Table S1 Stromal Score, Immune Score, and ESTIMATE Score

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0T5-01A-21R-A084-07	361.8755	116.516	478.3916
TCGA-A2-A0EM-01A-11R-A034-07	737.4148	125.7191	863.1339
TCGA-BH-A0BJ-01A-11R-A056-07	918.8147	729.4806	1648.295
TCGA-A7-A0DC-01B-04R-A22O-07	80.78604	-446.069	-365.283
TCGA-D8-A146-01A-31R-A115-07	1129.168	645.8598	1775.028
TCGA-B6-A0X7-01A-11R-A10J-07	691.0138	-123.354	567.6598
TCGA-A2-A0EU-01A-22R-A056-07	210.5296	-44.8378	165.6918
TCGA-AO-A0J9-01A-11R-A034-07	1394.553	1791.937	3186.49
TCGA-A2-A0YG-01A-21R-A109-07	-183.985	58.6547	-125.331
TCGA-E2-A1B4-01A-11R-A12P-07	-30.6976	-289.616	-320.314
TCGA-C8-A130-01A-31R-A115-07	508.0449	269.0979	777.1428
TCGA-OL-A5RW-01A-11R-A28M-07	-224.903	547.8998	322.9967
TCGA-E2-A14U-01A-11R-A22K-07	-529.411	-146.224	-675.635
TCGA-EW-A6SB-01A-12R-A32P-07	-465.344	2283.752	1818.408
TCGA-A2-A3XV-01A-21R-A239-07	210.2683	467.1782	677.4465
TCGA-A2-A3XW-01A-11R-A239-07	529.9273	1329.916	1859.843
TCGA-AC-A3HN-01A-11R-A213-07	1424.561	1306.89	2731.451
TCGA-A8-A09R-01A-11R-A00Z-07	778.5743	1030.722	1809.296
TCGA-A2-A3KD-01A-12R-A213-07	252.3715	264.3228	516.6943
TCGA-AO-A0JG-01A-31R-A084-07	622.2924	1283.13	1905.422
TCGA-B6-A1KI-01A-11R-A14M-07	635.4534	-383.228	252.2255
TCGA-E9-A2JT-01A-22R-A18M-07	999.6288	3153.895	4153.524
TCGA-BH-A0DV-01A-21R-A12P-07	1806.537	959.1447	2765.682
TCGA-BH-A0HA-01A-11R-A12P-07	1358.034	1185.065	2543.098
TCGA-A8-A084-01A-21R-A00Z-07	150.3536	-127.875	22.47875
TCGA-AC-A3EH-01A-22R-A22K-07	244.4624	286.9589	531.4213
TCGA-C8-A12Y-01A-11R-A12D-07	382.3806	347.3721	729.7527
TCGA-AN-A0XP-01A-11R-A109-07	483.9926	49.43273	533.4253
TCGA-A8-A07B-01A-11R-A00Z-07	574.7005	4.713155	579.4137
TCGA-E2-A14N-01A-31R-A137-07	-644.536	861.1031	216.5675
TCGA-AO-A1KS-01A-11R-A13Q-07	259.8816	220.593	480.4747
TCGA-A8-A07F-01A-11R-A00Z-07	434.6468	477.2505	911.8974
TCGA-GM-A3XL-01A-11R-A22U-07	-598.119	1476.801	878.6814
TCGA-S3-A6ZG-01A-22R-A32P-07	145.3673	556.5355	701.9028
TCGA-AC-A2QH-01B-04R-A22O-07	67.16175	-901.699	-834.538
TCGA-AR-A24S-01A-11R-A169-07	1476.478	1627.385	3103.863
TCGA-E2-A574-01A-11R-A29R-07	-1189.05	-741.069	-1930.12
TCGA-EW-A1PG-01A-11R-A144-07	847.732	145.5475	993.2795
TCGA-D8-A1XR-01A-11R-A14M-07	128.4862	-97.4491	31.03715
TCGA-AR-A1AP-01A-11R-A12P-07	609.0522	854.332	1463.384
TCGA-D8-A73X-01A-11R-A32P-07	643.7873	273.1571	916.9444
TCGA-EW-A1J1-01A-11R-A13Q-07	72.74654	939.4384	1012.185

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AO-A12D-01A-11R-A115-07	1153.618	1706.319	2859.937
TCGA-BH-A0DI-01A-21R-A12P-07	1551.649	1121.563	2673.212
TCGA-E2-A10C-01A-21R-A10J-07	147.3146	1288.139	1435.453
TCGA-GM-A3XG-01A-31R-A24H-07	-143.655	-220.076	-363.731
TCGA-AR-A1AT-01A-11R-A12P-07	544.9239	1745.438	2290.362
TCGA-B6-A40B-01A-11R-A239-07	465.2434	277.3508	742.5942
TCGA-A8-A07J-01A-11R-A00Z-07	1715.338	1539.943	3255.281
TCGA-AO-A0JJ-01A-11R-A056-07	1360.918	1710.694	3071.612
TCGA-E9-A1R0-01A-22R-A16F-07	728.3165	617.1971	1345.514
TCGA-B6-A400-01A-11R-A239-07	411.8958	988.1592	1400.055
TCGA-E9-A3QA-01A-61R-A22K-07	339.648	2235.786	2575.434
TCGA-D8-A27G-01A-11R-A16F-07	1027.899	992.0367	2019.936
TCGA-AR-A2LH-01A-31R-A18M-07	781.1572	2081.253	2862.411
TCGA-BH-A202-01A-11R-A14M-07	525.8503	1054.462	1580.312
TCGA-A2-A0T2-01A-11R-A084-07	137.8387	525.3759	663.2146
TCGA-D8-A1XQ-01A-11R-A14M-07	619.707	1526.191	2145.898
TCGA-A8-A08Z-01A-21R-A00Z-07	1547.362	1198.675	2746.037
TCGA-BH-A1EU-01A-11R-A137-07	1490.766	1883.253	3374.019
TCGA-B6-A0RG-01A-11R-A056-07	75.47074	-353.736	-278.266
TCGA-GM-A2DM-01A-11R-A180-07	-339.439	659.2388	319.8
TCGA-LL-A5YN-01A-11R-A28M-07	282.8581	2379.386	2662.244
TCGA-E2-A1LB-01A-11R-A144-07	408.0456	45.74156	453.7872
TCGA-AQ-A1H2-01A-11R-A13Q-07	-151.667	296.7351	145.0681
TCGA-D8-A1Y1-01A-21R-A14M-07	1109.297	682.2302	1791.527
TCGA-AO-A12A-01A-21R-A115-07	745.3168	641.4136	1386.73
TCGA-AN-A0XN-01A-21R-A109-07	1763.775	1297.679	3061.454
TCGA-PE-A5DE-01A-11R-A27Q-07	661.7617	2569.01	3230.772
TCGA-A8-A075-01A-11R-A084-07	585.9835	1008.529	1594.512
TCGA-LL-A441-01A-11R-A24H-07	390.171	2270.998	2661.169
TCGA-BH-A0W3-01A-11R-A109-07	-414.636	87.9287	-326.707
TCGA-A2-A04V-01A-21R-A034-07	777.8492	439.788	1217.637
TCGA-V7-A7HQ-01A-11R-A33J-07	233.9656	431.396	665.3616
TCGA-BH-A28Q-01A-11R-A16F-07	486.9517	189.8219	676.7736
TCGA-BH-A1FH-01A-12R-A13Q-07	1637.287	436.6379	2073.925
TCGA-E9-A1NE-01A-21R-A14M-07	1074.461	2422.051	3496.512
TCGA-C8-A26V-01A-11R-A16F-07	118.9315	426.295	545.2266
TCGA-AC-A6IW-01A-12R-A33J-07	-128.132	2346.01	2217.879
TCGA-A1-A0SJ-01A-11R-A084-07	542.7676	191.6562	734.4238
TCGA-XX-A899-01A-11R-A36F-07	1234.232	1926.136	3160.368
TCGA-A2-A0SY-01A-31R-A084-07	1205.578	1261.003	2466.581
TCGA-A2-A0CS-01A-11R-A115-07	661.6039	509.7883	1171.392
TCGA-BH-A1F6-01A-11R-A13Q-07	440.3261	1285.562	1725.888

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A8-A07W-01A-11R-A00Z-07	388.4326	570.3982	958.8308
TCGA-BH-A0HP-01A-12R-A084-07	768.0473	694.2077	1462.255
TCGA-B6-A0IJ-01A-11R-A034-07	-165.631	1963.972	1798.341
TCGA-E2-A1LS-01A-12R-A157-07	-349.069	-258.425	-607.494
TCGA-A2-A0CY-01A-12R-A034-07	-1029.71	-480.293	-1510
TCGA-A7-A26G-01A-21R-A169-07	1581.4	1366.099	2947.498
TCGA-EW-A424-01A-11R-A24H-07	423.2034	-293.974	129.2295
TCGA-B6-A409-01A-11R-A24H-07	-115.004	437.6168	322.6128
TCGA-WT-AB44-01A-11R-A41B-07	632.333	496.1537	1128.487
TCGA-EW-A6SC-01A-12R-A32P-07	1012.236	776.2925	1788.529
TCGA-AR-A256-01A-11R-A169-07	-84.4778	391.5988	307.121
TCGA-E2-A1IG-01A-11R-A144-07	908.3135	223.4988	1131.812
TCGA-EW-A1J5-01A-11R-A13Q-07	501.9921	1600.229	2102.221
TCGA-AR-A1AU-01A-11R-A12P-07	550.7963	89.10184	639.8981
TCGA-AC-A8OP-01A-11R-A36F-07	463.3341	391.3467	854.6808
TCGA-A8-A09Z-01A-11R-A00Z-07	-103.45	1214.572	1111.122
TCGA-BH-A18V-06A-11R-A213-07	272.8575	2513.511	2786.368
TCGA-OL-A66P-01A-11R-A31O-07	1071.928	2659.712	3731.64
TCGA-GM-A5PV-01A-11R-A28M-07	-572.953	550.8572	-22.0963
TCGA-B6-A0WW-01A-11R-A109-07	366.9796	-66.8262	300.1534
TCGA-A2-A04R-01A-41R-A109-07	25.77812	-578.823	-553.044
TCGA-A2-A1FW-01A-11R-A13Q-07	287.9343	-116.673	171.2618
TCGA-C8-A137-01A-11R-A115-07	101.3988	-589.126	-487.727
TCGA-AR-A24X-01A-11R-A169-07	580.9309	198.9324	779.8634
TCGA-BH-A0B2-01A-11R-A10J-07	1514.663	1822.69	3337.353
TCGA-C8-A12K-01A-21R-A115-07	556.8192	2421.228	2978.048
TCGA-BH-A0HB-01A-11R-A056-07	484.0993	1254.427	1738.526
TCGA-E9-A1NH-01A-11R-A14D-07	1229.968	669.7852	1899.753
TCGA-E2-A1LA-01A-11R-A144-07	670.4923	1790.947	2461.439
TCGA-A2-A0EV-01A-11R-A034-07	961.3979	1086.084	2047.481
TCGA-A2-A0SX-01A-12R-A084-07	854.3795	1999.044	2853.423
TCGA-A2-A04Y-01A-21R-A034-07	406.7688	1334.534	1741.303
TCGA-A2-A1FZ-01A-51R-A14D-07	1119.632	832.2423	1951.874
TCGA-E2-A573-01A-11R-A29R-07	-50.7302	1887.077	1836.347
TCGA-A7-A26I-01B-06R-A22O-07	1463.973	725.3403	2189.313
TCGA-C8-A138-01A-11R-A115-07	1113.166	1728.463	2841.629
TCGA-A8-A095-01A-11R-A00Z-07	275.2889	240.2848	515.5737
TCGA-EW-A1P3-01A-11R-A144-07	420.2453	423.5587	843.8041
TCGA-D8-A27H-01A-11R-A16F-07	639.7175	302.074	941.7916
TCGA-BH-A1FC-01A-11R-A13Q-07	-49.1757	1567.677	1518.501
TCGA-B6-A0WX-01A-11R-A109-07	1015.845	932.006	1947.852
TCGA-D8-A143-01A-11R-A115-07	-376.788	574.1614	197.3738

