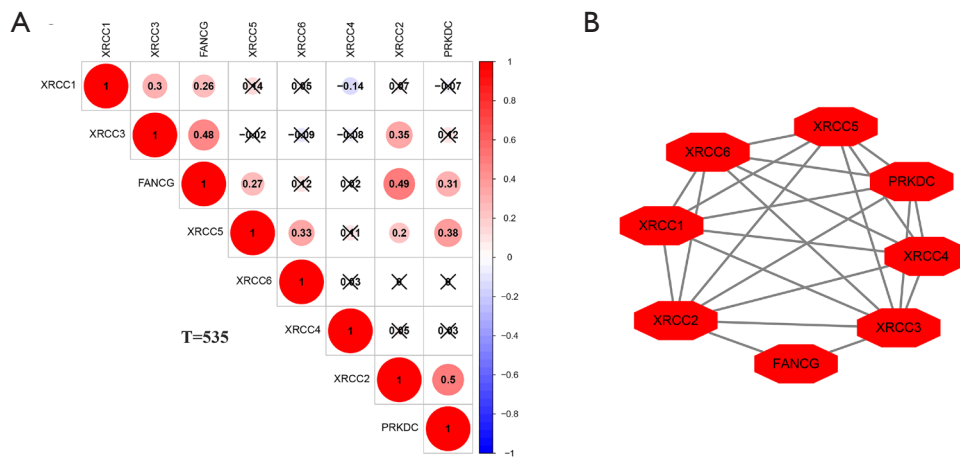


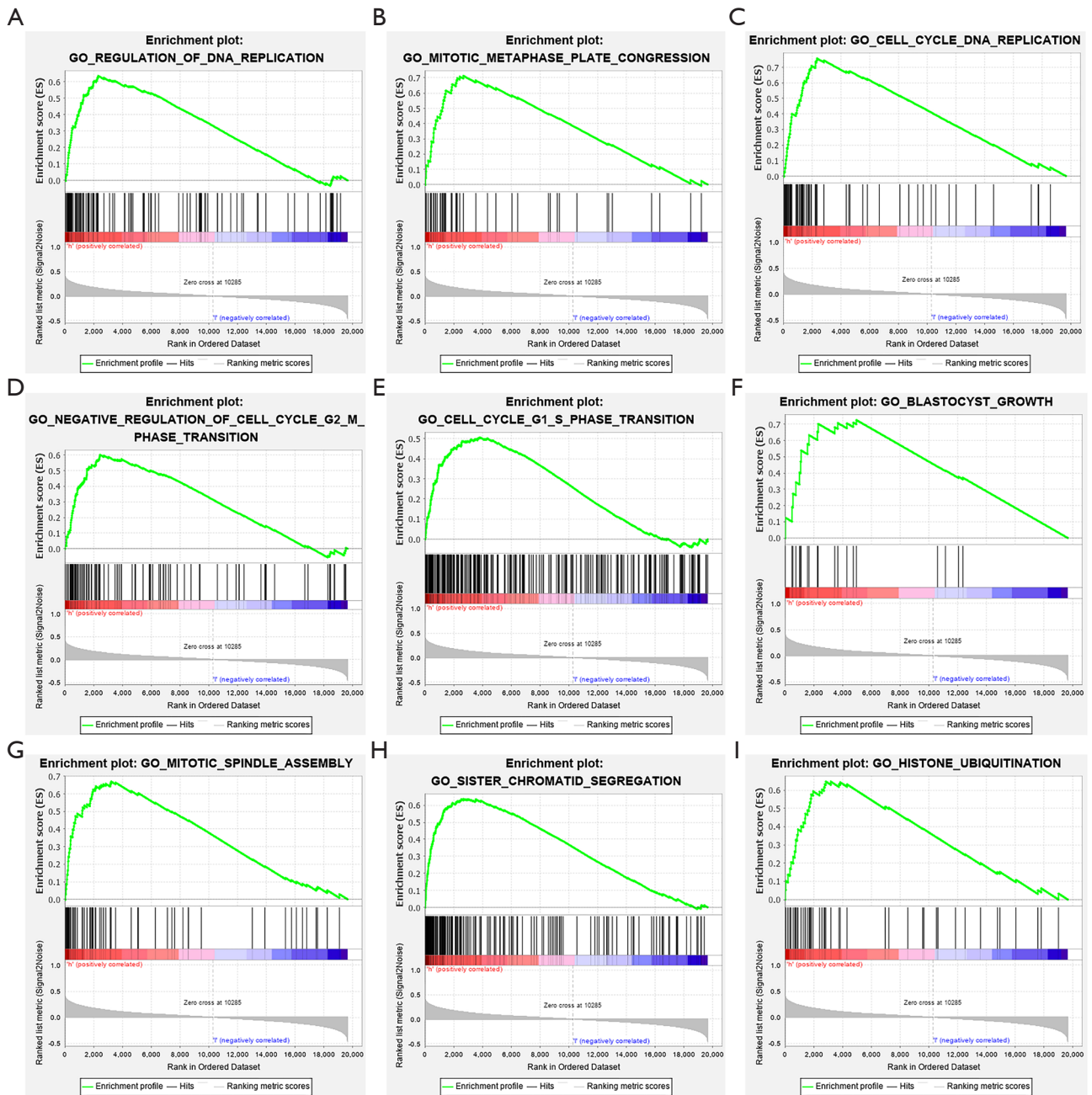
**Figure S1** Expression level of XRCC family members in pan-cancer tissues in the Oncomine database. (A) XRCC1; (B) XRCC6; (C) XRCC2; (D) XRCC3; (E) FANCG; (F) XRCC4; (G) XRCC5; (H) PRKDC.



