



Appendix 1. The PCA plot before batch effect removal. (A) The PCA plot after batch effect removal (B) Two types of samples from 2 different datasets were shown on this figure. Different colors indicated different datasets, while different symbols represented sample types (Normal liver and tumor). (C) Average silhouette width between the two molecular subtypes.

Appendix 2. Basic Information of Series Used for Estimating Immune Scores

Patient ID	Sample ID	Project ID	Age	Gender	OS_months	OS_event
1	GSM1948560	GSE75271	0.7	Maleale	1.71	0
2	GSM1948561	GSE75271	1.6	Female	10.37	0
3	GSM1948562	GSE75271	2.3	Male	0.59	1
4	GSM1948563	GSE75271	0.4	Female	2.51	0
5	GSM1948564	GSE75271	8.8	Female	0.09	1
6	GSM1948565	GSE75271	1.8	Male	0.4	0
7	GSM1948567	GSE75271	1.8	Male	3.41	0
8	GSM1948568	GSE75271	2.3	Female	1.31	0

9	GSM1948569	GSE75271	1	Female	12.79	0
10	GSM1948570	GSE75271	0.9	Male	2.26	0
11	GSM1948571	GSE75271	1.2	Male	1.65	0
12	GSM1948572	GSE75271	0.4	Male	8.48	0
13	GSM1948573	GSE75271	1.5	Male	7.48	0
14	GSM1948575	GSE75271	1.3	Female	1	1
15	GSM1948576	GSE75271	1.8	Male	0.24	0
16	GSM1948578	GSE75271	0.6	Female	10.83	0
17	GSM1948580	GSE75271	1.3	Female	9.99	0
18	GSM1948581	GSE75271	3	Female	8.75	0

19	GSM1948584	GSE75271	1.3	Male	0.45	1
20	GSM1948585	GSE75271	1.2	Male	7.53	0
21	GSM1948586	GSE75271	0.9	Female	2.03	0
22	GSM1948588	GSE75271	2.8	Male	2	0
23	GSM1948589	GSE75271	0.8	Female	0.08	0
24	GSM1948590	GSE75271	6.7	Female	0.42	1
25	GSM1948591	GSE75271	1.5	Female	0.84	1
26	GSM1948592	GSE75271	1.3	Female	2.64	0
27	GSM1948593	GSE75271	2.1	Female	8.49	0
28	GSM1948594	GSE75271	2.8	Female	9.79	0

29	GSM1948595	GSE75271	2.3	Male	8.94	0
30	GSM1948596	GSE75271	1.4	Male	8.3	0
31	GSM1948597	GSE75271	1.45	Male	1.77	1
32	GSM1948598	GSE75271	1.3	Male	0.48	1
33	GSM1948602	GSE75271	1.1	Female	4.5	0
34	GSM1948603	GSE75271	3.7	Male	0.26	0
35	GSM1948604	GSE75271	1.6	Male	2.3	0
36	GSM1948605	GSE75271	0.4	Male	2	0
37	GSM1948606	GSE75271	1.6	Male	1.63	0
38	GSM1948607	GSE75271	3.2	Male	10.59	0

39	GSM1948608	GSE75271	1.8	Male	9.21	0
40	GSM1948609	GSE75271	0.4	Male	9.91	0
41	GSM1948610	GSE75271	2.6	Female	1.55	0
42	GSM1948611	GSE75271	1.3	Female	1.19	0
43	GSM1948612	GSE75271	1.9	Female	1.21	0
44	GSM1948613	GSE75271	1	Female	1.35	0
45	HB5	E-MEXP-1851	7	Male	2	1
46	HB11	E-MEXP-1851	1.5	Female	1.75	1
47	HB28	E-MEXP-1851	2.83	Male	10	0
48	HB33	E-MEXP-1851	1	Male	0.29	1

49	HB48	E-MEXP-1851	6	Male	0.75	1
50	HB49	E-MEXP-1851	1.25	Female	0.5	1
51	HB54	E-MEXP-1851	0.83	Male	4.083	0
52	HB59	E-MEXP-1851	2	Female	6	0
53	HB60	E-MEXP-1851	2.5	Female	5.25	0
54	HB62	E-MEXP-1851	1.33	Male	5.75	0
55	HB63	E-MEXP-1851	17	Male	8	0
56	HB69	E-MEXP-1851	2.08	Male	5.583	0
57	HB70	E-MEXP-1851	3.5	Female	4.417	0
58	HB72	E-MEXP-1851	1.33	Female	0.792	1

59	HB73	E-MEXP-1851	2	Female	1.33	1
60	HB74	E-MEXP-1851	8	Male	2.917	0
61	HB75	E-MEXP-1851	1.75	Male	3.417	0
62	HB78	E-MEXP-1851	10.5	Male	2.667	0
63	HB79	E-MEXP-1851	12	Male	4.5	0
64	HB80	E-MEXP-1851	15	Male	1.667	1
65	HB81	E-MEXP-1851	1.83	Male	3	0
66	HB82	E-MEXP-1851	10	Male	5.25	0
67	HB83	E-MEXP-1851	1.25	Male	4.417	0
68	HB86	E-MEXP-1851	0.1	Male	5.5	0

Appendix 3. The Four Types Score Calculated Form ESTIMATE

Patient ID	Sample ID	StromalScore	ImmuneScore	ESTIMATEScore	TumorPurity
1	GSM1948560	-339.2052796	520.6282249	181.4229453	0.8070732
2	GSM1948561	-835.0526281	693.7755376	-141.2770904	0.8341264
3	GSM1948562	732.1400696	1438.073542	2170.213611	0.6029924
4	GSM1948563	-746.8715217	-135.3222271	-882.1937488	0.8890679
5	GSM1948564	-811.6009801	-212.8030935	-1024.404074	0.8984295
6	GSM1948565	-532.5433835	-137.8377237	-670.3811072	0.8744075
7	GSM1948567	558.657255	1342.457612	1901.114867	0.6340254
8	GSM1948568	-806.0161724	468.8204593	-337.1957132	0.8496417
9	GSM1948569	-314.0332121	179.0071045	-135.0261076	0.8336199

10	GSM1948570	-327.298754	-8.092744	-335.391499	0.849502
11	GSM1948571	107.7113923	885.862394	993.5737862	0.7311213
12	GSM1948572	-297.0230513	572.4950374	275.4719861	0.7988452
13	GSM1948573	-735.2535381	-273.4245442	-1008.678082	0.8974134
14	GSM1948575	-244.2297223	47.7520961	-196.4776263	0.8385682
15	GSM1948576	1372.848264	793.3703477	2166.218612	0.6034602
16	GSM1948578	-597.2013842	112.3774192	-484.823965	0.8608693
17	GSM1948580	-593.3328512	614.5192612	21.1864101	0.8207366
18	GSM1948581	-497.8739093	-26.0153717	-523.8892809	0.8637729
19	GSM1948584	1061.352762	198.8240446	1260.176806	0.7038691
20	GSM1948585	-449.3426916	458.1478343	8.8051428	0.8217736

21	GSM1948586	-497.330434	-209.0278493	-706.3582833	0.8769576
22	GSM1948588	98.7295474	945.4136638	1044.143211	0.7260369
23	GSM1948589	-496.1379305	233.8004849	-262.3374456	0.8437957
24	GSM1948590	-704.9386071	-387.8469897	-1092.785597	0.9027918
25	GSM1948591	-734.7811101	-222.5343912	-957.3155012	0.8940616
26	GSM1948592	235.7314186	-171.8679463	63.8634723	0.8171416
27	GSM1948593	-348.6138293	-365.1380344	-713.7518636	0.8774786
28	GSM1948594	-224.8775081	209.1609022	-15.716606	0.8238193
29	GSM1948595	-454.1720884	-411.5382647	-865.7103531	0.8879577
30	GSM1948596	-632.0491219	148.8688838	-483.1802381	0.8607465
31	GSM1948597	-428.3792844	-237.2111983	-665.5904827	0.8740661

32	GSM1948598	-555.2067525	72.7933638	-482.4133887	0.8606892
33	GSM1948602	-139.4671049	-200.491024	-339.9581289	0.8498555
34	GSM1948603	-769.5404581	-136.0219721	-905.5624302	0.8906329
35	GSM1948604	-202.2626279	277.0279318	74.7653039	0.8162181
36	GSM1948605	-507.0612507	354.4966295	-152.5646211	0.8350391
37	GSM1948606	-485.7743066	22.4168666	-463.3574399	0.8592617
38	GSM1948607	-202.1571421	635.4977115	433.3405694	0.7846924
39	GSM1948608	-31.6339791	1010.620248	978.9862684	0.7325805
40	GSM1948609	-56.2447815	464.2632331	408.0184515	0.7869911
41	GSM1948610	-891.9635171	200.4055996	-691.5579176	0.8759115
42	GSM1948611	-337.6548976	-93.6819701	-431.3368677	0.8568479

43	GSM1948612	-935.1778914	-119.8393281	-1055.01722	0.9003936
44	GSM1948613	-946.9467622	-197.8471389	-1144.793901	0.9060488
45	HB5	-396.7957939	-57.8738668	-454.6696607	0.8586087
46	HB11	686.5870703	1141.08019	1827.66726	0.6423256
47	HB28	-749.671181	-220.9218	-970.59298	0.894933
48	HB33	-487.1428165	-329.5356656	-816.678482	0.8846245
49	HB48	-696.1211574	-319.7145971	-1015.835755	0.8978765
50	HB49	-245.5563713	473.4292439	227.8728726	0.8030286
51	HB54	-705.30992	-413.98191	-1119.2918	0.9044583
52	HB59	-244.30176	-126.92903	-371.23079	0.8522658
53	HB60	425.631313	883.60383	1309.23514	0.6987357

54	HB62	468.261386	839.575542	1307.83693	0.6988825
55	HB63	-1020.251	-618.04028	-1638.2913	0.9343003
56	HB69	416.824049	1145.3637	1562.18775	0.6716977
57	HB70	861.683441	1643.62593	2505.30937	0.5630392
58	HB72	-636.98987	-34.710802	-671.70068	0.8745015
59	HB73	-987.73446	50.6485532	-937.08591	0.8927275
60	HB74	-482.45399	-219.19967	-701.65366	0.8766255
61	HB75	-66.825796	548.068478	481.242681	0.7803143
62	HB78	142.245569	1325.62662	1467.87219	0.6818893
63	HB79	-537.53168	-270.9742	-808.50588	0.8840644
64	HB80	-1022.2562	-822.0361	-1844.2923	0.9446512

65	HB81	272.456359	705.410829	977.867188	0.7326923
66	HB82	-1015.2695	-153.2309	-1168.5004	0.9075159
67	HB83	-124.07215	1089.61754	965.545388	0.733922
68	HB86	-879.46274	-299.20572	-1178.6685	0.9081418

Appendix 4. The Gene Expression in Black Module

Gene Symbols	GSM1948560	GSM1948561	GSM1948562	GSM1948563	GSM1948564	GSM1948565	GSM1948567	GSM1948568	GSM1948569	GSM1948570
CCL5	7.136	6.806	8.297	5.158	4.098	5.274	5.973	6.369	6.937	7.379
HLA-E	8.995	9.681	10.540	8.784	8.263	8.916	9.366	8.999	9.312	9.639
B2M	12.900	13.001	13.485	12.702	12.460	13.285	12.796	12.900	13.066	13.485
GBP1	7.186	8.159	8.172	7.068	4.886	6.927	8.007	7.442	7.758	8.828
TAP1	7.112	8.838	7.632	6.906	5.951	6.740	7.835	7.193	7.305	8.714
IRF1	6.806	7.684	7.884	6.724	5.805	6.736	7.490	6.638	7.154	7.837
PSMB10	7.921	8.019	8.274	7.521	6.538	7.157	7.286	7.462	7.428	8.324
CXCL9	7.357	9.227	6.816	6.320	5.086	6.592	9.067	7.096	7.481	9.669
PLAAT4	7.141	7.272	8.635	7.172	5.249	6.487	7.784	6.792	7.095	7.967
PSMB9	7.677	9.012	9.033	7.198	5.763	7.259	8.545	6.753	6.958	8.621
HLA-F	9.282	10.336	9.943	9.099	8.270	9.421	9.650	9.150	9.209	10.252
BTN3A3	6.096	6.343	6.760	5.665	5.061	5.404	6.706	5.226	6.708	6.670
LCK	6.800	5.496	5.212	4.856	4.507	4.903	4.770	4.602	5.040	4.814
PTPRCAP	6.459	6.334	6.668	5.832	5.670	6.149	6.093	5.967	6.534	6.529
CXCL13	3.635	5.001	6.091	3.399	3.118	3.346	3.809	3.526	3.707	5.819

RASGRP1	6.075	4.823	5.136	3.597	3.335	4.321	4.286	4.677	4.557	5.499
CD8A	7.755	6.521	7.043	5.382	5.623	5.455	6.053	6.470	5.966	6.613
IL7R	6.767	4.989	5.972	4.491	4.720	4.607	4.912	5.238	5.156	5.699
TRAF3IP3	4.983	5.107	5.616	4.831	4.810	4.892	5.053	4.758	4.725	5.093
CD2	7.143	6.336	6.167	5.143	5.407	5.166	6.055	5.992	5.636	6.809
CASP1	6.183	6.729	6.730	6.147	4.081	5.877	6.681	5.329	6.328	6.353
PTPN22	4.727	4.320	4.186	4.214	3.913	3.711	4.125	3.938	4.360	4.398
HCP5	5.592	6.914	6.253	4.945	4.723	5.319	5.684	5.296	5.833	6.577
CD27	5.261	6.116	5.712	5.212	5.077	5.226	5.299	5.444	5.644	5.673
CCR7	4.326	4.096	4.638	3.864	3.991	4.036	4.201	4.162	4.086	4.599
GZMK	6.098	6.424	7.697	5.206	7.752	5.545	6.105	5.926	6.499	7.407
CRTAM	3.563	3.825	4.327	3.438	3.558	3.386	3.580	3.319	3.472	3.808
CXCR6	5.196	5.242	5.480	5.167	5.056	5.202	5.142	5.244	5.413	5.752
GPR171	4.625	4.593	4.583	4.014	3.630	4.194	4.242	4.254	4.461	4.299
HLA-B	11.444	12.384	11.974	10.647	9.856	10.729	11.726	9.879	10.278	11.558
HLA-C	11.679	12.595	12.503	11.315	10.312	11.322	12.255	11.304	11.058	12.244
PSMB8	8.040	8.793	8.586	7.375	5.739	7.178	8.043	6.602	7.136	8.208
CYTIP	5.714	5.208	6.377	4.314	5.121	4.274	5.623	5.477	5.053	6.487