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-B6-A0WY-01A-11R-A109-07	687.9765	522.7469	1210.723
TCGA-A1-A0SK-01A-12R-A084-07	-1406.32	-1277.91	-2684.23
TCGA-A8-A06Q-01A-11R-A034-07	-1015.94	-478.796	-1494.74
TCGA-AC-A6NO-01A-12R-A33J-07	-49.4157	-184.465	-233.881
TCGA-A2-A0YC-01A-11R-A109-07	673.3218	590.4945	1263.816
TCGA-E9-A1R6-01A-11R-A14D-07	151.7173	-121.44	30.27686
TCGA-A1-A0SE-01A-11R-A084-07	625.7867	-39.9417	585.845
TCGA-BH-A1EY-01A-11R-A13Q-07	1330.253	1534.707	2864.96
TCGA-AC-A6IV-01A-12R-A33J-07	1719.387	1882.093	3601.48
TCGA-E2-A1LG-01A-21R-A14M-07	-1030.22	241.6964	-788.519
TCGA-AO-A12C-01A-11R-A10J-07	1125.79	-92.2491	1033.541
TCGA-GM-A4E0-01A-12R-A266-07	1572.667	1964.752	3537.418
TCGA-B6-A0IQ-01A-11R-A034-07	-648.453	415.7192	-232.734
TCGA-E9-A1ND-01A-11R-A144-07	669.3226	2250.225	2919.548
TCGA-A2-A3XS-01A-11R-A22U-07	127.9893	868.3823	996.3716
TCGA-EW-A1OX-01A-11R-A144-07	-1309.35	-1182.02	-2491.36
TCGA-D8-A1XK-01A-21R-A14M-07	-436.216	940.1244	503.9082
TCGA-AR-A24L-01A-11R-A169-07	1000.082	95.95828	1096.041
TCGA-A8-A07Z-01A-11R-A00Z-07	-283.818	627.8333	344.0156
TCGA-BH-A0C0-01A-21R-A056-07	391.4934	2297.431	2688.924
TCGA-S3-AA14-01A-11R-A41B-07	762.4901	-76.9662	685.5239
TCGA-E2-A1BC-01A-11R-A12P-07	901.1329	-184.434	716.6985
TCGA-AC-A8OR-01A-21R-A41B-07	-944.32	250.4118	-693.908
TCGA-E2-A15M-01A-11R-A12D-07	1661.271	2043.78	3705.051
TCGA-B6-A0RL-01A-11R-A084-07	-2065.59	-851.28	-2916.86
TCGA-BH-AB28-01A-31R-A41B-07	522.7143	985.512	1508.226
TCGA-AN-A0XO-01A-11R-A109-07	268.1636	-695.441	-427.278
TCGA-B6-A0X4-01A-11R-A109-07	-1263.07	-937.952	-2201.02
TCGA-A8-A093-01A-11R-A00Z-07	646.9976	-356.164	290.8335
TCGA-D8-A1JL-01A-11R-A13Q-07	1019.591	1744.865	2764.456
TCGA-LL-A5YP-01A-21R-A28M-07	1163.543	967.609	2131.152
TCGA-A2-A0CP-01A-11R-A034-07	1043.887	419.4613	1463.348
TCGA-EW-A1J6-01A-11R-A13Q-07	-118.2	1224.481	1106.282
TCGA-E2-A14R-01A-11R-A115-07	-381.033	1394.596	1013.563
TCGA-EW-A1OV-01A-11R-A144-07	944.881	2656.988	3601.869
TCGA-A2-A0CX-01A-21R-A00Z-07	1022.41	982.3927	2004.802
TCGA-A7-A13E-01A-11R-A277-07	-31.1087	-523.689	-554.798
TCGA-A8-A08F-01A-11R-A00Z-07	847.1192	1482.767	2329.886
TCGA-A7-A13E-01A-11R-A12P-07	-207.958	-415.458	-623.416
TCGA-E9-A1RG-01A-11R-A14D-07	295.3415	724.7952	1020.137
TCGA-E2-A15E-06A-11R-A12D-07	-507.233	606.8605	99.6278
TCGA-A1-A0SQ-01A-21R-A144-07	-86.1776	165.9144	79.73678

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-EW-A1PD-01A-11R-A144-07	841.7623	62.31857	904.0809
TCGA-BH-A0HN-01A-11R-A10U-07	-719.199	22.39037	-696.808
TCGA-E2-A1IU-01A-11R-A14D-07	-162.535	342.4605	179.9251
TCGA-BH-A0BO-01A-23R-A12D-07	1349.32	1182.797	2532.117
TCGA-E2-A1IJ-01A-11R-A144-07	1547.484	1517.192	3064.677
TCGA-A2-A0ES-01A-11R-A115-07	1029.688	717.593	1747.281
TCGA-AO-A12B-01A-11R-A10J-07	-476.558	-35.3909	-511.949
TCGA-BH-A0E9-01B-11R-A115-07	365.8746	518.0013	883.8759
TCGA-BH-A0BP-01A-11R-A115-07	1167.502	351.6442	1519.146
TCGA-E2-A153-01A-12R-A12D-07	1528.418	714.3235	2242.741
TCGA-PL-A8LZ-01A-31R-A36F-07	1156.856	2070.839	3227.695
TCGA-E9-A5UP-01A-11R-A28M-07	-1229.37	214.0843	-1015.29
TCGA-AC-A2FG-01A-11R-A17B-07	354.592	185.3607	539.9527
TCGA-AR-A5QN-01A-12R-A28M-07	637.5483	680.986	1318.534
TCGA-AR-A252-01A-11R-A169-07	1268.562	2454.741	3723.304
TCGA-A8-A08C-01A-11R-A00Z-07	-29.1073	-69.8781	-98.9855
TCGA-D8-A1X8-01A-11R-A14M-07	871.0312	908.3257	1779.357
TCGA-A8-A06X-01A-21R-A00Z-07	297.5506	580.1077	877.6583
TCGA-LL-A50Y-01A-11R-A266-07	39.87822	978.4835	1018.362
TCGA-AN-A049-01A-21R-A00Z-07	776.368	797.5021	1573.87
TCGA-E2-A14W-01A-11R-A12D-07	-441.193	-667.629	-1108.82
TCGA-LD-A9QF-01A-32R-A41B-07	1450.655	2702.04	4152.695
TCGA-D8-A1J8-01A-11R-A13Q-07	775.6169	1538.27	2313.887
TCGA-C8-A275-01A-21R-A16F-07	480.5224	1818.837	2299.36
TCGA-A2-A0YD-01A-11R-A109-07	1482.062	1228.6	2710.663
TCGA-D8-A1JH-01A-11R-A13Q-07	1244.314	973.0456	2217.36
TCGA-D8-A1X9-01A-12R-A157-07	888.3113	757.4187	1645.73
TCGA-E9-A2JS-01A-11R-A180-07	224.2512	37.33185	261.5831
TCGA-AC-A3W5-01A-11R-A22K-07	1464.596	1794.904	3259.5
TCGA-BH-A0C7-01B-11R-A115-07	192.5979	363.468	556.0659
TCGA-AQ-A0Y5-01A-11R-A14M-07	1075.909	335.6985	1411.608
TCGA-A7-A0CD-01A-11R-A00Z-07	71.0026	-277.182	-206.179
TCGA-A8-A08A-01A-11R-A32Y-07	634.6686	778.2095	1412.878
TCGA-A7-A26E-01A-11R-A277-07	1151.604	430.6097	1582.213
TCGA-A8-A09V-01A-11R-A034-07	601.0987	-354.256	246.8428
TCGA-A8-A09K-01A-11R-A00Z-07	-635.614	759.4953	123.881
TCGA-EW-A1IW-01A-11R-A13Q-07	659.6737	578.3143	1237.988
TCGA-C8-A1HF-01A-11R-A137-07	945.2386	1554.357	2499.596
TCGA-AO-A0JI-01A-21R-A056-07	-505.374	-131.136	-636.51
TCGA-D8-A3Z6-01A-11R-A239-07	506.7844	48.90931	555.6937
TCGA-AO-A126-01A-11R-A10J-07	1101.996	622.5388	1724.535
TCGA-E9-A1N3-01A-12R-A157-07	-545.368	-598.082	-1143.45

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AN-A04A-01A-21R-A034-07	966.894	229.357	1196.251
TCGA-E9-A3X8-01A-31R-A22U-07	940.6986	1521.968	2462.667
TCGA-D8-A27N-01A-11R-A16F-07	1184.871	1152.74	2337.611
TCGA-AR-A0U2-01A-11R-A109-07	-302.459	427.6234	125.1645
TCGA-AO-A0JA-01A-11R-A056-07	1235.396	805.6188	2041.015
TCGA-D8-A147-01A-11R-A115-07	-71.7452	914.9718	843.2266
TCGA-D8-A1JJ-01A-31R-A14M-07	896.9031	498.0246	1394.928
TCGA-EW-A1IX-01A-12R-A144-07	1173.113	529.0541	1702.168
TCGA-A8-A09N-01A-11R-A00Z-07	315.5094	213.6354	529.1447
TCGA-A7-A0CH-01A-21R-A00Z-07	362.8301	-15.2656	347.5645
TCGA-E2-A1IE-01A-11R-A13Q-07	-359.751	-738.322	-1098.07
TCGA-A7-A5ZX-01A-12R-A29R-07	748.17	-9.17635	738.9937
TCGA-A2-A4S3-01A-21R-A266-07	14.63644	997.394	1012.03
TCGA-BH-A1EO-01A-11R-A137-07	1762.219	1118.919	2881.137
TCGA-D8-A4Z1-01A-21R-A266-07	750.1418	450.6213	1200.763
TCGA-GI-A2C9-01A-11R-A21T-07	343.457	554.6482	898.1052
TCGA-Z7-A8R5-01A-42R-A41B-07	619.4029	1605.758	2225.161
TCGA-EW-A1P7-01A-21R-A144-07	1162.052	2643.359	3805.412
TCGA-A7-A13G-01B-04R-A22O-07	605.4785	110.9201	716.3985
TCGA-OL-A66O-01A-11R-A31O-07	-187.004	-297.803	-484.807
TCGA-A8-A083-01A-21R-A00Z-07	-784.433	-177.329	-961.762
TCGA-A2-A0D3-01A-11R-A115-07	-192.06	471.7465	279.687
TCGA-E9-A54X-01A-11R-A266-07	-1780.33	-1063.68	-2844.01
TCGA-D8-A1XU-01A-11R-A14M-07	944.911	517.51	1462.421
TCGA-A8-A07I-01A-11R-A00Z-07	1035.246	812.1313	1847.377
TCGA-E9-A54Y-01A-11R-A466-07	-1135.78	119.9451	-1015.84
TCGA-EW-A2FR-01A-11R-A21T-07	1639.411	782.6616	2422.073
TCGA-S3-A6ZH-01A-22R-A32P-07	-471.72	181.8559	-289.864
TCGA-BH-A18J-01A-11R-A12D-07	667.179	157.8159	824.995
TCGA-D8-A1JD-01A-11R-A13Q-07	1109.967	786.6338	1896.601
TCGA-BH-A0HF-01A-11R-A056-07	1098.827	1070.458	2169.285
TCGA-BH-A1FL-01A-11R-A13Q-07	149.3124	-123.863	25.44899
TCGA-BH-A1FG-01A-11R-A13Q-07	-69.5993	118.75	49.15071
TCGA-BH-A0E7-01A-11R-A034-07	39.3071	-470.015	-430.708
TCGA-BH-A1FR-01A-11R-A13Q-07	11.334	679.1332	690.4672
TCGA-BH-A18L-01A-32R-A12D-07	-663.499	-211.824	-875.323
TCGA-A7-A3IZ-01A-11R-A213-07	-379.409	-161.605	-541.014
TCGA-E2-A15P-01A-11R-A115-07	328.356	-77.2418	251.1141
TCGA-A8-A0A9-01A-11R-A00Z-07	518.4433	449.8194	968.2627
TCGA-A8-A06T-01A-11R-A00Z-07	330.2796	495.2692	825.5489
TCGA-E2-A15G-01A-11R-A12D-07	-155.832	-50.7488	-206.581
TCGA-OL-A5RZ-01A-11R-A28M-07	-492.286	-327.783	-820.07

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AR-A0TQ-01A-11R-A084-07	296.1889	1234.756	1530.945
TCGA-B6-A1KN-01A-11R-A13Q-07	305.4478	233.7023	539.1501
TCGA-E2-A1II-01A-11R-A144-07	72.37907	2480.916	2553.295
TCGA-AN-A03X-01A-21R-A00Z-07	1435.065	678.4071	2113.473
TCGA-A8-A08I-01A-11R-A00Z-07	-4.22019	2248.734	2244.514
TCGA-E2-A107-01A-11R-A10J-07	-491.631	-19.4475	-511.078
TCGA-A2-A0SW-01A-11R-A084-07	785.1372	1738.339	2523.476
TCGA-A7-A26F-01B-04R-A22O-07	1326.332	1413.063	2739.395
TCGA-D8-A1X6-01A-11R-A14M-07	256.4846	901.6953	1158.18
TCGA-AR-A254-01A-21R-A169-07	1247.876	1548.961	2796.837
TCGA-D8-A1XD-01A-11R-A14D-07	486.3181	-755.25	-268.932
TCGA-E9-A1NG-01A-21R-A14M-07	1888.971	1294.951	3183.922
TCGA-GM-A2DN-01A-11R-A180-07	674.9074	1947.084	2621.992
TCGA-A7-A6VX-01A-12R-A33J-07	582.5163	177.2964	759.8127
TCGA-E2-A1BD-01A-11R-A12P-07	352.6932	36.68973	389.3829
TCGA-E2-A154-01A-11R-A115-07	308.8831	-337.97	-29.0872
TCGA-A7-A13D-01B-04R-A277-07	104.4985	-650.299	-545.8
TCGA-EW-A2FS-01A-11R-A17B-07	125.8324	831.4449	957.2773
TCGA-OL-A66J-01A-11R-A29R-07	806.8557	474.6893	1281.545
TCGA-BH-A0DG-01A-21R-A12P-07	1395.844	1186.16	2582.004
TCGA-B6-A0IK-01A-12R-A056-07	5.711782	423.4338	429.1455
TCGA-EW-A3E8-01B-11R-A24H-07	897.4978	1715.145	2612.643
TCGA-E2-A14P-01A-31R-A12D-07	-400.485	666.5173	266.0323
TCGA-E9-A1N6-01A-11R-A144-07	948.1762	431.411	1379.587
TCGA-BH-A18G-01A-11R-A12D-07	186.3325	488.8252	675.1577
TCGA-A8-A0A2-01A-11R-A034-07	695.8743	663.9198	1359.794
TCGA-C8-A12N-01A-11R-A115-07	1088.538	766.5044	1855.043
TCGA-E9-A1N5-01A-11R-A14D-07	1145.997	1084.947	2230.945
TCGA-LL-A9Q3-01A-11R-A41B-07	327.642	925.4558	1253.098
TCGA-E9-A1R5-01A-11R-A14M-07	608.1203	-65.5964	542.5239
TCGA-AO-A0J8-01A-21R-A034-07	503.1499	894.6839	1397.834
TCGA-D8-A1XV-01A-11R-A14M-07	-622.492	-450.871	-1073.36
TCGA-BH-A0BV-01A-11R-A00Z-07	970.1175	1087.952	2058.069
TCGA-AO-A1KP-01A-11R-A13Q-07	-486.84	-683.072	-1169.91
TCGA-BH-A0HO-01A-11R-A034-07	499.0569	865.3911	1364.448
TCGA-UL-AAZ6-01A-11R-A41B-07	-761.013	62.19552	-698.818
TCGA-E9-A1N8-01A-11R-A144-07	-718.558	-488.607	-1207.17
TCGA-MS-A51U-01A-31R-A266-07	820.0385	679.6545	1499.693
TCGA-AR-A2LO-01A-31R-A18M-07	827.5023	1457.04	2284.543
TCGA-C8-A1HG-01A-11R-A137-07	485.5804	1462.483	1948.063
TCGA-BH-A0H0-01A-11R-A056-07	-464.408	-191.536	-655.943
TCGA-UU-A93S-01A-21R-A41B-07	-776.773	380.9216	-395.852

