S. Table 1: List of PCR primers used for generation of ORF sequencing library.

		Sequence
First Round	ORF_F1	ACTGGCTTTATATATCTTGTGGAAAGG
	ORF_F2	CAGTGCTTTATATATCTTGTGGAAAGG
	ORF_F3	TGACGCTTTATATATCTTGTGGAAAGG
	ORF_F4	GTCAGCTTTATATATCTTGTGGAAAGG
	ORF_R1	ACTGGTAATCCAGAGGTTGATTGTC
	ORF_R2	CAGTGTAATCCAGAGGTTGATTGTC
	ORF_R3	TGACGTAATCCAGAGGTTGATTGTC
	ORF_R4	GTCAGTAATCCAGAGGTTGATTGTC
Second Round	AmpFW_	5’-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTTTATATATC-3’
	AmpRV_	5’-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTAATCCAGAGG-3’

S. Table 2: List of western blot antibodies used in this study.

Antibody	Company	Catalog Number	Dilution
AKT	Cell Signaling Technology	4685	1:1000
pAKT S473	Cell Signaling Technology	9271	1:1000
β-actin	Cell Signaling Technology	3700	1:1000
IFNγ	Cell Signaling Technology	8455	1:1000
PD-L1	Cell Signaling Technology	13684	1:1000
pSTAT1 Y701	Cell Signaling Technology	9167	1:1000
pSTAT1 S727	Cell Signaling Technology	8826	1:1000
STAT1	Cell Signaling Technology	14994	1:1000
V5 Tag	Cell Signaling Technology	80076	1:1000

S. Table 3: List of qPCR primers used in this study.

Target	Forward Primer (5’→3’)	Reverse Primer (5’→3’)
B3GAT1	GTAATGAGGAGCCGTGGGTG	GTCACTGCCCTCATCCTTATGT
CHSY	TCCGAGCTGAAGCGAGCG	ACAGATGTGTCAGAACCCTCAC
DDX21	CTGAACCGGACTGTAACCCC	TCACTCCTCGGCCTTTGAGA
FGF2	GAGCGACCCTCACATCAAGCTA	CGTTTCAGTGCCACATACCAA
FGFR1	AACCAAACCGTATGCCCGTA	TGCTGCCGTACTCATTCTCC
FGFR2	TGACCAAACGTATCCCCCTG	TGCCCAGTGTCAGCTTATCTC
FGFR3	CCTCGGGAGATGACGAAGAC	CTGATGCCGCAGCTTGATG
FGFR4	TGCAGAATCTCACCTTGATTACA	TGTGTCCAGTAGGGTGCTTG
GALNT14	ACCTGAAGTGCAGACCCCTA	AGCAGTGTGCATCTGACTTG
HECW2	CTTAGAACTCCAGACCCGCC	ACAGATTTTTATCTCCGGTTCCA
IFNA1	ACTCATACACCAGGTCACGC	CAGTGTAAAGGTGCACATGACG
IFNB1	GCACTGGCTGGAATGAGACTA	CACTCTGACTATGGTCCAGGC
MYC	TACAACACCCGAGCAAGGAC	CTAACGTTGAGGGGCATCGT
NOP56	TTCGTCTGGTGGCCTTTTGT	GAAGTGCAGACGAACTCCTCG
ODC1	TGTTTTTGACATGGGGGCTG	TGTCCAACGCTGGGTTGATT
ST3GAL6	GTGTTTACTTCTGCCGCCTG	CATGGCTGGCTCACCTTTCG
ST6GALNAC5	TGGCGGACCACAAGGAAGATA	TAAAGCGGTGATGACTGCCC

S. Table 4: Sanger sequencing of selected clones serially sorted for PD-L1^{high} expression.

Clone #	ORF
A	SLC10A7
B	CTH
1	SENP8
2	SENP8
3	PPIAL4G
4	CNR2
5	DPF3
6	TMEM25
7	ZNF550

S. Table 5: Enriched ORFs in PD-L1^{high} sorted population.

Barcode	Gene	Unsorted Read Count	PD-L1^{high} Read Count	Total Read Count Normalized Ratio	Log2 Normalized Ratio
ACTTCATCAGCAGTGAGAATTCCA	ERO1L	7	10889	1208	10.2
CACGACGACATGGGTTATATCGAA	NUP85	3	4378	1134	10.1
AGATCAACGCGCCCATACGCACAT	OR2L2	15	19065	987	9.9
GCAGGATATTGGTTACATCGACCT	TDP2	120	111075	719	9.5
CCGAACACCCTCTAACTCGGCCTC	ATF7	352	290057	640	9.3
AAGAATATGTGGTAGTGCTTGATG	AMT	48	29441	476	8.9
TGTACACTCGGTGTGATTTGTAGT	GSTO1	245	146097	463	8.9
GATCGTATTAACTAGGCTAATGGC	SPACA3	5	2513	390	8.6
AATTCCCATTGTGATTGGGCCTGC	ZNF101	52	19317	289	8.2
ACCACTAAGGGACAGCAAACCTTC	HNF4G	158	53187	261	8.0
TGGCTCATAGCACCATACCCTCCT	PPP1R2	99	31497	247	7.9
CTTAGTCTTCATCCTCGTCTTATT	FAM209A	1	293	228	7.8
ATGAGCCTTATTGGAGGCTGAAAT	LINC00242	129	33748	203	7.7
CCACCTTCCCACCCTCACGAACGA	ENOSF1	9	2159	186	7.5
AGAAGGCACGCTTCAGCCGCGCCG	ZFHX2	216	48351	174	7.4
ATTATGTTTAGAACTAATATCTAG	ZNF581	132	28361	167	7.4
AACCGATGCCTTAAAGGGTAGTCC	TALDO1	29	5796	155	7.3
TGTACCCGCGAGTCTCCACACCGT	HTR2C	1	178	138	7.1
TTTAAGATTTCTGGGCTTCCCCCT	ABHD12B	5	850	132	7.0
ACTAAATTCAGTGATGCCACATAC	C8G	93	15030	126	7.0
TAAGCGAATAGTACCAGGGGTTGA	DNASE1L1	88	13212	117	6.9
CAGTGACTTATCGTATTTGTCTGA	DNM1	2	290	113	6.8
CTGATTCAGACAACGAGCATCAAC	CTSL1	125	16125	100	6.6
TCTCTTGGGAGGTGCATTCGATCA	PPIAL4G	122	15117	96	6.6
GCCCATCCAGCATGGCGGATTCCC	EFNA1	87	10319	92	6.5
ACAGCACTAGCAGGAACCTGGACT	TMED4	203	22053	84	6.4
CAACACGAGGCCATACATTGCTTA	PRKAA1	23	2471	83	6.4
TCATTGCTGTACATCTAGAGTTCG	S100A1	6	618	80	6.3
CTGTATAGACTGGCCGTCGAACTT	KRT23	12	1225	79	6.3
ATCGCTCCCTTCACAGTAAGCATA	C1ORF49	53	5353	78	6.3
TAGACGGTTTTATACGCTCAGCCA	EFHD1	100	9775	76	6.2
TAGAGGAAAGAATACAGGATCTAC	DLX6-AS1	397	38327	75	6.2
TAACTTGACGAAAGGACCCTGTGC	EIF4B	14	1328	74	6.2
CAAATCGCCTGACCCCAATAAAGA	BOD1P	12	1095	71	6.1
AACCCGCAACATGCCCGGTGGTCA	CPEB1	5	436	68	6.1
TAGTACCAAAAGCTTAACAGCGTT	ATCAY	26	2176	65	6.0
CTAGACATACATGATGCGGCACCT	ADORA2B	92	7575	64	6.0
CTATAAGAGCTCAATCACTGCGGA	TCN1	10	804	62	6.0

TTAGCTCCGTGCCGCGATATGAAA	BDNF	36	2867	62	6.0
AGAGTCCATTCTCCCACTATGCCC	REP15	227	17349	59	5.9
ACTTTTCCCGCTTGTCCTGCCCCC	GRK6	1	74	57	5.8
CCTGTTTCCCCCGACCCTGAGTCG	RASA3	2	138	54	5.7
AATTAACTGTTCATCCGAGTCTTT	ZCCHC9	1	68	53	5.7
GTGTTCCCCGCGGTCTGGCGAACG	TP73-AS1	81	5274	51	5.7
TTAACTTCAATTCTCTTTTTAATT	DIMT1	21	1294	48	5.6
CCTGGTTGCCCCTCTAGGGCTTGA	DPY19L2P1	151	8998	46	5.5
GCCACTTTGTAGGCGCCATTCGAC	CAPN1	1	59	46	5.5
CACTATATCAATGTTTCCATTCGT	FAM78A	8	462	45	5.5
TACCTGATAATGGCACCATGCAAA	DEFB129	259	13571	41	5.3
CCAATCAACCGGGCCCCGAAACTC	CDK16	10	522	41	5.3
CACCCTATCGTCGAGGTCGACTGC	PRAMEF5	63	3288	41	5.3
TCAGCCTACCATCAACTTCGTATT	SET	1	51	40	5.3
AAGCTGGGATTACTTCTGTACGGC	EEF1G	133	6536	38	5.3
AAGTGGGAGAGTAAGTGCCTGGTC	PRB4	371	18019	38	5.2
TTCGTACTCCGGTTCCTGTGCTTC	RHOG	213	10224	37	5.2
GGCATATGTCCTGACATCTGGCAG	CHIA	111	5244	37	5.2
CCGCATAAGGCCAGATCGGTGCTC	CAMLG	43	1997	36	5.2
GATACCATACGACATCCTGTTCAC	CCNL1	13	598	36	5.2
ACCTACCTCCTGACACATCAACTT	CNBP	216	9539	34	5.1
CCTCACAGTACTTGCCATCCTGAC	RBX1	278	11605	32	5.0
AGCAGAACCCTTAAAAGCTCGAGT	CST8	227	9049	31	5.0
TGTTGAATCGGTAACGATGACCTG	CDX4	24	942	30	4.9
TGCCCGTGTTCTCCATCAGGTTTA	TRIM72	1	39	30	4.9
AACTATTAGTGCCCGAGTCATCCC	CD82	57	2195	30	4.9
GTTTGTTCTAAACATTGCGACATC	ZNF578	9	339	29	4.9
TACACACCCTTCTTAGCCATTCAT	***NFKBIA***	242	9003	29	4.9
TCGGAAACCAGAACTATTAGTATA	RHPN1	3	111	29	4.8
CTACAATTTCTGTTCTGCACCTTA	ASIC1	18	659	28	4.8
TCCAACACAGCGAGCCTCTTGGCT	TNFSF11	79	2841	28	4.8
CACGCCCACCCGTGCCAGGACTAC	OR7E91P	45	1617	28	4.8
TCAAGATACCCTTGACCAAATGTT	ZNF550	25	883	27	4.8
ATTAACAACCATCCTGTCCTGGCC	C1QTNF2	255	8720	27	4.7
TTTAGACTGGTTTTGTAAGAGACC	UFSP1	152	5090	26	4.7
ACCGAGTCCGAATAGTTTATTCAG	HOOK1	23	764	26	4.7
GTCAACTGGGGCATCTGGCACCTC	ARHGEF26	222	7316	26	4.7
AGCTCAATCAACTCAACCTTACAA	KLRC1	101	3228	25	4.6
CCCTATGAAGGCCTGAAGCGGGCA	METTL21A	464	14778	25	4.6
GCACCGATACCGATCCCCCCAATC	GALNT10	147	4385	23	4.5
GTAGGTGCAAACGCGAGACAGACC	MAS1	168	4858	22	4.5
TTCAAAGAACAGGAACGGGCTCAT	FMN1	33	943	22	4.5
CTGGCATGCTAACCAAGTACACGC	CDH26	306	8694	22	4.5
CAAAGGCCTAAGAGGACAGAGAGT	ORAI1	185	5160	22	4.4