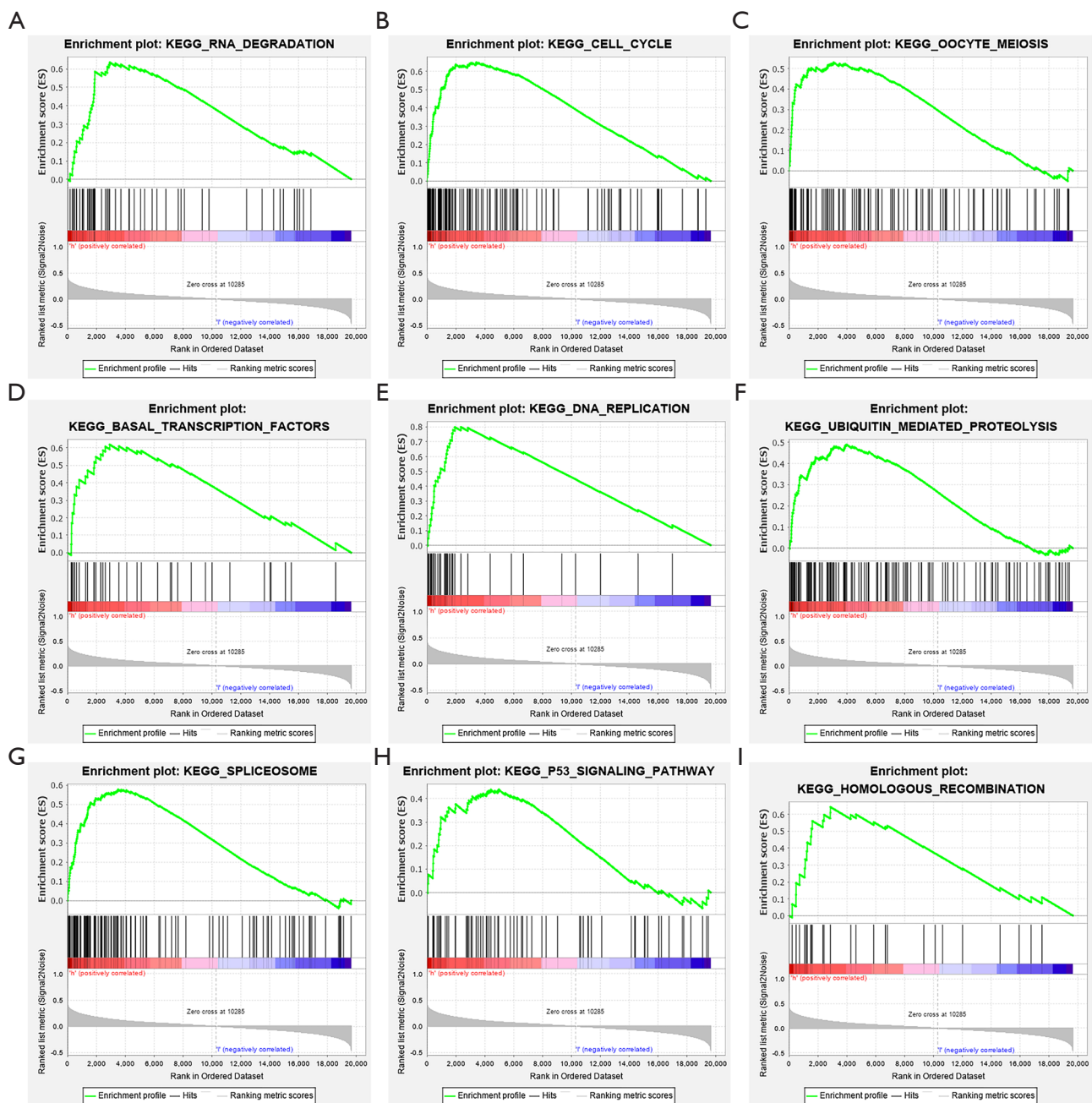
**Figure S2** Correlation and functional relationship of the eight members of the *XRCC* family. (A) Correlation analysis; (B) PPI network. PPI, protein-protein interaction.