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AR-A2LK-01A-11R-A180-07	537.4697	410.2841	947.7538
TCGA-C8-A274-01A-11R-A16F-07	-412.09	-12.6178	-424.707
TCGA-E2-A15A-01A-11R-A12D-07	612.8599	900.2486	1513.108
TCGA-A8-A08B-01A-11R-A00Z-07	-522.119	665.9271	143.8083
TCGA-A8-A06N-01A-11R-A00Z-07	-1517.94	-546.535	-2064.48
TCGA-B6-A1KF-01A-11R-A13Q-07	-192.636	-834.331	-1026.97
TCGA-AR-A24T-01A-11R-A169-07	1513.777	721.9456	2235.722
TCGA-D8-A1X7-01A-11R-A14M-07	425.6273	89.74614	515.3735
TCGA-AC-A3QQ-01B-06R-A22O-07	1032.808	756.4496	1789.257
TCGA-BH-A6R9-01A-21R-A32P-07	2106.169	1964.822	4070.991
TCGA-B6-A0RM-01A-11R-A084-07	-389.169	-345.133	-734.302
TCGA-5T-A9QA-01A-11R-A41B-07	-1463.8	-349.54	-1813.34
TCGA-A8-A085-01A-11R-A00Z-07	199.8931	-685.624	-485.731
TCGA-E2-A159-01A-11R-A115-07	549.1572	1837.364	2386.521
TCGA-AC-A2B8-01A-11R-A17B-07	1284.619	1171.917	2456.536
TCGA-C8-A12Z-01A-11R-A115-07	-84.0037	-310.433	-394.437
TCGA-E9-A229-01A-31R-A157-07	1483.161	953.6353	2436.796
TCGA-PE-A5DC-01A-12R-A27Q-07	-83.6901	123.7811	40.09093
TCGA-AO-A03V-01A-11R-A115-07	-5.01483	-17.5613	-22.5762
TCGA-BH-A1EW-01A-11R-A137-07	446.4243	978.4268	1424.851
TCGA-AC-A2BK-01A-11R-A21T-07	-1321.35	-686.015	-2007.36
TCGA-E2-A1LH-01A-11R-A14D-07	596.9906	2228.104	2825.095
TCGA-BH-A0HK-01A-11R-A056-07	744.0624	538.8814	1282.944
TCGA-AC-A3BB-01A-21R-A19W-07	1237.046	1826.081	3063.127
TCGA-AR-A1AR-01A-31R-A137-07	1090.462	1881.448	2971.911
TCGA-GM-A3NW-01A-21R-A22K-07	-35.2085	298.5093	263.3008
TCGA-AN-A04C-01A-21R-A034-07	-280.731	444.7691	164.0385
TCGA-A2-A25D-01A-12R-A16F-07	564.4129	1974.605	2539.018
TCGA-C8-A273-01A-11R-A16F-07	608.8667	161.6921	770.5589
TCGA-C8-A131-01A-11R-A115-07	570.3256	763.4247	1333.75
TCGA-AC-A2QI-01A-12R-A19W-07	1009.078	1042.318	2051.396
TCGA-AC-A2FM-01A-11R-A19W-07	-92.798	-475.171	-567.969
TCGA-AO-A1KQ-01A-11R-A13Q-07	313.5107	1134.919	1448.43
TCGA-C8-A133-01A-32R-A12D-07	-1180.78	-174.885	-1355.67
TCGA-D8-A1XM-01A-21R-A14M-07	1192.506	1270.396	2462.902
TCGA-AN-A0XL-01A-11R-A10J-07	1108.434	126.2597	1234.694
TCGA-C8-A12T-01A-11R-A115-07	911.0357	442.6516	1353.687
TCGA-E2-A15O-01A-11R-A115-07	-502.745	-35.6848	-538.43
TCGA-OL-A5RU-01A-11R-A28M-07	364.8265	1642.756	2007.583
TCGA-AN-A046-01A-21R-A034-07	903.3392	1515.551	2418.89
TCGA-AN-A0FK-01A-11R-A034-07	54.1933	5.054238	59.24754
TCGA-D8-A27M-01A-11R-A16F-07	1145.803	2035.197	3181

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0YF-01A-21R-A109-07	173.4318	638.5214	811.9533
TCGA-A8-A08P-01A-11R-A00Z-07	1046.999	1813.959	2860.958
TCGA-AO-A12H-01A-11R-A115-07	-78.6807	159.2628	80.58207
TCGA-D8-A1XL-01A-11R-A14M-07	209.9127	1671.025	1880.938
TCGA-E9-A1NI-01A-11R-A14D-07	735.979	197.3277	933.3067
TCGA-A2-A0YH-01A-11R-A109-07	1141.447	1698.336	2839.783
TCGA-A2-A04Q-01A-21R-A034-07	1012.099	2765.754	3777.853
TCGA-BH-A42V-01A-11R-A24H-07	765.0166	933.5393	1698.556
TCGA-D8-A1JN-01A-11R-A13Q-07	-927.665	128.0942	-799.571
TCGA-A2-A0CK-01A-11R-A22K-07	508.8867	720.8016	1229.688
TCGA-BH-A0BQ-01A-21R-A115-07	1142.005	1083.591	2225.596
TCGA-BH-A0DK-01A-21R-A056-07	1380.024	1952.503	3332.527
TCGA-AR-A24W-01A-11R-A169-07	708.9092	-147.423	561.4865
TCGA-A8-A07G-01A-11R-A034-07	1208.918	607.3049	1816.223
TCGA-A2-A0CT-01A-31R-A056-07	-167.11	-51.2179	-218.328
TCGA-B6-A0IN-01A-11R-A034-07	997.7566	1524.57	2522.327
TCGA-A2-A0CU-01A-12R-A034-07	242.0714	-147.016	95.05559
TCGA-B6-A0RN-01A-12R-A084-07	691.916	-174.624	517.2917
TCGA-A2-A0SV-01A-11R-A084-07	841.0259	1187.973	2028.999
TCGA-E2-A15K-06A-11R-A12P-07	-1179.49	-133.75	-1313.24
TCGA-A7-A26H-01A-11R-A169-07	1021.029	840.6603	1861.689
TCGA-C8-A12V-01A-11R-A115-07	833.1775	2956.843	3790.02
TCGA-A8-A082-01A-11R-A00Z-07	287.748	353.3295	641.0776
TCGA-E2-A1L6-01A-11R-A13Q-07	480.304	404.5206	884.8246
TCGA-A1-A0SM-01A-11R-A084-07	912.0325	469.8834	1381.916
TCGA-E2-A1B5-01A-21R-A12P-07	849.1319	2645.375	3494.507
TCGA-E2-A2P6-01A-11R-A19W-07	72.17081	423.0387	495.2095
TCGA-D8-A1JI-01A-11R-A13Q-07	-367.765	6.879369	-360.886
TCGA-S3-AA17-01A-11R-A41B-07	576.549	2380.767	2957.316
TCGA-B6-A40C-01A-11R-A239-07	781.2876	653.3194	1434.607
TCGA-A8-A091-01A-11R-A00Z-07	169.177	117.6703	286.8473
TCGA-AC-A7VC-01A-11R-A352-07	954.591	653.3246	1607.916
TCGA-AR-A1AO-01A-11R-A12P-07	1625.519	2693.983	4319.502
TCGA-AO-A1KR-01A-12R-A144-07	-919.954	454.4652	-465.489
TCGA-A8-A06Y-01A-21R-A00Z-07	-849.514	-535.032	-1384.55
TCGA-BH-A1FE-01A-11R-A13Q-07	1194.594	1567.315	2761.909
TCGA-E9-A3HO-01A-11R-A213-07	-155.433	822.8983	667.4657
TCGA-A2-A3Y0-01A-11R-A239-07	-349.147	1429.845	1080.697
TCGA-BH-A0H9-01A-11R-A056-07	-42.3523	-60.3187	-102.671
TCGA-GM-A2DF-01A-11R-A180-07	582.3275	1706.133	2288.461
TCGA-D8-A1JF-01A-11R-A13Q-07	808.0212	534.7868	1342.808

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-E9-A1RH-01A-21R-A169-07	272.8545	129.3158	402.1704
TCGA-AO-A0J2-01A-11R-A034-07	-200.919	1074.81	873.8908
TCGA-B6-A0IP-01A-11R-A034-07	48.37279	371.1902	419.563
TCGA-BH-A0GY-01A-11R-A056-07	426.4957	707.6625	1134.158
TCGA-A7-A6VY-01A-12R-A33J-07	572.1738	1479.049	2051.223
TCGA-E2-A15K-01A-11R-A12P-07	359.651	1261.519	1621.17
TCGA-D8-A1JE-01A-11R-A13Q-07	1456.41	778.9514	2235.361
TCGA-LL-A440-01A-11R-A24H-07	1646.531	1668.589	3315.12
TCGA-BH-A0BR-01A-21R-A115-07	1395.899	1118.376	2514.275
TCGA-D8-A1J9-01A-11R-A13Q-07	835.4996	525.2199	1360.719
TCGA-B6-A0RV-01A-11R-A084-07	125.3533	848.541	973.8943
TCGA-E9-A5UO-01A-11R-A28M-07	-1185.38	-768.869	-1954.25
TCGA-BH-A0C3-01A-21R-A12P-07	1329.285	1225.316	2554.601
TCGA-JL-A3YW-01A-12R-A239-07	1550.597	1735.731	3286.329
TCGA-B6-A0I8-01A-11R-A034-07	198.9268	-455.099	-256.172
TCGA-E2-A10F-01A-11R-A10J-07	1327.489	1319.296	2646.785
TCGA-AN-A0FW-01A-11R-A034-07	378.375	245.0547	623.4298
TCGA-AR-A1AL-01A-21R-A12P-07	982.5787	640.9186	1623.497
TCGA-BH-A1F2-01A-31R-A13Q-07	1087.943	301.727	1389.67
TCGA-BH-A0EB-01A-11R-A034-07	1293.988	1532.985	2826.972
TCGA-B6-A402-01A-11R-A239-07	-428.766	-352.656	-781.422
TCGA-AC-A2FF-01A-11R-A17B-07	1615.571	1478.603	3094.174
TCGA-E2-A15F-01A-11R-A115-07	-109.959	156.5899	46.63054
TCGA-AO-A03R-01A-21R-A034-07	88.29943	1242.222	1330.522
TCGA-E2-A15S-01A-11R-A115-07	-877.33	-800.121	-1677.45
TCGA-BH-A0B5-01A-11R-A12P-07	638.2503	757.0109	1395.261
TCGA-E9-A1RB-01A-11R-A157-07	21.46747	149.4424	170.9098
TCGA-OL-A66N-01A-12R-A31O-07	691.9623	1097.497	1789.459
TCGA-4H-AAAK-01A-12R-A41B-07	1150.833	528.3564	1679.189
TCGA-A7-A0CJ-01A-21R-A00Z-07	-421.907	41.61098	-380.296
TCGA-BH-A0W4-01A-11R-A109-07	531.8684	-265.717	266.1516
TCGA-BH-A0BT-01A-11R-A12P-07	396.2768	533.7987	930.0756
TCGA-C8-A135-01A-11R-A115-07	697.1139	845.9094	1543.023
TCGA-A8-A09X-01A-11R-A00Z-07	1116.332	1736.487	2852.82
TCGA-A2-A04N-01A-11R-A115-07	871.8746	221.6774	1093.552
TCGA-E9-A244-01A-11R-A169-07	7.459725	9.75598	17.2157
TCGA-AN-A0FL-01A-11R-A034-07	-589.75	-254.751	-844.501
TCGA-AN-A0AS-01A-11R-A00Z-07	945.8897	695.586	1641.476
TCGA-BH-A0E1-01A-11R-A056-07	267.0232	-173.582	93.44127
TCGA-D8-A27I-01A-11R-A16F-07	1348.811	1334.623	2683.433
TCGA-C8-A1HE-01A-11R-A13Q-07	134.6316	240.5281	375.1597
TCGA-BH-A0DL-01A-11R-A115-07	106.5185	1909.096	2015.614

