:0043234~protein complex	23	0.038755	0.006172
GOTERM_BP_DIRECT	GO:0006810~transport	20	0.0337	0.006308
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	12	0.02022	0.007416
GOTERM_MF_DIRECT	GO:0005499~vitamin D binding	3	0.005055	0.007839
GOTERM_BP_DIRECT	GO:0032225~regulation of synaptic transmission, dopaminergic	3	0.005055	0.007888
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	10	0.01685	0.008137
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	14	0.02359	0.008315
GOTERM_BP_DIRECT	GO:0007613~memory	7	0.011795	0.008914
GOTERM_BP_DIRECT	GO:0050909~sensory perception of taste	5	0.008425	0.009274
GOTERM_MF_DIRECT	GO:0008236~serine-type peptidase activity	7	0.011795	0.009476
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	33	0.055605	0.009902
GOTERM_MF_DIRECT	GO:0005229~intracellular calcium activated chloride channel activity	4	0.00674	0.0101
GOTERM_MF_DIRECT	GO:0005184~neuropeptide hormone	5	0.008425	0.010347

	activity			
GOTERM_BP_DIRECT	GO:0098532~histone H3-K27 trimethylation	3	0.005055	0.011607
GOTERM_MF_DIRECT	GO:0003677~DNA binding	65	0.109525	0.011666
GOTERM_BP_DIRECT	GO:0018149~peptide cross-linking	6	0.01011	0.014458
GOTERM_BP_DIRECT	GO:0006776~vitamin A metabolic process	3	0.005055	0.01594
GOTERM_BP_DIRECT	GO:0042472~inner ear morphogenesis	6	0.01011	0.016926
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	13	0.021905	0.017825
GOTERM_BP_DIRECT	GO:1902476~chloride transmembrane transport	8	0.01348	0.018249
GOTERM_BP_DIRECT	GO:0007010~cytoskeleton organization	11	0.018535	0.018873
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membrane	12	0.02022	0.019033
GOTERM_MF_DIRECT	GO:0005254~chloride channel activity	6	0.01011	0.019415
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	8	0.01348	0.01978
GOTERM_BP_DIRECT	GO:0016584~nucleosome positioning	3	0.005055	0.02085
GOTERM_MF_DIRECT	GO:0008146~sulfotransferase activity	5	0.008425	0.021305
GOTERM_BP_DIRECT	GO:0035902~response to immobilization stress	4	0.00674	0.021751
GOTERM_BP_DIRECT	GO:0032094~response to food	4	0.00674	0.021751
GOTERM_CC_DIRECT	GO:0042599~lamellar body	3	0.005055	0.021949
GOTERM_BP_DIRECT	GO:0070588~calcium ion transmembrane transport	9	0.015165	0.022334
GOTERM_BP_DIRECT	GO:0030216~keratinocyte differentiation	7	0.011795	0.022672
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	8	0.01348	0.024354
GOTERM_MF_DIRECT	GO:0005104~fibroblast growth factor receptor binding	4	0.00674	0.024451
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	6	0.01011	0.02564
GOTERM_MF_DIRECT	GO:0004983~neuropeptide Y receptor activity	3	0.005055	0.026141
GOTERM_BP_DIRECT	GO:0072488~ammonium transmembrane transport	3	0.005055	0.026299
GOTERM_BP_DIRECT	GO:0035095~behavioral response to nicotine	3	0.005055	0.026299
GOTERM_BP_DIRECT	GO:0006814~sodium ion transport	7	0.011795	0.029884
GOTERM_BP_DIRECT	GO:0008306~associative learning	4	0.00674	0.031062
GOTERM_BP_DIRECT	GO:0001523~retinoid metabolic process	6	0.01011	0.031432
GOTERM_MF_DIRECT	GO:0035240~dopamine binding	3	0.005055	0.032061
GOTERM_BP_DIRECT	GO:0042359~vitamin D metabolic process	3	0.005055	0.032253
GOTERM_BP_DIRECT	GO:0051965~positive regulation of synapse assembly	6	0.01011	0.033407
GOTERM_BP_DIRECT	GO:0019433~triglyceride catabolic process	4	0.00674	0.03456
GOTERM_BP_DIRECT	GO:0008202~steroid metabolic process	5	0.008425	0.035174
GOTERM_BP_DIRECT	GO:0015701~bicarbonate transport	5	0.008425	0.037839
GOTERM_BP_DIRECT	GO:0007274~neuromuscular synaptic transmission	4	0.00674	0.038252

