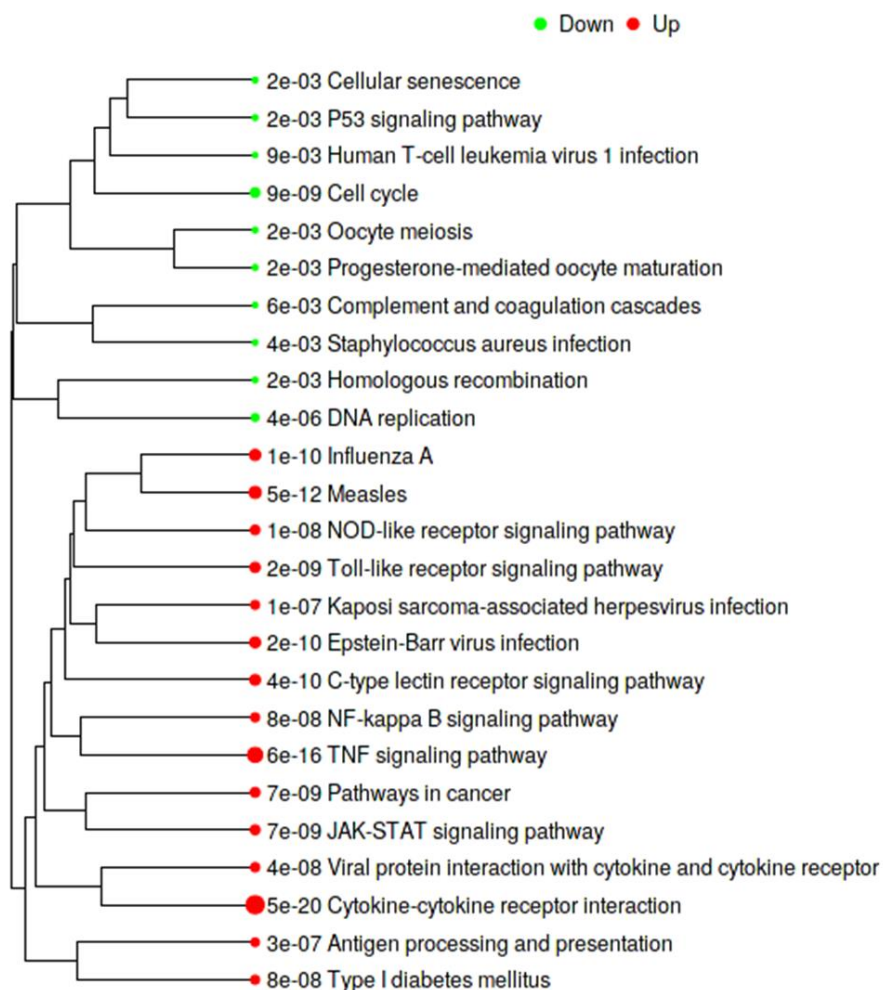


## **Supplementary Materials**

Gene set enrichment analysis reveals that Fucoïdan induces type I IFN pathways in BMDC

**Figure S1.**



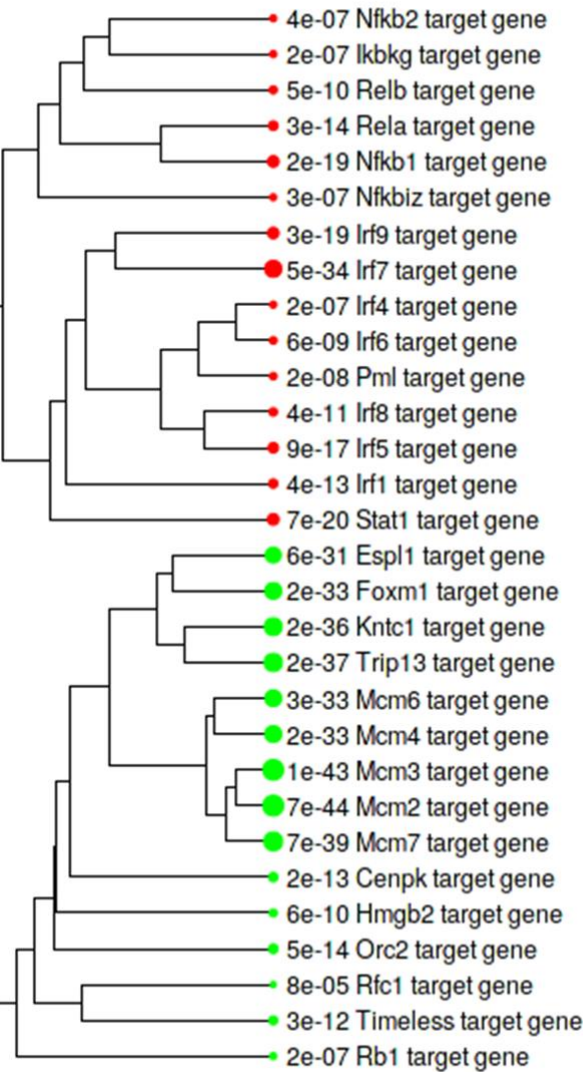
**Figure S1.** Visualization of the relationships between enriched KEGG pathways in DEGs using hierarchical clustering tree