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AQ-A7U7-01A-22R-A352-07	1627.254	2614.509	4241.763
TCGA-E2-A14Q-01A-11R-A12D-07	195.4108	199.6547	395.0655
TCGA-AO-A12E-01A-11R-A10J-07	582.8914	680.6227	1263.514
TCGA-C8-A8HP-01A-11R-A36F-07	439.7177	1769.667	2209.385
TCGA-BH-A1EX-01A-11R-A13Q-07	1077.812	902.1673	1979.979
TCGA-AO-A0JC-01A-11R-A056-07	701.9085	3672.572	4374.48
TCGA-BH-A0BM-01A-11R-A056-07	751.0524	249.7343	1000.787
TCGA-A7-A3RF-01A-11R-A22K-07	-260.699	-451.449	-712.147
TCGA-AQ-A04L-01B-21R-A10J-07	475.1579	134.2401	609.3981
TCGA-AC-A23E-01A-11R-A157-07	1617.035	733.9818	2351.017
TCGA-E2-A572-01A-13R-A31O-07	-620.858	156.1652	-464.693
TCGA-E2-A1LK-01A-21R-A14D-07	-1049.31	139.4484	-909.857
TCGA-BH-A0C1-01B-11R-A12D-07	740.5608	849.7702	1590.331
TCGA-A1-A0SH-01A-11R-A084-07	1514.031	400.4648	1914.496
TCGA-LL-A8F5-01A-11R-A36F-07	19.62501	1103.509	1123.134
TCGA-BH-A1FN-01A-11R-A13Q-07	381.4059	112.5716	493.9775
TCGA-OK-A5Q2-01A-11R-A27Q-07	700.0521	1420.35	2120.402
TCGA-EW-A1OZ-01A-11R-A144-07	653.7616	730.5923	1384.354
TCGA-GM-A3NY-01A-11R-A21T-07	152.2355	317.6782	469.9137
TCGA-BH-A0HU-01A-11R-A034-07	-311.013	7.70059	-303.312
TCGA-A8-A06O-01A-11R-A00Z-07	465.5005	473.4211	938.9216
TCGA-GM-A2DL-01A-11R-A18M-07	1192.773	802.6466	1995.42
TCGA-OL-A66L-01A-12R-A31O-07	894.8982	1394.557	2289.455
TCGA-BH-A5IZ-01A-11R-A27Q-07	-385.122	269.5012	-115.621
TCGA-A2-A0T4-01A-31R-A084-07	1221.45	1232.871	2454.321
TCGA-E2-A1IK-01A-11R-A144-07	-151.314	1174.666	1023.351
TCGA-A8-A09T-01A-11R-A00Z-07	567.5435	336.0982	903.6417
TCGA-E2-A1B6-01A-31R-A12P-07	67.83951	2799.006	2866.845
TCGA-AR-A24O-01A-11R-A169-07	1606.662	1175.783	2782.445
TCGA-D8-A1JM-01A-11R-A13Q-07	-1234.56	141.4302	-1093.13
TCGA-A2-A04P-01A-31R-A034-07	380.1929	1285.486	1665.679
TCGA-D8-A1XS-01A-11R-A14M-07	817.4659	352.2442	1169.71
TCGA-C8-A26Y-01A-11R-A16F-07	-668.467	515.8996	-152.567
TCGA-B6-A2IU-01A-32R-A18M-07	-247.622	-322.476	-570.098
TCGA-AQ-A54O-01A-11R-A266-07	-149.626	613.9511	464.3255
TCGA-AC-A62V-01A-11R-A31O-07	247.0104	255.4636	502.474
TCGA-D8-A1JC-01A-11R-A13Q-07	614.4136	660.1372	1274.551
TCGA-B6-A0IB-01A-11R-A034-07	-668.498	-728.912	-1397.41
TCGA-D8-A1XF-01A-11R-A14D-07	-848.746	-399.854	-1248.6
TCGA-E2-A15E-01A-11R-A12D-07	216.3034	-426.175	-209.872
TCGA-E2-A10A-01A-21R-A115-07	212.2516	278.3571	490.6087
TCGA-AR-A0TV-01A-21R-A084-07	-196.123	1271.524	1075.401

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AO-A129-01A-21R-A10J-07	277.0341	1586.026	1863.06
TCGA-AO-A0JE-01A-11R-A056-07	1509.47	1738.304	3247.774
TCGA-E2-A155-01A-11R-A12D-07	-503.67	-583.583	-1087.25
TCGA-A2-A0ET-01A-31R-A034-07	-694.436	440.1853	-254.25
TCGA-BH-A0EE-01A-11R-A034-07	-1087.33	742.2632	-345.069
TCGA-BH-A0B0-01A-21R-A115-07	1176.52	1331.177	2507.698
TCGA-BH-A18R-01A-11R-A12D-07	-200.751	376.6011	175.8498
TCGA-BH-A0AZ-01A-21R-A12P-07	1674.43	726.3399	2400.77
TCGA-GI-A2C8-01A-11R-A16F-07	1515.506	1195.235	2710.741
TCGA-GM-A3XN-01A-12R-A22U-07	1215.533	1125.132	2340.665
TCGA-EW-A1IY-01A-11R-A13Q-07	1213.353	1607.799	2821.153
TCGA-AN-A0XT-01A-11R-A109-07	103.5683	-70.3559	33.21241
TCGA-S3-A6ZF-01A-32R-A32P-07	315.5398	805.0783	1120.618
TCGA-OL-A66I-01A-21R-A29R-07	989.126	2677.521	3666.647
TCGA-E2-A9RU-01A-11R-A41B-07	299.3331	517.2123	816.5454
TCGA-E2-A1B1-01A-21R-A12P-07	1508.528	1626.312	3134.84
TCGA-A2-A04W-01A-31R-A115-07	632.4285	300.521	932.9496
TCGA-E2-A14X-01A-11R-A115-07	88.94032	1284.196	1373.136
TCGA-BH-A0DT-01A-21R-A12D-07	745.2452	823.5593	1568.805
TCGA-B6-A0IC-01A-11R-A034-07	-1539.98	-479.891	-2019.87
TCGA-AR-A0TU-01A-31R-A109-07	-687.236	1206.421	519.1851
TCGA-AR-A2LJ-01A-12R-A19W-07	1060.36	1865.057	2925.417
TCGA-E9-A22A-01A-11R-A157-07	1672.066	1583.114	3255.18
TCGA-E2-A1IN-01A-11R-A13Q-07	1114.23	109.2306	1223.46
TCGA-E2-A15R-01A-11R-A115-07	-506.843	-863.543	-1370.39
TCGA-B6-A0WT-01A-11R-A109-07	666.4318	-56.9762	609.4556
TCGA-AR-A2LM-01A-11R-A180-07	1163.349	550.6785	1714.028
TCGA-A2-A0YK-01A-22R-A109-07	1264.906	2135.919	3400.825
TCGA-AR-A0TZ-01A-12R-A084-07	97.28027	-142.661	-45.3807
TCGA-AN-A0XS-01A-22R-A109-07	1131.336	1196.099	2327.435
TCGA-BH-A42U-01A-12R-A24H-07	712.6805	1407.938	2120.618
TCGA-D8-A1Y2-01A-11R-A157-07	1709.525	2239.124	3948.649
TCGA-A2-A0T1-01A-21R-A084-07	1393.135	2146.91	3540.044
TCGA-A8-A07R-01A-21R-A034-07	-635.922	-159.932	-795.854
TCGA-A2-A0CQ-01A-21R-A034-07	-63.7033	755.6686	691.9652
TCGA-B6-A0X1-01A-11R-A109-07	-602.932	1098.577	495.6451
TCGA-EW-A1PE-01A-11R-A144-07	959.8381	1455.833	2415.671
TCGA-E2-A105-01A-11R-A10J-07	-487.449	-357.277	-844.726
TCGA-E2-A3DX-01A-21R-A213-07	1523.438	1987.279	3510.717
TCGA-LL-A442-01A-11R-A24H-07	-327.71	599.6283	271.9179
TCGA-GM-A2DH-01A-11R-A180-07	-41.9396	1608.152	1566.212
TCGA-BH-A0B7-01A-12R-A115-07	1036.709	1688.354	2725.062

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A1F5-01A-12R-A13Q-07	120.5441	-238.441	-117.897
TCGA-A2-A3XZ-01A-42R-A239-07	92.38918	1883.586	1975.975
TCGA-A7-A0DB-01C-02R-A277-07	1163.98	138.5772	1302.557
TCGA-Z7-A8R6-01A-11R-A41B-07	-98.5055	181.559	83.05344
TCGA-OL-A6VQ-01A-12R-A41B-07	942.2669	670.6117	1612.879
TCGA-BH-A0W5-01A-11R-A109-07	979.7997	2093.378	3073.178
TCGA-AN-A0FJ-01A-11R-A00Z-07	179.1662	6.508184	185.6744
TCGA-BH-A28O-01A-11R-A22K-07	1081.86	548.1975	1630.057
TCGA-AR-A5QP-01A-11R-A28M-07	568.0603	377.7524	945.8126
TCGA-LL-A6FP-01A-11R-A31O-07	-1045.65	-489.328	-1534.97
TCGA-C8-A12X-01A-11R-A115-07	74.77738	357.3881	432.1655
TCGA-B6-A0I6-01A-11R-A034-07	290.093	-80.6433	209.4497
TCGA-AC-A2FE-01A-11R-A19W-07	1122.768	2044.423	3167.192
TCGA-A7-A13F-01A-11R-A12P-07	105.4052	208.7168	314.122
TCGA-AC-A6IX-01A-12R-A32P-07	1144.207	1000.226	2144.433
TCGA-D8-A1JS-01A-11R-A13Q-07	-1014.67	-296.948	-1311.61
TCGA-AC-A6IX-06A-11R-A32P-07	122.5068	1925.096	2047.603
TCGA-B6-A0WZ-01A-11R-A109-07	-2.56319	-275.545	-278.108
TCGA-AR-A0TW-01A-11R-A084-07	161.4651	1208.318	1369.783
TCGA-AO-A0J7-01A-11R-A034-07	-363.883	-482.582	-846.465
TCGA-AN-A0XR-01A-11R-A109-07	-194.177	-301.203	-495.379
TCGA-AQ-A04H-01B-11R-A10J-07	-146.855	-192.393	-339.249
TCGA-A2-A0CW-01A-21R-A115-07	-463.577	543.8826	80.30527
TCGA-E2-A15T-01A-11R-A115-07	-659.168	-568.555	-1227.72
TCGA-E2-A14T-01A-11R-A115-07	-71.8007	309.3122	237.5115
TCGA-AR-A255-01A-11R-A169-07	1169.103	962.3101	2131.413
TCGA-BH-A18H-01A-11R-A12D-07	546.5554	1848.304	2394.859
TCGA-A8-A07P-01A-11R-A00Z-07	583.4555	485.8967	1069.352
TCGA-D8-A1JK-01A-11R-A13Q-07	917.8517	1687.361	2605.213
TCGA-BH-A0DP-01A-21R-A056-07	954.3696	1028.307	1982.676
TCGA-BH-A0H3-01A-11R-A12P-07	1102.593	748.5467	1851.14
TCGA-AR-A0TS-01A-11R-A115-07	635.7285	2182.786	2818.514
TCGA-E9-A22B-01A-11R-A157-07	960.589	503.5976	1464.187
TCGA-A2-A0SU-01A-11R-A084-07	436.689	529.3933	966.0823
TCGA-B6-A0WS-01A-11R-A115-07	911.1775	1450.921	2362.099
TCGA-BH-A0H5-01A-21R-A115-07	822.9571	3071.227	3894.184
TCGA-AR-A251-01A-12R-A169-07	157.8719	262.5329	420.4048
TCGA-BH-A203-01A-12R-A169-07	341.7357	1056.522	1398.258
TCGA-LL-A6FR-01A-12R-A31O-07	401.3968	256.0778	657.4746
TCGA-AR-A0TT-01A-31R-A084-07	1284.974	2562.753	3847.727
TCGA-A2-A3XU-01A-12R-A22U-07	-1136.4	-673.145	-1809.55
TCGA-E9-A1RC-01A-11R-A157-07	-80.1232	-505.341	-585.464

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-OL-A5S0-01A-11R-A28M-07	755.9052	1267.145	2023.05
TCGA-A1-A0SI-01A-11R-A144-07	1336.878	1127.83	2464.707
TCGA-AO-A0JL-01A-11R-A056-07	8.92155	-14.4606	-5.53904
TCGA-C8-A12L-01A-11R-A115-07	-298.575	281.9975	-16.5774
TCGA-A1-A0SD-01A-11R-A115-07	897.9876	448.4575	1346.445
TCGA-BH-A0HL-01A-11R-A10U-07	-1040.79	-1123.32	-2164.11
TCGA-EW-A1P0-01A-11R-A144-07	185.7129	344.6405	530.3534
TCGA-A2-A0T7-01A-21R-A084-07	765.3267	464.0035	1229.33
TCGA-A8-A086-01A-11R-A00Z-07	912.5523	111.7766	1024.329
TCGA-AR-A0TX-01A-11R-A084-07	937.7344	1785.05	2722.785
TCGA-A2-A1FX-01A-11R-A13Q-07	703.9401	621.4645	1325.405
TCGA-A2-A0YL-01A-21R-A109-07	894.5677	730.2851	1624.853
TCGA-AO-A0JB-01A-11R-A32Y-07	298.3392	644.7256	943.0648
TCGA-PE-A5DD-01A-12R-A27Q-07	679.081	884.8451	1563.926
TCGA-A2-A3XX-01A-21R-A239-07	75.7561	777.0301	852.7862
TCGA-A2-A1G1-01A-21R-A13Q-07	945.6563	1441.786	2387.443
TCGA-C8-A12P-01A-11R-A115-07	835.966	634.3436	1470.31
TCGA-A2-A25F-01A-11R-A169-07	2025.063	3330.563	5355.625
TCGA-AR-A1AS-01A-11R-A12P-07	105.9054	103.9979	209.9033
TCGA-BH-A0DX-01A-11R-A115-07	1318.567	1219.951	2538.518
TCGA-BH-A0B3-01A-11R-A056-07	623.6845	1349.342	1973.026
TCGA-A8-A0AB-01A-11R-A034-07	-225.123	-788.358	-1013.48
TCGA-AN-A0FD-01A-11R-A034-07	960.0156	570.4925	1530.508
TCGA-BH-A0E0-01A-11R-A056-07	-690.063	343.1055	-346.957
TCGA-EW-A1P6-01A-11R-A144-07	601.3752	-33.8744	567.5008
TCGA-C8-A1HN-01A-11R-A137-07	25.37219	219.7926	245.1648
TCGA-BH-A1ES-06A-12R-A24H-07	-778.799	-297.407	-1076.21
TCGA-BH-A0DD-01A-31R-A12P-07	-51.5225	61.66404	10.1415
TCGA-AC-A2FK-01A-12R-A180-07	387.5003	624.514	1012.014
TCGA-E9-A227-01A-11R-A157-07	822.152	1377.997	2200.149
TCGA-A7-A4SB-01A-21R-A266-07	66.73792	-412.844	-346.106
TCGA-AN-A0FN-01A-11R-A034-07	2109.483	2164.239	4273.722
TCGA-A2-A0EX-01A-21R-A034-07	995.839	543.7979	1539.637
TCGA-AR-A24M-01A-11R-A169-07	958.1618	290.7916	1248.953
TCGA-A7-A5ZW-01A-12R-A29R-07	1312.818	759.2034	2072.021
TCGA-BH-A0WA-01A-11R-A109-07	187.1007	362.8875	549.9882
TCGA-AR-A24V-01A-21R-A169-07	1544.23	852.8681	2397.098
TCGA-A2-A4S0-01A-21R-A266-07	-513.76	-285.982	-799.742
TCGA-AC-A62Y-01A-11R-A29R-07	634.0315	1285.572	1919.603
TCGA-AR-A1AY-01A-21R-A12P-07	-116.704	6.020758	-110.683
TCGA-E2-A1IF-01A-11R-A144-07	855.2292	547.1291	1402.358
TCGA-C8-A26X-01A-31R-A16F-07	1256.999	2099.988	3356.986