**Table S1** Genes of the XRCC family were involved in molecular biological functions

Type	GO	Description	P
BP	GO:0006302	Double-strand break repair	2.94E-11
BP	GO:0006281	DNA repair	3.49E-11
BP	GO:0006310	DNA recombination	3.49E-11
BP	GO:0010212	Response to ionizing radiation	7.62E-10
BP	GO:0009314	Response to radiation	1.68E-09
BP	GO:0006303	Double-strand break repair via nonhomologous end joining	2.33E-09
BP	GO:0009628	Response to abiotic stimulus	4.44E-09
BP	GO:0000723	Telomere maintenance	1.31E-08
BP	GO:0010165	Response to X-ray	3.56E-08
BP	GO:0010332	Response to gamma radiation	2.12E-07
BP	GO:0075713	Establishment of integrated proviral latency	2.84E-07
BP	GO:0006266	DNA ligation	1.33E-06
BP	GO:0006312	Mitotic recombination	2.32E-06
BP	GO:0071475	Cellular hyperosmotic salinity response	3.91E-05
BP	GO:0032481	Positive regulation of type I interferon production	5.69E-05
BP	GO:0000707	Meiotic DNA recombinase assembly	0.00012
BP	GO:0000724	Double-strand break repair via homologous recombination	0.00012
BP	GO:0051351	Positive regulation of ligase activity	0.00012
BP	GO:0042148	Strand invasion	0.00013
BP	GO:0000722	Telomere maintenance via recombination	0.00019
BP	GO:0051103	DNA ligation involved in DNA repair	0.00019
BP	GO:0071481	Cellular response to X-ray	0.00019
BP	GO:0048660	Regulation of smooth muscle cell proliferation	0.00021
BP	GO:0006996	Organelle organization	0.00024
BP	GO:0002218	Activation of innate immune response	0.00057
BP	GO:0071480	Cellular response to gamma radiation	0.00069
BP	GO:0007420	Brain development	0.00087
BP	GO:0032205	Negative regulation of telomere maintenance	0.0012
BP	GO:0007131	Reciprocal meiotic recombination	0.0017
BP	GO:0036297	Interstrand cross-link repair	0.0017
BP	GO:0032508	DNA duplex unwinding	0.002
BP	GO:0033044	Regulation of chromosome organization	0.002
BP	GO:0001756	Somitogenesis	0.0027
BP	GO:0043902	Positive regulation of multi-organism process	0.0035
BP	GO:0002244	Hematopoietic progenitor cell differentiation	0.0037
BP	GO:0007399	Nervous system development	0.0054
BP	GO:0080134	Regulation of response to stress	0.0074
BP	GO:0022414	Reproductive process	0.0083
BP	GO:0043085	Positive regulation of catalytic activity	0.0086
BP	GO:0051704	Multi-organism process	0.0086
BP	GO:0048731	System development	0.01
BP	GO:0045087	Innate immune response	0.0114
BP	GO:0051240	Positive regulation of multicellular organismal process	0.0118
BP	GO:0048513	Animal organ development	0.015
BP	GO:0051054	Positive regulation of DNA metabolic process	0.0163
BP	GO:0031399	Regulation of protein modification process	0.0169
BP	GO:0045935	Positive regulation of nucleobase-containing compound metabolic process	0.0176