**Table S1. Enriched TF Target gene sets among DEGs**

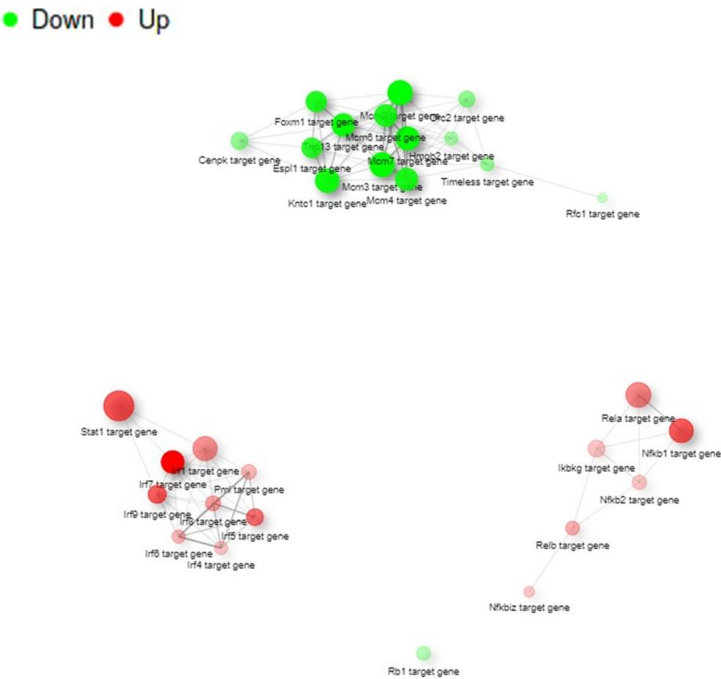
<b>Direction</b>	<b>Pathways</b>	<b>nGenes</b>	<b>adj.Pval</b>
Down	Mcm2 target gene	56	6.70E-44
Regulated	Mcm3 target gene	56	1.10E-43
	Mcm7 target gene	51	6.70E-39
	Trip13 target gene	47	1.60E-37
	Kntc1 target gene	54	2.30E-36
	Foxm1 target gene	37	1.60E-33
	Mcm4 target gene	45	1.60E-33
	Mcm6 target gene	44	2.80E-33
	Espl1 target gene	35	6.10E-31
	Orc2 target gene	20	4.80E-14
	Cenpk target gene	24	2.30E-13
	Timeless target gene	14	2.80E-12
	Hmgb2 target gene	14	5.60E-10
	Rb1 target gene	16	2.10E-07
	Rfc1 target gene	7	7.80E-05
Up	Irf7 target gene	49	5.10E-34
Regulated	Stat1 target gene	100	7.30E-20
	Nfkb1 target gene	54	1.70E-19
	Irf9 target gene	28	3.20E-19
	Irf5 target gene	24	9.10E-17
	Rela target gene	59	3.10E-14
	Irf1 target gene	56	4.50E-13
	Irf8 target gene	18	4.20E-11
	Relb target gene	14	4.90E-10
	Irf6 target gene	14	6.10E-09
	Pml target gene	18	1.80E-08
	Ikbkg target gene	23	1.70E-07
	Irf4 target gene	14	2.20E-07
	Nfkbiz target gene	9	3.40E-07
	Nfkb2 target gene	16	4.00E-07

Figure S2.