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A0HW-01A-11R-A034-07	-1159.13	-994.707	-2153.83
TCGA-S3-AA10-01A-21R-A41B-07	297.2685	2313.035	2610.303
TCGA-BH-A201-01A-11R-A14M-07	899.2896	1.501701	900.7913
TCGA-A8-A08T-01A-21R-A00Z-07	378.5585	98.64183	477.2003
TCGA-BH-A0HQ-01A-11R-A034-07	609.6994	44.91707	654.6165
TCGA-AO-A0J4-01A-11R-A034-07	211.2342	1423.836	1635.071
TCGA-D8-A1XC-01A-11R-A14D-07	-948.68	-347.426	-1296.11
TCGA-3C-AALJ-01A-31R-A41B-07	508.1145	1144.377	1652.492
TCGA-BH-A209-01A-11R-A157-07	539.8323	2384.329	2924.161
TCGA-BH-A18P-01A-11R-A12D-07	347.1617	329.8238	676.9855
TCGA-AR-A1AW-01A-21R-A12P-07	1179.695	3087.187	4266.882
TCGA-BH-A1FJ-01A-11R-A13Q-07	-338.83	-564.255	-903.085
TCGA-A2-A0CZ-01A-11R-A034-07	1454.083	1187.103	2641.186
TCGA-A2-A0ST-01A-12R-A084-07	653.3262	3028.762	3682.088
TCGA-AC-A4ZE-01A-11R-A41B-07	-94.4751	-39.3839	-133.859
TCGA-AO-A12G-01A-11R-A10J-07	738.5308	421.1004	1159.631
TCGA-E9-A1RA-01A-11R-A14D-07	384.7664	463.0363	847.8027
TCGA-A1-A0SG-01A-11R-A144-07	647.4868	587.9347	1235.422
TCGA-A7-A4SD-01A-11R-A266-07	495.9436	1399.437	1895.381
TCGA-EW-A6SD-01A-12R-A33J-07	420.6123	1230.251	1650.863
TCGA-E2-A14V-01A-11R-A12D-07	-216.415	-285.371	-501.785
TCGA-E9-A226-01A-21R-A157-07	797.9951	-72.8177	725.1774
TCGA-A8-A09B-01A-11R-A00Z-07	427.4128	72.81319	500.226
TCGA-E2-A156-01A-11R-A12D-07	-727.092	-365.934	-1093.03
TCGA-A8-A08H-01A-21R-A00Z-07	1919.957	2566.119	4486.076
TCGA-BH-A0DQ-01A-11R-A084-07	1368.56	548.5919	1917.152
TCGA-AO-A1KT-01A-11R-A13Q-07	768.1988	539.329	1307.528
TCGA-AC-A8OQ-01A-11R-A41B-07	876.3415	1517.855	2394.197
TCGA-B6-A0X0-01A-21R-A115-07	-737.454	-281.364	-1018.82
TCGA-A7-A4SA-01A-11R-A266-07	793.8767	1650.843	2444.719
TCGA-AC-A3W6-01A-12R-A22K-07	1514.684	1669.29	3183.974
TCGA-E2-A158-01A-11R-A12D-07	-1168.01	-401.355	-1569.36
TCGA-AO-A0J5-01A-11R-A034-07	1308.896	304.502	1613.398
TCGA-A8-A06Z-01A-11R-A00Z-07	-639.718	-155.581	-795.299
TCGA-A8-A09E-01A-11R-A00Z-07	-203.949	-239.803	-443.752
TCGA-AR-A2LR-01A-12R-A18M-07	739.3271	-1.55485	737.7722
TCGA-A2-A0D1-01A-11R-A034-07	-295.214	-366.353	-661.567
TCGA-D8-A1XT-01A-11R-A14M-07	1174.823	882.3971	2057.22
TCGA-WT-AB41-01A-11R-A41B-07	249.0038	2264.202	2513.206
TCGA-AO-A0JF-01A-11R-A056-07	1616.348	1199.019	2815.367
TCGA-BH-A1F0-01A-11R-A137-07	1389.358	2497.862	3887.22
TCGA-D8-A1XJ-01A-11R-A14M-07	366.6069	17.66356	384.2705

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-E9-A1RD-01A-11R-A157-07	489.222	204.7444	693.9664
TCGA-EW-A3U0-01A-11R-A22K-07	999.9527	2696.632	3696.585
TCGA-AC-A2QJ-01A-12R-A19W-07	1254.487	1956.35	3210.837
TCGA-E9-A1N4-01A-11R-A14M-07	1022.581	1435.724	2458.305
TCGA-C8-A1HO-01A-11R-A13Q-07	-134.2	-218.157	-352.357
TCGA-A8-A08G-01A-11R-A00Z-07	424.749	503.5932	928.3421
TCGA-GM-A2DD-01A-11R-A180-07	1249.25	2302.757	3552.006
TCGA-C8-A26W-01A-11R-A16F-07	660.1169	1095.1	1755.216
TCGA-LQ-A4E4-01A-11R-A266-07	-147.797	-515.605	-663.403
TCGA-C8-A12W-01A-11R-A115-07	990.2119	733.7251	1723.937
TCGA-BH-A18I-01A-11R-A12D-07	1413.6	1260.241	2673.841
TCGA-AC-A62X-01A-11R-A29R-07	-854.854	-283.179	-1138.03
TCGA-A8-A09Q-01A-11R-A00Z-07	906.2845	1477.412	2383.697
TCGA-BH-A0B6-01A-11R-A19W-07	1033.296	2592.293	3625.589
TCGA-BH-A8FY-01A-11R-A36F-07	-695.887	196.7842	-499.103
TCGA-A7-A26E-01B-06R-A277-07	1148.99	453.3545	1602.345
TCGA-D8-A27E-01A-11R-A16F-07	-14.2502	301.6555	287.4053
TCGA-AC-A3W7-01A-11R-A22K-07	559.2791	187.2385	746.5177
TCGA-E2-A15H-01A-11R-A12D-07	127.5582	-142.524	-14.9655
TCGA-B6-A0I2-01A-11R-A034-07	-332.881	2019.57	1686.689
TCGA-B6-A0IE-01A-11R-A034-07	84.362	-45.8996	38.46237
TCGA-AQ-A1H3-01A-31R-A13Q-07	839.4353	715.7597	1555.195
TCGA-BH-A0BC-01A-22R-A084-07	1112.558	1535.932	2648.489
TCGA-AR-A0U4-01A-11R-A109-07	629.5442	2164.562	2794.106
TCGA-LL-A7SZ-01A-32R-A352-07	544.834	2036.24	2581.074
TCGA-A7-A13D-01A-13R-A277-07	41.17683	-385.465	-344.289
TCGA-GM-A2DK-01A-21R-A180-07	807.7075	944.96	1752.667
TCGA-AN-A0FZ-01A-11R-A034-07	158.5832	-351.501	-192.918
TCGA-AN-A0AT-01A-11R-A034-07	-479.205	509.2958	30.09061
TCGA-BH-A0GZ-01A-11R-A056-07	670.5231	152.734	823.2571
TCGA-A7-A26E-01A-11R-A169-07	905.2366	186.3171	1091.554
TCGA-A7-A5ZV-01A-11R-A28M-07	-365.996	583.3078	217.3116
TCGA-A7-A4SC-01A-12R-A266-07	751.5316	641.9556	1393.487
TCGA-AN-A0FT-01A-11R-A034-07	773.5763	641.4723	1415.049
TCGA-A2-A1G0-01A-11R-A13Q-07	975.729	855.5105	1831.24
TCGA-A8-A08X-01A-21R-A00Z-07	1100.633	1375.379	2476.013
TCGA-A7-A13E-01B-06R-A277-07	1289.183	1509.585	2798.768
TCGA-D8-A1XA-01A-11R-A14D-07	254.5209	245.4157	499.9365
TCGA-D8-A27F-01A-11R-A16F-07	461.0445	181.9832	643.0277
TCGA-BH-A208-01A-11R-A157-07	2068.331	762.1649	2830.496
TCGA-A7-A13H-01A-11R-A22K-07	736.7682	1598.352	2335.12
TCGA-E2-A10E-01A-21R-A10J-07	88.57744	298.4154	386.9929

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A1-A0SO-01A-22R-A084-07	-1129.73	-583.059	-1712.79
TCGA-E9-A22H-01A-11R-A157-07	-85.067	477.937	392.8699
TCGA-D8-A1XZ-01A-11R-A14M-07	682.761	754.1715	1436.933
TCGA-D8-A1XO-01A-11R-A14M-07	1146.792	782.6289	1929.42
TCGA-C8-A1HJ-01A-11R-A13Q-07	-263.133	133.7804	-129.352
TCGA-B6-A0IH-01A-11R-A115-07	963.0788	1045.692	2008.771
TCGA-GM-A2DC-01A-11R-A18M-07	-259.189	5.94529	-253.244
TCGA-A1-A0SB-01A-11R-A144-07	-366.731	-1064.42	-1431.16
TCGA-AO-A03P-01A-11R-A00Z-07	87.27544	-19.8291	67.44632
TCGA-E2-A15L-01A-11R-A12D-07	535.3498	-95.2432	440.1066
TCGA-A2-A25C-01A-11R-A169-07	665.3412	431.3032	1096.644
TCGA-D8-A1X5-01A-11R-A14D-07	784.1902	780.163	1564.353
TCGA-B6-A0RT-01A-21R-A084-07	947.3707	3126.038	4073.409
TCGA-LL-A73Y-01A-11R-A33J-07	725.5302	1136.015	1861.545
TCGA-A2-A0CO-01A-13R-A22K-07	1114.083	1926.567	3040.65
TCGA-A8-A0A7-01A-11R-A00Z-07	1527.586	2753.51	4281.096
TCGA-AO-A03N-01B-11R-A10J-07	410.0172	62.81878	472.8359
TCGA-AR-A0TR-01A-11R-A084-07	-1221.66	-96.8081	-1318.46
TCGA-BH-A1FU-01A-11R-A14D-07	1206.157	1023.288	2229.445
TCGA-C8-A1HM-01A-12R-A137-07	13.77551	2169.838	2183.613
TCGA-AQ-A54N-01A-11R-A266-07	-1433.08	37.30281	-1395.77
TCGA-A2-A0CM-01A-31R-A034-07	681.5476	1728.242	2409.79
TCGA-AR-A2LN-01A-21R-A18M-07	1418.376	909.4092	2327.785
TCGA-BH-A0BD-01A-11R-A034-07	754.0753	1116.901	1870.976
TCGA-A2-A3XT-01A-11R-A22U-07	283.6683	1709.613	1993.281
TCGA-A7-A4SF-01A-11R-A266-07	-137.428	338.0649	200.6367
TCGA-A2-A0T0-01A-22R-A084-07	398.4611	548.1414	946.6025
TCGA-BH-A0AW-01A-11R-A056-07	1136.314	2243.975	3380.289
TCGA-A7-A425-01A-11R-A24H-07	762.0663	971.3269	1733.393
TCGA-D8-A13Z-01A-11R-A115-07	637.8675	1179.137	1817.004
TCGA-LD-A66U-01A-11R-A31O-07	682.2014	1428.589	2110.791
TCGA-A8-A079-01A-21R-A00Z-07	-250.388	263.1151	12.72694
TCGA-EW-A6S9-01A-22R-A33J-07	633.1273	127.0777	760.205
TCGA-BH-A0DO-01B-11R-A12D-07	167.1955	-107.012	60.18328
TCGA-B6-A401-01A-11R-A239-07	459.7458	996.8263	1456.572
TCGA-3C-AAAU-01A-11R-A41B-07	-628.397	-491.601	-1120
TCGA-A7-A2KD-01A-31R-A21T-07	946.0329	1101.539	2047.572
TCGA-AR-A1AX-01A-11R-A12P-07	930.8421	2244.811	3175.654
TCGA-A2-A0YJ-01A-11R-A109-07	-653.773	-338.038	-991.811
TCGA-A8-A08O-01A-21R-A056-07	484.6263	-406.705	77.92116
TCGA-BH-A0B8-01A-21R-A056-07	230.9847	41.26919	272.2539
TCGA-A2-A0D2-01A-21R-A034-07	223.7987	1139.734	1363.533