TCTTGCTACCGGTGACATTCTCCG	KCNJ15	51	1420	22	4.4
TGAATTGTCGCCCCCAGATACACC	ZCCHC10	208	5745	21	4.4
GCCTAATTCGTGACGTCCCCAAAT	DCLRE1B	10	276	21	4.4
TTGCCGAACCGCGCACTCAGAATC	PIAS4	15	385	20	4.3
ACGCGCCCGATCCCCACTTCCAAT	ANXA11	74	1865	20	4.3
ATAGAACGTGACCAATCGTTGTTT	PIPOX	20	491	19	4.3
GCTGTAGTGTGCCCGCTGAGGCCT	PRKCZ	9	218	19	4.2
ACCAGAATGATACCTTGATCTCAC	GPBAR1	8	191	19	4.2
GTGATACCTCCTTCTCCCGACCCA	ASPDH	65	1547	18	4.2
CCATTCCACCTAGAGAATTTATAC	P2RX2	1	23	18	4.2
CGTCATTATATTCCTCTCCAGGAT	KIAA0284	55	1233	17	4.1
ACTTCCTGGAGAGGGGCTAACAGT	WBP2NL	200	4481	17	4.1
CTTAATAAGTCGAAATCCGAGGAC	GPR139	13	290	17	4.1
TGGCCCATCAAACGAGCCTTATTT	AKR1B1	46	1011	17	4.1
GAGGATGTCACACCACGATATCAT	SLC22A11	27	581	17	4.1
CTTGCCCCCATCACCCATATTTCT	CMTM2	339	7270	17	4.1
ACACCGGTCTGCTCCCGATCGGGC	TNFAIP2	85	1805	16	4.0
TCGACGGACATGGGAAAGATCAAC	REEP5	142	2956	16	4.0
AACCTTACTAATAGCTTGGTTGCC	CCDC138	9	187	16	4.0
AGCAATCTTACCGGAGCAGTTACA	CEACAM8	18	373	16	4.0
TCAGAGCAATATCCCATAATCAGT	RUVBL1	109	2242	16	4.0
TTGATTTCCAGTGCGAGAAGACCG	HMX2	16	316	15	3.9
ATTGTCAATGGTTTGATCTCAGCA	FOS	99	1952	15	3.9
TTCCGCCCTGTATTCCGGTACGTC	ENTPD2	8	156	15	3.9
TATATGTCTGAATACTCCGATCAG	OR14J1	4	78	15	3.9
AAGCACATCCGTTGTGCGCACAGA	BAMBI	19	359	15	3.9
ATCGAGGGTCCACGTACCTGTACT	RABL2A	113	2132	15	3.9
CATCACATATAAATGAGGACATGG	STRN	10	184	14	3.8
ACCTTAGACGCTCCTTTTCGCTGA	TAC1	97	1764	14	3.8
TCTCATCTGTCCCTGGCCCCGTAA	TERF2IP	16	285	14	3.8
ACGCCGAGATCCGCATAAGCCGTA	GLO1	76	1350	14	3.8
CCATCCTTACCAGAAACAACTCCC	UBE2W	102	1800	14	3.8
ATCACAACTATCGTTATTTACCGC	KCNAB2	11	194	14	3.8
GGTCGAATGGTCGCATTAGATTCC	HIST2H2AA3	91	1592	14	3.8
CATCATTCGCCTCTATCAACAATA	ZNRD1	82	1424	13	3.8
ACTTGCATCCTGCCCCAGAGGCTG	OR56B1	8	132	13	3.7
TCTGAAAAACTCCGAAATAGCAGA	HINFP	47	768	13	3.7
AACTACTATGGGGCCTTGCACCTT	RHBDD2	160	2599	13	3.7
TCGACAGCACTCACGGGTTAGCAG	LINC00482	48	767	12	3.6
TAATTAACCGTTTGAACTGCAACT	SAMD10	44	690	12	3.6
ACTGAGCAAGTCCCCCTTCCTATA	C7ORF42	112	1755	12	3.6
GTTCGGAGAGGCTCTATGGTTGGG	DUSP10	61	953	12	3.6
CAGCCTTAAACAGACTTCATAAGC	HSPA8	56	865	12	3.6
CCGCAGGTCTTCTGTTTTTAGGAT	FAM71B	17	262	12	3.6
TTCTAACCCCTTTGTAGACCAATG	HIST2H2BA	443	6778	12	3.6

CTGAGGCAGCGTCGGCTATTCGCA	MST4	217	3280	12	3.6
AGCCAATTATCCTGTTGTGTCCCG	ANAPC16	222	3188	11	3.5
GTTCGCTAAATCCGTTCTCCCGGC	LRRC52	74	1061	11	3.5
ACGCTCAATGAGTGCACGCTCACC	PCSK9	94	1324	11	3.5
TTGTCTTCTATTATGAGTTGCGTA	CXCL5	43	596	11	3.4
GCTTCTCTAGTGAAAGTAATTTTG	FMR1	14	189	10	3.4
ATAACCAAGTTATGGAAACAGGCC	CPSF4	97	1305	10	3.4
GGGACCATAATGGCGATCCATTAG	AREG	6	80	10	3.4
TCCCGTGTGAATATTTTGGCCTTT	DHPS	68	903	10	3.4
AGTTGTGCCCCTCGGAGTGCGCCA	GPAA1	2	26	10	3.3
CCTAGACTGTACCTCCCATGGACC	COQ4	219	2814	10	3.3
TAGTGTTCCCTCCATCTATCGAAG	TMPRSS12	6	77	10	3.3
GTAGTACAATACCCCGAGTCGGAA	GJA4	35	443	10	3.3
CATGCGCTACTTAATTGAAGTGCC	BCMO1	13	163	10	3.3
TTATATTCCCAGTAGGGCTAGGAG	CLDN7	12	148	10	3.3
ACGATCAACCTGCGTTTTCCCGCA	APOPT1	175	2091	9	3.2
CGCAGGTTGCACAGAATGCTCGGT	EPB41L1	27	319	9	3.2
CGGCATTCCGTCAATTGCCGAACT	PMCH	67	777	9	3.2
CGCAAATACTTTCGGATGGCATCC	C1ORF64	212	2424	9	3.2
TCAGTACTAGGAAGGTCTCTACGA	MAX	73	828	9	3.1
GTCCGTTTAAGAACGTTTCGGCAC	C11ORF31	158	1789	9	3.1
TTATCATTCTGGGGATGGCAGGAG	PLEKHB2	124	1401	9	3.1
CCCTCCCAGTGTTGACTGTATTCC	GCNT3	60	667	9	3.1
GGGCGTGAGATAAAAGTGTAAAAT	MTERFD2	85	929	8	3.1
TAGGGTATAATAGATGATCCTGCC	ST6GALNAC6	29	315	8	3.1
CTTAGCCAATGGGTGCATCCGTGG	OR51G2	18	195	8	3.1
AGCAGACGTTGCATGCGCAATTCA	RANBP10	67	718	8	3.1
CCGCAGTCCCCTTCGCCGGAGATC	GFOD2	42	446	8	3.0
GCATGGGCCGAGCGCATTTCGCGG	FAM27E2	275	2793	8	3.0
ATTCGCGGCTATGCAGGGGCACTA	RHBDL2	5	49	8	2.9
CATAGTAGCGCACTACAGTTTAGC	REEP6	26	251	7	2.9
ACTTCGACGTCTGGAACCAGTCTC	C1ORF158	90	857	7	2.9
TTTGGCATCCCCCCTGTAGTGCGC	ZNF689	71	675	7	2.9
ACAGGATACATGATTACATGCCCC	SHMT1	11	102	7	2.8
TCTAAACGAACGCATCCCTGCCCT	PF4V1	34	313	7	2.8
TATAAGGCACCCAATAACCGAGAT	RORB	70	638	7	2.8
CTGCGACGCGGTACTGACGAATAT	C11ORF63	74	659	7	2.8
ACTGGGTCACAGTAGTGATTACCC	TGIF2	317	2810	7	2.8
CTTCGTGACAATACCTTTCGGAAT	CDK2	11	97	7	2.8
GCCCAGCTACACAACCAAGTTGCC	PYY	488	4288	7	2.8
GGGTCAGTAGTGGATGTACCAGTA	LOC554223	53	457	7	2.7
GCAAAGACACGTAGACGATAAGCC	FAM83A	62	515	6	2.7
ACACAAACGCTCATCAGCCCTGGC	CD300LB	127	1048	6	2.7
TGACGTCCGTCCCAGACCGTCTGC	GRB7	39	314	6	2.6

GAATTTGTCGACGTGCTTTGAGGA	TRIM52	65	521	6	2.6
CATATCACCAAATTTATTCCGAAC	KIRREL3-AS3	107	851	6	2.6
TTGACTTTGATGTATCAGATCTAC	***CD300C***	162	1253	6	2.6
ACAAATTCCGAGATAGACGTCCAA	DCTN3	127	981	6	2.6
CCAGAATTACGCACTTGTCGATGT	SLC39A7	45	345	6	2.6
TCTCAGTCTCCACTCGTCTTGAGA	SUOX	50	376	6	2.5
ACAAGATATTAACGCTCGGCTGGA	KIAA1467	19	139	6	2.5
ATGACTGTGTTAGGCGGCTCACGG	TIMM17A	128	915	6	2.5
TAGTATGACGCGAGCAGTTCTAAA	SH2D2A	123	871	6	2.5
CACTTATCGGGGTCATTCGAGGTC	ZCCHC2	44	310	5	2.5
TATCCCCCCTGGAGTCGCAGTCCT	LOC541471	399	2808	5	2.5
AATGATGTAGTCCGTCATCCTCAA	LINGO1	3	21	5	2.4
TTCCCCGTTCCTAGAAGGGGCAAA	CHRM5	2	14	5	2.4
TCCCGAGATTACATTTCAGACAAT	ADA	48	335	5	2.4
CGTTCACGTCATAGCGTTCCCGAA	AKR1C2	31	215	5	2.4
CAAGAGCTACGATCTACTCCCCCA	NR1D2	47	321	5	2.4
GACGGCAACTTCGGGAATCACTAG	PNMT	124	839	5	2.4
CACGCCAAAGAAACCTCGAAGCTG	CHCHD7	680	4594	5	2.4
AGTAGGTTCAACCGCAAACAGATC	NOA1	19	126	5	2.4
GTCAACGACCTAAGGAACTCGTGC	LAIR1	21	138	5	2.4
AAAAATGGGCGCTCTGAGACACAC	ZNF680	11	72	5	2.3
TGTAGAAGTTTCTGGATAAGCCAC	SLC50A1	130	849	5	2.3
GTGCTGACATCTAACCCGTCTAGA	HAND1	62	402	5	2.3
TCGTTAGTTGTCAAATGCCAAACC	STK32C	5	32	5	2.3
TGTCCCCATCACCATGAGTGCCGT	VMAC	146	933	5	2.3
ATGCTGGGAAGCGATAATCGCGTA	BCCIP	44	277	5	2.3
CAATCGACGCTAAAGTGACCAGGA	RPL14	158	982	5	2.3
TGGCGCATCCTAAAGTGTAAGATT	HSBP1	126	779	5	2.3
ATACCCTGTCGGTTGGTCAATCAC	ULK4	8	49	5	2.3
CACCTCATGGGGCGTAAGCCCAGG	CA6	168	1028	5	2.2
AATGCGTTCGTGACACTTACGCCT	PSMC4	5	30	5	2.2
CTTTCAGGTTGCACAGCGGACTTC	PRAMEF10	50	297	5	2.2
GTGCCCACCTTTAGACGTAATGGC	PPP1R1A	274	1610	5	2.2
TTCATTACCATAACTCGGTGGCCA	CCDC114	48	279	5	2.2
TGCTTTCTGCCCCCGTATTAGTAG	HSPB6	130	746	4	2.2
CCGTATATTTCTATTTATTTATCG	TGS1	25	141	4	2.1
GATTATACTTTCACGTGGACACGA	IGHD	60	337	4	2.1
CTGACGTGCCCTAATTCCCTGTGC	NDUFA10	75	421	4	2.1
GGACACTACTCCGTAAAGGTACGT	MPZL1	51	285	4	2.1
TGACAGTGGCCAGGCGACCCGCCG	LOC339535	17	95	4	2.1
GTGCACCCAGGGCCGTGACTGGAG	TMEM25	119	660	4	2.1
GTTCCAGTTGCCGCGCCGGGGTGC	NAALADL2	101	556	4	2.1
CCTCTGTCACAGGTACTCTCTGTT	CTC1	43	235	4	2.1
ATGGGTTCTGTAGGGCCGCCGCAA	ZDHHC15	158	859	4	2.1
ATAACCATTGAGGGTAATTTTTAC	C7ORF49	83	450	4	2.1