A



B



**Figure S2.** Visualization of the relationships between enriched TF target gene sets in DEGs using (A) tree and (B) network

**Table S2. Virus-specific immune pathways enriched in fucoidan-treated BMDCs**

NAME	SIZE	NES	NOM p-val	FDR q-val
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_CALU3_CELLS_UP	277	2.36	0.000	0.000
BLANCO_MELO_RESPIRATORY_SYNCYTIAL_VIRUS_INFECTION_A594_CELLS_UP	242	2.33	0.000	0.000
BLANCO_MELO_HUMAN_PARAINFLUENZA_VIRUS_3_INFECTION_A594_CELLS_UP	165	2.32	0.000	0.000
BLANCO_MELO_COVID19_BRONCHIAL_EPITHELIAL_CELLS_SARS_COV_2_INFECTION_UP	121	2.30	0.000	0.000
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_INFLUENZA_A_INFECTION_UP	110	2.00	0.000	0.003
WP_SARSCOV2_INNATE_IMMUNITY_EVASION_AND_CELLSPECIFIC_IMMUNE_RESPONSE	62	1.92	0.000	0.008
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_A594_ACE2_EXPRESSING_CELLS_UP	400	1.92	0.000	0.009
BLANCO_MELO_COVID19_SARS_COV_2_LOW_MOI_INFECTION_A594_ACE2_EXPRESSING_CELLS_UP	119	1.88	0.000	0.014
ZHU_CMV_8_HR_UP	35	1.86	0.000	0.016
WP_SARS_CORONAVIRUS_AND_INNATE_IMMUNITY	27	1.83	0.000	0.022
WP_HOSTPATHOGEN_INTERACTION_OF_HUMAN_CORONA_VIRUSES_IN_INTERFERON_INDUCTION	32	1.82	0.000	0.023
WP_TYPE_I_INTERFERON_INDUCTION_AND_SIGNALING_DURING_SARSCOV2_INFECTION	28	1.82	0.005	0.024
BROWNE_HCMV_INFECTION_4HR_UP	45	1.79	0.005	0.029
VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP	157	1.73	0.000	0.041
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_A594_ACE2_EXPRESSING_CELLS_RUXOLITINIB_UP	342	1.71	0.000	0.049
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_A594_CELLS_UP	71	1.69	0.000	0.052
BROWNE_HCMV_INFECTION_6HR_UP	56	1.69	0.006	0.053
WP_STING_PATHWAY_IN_KAWASAKILIKE_DISEASE_AND_COVID19	18	1.63	0.007	0.076
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	42	1.61	0.006	0.083
DORN_ADENOVIRUS_INFECTION_24HR_DN	38	1.57	0.017	0.098
DORN_ADENOVIRUS_INFECTION_32HR_DN	36	1.56	0.016	0.103
DORN_ADENOVIRUS_INFECTION_48HR_DN	37	1.56	0.016	0.103
DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	258	1.51	0.000	0.122
ZHU_CMV_ALL_UP	100	1.47	0.003	0.145
DORN_ADENOVIRUS_INFECTION_12HR_UP	25	1.41	0.056	0.178
BROWNE_HCMV_INFECTION_12HR_UP	93	1.40	0.009	0.180
BLANCO_MELO_MERS_COV_INFECTION_MCR5_CELLS_DN	24	1.41	0.040	0.180
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	19	1.34	0.098	0.225
WP_EBOLA_VIRUS_PATHWAY_ON_HOST	103	1.33	0.013	0.229