GOTERM_BP_DIRECT	GO:0007399~nervous system development	15	0.025275	0.04038
GOTERM_MF_DIRECT	GO:0042056~chemoattractant activity	4	0.00674	0.0418
GOTERM_MF_DIRECT	GO:0015254~glycerol channel activity	3	0.005055	0.045275
GOTERM_BP_DIRECT	GO:0021846~cell proliferation in forebrain	3	0.005055	0.045541
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	9	0.015165	0.045808
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	23	0.038755	0.046034
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	5	0.008425	0.046508
GOTERM_BP_DIRECT	GO:0008203~cholesterol metabolic process	6	0.01011	0.046862
GOTERM_BP_DIRECT	GO:0031424~keratinization	5	0.008425	0.049623

Table S9. Survival analysis of DEG between high- and low-STXBP5-AS1 expression groups (Only gene list with P<0.05 is shown).

ID	P value	HR	Low 95%CI	High 95%CI
COX8C	0.002984	1.89384	1.24246	2.886715
KRT3	0.003443	1.890205	1.233775	2.89589
COLEC10	0.00769	0.561302	0.367089	0.858267
LUZP2	0.008279	0.563532	0.368157	0.862591
B3GNT6	0.008328	0.561804	0.366072	0.86219
CLCA1	0.011671	0.576876	0.376188	0.884628
GIF	0.011941	0.582207	0.381873	0.887637
VSTM2A	0.012051	0.578595	0.377458	0.886911
GLYATL2	0.013554	0.594046	0.392883	0.898208
HOXC13	0.016032	1.687068	1.102235	2.582206
ITLN1	0.017858	0.597059	0.389648	0.914874
GFY	0.017878	1.655044	1.09072	2.511341
CPN1	0.018671	0.605364	0.398446	0.919737
ITLN2	0.020521	0.611212	0.403	0.926995
GCG	0.021027	0.613834	0.40553	0.929133
DPCR1	0.021535	1.643644	1.075927	2.51092
GPR15	0.023106	0.609272	0.397329	0.934269
C19orf81	0.023211	1.619302	1.068034	2.455107
SLC38A8	0.025795	1.599945	1.058419	2.418535
REP15	0.029968	0.62727	0.411677	0.955768
ATOH1	0.0323	0.621861	0.402535	0.96069
HIST1H4F	0.033227	0.636932	0.420503	0.964756
HIST1H2BO	0.034221	1.577314	1.034477	2.405002
APOF	0.034271	0.639258	0.422431	0.967378
PAGE2	0.035262	1.561772	1.031263	2.365189
FTCD	0.037752	1.547991	1.025036	2.337749
UNC5D	0.040487	0.642471	0.420759	0.98101
PNLDC1	0.045544	1.534386	1.008522	2.334447
GPR83	0.049187	1.520442	1.001493	2.308298

Table S10. Gene signatures of nine immune cells list.

Immune cells	Gene list
Naïve T-Cell	CCR7,LEF1,TCF7,SELL
Effector T-Cell	CX3CR1,FGFBP2,FCGR3A
Effector memory T-Cell	PDCD1,DUSP4,GZMK,GZMA,IFNG
Central memory T-Cell	CCR7, SELL, IL7R
Resident memory T-Cell	CD69,ITGAE,CXCR6,MYADM
Exhausted T-Cell	HAVCR2,TIGIT,LAG3,PDCD1,CXCL13 LAYN
Resting Treg T-Cell	FOXP3,IL2RA
Effector Treg T-Cell	FOXP3,CTLA4,CCR8,TNFRSF9
Th1-like	CXCL13,HAVCR2,IFNG,CXCR3,BHLHE40,CD4