BP	GO:0048522	Positive regulation of cellular process	0.0207
BP	GO:0022402	Cell cycle process	0.0213
BP	GO:0045321	Leukocyte activation	0.0213
BP	GO:0048584	Positive regulation of response to stimulus	0.0268
BP	GO:1901990	Regulation of mitotic cell cycle phase transition	0.0354
BP	GO:0051172	Negative regulation of nitrogen compound metabolic process	0.0381
BP	GO:0031324	Negative regulation of cellular metabolic process	0.0454
BP	GO:0050769	Positive regulation of neurogenesis	0.0469
BP	GO:0051094	Positive regulation of developmental process	0.0475
MF	GO:0140097	Catalytic activity, acting on DNA	2.35E-07
MF	GO:0003684	Damaged DNA binding	3.37E-07
MF	GO:0008094	DNA-dependent ATPase activity	3.37E-07
MF	GO:0003677	DNA binding	6.46E-05
MF	GO:0000150	Recombinase activity	0.0001
MF	GO:0003690	Double-stranded DNA binding	0.0001
MF	GO:0008022	Protein C-terminus binding	0.00044
MF	GO:0005524	ATP binding	0.00074
MF	GO:0042162	Telomeric DNA binding	0.00074
MF	GO:0003678	DNA helicase activity	0.00078
MF	GO:0008144	Drug binding	0.00088
MF	GO:0003697	Single-stranded DNA binding	0.0019
MF	GO:0016787	Hydrolase activity	0.003
MF	GO:0003824	Catalytic activity	0.0188
MF	GO:0005488	Binding	0.0385
CC	GO:1990391	DNA repair complex	6.40E-11
CC	GO:0070419	Nonhomologous end joining complex	2.57E-10
CC	GO:0000784	Nuclear chromosome, telomeric region	8.13E-08
CC	GO:0005654	Nucleoplasm	1.10E-05
CC	GO:0043564	Ku70:Ku80 complex	1.10E-05
CC	GO:0005958	DNA-dependent protein kinase-DNA ligase 4 complex	1.97E-05
CC	GO:0033063	Rad51B-Rad51C-Rad51D-XRCC2 complex	2.58E-05
CC	GO:0005730	Nucleolus	6.28E-05
CC	GO:0005694	Chromosome	6.31E-05
CC	GO:0032991	Protein-containing complex	6.31E-05
CC	GO:0000783	Nuclear telomere cap complex	6.43E-05
CC	GO:0032993	Protein-DNA complex	0.00015
CC	GO:0043232	Intracellular non-membrane-bounded organelle	0.00028
CC	GO:0005657	Replication fork	0.00056
CC	GO:0005829	Cytosol	0.0111
CC	GO:0005667	Transcription regulator complex	0.0162
CC	GO:0034774	Secretory granule lumen	0.0162



**Figure S3** The biological functions involved in the high-risk model.



**Figure S4** The signaling pathways involved in the high-risk model.

Table S2 XRCC4, XRCC5, and XRCC6 were related to the immune genes

XRCC4	cor	P	XRCC5	cor	P	XRCC6	cor	P
CX3CL1	0.025	0.568931297	CX3CL1	-0.292	5.98E-12	CX3CL1	-0.023	0.591492333
CCL26	0.233	4.99E-08	CCL26	0.057	0.186796344	CCL26	-0.024	0.585938933
TNFRSF17	0.169	8.17E-05	TNFRSF17	-0.06	0.165506718	TNFRSF17	-0.157	0.000265563
TNFRSF9	0.248	5.77E-09	TNFRSF9	-0.045	0.302695211	TNFRSF9	-0.128	0.003092972
PVR	0.004	0.920944752	PVR	0.221	2.55E-07	PVR	0.082	0.059349591