ACCCGAATAACATGTAATCTCCCT	EIF5A	68	364	4	2.1
ATAATCAGGGTGTGCCGATCCTGC	PPYR1	76	402	4	2.0
TCTTGAACCTCGAGATTATGACTC	SLC25A44	57	299	4	2.0
ACTATAGCACACTGAAGGTTTGAA	LIMK2	21	110	4	2.0
TATTTAGCACGCAAGAGCCGGAAC	GABRA5	13	68	4	2.0
CAAGTCCCGCTACGTGAGCGCCAA	OR2T2	16	83	4	2.0
ACACATTGTTACCGCCACGTTGAG	RPL15	83	429	4	2.0
GTGGCGCCAAGTCGCAATGGACTC	DNAJC7	12	62	4	2.0
CGCACATCAAGTCCCCAGTTCGTG	SYNGR1	141	714	4	2.0
GTCTCCTATTTACTACCTCCCTCC	TNFSF18	96	484	4	2.0
AGGTTTAAGGCTCCGCATCTAATC	CHCHD2	3	15	4	2.0
GGGGGATCTACGATATGACAGGCG	SLC25A22	62	307	4	1.9
CCCCCAATCGTGCTCCTTCACCTG	HN1L	52	257	4	1.9
TCTCAGCTTTCATATGACGGCCAC	DAP3	34	167	4	1.9
AAAAAAGTCGCCATGCCAGAACAA	SEMA4C	29	142	4	1.9
TTAAGGGTAACATGGCTACGCACT	UTP23	185	893	4	1.9
GCAGGCCTTACTGTACTCCTCAAG	ALG2	137	659	4	1.9
CATCTACGCACTTAACAACACTCT	DDX19A	101	483	4	1.9
ATCCGACAGTATGCGCCCTAGTGA	ECD	18	86	4	1.9
TTGTTCTAGCATATTTTATTACAA	42990	32	151	4	1.9
GTCATGATTAGTTTTATACGATGT	CHRM4	14	66	4	1.9
GTACTCCTACCTTATTCTCGACCG	DNAJB1	49	231	4	1.9
GTGCGGCTGTAGGATGTCGGGCCA	TSPAN15	9	42	4	1.9
GGTTCACAGTTTTTGAACTCAACC	CHI3L2	43	200	4	1.9
AAACTGTACGAACGTCTATCCGGT	SNAPC2	14	65	4	1.9
GGCTCATATTGGCAGGAGAAGAAG	CBFA2T2	130	603	4	1.8
ATATGCAGTGAATTAAGGCGATCA	SIVA1	218	998	4	1.8
TTCCTAAATACAGTTACCTAACCA	CATSPER4	35	160	4	1.8
GGACACGGGCGTGCCCGATTCACG	CCDC65	16	73	4	1.8
TCCTCGGTTTCTGACTGATCCCCC	GPR20	60	273	4	1.8
CTTTCCGCGGCGGTGGCGCCGTTG	GPER	5	22	3	1.8
CTGAAATGTTCCCGTACGGGTACG	CER1	199	875	3	1.8
CGATACCATTACCGACTTTCAATC	WISP2	58	254	3	1.8
TTCCAATAACGCTAAGACGACGGG	PARVG	55	240	3	1.8
GACCTACGAGGTCAGACATACTCG	RPS2	27	117	3	1.8
AGGACAGAGCCAACGAAAACGGAT	AIPL1	42	181	3	1.7
AGTATCTCTCAGCGAAATAGTGAC	ZCRB1	25	107	3	1.7
TACACGATACCCCGTGCTGAGACC	C1ORF87	44	187	3	1.7
TGGCCGTGCGGCGTCAATTGTCCA	RAB28	59	250	3	1.7
CCAACCCCTACGACAGTCGAGTGC	SUCNR1	225	946	3	1.7
AGAGGTTTGCTATCCCGTCCTCCG	EBAG9	114	475	3	1.7
ACGTTGCATCCCAAGCTTTGAGAG	CCDC146	72	298	3	1.7
TCATGTTACCATGCAAAAGTGATG	NUDT3	134	550	3	1.7
GCTCGCCCGCTCGGCTTAGGCTCA	WHAMMP3	29	119	3	1.7

TGACTTCAAATGTACGGAAGGTAA	C10ORF125	143	583	3	1.7
TGGCCCACCCGCCCTTACGGCATA	C7ORF34	500	2029	3	1.7
TGGTCAGTCATACAACAGGCAGAC	EXOC2	2	8	3	1.6
CCCATCTACTAGCATTGGGAGGTT	C12ORF4	1	4	3	1.6
CGTGCCTCGTCCCGATTTAGCTAT	GPR82	1	4	3	1.6
GCCCTCTAAAAATCTACTTCAGCC	TSPYL1	13	51	3	1.6
ATCACATGGAGAGCAATGTTGACC	CYCS	574	2244	3	1.6
ACCCCCATCCAACTTCCGGATCTA	MFF	11	43	3	1.6
CTAAGGACACAGGCTCCACGAAAT	CPA3	111	432	3	1.6
CTCTGAGACGCTGCAATCGACGAT	TMEM35	224	869	3	1.6
ACCTAGTCTGGCCTCACGTTAAGG	TMOD3	156	605	3	1.6
GCACGGCCCGTAGCCCTATCGCCC	FAM27L	71	272	3	1.6
TCTCAATACCCAATGCCCTTTTTG	ATG10	181	684	3	1.6
GCACAGTCTCAGAGTGCCACAACC	TAS2R3	331	1247	3	1.5
TGTGGTTCTCGGCCTTCACAGGTC	RPL14	240	899	3	1.5
CCAAGGACAAAGTCTAGAGAGCCT	EIF4E2	69	256	3	1.5
TATTACCGGGCCGTATTAGTTGAA	TEX2	31	115	3	1.5
CTTAAAACAACCCATCCTCCGGTG	PRAF2	102	375	3	1.5
GTGACGGTAGCCACATGTTCCTGC	RPL19	151	554	3	1.5
AGCTTAGCACTATAGGTAGCTATC	OSTM1	3	11	3	1.5
GCGGAGATACGACCCTACCACACC	COX4I2	232	846	3	1.5
CGCGGTAAGCACCTCATGCGCCGC	CEPT1	70	254	3	1.5
ACATCAGTACCCCCGCAGATCGTC	DMWD	128	463	3	1.5
TTCGCTAATCATTAAAAAAACGGA	NAGS	29	104	3	1.5
CGGACTTCGCGTGCGTAGGTCTTC	FGR	7	25	3	1.5
GCAATAACTGAACTTGTACAATAA	TYRP1	42	149	3	1.5
GCCGCTTTTGGATGTACCGAGTTG	C17ORF53	58	205	3	1.5
TGCCGCCATCCGATTAAGTCCCAT	TRIM13	31	109	3	1.4
TCGTAACGCCAGGTATCTCGGGTA	PCK1	4	14	3	1.4
CGAACTACTTACCTAATCGTGGGA	MST1R	141	493	3	1.4
CTTGTTCGTCGTGTTAGGATCGTT	CCDC42	70	244	3	1.4
TAAAGTCTGCATATGCCAAGCTGG	SNAP47	188	645	3	1.4
TTTTTAGACCATACGTGGGATTTT	GSTA1	14	48	3	1.4
CAACCTGAGAGTGTTGACCGAAGA	C14ORF79	319	1074	3	1.4
TGATAGCCGAGTGACCACCTTTTT	NRIP3	196	656	3	1.4
TAACCAACTCCCCTGTGCTCTGGG	SEC61B	86	287	3	1.4
GGCTTATTAGGACTCATCGCGCCC	TXLNA	3	10	3	1.4
TTTCTTGGCTTGCACTGTGACCGC	NUDT14	99	330	3	1.4
CCCAGTGGGGTCCGGGTCAACTCG	TMEM206	16	53	3	1.4
ATCATTCGCACAACCACGAACTCA	CCL4	1293	4240	3	1.3
AAAACGCGAACATGTACCTCGCAC	DGUOK	31	101	3	1.3
TGCCTTGCCGTAGTCAAACTCACC	ZNF416	8	26	3	1.3
AACGCCAAACCATATGCACCGTCC	C3AR1	56	182	3	1.3
AAGTCTATCAAAAGTCCCATCACT	ACPP	30	97	3	1.3
GCTGACCAGAAACTCTGACTATTT	LACRT	220	708	2	1.3

ATCACAGGCGGCGTAGCCGACCCG	BMS1P5	253	813	2	1.3
GATGCGGTGTGACGGATGTTCCCA	GOLGA7	183	587	2	1.3
GATTTGCACCTTAGACAGGGGGTC	TOLLIP	118	376	2	1.3
ACAGGTGTTTTGGCCGACTACTAA	C15ORF53	102	325	2	1.3
ATCCAAATGCGCGCCAGTTGCCTA	MRPS11	170	530	2	1.3
TCAGGGACACTTACAAGCCGGCGT	LINC00518	103	321	2	1.3
ATCAGACACGCCTATCCTACGAGG	SPATA8	161	501	2	1.3
GCTGCTAGCTATCAAGTTAAAATT	C22ORF31	53	162	2	1.2
CCGGCGTACCTCCTACCTAACATT	MRPL43	126	383	2	1.2
AAATCCTAGTAACGCCCCAATATA	RIMKLA	56	168	2	1.2
TCTCAATATACGGCGGTAAGTGCG	NANOG	1	3	2	1.2
CTTGTACGTCAGTAGATCATTTTC	WDR18	1	3	2	1.2
TGTCTCGTCCCATTAAAGGTGTCG	TREML2	1	3	2	1.2
CCTGGACACAATCTCTGCAAATTA	JPH1	25	74	2	1.2
TGCAGCTTTACAACATGCACTCTG	PDE6D	136	401	2	1.2
TTCGACGTAGATCTATGGGCGTGC	ANKRD49	70	206	2	1.2
CGTGTTGAAGCGCTGCGCAGTTTG	NPR3	82	240	2	1.2
GAAAACAGTATACCGCTGCCGACG	TRIB2	24	70	2	1.2
GTGTCATGCCCCCCGTTTACCGTT	PPIE	24	70	2	1.2
AAATTACCTACGATATTCCTATGA	GPR162	71	207	2	1.2
CTTGACCCATCCGACATATTACTC	MB21D1	101	294	2	1.2
CAGAGTACTCCGAGACTACAGGTC	C2ORF73	138	399	2	1.2
GTTGGCCATCACCTACGCAATTAC	CCDC28B	226	638	2	1.1
TCGATGTTAACGCCTCGAGCACTT	SLC25A10	106	299	2	1.1
GGACCCGAACGTCACTGCTATACC	DAD1	9	25	2	1.1
GAGACGCCGTACGACATTTTTAAA	PPIL1	28	76	2	1.1
GGCGAACTGTGAGTTTGTTGCACC	IL28A	258	684	2	1.0
TAGCGCTCCGCATCATCGACTTGC	TXNDC11	74	195	2	1.0
AAATTTGTATGCCACCGTCGCCTA	***FGF6***	352	921	2	1.0
TACTAAATTCACTGAAACCATTAC	***IL17A***	504	1309	2	1.0