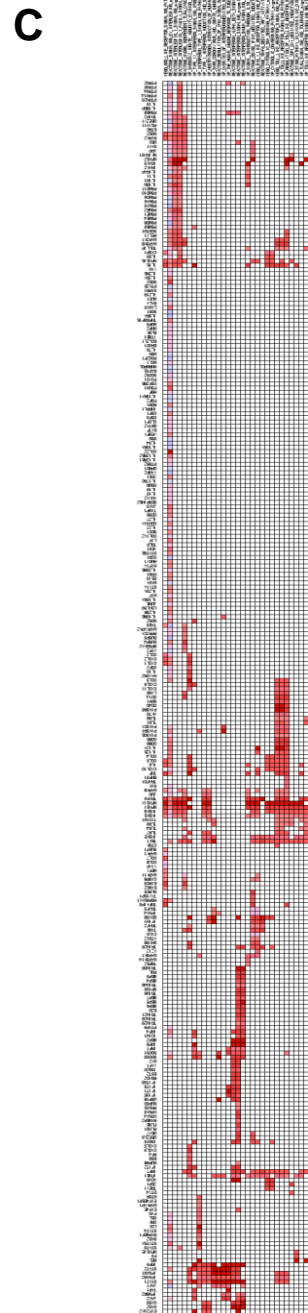
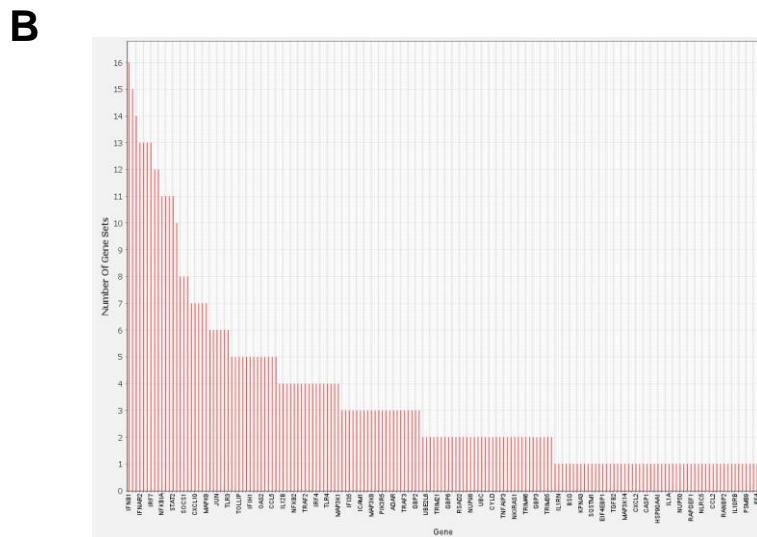
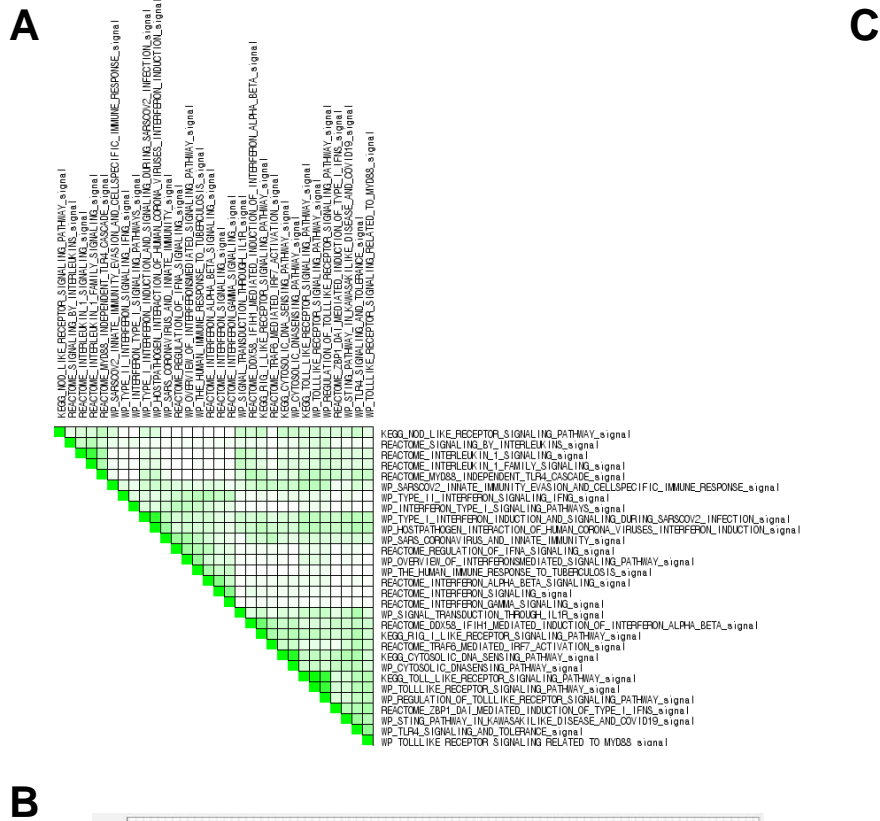
**Table S3. PRR signaling pathways enriched in fucoidan-treated BMDCs**