XRCC5	0.175	4.87E-05	XRCC5	1	0	XRCC5	0.357	1.46E-17
CXCL2	-0.035	0.419462461	CXCL2	-0.264	5.44E-10	CXCL2	-0.214	5.75E-07
LAG3	-0.008	0.852057213	LAG3	-0.065	0.133636238	LAG3	-0.149	0.000538555
CD40	0.129	0.002888207	CD40	-0.176	4.39E-05	CD40	-0.065	0.130786826
TNFSF13B	0.262	7.13E-10	TNFSF13B	-0.012	0.784919029	TNFSF13B	-0.149	0.000527802
CCL22	0.062	0.152716365	CCL22	-0.163	0.000151071	CCL22	-0.002	0.96585854
CCL17	0.034	0.434880902	CCL17	-0.257	1.53E-09	CCL17	0.021	0.620604918
CD276	-0.007	0.867022858	CD276	0.109	0.011950511	CD276	0.223	1.97E-07
CCL24	0.212	7.08E-07	CCL24	0.118	0.00614055	CCL24	0.03	0.49395181
TGFB1	0.276	8.77E-11	TGFB1	0.206	1.61E-06	TGFB1	-0.188	1.19E-05
CXCL12	0.121	0.004992095	CXCL12	-0.116	0.007292657	CXCL12	-0.143	0.000877105
CCL7	0.249	5.53E-09	CCL7	0.085	0.05048319	CCL7	0.057	0.185472508
CCL2	0.235	3.66E-08	CCL2	-0.08	0.063822772	CCL2	-0.049	0.254718295
CCL8	0.253	3.06E-09	CCL8	0.07	0.107334423	CCL8	0.023	0.60019873
CCL1	0.105	0.014715748	CCL1	-0.061	0.158268068	CCL1	0.027	0.535593895
ULBP1	-0.035	0.421271558	ULBP1	0.013	0.761033993	ULBP1	0.035	0.423845066
CCR6	0.099	0.021528102	CCR6	-0.124	0.003963097	CCR6	-0.274	1.24E-10
CD86	0.28	4.48E-11	CD86	-0.071	0.101435478	CD86	-0.156	0.000293129
HHLA2	0.055	0.20585345	HHLA2	-0.138	0.001384266	HHLA2	0.011	0.795640807
CCL20	0.118	0.006493886	CCL20	0.036	0.408983419	CCL20	-0.039	0.364853416
CD48	0.163	0.00015073	CD48	-0.101	0.019605336	CD48	-0.142	0.000978132
CD160	0.116	0.007319177	CD160	-0.144	0.000848341	CD160	-0.525	2.71E-39
TNFSF4	0.424	8.72E-25	TNFSF4	0.098	0.022970244	TNFSF4	-0.155	0.000312759
CD274	0.247	7.21E-09	CD274	-0.078	0.070230227	CD274	-0.175	4.80E-05
TNFSF18	0.216	4.42E-07	TNFSF18	0.04	0.361341843	TNFSF18	-0.074	0.08598465
TNFRSF8	0.065	0.132654552	TNFRSF8	-0.062	0.149570582	TNFRSF8	-0.1	0.020539666
CD80	0.306	4.62E-13	CD80	-0.096	0.027015198	CD80	-0.302	1.01E-12
CCR2	0.186	1.47E-05	CCR2	-0.115	0.007703775	CCR2	-0.21	9.64E-07
CXCR4	0.14	0.001129742	CXCR4	-0.086	0.047195645	CXCR4	-0.201	2.74E-06
CD244	0.123	0.004337248	CD244	-0.104	0.016244471	CD244	-0.205	1.68E-06
CXCL6	0.09	0.036807951	CXCL6	0.051	0.243105359	CXCL6	-0.077	0.075924369
KIR2DL1	0.015	0.725185178	KIR2DL1	0.062	0.152641661	KIR2DL1	-0.017	0.70244992
TNFSF9	0.176	4.23E-05	TNFSF9	-0.139	0.001241306	TNFSF9	0.11	0.010826689
CD70	0.127	0.00335312	CD70	-0.015	0.728667018	CD70	0.033	0.444863555
TNFSF14	0.018	0.679743896	TNFSF14	-0.208	1.25E-06	TNFSF14	-0.271	1.86E-10
CCR7	-0.022	0.604451231	CCR7	-0.214	5.73E-07	CCR7	-0.199	3.40E-06
KDR	0.05	0.243942206	KDR	-0.043	0.318860255	KDR	-0.104	0.016601791
ADORA2A	-0.039	0.367768047	ADORA2A	-0.197	4.48E-06	ADORA2A	-0.298	2.10E-12