TRAC	6.430	6.352	7.122	6.087	5.309	5.866	5.900	6.269	6.748	7.345
CD69	5.024	4.153	6.155	3.301	3.415	3.775	4.096	5.093	4.650	4.964
CD247	6.022	5.597	5.204	4.404	4.851	4.905	5.210	4.447	5.386	5.723
GPR18	4.064	4.417	4.740	3.772	3.841	4.232	3.729	3.889	3.848	4.041
HLA-G	9.623	10.082	9.702	9.125	8.601	9.495	10.002	8.574	9.061	10.127
TRBC1	9.592	7.154	7.721	5.939	5.388	6.317	6.986	6.897	6.666	7.611
ITK	6.367	4.753	5.314	4.091	3.938	4.121	4.176	3.945	4.083	4.586
JCHAIN	4.958	5.246	6.675	4.191	4.336	4.359	5.766	6.068	3.790	5.929
TRIM22	7.515	7.460	9.886	7.028	6.621	7.317	7.379	6.569	7.370	8.601
CD3D	7.450	6.130	6.425	5.835	5.601	5.705	5.722	5.848	6.191	6.586
HLA-J	8.502	9.002	9.145	8.424	7.311	8.525	8.719	8.073	8.607	8.766
SIRPG	4.168	4.463	4.670	3.755	4.053	4.021	4.212	4.115	4.636	5.079
FCMR	5.575	5.285	5.795	5.331	5.073	5.204	5.342	4.627	5.018	6.033
RERGL	3.744	3.799	5.397	3.814	3.440	3.612	3.569	3.852	3.782	3.754
PTPRC	4.238	4.281	4.662	4.125	4.557	4.004	3.950	5.023	4.245	4.647
DOCK2	3.684	4.347	4.194	4.111	4.023	4.668	3.788	4.021	4.328	4.180
DSE	4.498	4.191	4.244	4.323	4.089	4.072	4.241	4.465	4.574	4.262
PTPRE	4.003	3.927	4.682	3.784	4.298	3.730	4.323	4.300	4.173	4.031

TRAF5	3.827	4.167	4.230	4.259	3.917	4.100	3.918	3.894	4.000	4.002
TGFB1	5.480	5.756	5.413	5.751	5.621	5.554	5.830	5.944	5.718	6.147
GAS1	4.605	4.299	5.001	4.473	4.603	4.462	4.378	3.621	3.647	3.788
PTGER4	5.200	5.003	4.991	4.818	5.062	5.285	4.968	4.683	5.256	4.758
GPNMB	5.582	5.362	6.561	4.815	5.782	4.595	6.216	7.068	5.286	6.755
CLEC7A	4.879	4.866	5.380	4.859	4.995	4.574	5.170	4.830	4.897	5.019
FCER1G	7.390	9.151	9.602	6.256	9.977	6.308	7.822	6.960	5.611	7.673
ITGB2	6.860	7.144	7.866	6.778	6.511	6.442	7.211	6.597	6.359	7.253
SAMSN1	5.041	5.481	5.700	4.926	5.103	4.599	5.195	4.810	4.642	5.423
MS4A4A	5.480	5.696	6.342	5.421	5.238	4.375	6.241	4.599	4.151	5.621
WARS1	7.249	7.954	7.968	6.952	6.920	7.302	7.761	6.892	6.562	7.341
HLA-DPB1	9.850	9.958	11.012	9.150	8.319	9.100	10.575	8.911	9.417	10.414
LGMN	9.023	9.541	9.695	9.055	8.757	9.141	9.263	8.718	8.729	9.938
LAPTM5	8.747	9.839	9.933	7.971	8.803	7.724	9.056	8.544	7.829	9.011
ARPC1B	8.667	9.768	9.927	8.306	9.283	8.759	9.089	9.113	8.519	10.022
LYN	6.604	7.867	8.630	6.248	5.985	7.184	7.191	7.281	6.788	7.960
CTSS	6.687	7.787	9.109	6.535	6.160	5.837	7.784	7.178	6.573	7.757
CIQB	8.349	9.415	10.197	8.230	8.070	7.066	8.803	8.156	7.512	9.581

HCLS1	6.885	7.252	8.780	6.417	6.779	6.428	6.717	6.624	6.045	7.582
CSF1R	6.877	7.603	8.757	7.072	6.753	6.607	7.177	7.121	6.371	7.910
LGALS9	6.266	7.088	7.849	6.477	6.864	6.502	6.627	6.991	6.593	7.306
AP1S2	6.271	6.156	6.916	6.270	6.336	6.374	6.131	6.498	6.534	6.789
CD53	7.914	8.782	9.246	7.607	7.498	7.117	8.338	8.390	7.264	8.970
CD163	7.720	7.209	10.309	8.093	8.770	6.778	8.047	7.969	6.728	9.040
CYBB	5.634	6.710	7.225	5.440	5.201	5.803	6.112	5.977	6.502	6.809
HLA-DMB	7.153	7.120	8.547	7.038	6.808	7.070	7.699	7.311	7.262	8.124
FCGR3B	5.986	6.406	7.652	5.652	5.767	5.092	6.174	5.359	5.345	6.464
IRF8	7.608	7.941	8.749	7.768	7.573	7.875	7.718	7.400	7.845	8.315
IL2RG	6.343	5.958	6.359	5.325	5.196	5.578	5.315	5.504	5.046	5.470
CD48	7.101	7.500	7.911	6.211	5.863	6.572	7.301	6.792	6.804	7.674
TYROBP	7.499	8.789	9.923	7.501	7.420	6.670	8.012	8.557	7.263	8.913
ALOX5AP	6.484	6.007	6.984	5.837	5.577	5.758	5.738	5.434	5.293	5.643
CD37	5.182	5.040	5.387	4.612	4.401	4.265	4.697	4.679	4.083	4.756
GMFG	7.701	7.213	8.678	6.853	6.691	7.049	7.019	6.474	7.226	7.447
MRC1	6.856	6.492	10.118	7.544	7.862	7.973	7.255	7.697	7.178	7.346
MYO5A	4.017	3.972	5.073	3.636	3.869	3.598	4.012	4.479	3.402	4.228

SELL	6.499	5.512	6.291	5.147	4.957	5.150	5.961	5.370	4.962	6.226
SLC7A7	6.410	7.163	8.718	6.223	6.231	6.270	6.500	6.764	6.335	7.512
CD52	6.425	6.096	7.521	6.106	5.880	6.404	6.852	6.650	6.144	7.525
EVI2A	5.932	5.189	6.560	4.448	5.351	4.380	5.522	5.725	4.986	6.323
FOLR2	7.238	7.337	8.715	7.374	7.147	6.894	7.519	7.942	7.343	8.219
IL10RA	6.799	7.043	8.330	6.178	6.117	5.805	6.641	6.281	5.977	6.995
SASH3	6.570	6.235	6.975	5.271	5.410	5.894	5.766	5.931	5.842	6.866
MNDA	5.927	5.777	7.155	4.292	4.530	5.224	5.884	5.413	5.034	5.786
CCR1	6.016	6.603	7.576	6.032	5.690	5.361	6.520	7.026	5.754	7.286
NCF4	5.800	5.823	6.475	5.643	5.182	5.484	5.495	5.349	4.827	5.687
CSF2RB	5.776	6.306	6.584	4.937	4.850	5.594	6.102	5.445	4.287	6.484
LCP2	5.889	6.685	7.836	5.195	4.961	5.274	5.992	6.251	5.311	6.658
AOAH	5.417	5.918	6.788	5.760	5.372	5.280	5.974	5.748	5.739	6.268
LY86	6.448	6.593	7.804	6.251	6.135	6.255	6.552	6.431	5.896	6.874
VAV1	5.252	5.356	6.012	4.690	4.689	4.871	5.088	5.306	4.618	5.632
IL18	3.457	3.875	5.602	3.326	3.316	3.272	4.017	3.895	2.921	3.833
IGSF6	5.227	6.221	7.332	5.097	5.190	4.611	5.819	6.233	5.638	6.551
LY96	5.407	5.913	7.824	5.532	5.653	4.713	6.598	5.593	5.008	6.528

TFEC	4.028	4.519	5.142	4.047	4.160	3.568	4.326	3.677	3.344	4.935
SYK	6.240	6.353	6.520	5.180	4.978	5.447	5.303	5.599	5.062	5.767
THEMIS2	6.023	6.763	7.343	5.636	5.572	5.681	6.268	6.215	5.843	7.206
LILRB2	5.815	6.759	7.259	6.287	6.275	5.938	6.669	6.614	6.414	7.082
PRKCB	6.271	6.165	6.786	4.467	4.288	4.443	4.948	4.766	4.886	5.576
HCK	5.675	6.929	7.308	6.025	5.420	5.601	6.559	6.284	5.326	6.939
FAM49A	5.687	6.286	6.411	5.399	6.304	5.247	5.761	5.590	5.255	6.181
TBXAS1	5.373	5.551	6.176	5.431	5.828	5.216	5.292	5.451	5.013	5.354
TNFAIP8	5.892	6.428	7.352	5.450	4.975	4.605	6.016	5.790	4.530	6.793
LCP1	7.788	8.190	8.845	7.347	7.072	7.338	8.017	7.167	7.275	7.548
HLA-DRA	9.985	10.561	11.485	9.501	8.152	9.717	10.795	8.625	9.218	10.669
CORO1A	7.730	7.831	8.093	6.164	5.747	6.215	6.863	6.782	6.232	7.327
NCKAP1L	6.560	6.906	7.540	6.469	5.948	5.818	6.384	6.414	5.972	7.249
C3AR1	6.178	7.032	7.841	6.424	5.723	5.783	6.925	6.462	6.117	7.278
CD300A	6.344	6.825	8.232	5.906	6.427	5.941	6.421	6.862	5.677	7.081
NCF2	5.117	6.006	6.695	4.741	5.596	5.119	5.727	5.823	5.242	5.990
TLR1	3.961	4.850	5.806	3.824	3.327	3.297	4.748	4.156	3.797	4.260
LST1	6.988	7.902	8.814	6.838	6.713	6.926	7.459	6.812	6.959	7.233

EVI2B	5.958	6.168	7.635	5.258	5.448	5.458	5.952	5.630	5.265	6.341
HLA-DPA1	10.315	9.948	12.270	10.307	9.238	10.233	9.973	10.890	9.875	11.946
CLIC2	4.640	4.710	6.421	4.539	4.336	4.348	4.689	4.763	4.738	4.903
RNASE6	6.580	6.524	8.111	6.766	6.762	6.228	6.831	7.253	5.931	7.814
MYO1F	6.599	6.919	7.660	6.600	6.515	6.515	6.594	6.986	6.512	7.475
NKG7	5.213	5.840	6.513	4.800	4.462	5.107	6.116	5.126	4.726	5.933
GPR65	4.550	5.371	6.478	4.578	4.520	4.380	5.112	4.874	4.371	5.210
CD72	5.706	6.105	6.604	4.880	5.003	4.961	5.764	5.169	5.442	5.939
HLA-DMA	7.428	8.076	9.108	7.237	6.583	7.052	8.495	7.312	6.637	8.817
NAGK	8.201	8.689	9.135	8.255	7.848	8.108	8.488	7.850	7.802	8.746
C1QA	8.535	9.561	10.737	8.758	8.453	8.149	8.843	8.863	7.952	9.717
PLAC8	6.707	6.558	9.431	5.380	5.393	6.173	5.877	5.484	5.405	6.653
GIMAP4	5.888	6.339	7.882	6.300	5.709	6.498	5.987	5.936	6.170	7.030
ADAP2	6.189	7.472	8.079	6.150	5.960	5.560	6.348	6.822	5.921	7.445
DPEP2	4.975	4.798	5.778	5.024	5.103	4.764	4.820	4.765	4.971	5.201
ADA2	7.840	8.062	9.172	7.606	6.893	6.839	7.692	7.539	6.843	8.677
MS4A6A	6.744	6.896	10.240	7.106	6.989	6.680	6.678	7.748	6.033	7.975
CLEC4A	4.309	5.130	6.285	4.432	4.924	4.606	5.098	4.350	4.458	5.208

P2RY13	4.183	4.294	6.899	4.827	4.413	4.792	4.502	4.363	4.406	4.833
ATP8B4	3.959	3.895	5.458	3.606	3.810	3.599	3.871	3.970	3.667	3.811
SH3BGRL3	7.987	8.982	9.453	7.946	7.668	8.027	8.060	8.614	7.547	8.517
SREBF2	8.147	7.948	7.390	8.297	8.005	8.061	7.928	8.431	8.365	7.836
ERG28	10.151	9.950	8.770	9.884	10.180	10.054	9.141	9.900	9.994	9.402

Gene Symbols	GSM1948571	GSM1948572	GSM1948573	GSM1948575	GSM1948576	GSM1948578	GSM1948580	GSM1948581	GSM1948584	GSM1948585
CCL5	4.858	5.027	6.045	5.427	6.368	5.195	6.152	5.398	5.496	6.670
HLA-E	9.146	8.904	9.541	8.575	9.501	9.453	9.334	10.144	9.902	9.761
B2M	12.835	13.128	12.970	13.112	13.128	13.216	13.164	13.424	13.692	13.562
GBP1	7.902	8.001	7.554	6.345	7.922	6.296	7.723	9.351	9.375	7.564
TAP1	7.351	8.025	7.177	7.353	8.482	7.693	7.465	8.947	8.024	8.756
IRF1	7.010	6.482	7.167	6.753	7.010	6.223	7.085	8.579	7.137	7.663
PSMB10	7.916	7.187	8.098	7.293	8.045	7.000	7.674	7.989	6.695	8.037
CXCL9	8.516	7.113	6.894	6.932	8.549	7.534	8.259	8.176	6.309	8.910
PLAAT4	7.043	6.493	7.718	6.285	7.258	6.519	7.376	7.664	6.359	8.437
PSMB9	7.144	6.855	7.631	6.969	8.537	6.842	7.749	8.723	7.207	9.017
HLA-F	9.090	8.909	9.190	8.962	10.215	9.338	9.863	9.921	9.767	10.288

BTN3A3	5.415	5.795	5.980	5.489	6.749	5.773	6.391	5.825	5.699	6.643
LCK	4.484	4.698	4.894	4.689	5.311	4.270	5.135	4.575	4.300	5.256
PTPRCAP	5.927	6.222	5.844	5.855	6.488	5.211	6.071	6.436	5.671	6.443
CXCL13	3.144	3.663	3.151	3.715	5.435	3.409	4.211	3.438	3.317	5.046
RASGRP1	4.489	3.650	4.392	3.997	4.942	4.030	4.796	4.527	4.028	5.362
CD8A	5.316	4.893	5.945	6.580	6.314	5.481	6.127	5.341	5.759	6.931
IL7R	5.053	4.716	5.196	4.777	5.588	5.488	5.150	5.680	5.903	5.440
TRAF3IP3	4.562	4.312	4.651	4.695	4.668	4.427	4.842	5.239	4.296	5.259
CD2	5.461	5.336	4.761	5.817	6.356	4.932	5.863	5.631	5.373	6.554
CASP1	6.054	5.576	6.745	5.976	6.475	5.565	6.646	6.600	5.784	7.046
PTPN22	4.230	3.723	3.644	4.048	4.719	4.206	4.110	4.819	4.035	4.174
HCP5	5.220	5.978	5.334	5.885	7.050	5.193	5.967	5.983	5.767	6.852
CD27	4.924	5.180	4.721	5.196	5.637	5.525	5.504	5.895	5.235	6.507
CCR7	4.547	3.870	4.172	3.376	3.857	3.924	4.397	4.072	3.799	4.585
GZMK	5.361	5.198	6.071	5.337	6.557	5.340	6.170	5.743	5.783	6.662
CRTAM	3.467	3.172	3.215	3.849	4.082	3.076	3.686	3.616	4.070	4.297
CXCR6	5.211	5.080	5.539	5.007	5.177	4.660	5.280	5.242	5.230	5.284
GPR171	4.285	4.328	4.323	3.747	3.962	4.588	4.830	5.238	4.656	4.831