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-5L-AAT0-01A-12R-A41B-07	1088.982	1299.854	2388.836
TCGA-A2-A0EW-01A-21R-A115-07	1339.088	985.9865	2325.075
TCGA-AR-A0TY-01A-12R-A115-07	-362.611	-203.469	-566.08
TCGA-A2-A3KC-01A-11R-A213-07	1074.267	781.5876	1855.854
TCGA-BH-A0BG-01A-11R-A115-07	116.4027	1594.355	1710.758
TCGA-AR-A24U-01A-11R-A169-07	1268.507	1924.653	3193.16
TCGA-A8-A096-01A-11R-A00Z-07	1407.314	1773.404	3180.718
TCGA-A8-A09G-01A-21R-A00Z-07	162.731	1106.234	1268.965
TCGA-B6-A0WV-01A-11R-A109-07	-704.441	-968.83	-1673.27
TCGA-AR-A1AK-01A-21R-A12P-07	1073.773	1677.362	2751.135
TCGA-A1-A0SF-01A-11R-A144-07	541.2882	927.2839	1468.572
TCGA-BH-A0RX-01A-21R-A084-07	1237.272	2230.181	3467.452
TCGA-E2-A109-01A-11R-A10J-07	275.9186	199.3477	475.2663
TCGA-B6-A0I1-01A-11R-A21T-07	-1148.59	-492.446	-1641.03
TCGA-E9-A22D-01A-11R-A157-07	624.8519	2561.58	3186.432
TCGA-A8-A0AD-01A-11R-A056-07	1008.874	816.7859	1825.66
TCGA-D8-A73W-01A-22R-A352-07	948.6209	1054.234	2002.855
TCGA-E9-A1R7-01A-11R-A14M-07	-304.843	-550.292	-855.136
TCGA-BH-A0W7-01A-11R-A115-07	1191.2	1763.419	2954.619
TCGA-BH-A6R8-01A-21R-A33J-07	-26.8333	934.1934	907.3601
TCGA-AC-A2FB-01A-11R-A17B-07	907.0175	2399.569	3306.587
TCGA-AN-A0XU-01A-11R-A109-07	-610.211	684.122	73.91141
TCGA-E2-A1IH-01A-11R-A13Q-07	1664.305	2010.938	3675.243
TCGA-A7-A6VW-01A-21R-A33J-07	-34.6628	870.6263	835.9635
TCGA-E2-A570-01A-11R-A29R-07	836.755	77.10732	913.8623
TCGA-E2-A56Z-01A-12R-A29R-07	-265.966	-87.0753	-353.041
TCGA-BH-A1EV-01A-11R-A137-07	512.2499	-202.366	309.8842
TCGA-A7-A6VV-01A-22R-A33J-07	935.3193	998.2184	1933.538
TCGA-AN-A0AK-01A-21R-A00Z-07	-410.237	239.2564	-170.981
TCGA-AO-A125-01A-11R-A10J-07	-1419.26	-470.349	-1889.61
TCGA-A8-A0A4-01A-11R-A00Z-07	579.5445	-187.935	391.6093
TCGA-A2-A3XY-01A-11R-A239-07	1089.634	1577.641	2667.275
TCGA-EW-A1OW-01A-21R-A144-07	566.0716	482.024	1048.096
TCGA-A8-A09M-01A-11R-A00Z-07	238.2622	1223.784	1462.046
TCGA-A2-A0EP-01A-52R-A22U-07	1901.568	3083.962	4985.53
TCGA-A7-A426-01A-22R-A24H-07	645.0027	599.1148	1244.118
TCGA-A2-A0CV-01A-31R-A115-07	923.5815	1019.963	1943.545
TCGA-B6-A0RH-01A-21R-A115-07	658.252	298.7831	957.0351
TCGA-GM-A5PX-01A-12R-A28M-07	979.0288	557.6407	1536.669
TCGA-A7-A0CE-01A-11R-A00Z-07	-379.473	-36.0469	-415.52
TCGA-E9-A5FK-01A-11R-A27Q-07	795.9814	2419.77	3215.752
TCGA-OL-A6VR-01A-32R-A33J-07	-864.162	-419.978	-1284.14

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-B6-A0RE-01A-11R-A056-07	-236.415	125.7877	-110.627
TCGA-AO-A03T-01A-21R-A034-07	-252.219	702.8875	450.6681
TCGA-E2-A1L8-01A-11R-A13Q-07	740.505	455.1936	1195.699
TCGA-AR-A24Q-01A-12R-A169-07	825.9828	945.5791	1771.562
TCGA-BH-A0AV-01A-31R-A115-07	1199.454	592.1266	1791.581
TCGA-BH-A0HI-01A-11R-A084-07	713.3177	472.6526	1185.97
TCGA-B6-A0RU-01A-11R-A084-07	225.2625	-152.824	72.43818
TCGA-E9-A1R2-01A-11R-A14D-07	343.9285	458.5513	802.4798
TCGA-BH-A204-01A-11R-A157-07	246.254	-446.021	-199.767
TCGA-AR-A1AJ-01A-21R-A12P-07	1228.745	2640.199	3868.945
TCGA-AN-A0FV-01A-11R-A00Z-07	486.4739	-138.877	347.5971
TCGA-BH-A0BZ-01A-31R-A12P-07	1303.395	1804.42	3107.815
TCGA-E9-A247-01A-11R-A169-07	-288.373	-416.735	-705.108
TCGA-AC-A23C-01A-12R-A169-07	749.6747	884.9533	1634.628
TCGA-A1-A0SN-01A-11R-A144-07	882.1153	1126.598	2008.713
TCGA-A7-A0D9-01A-31R-A056-07	82.8946	-441.306	-358.411
TCGA-AN-A041-01A-11R-A034-07	829.5652	208.9613	1038.526
TCGA-BH-A1FE-06A-11R-A213-07	1182.315	511.6504	1693.965
TCGA-BH-A0B9-01A-11R-A056-07	-678.169	1711.561	1033.392
TCGA-AO-A128-01A-11R-A10J-07	620.8024	3055.547	3676.349
TCGA-AR-A0U0-01A-11R-A109-07	148.7198	1810.755	1959.474
TCGA-C8-A12Q-01A-11R-A115-07	741.4946	777.8372	1519.332
TCGA-S3-AA0Z-01A-11R-A41B-07	-191.799	1117.207	925.4082
TCGA-BH-A1F8-01A-11R-A13Q-07	317.1473	109.4608	426.6081
TCGA-AC-A5XU-01A-11R-A28M-07	531.805	14.44495	546.25
TCGA-AC-A2FO-01A-11R-A180-07	1136.151	1659.959	2796.11
TCGA-A7-A0DB-01A-11R-A00Z-07	871.518	755.4778	1626.996
TCGA-AR-A0TP-01A-11R-A084-07	-617.339	-654.418	-1271.76
TCGA-AO-A03O-01A-11R-A00Z-07	-162.289	906.545	744.2564
TCGA-OL-A66H-01A-11R-A29R-07	593.698	1401.583	1995.281
TCGA-D8-A27R-01A-11R-A16F-07	652.4078	905.3357	1557.743
TCGA-A2-A4RW-01A-21R-A266-07	661.9914	552.3733	1214.365
TCGA-AN-A0G0-01A-11R-A034-07	-91.9706	99.91624	7.945662
TCGA-C8-A134-01A-11R-A115-07	-64.9455	1164.388	1099.443
TCGA-A2-A25A-01A-12R-A16F-07	1371.669	1129.97	2501.639
TCGA-A1-A0SP-01A-11R-A084-07	-27.631	1073.946	1046.315
TCGA-EW-A1OY-01A-11R-A144-07	-114.003	219.8998	105.8971
TCGA-A8-A081-01A-11R-A00Z-07	-344.492	1203.221	858.7284
TCGA-D8-A73U-01A-11R-A33J-07	1595.865	2985.229	4581.094
TCGA-BH-A0BL-01A-11R-A115-07	1486.025	1752.169	3238.193
TCGA-AR-A24P-01A-11R-A169-07	920.2539	351.9361	1272.19
TCGA-D8-A140-01A-11R-A115-07	321.6286	704.2887	1025.917

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-D8-A27L-01A-11R-A16F-07	1162.418	979.6747	2142.093
TCGA-EW-A1PC-01B-11R-A21T-07	-354.512	-346.377	-700.888
TCGA-BH-A18M-01A-11R-A12D-07	1036.823	528.6924	1565.515
TCGA-AR-A5QM-01A-11R-A27Q-07	932.14	1101.055	2033.195
TCGA-E9-A1RI-01A-11R-A169-07	1289.876	449.4842	1739.361
TCGA-A8-A08R-01A-11R-A034-07	569.6026	1474.146	2043.749
TCGA-AN-A0FS-01A-11R-A034-07	881.1838	-16.4002	864.7836
TCGA-BH-A8G0-01A-11R-A352-07	1337.062	1801.328	3138.391
TCGA-C8-A12O-01A-11R-A115-07	1182.415	859.7651	2042.18
TCGA-E9-A1R4-01A-21R-A14D-07	597.5154	1703.144	2300.66
TCGA-AN-A0AJ-01A-11R-A00Z-07	366.2583	1407.873	1774.131
TCGA-BH-A0HY-01A-11R-A056-07	320.8468	-309.316	11.53074
TCGA-AC-A5XS-01A-11R-A29R-07	812.9374	1636.74	2449.678
TCGA-BH-A0AU-01A-11R-A12P-07	688.9994	547.443	1236.442
TCGA-EW-A1P1-01A-31R-A14D-07	1645.574	1519.397	3164.971
TCGA-E9-A22E-01A-11R-A157-07	1910.63	1205.026	3115.656
TCGA-BH-A0E2-01A-11R-A056-07	728.0152	366.7327	1094.748
TCGA-OL-A5RV-01A-12R-A28M-07	45.88011	-67.9637	-22.0836
TCGA-E9-A245-01A-22R-A16F-07	-216.921	-271.127	-488.048
TCGA-D8-A1Y3-01A-11R-A157-07	161.3131	1254.449	1415.762
TCGA-A8-A07L-01A-11R-A00Z-07	219.1686	-334.858	-115.689
TCGA-AC-A23H-01A-11R-A157-07	206.5002	-177.458	29.04187
TCGA-BH-A0HX-01A-21R-A056-07	651.7482	364.9702	1016.718
TCGA-AC-A3QP-01A-11R-A22U-07	1072.898	1334.68	2407.578
TCGA-S3-AA12-01A-11R-A41B-07	-407.213	-283.687	-690.9
TCGA-E2-A1IO-01A-11R-A144-07	1318.252	940.1925	2258.445
TCGA-E9-A22G-01A-11R-A157-07	-947.017	123.9563	-823.06
TCGA-E9-A1NA-01A-11R-A144-07	945.5398	1009.572	1955.111
TCGA-B6-A0IA-01A-11R-A034-07	-841.613	-299.725	-1141.34
TCGA-AC-A3TN-01A-11R-A22K-07	91.51009	144.2376	235.7477
TCGA-AO-A03M-01B-11R-A10J-07	324.9524	1533.292	1858.245
TCGA-E2-A15C-01A-31R-A12D-07	650.4034	267.952	918.3554
TCGA-AR-A0U3-01A-11R-A109-07	-496.348	100.8246	-395.524
TCGA-EW-A1PB-01A-11R-A144-07	147.0918	2455.77	2602.862
TCGA-OL-A66K-01A-11R-A29R-07	621.3392	26.96036	648.2996
TCGA-EW-A1J3-01A-11R-A13Q-07	179.2221	170.4062	349.6283
TCGA-A8-A076-01A-21R-A00Z-07	881.7204	611.911	1493.631
TCGA-B6-A0RQ-01A-11R-A115-07	-110.535	-357.827	-468.362
TCGA-C8-A12U-01A-11R-A115-07	-789.09	895.9795	106.8895
TCGA-A2-A0EQ-01A-11R-A034-07	381.0849	2310.012	2691.097
TCGA-BH-A1FB-01A-11R-A13Q-07	1351.213	1769.579	3120.792
TCGA-BH-A2L8-01A-11R-A18M-07	962.979	2076.272	3039.251

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A8FZ-01A-11R-A352-07	1103.02	1784.833	2887.853
TCGA-A8-A06R-01A-11R-A00Z-07	1073.294	1063.906	2137.2
TCGA-BH-A18Q-01A-12R-A12D-07	-24.125	796.8441	772.7191
TCGA-E9-A248-01A-11R-A169-07	413.0591	2069.897	2482.956
TCGA-A8-A0A6-01A-12R-A056-07	724.036	1823.306	2547.342
TCGA-LL-A7T0-01A-31R-A352-07	8.281051	710.4948	718.7758
TCGA-EW-A1P4-01A-21R-A144-07	151.469	1573.023	1724.492
TCGA-C8-A3M8-01A-11R-A213-07	180.6251	-218.361	-37.7361
TCGA-A2-A0YE-01A-11R-A109-07	-27.6124	-234.458	-262.07
TCGA-EW-A1P8-01A-11R-A144-07	260.4594	1396.026	1656.486
TCGA-E2-A15A-06A-11R-A12D-07	342.8426	1728.13	2070.972
TCGA-3C-AALK-01A-11R-A41B-07	921.7338	593.955	1515.689
TCGA-OL-A5D7-01A-11R-A27Q-07	-432.471	1779.625	1347.154
TCGA-XX-A89A-01A-11R-A36F-07	1764.481	1737.498	3501.979
TCGA-GM-A2DO-01A-11R-A18M-07	197.35	3073.61	3270.96
TCGA-E2-A14O-01A-31R-A115-07	-123.272	157.2245	33.95272
TCGA-D8-A27P-01A-11R-A16F-07	187.8482	-224.496	-36.6476
TCGA-E2-A1AZ-01A-11R-A12P-07	974.8927	1511.382	2486.275
TCGA-LL-A5YL-01A-12R-A29R-07	466.2993	1192.41	1658.709
TCGA-A2-A1G6-01A-11R-A13Q-07	550.8594	604.3526	1155.212
TCGA-BH-A0EI-01A-11R-A115-07	868.1544	-210.159	657.9953
TCGA-A2-A0T6-01A-11R-A084-07	1670.695	1417.19	3087.885
TCGA-A2-A1FV-01A-11R-A13Q-07	122.5499	-608.74	-486.19
TCGA-E2-A2P5-01A-11R-A19W-07	375.3251	274.5978	649.9229
TCGA-E9-A6HE-01A-11R-A31O-07	718.9059	902.9974	1621.903
TCGA-E2-A108-01A-13R-A10J-07	1942.987	2704.442	4647.43
TCGA-LD-A7W6-01A-81R-A352-07	243.0749	439.3715	682.4464
TCGA-BH-A1ES-01A-11R-A137-07	419.5377	-609.581	-190.043
TCGA-D8-A1JU-01A-11R-A13Q-07	1794.007	1067.397	2861.404
TCGA-E2-A14Z-01A-11R-A115-07	746.0742	1824.092	2570.166
TCGA-A2-A0ER-01A-21R-A034-07	-168.46	171.1949	2.7351
TCGA-OL-A6VO-01A-12R-A33J-07	-473.337	503.6326	30.29553
TCGA-AR-A24K-01A-11R-A169-07	-151.45	-565.872	-717.322
TCGA-B6-A0X5-01A-21R-A109-07	-398.761	-294.71	-693.471
TCGA-A2-A25E-01A-11R-A169-07	149.6723	-12.8447	136.8276
TCGA-B6-A0IM-01A-11R-A034-07	373.5572	-45.2946	328.2626
TCGA-LL-A740-01A-21R-A32P-07	1044.732	683.1956	1727.928
TCGA-LL-A5YM-01A-11R-A28M-07	123.3167	544.0642	667.3809
TCGA-JL-A3YX-01A-11R-A22U-07	-56.2291	-282.849	-339.078
TCGA-D8-A1JA-01A-11R-A13Q-07	758.6791	299.531	1058.21
TCGA-A8-A07S-01A-11R-A034-07	199.5905	215.3809	414.9714
TCGA-A8-A090-01A-11R-A00Z-07	690.7509	822.3706	1513.121