S. Table 6: Gene family annotation of overrepresented genes in our genome-wide ORF screen.

Gene Family Annotation	**Cytokines and Growth Factors**	**Transcription Factors**	**Homeodomain Proteins**	**Cell Differentiation Markers**	**Protein Kinases**	**Translocated Cancer Genes**	**Oncogenes**	**Tumor Suppressors**
Tumor Suppressors	0	0	0	0	0	0	0	0
Oncogenes	0	1	0	0	0	3	3	
Translocated Cancer Genes	0	1	0	0	0	3		
Protein Kinases	0	0	0	1	12			
Cell Differentiation Markers	1	0	0	7				
Homeodomain Proteins	0	5	5					
Transcription Factors	0	20						
Cytokines and Growth Factors	18							

S. Table 7: GSEA of cellular pathways enriched in PD-L1^{high} cells.

Enriched Gene Set Name	No. Genes in Gene Set (K)	No. Genes in Overlap (k)	*p*-Value	FDR q-value
GO_RESPONSE_TO_EXTERNAL_STIMULUS	1821	43	2.99E-12	6.63E-09
GO_CELL_CELL_SIGNALING	767	26	4.44E-11	4.93E-08
GO_REGULATION_OF_RESPONSE_TO_STRESS	1468	36	7.36E-11	5.44E-08
GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1403	34	3.50E-10	1.55E-07
HALLMARK_MYC_TARGETS_V1	200	7	5.31E-04	1.33E-02
HALLMARK_TNFA_SIGNALING_VIA_NFKB	200	7	5.31E-04	1.33E-02

S. Table 8: RNA-seq GSEA for INFγ-treated and FGF2-treated UM-SCC-14a cells identified 168 and 121 positively correlated gene sets, respectively, and 1 and 3 negatively correlated genes sets, respectively.

Correlation	IFNγ_Control	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
Negative	KRAS.LUNG_UP.V1_DN	140	-0.7433987	-1.8223642	0	0.0051953	0.007
Positive	HALLMARK_INTERFERON_GAMMA_RESPONSE	198	0.90554595	2.2204711	0	0	0
Positive	HALLMARK_INTERFERON_ALPHA_RESPONSE	95	0.9612267	2.1719477	0	0	0
Positive	GO_RIBOSOME_BIOGENESIS	264	0.84289455	2.137643	0	0	0
Positive	GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	454	0.80612314	2.1235926	0	0	0
Positive	HALLMARK_MYC_TARGETS_V1	197	0.85763717	2.098156	0	0	0
Positive	GO_NCRNA_METABOLIC_PROCESS	428	0.7894097	2.0703828	0	0	0
Positive	GO_DEFENSE_RESPONSE_TO_VIRUS	231	0.830162	2.0657225	0	0	0

Positive	GO_RRNA_METABOLIC_PROCESS	194	0.8365136	2.0526576	0	0	0
Positive	GO_NCRNA_PROCESSING	352	0.7943593	2.0520508	0	0	0
Positive	GO_RESPONSE_TO_INTERFERON_GAMMA	192	0.8347406	2.0390162	0	0	0
Positive	GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	87	0.9038718	2.0353277	0	0	0
Positive	GO_RESPONSE_TO_VIRUS	314	0.7923952	2.0324743	0	0	0
Positive	GO_RESPONSE_TO_TYPE_I_INTERFERON	95	0.88454956	2.0047338	0	0	0
Positive	GO_MITOCHONDRIAL_GENE_EXPRESSION	151	0.8299274	2.000083	0	0	0
Positive	HALLMARK_ALLOGRAFT_REJECTION	199	0.8181267	1.9989552	0	0	0
Positive	GO_MRNA_TRANSPORT	147	0.8146503	1.9499222	0	0	0
Positive	GO_MITOCHONDRIAL_TRANSLATION	129	0.835553	1.9442384	0	0	0
Positive	GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	160	0.800192	1.9383287	0	0	0
Positive	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	118	0.82819223	1.9348161	0	0	0

Positive	GO_RNA_EXPORT_FROM_NUCLEUS	136	0.8188273	1.9322176	0	0	0
Positive	GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	192	0.78919905	1.9280034	0	0	0
Positive	GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	268	0.76488715	1.9277563	0	0	0
Positive	GO_VIRAL_GENE_EXPRESSION	189	0.79552704	1.9270865	0	0	0
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION	219	0.7741375	1.9209396	0	0	0
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	184	0.79390395	1.9189066	0	0	0
Positive	GO_RNA_LOCALIZATION	225	0.7706364	1.9148464	0	0	0
Positive	GO_TRANSLATIONAL_TERMINATION	102	0.8405553	1.9134037	0	0	0
Positive	GO_ESTABLISHMENT_OF_RNA_LOCALIZATION	192	0.7841347	1.9093522	0	0	0
Positive	GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	60	0.88311917	1.9008884	0	0	0
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	79	0.8603635	1.8896902	0	0	0
Positive	GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	364	0.73371243	1.8879664	0	0	0

Positive	HALLMARK_E2F_TARGETS	197	0.77368	1.8832386	0	3.86E-05	0.001
Positive	GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	81	0.84312487	1.8800665	0	3.74E-05	0.001
Positive	CSR_EARLY_UP.V1_UP	144	0.78377974	1.8797913	0	3.63E-05	0.001
Positive	GO_MRNA_EXPORT_FROM_NUCLEUS	110	0.8072395	1.8720449	0	3.53E-05	0.001
Positive	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	115	0.8019684	1.8690088	0	3.43E-05	0.001
Positive	GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	100	0.8191012	1.868452	0	3.34E-05	0.001
Positive	HALLMARK_MYC_TARGETS_V2	58	0.8816229	1.8677616	0	3.25E-05	0.001
Positive	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	156	0.7779789	1.8636589	0	3.17E-05	0.001
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	95	0.82904613	1.8615639	0	3.09E-05	0.001
Positive	GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	67	0.8551836	1.8603039	0	3.01E-05	0.001
Positive	GO_NUCLEAR_EXPORT	194	0.75093067	1.8566462	0	2.94E-05	0.001
Positive	GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	290	0.73200166	1.8512741	0	2.87E-05	0.001

Positive	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	87	0.83585715	1.851093	0	2.81E-05	0.001
Positive	GO_RNA_CATABOLIC_PROCESS	380	0.7138684	1.8489683	0	2.74E-05	0.001
Positive	GO_TRNA_METABOLIC_PROCESS	172	0.76336825	1.8485299	0	2.68E-05	0.001
Positive	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	102	0.81116	1.8419433	0	2.63E-05	0.001
Positive	GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	71	0.8417486	1.8370137	0	2.57E-05	0.001
Positive	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	98	0.80859894	1.836243	0	2.52E-05	0.001
Positive	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	101	0.79884404	1.8311089	0	4.95E-05	0.002
Positive	GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	426	0.69595015	1.8302764	0	4.85E-05	0.002
Positive	LTE2_UP.V1_DN	188	0.74373907	1.827929	0	1.19E-04	0.005
Positive	GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	66	0.8676449	1.8250657	0	1.17E-04	0.005
Positive	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	93	0.8039506	1.8244761	0	1.15E-04	0.005
Positive	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	139	0.762666	1.8241919	0	1.13E-04	0.005

Positive	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	338	0.70853966	1.8201495	0	1.54E-04	0.007
Positive	GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROUGH_PARASITISM	219	0.72928363	1.8119262	0	2.16E-04	0.01
Positive	GO_RNA_3_END_PROCESSING	136	0.7802188	1.8105692	0	2.33E-04	0.011
Positive	GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	32	0.92628205	1.798591	0	2.91E-04	0.014
Positive	GO_RNA_SPLICING	447	0.6888717	1.796681	0	3.06E-04	0.015
Positive	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	45	0.8829626	1.7949487	0	3.21E-04	0.016
Positive	GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	168	0.73940355	1.7927266	0	3.16E-04	0.016
Positive	GO_REGULATION_OF_VIRAL_LIFE_CYCLE	137	0.7612554	1.7926422	0	3.11E-04	0.016
Positive	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA	74	0.8175832	1.79003	0	3.64E-04	0.019
Positive	GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	146	0.7462191	1.7890184	0	3.58E-04	0.019
Positive	GO_DNA_REPLICATION	261	0.71207047	1.7888429	0	3.71E-04	0.02
Positive	GO_DNA_DEPENDENT_DNA_REPLICATION	139	0.75642145	1.7864088	0	4.20E-04	0.023

Positive	GO_MATURATION_OF_SSU_RRNA	42	0.88631976	1.7862648	0	4.14E-04	0.023
Positive	GO_TRANSLATIONAL_INITIATION	190	0.7271442	1.7851684	0	4.08E-04	0.023
Positive	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	209	0.71691453	1.7774522	0	4.56E-04	0.026
Positive	GO_RIBOSOME_ASSEMBLY	56	0.84800684	1.7737372	0	4.66E-04	0.027
Positive	GO_VIRAL_LIFE_CYCLE	311	0.686978	1.7679743	0	6.64E-04	0.039
Positive	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	443	0.6774748	1.7673198	0	6.55E-04	0.039
Positive	GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	75	0.8142054	1.7664214	0	6.46E-04	0.039
Positive	GO_LYMPHOCYTE_MEDIATED_IMMUNITY	331	0.6884443	1.7647889	0	6.54E-04	0.04
Positive	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	128	0.75241995	1.7639073	0	6.78E-04	0.042
Positive	GO_TRNA_PROCESSING	125	0.7581596	1.7638146	0	6.69E-04	0.042
Positive	GO_TYPE_I_INTERFERON_PRODUCTION	122	0.7581666	1.7608929	0	8.02E-04	0.049
Positive	GO_VIRAL_GENOME_REPLICATION	114	0.7683618	1.7606432	0	8.07E-04	0.05

Positive	GO_REGULATION_OF_CELL_KILLING	90	0.78268296	1.7585076	0	8.74E-04	0.055
Positive	GO_TRANSLATIONAL_ELONGATION	129	0.74324775	1.7570441	0	8.94E-04	0.057
Positive	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	55	0.83777434	1.7547866	0	9.58E-04	0.062
Positive	GO_MRNA_3_END_PROCESSING	96	0.77559173	1.7532697	0	0.0010058	0.066
Positive	GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	299	0.6853404	1.752289	0	0.00106667	0.071
Positive	GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	52	0.8334717	1.751808	0	0.00109757	0.074
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II	98	0.7658767	1.7508564	0	0.00114194	0.078
Positive	HALLMARK_INFLAMMATORY_RESPONSE	197	0.714351	1.7507513	0	0.00112882	0.078
Positive	GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	78	0.80041754	1.749302	0	0.00121315	0.084
Positive	GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	32	0.9111876	1.745603	0	0.00139161	0.097
Positive	GO_POSITIVE_REGULATION_OF_CELL_KILLING	65	0.80126864	1.7450265	0	0.00140281	0.099
Positive	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	284	0.69059545	1.74496	0	0.00138739	0.099