HLA-B	10.508	10.295	10.599	10.452	11.751	10.328	11.419	10.881	10.890	11.759
HLA-C	11.257	11.622	11.154	11.485	12.320	12.048	12.220	12.685	12.295	12.623
PSMB8	7.213	6.935	7.616	7.439	8.609	6.927	7.686	7.743	6.820	8.569
CYTIP	5.026	4.599	4.875	5.068	5.665	5.017	4.810	4.485	5.112	5.166
TRAC	6.223	5.112	5.705	5.664	6.240	5.898	6.602	6.199	6.058	6.926
CD69	4.481	3.924	4.571	3.865	5.060	4.238	4.477	4.853	4.611	5.200
CD247	4.690	4.820	5.235	4.774	5.334	4.693	5.116	5.133	5.226	5.323
GPR18	3.930	4.212	3.900	3.807	3.889	3.963	4.188	4.453	3.883	4.660
HLA-G	9.140	8.947	9.371	8.801	9.765	8.969	9.486	9.286	9.317	9.381
TRBC1	6.154	6.141	6.154	6.286	7.396	6.492	7.644	6.797	6.049	8.362
ITK	3.949	4.057	4.526	3.811	4.937	4.497	4.887	4.637	5.174	5.176
JCHAIN	3.518	4.090	4.207	3.917	4.958	3.848	4.433	4.011	3.407	6.335
TRIM22	7.547	6.283	7.740	6.831	7.858	7.212	7.323	9.814	8.818	7.644
CD3D	5.607	5.664	5.855	6.111	6.663	5.809	6.294	6.013	5.581	6.680
HLA-J	8.068	8.215	8.076	7.812	8.513	8.389	8.846	8.714	8.899	9.149
SIRPG	4.510	3.887	4.003	3.833	4.957	4.142	4.415	4.875	4.242	4.971
FCMR	5.128	4.788	5.223	5.168	5.767	4.953	5.879	5.057	5.313	6.279
RERGL	3.668	3.174	3.997	3.810	3.532	3.750	3.726	3.750	3.353	3.851

PTPRC	4.153	5.126	4.494	4.104	4.134	3.993	4.749	4.385	4.428	4.138
DOCK2	4.722	4.419	3.980	4.658	3.955	3.747	4.225	4.121	3.939	3.823
DSE	4.693	4.385	4.215	4.508	4.035	4.104	4.224	3.931	3.996	3.809
PTPRE	4.208	4.997	4.148	4.165	4.749	3.902	4.072	3.944	3.925	3.798
TRAF5	4.073	4.266	3.741	4.623	3.742	3.960	3.785	3.874	4.256	3.646
TGFB1	6.208	6.436	5.842	6.217	5.807	5.588	5.222	5.717	5.943	5.015
GAS1	4.213	4.092	4.025	4.696	4.207	3.790	4.343	3.917	3.602	3.494
PTGER4	5.005	4.481	4.750	5.937	5.266	4.125	5.015	5.137	4.476	4.278
GPNMB	6.356	5.192	4.993	6.680	7.160	6.501	5.453	4.500	8.324	5.654
CLEC7A	5.265	4.691	4.462	5.304	5.496	4.500	4.437	4.710	4.254	4.422
FCER1G	7.765	6.015	6.294	7.442	8.723	6.961	7.101	5.420	6.080	7.386
ITGB2	7.329	5.623	6.029	7.201	7.155	5.872	6.659	5.555	5.846	6.756
SAMSN1	5.497	4.501	4.532	5.324	5.869	4.728	5.005	4.330	4.579	4.917
MS4A4A	6.124	4.017	4.349	6.045	6.905	4.823	5.451	3.891	4.299	4.563
WARS1	6.840	6.395	7.015	6.907	7.463	6.927	6.995	7.022	7.089	7.301
HLA-DPB1	10.769	8.718	10.295	9.338	10.575	10.622	9.846	8.600	9.450	10.208
LGMN	9.998	8.174	8.898	9.976	10.285	8.862	9.025	7.837	9.199	8.635
LAPTM5	8.914	7.778	8.086	8.940	9.617	8.558	8.193	6.913	8.135	8.579

ARPC1B	9.534	8.382	8.855	9.249	9.749	8.530	9.292	8.436	8.994	9.077
LYN	7.408	6.602	7.051	7.388	7.607	6.014	7.131	6.305	6.653	7.169
CTSS	7.466	7.281	6.591	7.085	7.608	6.205	6.952	5.941	6.595	6.948
CIQB	9.148	7.503	8.084	8.433	9.768	8.247	8.709	5.758	7.919	8.205
HCLS1	6.996	6.182	6.941	6.671	6.792	6.251	6.863	5.805	7.120	7.263
CSF1R	7.556	7.166	7.100	7.425	7.822	7.456	7.289	6.398	7.513	6.928
LGALS9	6.676	6.603	6.920	6.876	6.521	6.596	6.588	7.244	6.625	6.567
AP1S2	6.353	6.272	6.349	6.707	6.682	6.031	6.422	6.385	7.038	6.419
CD53	8.559	6.998	7.655	8.428	8.575	7.996	7.869	7.674	8.016	8.195
CD163	8.421	6.856	7.831	9.087	8.586	8.395	7.623	6.273	8.424	7.896
CYBB	7.069	5.506	5.671	6.984	6.778	5.410	6.420	5.318	5.041	5.626
HLA-DMB	8.345	6.316	7.263	7.040	8.124	7.405	7.145	7.255	7.588	7.349
FCGR3B	6.858	5.616	5.596	5.574	6.270	6.141	5.826	4.737	5.004	5.688
IRF8	8.071	7.366	7.782	7.596	8.111	7.560	7.943	8.245	6.903	7.870
IL2RG	5.162	4.774	5.173	5.125	5.724	5.406	5.367	5.462	5.158	5.555
CD48	7.217	5.789	6.571	6.425	7.405	6.483	6.848	7.116	6.652	7.533
TYROBP	8.720	6.880	7.744	8.585	9.074	8.081	8.074	6.723	8.274	8.078
ALOX5AP	6.710	4.738	5.523	6.309	5.921	5.581	5.864	5.659	5.553	5.704

CD37	4.645	4.764	4.504	4.191	4.923	3.626	4.592	3.496	4.053	4.529
GMFG	7.810	6.447	7.060	7.404	7.369	7.156	6.793	5.953	7.734	7.274
MRC1	7.624	6.418	7.443	9.209	7.715	7.181	7.370	5.177	8.424	6.225
MYO5A	4.750	3.559	3.278	5.023	4.511	4.168	4.287	3.333	4.703	3.802
SELL	6.271	4.684	4.958	5.292	5.871	4.076	5.828	4.956	4.881	5.754
SLC7A7	6.969	6.104	6.201	7.128	7.533	7.258	6.867	6.222	6.737	6.571
CD52	5.920	5.892	6.258	5.720	6.556	5.786	6.484	5.898	5.562	6.905
EVI2A	5.987	4.249	4.612	5.921	6.064	5.775	5.875	4.003	6.152	5.665
FOLR2	7.436	6.875	7.269	8.033	8.263	7.327	7.538	7.214	7.916	7.370
IL10RA	7.025	6.314	8.425	6.861	7.102	6.894	6.228	6.539	6.682	6.897
SASH3	6.019	5.150	5.447	6.202	5.942	5.427	5.691	6.321	5.948	5.917
MNDA	7.199	4.182	5.002	5.269	5.860	4.780	5.361	5.440	4.306	5.354
CCR1	7.027	5.854	6.151	6.993	6.795	5.862	6.431	6.527	6.335	6.524
NCF4	5.792	4.947	5.208	5.478	5.661	5.439	5.632	5.135	5.496	5.732
CSF2RB	5.955	5.338	5.183	5.614	6.116	5.234	6.136	4.515	5.935	5.897
LCP2	6.292	4.842	5.807	6.405	6.637	5.002	6.125	5.111	6.334	6.284
AOAH	6.246	5.608	5.852	6.110	6.554	5.640	5.990	5.778	5.464	5.716
LY86	6.875	6.446	6.520	7.089	6.750	6.611	6.182	7.128	7.187	6.650

VAV1	5.795	4.810	4.676	5.193	5.391	4.610	4.966	4.694	4.848	5.099
IL18	4.363	3.387	3.004	4.164	4.981	3.245	4.005	3.107	3.622	3.574
IGSF6	6.846	4.956	5.286	6.583	6.599	5.339	6.146	5.788	6.099	5.858
LY96	6.400	4.290	5.600	6.120	6.406	5.512	6.083	3.535	6.734	5.371
TFEC	4.814	3.729	3.715	4.209	4.695	3.822	4.323	3.584	4.205	4.809
SYK	6.302	5.937	4.881	6.648	5.583	5.725	5.823	4.881	5.024	5.648
THEMIS2	6.691	6.155	6.387	5.953	6.819	6.082	5.751	5.515	6.208	6.208
LILRB2	6.917	6.621	6.627	6.098	6.785	6.134	6.777	6.304	5.867	6.785
PRKCB	5.333	3.900	4.906	5.725	5.935	4.566	5.111	4.249	4.515	5.131
HCK	6.824	5.313	5.776	6.755	6.615	4.997	6.331	4.926	5.272	6.122
FAM49A	5.866	5.357	5.711	5.530	6.414	5.787	5.307	4.440	5.937	5.420
TBXAS1	6.112	5.144	5.335	5.442	5.703	5.501	5.628	4.755	5.356	5.282
TNFAIP8	5.875	5.517	5.006	6.311	6.337	5.922	6.178	5.228	6.169	6.436
LCP1	8.057	7.022	7.138	7.253	7.856	7.211	7.251	6.648	7.388	7.584
HLA-DRA	11.053	7.043	9.667	8.549	11.139	9.977	9.414	6.580	8.911	9.910
CORO1A	7.038	5.621	6.065	7.271	7.160	5.358	6.781	6.062	6.109	7.003
NCKAP1L	6.675	5.538	6.190	6.332	6.620	5.893	6.358	6.640	6.217	6.650
C3AR1	6.974	5.686	6.011	7.095	7.076	6.390	6.554	6.159	7.056	6.487

CD300A	6.871	5.853	6.171	6.798	6.943	7.493	6.386	6.747	6.599	6.901
NCF2	6.116	4.883	5.260	5.957	5.548	5.671	5.580	4.653	5.972	5.675
TLR1	4.848	3.415	3.707	4.984	4.582	3.695	4.259	2.980	3.469	3.877
LST1	7.844	7.002	7.272	6.757	7.556	6.607	6.943	6.822	6.073	6.908
EVI2B	6.517	4.856	5.247	6.184	6.311	4.779	5.849	4.034	4.874	5.687
HLA-DPA1	11.180	9.732	9.666	8.773	12.244	9.944	10.885	9.927	11.024	11.012
CLIC2	4.798	4.304	4.994	4.470	5.292	4.357	4.707	3.957	4.297	4.271
RNASE6	7.665	4.859	6.203	8.042	8.028	6.966	7.470	5.888	7.151	6.956
MYO1F	6.940	6.072	6.466	6.472	6.691	6.691	6.704	6.790	6.177	6.709
NKG7	5.702	4.701	5.531	4.723	5.657	4.780	5.360	4.584	4.954	5.989
GPR65	4.788	3.937	4.801	4.717	4.788	4.633	4.772	4.420	4.286	4.861
CD72	5.910	4.611	5.410	5.339	6.263	4.818	5.537	4.618	4.310	5.496
HLA-DMA	8.095	6.080	7.422	7.252	8.533	7.939	7.537	6.309	7.677	7.994
NAGK	8.483	7.253	8.047	8.068	8.446	8.332	8.032	7.575	8.671	8.548
C1QA	9.260	8.111	8.632	9.049	9.723	8.752	8.805	6.849	8.958	8.971
PLAC8	7.145	4.833	6.658	5.389	5.889	4.988	5.265	6.375	5.135	5.866
GIMAP4	6.428	5.388	6.337	6.207	6.369	5.509	6.230	5.566	6.116	5.859
ADAP2	6.647	5.738	6.642	7.412	6.896	6.630	6.452	6.257	6.027	6.605

DPEP2	5.147	4.429	4.785	4.933	5.168	4.805	5.206	4.968	4.871	4.838
ADA2	8.191	7.218	7.189	7.063	7.722	8.037	7.956	7.422	8.143	7.791
MS4A6A	7.813	7.126	6.790	7.927	7.671	7.902	7.127	6.546	7.852	7.616
CLEC4A	5.394	4.348	4.269	4.615	5.228	4.703	4.925	4.278	3.987	4.814
P2RY13	5.419	3.787	4.710	5.063	4.122	3.841	4.772	4.018	4.073	4.626
ATP8B4	3.733	3.149	3.459	4.232	3.674	3.745	3.894	3.792	4.237	3.999
SH3BGRL3	8.086	7.932	7.827	8.199	8.270	8.064	8.043	7.191	8.499	8.101
SREBF2	8.141	8.079	8.205	7.563	7.424	7.801	8.449	8.591	8.036	8.443
ERG28	9.814	9.996	9.760	9.113	9.068	9.224	10.319	9.650	9.308	10.240

Gene Symbols	GSM1948586	GSM1948588	GSM1948589	GSM1948590	GSM1948591	GSM1948592	GSM1948593	GSM1948594	GSM1948595	GSM1948596
CCL5	4.578	8.293	4.014	3.764	4.630	4.891	4.469	5.369	3.470	4.906
HLA-E	9.043	10.394	8.936	8.196	8.433	8.604	8.789	8.726	8.981	8.431
B2M	13.164	13.717	13.084	12.638	12.779	13.180	12.884	13.285	13.001	12.900
GBP1	7.936	8.623	7.911	5.547	6.231	5.866	6.901	6.704	6.064	6.804
TAP1	6.981	8.366	7.556	6.506	7.014	7.279	6.815	7.487	7.308	7.238
IRF1	6.625	8.016	7.362	5.935	6.256	6.262	6.210	6.616	6.569	6.232
PSMB10	7.246	8.304	7.430	7.020	7.196	6.685	7.431	7.339	7.125	7.347

CXCL9	8.158	10.137	7.416	5.823	7.204	5.815	5.375	7.799	5.866	6.277
PLAAT4	7.099	8.631	7.774	6.727	6.272	6.439	7.367	6.891	5.430	6.824
PSMB9	7.446	9.109	7.513	5.352	6.720	6.778	6.590	7.312	7.128	6.956
HLA-F	9.540	10.711	9.410	8.713	8.637	9.119	8.764	9.432	9.289	9.084
BTN3A3	6.220	6.938	6.091	5.650	5.632	5.500	6.704	6.048	5.241	6.191
LCK	4.664	4.857	4.334	4.285	4.625	4.409	4.498	4.638	4.381	4.787
PTPRCAP	5.744	6.372	6.503	5.695	5.529	5.778	5.959	6.133	6.342	5.683
CXCL13	3.518	5.282	3.081	3.472	3.326	3.367	3.299	3.487	3.184	3.346
RASGRP1	4.384	5.639	4.251	4.071	3.717	4.477	3.631	4.391	3.677	3.803
CD8A	5.052	7.664	5.516	5.414	7.390	5.791	4.939	5.896	5.673	5.360
IL7R	5.562	6.375	5.282	4.744	4.600	5.126	4.472	5.156	5.291	4.599
TRAF3IP3	4.977	5.337	4.702	4.502	4.808	4.557	4.859	5.034	4.676	4.849
CD2	5.103	6.906	5.310	4.726	4.961	5.425	4.551	5.790	5.028	5.667
CASP1	6.978	6.856	7.194	5.755	5.689	5.496	5.228	6.365	4.947	6.336
PTPN22	3.967	4.809	4.790	4.134	3.851	4.085	3.784	4.195	3.973	3.921
HCP5	5.676	6.384	4.958	4.581	4.932	5.071	5.275	5.115	5.095	5.614
CD27	5.251	5.508	5.044	5.009	5.197	5.312	5.154	5.422	5.109	5.095
CCR7	4.483	4.363	3.781	4.133	3.944	3.982	4.020	4.464	4.335	3.848