CCL25	0.079	0.066310209	CCL25	-0.032	0.466143467	CCL25	-0.086	0.046960161
IDO1	0.109	0.01149635	IDO1	0.033	0.450656196	IDO1	-0.054	0.211079429
VTCN1	-0.041	0.34718313	VTCN1	0.033	0.449533403	VTCN1	-0.017	0.69228404
IL2RA	0.237	2.80E-08	IL2RA	0.041	0.338378754	IL2RA	-0.099	0.022629607
KLRC1	0.247	7.43E-09	KLRC1	-0.019	0.656390121	KLRC1	-0.175	4.70E-05
HAVCR2	0.255	2.13E-09	HAVCR2	-0.124	0.004177175	HAVCR2	-0.147	0.000665012
NT5E	0.182	2.34E-05	NT5E	-0.03	0.488995346	NT5E	0.021	0.631090231
IL6	0.17	7.49E-05	IL6	0.02	0.645310115	IL6	-0.107	0.013552203
IL10	0.17	7.50E-05	IL10	-0.055	0.200896624	IL10	-0.101	0.019997271
CCL21	0.093	0.032215511	CCL21	-0.05	0.248700196	CCL21	0.039	0.369975764
ENTPD1	0.239	2.07E-08	ENTPD1	-0.051	0.239693681	ENTPD1	-0.347	1.42E-16
CXCL9	0.084	0.052169796	CXCL9	0.055	0.200980705	CXCL9	-0.115	0.007711904
CD27	0.046	0.28735872	CD27	-0.147	0.000675162	CD27	-0.138	0.001329469
XCL1	0.015	0.734176917	XCL1	0.136	0.001644228	XCL1	0.035	0.419901604
XCL2	0.12	0.005350195	XCL2	-0.051	0.23618319	XCL2	-0.095	0.02843227
CXCL14	0.064	0.13993607	CXCL14	-0.093	0.030958584	CXCL14	-0.067	0.119622165
CCL28	0.147	0.000664186	CCL28	-0.07	0.106788675	CCL28	-0.138	0.001430795
XRCC4	1	0	XRCC4	0.175	4.87E-05	XRCC4	0.003	0.946384078
CD96	0.098	0.023091268	CD96	-0.093	0.030606415	CD96	-0.254	2.54E-09
CXCL13	0.092	0.034174697	CXCL13	-0.021	0.62473293	CXCL13	-0.125	0.00388277
TNFRSF14	-0.142	0.000978329	TNFRSF14	-0.458	3.67E-29	TNFRSF14	-0.22	2.80E-07
TNFRSF13C	-0.051	0.235189406	TNFRSF13C	-0.106	0.013990073	TNFRSF13C	-0.206	1.54E-06
ICOSLG	-0.03	0.488753722	ICOSLG	-0.044	0.307766389	ICOSLG	-0.047	0.275085532
CXCR5	-0.034	0.43758992	CXCR5	-0.123	0.004469894	CXCR5	-0.132	0.002247667
IL6R	-0.179	3.14E-05	IL6R	-0.219	3.23E-07	IL6R	-0.093	0.03123836
CCR5	0.138	0.001415216	CCR5	-0.116	0.007136542	CCR5	-0.256	1.82E-09
CXCL16	-0.154	0.000349931	CXCL16	-0.218	3.55E-07	CXCL16	0.123	0.004295705
TNFSF13	-0.052	0.230723652	TNFSF13	-0.249	5.34E-09	TNFSF13	0.145	0.000751992
CXCR1	0.006	0.890843794	CXCR1	0.045	0.296525679	CXCR1	-0.05	0.252319994
CTLA4	0.159	0.000217081	CTLA4	-0.117	0.006760274	CTLA4	-0.292	5.50E-12
ICOS	0.218	3.59E-07	ICOS	-0.115	0.007588628	ICOS	-0.281	3.48E-11
CXCL3	0.03	0.487640536	CXCL3	-0.124	0.003947719	CXCL3	-0.164	0.000141255
CXCL5	0.21	9.58E-07	CXCL5	0.128	0.002911276	CXCL5	-0.049	0.254691705
CXCL1	0.044	0.309590843	CXCL1	-0.049	0.255340454	CXCL1	-0.136	0.001622125
CCR1	0.213	6.93E-07	CCR1	-0.091	0.034770103	CCR1	-0.135	0.001698474
RAET1E	0.091	0.035354522	RAET1E	0.12	0.005530295	RAET1E	0.022	0.615347732
B2M	0.274	1.07E-10	B2M	-0.04	0.359475197	B2M	-0.001	0.975203616