Positive	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	89	0.78508437	1.7449085	0	0.00137231	0.099
Positive	MYC_UP.V1_UP	165	0.72561896	1.74406	0	0.0014242	0.103
Positive	HALLMARK_G2M_CHECKPOINT	192	0.71929526	1.7433486	0	0.00142235	0.104
Positive	GO_T_CELL_MEDIATED_IMMUNITY	102	0.7632649	1.7432184	0	0.00140737	0.104
Positive	GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	88	0.7833804	1.7416139	0	0.00145668	0.109
Positive	GO_DNA_PACKAGING	202	0.7041768	1.7395071	0	0.00161884	0.122
Positive	GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	53	0.8291518	1.7372813	0	0.00171459	0.131
Positive	GO_DNA_CONFORMATION_CHANGE	294	0.6817527	1.7372763	0	0.00169727	0.131
Positive	GO_RNA_MODIFICATION	152	0.71934664	1.7344338	0	0.00182716	0.142
Positive	GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	170	0.7165446	1.7335583	0	0.00188123	0.148
Positive	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	234	0.6967978	1.7320914	0	0.001995	0.156
Positive	GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	61	0.8141772	1.7309469	0	0.00203478	0.16

Positive	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	196	0.70351386	1.7301751	0	0.00207476	0.164
Positive	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	491	0.6586912	1.7292226	0	0.00210176	0.166
Positive	GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	276	0.6865249	1.7282346	0	0.00216304	0.173
Positive	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	314	0.68060005	1.7276406	0	0.00216585	0.175
Positive	GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	195	0.7072849	1.7258484	0	0.00231687	0.186
Positive	GO_TELOMERE_ORGANIZATION	170	0.7090071	1.7244133	0	0.00238546	0.193
Positive	GO_REGULATION_OF_MRNA_PROCESSING	137	0.7350094	1.7230216	0	0.00241966	0.197
Positive	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	143	0.7285802	1.7222664	0	0.00245352	0.2
Positive	GO_REGULATION_OF_HEMOPOIESIS	463	0.6578959	1.7211392	0	0.00253052	0.206
Positive	HALLMARK_IL6_JAK_STAT3_SIGNALING	86	0.7642457	1.7205914	0	0.00257373	0.212
Positive	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	136	0.7268635	1.7200831	0	0.00261579	0.216
Positive	GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	384	0.6669863	1.7199521	0	0.00259304	0.216

Positive	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	25	0.92729497	1.715613	0	0.00291831	0.238
Positive	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	119	0.7393088	1.7104554	0	0.00327185	0.263
Positive	GO_DNA_BIOSYNTHETIC_PROCESS	181	0.704471	1.7102692	0	0.00327555	0.266
Positive	GO_RESPONSE_TO_INTERLEUKIN_1	194	0.6986005	1.7101656	0	0.00324802	0.266
Positive	GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	459	0.64797395	1.7061386	0	0.00365959	0.291
Positive	GO_REGULATION_OF_RNA_METABOLIC_PROCESS	218	0.6912218	1.7057811	0	0.00365971	0.293
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	21	0.96484506	1.7048018	0	0.00371086	0.299
Positive	GO_NCRNA_EXPORT_FROM_NUCLEUS	38	0.83934945	1.7038001	0	0.00378093	0.306
Positive	GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	476	0.65076715	1.7033758	0	0.00379065	0.308
Positive	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	213	0.6875589	1.7028387	0	0.00378998	0.31
Positive	GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	207	0.68680066	1.7027463	0	0.00377937	0.312
Positive	GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	168	0.71443176	1.7004303	0	0.00401955	0.331

Positive	GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	215	0.69049674	1.6989272	0	0.00414262	0.345
Positive	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	92	0.75495946	1.6986895	0	0.00414845	0.349
Positive	GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	100	0.7419375	1.6985424	0	0.00416389	0.351
Positive	GO_NIK_NF_KAPPAB_SIGNALING	171	0.7056006	1.6978	0	0.00418837	0.355
Positive	GO_INTERFERON_GAMMA_PRODUCTION	108	0.73660886	1.6916289	0	0.00484554	0.405
Positive	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	489	0.6397616	1.690962	0	0.00487348	0.408
Positive	GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	193	0.69039935	1.6901879	0	0.00489208	0.412
Positive	GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	282	0.6692534	1.6888759	0	0.00506579	0.424
Positive	HALLMARK_TNFA_SIGNALING_VIA_NFKB	198	0.690621	1.6888169	0	0.00505537	0.426
Positive	GO_REGULATION_OF_T_CELL_ACTIVATION	305	0.66297334	1.688533	0	0.00511757	0.433
Positive	GO_INTERACTION_WITH_SYMBIONT	79	0.7671075	1.6883881	0	0.00509844	0.433
Positive	GO_REGULATION_OF_T_CELL_DIFFERENTIATION	135	0.7154251	1.6809404	0	0.00620937	0.508

Positive	GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	113	0.7302917	1.6806239	0	0.00618226	0.509
Positive	GO_CHROMATIN_ASSEMBLY	161	0.7018444	1.6798458	0	0.00624268	0.516
Positive	GO_MRNA_SPLICE_SITE_SELECTION	47	0.8312149	1.6787411	0.00389105	0.00642323	0.527
Positive	GO_NUCLEAR_TRANSPORT	335	0.6570517	1.6767555	0	0.0066688	0.542
Positive	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	438	0.64186347	1.6760253	0	0.00677512	0.551
Positive	GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	267	0.6601057	1.6755631	0	0.00679603	0.553
Positive	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	270	0.6659956	1.6738914	0	0.00712744	0.578
Positive	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	75	0.7685833	1.6721886	0	0.00743042	0.596
Positive	GO_NUCLEOSOME_ORGANIZATION	177	0.6872437	1.6707528	0	0.00758689	0.606
Positive	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	54	0.7996938	1.6707222	0	0.00753597	0.606
Positive	GO_MULTI_ORGANISM_LOCALIZATION	69	0.772905	1.6704634	0	0.00751014	0.608
Positive	GO_T_CELL_ACTIVATION	449	0.63842577	1.6690421	0	0.0076891	0.615

Positive	GO_T_CELL_MEDIATED_CYTOTOXICITY	48	0.81392646	1.6684281	0	0.00775993	0.62
Positive	GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	82	0.75699025	1.6682272	0	0.00775726	0.622
Positive	GO_REGULATION_OF_GENE_SILENCING	148	0.7035502	1.6676139	0	0.00779379	0.628
Positive	GO_AMINO_ACID_ACTIVATION	48	0.81630445	1.6673872	0	0.00777543	0.63
Positive	CSR_LATE_UP.V1_UP	162	0.69054186	1.6656861	0	0.00807286	0.642
Positive	GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	370	0.64407015	1.664064	0	0.00841169	0.657
Positive	GO_MRNA_CIS_SPLICING_VIA_SPLICEOSOME	53	0.80125886	1.663705	0.00186916	0.00842829	0.661
Positive	GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	165	0.69054455	1.6630989	0	0.00849065	0.665
Positive	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	247	0.6629594	1.662756	0	0.00852135	0.668
Positive	GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	105	0.7196676	1.6617696	0.00369686	0.00868967	0.675
Positive	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	66	0.7761348	1.6613383	0.0034904	0.00875746	0.679
Positive	GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS	23	0.9147791	1.6611509	0	0.00873359	0.681

Positive	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	265	0.66122085	1.6609502	0	0.00871734	0.682
Positive	GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	91	0.74264836	1.6608021	0	0.0086942	0.684
Positive	GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	83	0.740774	1.660091	0	0.00881911	0.693
Positive	CAMP_UP.V1_UP	189	0.6863754	1.6587441	0	0.00897942	0.699
Positive	GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	100	0.73293465	1.6567699	0	0.00941497	0.718
Positive	GO_TRNA_TRANSPORT	35	0.8404555	1.6537002	0	0.01015671	0.743
Positive	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	218	0.6625311	1.6527159	0	0.01025574	0.746
Positive	GO_TRANSPORT_OF_VIRUS	57	0.76840055	1.6523752	0	0.01025289	0.746
Positive	GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	101	0.7295437	1.6513941	0	0.01045047	0.759
Positive	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	139	0.6909877	1.6493467	0	0.01092388	0.776
Positive	GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	248	0.6566741	1.6488787	0	0.01100218	0.778
Positive	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	35	0.8378284	1.648119	0	0.01114277	0.787

Positive	GO_TYPE_2_IMMUNE_RESPONSE	36	0.83796895	1.6455413	0	0.01175368	0.809
Positive	GO_LEUKOCYTE_CELL_CELL_ADHESION	327	0.63855815	1.6449139	0	0.01192895	0.819
Positive	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	43	0.80664575	1.6424822	0.006	0.01249659	0.833
Positive	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	142	0.69253606	1.6421102	0	0.01255079	0.835
Positive	GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	180	0.67302096	1.6388625	0	0.01338923	0.852
Positive	GO_IMMUNOGLOBULIN_PRODUCTION	180	0.6761469	1.6386665	0	0.0133694	0.855
Positive	GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	144	0.6886602	1.6382427	0	0.01343755	0.856
Positive	GO_MRNA_5_SPLICE_SITE_RECOGNITION	26	0.8781978	1.6378584	0.00201207	0.01351084	0.864
Positive	GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	260	0.6484348	1.6346395	0	0.01454581	0.886
Positive	GO_TRNA_MODIFICATION	82	0.7352399	1.6344475	0.00183824	0.01452668	0.887
Positive	GO_CELL_KILLING	159	0.68670785	1.6329918	0	0.01505991	0.896
Positive	GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	79	0.7403923	1.6321601	0.00180832	0.01525483	0.903

Positive	GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	172	0.6675382	1.6315975	0	0.01536961	0.904
Positive	GO_NON_RECOMBINATIONAL_REPAIR	85	0.73080593	1.6315249	0	0.015308	0.904
Positive	GO_LEUKOCYTE_PROLIFERATION	286	0.6482658	1.6311	0	0.01537532	0.905
Positive	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	99	0.7158688	1.6303872	0	0.01552072	0.908
Positive	GO_B_CELL_MEDIATED_IMMUNITY	200	0.6588324	1.6299905	0	0.01558717	0.911
Positive	GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	93	0.7257773	1.6284676	0.00178571	0.01611701	0.92
Positive	GO_MYELOID_DENDRITIC_CELL_ACTIVATION	29	0.85649455	1.627063	0.0059761	0.01660907	0.926
Positive	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_VIA_MHC_CLASS_IB	16	0.9650647	1.6268317	0	0.01664342	0.927
Positive	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	337	0.6358175	1.6267465	0	0.01657115	0.928
Positive	GO_DOUBLE_STRAND_BREAK_REPAIR	218	0.6571105	1.6266613	0	0.01650535	0.929
Positive	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	99	0.7185225	1.6248835	0	0.0172153	0.937
Positive	GO_RESPONSE_TO_INTERFERON_BETA	28	0.8629353	1.6243924	0.0019084	0.01728285	0.939

Positive	ERBB2_UP.V1_DN	184	0.66954523	1.6237798	0	0.01742936	0.944
Positive	GO_FC_RECEPTOR_SIGNALING_PATHWAY	239	0.6448382	1.623676	0	0.01742842	0.945
Positive	GO_MATURATION_OF_5_8S_RRNA	26	0.87121636	1.6235825	0.00957854	0.01739077	0.946
Positive	GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	92	0.7265316	1.6223769	0.00178571	0.01775722	0.947
Positive	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	24	0.8845819	1.6220642	0.00191571	0.01776621	0.947
Positive	GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	136	0.6882278	1.6214104	0	0.01784712	0.947
Positive	GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	29	0.8650532	1.6212981	0	0.01777819	0.948
Positive	GO_DENDRITIC_CELL_DIFFERENTIATION	41	0.8120865	1.6204835	0.00196464	0.01797643	0.951
Positive	GO_T_CELL_DIFFERENTIATION	232	0.6474248	1.6204323	0	0.01789589	0.951
Positive	GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	187	0.6600424	1.6193717	0	0.01823904	0.957
Positive	GO_PROTEIN_POLYUBIQUITINATION	298	0.634874	1.6190115	0	0.01827527	0.957
Positive	GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	34	0.83439696	1.6166432	0.00379507	0.01911972	0.969