GZMK	4.973	8.001	5.655	5.201	7.447	5.110	5.162	5.614	5.548	5.856
CRTAM	3.519	4.134	3.583	3.457	3.481	3.395	3.389	3.630	3.404	3.644
CXCR6	5.181	5.833	4.945	4.934	5.044	4.746	4.926	5.017	5.176	5.059
GPR171	4.331	5.607	4.156	3.945	3.831	3.839	4.226	4.242	4.106	3.839
HLA-B	10.726	11.822	10.307	9.663	10.225	10.309	10.118	10.729	10.199	10.460
HLA-C	11.705	12.900	11.089	10.672	11.273	11.847	11.278	11.983	11.594	11.268
PSMB8	7.499	8.281	7.366	5.751	6.765	6.620	7.471	7.140	6.968	7.777
CYTIP	4.974	6.014	4.115	4.074	5.177	4.516	4.109	4.324	4.519	4.679
TRAC	5.962	7.309	5.356	5.659	5.843	5.946	5.716	6.374	5.975	6.000
CD69	4.420	6.565	3.476	3.395	3.515	4.158	3.319	3.959	2.874	3.430
CD247	4.939	5.483	5.269	4.789	4.790	4.981	4.836	5.272	5.419	4.901
GPR18	4.171	4.962	4.455	3.523	3.861	3.896	3.656	3.929	3.913	4.067
HLA-G	9.290	9.830	9.045	8.954	8.887	8.565	8.912	9.297	8.719	9.228
TRBC1	6.515	8.295	6.105	5.578	6.065	6.061	5.793	6.649	5.613	6.683
ITK	4.387	5.423	4.236	3.884	4.007	4.184	4.126	4.487	4.297	4.288
JCHAIN	4.323	7.006	4.205	3.045	3.987	4.473	3.415	4.417	2.720	3.014
TRIM22	7.357	8.753	7.687	6.195	6.510	7.396	7.090	7.710	6.205	7.209
CD3D	5.513	6.426	5.097	5.164	5.123	4.948	5.620	5.709	4.819	5.781

HLA-J	8.690	9.119	8.780	8.236	7.875	8.237	8.094	8.435	8.658	8.005
SIRPG	4.248	4.591	4.272	4.337	3.930	4.220	3.982	4.533	4.409	4.064
FCMR	5.365	6.224	5.562	4.753	4.952	5.009	5.144	5.213	5.588	5.286
RERGL	3.811	3.871	3.724	3.363	3.429	3.261	3.358	3.251	3.476	3.983
PTPRC	4.310	4.152	4.070	4.001	4.426	4.328	4.641	4.252	4.318	4.060
DOCK2	3.580	3.925	3.858	4.031	3.706	3.773	3.549	3.742	3.846	4.084
DSE	4.133	4.086	4.271	4.122	3.961	3.929	4.112	4.100	4.186	4.659
PTPRE	3.940	4.703	4.272	4.492	4.146	4.066	4.158	4.331	4.226	4.105
TRAF5	3.551	4.030	3.571	3.956	3.550	3.865	3.498	3.872	3.897	3.795
TGFB1	5.513	5.470	6.038	5.953	5.550	5.475	5.430	5.270	5.476	5.721
GAS1	4.110	4.051	3.821	3.585	4.298	3.727	4.249	3.725	3.823	4.235
PTGER4	5.190	4.426	4.887	5.021	5.001	4.450	5.086	4.999	4.439	4.803
GPNMB	4.418	5.249	4.587	5.290	5.790	5.976	5.039	5.541	5.381	7.223
CLEC7A	4.605	4.883	4.569	4.336	4.656	4.250	4.524	4.502	4.235	5.301
FCER1G	5.639	7.449	5.996	6.481	8.223	6.229	5.521	7.158	5.791	7.294
ITGB2	5.965	7.299	6.175	6.459	6.189	5.501	6.081	6.655	5.282	6.907
SAMSN1	4.704	5.153	5.152	4.390	4.721	4.298	4.474	4.827	4.394	5.248
MS4A4A	3.966	5.158	3.647	4.081	5.597	4.036	4.441	5.270	3.820	6.231

WARS1	7.019	7.467	7.107	6.980	7.075	7.215	6.913	7.195	7.013	6.998
HLA-DPB1	9.226	11.814	9.772	8.519	9.511	9.551	8.402	10.265	9.432	9.429
LG MN	8.658	8.871	8.629	9.043	9.206	8.420	8.257	9.661	8.199	9.377
LAP TM5	7.401	8.238	7.843	8.254	8.095	7.967	7.558	8.405	7.869	8.638
ARPC1B	8.085	8.977	8.549	8.668	8.838	9.511	8.729	9.227	8.746	9.176
LYN	6.313	7.383	6.294	6.704	6.281	6.596	6.829	6.820	6.023	7.127
CTSS	6.311	6.931	6.353	6.026	6.481	6.686	5.777	7.525	6.202	7.521
C1QB	5.869	8.953	7.561	7.282	7.675	6.562	6.893	9.013	6.475	8.375
HCLS1	6.118	7.594	6.618	6.123	6.199	6.679	6.251	6.833	5.744	7.018
CSF1R	6.578	7.862	7.181	7.375	6.594	6.925	6.502	7.611	7.423	7.479
LGALS9	6.723	6.701	6.165	6.414	6.215	6.458	6.331	6.703	6.423	6.210
AP1S2	6.189	6.611	6.218	5.921	6.504	6.504	5.948	5.911	5.952	6.518
CD53	7.216	8.817	7.743	7.780	7.495	7.298	6.828	8.302	7.577	8.205
CD163	6.096	8.314	7.467	8.332	7.554	7.566	6.907	8.546	6.572	8.436
CYBB	5.592	6.070	5.770	5.454	5.613	4.848	5.613	5.932	5.011	7.160
HLA-DMB	6.793	8.794	7.778	6.872	7.292	6.808	6.540	7.988	6.864	7.434
FCGR3B	5.148	5.864	5.489	5.472	5.668	5.639	5.267	5.885	4.981	5.804
IRF8	7.615	7.951	7.595	7.561	7.905	6.844	7.418	8.127	7.457	7.834

IL2RG	4.920	5.426	4.830	5.210	5.145	4.936	5.246	5.154	5.070	5.130
CD48	6.514	8.105	7.289	6.217	6.336	6.451	6.167	7.021	7.014	6.490
TYROBP	6.327	8.540	7.977	7.818	7.370	7.408	6.481	8.187	5.781	8.217
ALOX5AP	5.590	6.355	6.255	5.569	6.033	5.310	5.601	5.219	5.421	5.754
CD37	4.101	4.402	3.761	3.986	3.955	3.921	4.051	3.964	4.132	4.255
GMFG	6.746	7.884	6.974	6.158	6.671	7.181	6.891	6.877	6.403	7.029
MRC1	6.430	8.402	6.276	7.105	6.792	6.865	7.046	7.222	6.283	7.863
MYO5A	3.391	3.922	3.496	3.324	3.832	4.027	3.603	3.523	3.584	4.475
SELL	5.764	5.906	5.580	4.083	5.196	5.303	4.074	5.227	5.152	4.975
SLC7A7	5.976	7.209	6.297	7.017	6.341	7.100	6.278	7.275	6.625	7.118
CD52	5.831	7.688	5.103	5.646	5.615	5.807	4.936	6.605	4.718	6.003
EVI2A	4.650	6.308	4.814	4.258	5.065	5.435	4.285	4.863	3.989	5.441
FOLR2	6.960	7.729	7.232	7.402	7.066	6.747	6.892	7.371	6.620	7.772
IL10RA	6.958	7.510	6.971	6.310	6.328	6.175	6.097	7.366	5.424	6.620
SASH3	5.763	6.490	6.320	5.753	5.398	5.448	5.540	5.896	5.747	5.793
MNDA	5.102	6.418	6.618	4.158	5.192	4.898	4.731	4.667	4.686	4.987
CCR1	5.242	7.030	6.090	6.209	5.707	5.874	5.191	6.511	5.649	6.648
NCF4	5.102	6.129	5.835	5.516	5.506	5.300	5.480	5.655	5.145	6.145

CSF2RB	5.257	6.565	5.515	4.878	5.665	5.397	5.169	6.183	4.796	6.191
LCP2	5.012	7.001	5.172	5.252	5.657	5.462	4.687	6.369	4.639	6.262
AOAH	5.321	6.397	5.849	5.118	5.676	5.161	5.519	5.963	4.361	6.205
LY86	6.054	7.114	7.178	6.812	6.348	6.515	5.935	6.870	6.681	6.863
VAV1	4.625	5.274	4.688	4.674	4.802	4.740	4.754	5.193	4.505	5.384
IL18	3.076	3.668	3.399	3.318	3.629	3.451	3.436	4.045	3.159	3.801
IGSF6	4.657	6.734	5.264	5.165	5.585	4.977	4.937	6.521	4.773	6.750
LY96	4.834	6.355	4.821	5.056	5.748	6.314	5.422	5.759	4.457	6.202
TFEC	4.131	4.945	3.940	4.051	4.196	4.025	3.664	4.360	3.929	4.936
SYK	4.850	5.627	5.932	5.166	5.601	5.943	4.964	5.521	4.947	6.006
THEMIS2	5.386	6.586	5.667	5.682	5.756	5.728	5.524	5.798	4.890	5.747
LILRB2	6.318	6.826	6.509	6.097	5.906	5.975	6.232	6.771	6.068	5.955
PRKCB	4.467	5.743	4.858	4.122	4.747	4.628	4.405	5.610	4.234	5.319
HCK	4.603	6.175	5.105	5.520	5.746	5.768	5.344	6.379	4.868	6.136
FAM49A	5.311	5.520	5.000	4.958	5.678	4.906	4.997	5.175	4.729	5.434
TBXAS1	5.428	5.515	5.066	5.097	5.054	5.214	5.182	5.280	4.719	5.664
TNFAIP8	4.660	6.369	5.520	5.886	6.075	6.642	4.974	6.114	5.426	6.421
LCP1	7.015	8.202	7.957	6.932	7.043	7.002	7.108	7.984	7.052	7.084

HLA-DRA	8.622	11.795	9.222	7.324	9.395	8.884	8.122	9.908	7.290	9.933
CORO1A	5.596	7.283	6.131	5.599	6.069	6.222	5.478	5.875	5.221	6.489
NCKAP1L	5.893	6.777	6.657	6.155	6.105	5.986	5.844	6.294	5.935	6.563
C3AR1	5.576	6.736	6.415	6.547	6.476	6.062	6.013	6.740	6.123	6.710
CD300A	5.621	7.102	6.588	6.447	6.249	6.367	5.867	6.808	6.504	6.623
NCF2	5.092	6.670	5.922	5.867	5.325	5.632	5.484	5.675	6.090	6.081
TLR1	3.038	4.105	3.388	3.430	4.029	3.655	3.707	3.986	3.327	4.487
LST1	6.470	7.661	7.113	6.336	6.740	6.163	6.585	6.889	5.949	6.982
EVI2B	4.376	6.762	5.676	4.947	5.095	4.870	4.880	5.823	4.370	5.862
HLA-DPA1	8.413	11.776	10.043	8.956	10.235	10.160	9.109	10.972	9.287	10.828
CLIC2	4.070	5.572	3.882	3.709	4.411	4.001	4.469	4.526	3.325	5.119
RNASE6	5.721	7.193	6.546	6.243	6.521	6.199	5.972	6.455	5.859	7.445
MYO1F	6.499	7.057	7.314	6.451	6.270	6.958	6.387	6.788	6.197	6.537
NKG7	4.975	6.046	5.538	4.402	4.524	4.580	4.616	5.171	4.487	4.740
GPR65	4.388	5.820	4.675	4.503	4.848	4.719	4.607	4.789	4.394	5.253
CD72	4.833	5.720	5.057	4.415	4.911	4.362	4.725	5.619	4.337	4.880
HLA-DMA	6.756	9.931	6.975	6.470	7.181	6.857	6.475	7.798	6.056	7.684
NAGK	7.824	8.130	7.978	8.085	8.308	8.468	8.091	8.575	8.281	8.509

C1QA	6.799	9.156	8.370	8.061	8.022	7.571	7.553	9.407	6.696	8.636
PLAC8	5.558	7.285	7.174	5.769	5.066	5.944	5.157	5.444	5.285	5.372
GIMAP4	5.325	6.875	5.844	5.083	5.927	5.872	6.165	6.046	5.442	6.170
ADAP2	5.629	6.566	6.800	7.016	6.515	6.316	6.106	6.974	6.429	7.006
DPEP2	4.628	5.049	5.337	4.747	4.788	4.620	4.504	4.735	4.558	4.968
ADA2	6.654	8.347	8.057	7.125	6.772	7.733	6.852	8.314	6.841	7.263
MS4A6A	5.915	8.181	7.265	6.883	7.033	7.319	6.661	7.767	6.878	7.703
CLEC4A	4.057	5.427	4.053	4.166	5.014	4.836	4.538	4.346	4.115	5.109
P2RY13	3.989	5.841	4.255	3.901	4.307	4.290	4.492	4.857	4.166	5.270
ATP8B4	4.285	4.410	4.452	3.519	3.884	3.325	4.073	3.885	3.590	4.363
SH3BGRL3	7.141	8.039	7.291	7.788	7.410	8.434	7.351	7.609	7.597	7.583
SREBF2	8.460	8.255	8.539	7.984	7.517	7.756	7.752	8.077	8.403	7.577
ERG28	10.254	9.785	10.028	9.620	9.854	9.105	9.364	9.884	9.558	9.621

Gene Symbols	GSM1948597	GSM1948598	GSM1948602	GSM1948603	GSM1948604	GSM1948605	GSM1948606	GSM1948607	GSM1948608	GSM1948609
CCL5	4.148	4.237	4.022	4.547	6.259	4.624	5.494	6.249	7.898	6.369
HLA-E	8.766	9.222	8.742	8.423	10.178	8.219	9.240	9.342	9.956	9.254
B2M	12.582	13.145	13.164	12.028	13.466	13.128	13.267	13.364	13.534	13.164