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A8-A09D-01A-11R-A00Z-07	1498.793	1021.963	2520.756
TCGA-BH-A0AY-01A-21R-A00Z-07	1375.534	1153.168	2528.702
TCGA-B6-A0I5-01A-11R-A034-07	334.4097	698.0978	1032.508
TCGA-AO-A124-01A-11R-A10J-07	-746.365	177.4029	-568.962
TCGA-OL-A97C-01A-32R-A41B-07	490.6302	724.4907	1215.121
TCGA-E9-A249-01A-11R-A169-07	-184.717	130.8408	-53.8763
TCGA-E2-A1LE-01A-12R-A19W-07	1226.15	1513.458	2739.608
TCGA-AR-A2LQ-01A-22R-A18M-07	1713.118	782.3614	2495.479
TCGA-A8-A08L-01A-11R-A00Z-07	157.7085	1116.836	1274.545
TCGA-AR-A24Z-01A-11R-A169-07	-112.733	100.5104	-12.2227
TCGA-AR-A24N-01A-11R-A169-07	554.0422	157.6162	711.6584
TCGA-A8-A07U-01A-11R-A034-07	849.9227	2362.488	3212.411
TCGA-B6-A0RP-01A-21R-A084-07	970.8318	742.3626	1713.194
TCGA-BH-A0BW-01A-11R-A115-07	288.3453	1849.017	2137.362
TCGA-A2-A0YT-01A-11R-A109-07	-162.411	152.3484	-10.0631
TCGA-PL-A8LY-01A-11R-A41B-07	-600.819	275.114	-325.705
TCGA-AC-A3OD-01B-06R-A22O-07	1073.924	2171.455	3245.379
TCGA-BH-A0BF-01A-21R-A12P-07	1769.559	2374.354	4143.913
TCGA-A8-A0A1-01A-11R-A00Z-07	1133.912	1757.1	2891.012
TCGA-5L-AAT1-01A-12R-A41B-07	985.8195	2050.83	3036.649
TCGA-A8-A092-01A-11R-A00Z-07	207.4417	178.9112	386.3528
TCGA-A2-A0CL-01A-11R-A115-07	1377.688	2810.275	4187.963
TCGA-GM-A2DI-01A-31R-A18M-07	1392.171	2664.815	4056.986
TCGA-AN-A0XV-01A-11R-A109-07	793.6113	592.4079	1386.019
TCGA-HN-A2NL-01A-11R-A18M-07	-825.541	616.8804	-208.66
TCGA-E2-A15J-01A-11R-A12P-07	-294.615	-172.522	-467.137
TCGA-E2-A106-01A-11R-A10J-07	-540.817	-574.854	-1115.67
TCGA-D8-A1JG-01B-11R-A13Q-07	865.7544	1347.324	2213.079
TCGA-E9-A1R3-01A-31R-A14M-07	948.7981	995.9155	1944.714
TCGA-BH-A18U-01A-21R-A12D-07	499.5201	516.3812	1015.901
TCGA-E2-A1L9-01A-11R-A13Q-07	1416.114	914.9735	2331.087
TCGA-A7-A3J0-01A-11R-A213-07	-651.251	421.6714	-229.58
TCGA-BH-A0E6-01A-11R-A034-07	-16.7246	875.1611	858.4366
TCGA-AN-A0FX-01A-11R-A034-07	279.9482	-179.387	100.5613
TCGA-A2-A1G4-01A-11R-A13Q-07	-352.643	175.6484	-176.994
TCGA-AO-A0J6-01A-11R-A034-07	-684.298	1313.266	628.9678
TCGA-W8-A86G-01A-21R-A36F-07	215.7305	-445.943	-230.213
TCGA-AC-A2BM-01A-11R-A21T-07	103.0187	761.9579	864.9767
TCGA-C8-A3M7-01A-12R-A21T-07	752.6987	551.0641	1303.763
TCGA-D8-A145-01A-11R-A115-07	877.1933	547.6363	1424.83
TCGA-3C-AALI-01A-11R-A41B-07	234.6229	1145.596	1380.219
TCGA-EW-A1IZ-01A-11R-A13Q-07	252.1322	2435.123	2687.255

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-A2-A0EN-01A-13R-A084-07	1540.088	2151.644	3691.732
TCGA-HN-A2OB-01A-21R-A27Q-07	1250.846	280.1424	1530.988
TCGA-AN-A0FY-01A-11R-A034-07	462.3564	-27.9313	434.425
TCGA-AO-A1KO-01A-31R-A13Q-07	281.6827	46.21256	327.8953
TCGA-C8-A1HL-01A-11R-A137-07	778.2094	396.0358	1174.245
TCGA-BH-A18S-01A-11R-A12D-07	-324.243	108.8449	-215.398
TCGA-C8-A27A-01A-11R-A169-07	-493.582	-424.128	-917.71
TCGA-AN-A04D-01A-21R-A034-07	-1102.63	-778.19	-1880.82
TCGA-BH-A42T-01A-11R-A24H-07	394.0191	812.0634	1206.083
TCGA-E9-A1RF-01A-11R-A157-07	1032.784	1341.461	2374.246
TCGA-BH-A18N-01A-11R-A12D-07	32.59187	-62.5523	-29.9604
TCGA-AN-A0FF-01A-11R-A034-07	604.7918	977.7231	1582.515
TCGA-C8-A12M-01A-11R-A115-07	-334.66	-8.58491	-343.244
TCGA-E2-A15I-01A-21R-A137-07	382.2514	911.8453	1294.097
TCGA-D8-A1XG-01A-11R-A14D-07	-34.7014	-104.309	-139.01
TCGA-C8-A1HI-01A-11R-A137-07	292.5962	73.74994	366.3461
TCGA-EW-A2FV-01A-11R-A17B-07	649.438	1104.496	1753.934
TCGA-B6-A0RS-01A-11R-A084-07	382.2575	1115.728	1497.985
TCGA-BH-A0B4-01A-11R-A00Z-07	1132.78	815.4244	1948.204
TCGA-C8-A278-01A-11R-A169-07	1217.648	1723.384	2941.031
TCGA-A2-A4RY-01A-31R-A266-07	808.5705	797.0441	1605.615
TCGA-A8-A08S-01A-11R-A034-07	84.80927	223.0109	307.8202
TCGA-AR-A2LL-01A-11R-A180-07	280.5886	721.8692	1002.458
TCGA-A2-A04X-01A-21R-A034-07	338.2693	1719.398	2057.667
TCGA-A8-A09A-01A-11R-A00Z-07	898.1088	537.3706	1435.479
TCGA-D8-A142-01A-11R-A115-07	983.989	818.03	1802.019
TCGA-EW-A2FW-01A-11R-A17B-07	121.8171	-162.716	-40.8986
TCGA-AC-A23G-01A-11R-A213-07	1745.625	1097.803	2843.428
TCGA-E2-A1LL-01A-11R-A144-07	-494.739	-145.237	-639.976
TCGA-EW-A6SA-01A-21R-A32P-07	-879.365	-997.372	-1876.74
TCGA-E2-A1IL-01A-11R-A14D-07	605.5253	-185.318	420.2069
TCGA-D8-A1XB-01A-11R-A14D-07	908.4237	-46.1767	862.247
TCGA-AC-A3TM-01A-11R-A22K-07	200.6479	886.3429	1086.991
TCGA-AR-A1AI-01A-11R-A12P-07	-270.289	1803.233	1532.944
TCGA-AC-A8OS-01A-12R-A41B-07	1106.788	1095.774	2202.562
TCGA-OL-A5RX-01A-11R-A28M-07	272.9918	567.7486	840.7404
TCGA-AO-A0J3-01A-11R-A034-07	-951.251	-408.069	-1359.32
TCGA-E9-A295-01A-11R-A16F-07	551.6853	253.8996	805.5849
TCGA-LL-A73Z-01A-11R-A32P-07	923.4781	1368.9	2292.378
TCGA-AR-A250-01A-31R-A169-07	1279.446	953.7778	2233.224
TCGA-A2-A0YI-01A-31R-A10J-07	1132.268	1787.522	2919.79
TCGA-BH-A0DH-01A-11R-A084-07	191.543	479.8495	671.3925

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-D8-A27W-01A-11R-A16F-07	537.6674	565.9388	1103.606
TCGA-AR-A1AN-01A-11R-A12P-07	1136.585	627.1317	1763.717
TCGA-B6-A3ZX-01A-11R-A239-07	198.6427	2502.26	2700.902
TCGA-AR-A1AQ-01A-11R-A12P-07	485.5663	1988.832	2474.399
TCGA-E9-A1NF-01A-11R-A14D-07	1774.905	870.1714	2645.076
TCGA-A7-A0DB-01A-11R-A277-07	1195.261	717.4106	1912.672
TCGA-BH-A0EA-01A-11R-A115-07	885.0061	503.2001	1388.206
TCGA-EW-A1PF-01A-11R-A144-07	1099.357	715.7033	1815.061
TCGA-E9-A3Q9-01A-11R-A21T-07	418.1703	1091.197	1509.368
TCGA-D8-A27K-01A-11R-A16F-07	638.3432	838.2782	1476.621
TCGA-OL-A5RY-01A-21R-A28M-07	1333.745	2388.954	3722.7
TCGA-LD-A74U-01A-13R-A33J-07	1144.366	1060.71	2205.075
TCGA-B6-A408-01A-12R-A24H-07	710.4715	1367.594	2078.066
TCGA-AR-A24R-01A-11R-A169-07	345.4299	663.9052	1009.335
TCGA-EW-A1P5-01A-11R-A144-07	178.3584	994.0958	1172.454
TCGA-GM-A2DB-01A-31R-A18M-07	-430.024	1055.994	625.9693
TCGA-A8-A07C-01A-11R-A034-07	67.34505	845.39	912.7351
TCGA-AR-A1AM-01A-41R-A22K-07	687.7306	706.481	1394.212
TCGA-BH-A0DZ-01A-11R-A00Z-07	1292.436	1094.562	2386.997
TCGA-A2-A259-01A-11R-A16F-07	804.241	957.7424	1761.983
TCGA-A7-A56D-01A-11R-A27Q-07	826.9756	1065.11	1892.086
TCGA-AR-A1AH-01A-11R-A12D-07	-446.507	-379.378	-825.885
TCGA-A8-A09I-01A-22R-A034-07	547.9132	1095.846	1643.76
TCGA-BH-A1FD-01A-11R-A13Q-07	577.8286	295.1973	873.0259
TCGA-AO-A0JD-01A-11R-A056-07	-710.404	485.4039	-225
TCGA-GM-A2DA-01A-11R-A18M-07	1035.633	1597.37	2633.004
TCGA-EW-A1J2-01A-21R-A13Q-07	1236.721	1024.335	2261.056
TCGA-D8-A1XY-01A-11R-A14M-07	1028.686	181.4297	1210.115
TCGA-BH-A1EN-01A-11R-A13Q-07	347.8897	-102.727	245.1629
TCGA-C8-A26Z-01A-11R-A16F-07	134.3686	-395.78	-261.412
TCGA-D8-A1JB-01A-11R-A13Q-07	744.6621	1911.992	2656.654
TCGA-BH-A0DS-01A-11R-A056-07	824.4646	1096.059	1920.523
TCGA-PL-A8LX-01A-11R-A41B-07	-344.266	400.3515	56.08547
TCGA-A2-A0T3-01A-21R-A115-07	-264.529	-436.67	-701.199
TCGA-BH-A1ET-01A-11R-A137-07	655.5713	401.4169	1056.988
TCGA-AN-A03Y-01A-21R-A00Z-07	51.04332	529.9174	580.9608
TCGA-A7-A3IY-01A-21R-A21T-07	984.5914	1380.34	2364.932
TCGA-BH-A18F-01A-11R-A12D-07	975.4634	849.9154	1825.379
TCGA-AO-A03U-01B-21R-A10J-07	1108.084	1986.15	3094.234
TCGA-A8-A07O-01A-11R-A00Z-07	-233.832	767.0534	533.2213
TCGA-LL-A6FQ-01A-11R-A31O-07	17.30215	619.5616	636.8638
TCGA-E9-A24A-01A-11R-A169-07	1151.486	1165.733	2317.219