Positive	GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	126	0.6932677	1.6150527	0	0.01969351	0.97
Positive	GO_POSTREPLICATION_REPAIR	49	0.77526766	1.613974	0.00542496	0.02006262	0.972
Positive	GO_LYMPHOCYTE_HOMEOSTASIS	62	0.7553671	1.6131753	0.00533808	0.0202506	0.974
Positive	PTEN_DN.V1_DN	174	0.66020656	1.611988	0	0.02068601	0.977
Positive	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	30	0.86070865	1.6105955	0.00198413	0.02131553	0.98
Positive	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	439	0.61279005	1.6085228	0	0.02229291	0.984
Positive	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	64	0.7537569	1.6068453	0.0018622	0.0230013	0.986
Positive	GO_REGULATION_OF_DNA_METABOLIC_PROCESS	267	0.63546395	1.6066439	0	0.02303164	0.986
Positive	GO_CHROMOSOME_SEGREGATION	291	0.6356618	1.6065612	0.00176367	0.02298811	0.987
Positive	GO_CELLULAR_RESPONSE_TO_VIRUS	47	0.77858204	1.6062541	0.00373832	0.02301765	0.99
Positive	GO_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	56	0.77044314	1.6053866	0.00365631	0.02335582	0.992
Positive	GO_CELL_CYCLE_DNA_REPLICATION	62	0.75655377	1.603857	0.00367647	0.02399372	0.992

Positive	GO_NCRNA_TRANSCRIPTION	97	0.708391	1.603511	0.00197239	0.02407341	0.993
Positive	GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	41	0.7933855	1.6008588	0.00543478	0.02533406	0.994
Positive	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	139	0.68284476	1.6006035	0	0.02535295	0.994
Positive	GO_REGULATION_OF_VIRAL_TRANSCRIPTION	64	0.74604887	1.6001797	0.00375235	0.02546308	0.995
Positive	GO_RESPONSE_TO_DSRNA	53	0.77099305	1.5986838	0.00576923	0.02612163	0.996
Positive	GO_TRANSLESION_SYNTHESIS	38	0.79445153	1.5971978	0.00571429	0.02681002	0.997
Positive	GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION	30	0.8502664	1.5968673	0.00187266	0.02687066	0.997
Positive	GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	46	0.7867172	1.5959448	0.00548446	0.02729124	0.997
Positive	VEGF_A_UP.V1_DN	190	0.6625285	1.5950946	0	0.02766525	0.997
Positive	GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	73	0.7283283	1.5942577	0.00366972	0.02807831	0.997
Positive	GO_RESPONSE_TO_GAMMA_RADIATION	53	0.76079875	1.5929478	0.00195313	0.02875005	0.998
Positive	GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.8890183	1.5928996	0.00187617	0.02864869	0.998

Positive	GO_RNA_5_END_PROCESSING	21	0.8789744	1.5916674	0.00795229	0.02918312	1
Positive	GO_POSITIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION_INVOLVED_IN_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_SIGNALING_PATHWAY	31	0.84551513	1.5913233	0.0035461	0.02924635	1
Positive	GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	49	0.77639294	1.5910772	0.00572519	0.02928306	1
Positive	GO_RNA_CAPPING	32	0.8285141	1.5910633	0.00381679	0.02917617	1
Positive	GO_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	179	0.65021574	1.5907775	0	0.02920274	1
Positive	GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	303	0.62596273	1.5899729	0	0.02948928	1
Positive	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	78	0.7208499	1.5897795	0.00373134	0.02945343	1
Positive	GO_TOLERANCE_INDUCTION	24	0.85945004	1.5882366	0.00189036	0.03025085	1
Positive	GO_ALPHA_BETA_T_CELL_ACTIVATION	134	0.677799	1.5879756	0	0.03030336	1
Positive	GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	128	0.66776603	1.5867345	0.00179856	0.03083519	1
Positive	GO_POSITIVE_T_CELL_SELECTION	35	0.81868786	1.5862341	0.00754717	0.03099988	1
Positive	GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION_OF_STAT_PROTEIN	23	0.8669631	1.5860394	0.00803213	0.03100369	1

Positive	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I	61	0.75011957	1.5859946	0.00548446	0.03091326	1
Positive	GO_CELLULAR_DEFENSE_RESPONSE	52	0.76714253	1.5855929	0.0037594	0.03102538	1
Positive	GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	191	0.64478624	1.5850143	0	0.03122483	1
Positive	GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	47	0.7747868	1.5850048	0.0077821	0.03110529	1
Positive	GO_INTERFERON_ALPHA_PRODUCTION	30	0.82837516	1.5849712	0.01509434	0.03101111	1
Positive	GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	107	0.703545	1.5846031	0.00190476	0.03110129	1
Positive	GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	33	0.80968297	1.5841563	0.00980392	0.03128775	1
Positive	GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	27	0.8470135	1.5840019	0.00978474	0.03127576	1
Positive	GO_T_CELL_PROLIFERATION	175	0.6499488	1.5838779	0.0017452	0.0312256	1
Positive	GO_RESPONSE_TO_INTERLEUKIN_7	39	0.7943622	1.5830628	0.00392927	0.03160154	1
Positive	GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	115	0.69093543	1.5827565	0	0.03165021	1
Positive	GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	63	0.75002396	1.5820128	0.00387597	0.0319824	1

Positive	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	122	0.68082654	1.58178	0	0.03204396	1
Positive	MEL18_DN.V1_UP	136	0.66620606	1.5806875	0	0.03255099	1
Positive	GO_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	256	0.6250968	1.5806057	0	0.0324831	1
Positive	GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	111	0.68678087	1.5800483	0	0.03269067	1
Positive	GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	158	0.65764457	1.5769624	0	0.03455719	1
Positive	GO_RESPONSE_TO_IONIZING_RADIATION	142	0.6692011	1.5764866	0	0.03476962	1
Positive	GO_NUCLEUS_ORGANIZATION	125	0.67704755	1.5762577	0	0.03479126	1
Positive	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	207	0.6436104	1.5762193	0	0.03468393	1
Positive	GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	179	0.6500772	1.5759479	0	0.03471058	1
Positive	GO_ANTIMICROBIAL_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_ANTIMICROBIAL_PEPTIDE	72	0.72814035	1.5753165	0.0037594	0.0349741	1
Positive	GO_DNA_REPLICATION_INITIATION	37	0.8004648	1.5750884	0.00587084	0.03497624	1
Positive	GO_NCRNA_CATABOLIC_PROCESS	27	0.8346705	1.5745391	0.006	0.03527354	1

Positive	GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	30	0.8283312	1.5735061	0.00189753	0.03578864	1
Positive	GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	457	0.6013316	1.572896	0	0.03609826	1
Positive	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	53	0.7587664	1.5723917	0.00378788	0.03627125	1
Positive	GO_PROTEIN_FOLDING	218	0.6388084	1.5719377	0	0.03643833	1
Positive	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	305	0.6123591	1.5707741	0	0.03717762	1
Positive	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	62	0.7323327	1.5698891	0.00729927	0.03766453	1
Positive	GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	200	0.64442086	1.5696151	0	0.03771395	1
Positive	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROMOTER	30	0.85013384	1.5690522	0.00555556	0.03792532	1
Positive	GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	109	0.677867	1.5687336	0.005386	0.0379961	1
Positive	GO_NEGATIVE_REGULATION_OF_CELL_KILLING	21	0.8891916	1.5686661	0.00779727	0.03791349	1
Positive	BMI1_DN_MEL18_DN.V1_UP	141	0.6579913	1.5681403	0	0.03818316	1
Positive	GO_CYTOPLASMIC_TRANSLATION	93	0.7020798	1.5676738	0.00522648	0.0383299	1

Positive	GO_REGULATION_OF_MONOCYTE_DIFFERENTIATION	21	0.8887684	1.5666565	0.00185185	0.03882586	1
Positive	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	75	0.7175089	1.5654321	0.00369686	0.03952517	1
Positive	GO_B_CELL_HOMEOSTASIS	29	0.8351454	1.5652108	0.00595238	0.0395412	1
Positive	GO_PROGRAMMED_NECROTIC_CELL_DEATH	47	0.7708904	1.5650296	0.00738007	0.0395149	1
Positive	GO_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	316	0.61541337	1.564991	0	0.03938635	1
Positive	GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	21	0.87965626	1.5645499	0.00197628	0.03953839	1
Positive	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	99	0.69396377	1.5640824	0.00374532	0.03966898	1
Positive	GO_NUCLEAR_DNA_REPLICATION	54	0.75944287	1.5637494	0.00925926	0.03976886	1
Positive	GO_T_HELPER_17_TYPE_IMMUNE_RESPONSE	28	0.83000433	1.562667	0.00545455	0.04046395	1
Positive	GO_NCRNA_3_END_PROCESSING	37	0.80183	1.5623124	0.00208333	0.04051767	1
Positive	GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	39	0.7912643	1.5621449	0.0056926	0.0405258	1
Positive	GO_REGULATION_OF_INFLAMMATORY_RESPONSE	343	0.6040947	1.5619123	0	0.04056355	1

Positive	GO_DNA_RECOMBINATION	263	0.6219674	1.5616796	0.00172712	0.04060045	1
Positive	GO_REGULATION_OF_CELL_CELL_ADHESION	386	0.6005968	1.5615287	0	0.04055032	1
Positive	GO_RESPONSE_TO_INTERLEUKIN_12	50	0.7480503	1.5600773	0.00914077	0.04141192	1
Positive	GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	146	0.6571284	1.5596571	0	0.04158886	1
Positive	GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	117	0.6718897	1.5594462	0	0.04159799	1
Positive	GO_T_CELL_CYTOKINE_PRODUCTION	39	0.7898879	1.5591397	0.00731261	0.0416966	1
Positive	GO_SISTER_CHROMATID_SEGREGATION	178	0.64363843	1.5588344	0	0.04177346	1
Positive	GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	41	0.7809731	1.5586789	0.00558659	0.04174893	1
Positive	GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	172	0.636081	1.5569239	0	0.04299128	1
Positive	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	47	0.7598614	1.5567881	0.00764818	0.04293875	1
Positive	GO_HISTONE_EXCHANGE	55	0.7497819	1.5559807	0.00344234	0.04340288	1
Positive	BMI1_DN.V1_UP	142	0.6593644	1.5547053	0.00178891	0.04415608	1

Positive	GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	102	0.6838056	1.554536	0.00181159	0.04416415	1
Positive	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	33	0.8020611	1.5538402	0.00735294	0.04458548	1
Positive	GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	110	0.6752669	1.5536914	0.00182815	0.04452462	1
Positive	GO_NUCLEAR_CHROMOSOME_SEGREGATION	240	0.6183649	1.5532932	0	0.0446888	1
Positive	GO_POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	69	0.7157826	1.5515084	0.00560748	0.04599967	1
Positive	GO_CENTROMERE_COMPLEX_ASSEMBLY	51	0.7561084	1.5509582	0.00919118	0.04623351	1
Positive	GO_REGULATION_OF_DNA_REPLICATION	102	0.6768263	1.550887	0.00185185	0.04616827	1
Positive	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	109	0.676373	1.5506496	0.00190114	0.04617659	1
Positive	GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	225	0.62659305	1.5500591	0	0.04649598	1
Positive	GO_RESPONSE_TO_CHEMOKINE	92	0.6885604	1.5498616	0.0018018	0.04652276	1
Positive	HALLMARK_IL2_STAT5_SIGNALING	196	0.63536996	1.5475441	0	0.04823072	1
Positive	GO_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	18	0.8888893	1.5475013	0.00974659	0.04812944	1