GBP1	7.479	7.869	7.365	6.794	8.398	6.051	7.214	7.016	8.353	7.525
TAP1	6.759	7.967	7.053	6.999	7.978	7.041	7.245	7.969	8.977	7.927
IRF1	6.325	6.635	6.481	6.431	7.233	6.157	6.899	7.296	7.832	7.103
PSMB10	7.016	7.201	6.930	7.140	7.924	7.176	7.410	7.952	8.103	7.911
CXCL9	5.358	5.321	6.340	5.847	9.030	5.331	7.264	7.100	9.854	8.693
PLAAT4	6.481	7.443	6.519	5.665	8.281	5.469	6.702	8.098	8.525	7.488
PSMB9	6.747	7.902	6.672	6.972	8.314	6.368	6.893	8.379	9.210	8.232
HLA-F	9.237	9.185	8.879	8.510	9.834	8.843	9.348	9.642	10.741	9.754
BTN3A3	5.739	6.238	5.417	5.372	6.539	5.498	5.925	5.936	7.076	6.325
LCK	4.606	4.423	4.669	4.217	4.613	4.670	4.733	4.681	5.302	4.711
PTPRCAP	5.722	5.704	5.598	5.764	6.071	5.809	5.837	6.331	6.452	5.893
CXCL13	3.258	3.190	3.322	3.223	3.485	3.305	3.625	3.469	7.375	4.742
RASGRP1	3.664	3.755	3.940	3.537	4.104	4.025	4.575	4.286	6.024	4.943
CD8A	5.877	6.139	5.313	5.214	5.464	5.344	5.654	6.266	7.644	5.886
IL7R	5.011	4.669	5.137	4.746	5.508	4.932	5.145	5.560	5.353	4.632
TRAF3IP3	4.733	4.596	4.925	4.792	5.214	4.669	4.707	5.001	5.724	4.990
CD2	5.066	5.212	5.542	5.399	5.325	4.473	5.434	5.709	7.208	5.813
CASP1	6.384	6.328	5.992	5.838	6.435	6.029	6.880	6.366	7.657	6.999

PTPN22	4.302	3.858	4.033	4.114	4.316	4.421	4.370	4.440	5.010	4.361
HCP5	5.382	5.597	5.290	4.750	6.125	4.495	5.193	5.299	7.161	6.242
CD27	4.875	5.045	5.499	5.159	5.567	5.133	5.463	5.333	5.925	5.577
CCR7	4.000	4.145	4.506	4.145	4.545	4.041	4.257	4.223	5.714	4.212
GZMK	5.377	6.730	4.948	5.309	5.463	5.324	5.598	5.863	7.606	6.458
CRTAM	3.328	3.611	3.670	3.463	3.623	3.838	3.374	4.421	4.606	3.911
CXCR6	5.070	4.980	5.011	5.006	5.147	4.786	5.196	5.532	5.733	5.287
GPR171	3.732	4.021	4.049	4.199	4.382	3.944	4.623	4.235	5.997	4.799
HLA-B	10.540	10.503	10.233	9.684	11.094	9.931	10.758	10.773	12.220	11.289
HLA-C	11.373	12.005	11.081	10.364	12.270	11.510	12.017	12.005	12.255	12.017
PSMB8	6.884	7.379	6.818	7.066	7.675	7.395	7.554	7.739	8.702	8.229
CYTIP	4.529	4.646	4.765	4.311	5.075	4.862	4.576	4.777	6.258	5.101
TRAC	5.649	5.426	5.944	5.657	6.244	5.217	6.337	6.515	7.761	6.511
CD69	3.891	3.137	4.409	4.148	4.510	3.543	4.376	3.869	5.237	5.521
CD247	4.762	4.919	4.930	5.063	5.671	5.093	4.936	5.549	5.814	5.253
GPR18	3.712	3.940	3.984	3.722	4.348	3.661	4.089	4.197	5.562	4.383
HLA-G	9.206	8.963	8.822	8.479	9.417	9.206	9.050	9.458	10.104	9.568
TRBC1	5.784	5.320	6.802	5.864	6.264	5.719	6.566	6.957	8.125	6.714

ITK	3.961	4.198	4.434	4.273	4.613	3.885	4.573	4.637	6.096	4.564
JCHAIN	4.468	5.181	3.293	2.870	4.889	3.099	4.369	5.646	6.445	4.735
TRIM22	7.392	8.351	7.339	6.477	8.857	6.129	7.078	8.646	9.390	7.884
CD3D	5.570	5.216	5.442	5.542	5.556	5.572	5.631	6.309	6.306	5.882
HLA-J	8.382	8.079	8.355	8.153	8.503	8.371	8.380	8.687	9.325	8.659
SIRPG	4.090	4.196	4.272	4.488	3.884	3.974	4.481	4.501	5.045	4.561
FCMR	5.034	5.224	5.036	4.871	5.321	4.871	5.279	5.531	6.428	5.418
RERGL	3.366	3.407	3.365	3.381	4.175	3.581	3.769	3.815	3.897	3.423
PTPRC	4.117	4.138	4.289	4.456	4.124	3.995	4.333	4.593	4.192	4.230
DOCK2	3.839	4.014	3.902	4.138	4.016	3.862	4.054	4.011	3.967	3.858
DSE	3.786	3.712	4.105	3.946	4.020	3.760	3.950	4.058	4.341	3.895
PTPRE	4.202	3.965	4.025	4.271	4.338	4.422	4.091	4.024	4.258	4.057
TRAF5	3.951	3.682	4.277	3.780	3.671	3.841	3.556	4.215	3.666	3.733
TGFB1	5.469	5.546	5.571	5.606	5.774	5.601	5.365	5.796	5.410	5.640
GAS1	3.935	4.320	4.031	4.116	3.763	4.124	4.256	3.722	3.986	4.103
PTGER4	4.893	5.099	5.026	4.901	4.998	4.751	4.708	5.015	4.735	4.969
GPNMB	5.200	5.287	4.977	4.830	4.497	7.351	5.033	8.898	6.439	5.736
CLEC7A	4.347	4.530	4.373	4.632	4.804	4.688	4.557	4.785	5.384	4.612

FCER1G	6.258	7.351	5.915	9.642	6.509	8.597	7.023	7.339	7.556	7.623
ITGB2	5.889	6.566	5.615	6.420	6.332	7.877	6.146	6.545	7.573	6.804
SAMSN1	4.397	4.783	4.302	4.561	4.344	5.083	4.881	4.996	5.329	5.083
MS4A4A	4.521	5.381	4.379	5.213	4.380	6.544	4.821	5.263	6.151	6.110
WARS1	6.853	7.510	7.085	7.052	7.503	7.289	7.081	7.291	7.611	7.138
HLA-DPB1	9.095	8.536	9.709	8.421	10.099	6.872	9.157	11.139	10.744	9.846
LGMN	8.654	9.177	8.352	9.276	8.507	9.406	8.867	9.428	9.009	9.207
LAPTM5	7.902	8.262	7.551	8.230	7.751	9.534	7.898	9.062	8.421	8.407
ARPC1B	8.679	8.704	8.224	9.158	8.397	9.608	8.966	9.203	8.978	9.177
LYN	6.418	7.159	6.685	6.889	7.466	6.933	7.180	7.677	7.526	7.225
CTSS	6.338	6.880	6.035	6.620	7.077	7.067	6.897	8.253	7.805	7.308
C1QB	6.645	8.236	6.294	7.779	7.632	8.826	7.837	8.498	8.433	8.576
HCLS1	6.000	6.532	6.575	6.517	7.147	6.884	6.811	7.674	7.908	7.381
CSF1R	6.838	6.925	6.626	7.607	7.362	8.195	6.940	7.569	7.166	7.309
LGALS9	6.535	7.124	6.501	6.399	6.629	7.015	6.450	7.333	6.411	6.529
AP1S2	6.199	6.210	6.131	6.747	6.138	6.918	6.299	6.320	6.267	6.596
CD53	7.435	7.964	7.457	7.945	8.017	8.987	7.710	9.109	8.646	8.133
CD163	7.099	8.493	6.732	8.418	7.397	11.008	7.234	8.948	7.888	8.372

CYBB	5.773	5.936	5.208	6.596	5.840	6.699	5.825	6.134	6.506	5.950
HLA-DMB	6.955	6.727	7.015	6.980	7.492	6.296	6.827	8.780	8.255	7.457
FCGR3B	5.385	6.128	5.124	5.561	6.209	6.426	5.795	5.509	6.178	6.387
IRF8	7.689	7.789	7.827	7.266	8.111	8.182	7.855	8.562	8.514	8.210
IL2RG	4.938	5.568	5.352	5.446	5.425	5.005	5.235	5.605	6.239	5.243
CD48	6.223	6.625	6.629	6.585	6.894	7.037	6.750	8.309	7.759	7.298
TYROBP	7.230	7.979	6.733	7.872	7.605	9.426	7.588	9.474	8.158	8.283
ALOX5AP	5.789	5.262	5.478	5.792	5.268	7.018	5.328	5.711	6.600	5.802
CD37	3.936	3.978	4.215	4.150	4.237	4.054	3.995	4.543	4.653	3.987
GMFG	6.644	6.899	6.495	6.621	7.099	7.129	6.719	7.330	7.612	7.375
MRC1	6.829	6.929	7.004	7.517	7.753	8.821	6.814	7.799	8.053	7.265
MYO5A	3.549	3.494	3.531	3.709	3.768	4.430	3.875	3.910	5.104	3.852
SELL	5.381	5.711	5.092	4.983	5.621	4.888	5.116	5.902	6.437	5.402
SLC7A7	6.263	6.895	6.237	6.469	6.838	7.834	6.524	7.552	7.014	7.164
CD52	5.421	6.112	5.536	5.185	6.133	5.460	5.764	7.534	7.988	6.218
EVI2A	4.630	4.769	4.634	5.235	4.833	5.935	5.133	5.315	6.590	5.611
FOLR2	7.194	7.297	6.894	7.720	7.232	8.039	7.003	7.381	7.360	7.492
IL10RA	6.348	6.112	5.945	6.693	7.138	7.048	6.552	7.372	7.590	6.834

SASH3	5.381	5.500	5.598	5.628	6.043	6.298	5.587	6.312	6.457	5.573
MNDA	4.331	5.594	4.524	4.760	5.631	5.763	4.612	5.488	6.345	5.389
CCR1	5.782	7.108	5.924	6.633	6.639	7.698	6.110	7.310	6.334	6.492
NCF4	5.617	5.562	5.470	5.981	5.724	6.218	5.484	5.814	5.789	6.107
CSF2RB	5.052	5.484	5.800	5.698	5.755	5.757	5.630	6.280	6.882	6.465
LCP2	5.148	5.607	4.914	5.636	6.289	5.862	6.318	5.869	7.060	6.454
AOAH	5.250	5.488	5.099	5.712	6.042	5.511	5.530	5.976	6.514	6.330
LY86	6.317	6.630	6.493	6.712	6.695	7.299	6.209	7.471	6.713	6.713
VAV1	4.735	4.633	4.596	4.821	4.947	4.673	4.752	4.844	5.083	5.073
IL18	3.568	3.358	3.423	3.318	3.379	3.781	3.533	3.667	4.340	4.191
IGSF6	5.142	5.806	4.683	5.607	5.584	5.396	5.825	7.318	6.416	5.809
LY96	5.964	6.494	4.949	5.596	5.198	6.520	5.174	6.297	6.811	6.423
TFEC	3.809	4.382	3.713	4.194	3.994	4.684	4.220	4.489	5.412	4.529
SYK	5.543	5.452	5.599	5.234	4.940	5.900	5.451	5.321	6.212	5.540
THEMIS2	5.557	5.482	5.514	5.844	5.458	6.143	5.658	5.991	6.028	6.143
LILRB2	5.805	6.572	5.781	6.379	6.691	6.777	6.464	6.967	6.144	6.601
PRKCB	4.362	4.523	4.533	4.523	4.667	4.837	4.447	5.024	6.223	5.550
HCK	5.448	5.743	5.219	5.689	6.159	6.587	5.789	5.905	6.067	6.126

FAM49A	5.019	5.619	4.853	5.013	5.030	5.217	4.874	4.920	5.788	5.418
TBXAS1	5.065	5.034	5.116	5.438	5.342	5.784	5.234	5.149	5.416	5.458
TNFAIP8	5.558	5.362	5.315	5.864	5.068	6.660	6.212	5.500	6.900	6.426
LCP1	6.708	7.514	6.816	7.391	7.387	7.642	7.064	8.152	7.981	7.703
HLA-DRA	9.074	8.709	9.062	8.336	9.651	7.250	8.808	10.929	11.572	10.269
CORO1A	5.628	6.301	5.214	6.265	6.271	7.043	6.197	6.527	7.273	6.375
NCKAP1L	6.022	6.300	6.088	6.254	6.539	7.014	6.349	7.207	6.887	6.691
C3AR1	6.153	6.892	5.917	6.934	6.420	6.967	6.347	7.155	6.728	6.663
CD300A	5.412	6.555	6.131	6.463	7.029	7.914	6.483	7.394	6.459	6.527
NCF2	5.811	5.858	5.209	5.669	5.541	6.678	5.321	6.864	6.331	5.679
TLR1	4.124	3.449	3.268	3.955	3.872	4.539	3.742	3.989	4.613	4.021
LST1	6.726	6.631	6.602	6.798	7.016	7.027	6.804	7.680	7.241	7.178
EVI2B	4.591	5.427	4.639	5.115	5.309	5.646	5.353	5.686	6.710	5.648
HLA-DPA1	9.976	9.733	9.943	9.717	9.728	7.878	10.877	10.961	11.776	11.193
CLIC2	3.573	4.369	4.134	4.169	4.943	3.300	4.482	4.243	6.173	5.374
RNASE6	6.059	6.670	5.841	6.440	6.163	7.507	6.089	6.963	7.604	7.283
MYO1F	6.589	6.621	6.466	6.579	6.893	7.160	6.380	7.181	6.861	6.852
NKG7	4.582	4.791	4.746	4.384	5.783	4.912	5.480	5.280	6.591	5.535

GPR65	4.227	4.868	4.476	4.524	4.811	5.309	4.751	5.040	5.676	5.247
CD72	4.447	4.772	4.807	4.596	5.031	4.281	5.370	5.011	6.223	5.854
HLA-DMA	6.871	7.097	6.433	6.920	8.127	6.705	7.095	8.838	8.918	7.665
NAGK	8.475	8.610	7.776	8.178	8.501	8.247	8.012	8.523	8.642	8.378
C1QA	7.661	8.473	7.017	8.317	8.199	9.172	8.104	9.014	8.789	9.052
PLAC8	5.202	6.439	5.146	5.206	6.963	6.039	5.373	6.019	6.934	6.361
GIMAP4	5.437	6.500	6.007	5.393	7.019	5.804	5.883	6.432	7.297	6.524
ADAP2	6.251	6.799	6.095	6.765	6.802	8.202	6.604	6.774	6.758	6.855
DPEP2	4.435	4.727	4.776	5.170	5.138	4.831	4.530	5.318	4.994	4.958
ADA2	6.605	8.319	6.743	6.879	7.875	6.794	7.243	9.528	8.320	7.918
MS4A6A	6.943	7.410	6.823	7.421	8.227	8.240	7.218	8.199	7.608	7.799
CLEC4A	4.526	4.413	4.548	4.472	4.896	4.353	4.511	4.814	5.622	4.860
P2RY13	4.259	4.715	4.338	4.255	4.774	3.917	4.628	4.776	5.745	4.396
ATP8B4	3.773	3.831	3.959	3.792	3.915	3.900	3.762	4.023	4.576	4.459
SH3BGRL3	7.267	7.591	7.083	7.219	7.400	8.324	7.807	7.982	7.984	7.828
SREBF2	7.616	8.594	8.537	8.644	8.340	7.132	8.016	8.212	7.960	7.830
ERG28	9.348	10.217	10.242	9.226	9.977	8.653	9.629	8.970	9.790	9.829