NAME	SIZE	NES	NOM p-val	FDR q-val
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	63	1.76	0.003	0.036
WP_TOLLLIKE_RECEPTOR_SIGNALING_PATHWAY	99	1.74	0.000	0.039
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	97	1.73	0.000	0.041
WP_FIBRIN_COMPLEMENT_RECEPTOR_3_SIGNALING_PATHWAY	42	1.70	0.000	0.051
REACTOME_BINDING_AND_UPTAKE_OF_LIGANDS_BY_SCAVENGER_RECEPTORS	36	1.65	0.003	0.071
WP_REGULATION_OF_TOLLLIKE_RECEPTOR_SIGNALING_PATHWAY	137	1.63	0.000	0.076
WP_STING_PATHWAY_IN_KAWASAKILIKE_DISEASE_AND_COVID19	18	1.63	0.007	0.076
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	49	1.63	0.006	0.076
WP_NOVEL_INTRACELLULAR_COMPONENTS_OF_RIGILIKE_RECEPTOR_RLR_PATHWAY	57	1.59	0.003	0.088
WP_TLR4_SIGNALING_AND_TOLERANCE	28	1.54	0.018	0.110
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	53	1.53	0.003	0.111
REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	60	1.49	0.012	0.131
REACTOME_CLEC7A_DECTIN_1_SIGNALING	97	1.46	0.003	0.151
WP_CYTOSOLIC_DNASENSING_PATHWAY	65	1.44	0.009	0.163
REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	18	1.40	0.079	0.180
WP_TOLLLIKE_RECEPTOR_SIGNALING_RELATED_TO_MXD88	32	1.36	0.055	0.207
REACTOME_TOLL_LIKE_RECEPTOR_TLR1_TLR2_CASCADE	100	1.35	0.010	0.217
REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	148	1.30	0.004	0.249
REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	92	1.30	0.031	0.249

**Table S4. Leading edge genes within representative enrichment plots shown in Fig. 4b**

<b>(Left)</b>		<b>(Middle)</b>		<b>(Right)</b>	
<b>GENE</b>	<b>NA RUNNING ME ES</b>	<b>GENE</b>	<b>NA RUNNING ME ES</b>	<b>GENE</b>	<b>NA RUNNING ME ES</b>
ADAR	0.023	NFKBIA	0.068	IRF9	0.066
IRF8	0.057	TRAF6	0.119	DDX58	0.151
OAS2	0.085	NFKB1	0.175	STAT1	0.232
GBP2	0.115	OAS2	0.219	IFIH1	0.306
IRF9	0.146	IRF9	0.267	STAT2	0.378
STAT1	0.173	EIF2AK2	0.312	TBK1	0.442
OAS3	0.201	STAT1	0.359	IFNAR1	0.515
XAF1	0.224	OAS3	0.404	IKBKE	0.53
STAT2	0.249	STAT2	0.44	IFNAR2	0.574
SOCS3	0.276	TLR7	0.484	IFNB1	0.616
IFIT1	0.301	TBK1	0.517	TLR3	0.659
IRF4	0.326	IFNAR1	0.559	TICAM1	0.685
USP18	0.354	TREML4	0.597	JAK1	0.693
ISG15	0.378	IKBKG	0.636	TRAF3	0.69
RSAD2	0.405	IKBKE	0.633	IFNA4	0.712
MX2	0.431	IFNAR2	0.654		
IFNAR1	0.458	JUN	0.658		
IRF7	0.484	MAPK8	0.678		
IFIT2	0.509	IKBKB	0.701		
IFIT3	0.531				
BST2	0.55				
IFI35	0.573				
SOCS1	0.587				
ISG20	0.607				
IFITM3	0.61				
IFNAR2	0.623				
IFNB1	0.633				
IRF1	0.648				
PSMB8	0.663				