Positive	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	17	0.9134732	1.547221	0.00409836	0.04818996	1
Positive	GO_LYMPHOCYTE_DIFFERENTIATION	342	0.60378873	1.5468444	0	0.04838007	1
Correlation	FGF2_Control	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
Negative	KRAS.LUNG_UP.V1_DN	140	-0.77582663	-1.9381864	0	0	0
Negative	KRAS.600_UP.V1_DN	272	-0.6982987	-1.87687	0	6.05E-04	0.002
Negative	KRAS.600.LUNG.BREAST_UP.V1_DN	275	-0.67471427	-1.8261286	0	0.00401092	0.02
Negative	KRAS.LUNG.BREAST_UP.V1_DN	137	-0.7190784	-1.7967504	0	0.01100573	0.072
Negative	KRAS.300_UP.V1_DN	135	-0.70128334	-1.7674538	0	0.02242189	0.175
Positive	HALLMARK_MYC_TARGETS_V1	197	0.8882303	2.1376314	0	0	0

Positive	GO_RIBOSOME_BIOGENESIS	264	0.8613736	2.1171236	0	0	0
Positive	GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	454	0.82600915	2.1006813	0	0	0
Positive	GO_NCRNA_METABOLIC_PROCESS	428	0.8258835	2.0846767	0	0	0
Positive	GO_NCRNA_PROCESSING	352	0.8313273	2.0805058	0	0	0
Positive	GO_RRNA_METABOLIC_PROCESS	194	0.8563418	2.057439	0	0	0
Positive	HALLMARK_E2F_TARGETS	197	0.8215042	1.9815567	0	0	0
Positive	GO_MITOCHONDRIAL_GENE_EXPRESSION	151	0.8458019	1.9805963	0	0	0
Positive	GO_MITOCHONDRIAL_TRANSLATION	129	0.8505818	1.9555104	0	0	0
Positive	GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	268	0.79622877	1.9548925	0	0	0
Positive	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	102	0.8803201	1.9531101	0	0	0
Positive	GO_TRANSLATIONAL_INITIATION	190	0.81442815	1.9489046	0	0	0
Positive	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	118	0.8591481	1.9396626	0	0	0

Positive	GO_TRNA_METABOLIC_PROCESS	172	0.810916	1.9319206	0	0	0
Positive	GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	364	0.7649295	1.9155345	0	0	0
Positive	GO_RNA_EXPORT_FROM_NUCLEUS	136	0.82730263	1.9128438	0	0	0
Positive	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	115	0.8485687	1.9120183	0	0	0
Positive	GO_TRANSLATIONAL_TERMINATION	102	0.8524586	1.9011234	0	0	0
Positive	HALLMARK_MYC_TARGETS_V2	58	0.9074457	1.8977801	0	0	0
Positive	GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	66	0.8924492	1.8897505	0	0	0
Positive	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	87	0.8569772	1.8894997	0	0	0
Positive	HALLMARK_G2M_CHECKPOINT	192	0.7871618	1.8860937	0	0	0
Positive	GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	276	0.76731974	1.8782425	0	0	0
Positive	GO_DNA_CONFORMATION_CHANGE	294	0.7536664	1.8736281	0	0	0
Positive	GO_RNA_3_END_PROCESSING	136	0.79742235	1.8696054	0	0	0

Positive	GO_RNA_SPLICING	447	0.73679644	1.8651861	0	0	0
Positive	GO_VIRAL_GENE_EXPRESSION	189	0.78723896	1.86406435	0	0	0
Positive	GO_TRNA_PROCESSING	125	0.81260836	1.85783662	0	0	0
Positive	GO_MRNA_EXPORT_FROM_NUCLEUS	110	0.81815714	1.85218892	0	0	0
Positive	CSR_EARLY_UP.V1_UP	144	0.801807	1.8514453	0	0	0
Positive	GO_NUCLEOSOME_ORGANIZATION	177	0.7835047	1.8475046	0	0	0
Positive	GO_RIBOSOME_ASSEMBLY	56	0.8893816	1.846356	0	0	0
Positive	GO_NUCLEAR_EXPORT	194	0.7664079	1.8425521	0	0	0
Positive	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	139	0.79356027	1.8425175	0	0	0
Positive	GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	71	0.8527359	1.8374302	0	0	0
Positive	GO_DNA_PACKAGING	202	0.76607734	1.830198	0	0	0
Positive	GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	60	0.8751431	1.8276933	0	0	0

Positive	MYC_UP.V1_UP	165	0.7760886	1.8273318	0	0	0
Positive	CSR_LATE_UP.V1_UP	162	0.7718832	1.8229833	0	0	0
Positive	GO_RNA_LOCALIZATION	225	0.75548875	1.8186074	0	0	0
Positive	GO_CHROMATIN_ASSEMBLY	161	0.7685683	1.8175946	0	0	0
Positive	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	196	0.7473979	1.8049563	0	2.93E-05	0.001
Positive	VEGF_A_UP.V1_DN	190	0.75462705	1.804688	0	2.86E-05	0.001
Positive	GO_TELOMERE_ORGANIZATION	170	0.7628874	1.8044596	0	2.80E-05	0.001
Positive	GO_RNA_CATABOLIC_PROCESS	380	0.7087321	1.7842686	0	5.45E-05	0.002
Positive	GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	187	0.75153625	1.7825218	0	5.33E-05	0.002
Positive	GO_CYTOPLASMIC_TRANSLATION	93	0.80360293	1.7806782	0	5.21E-05	0.002
Positive	GO_TRANSLATIONAL_ELONGATION	129	0.7743524	1.7771695	0	5.10E-05	0.002
Positive	GO_MRNA_3_END_PROCESSING	96	0.7858801	1.7651681	0	1.24E-04	0.005

Positive	GO_DNA_REPLICATION	261	0.71518916	1.7651165	0	1.22E-04	0.005
Positive	GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	105	0.78279436	1.761687	0	1.19E-04	0.005
Positive	GO_TRNA_MODIFICATION	82	0.80498284	1.7590258	0	1.40E-04	0.006
Positive	GO_ESTABLISHMENT_OF_RNA_LOCALIZATION	192	0.74676627	1.7542531	0	1.83E-04	0.008
Positive	GO_ATP_DEPENDENT_CHROMATIN_REMODELING	78	0.80238074	1.751815	0	2.02E-04	0.009
Positive	GO_NCRNA_TRANSCRIPTION	97	0.7813593	1.7518033	0	1.98E-04	0.009
Positive	GO_CHROMOSOME_SEGREGATION	291	0.7053473	1.741984	0	3.46E-04	0.016
Positive	GO_MRNA_TRANSPORT	147	0.7393894	1.7419739	0	3.40E-04	0.016
Positive	GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	53	0.8535504	1.741522	0	3.34E-04	0.016
Positive	GO_MITOTIC_NUCLEAR_DIVISION	273	0.70681345	1.7408998	0	3.28E-04	0.016
Positive	GO_NUCLEAR_TRANSPORT	335	0.69397366	1.7354246	0	3.63E-04	0.018
Positive	GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	113	0.7566006	1.7353755	0	3.57E-04	0.018

Positive	GO_PROTEIN_TARGETING_TO_MEMBRANE	191	0.7274198	1.7349359	0	3.71E-04	0.019
Positive	GO_RNA_MODIFICATION	152	0.73006886	1.7306435	0	4.60E-04	0.024
Positive	GO_DNA_DEPENDENT_DNA_REPLICATION	139	0.74695235	1.7303845	0	4.53E-04	0.024
Positive	GO_REGULATION_OF_GENE_SILENCING	148	0.7429648	1.7267243	0	5.39E-04	0.029
Positive	GO_CENTROMERE_COMPLEX_ASSEMBLY	51	0.8217934	1.7196227	0	7.33E-04	0.039
Positive	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	75	0.7952272	1.7157288	0	8.12E-04	0.044
Positive	GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	144	0.73268783	1.7150116	0	8.18E-04	0.045
Positive	GO_NUCLEUS_ORGANIZATION	125	0.7480515	1.7082949	0	9.64E-04	0.054
Positive	GO_MATURATION_OF_SSU_RRNA	42	0.8751695	1.7064301	0	0.0010367	0.059
Positive	GO_REGULATION_OF_MRNA_PROCESSING	137	0.7337583	1.6981843	0	0.00134848	0.077
Positive	GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	209	0.6947516	1.6931102	0	0.00149826	0.086
Positive	GO_SISTER_CHROMATID_SEGREGATION	178	0.7117552	1.687063	0	0.00184367	0.107

Positive	GO_NUCLEAR_CHROMOSOME_SEGREGATION	240	0.6902407	1.68239	0	0.00201517	0.119
Positive	GO_NCRNA_EXPORT_FROM_NUCLEUS	38	0.85644233	1.6821171	0	0.0019883	0.119
Positive	GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	102	0.74557024	1.6788954	0	0.00225117	0.137
Positive	GO_HISTONE_EXCHANGE	55	0.8108608	1.6785281	0	0.00223772	0.138
Positive	GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	100	0.7529516	1.6768435	0	0.00236466	0.147
Positive	GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	282	0.67791724	1.6739255	0	0.0026717	0.162
Positive	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	489	0.6535058	1.6729494	0	0.00269885	0.166
Positive	GO_REGULATION_OF_RNA_METABOLIC_PROCESS	218	0.6950696	1.6704874	0	0.0028147	0.175
Positive	GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	29	0.9031338	1.6701258	0	0.00282464	0.178
Positive	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	234	0.68773764	1.6700939	0	0.00279061	0.178
Positive	GO_MATURATION_OF_5_8S_RRNA	26	0.9055649	1.6680235	0	0.0030022	0.193
Positive	GO_DNA_BIOSYNTHETIC_PROCESS	181	0.70207864	1.667802	0	0.00299532	0.195

Positive	GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	79	0.76661694	1.6665936	0	0.00304537	0.201
Positive	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	78	0.76263934	1.6636914	0.00151057	0.00345725	0.225
Positive	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I	61	0.7865813	1.6635834	0	0.0034318	0.226
Positive	GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	32	0.8880749	1.6624378	0	0.00352907	0.234
Positive	GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	73	0.77273345	1.660791	0	0.00367751	0.245
Positive	GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	52	0.8158347	1.6603299	0	0.00373059	0.251
Positive	KRAS.600_UP.V1_UP	274	0.6707023	1.6551499	0	0.00448061	0.297
Positive	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	143	0.7153987	1.6540773	0	0.0045499	0.303
Positive	KRAS.50_UP.V1_UP	48	0.80800605	1.6537927	0	0.00454028	0.304
Positive	GO_TRNA_TRANSPORT	35	0.8601918	1.6535892	0	0.00451822	0.306
Positive	GO_NCRNA_3_END_PROCESSING	37	0.8489178	1.6530057	0.00163399	0.00458518	0.311
Positive	GO_CHROMATIN_ORGANIZATION_INVOLVED_IN_REGULATION_OF_TRANSCRIPTION	124	0.72009045	1.6522368	0	0.00459991	0.315