Gene Symbols	GSM1948610	GSM1948611	GSM1948612	GSM1948613	HB11	HB28	HB33	HB48	HB49	HB5
CCL5	6.657	4.378	4.271	4.089	7.115	4.536	4.355	5.036	6.355	5.111
HLA-E	9.653	9.476	8.713	8.076	10.452	8.539	8.564	9.539	9.448	8.451
B2M	13.639	13.485	13.052	12.835	13.717	13.084	12.611	12.884	13.562	13.052
GBP1	8.326	8.734	6.374	5.048	8.416	7.563	6.111	6.772	8.820	5.615
TAP1	9.523	8.008	7.620	6.904	9.388	7.290	6.805	7.570	8.250	6.552
IRF1	7.755	7.254	6.354	5.682	7.727	6.617	6.801	6.722	7.855	6.747
PSMB10	8.022	7.732	7.067	7.427	8.057	6.721	6.380	7.262	7.779	6.698
CXCL9	10.160	9.800	5.605	6.189	8.197	6.618	6.274	6.782	9.038	5.811
PLAAT4	7.568	8.185	6.144	5.702	8.643	6.015	4.839	7.053	7.811	6.339
PSMB9	9.316	8.530	6.799	6.308	9.236	6.755	6.454	7.706	7.946	7.524
HLA-F	10.957	9.253	9.294	9.072	10.961	9.001	8.171	9.574	9.927	8.731
BTN3A3	7.452	6.042	6.300	4.943	7.430	5.560	5.391	6.033	5.711	5.642
LCK	4.769	4.540	4.762	4.342	5.247	4.286	4.266	4.395	4.712	4.534
PTPRCAP	5.939	6.182	5.486	5.968	6.251	5.819	5.870	5.525	6.890	5.824
CXCL13	5.403	3.349	3.400	3.202	3.609	3.693	3.684	3.355	3.593	3.915
RASGRP1	5.330	3.902	3.995	3.741	4.829	3.957	4.001	3.937	4.431	3.939
CD8A	6.617	5.677	5.234	5.466	5.943	5.406	5.496	5.892	6.936	6.152

IL7R	4.715	5.278	5.134	4.789	5.304	4.670	4.547	4.713	5.673	4.542
TRAF3IP3	5.113	4.919	4.568	4.652	5.220	4.594	4.897	4.919	4.736	4.799
CD2	6.192	4.851	5.135	5.046	6.393	5.022	5.137	5.308	6.164	5.226
CASP1	6.749	6.926	5.893	5.427	7.558	5.983	5.339	5.777	6.432	5.652
PTPN22	4.277	3.845	4.370	3.998	4.858	4.033	4.026	4.105	4.165	3.991
HCP5	8.047	5.547	5.521	4.669	7.104	5.587	5.024	5.176	6.041	5.430
CD27	5.738	5.362	5.414	5.257	5.885	5.180	5.282	5.420	5.546	5.209
CCR7	4.437	4.474	4.431	4.033	4.985	3.948	3.790	3.775	4.227	4.151
GZMK	6.682	5.132	5.312	5.831	6.921	5.445	5.595	5.522	6.617	5.815
CRTAM	4.506	3.588	3.564	3.432	3.692	3.580	3.475	3.248	3.676	3.625
CXCR6	5.221	4.874	4.819	4.877	5.315	5.350	4.951	4.988	5.332	5.062
GPR171	4.500	4.369	3.693	4.241	5.069	4.116	4.063	3.954	4.230	4.111
HLA-B	12.255	10.748	10.593	10.455	12.283	9.799	9.659	10.587	11.278	9.971
HLA-C	13.066	11.720	11.866	10.463	12.985	11.203	10.877	11.759	12.330	11.067
PSMB8	8.733	7.872	7.389	6.582	8.882	7.041	5.819	7.795	7.455	7.084
CYTIP	5.073	4.218	4.459	4.518	6.125	4.716	4.466	4.577	5.135	4.523
TRAC	6.921	6.151	5.657	5.586	6.677	5.680	5.486	5.426	6.761	5.876
CD69	4.411	4.192	3.462	3.383	5.357	4.080	3.791	3.937	4.211	3.777

CD247	5.341	5.292	5.003	4.951	5.671	4.930	4.887	5.044	5.174	4.980
GPR18	4.267	4.218	3.716	3.772	4.736	4.087	4.015	3.884	4.063	3.932
HLA-G	9.458	9.178	9.192	9.218	10.546	8.753	8.582	9.360	9.664	8.727
TRBC1	7.579	6.025	5.721	5.510	7.200	5.885	6.241	6.020	7.769	5.783
ITK	4.799	4.069	4.044	4.001	5.351	4.323	4.139	4.369	4.317	4.133
JCHAIN	3.441	4.024	3.591	3.342	5.223	4.242	3.885	4.095	4.376	4.014
TRIM22	7.744	8.557	6.393	6.316	10.201	7.655	7.012	6.929	8.444	7.266
CD3D	6.215	5.203	4.957	5.285	6.170	5.502	5.275	5.736	6.003	5.633
HLA-J	9.245	8.238	8.613	8.255	9.294	7.994	7.910	8.613	8.922	7.884
SIRPG	4.826	4.003	4.239	4.273	4.398	3.912	4.038	4.185	4.295	4.199
FCMR	5.294	5.213	4.860	5.038	5.465	5.291	5.321	5.324	5.853	5.453
RERGL	3.376	3.961	3.523	3.393	3.752	3.473	3.519	3.419	3.717	3.472
PTPRC	4.484	4.006	4.348	4.144	5.242	3.724	3.573	3.981	4.368	3.757
DOCK2	3.815	3.887	4.027	4.227	4.983	3.538	3.539	3.635	3.852	3.567
DSE	4.135	3.843	3.928	3.984	5.628	3.336	3.928	3.455	3.763	3.460
PTPRE	4.236	4.366	3.795	4.176	5.806	3.914	4.218	3.685	3.697	3.737
TRAF5	4.100	3.918	4.093	3.801	4.862	3.650	3.834	3.865	3.381	3.905
TGFB1	5.842	6.070	5.597	5.680	6.894	4.979	6.381	5.278	5.406	4.910

GAS1	4.097	4.138	3.963	3.890	4.325	3.713	3.980	3.665	3.651	4.376
PTGER4	4.838	4.974	5.548	4.956	6.069	4.397	4.418	5.231	4.518	4.626
GPNMB	4.574	4.674	4.943	5.600	6.810	6.303	4.510	4.280	5.627	5.933
CLEC7A	4.542	4.267	4.392	4.532	5.432	4.436	4.413	4.339	4.388	4.497
FCER1G	6.384	6.043	6.873	7.437	8.442	6.424	6.491	6.059	7.459	6.942
ITGB2	6.185	5.991	6.231	6.487	7.593	6.133	5.817	5.859	6.433	5.886
SAMSN1	4.851	4.402	4.761	4.826	6.167	4.432	4.478	4.467	4.410	4.655
MS4A4A	4.118	4.283	4.690	5.554	7.585	5.307	4.636	4.352	4.270	4.510
WARS1	7.226	7.449	6.816	7.266	8.214	7.069	7.154	6.966	7.582	6.726
HLA-DPB1	9.524	8.920	9.674	9.303	10.166	9.018	9.109	8.397	10.328	9.240
LGMN	8.334	8.233	8.788	9.074	9.471	8.887	8.853	7.897	9.227	9.222
LAPTM5	7.730	8.050	8.215	8.663	9.056	8.253	7.956	7.693	8.515	7.770
ARPC1B	8.590	8.484	8.804	8.852	9.541	8.913	9.148	8.591	8.989	8.627
LYN	6.983	7.476	6.579	5.872	7.421	6.167	6.967	6.665	7.179	7.275
CTSS	7.496	6.743	6.220	6.346	7.673	7.308	5.732	6.464	7.255	7.121
C1QB	7.715	6.541	7.162	7.851	10.144	7.153	7.112	7.567	9.111	7.606
HCLS1	6.764	6.167	6.525	6.309	8.077	6.135	6.459	6.104	7.075	6.608
CSF1R	6.577	6.613	7.211	7.086	8.049	6.689	7.071	7.192	7.437	6.636

LGALS9	6.628	6.213	6.535	6.499	7.771	6.497	6.220	6.344	6.883	6.550
AP1S2	5.996	6.197	6.158	6.470	6.409	6.104	5.829	6.340	6.276	5.979
CD53	7.880	7.379	8.025	7.936	9.059	7.914	7.393	7.384	8.249	7.852
CD163	6.319	6.612	7.971	7.995	9.571	7.264	7.125	6.753	8.605	7.698
CYBB	6.070	5.620	5.252	6.022	6.337	5.168	5.799	5.359	6.472	5.625
HLA-DMB	6.980	6.890	6.852	7.357	7.953	7.189	7.032	6.787	7.892	7.355
FCGR3B	5.358	5.308	5.378	5.897	6.596	5.049	5.038	5.472	6.535	5.901
IRF8	7.309	7.816	7.334	8.009	8.209	7.361	7.028	7.275	8.061	7.003
IL2RG	5.576	4.924	5.258	4.889	6.155	5.093	4.805	4.973	5.346	4.816
CD48	6.904	6.825	6.480	6.564	7.158	6.642	6.394	6.419	7.466	6.718
TYROBP	7.381	6.267	7.883	7.862	9.248	7.207	7.187	6.890	8.084	7.368
ALOX5AP	5.447	5.474	5.834	5.872	6.636	5.779	5.769	5.176	5.913	5.614
CD37	4.296	3.995	3.658	3.882	4.966	3.865	3.688	3.892	4.460	3.759
GMFG	6.293	6.858	6.708	6.750	7.687	6.306	6.341	6.193	7.319	6.877
MRC1	6.112	7.322	6.963	7.386	8.790	7.028	7.440	5.861	7.453	6.989
MYO5A	4.001	3.229	3.322	3.656	5.089	3.728	3.733	3.759	3.682	3.733
SELL	5.747	5.219	5.235	4.364	6.907	4.713	4.877	4.603	5.860	5.513
SLC7A7	6.467	6.486	6.509	6.989	7.062	6.652	6.499	6.388	7.771	6.924

CD52	6.116	5.413	5.827	5.920	6.268	4.875	5.536	5.299	6.953	5.932
EVI2A	5.050	4.575	4.535	4.733	6.542	4.892	4.689	4.886	5.014	5.023
FOLR2	6.616	6.588	7.182	7.283	7.514	7.019	7.579	7.101	8.220	7.603
IL10RA	6.423	8.061	6.006	6.364	7.331	5.756	6.089	6.236	7.502	6.291
SASH3	5.992	5.894	5.557	5.624	6.163	5.650	5.305	5.712	6.737	5.802
MNDA	4.775	4.572	5.035	4.985	7.729	4.744	4.460	4.844	4.938	5.004
CCR1	6.063	5.472	6.470	6.380	8.019	5.958	5.530	5.499	6.767	6.484
NCF4	5.655	5.557	5.384	5.738	6.508	5.536	5.505	5.248	5.410	5.867
CSF2RB	5.721	5.410	5.483	5.665	6.746	5.516	5.398	5.206	4.891	5.199
LCP2	6.254	5.321	4.859	4.980	6.930	5.473	4.672	5.107	6.571	5.507
AOAH	5.520	5.394	5.554	5.787	6.215	5.478	5.309	5.343	6.396	5.340
LY86	6.004	6.502	6.785	6.731	7.027	6.688	6.602	6.172	6.668	6.865
VAV1	4.809	4.410	4.875	4.842	5.183	4.803	4.560	4.630	5.157	4.733
IL18	3.653	3.061	3.169	3.367	3.939	3.648	3.341	3.529	3.665	3.449
IGSF6	6.067	4.671	5.343	5.719	6.308	5.628	5.142	5.370	6.318	5.415
LY96	4.795	5.069	5.480	5.623	7.340	5.148	4.671	5.085	4.924	5.916
TFEC	4.146	3.920	4.056	4.239	5.595	4.035	3.898	3.909	4.014	3.917
SYK	5.425	4.622	5.410	5.209	6.768	5.264	5.295	5.338	5.162	5.302

THEMIS2	5.720	5.620	5.468	6.058	7.160	5.364	5.969	5.510	5.532	5.372
LILRB2	6.631	6.122	5.949	6.212	6.961	6.223	6.167	6.414	6.709	6.249
PRKCB	5.101	4.449	4.691	4.874	6.158	4.361	4.699	4.310	4.816	4.466
HCK	5.819	5.208	5.301	5.761	6.920	5.740	5.350	5.229	5.676	5.463
FAM49A	5.261	4.899	4.909	5.260	6.117	5.338	5.556	5.199	5.144	5.030
TBXAS1	5.196	5.070	5.207	5.329	5.653	5.014	5.292	4.964	5.385	4.754
TNFAIP8	6.212	5.073	5.769	5.615	7.063	5.562	5.293	5.295	5.146	5.213
LCP1	7.144	7.456	6.957	7.198	7.594	7.109	7.465	7.388	8.003	7.702
HLA-DRA	9.068	9.047	9.307	9.568	11.139	9.014	8.127	8.442	9.837	8.879
CORO1A	6.564	5.491	5.816	6.202	7.311	5.715	6.050	5.835	6.238	5.958
NCKAP1L	6.441	6.351	6.235	6.107	6.696	6.447	6.244	6.239	6.391	6.403
C3AR1	5.827	5.802	6.875	6.600	7.541	6.078	6.245	5.675	6.942	6.187
CD300A	6.335	6.091	6.335	6.986	7.498	6.254	6.163	6.510	6.793	6.987
NCF2	5.734	5.253	5.550	5.705	6.799	5.707	5.401	5.273	5.620	5.235
TLR1	4.372	3.623	3.511	3.590	4.805	3.442	3.679	3.949	3.725	3.857
LST1	6.734	6.815	6.454	6.634	7.013	6.686	6.997	6.972	7.385	7.158
EVI2B	5.231	4.809	4.923	4.685	6.776	4.841	4.903	4.735	5.431	5.230
HLA-DPA1	10.659	10.112	9.580	10.248	11.856	10.351	9.438	9.720	10.708	10.004

CLIC2	4.308	4.409	3.594	4.078	5.658	3.876	4.278	4.142	4.127	4.379
RNASE6	5.953	5.616	6.081	7.169	7.848	6.510	6.114	5.961	5.983	6.495
MYO1F	6.762	6.531	6.463	6.393	6.838	6.458	6.872	6.464	6.749	6.600
NKG7	5.779	5.411	5.020	4.468	5.676	4.622	4.759	4.664	5.193	4.765
GPR65	4.477	4.648	4.603	4.490	5.729	4.424	4.505	4.370	4.461	4.444
CD72	5.255	4.514	4.447	4.366	6.217	4.314	4.920	4.635	5.301	5.207
HLA-DMA	8.034	6.216	7.206	7.207	8.344	7.383	6.705	6.259	7.753	6.928
NAGK	8.188	7.965	8.468	7.881	9.039	8.322	8.012	8.156	8.198	7.972
C1QA	7.910	7.108	7.714	8.230	10.096	7.668	8.253	8.097	9.354	8.164
PLAC8	5.609	5.643	5.029	5.905	8.052	4.878	5.623	4.641	6.361	5.565
GIMAP4	6.087	6.039	5.198	5.559	7.479	5.563	5.523	5.546	6.208	6.422
ADAP2	6.186	5.910	6.701	6.608	6.878	6.267	6.527	6.281	6.777	6.512
DPEP2	4.815	4.891	4.714	4.849	4.691	4.789	4.563	4.962	4.754	4.883
ADA2	7.765	7.382	7.030	7.020	8.162	7.402	8.015	6.646	7.981	7.604
MS4A6A	6.922	6.631	7.283	7.313	8.693	7.218	7.204	6.626	8.047	7.596
CLEC4A	5.228	4.694	4.384	4.922	5.120	4.489	4.386	4.309	4.537	4.851
P2RY13	4.393	3.946	3.748	3.805	5.374	4.403	4.417	4.023	4.377	4.891
ATP8B4	3.850	3.677	3.599	3.788	4.347	3.825	3.650	3.903	3.722	3.709