**Figure S3.** Leading edge analysis of cluster A1 enriched genes





**Table S5. GSEA of TF targets in fucoidan vs control BMDCs**

<b>NAME</b>	<b>SIZE</b>	<b>NES</b>	<b>NOM p-val</b>	<b>FDR q-val</b>
ICSBP_Q6	239	1.69	0	0.09
IRF2_01	119	1.6	0	0.116
NFKB_Q6_01	228	1.41	0	0.127
NFKAPPAB_01	241	1.41	0	0.135
CREL_01	248	1.46	0.004	0.135
STTTTCRNTTT_IRF_Q6	178	1.43	0	0.136
STAT5A_01	236	1.38	0	0.136
ARP1_01	149	1.37	0.008	0.138
NFKB_Q6	242	1.42	0	0.139
SREBP1_Q6	235	1.38	0.005	0.139
GGGNNTTCC_NFKB_Q6_01	127	1.47	0	0.141
IRF1_01	228	1.39	0.004	0.142
NFAT_Q6	224	1.36	0	0.142
IRF7_01	237	1.54	0	0.143
NFKB_C	249	1.43	0	0.146
IRF_Q6	229	1.36	0.005	0.147
EN1_01	107	1.38	0.009	0.148
E2F_Q6	210	-1.81	0	0.001
E2F1_Q3	221	-1.82	0	0.001
E2F1DP1RB_01	209	-1.78	0	0.001
E2F_Q4	213	-1.79	0	0.001
SGCGSSAAA_E2F1DP2_01	150	-1.83	0	0.001
E2F_02	214	-1.74	0	0.001
E2F_Q3	205	-1.83	0	0.001
E2F4DP2_01	214	-1.73	0	0.001
E2F1_Q4_01	208	-1.77	0	0.001
E2F1DP1_01	214	-1.74	0	0.001
E2F4DP1_01	216	-1.83	0	0.001
E2F_Q4_01	216	-1.75	0	0.001
E2F1DP2_01	214	-1.72	0	0.002
E2F1_Q6	212	-1.83	0	0.002
E2F_Q3_01	214	-1.87	0	0.002
E2F_Q6_01	218	-1.68	0	0.002
E2F1_Q6_01	223	-1.66	0	0.003
E2F_03	229	-1.61	0	0.005
E2F1_Q4	232	-1.61	0	0.005
E2F1_Q3_01	231	-1.54	0	0.015
KTGGYRSGAA_UNKNOWN	70	-1.4	0.016	0.094
NFY_C	218	-1.4	0.001	0.097

**Table S6. Leading edge genes within LINDSTEDT DC maturation gene set enrichment plots in Fig. 5a**

<b>A</b>		<b>B</b>		<b>C</b>	
<b>GENE NAME</b>	<b>RUNNING ES</b>	<b>GENE NAME</b>	<b>RUNNING ES</b>	<b>GENE NAME</b>	<b>RUNNING ES</b>
LAD1	0.050	NR4A3	0.053	LAD1	0.050
COL14A1	0.091	NFKBIA	0.087	COL14A1	0.091
STAT5A	0.132	REL	0.122	STAT5A	0.132
ENPP4	0.169	NFKB2	0.156	ENPP4	0.169
TNFSF4	0.203	TNIP1	0.190	TNFSF4	0.203
LY75	0.233	CD83	0.215	LY75	0.233
SYNGR3	0.265	CD80	0.244	SYNGR3	0.265
STK39	0.292	MARCKSL1	0.273	STK39	0.292
CD86	0.320	NFKB1	0.302	CD86	0.320
CD200	0.341	PSME2	0.330	CD200	0.341
LGALS9	0.349	BIRC3	0.356	LGALS9	0.349
ATF3	0.372	CYTIP	0.384	ATF3	0.372
TNFRSF11B	0.395	TNFAIP3	0.412	TNFRSF11B	0.395
SEMA7A	0.416	DUSP4	0.438	SEMA7A	0.416
NID1	0.434	CFLAR	0.464	NID1	0.434
STAT3	0.446	TRAF1	0.482	STAT3	0.446
FOXO1	0.467	TNFRSF9	0.503	FOXO1	0.467
NFIL3	0.478	SLAMF1	0.522	NFIL3	0.478
FERMT2	0.496	IL2RA	0.545	FERMT2	0.496
TRAFFD1	0.509	IL15RA	0.568	TRAFFD1	0.509
SOCS2	0.525	TAP1	0.581	SOCS2	0.525
ARID5A	0.538	SDC4	0.602	ARID5A	0.538
GTF2E2	0.550	JRK	0.624	GTF2E2	0.550
PLAGL1	0.566	ADM	0.644	PLAGL1	0.566
S1PR1	0.577	USP12	0.663	S1PR1	0.577
PRKAR2B	0.582	BTG1	0.678	PRKAR2B	0.582
FLT3	0.578	OPTN	0.694	FLT3	0.578
MUC1	0.583	TNFAIP2	0.697	MUC1	0.583
TNFRSF11A	0.583	MAP3K14	0.715	TNFRSF11A	0.583
ROCK2	0.589	PDGFA	0.718	ROCK2	0.589
JAK1	0.595	ID2	0.734	JAK1	0.595
		PNRC1	0.745		
		HIVEP1	0.747		