Positive	GO_AMINO_ACID_ACTIVATION	48	0.8139292	1.6516396	0	0.0046274	0.319
Positive	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	90	0.74808604	1.6516339	0	0.00458066	0.319
Positive	GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	132	0.71023875	1.650234	0	0.00474047	0.333
Positive	E2F1_UP.V1_UP	177	0.69485474	1.6487702	0	0.00493305	0.347
Positive	GO_PROTEIN_FOLDING	218	0.68629754	1.6478361	0	0.00511125	0.36
Positive	RPS14_DN.V1_DN	178	0.6919759	1.6469218	0	0.00521512	0.372
Positive	GO_MULTI_ORGANISM_LOCALIZATION	69	0.7645204	1.6463453	0	0.00524574	0.377
Positive	GO_CHROMATIN_SILENCING_AT_RDNA	40	0.8325039	1.6415066	0	0.00633855	0.43
Positive	GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	207	0.68054944	1.6407014	0	0.00647296	0.437
Positive	GO_SNRNA_TRANSCRIPTION	67	0.7746329	1.6382086	0	0.00701252	0.472
Positive	KRAS.300_UP.V1_UP	141	0.7024808	1.6369445	0	0.0072728	0.487
Positive	GO_CHROMOSOME_LOCALIZATION	71	0.7716036	1.6368382	0	0.00721709	0.488

Positive	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	313	0.6579502	1.6362166	0	0.00719573	0.489
Positive	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	98	0.73655045	1.6334805	0	0.00796175	0.532
Positive	GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	41	0.8259129	1.6308765	0	0.00846542	0.557
Positive	GO_TRANSPORT_OF_VIRUS	57	0.78010046	1.6298196	0.00309119	0.00868032	0.572
Positive	GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	66	0.76644164	1.6265811	0	0.00941312	0.605
Positive	GO_CHROMATIN_REMODELING_AT_CENTROMERE	43	0.8235702	1.625965	0.0015949	0.00955264	0.612
Positive	GO_NUCLEOTIDE_EXCISION_REPAIR	108	0.7176641	1.6254656	0.00306279	0.00962674	0.617
Positive	MEL18_DN.V1_UP	136	0.70327014	1.6250697	0	0.00963801	0.621
Positive	GO_REGULATION_OF_DNA_REPLICATION	102	0.7301626	1.6248801	0	0.00958695	0.623
Positive	GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	81	0.75235975	1.6242986	0	0.00960917	0.627
Positive	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	77	0.7501906	1.6241151	0	0.00957946	0.629
Positive	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	109	0.71545017	1.6238085	0	0.00964082	0.636

Positive	GO_REGULATION_OF_DNA_METABOLIC_PROCESS	267	0.663308	1.6182345	0	0.01105159	0.688
Positive	GO_PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY	315	0.65097386	1.6157043	0	0.0118191	0.718
Positive	GO_DNA_REPLICATION_INITIATION	37	0.82977563	1.6154686	0	0.01179258	0.72
Positive	GO_REGULATION_OF_CHROMOSOME_SEGREGATION	99	0.7225522	1.614899	0.00150602	0.01187234	0.726
Positive	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	120	0.6973619	1.6148217	0	0.01183594	0.73
Positive	GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	61	0.76930624	1.613727	0	0.01219195	0.74
Positive	GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	69	0.7601232	1.6129497	0	0.01229601	0.748
Positive	HALLMARK_OXIDATIVE_PHOSPHORYLATION	184	0.67935675	1.6122321	0	0.01243566	0.758
Positive	GO_DNA_GEOMETRIC_CHANGE	91	0.7275163	1.6111825	0.00154321	0.01268521	0.765
Positive	GO_METAPHASE_PLATE_CONGRESSION	56	0.7790876	1.610703	0	0.0127551	0.772
Positive	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	218	0.66590774	1.6105777	0	0.01270463	0.774
Positive	GO_RNA_METHYLATION	72	0.7460393	1.6101243	0	0.01277367	0.778

Positive	GO_SPINDLE_ORGANIZATION	161	0.6829897	1.6099087	0	0.01274182	0.78
Positive	GO_REGULATION_OF_RNA_SPLICING	135	0.70042187	1.609038	0	0.01298855	0.789
Positive	GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	32	0.8440627	1.6077223	0	0.01352598	0.8
Positive	BMI1_DN_MEL18_DN.V1_UP	141	0.69376737	1.6076881	0	0.01342725	0.8
Positive	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TELOMERIC_REGION	28	0.8696917	1.6064986	0.00168919	0.01371711	0.808
Positive	GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	34	0.8432496	1.6059943	0	0.01386165	0.812
Positive	GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION	30	0.87274003	1.6038986	0.00483871	0.01470598	0.836
Positive	GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	110	0.70399785	1.6032664	0	0.01489446	0.839
Positive	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_I_PROMOTER	35	0.83088285	1.6025904	0.00156986	0.01498641	0.843
Positive	GO_RNA_CAPPING	32	0.84481853	1.6025645	0	0.01489861	0.844
Positive	GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	21	0.92467767	1.6024816	0	0.01482042	0.845
Positive	GO_REGULATION_OF_TELOMERE_MAINTENANCE	76	0.7415315	1.6019211	0.0030722	0.01494503	0.85

Positive	GO_RNA_POLYADENYLATION	42	0.80506384	1.6008149	0	0.01523386	0.856
Positive	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROMOTER	30	0.8570867	1.5999541	0.00163666	0.0154932	0.866
Positive	GO_CYTOPLASMIC_TRANSLATIONAL_INITIATION	30	0.8482898	1.5968685	0	0.01678059	0.889
Positive	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	284	0.64357764	1.596719	0	0.01671661	0.89
Positive	GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	140	0.6873921	1.596278	0.001443	0.01678321	0.893
Positive	GO_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	164	0.67430466	1.5926843	0	0.01810115	0.906
Positive	GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	21	0.9246778	1.5922726	0.00164204	0.01819803	0.907
Positive	GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	92	0.7292532	1.5903546	0.00289436	0.01906145	0.918
Positive	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	61	0.75503105	1.5903459	0.00320513	0.01893768	0.918
Positive	GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	172	0.67953336	1.5898552	0	0.01904999	0.921
Positive	GO_SNRNA_PROCESSING	28	0.85513026	1.5884355	0	0.01956663	0.928
Positive	GO_PROTEIN_TARGETING_TO_MITOCHONDRION	94	0.7045638	1.5864625	0	0.02031525	0.931

Positive	GO_MATURATION_OF_LSU_RRNA	19	0.9310817	1.5857543	0	0.02058635	0.934
Positive	GO_REGULATION_OF_NUCLEAR_DIVISION	204	0.6584597	1.5856901	0	0.02048758	0.936
Positive	GO_NEGATIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	48	0.7759637	1.5854704	0.00302115	0.02047338	0.937
Positive	GO_POSITIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION_INVOLVED_IN_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_SIGNALING_PATHWAY	31	0.85339105	1.5849618	0	0.02058061	0.937
Positive	GO_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	52	0.77013695	1.584389	0	0.0207153	0.939
Positive	GO_RESPONSE_TO_HEAT	172	0.6652299	1.5823165	0	0.02182322	0.952
Positive	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	35	0.8198423	1.5801606	0	0.02285907	0.96
Positive	GO_DOUBLE_STRAND_BREAK_REPAIR	218	0.65647256	1.5782304	0	0.0236857	0.966
Positive	HALLMARK_DNA_REPAIR	148	0.67448384	1.577298	0	0.02408995	0.966
Positive	GO_SPINDLE_ASSEMBLY	103	0.7041898	1.5770713	0	0.02408318	0.966
Positive	GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	59	0.76095355	1.5756739	0.00154321	0.02456021	0.967
Positive	GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	244	0.6486476	1.5746485	0	0.02504786	0.969

Positive	GO_ORGANELLE_FISSION	433	0.61594635	1.5719799	0	0.02646919	0.976
Positive	GO_OXIDATIVE_PHOSPHORYLATION	119	0.68812704	1.5707544	0	0.02708778	0.979
Positive	GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	325	0.62944585	1.5704048	0	0.02712092	0.979
Positive	GO_NON_RECOMBINATIONAL_REPAIR	85	0.71917796	1.5699334	0.00290698	0.02730055	0.979
Positive	KRAS.LUNG_UP.V1_UP	135	0.6823618	1.5684451	0.00143472	0.02806452	0.98
Positive	GO_POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	69	0.727674	1.5679238	0.00311526	0.02822348	0.981
Positive	GO_MITOTIC_METAPHASE_PLATE_CONGRESSION	44	0.7788939	1.5670682	0.00159744	0.02868408	0.982
Positive	GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	260	0.6377466	1.566945	0	0.02857678	0.982
Positive	GO_MACROMOLECULE_METHYLATION	275	0.6361373	1.5652864	0	0.02952778	0.985
Positive	GO_CELL_CYCLE_DNA_REPLICATION	62	0.74493724	1.5621085	0.00468019	0.03168878	0.99
Positive	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	50	0.75558466	1.5607074	0.00625978	0.03247551	0.992
Positive	GO_NEGATIVE_REGULATION_OF_RNA_SPLICING	25	0.8531647	1.5605124	0.00506757	0.03243004	0.992

Positive	GO_CHROMATIN_REMODELING	168	0.6599424	1.5604421	0	0.03229861	0.992
Positive	GO_PROTEIN_HETEROTETRAMERIZATION	53	0.7579752	1.5556654	0.0031746	0.03583632	0.998
Positive	GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX_ASSEMBLY	26	0.8436825	1.5553508	0.00507614	0.0359056	0.998
Positive	GO_PROTEIN_TARGETING	412	0.61465424	1.55293	0	0.03780246	0.998
Positive	GO_NEGATIVE_REGULATION_OF_MRNA_PROCESSING	29	0.8373018	1.5528204	0	0.03767781	0.998
Positive	GO_RNA_5_END_PROCESSING	21	0.8836792	1.5495642	0.00165837	0.04004541	0.999
Positive	GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	77	0.7058567	1.5491294	0.00298507	0.04020634	0.999
Positive	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	37	0.8029952	1.5479534	0.00332779	0.04091173	0.999
Positive	GO_TELOMERE_CAPPING	52	0.7505662	1.54777	0.0030581	0.04091924	0.999
Positive	GO_NEGATIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	147	0.66106653	1.5466932	0	0.04168241	0.999
Positive	GO_CHROMOSOME_CONDENSATION	41	0.78924066	1.5455477	0	0.04253998	0.999
Positive	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	107	0.6873413	1.5451977	0.0014245	0.04263448	0.999

Positive	GO_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	278	0.6277922	1.5445786	0	0.04290196	0.999
Positive	GO_INTERACTION_WITH_SYMBIONT	79	0.7117407	1.5440521	0.0015949	0.04313536	0.999
Positive	GO_TELOMERASE_RNA_LOCALIZATION	19	0.8920303	1.5431556	0	0.0437072	1
Positive	GO_POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BODY	15	0.94005924	1.5412396	0.00172712	0.0452712	1
Positive	GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	44	0.7747746	1.5412024	0.00491803	0.04507923	1
Positive	GO_DNA_RECOMBINATION	263	0.62655056	1.540815	0	0.04515132	1
Positive	GO_CELLULAR_RESPONSE_TO_HEAT	131	0.6775538	1.5399349	0	0.04574508	1
Positive	GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	146	0.65797585	1.5393602	0.00136799	0.04603612	1
Positive	GO_RESPONSE_TO_INTERLEUKIN_7	39	0.7793739	1.5381489	0.00831947	0.04706299	1
Positive	GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	193	0.6383027	1.538091	0	0.04689087	1
Positive	GO_INTERSTRAND_CROSS_LINK_REPAIR	48	0.745106	1.5370057	0.0046225	0.04777862	1
Positive	GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY	42	0.779456	1.5360017	0.00793651	0.04852704	1

Positive	GO_ALTERNATIVE_MRNA_SPLICING_VIA_SPLICEOSOME	76	0.7023584	1.5349722	0.00298507	0.04921557	1
Positive	GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	44	0.76853395	1.5341821	0.00163132	0.04979948	1