SH3BGRL3	7.515	7.109	7.558	7.667	8.446	7.685	7.498	7.414	8.039	7.173
SREBF2	8.030	8.486	7.723	7.789	8.010	8.463	8.160	8.541	8.586	7.172
ERG28	10.067	9.806	9.790	9.615	9.702	10.267	9.360	10.259	9.669	9.352

Gene Symbols	HB54	HB59	HB60	HB62	HB63	HB69	HB70	HB72	HB73
CCL5	5.067	5.935	5.693	5.934	4.584	8.757	8.754	5.067	4.433
HLA-E	8.441	9.031	10.089	9.848	9.020	10.222	10.555	8.726	8.841
B2M	12.763	13.399	13.562	12.868	12.651	13.562	13.717	12.638	12.667
GBP1	7.283	6.871	8.227	10.511	6.657	8.472	9.218	5.752	5.632
TAP1	7.083	6.998	7.887	10.354	7.034	7.706	8.550	6.938	6.885
IRF1	6.813	6.386	7.086	10.578	6.509	7.366	7.754	6.253	6.489
PSMB10	7.699	7.534	8.051	8.296	7.183	7.714	8.219	7.624	7.843
CXCL9	7.140	6.720	6.693	10.832	7.825	8.870	10.460	6.105	6.973
PLAAT4	7.127	6.727	7.624	7.938	6.244	8.138	8.822	6.515	6.416
PSMB9	7.127	7.054	8.054	8.667	6.069	8.427	9.393	6.568	6.276
HLA-F	9.145	9.505	10.144	9.669	9.237	10.331	10.359	8.722	8.638
BTN3A3	5.743	5.563	5.968	5.664	6.299	6.773	7.393	5.061	5.605
LCK	4.402	4.687	4.735	5.015	4.228	5.560	6.178	4.385	4.305

PTPRCAP	6.008	6.031	6.219	6.027	5.904	7.243	6.667	5.723	5.773
CXCL13	3.905	3.654	3.625	3.515	3.159	4.457	3.728	3.334	3.687
RASGRP1	4.251	4.078	4.220	4.557	3.956	5.190	6.202	4.089	3.919
CD8A	5.768	6.122	5.851	5.601	5.456	7.544	7.890	4.868	5.863
IL7R	4.741	4.865	5.667	5.436	4.900	6.440	6.111	4.820	4.709
TRAF3IP3	4.880	4.941	4.737	4.620	4.890	5.245	5.559	4.640	4.848
CD2	5.448	5.595	5.811	5.759	4.958	6.854	7.488	5.034	5.280
CASP1	6.043	6.284	7.174	6.326	5.687	7.314	7.599	5.665	5.890
PTPN22	3.998	4.043	4.100	4.310	3.906	4.465	5.287	4.254	4.090
HCP5	5.190	5.264	6.551	6.385	4.994	6.941	6.376	4.883	5.012
CD27	5.315	5.295	5.449	5.267	5.299	5.725	6.346	4.959	5.191
CCR7	3.991	3.985	4.124	5.308	4.128	4.901	5.079	4.019	4.013
GZMK	5.629	5.803	6.019	5.629	5.212	7.415	8.438	6.164	5.330
CRTAM	3.393	3.624	3.514	3.785	3.444	3.987	4.454	3.638	3.494
CXCR6	5.057	5.358	5.143	4.944	4.924	5.575	5.850	4.735	4.999
GPR171	4.234	4.206	4.428	5.447	3.837	4.645	5.632	3.968	4.081
HLA-B	10.104	10.972	11.822	11.223	10.118	11.964	12.244	10.222	10.185
HLA-C	11.121	11.915	12.868	11.895	11.408	12.763	13.001	10.893	10.846

PSMB8	7.504	7.277	8.142	8.600	6.661	7.896	8.607	6.516	7.442
CYTIP	4.546	4.499	5.265	5.881	4.824	5.099	7.145	4.955	5.159
TRAC	6.021	6.354	6.029	6.097	5.727	7.537	7.532	5.613	5.711
CD69	3.950	4.283	4.377	6.943	3.456	4.718	7.019	4.448	3.887
CD247	4.912	4.989	5.157	5.704	4.561	5.585	5.810	5.003	5.111
GPR18	3.814	3.906	4.208	3.996	3.949	4.392	4.901	3.977	3.753
HLA-G	8.693	9.189	9.666	9.390	9.068	10.112	10.127	8.758	8.794
TRBC1	6.449	6.771	6.847	6.499	5.998	8.377	8.490	5.831	5.872
ITK	4.105	4.342	4.461	4.648	4.368	5.101	6.056	4.277	4.447
JCHAIN	4.058	4.001	4.763	3.904	4.141	5.895	9.898	4.358	3.866
TRIM22	6.847	8.433	8.608	8.604	5.813	8.413	9.234	6.889	5.946
CD3D	5.559	5.670	5.591	5.821	5.574	7.000	7.114	5.483	5.499
HLA-J	8.310	8.475	9.113	8.172	8.442	9.219	9.604	7.928	7.932
SIRPG	4.542	4.256	4.501	4.410	3.811	4.807	4.725	4.058	4.315
FCMR	5.102	5.576	5.442	4.658	5.343	5.833	6.121	4.392	5.389
RERGL	3.596	3.602	3.834	3.816	3.538	4.221	5.181	3.580	3.526
PTPRC	3.838	3.763	4.702	4.457	3.592	5.340	5.740	3.999	4.292
DOCK2	3.577	3.693	4.616	4.186	3.445	4.355	5.392	3.965	3.949

DSE	3.587	3.875	4.868	5.179	3.555	4.633	5.356	4.077	3.496
PTPRE	3.495	4.075	4.228	5.470	3.661	4.882	5.463	3.958	3.979
TRAF5	3.134	3.756	4.227	4.502	3.216	4.686	4.628	4.245	4.028
TGFB1	5.049	5.337	6.543	6.604	5.759	6.355	6.822	5.748	5.310
GAS1	3.569	3.742	4.995	4.827	3.615	4.875	6.077	3.801	3.536
PTGER4	4.182	4.704	5.116	6.507	4.413	5.116	6.522	5.020	4.570
GPNMB	4.361	5.165	7.704	7.157	3.653	7.084	7.647	6.423	6.527
CLEC7A	4.284	4.541	5.395	4.896	3.797	4.843	5.765	4.721	4.783
FCER1G	5.302	6.108	8.282	6.923	5.184	7.951	7.847	7.320	7.879
ITGB2	5.518	6.235	7.101	6.876	5.546	7.508	7.930	6.697	7.272
SAMSN1	4.298	4.457	5.188	5.585	4.394	5.114	6.566	5.150	5.162
MS4A4A	3.815	4.144	7.079	5.426	3.625	5.148	7.262	5.179	6.148
WARS1	6.727	7.009	7.253	8.278	7.032	7.559	7.953	6.989	7.077
HLA-DPB1	9.473	9.377	11.012	10.195	9.127	11.278	11.610	9.074	9.354
LGMN	8.403	8.534	9.879	8.718	7.383	9.334	9.717	9.189	9.563
LAPTM5	7.021	8.005	9.286	8.884	6.555	9.222	9.458	8.380	8.700
ARPC1B	8.677	8.830	9.386	9.326	8.100	9.651	9.839	8.714	9.119
LYN	5.973	6.992	7.248	8.203	5.861	7.439	7.619	6.433	5.864

CTSS	5.135	7.145	8.484	6.344	5.636	7.693	8.580	6.648	6.668
C1QB	5.850	7.045	9.169	8.464	6.058	9.370	9.356	7.790	7.896
HCLS1	5.702	6.481	8.311	7.577	5.632	8.202	8.434	6.672	6.591
CSF1R	6.332	6.778	8.188	7.262	6.583	8.113	8.547	6.953	7.636
LGALS9	6.604	6.340	7.266	7.029	6.569	7.101	7.134	6.514	6.864
AP1S2	5.891	6.403	7.089	6.663	6.091	7.299	7.426	6.330	6.186
CD53	7.383	7.617	8.662	8.614	6.923	9.031	9.442	7.784	8.234
CD163	5.819	7.213	9.977	8.271	5.974	9.100	9.403	7.440	8.349
CYBB	5.433	5.442	6.249	6.005	4.938	7.304	6.442	5.783	6.162
HLA-DMB	6.655	6.929	8.569	7.384	6.431	8.295	8.938	6.953	6.948
FCGR3B	4.981	5.056	6.356	4.884	5.022	5.912	6.590	5.502	6.103
IRF8	7.940	7.465	8.406	8.970	7.472	8.672	9.273	7.402	7.716
IL2RG	5.061	5.006	5.817	6.022	4.767	6.270	6.631	5.028	5.347
CD48	6.408	6.948	7.497	7.399	6.219	8.060	8.030	6.470	6.707
TYROBP	6.380	7.232	9.176	8.620	6.414	9.047	9.378	7.663	8.337
ALOX5AP	5.213	5.397	6.338	5.243	5.400	6.780	7.298	6.360	5.596
CD37	3.869	3.717	5.033	4.717	4.040	4.618	5.563	4.537	4.219
GMFG	6.617	6.857	7.765	7.611	6.685	8.156	8.499	7.087	7.268

MRC1	6.125	7.193	8.816	8.460	5.703	9.025	9.354	7.008	7.606
MYO5A	3.682	3.582	4.246	4.037	3.543	3.972	4.660	3.943	3.594
SELL	4.925	5.426	5.784	5.463	4.257	5.883	6.806	5.372	4.856
SLC7A7	6.244	6.569	8.176	6.556	6.094	7.581	8.034	6.564	6.985
CD52	5.687	5.487	6.447	6.742	5.415	7.083	7.017	5.630	6.199
EVI2A	4.712	4.686	6.679	5.673	4.261	5.458	7.165	5.278	5.435
FOLR2	7.029	7.305	7.977	7.469	6.832	8.014	8.027	6.827	7.151
IL10RA	5.965	7.055	7.321	7.313	5.713	8.245	8.246	6.517	6.884
SASH3	5.703	5.791	5.880	5.879	5.511	6.610	6.866	5.529	5.689
MNDA	4.670	4.679	6.553	5.337	4.576	5.283	6.784	6.386	5.057
CCR1	5.579	6.021	7.250	7.191	5.555	6.466	7.126	6.482	6.491
NCF4	5.177	5.301	5.998	5.711	5.446	5.763	6.374	5.581	5.841
CSF2RB	4.938	5.428	5.593	7.209	5.446	6.419	6.804	6.142	5.650
LCP2	4.902	4.940	6.781	8.012	5.103	6.729	7.577	5.195	5.179
AOAH	5.034	5.351	6.547	5.882	5.295	6.439	6.681	5.848	5.819
LY86	6.534	6.540	7.642	7.090	6.168	6.976	7.538	6.242	6.747
VAV1	4.711	4.466	5.028	5.418	4.758	5.500	5.744	5.081	5.166
IL18	3.400	3.590	4.100	4.203	3.551	3.803	4.114	3.481	3.375

IGSF6	5.313	5.577	6.432	6.999	5.195	6.305	6.102	5.880	5.703
LY96	4.448	5.102	6.905	6.394	4.452	6.643	8.005	6.305	5.923
TFEC	3.795	4.055	4.473	5.281	3.932	4.071	5.183	4.340	4.240
SYK	5.126	5.042	6.015	6.167	4.727	5.463	6.558	5.841	5.406
THEMIS2	5.017	5.340	6.747	5.974	5.551	6.589	7.510	6.279	6.549
LILRB2	6.318	5.829	6.859	7.205	6.131	6.707	7.061	6.384	6.559
PRKCB	4.683	4.750	5.733	5.254	4.108	5.430	6.526	4.848	4.927
HCK	4.607	5.059	6.741	7.213	5.207	6.265	7.392	5.914	6.116
FAM49A	4.624	4.626	5.774	6.065	4.786	5.895	6.167	5.673	6.029
TBXAS1	5.058	5.006	6.256	5.919	4.858	5.446	6.137	5.582	5.865
TNFAIP8	4.987	5.338	6.278	8.333	4.850	6.663	7.637	5.887	5.750
LCP1	6.926	7.206	8.062	7.484	6.663	8.323	8.746	6.951	7.695
HLA-DRA	7.950	8.529	11.016	10.089	8.238	11.247	11.594	8.681	9.205
CORO1A	5.921	5.790	6.687	7.048	5.880	7.703	7.951	6.545	6.174
NCKAP1L	6.029	6.160	6.955	6.378	5.952	7.258	7.435	6.123	6.644
C3AR1	5.812	5.743	7.405	6.710	6.184	6.974	7.426	6.849	6.534
CD300A	6.309	6.380	7.710	6.242	5.695	7.019	7.824	5.989	7.063
NCF2	5.233	5.543	7.395	6.147	5.019	5.807	7.157	5.964	6.182

TLR1	3.793	3.907	4.500	4.277	3.650	4.199	5.259	4.055	3.884
LST1	6.731	6.768	7.214	7.136	6.946	7.957	7.865	6.806	6.861
EVI2B	5.159	5.356	6.382	4.856	4.756	6.762	7.895	5.555	5.465
HLA-DPA1	9.944	9.691	11.361	11.432	8.954	12.270	12.087	9.434	9.469
CLIC2	3.978	4.212	5.112	5.642	3.783	5.267	5.786	4.396	3.986
RNASE6	5.583	6.198	8.495	6.575	5.290	7.845	8.498	6.874	7.164
MYO1F	6.264	6.568	7.462	6.499	6.442	7.610	7.659	6.686	6.783
NKG7	4.968	4.991	5.071	5.383	4.833	6.287	6.207	5.207	4.499
GPR65	4.515	4.542	5.237	4.860	4.598	4.989	6.669	4.877	4.729
CD72	4.658	4.435	5.161	5.114	4.696	5.555	5.961	4.594	5.353
HLA-DMA	6.305	6.832	8.858	8.283	5.999	8.893	9.587	6.972	7.762
NAGK	7.934	7.971	8.634	8.478	7.662	8.450	9.049	8.338	8.692
C1QA	6.623	7.948	9.329	9.146	6.475	9.804	9.827	8.161	8.567
PLAC8	4.265	4.848	7.264	5.119	4.367	7.337	7.674	6.834	6.852
GIMAP4	5.801	6.276	7.113	5.822	5.814	7.624	7.591	5.420	5.377
ADAP2	6.136	6.447	7.431	6.783	5.642	7.827	7.981	6.311	6.974
DPEP2	4.874	4.684	5.782	4.713	4.702	5.212	5.455	4.948	5.182
ADA2	6.793	7.584	8.808	8.027	6.214	8.761	8.999	6.917	7.127