TMIGD2	0.102	0.018356154	TMIGD2	-0.098	0.02303364	TMIGD2	-0.102	0.018320314
CX3CR1	-0.021	0.625401388	CX3CR1	-0.221	2.35E-07	CX3CR1	-0.076	0.079903969
TAP1	0.158	0.000243567	TAP1	0.094	0.030043655	TAP1	0.039	0.368768465
LGALS9	-0.026	0.549176875	LGALS9	-0.235	3.97E-08	LGALS9	-0.038	0.386501579
CXCL10	0.241	1.55E-08	CXCL10	0.1	0.020707958	CXCL10	-0.038	0.382458495
CXCL11	0.191	8.69E-06	CXCL11	0.056	0.199108316	CXCL11	-0.039	0.364443135
CXCL8	0.28	4.38E-11	CXCL8	0.174	5.38E-05	CXCL8	0.014	0.741802874
CCL11	0.211	8.97E-07	CCL11	0.034	0.433707789	CCL11	-0.038	0.384018567
CXCR6	0.17	7.88E-05	CXCR6	-0.065	0.132557272	CXCR6	-0.261	9.39E-10
CCL19	-0.02	0.641061688	CCL19	-0.154	0.000336546	CCL19	-0.056	0.199618569
XCR1	-0.056	0.197612065	XCR1	-0.149	0.000529835	XCR1	-0.195	5.66E-06
CCR9	0.047	0.276958792	CCR9	-0.095	0.028781645	CCR9	-0.113	0.008798978
CD28	0.208	1.17E-06	CD28	-0.14	0.001163288	CD28	-0.341	4.80E-16
HLA-DQB1	0.008	0.849400934	HLA-DQB1	-0.305	5.44E-13	HLA-DQB1	-0.085	0.04908356
CCR8	0.259	1.21E-09	CCR8	0.007	0.869882953	CCR8	-0.132	0.002207012
CXCR2	0.044	0.312593351	CXCR2	-0.006	0.882801894	CXCR2	-0.115	0.007675023
CCL13	0.247	7.34E-09	CCL13	-0.171	7.09E-05	CCL13	0.059	0.174218653
TNFSF15	-0.129	0.002757172	TNFSF15	-0.074	0.086072179	TNFSF15	-0.035	0.422844781
TIGIT	0.121	0.004900923	TIGIT	-0.09	0.036624257	TIGIT	-0.301	1.25E-12
CSF1R	0.123	0.004502457	CSF1R	-0.158	0.000250205	CSF1R	-0.139	0.001299234
CCR3	0.021	0.620009698	CCR3	-0.04	0.36020986	CCR3	0.105	0.014920839
CCR4	0.102	0.018565906	CCR4	-0.146	0.000697664	CCR4	-0.237	2.84E-08
CCR10	-0.057	0.18778402	CCR10	-0.019	0.66747335	CCR10	-0.009	0.836408466
TMEM173	-0.075	0.08320565	TMEM173	-0.349	8.28E-17	TMEM173	-0.024	0.583184106
BTLA	0.135	0.001819738	BTLA	-0.133	0.002009577	BTLA	-0.387	1.62E-20
CXCR3	-0.024	0.581579106	CXCR3	-0.214	5.98E-07	CXCR3	-0.129	0.002694991
TNFRSF4	-0.012	0.786885943	TNFRSF4	-0.231	6.87E-08	TNFRSF4	-0.043	0.322560803
TNFRSF18	0.001	0.984421798	TNFRSF18	-0.21	9.03E-07	TNFRSF18	-0.027	0.534760723
PDCC1	0.008	0.859882922	PDCC1	-0.119	0.005876848	PDCC1	-0.163	0.000146595
CXCL17	-0.213	6.80E-07	CXCL17	-0.287	1.22E-11	CXCL17	-0.057	0.184694284
HLA-DRB1	0.053	0.224577668	HLA-DRB1	-0.307	3.79E-13	HLA-DRB1	-0.027	0.540222835
XRCC6	0.003	0.946384078	XRCC6	0.357	1.46E-17	XRCC6	1	0
HLA-DQA1	0.09	0.037806709	HLA-DQA1	-0.213	6.43E-07	HLA-DQA1	-0.14	0.001174679
PDCC1LG2	0.296	2.61E-12	PDCC1LG2	0.006	0.884529344	PDCC1LG2	-0.178	3.34E-05
HLA-DOA	0.044	0.305370162	HLA-DOA	-0.224	1.61E-07	HLA-DOA	-0.137	0.001459944
HLA-DMA	-0.026	0.545299624	HLA-DMA	-0.411	2.91E-23	HLA-DMA	-0.075	0.083843037
TAP2	0.115	0.007988396	TAP2	-0.058	0.178166234	TAP2	-0.194	5.87E-06
HLA-DRA	0.							