MS4A6A	6.284	7.108	9.323	6.830	6.026	8.793	9.067	6.744	7.358
CLEC4A	4.028	4.622	4.789	4.942	4.347	4.650	6.009	4.719	4.984
P2RY13	4.104	4.789	6.112	5.452	3.726	5.582	5.513	4.040	4.153
ATP8B4	3.711	3.899	4.444	4.009	3.597	4.361	5.665	3.978	3.896
SH3BGRL3	7.517	7.517	8.839	8.477	7.177	8.786	8.565	7.658	7.588
SREBF2	8.216	8.083	7.009	7.733	8.810	8.155	7.525	7.864	7.873
ERG28	9.581	10.091	8.356	9.686	10.341	9.873	9.163	9.785	9.140
Gene Symbols	HB74	HB75	HB78	HB79	HB80	HB81	HB82	HB83	HB86
CCL5	5.361	6.008	8.669	4.732	4.351	5.742	4.599	5.697	4.408
HLA-E	9.426	9.693	10.285	8.883	8.575	9.753	8.880	9.572	8.290
B2M	13.466	13.383	13.424	12.868	12.434	13.399	13.364	13.342	12.345
GBP1	7.355	8.714	8.408	8.393	6.263	7.635	7.883	7.148	6.034
TAP1	7.120	7.791	8.806	7.281	7.196	7.684	8.150	8.045	6.605
IRF1	7.172	7.084	7.199	7.172	5.874	6.999	6.664	6.929	6.195
PSMB10	7.972	8.012	7.492	6.900	6.528	7.750	6.988	8.134	7.188
CXCL9	7.780	8.780	9.447	6.125	5.340	6.296	7.054	6.667	4.909
PLAAT4	7.659	8.526	7.849	7.514	5.525	7.825	7.071	8.185	6.071

PSMB9	7.794	8.259	9.337	7.162	6.062	7.864	8.757	8.179	5.865
HLA-F	9.552	9.754	10.578	8.763	9.450	9.967	9.844	10.022	8.776
BTN3A3	6.123	6.725	7.301	6.455	6.372	6.342	6.885	5.998	5.465
LCK	4.614	5.071	6.037	4.358	4.268	4.832	4.359	5.019	4.347
PTPRCAP	6.107	6.251	7.252	6.050	5.726	5.986	5.824	6.350	5.877
CXCL13	3.784	3.686	4.779	4.038	3.564	3.962	3.632	4.604	3.633
RASGRP1	4.359	4.670	6.259	4.143	4.155	4.385	3.956	4.633	3.813
CD8A	5.950	5.730	7.568	5.554	5.458	5.216	5.517	5.427	5.467
IL7R	4.886	6.449	7.265	4.857	4.875	5.859	4.780	6.182	4.553
TRAF3IP3	4.978	4.804	5.551	4.658	4.448	4.875	4.727	5.266	4.502
CD2	5.128	5.131	7.335	5.194	5.113	5.494	4.844	6.038	4.780
CASP1	6.456	6.540	6.118	5.317	6.677	6.653	6.584	6.601	5.312
PTPN22	4.170	4.274	4.993	4.226	3.995	4.340	4.053	4.407	3.926
HCP5	5.727	6.158	6.528	5.146	4.904	5.769	5.746	6.063	4.950
CD27	5.371	5.427	6.483	5.053	5.314	5.307	5.245	5.449	5.102
CCR7	3.936	4.529	4.840	3.941	4.005	4.096	3.993	4.762	4.134
GZMK	5.809	6.115	8.008	5.456	5.469	5.886	5.189	5.773	5.058
CRTAM	3.552	3.533	3.840	3.304	3.276	3.511	3.655	3.797	3.568

CXCR6	5.087	5.192	5.702	5.176	5.186	5.223	5.084	5.307	4.894
GPR171	4.182	4.425	5.695	3.938	4.070	4.296	4.003	4.422	4.024
HLA-B	10.909	11.572	11.822	10.107	10.222	11.588	11.193	11.642	10.028
HLA-C	12.147	12.087	12.685	11.252	11.610	12.533	12.320	12.345	11.089
PSMB8	7.558	8.038	8.197	7.086	6.737	7.825	7.928	7.732	6.357
CYTIP	4.816	5.165	6.536	4.714	4.360	5.100	4.625	5.419	4.766
TRAC	6.140	6.591	7.293	5.858	5.543	6.099	5.572	6.311	5.548
CD69	4.213	4.394	5.257	3.795	3.837	4.554	3.877	4.554	3.854
CD247	5.378	5.100	6.050	4.850	4.759	4.932	5.049	5.396	4.853
GPR18	3.998	4.239	4.557	4.080	3.906	4.333	4.081	4.499	3.683
HLA-G	9.337	9.355	10.129	8.873	9.396	9.860	9.756	9.581	8.990
TRBC1	6.800	6.896	8.620	5.942	5.196	6.769	5.763	7.399	5.900
ITK	4.583	4.206	6.985	4.191	4.239	4.618	4.286	4.384	4.295
JCHAIN	4.750	4.159	4.999	4.098	3.997	4.305	3.917	5.607	3.822
TRIM22	7.520	8.333	8.614	6.951	6.043	8.664	7.946	8.270	5.633
CD3D	5.554	6.003	7.783	5.314	5.350	5.776	5.328	5.839	5.442
HLA-J	8.604	8.957	9.352	8.050	8.513	8.754	9.027	8.859	8.174
SIRPG	4.091	4.114	5.064	4.027	4.135	4.017	4.085	4.658	4.086

FCMR	5.277	5.474	6.436	4.866	4.854	5.217	4.915	5.266	5.172
RERGL	3.554	3.558	3.870	3.526	3.728	3.727	3.494	3.811	3.366
PTPRC	4.227	4.598	5.423	3.829	3.277	4.778	3.924	4.972	3.799
DOCK2	3.568	4.079	5.034	3.624	3.368	4.447	3.499	4.433	3.783
DSE	4.180	3.786	4.436	4.043	3.271	4.796	3.473	4.302	3.841
PTPRE	3.576	4.049	4.505	3.837	3.592	4.723	4.063	4.979	3.827
TRAF5	3.422	3.474	5.439	3.355	3.814	4.326	3.388	4.294	3.762
TGFB1	4.949	5.797	6.257	5.139	5.133	6.502	5.154	6.380	5.820
GAS1	3.604	4.607	4.607	3.685	3.588	5.098	3.556	3.930	3.695
PTGER4	4.669	5.190	5.533	4.446	4.519	5.728	4.292	5.376	4.231
GPNMB	4.406	6.262	6.397	4.419	3.724	7.064	5.570	7.150	4.921
CLEC7A	4.440	4.524	5.403	4.399	3.957	5.346	4.793	5.429	4.566
FCER1G	6.200	7.423	9.266	6.231	4.976	7.713	7.279	8.251	5.823
ITGB2	5.832	6.699	7.717	5.712	4.947	7.406	6.491	7.975	5.890
SAMSN1	4.504	5.233	5.844	4.390	4.275	5.115	4.539	5.508	4.531
MS4A4A	4.509	4.874	5.000	4.061	3.855	5.266	4.448	5.126	4.273
WARS1	7.004	7.477	7.812	6.821	6.885	7.304	7.139	7.276	6.754
HLA-DPB1	8.875	10.192	11.396	8.782	8.383	11.085	7.774	10.160	8.463

LGMN	8.611	9.002	9.169	7.868	8.076	9.645	8.540	9.424	8.558
LAPTM5	7.215	8.939	9.709	7.518	7.017	9.074	7.889	9.457	8.254
ARPC1B	7.893	9.270	9.372	8.332	8.559	9.374	8.238	9.739	8.356
LYN	6.034	7.592	7.700	6.795	6.032	7.492	7.122	8.417	6.851
CTSS	7.083	7.692	7.366	6.355	5.436	7.595	6.720	7.326	5.570
C1QB	7.909	8.572	8.433	6.834	5.081	8.339	7.177	9.039	7.429
HCLS1	6.223	6.987	8.283	6.348	5.519	7.714	6.308	7.733	6.326
CSF1R	7.219	7.290	7.663	6.534	6.258	7.552	6.717	7.576	6.732
LGALS9	6.196	7.075	7.060	5.915	5.988	7.143	6.836	7.368	6.811
AP1S2	6.100	6.519	6.793	5.847	5.757	6.831	6.499	7.157	6.107
CD53	7.585	8.130	8.912	7.208	6.831	8.019	7.963	8.832	7.271
CD163	7.724	8.280	7.984	7.668	5.649	8.361	7.136	8.830	7.501
CYBB	5.571	6.240	6.974	5.624	5.452	7.601	6.140	7.043	5.855
HLA-DMB	7.073	7.644	8.286	6.560	6.494	8.131	6.653	8.242	6.165
FCGR3B	5.633	6.744	5.755	5.886	4.947	6.790	5.312	6.324	5.991
IRF8	7.652	7.652	7.783	7.751	6.455	8.322	7.078	8.520	7.503
IL2RG	4.929	5.736	6.514	4.921	4.593	5.437	5.277	6.310	4.863
CD48	6.857	7.044	8.207	6.074	6.021	7.178	6.886	7.748	5.759

TYROBP	7.254	8.476	8.470	6.946	5.497	9.011	7.844	9.023	6.803
ALOX5AP	5.548	6.221	6.344	5.291	5.008	7.081	5.291	6.773	5.276
CD37	3.791	4.707	5.511	3.733	3.647	4.675	3.922	4.849	4.187
GMFG	6.596	7.487	7.979	6.212	6.002	7.362	6.102	7.743	7.005
MRC1	7.040	7.456	7.743	6.710	5.872	7.696	5.531	7.953	6.064
MYO5A	3.704	4.177	4.273	3.533	3.581	3.811	3.887	4.269	3.723
SELL	5.008	5.272	5.875	5.250	4.849	5.692	5.463	7.387	5.209
SLC7A7	6.411	6.702	7.396	6.082	5.860	7.339	6.624	7.347	6.319
CD52	5.952	6.953	8.291	5.475	5.207	6.801	6.404	7.771	5.515
EVI2A	4.845	5.513	6.370	4.893	4.278	6.536	4.992	5.922	4.328
FOLR2	7.151	8.152	7.715	7.269	6.655	7.484	6.500	7.820	7.159
IL10RA	6.542	6.648	7.983	5.740	5.534	7.068	6.193	7.212	5.876
SASH3	5.833	6.152	7.048	5.558	5.526	5.920	5.711	6.679	5.915
MNDA	4.765	5.852	5.901	4.898	4.531	6.276	5.358	6.866	4.999
CCR1	5.842	6.756	5.774	6.401	5.168	6.183	6.881	7.458	6.306
NCF4	5.283	5.711	6.031	5.245	5.086	6.196	5.811	6.214	5.653
CSF2RB	5.083	6.071	5.849	4.943	4.966	6.235	5.368	6.837	5.383
LCP2	5.280	6.021	6.892	5.423	4.791	6.522	5.468	6.416	5.405

AOAH	5.752	6.219	6.269	5.644	4.746	5.974	5.242	6.229	5.098
LY86	6.242	7.050	7.190	6.006	6.139	6.884	6.765	7.320	6.223
VAV1	4.931	5.032	5.022	4.332	4.359	5.024	4.729	5.066	4.778
IL18	3.506	3.437	3.642	3.606	3.349	4.595	3.293	3.857	3.320
IGSF6	5.394	5.581	6.015	5.297	5.368	5.916	6.036	7.123	5.237
LY96	5.064	5.396	6.395	4.996	4.301	6.269	5.322	7.121	4.861
TFEC	3.982	4.200	4.405	3.846	3.856	4.427	4.326	4.541	4.014
SYK	5.493	5.793	5.526	5.257	4.901	6.021	5.160	6.317	5.332
THEMIS2	5.397	6.399	7.082	5.160	5.201	7.018	5.628	6.357	5.547
LILRB2	5.865	6.703	6.555	6.024	5.768	6.680	6.462	6.906	6.032
PRKCB	4.427	5.220	5.456	4.441	3.927	4.493	4.410	6.245	4.665
HCK	5.082	6.299	6.465	5.159	4.605	6.312	5.779	6.842	5.376
FAM49A	5.260	5.608	5.577	5.043	4.678	5.597	5.276	5.904	5.176
TBXAS1	4.938	5.471	5.242	5.123	5.053	5.454	5.268	5.557	5.590
TNFAIP8	5.505	5.857	6.267	5.502	5.292	6.432	5.160	6.396	5.592
LCP1	7.285	7.632	8.188	6.787	6.668	7.773	7.315	7.884	6.712
HLA-DRA	9.058	10.118	11.315	8.114	7.145	10.952	7.802	10.479	6.978
CORO1A	6.189	6.843	8.024	5.693	5.377	7.322	5.936	7.679	5.864

NCKAP1L	6.261	5.958	7.116	5.877	5.740	6.710	6.478	7.352	6.118
C3AR1	6.323	6.933	6.751	5.982	5.663	6.856	6.581	6.774	6.441
CD300A	6.424	6.607	6.717	6.213	5.950	6.543	6.578	7.100	6.258
NCF2	5.191	5.923	5.821	5.153	6.006	6.836	6.221	6.325	5.044
TLR1	4.146	3.896	3.953	3.857	3.827	4.881	3.872	4.018	3.126
LST1	6.941	6.931	7.445	6.356	6.058	7.143	6.873	8.766	6.450
EVI2B	5.084	5.269	6.454	5.005	4.753	5.698	4.989	6.441	4.736
HLA-DPA1	10.367	11.144	11.814	9.237	8.144	11.049	9.478	11.524	8.446
CLIC2	4.515	4.944	4.780	3.947	3.859	4.984	4.302	5.537	5.055
RNASE6	6.351	7.003	7.727	5.976	5.604	7.610	6.293	7.357	6.096
MYO1F	6.743	6.842	7.439	6.417	6.056	7.020	6.772	7.591	6.186
NKG7	5.070	5.724	6.839	4.678	4.594	5.398	4.677	5.967	4.885
GPR65	4.596	4.743	5.284	4.691	4.669	5.335	4.670	4.891	4.457
CD72	4.610	5.946	5.466	4.572	4.602	5.173	4.865	5.979	4.763
HLA-DMA	7.475	7.934	8.933	6.344	6.127	8.436	6.216	8.286	5.855
NAGK	7.896	8.437	8.469	7.771	7.350	8.687	8.547	8.587	7.929
C1QA	8.203	9.205	9.465	7.622	6.363	9.326	7.631	9.635	8.396
PLAC8	5.354	6.148	5.992	5.703	4.650	6.227	6.632	7.983	5.328

GIMAP4	5.649	6.143	7.063	5.898	5.882	6.193	6.149	6.633	5.453
ADAP2	6.432	6.245	7.034	6.553	5.773	6.908	6.581	6.838	6.334
DPEP2	4.880	5.193	5.442	4.402	4.573	5.234	4.906	5.649	4.470
ADA2	7.110	8.386	8.848	6.613	6.409	8.328	7.322	8.986	7.666
MS4A6A	7.412	7.382	8.064	6.814	5.928	8.483	6.902	8.241	6.673
CLEC4A	4.429	4.892	5.003	4.488	4.234	5.361	4.347	4.924	4.377
P2RY13	4.477	4.117	4.696	4.199	3.871	5.129	4.390	5.778	4.356
ATP8B4	3.746	3.909	4.011	3.723	3.615	4.459	3.661	4.144	3.423
SH3BGRL3	7.167	8.313	8.672	7.652	7.230	8.346	7.703	9.135	8.123
SREBF2	7.776	8.052	7.476	8.367	7.983	8.066	8.947	8.008	8.218
ERG28	9.569	9.511	9.157	10.322	10.192	9.013	10.346	10.245	9.320