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-AC-A5EH-01A-11R-A28M-07	1015.118	872.7366	1887.854
TCGA-AR-A24H-01A-11R-A169-07	-178.575	637.8663	459.2911
TCGA-A8-A099-01A-11R-A00Z-07	298.1725	279.8523	578.0248
TCGA-D8-A27T-01A-11R-A16F-07	1278.63	1204.82	2483.451
TCGA-BH-A0H6-01A-21R-A056-07	659.5788	-151.338	508.2404
TCGA-A7-A0DC-01A-11R-A00Z-07	-946.213	-1011.82	-1958.03
TCGA-OL-A5D8-01A-11R-A27Q-07	26.29124	462.7266	489.0179
TCGA-A2-A0CR-01A-11R-A22K-07	1054.394	2747.267	3801.662
TCGA-EW-A1PA-01A-11R-A144-07	291.735	344.5474	636.2824
TCGA-B6-A0RI-01A-11R-A056-07	779.4208	334.4367	1113.858
TCGA-D8-A1Y0-01A-11R-A14M-07	989.6782	1308.813	2298.491
TCGA-B6-A0RO-01A-22R-A084-07	-423.048	-150.303	-573.351
TCGA-A2-A4S1-01A-21R-A266-07	1494.513	1834.707	3329.22
TCGA-AC-A3YI-01A-21R-A239-07	1170.917	809.808	1980.725
TCGA-A7-A13D-01A-13R-A12P-07	-39.1143	-223.312	-262.427
TCGA-D8-A27V-01A-12R-A17B-07	703.8121	75.96051	779.7726
TCGA-A2-A0D4-01A-11R-A00Z-07	-381.759	-506.206	-887.965
TCGA-B6-A0IG-01A-11R-A034-07	-98.7163	0.791701	-97.9246
TCGA-BH-A0B1-01A-12R-A056-07	627.4291	200.1607	827.5898
TCGA-AC-A7VB-01A-11R-A352-07	-918.916	-863.341	-1782.26
TCGA-A7-A26J-01B-02R-A277-07	1098.731	955.7106	2054.442
TCGA-E2-A10B-01A-11R-A10J-07	597.4535	447.0144	1044.468
TCGA-D8-A141-01A-11R-A115-07	1619.495	2180.746	3800.241
TCGA-C8-A1HK-01A-21R-A13Q-07	-280.329	135.9724	-144.356
TCGA-D8-A3Z5-01A-41R-A24H-07	-66.1206	-27.9168	-94.0374
TCGA-EW-A423-01A-11R-A24H-07	-144.906	997.8827	852.9764
TCGA-AR-A2LE-01A-11R-A180-07	158.2877	211.6336	369.9213
TCGA-A7-A4SE-01A-11R-A266-07	680.8561	337.51	1018.366
TCGA-AO-A12F-01A-11R-A115-07	494.8098	-125.777	369.033
TCGA-A7-A26J-01A-11R-A169-07	753.8377	344.939	1098.777
TCGA-A8-A06P-01A-11R-A00Z-07	1296.46	510.6509	1807.111
TCGA-AC-A3YJ-01A-11R-A22U-07	-229.558	804.0604	574.5026
TCGA-A2-A0EO-01A-11R-A034-07	1277.463	972.183	2249.646
TCGA-E2-A14Y-01A-21R-A12D-07	-578.929	-38.1955	-617.124
TCGA-E2-A152-01A-11R-A12D-07	1006.459	477.3252	1483.784
TCGA-BH-A5J0-01A-11R-A27Q-07	1159.633	1870.244	3029.878
TCGA-D8-A1JP-01A-11R-A13Q-07	1227.168	873.9578	2101.126
TCGA-AO-A03L-01A-41R-A056-07	767.0852	718.1652	1485.25
TCGA-AN-A0XW-01A-11R-A109-07	1579.78	1803.921	3383.701
TCGA-E9-A1QZ-01A-21R-A169-07	820.7735	1840.071	2660.844
TCGA-A8-A097-01A-11R-A034-07	919.9518	666.413	1586.365
TCGA-AR-A1AV-01A-21R-A12P-07	276.5305	40.62765	317.1582

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-BH-A18K-01A-11R-A12D-07	713.7209	205.7447	919.4656
TCGA-AQ-A04J-01A-02R-A034-07	978.9645	1897.641	2876.606
TCGA-OL-A5DA-01A-11R-A27Q-07	38.46988	347.3105	385.7804
TCGA-OL-A5D6-01A-21R-A27Q-07	1012.512	616.9078	1629.42
TCGA-B6-A0IO-01A-11R-A034-07	-525.476	248.7673	-276.709
TCGA-BH-A0H7-01A-13R-A056-07	822.6424	238.4276	1061.07
TCGA-E9-A1N9-01A-11R-A14D-07	373.5142	256.1196	629.6338
TCGA-AN-A0AM-01A-11R-A034-07	331.1679	921.8502	1253.018
TCGA-C8-A27B-01A-11R-A169-07	-132.478	1589.933	1457.455
TCGA-LL-A5YO-01A-21R-A28M-07	738.741	2816.414	3555.155
TCGA-A2-A25B-01A-11R-A169-07	666.632	636.7454	1303.377
TCGA-E9-A1NC-01A-21R-A26B-07	795.3441	1738.732	2534.076
TCGA-E2-A1LI-01A-12R-A157-07	-402.894	963.5521	560.6581
TCGA-E9-A1RE-01A-11R-A157-07	-105.176	-393.775	-498.952
TCGA-D8-A1JT-01A-31R-A13Q-07	-327.704	187.5496	-140.154
TCGA-A8-A06U-01A-11R-A00Z-07	-62.6942	632.5762	569.882
TCGA-C8-A8HR-01A-11R-A36F-07	1415.377	1560.755	2976.132
TCGA-A7-A0CG-01A-12R-A056-07	1229.529	1471.015	2700.545
TCGA-A2-A0D0-01A-11R-A00Z-07	-894.965	947.7314	52.76632
TCGA-D8-A13Y-01A-11R-A115-07	-934.393	-977.274	-1911.67
TCGA-B6-A0I9-01A-11R-A034-07	-369.575	299.1114	-70.4637
TCGA-A2-A04T-01A-21R-A034-07	-265.108	1169.003	903.8949
TCGA-E2-A150-01A-11R-A12D-07	484.1966	1046.641	1530.837
TCGA-AN-A0AR-01A-11R-A00Z-07	-776.076	-373.633	-1149.71
TCGA-C8-A8HQ-01A-11R-A36F-07	1021.922	1136.573	2158.495
TCGA-A8-A094-01A-11R-A00Z-07	735.357	1575.801	2311.158
TCGA-S3-AA15-01A-11R-A41B-07	1370.527	2492.983	3863.51
TCGA-B6-A1KC-01B-11R-A157-07	-282.12	-297.321	-579.441
TCGA-A2-A0YM-01A-11R-A109-07	170.0203	1081.479	1251.499
TCGA-AO-A0JM-01A-21R-A056-07	771.784	492.6522	1264.436
TCGA-AR-A5QQ-01A-11R-A28M-07	499.2073	2213.566	2712.773
TCGA-A8-A08J-01A-11R-A00Z-07	726.563	486.7599	1213.323
TCGA-E2-A1B0-01A-11R-A12P-07	648.7097	807.3876	1456.097
TCGA-S3-AA11-01A-31R-A41B-07	-399.49	-537.685	-937.175
TCGA-BH-A0DE-01A-11R-A115-07	1125.441	1030.508	2155.949
TCGA-BH-A1FM-01A-11R-A13Q-07	803.2553	31.96023	835.2155
TCGA-A8-A09W-01A-11R-A00Z-07	762.6519	573.9067	1336.559
TCGA-D8-A1XW-01A-11R-A14M-07	1144.116	1493.856	2637.972
TCGA-GM-A2D9-01A-11R-A18M-07	543.0226	646.3363	1189.359
TCGA-E2-A15D-01A-11R-A115-07	520.3371	362.2321	882.5692
TCGA-A7-A0DA-01A-31R-A115-07	422.7975	-31.9549	390.8426
TCGA-E2-A576-01A-11R-A31O-07	-46.0453	247.9733	201.928

Table S1 *(continued)*

Table S1 *(continued)*

ID	Stromal Score	Immune Score	ESTIMATE Score
TCGA-PL-A8LV-01A-21R-A41B-07	-38.1724	1031.531	993.3585
TCGA-A2-A4RX-01A-11R-A266-07	969.7661	892.3097	1862.076
TCGA-E9-A243-01A-21R-A169-07	1341.147	2789.554	4130.701
TCGA-A8-A07E-01A-11R-A034-07	1378.974	888.2013	2267.175
TCGA-E9-A228-01A-31R-A157-07	20.21764	244.6108	264.8284
TCGA-A2-A4S2-01A-12R-A266-07	620.1788	1369.798	1989.977
TCGA-A7-A3J1-01A-11R-A213-07	902.851	1746.58	2649.431
TCGA-EW-A1PH-01A-11R-A14M-07	-306.027	225.041	-80.9857
TCGA-A2-A04U-01A-11R-A115-07	-179.333	-235.656	-414.99
TCGA-C8-A132-01A-31R-A115-07	1089.54	1506.795	2596.335
TCGA-BH-A18T-01A-11R-A12D-07	-352.035	325.0774	-26.9576
TCGA-E2-A1L7-01A-11R-A144-07	346.2563	1446.559	1792.815
TCGA-A7-A26J-01A-11R-A277-07	673.7085	339.6911	1013.4
TCGA-BH-A0BA-01A-11R-A056-07	511.7026	490.2181	1001.921
TCGA-E9-A5FL-01A-11R-A27Q-07	318.9038	598.3258	917.2296
TCGA-BH-A18V-01A-11R-A12D-07	715.345	1291.534	2006.879
TCGA-AN-A0AL-01A-11R-A00Z-07	853.5801	1251.918	2105.498
TCGA-A2-A0EY-01A-11R-A034-07	344.6446	882.5369	1227.181

Table S2 DEGs based upon stromal scores

Gene	conMean	treatMean	logFC	P value	fdr
KCNH6	0.244936	0.051984	-2.23626	1.81E-05	3.29E-05
AEBP1	88.56828	222.7741	1.330719	8.50E-98	1.01E-95
ISM1	2.815568	5.892012	1.065334	8.52E-62	2.30E-60
SEC14L4	0.209085	0.099951	-1.0648	0.010777851	0.014627391
MMP3	4.128772	11.50347	1.478284	4.18E-58	9.65E-57
LRP1	11.24731	28.57202	1.345024	1.47E-122	9.53E-120
SCARF2	2.557794	5.516618	1.108884	4.77E-68	1.63E-66
CPA3	6.46058	14.57038	1.173303	1.31E-47	2.03E-46
KIF26B	1.782467	3.583796	1.007613	6.26E-66	1.94E-64
ANTXRL	0.190947	0.058239	-1.71311	0.016490042	0.021892867
SCARA5	0.384015	1.273912	1.730031	8.32E-31	6.87E-30
PCSK1N	5.329104	1.924885	-1.46912	0.005616738	0.007881505
CCL19	18.43253	39.47377	1.09864	1.07E-22	6.24E-22
MYOCD	0.050427	0.146077	1.534467	2.60E-35	2.53E-34
DNASE1L3	0.273994	0.564663	1.043247	1.36E-29	1.07E-28
TLR4	2.209909	5.009064	1.180554	3.35E-99	4.34E-97
MEDAG	1.937366	5.408507	1.481134	2.80E-83	1.73E-81
CH25H	0.958164	2.315362	1.272893	3.39E-56	7.35E-55
CXCL12	11.30704	29.66187	1.391388	8.30E-112	2.17E-109
LRRTM2	0.106684	0.254597	1.254875	8.17E-43	1.04E-41
C1QTNF7	0.225428	0.736774	1.708555	2.60E-62	7.12E-61
ADIPOQ	2.473261	10.4573	2.080023	7.92E-26	5.32E-25
CELF4	0.484387	0.118051	-2.03674	2.75E-08	6.38E-08
KLK3	0.172468	0.571526	1.72849	1.03E-20	5.38E-20
GLT8D2	3.317327	9.165257	1.466154	2.35E-123	1.60E-120
GIMAP8	2.221345	4.45722	1.00471	7.28E-68	2.45E-66
CTSE	0.160688	0.457464	1.509401	9.12E-08	2.03E-07
SLAMF6	1.459438	3.268533	1.16323	1.20E-36	1.23E-35
SPDYC	10.82922	2.146757	-2.3347	0.014530224	0.019410245
CD69	1.407135	3.287871	1.224394	1.88E-43	2.48E-42
MRGPRF	1.118384	2.952346	1.400446	3.51E-86	2.48E-84
CELF3	0.360735	0.090206	-1.99964	0.000131218	0.000221606
COL10A1	20.71633	65.06779	1.651175	5.69E-69	2.01E-67
BTLA	0.270116	0.622922	1.205473	1.17E-28	8.85E-28
CYP11A1	0.225828	2.206447	3.288428	1.61E-52	3.09E-51
FCRLA	0.440843	0.930342	1.077497	4.64E-26	3.14E-25
MXRA5	21.759	59.08938	1.441287	4.01E-113	1.16E-110
ICAM3	0.450747	0.927922	1.041684	1.35E-40	1.58E-39
CA10	0.08012	0.180581	1.172405	7.96E-05	0.000137408
CALHM5	0.636335	1.635364	1.361754	4.38E-133	7.45E-130
WIPF1	4.852727	10.36226	1.094471	1.47E-111	3.65E-109
COL16A1	8.245005	17.04573	1.047818	2.48E-65	7.59E-64

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
FAM57B	0.72143	0.314475	-1.19792	1.26E-08	3.02E-08
SLC8A2	0.562669	0.134726	-2.06226	0.002678175	0.003912596
FCRL1	0.173452	0.458912	1.403683	4.72E-18	2.14E-17
DPP4	1.218031	3.358975	1.463471	3.00E-96	3.21E-94
PPM1E	0.797705	0.264271	-1.59384	1.00E-11	3.04E-11
CCR5	2.38918	4.847795	1.020813	6.88E-43	8.81E-42
FAP	3.544912	10.0916	1.509334	3.26E-120	1.43E-117
FN1	177.4868	415.7963	1.228166	2.14E-69	7.68E-68
LRCH2	0.290851	0.630024	1.115126	3.25E-105	5.66E-103
KERA	0.350967	0.915955	1.383943	1.13E-85	7.81E-84
IKZF1	1.309711	2.849067	1.121241	3.64E-55	7.66E-54
OGN	5.021205	10.87321	1.114672	2.13E-74	9.36E-73
KRT10	26.45772	12.90371	-1.0359	0.000832003	0.001284586
ZNF366	0.376656	0.830672	1.141033	1.78E-58	4.17E-57
CTSG	0.814063	2.26958	1.479212	1.59E-41	1.93E-40
TM6SF1	0.847183	1.776877	1.068598	2.57E-90	2.15E-88
SRPX	5.297004	11.52635	1.121687	5.76E-92	5.15E-90
KCTD12	10.20215	22.80866	1.160709	1.66E-114	5.36E-112
COL8A2	8.422329	22.71467	1.431333	1.98E-89	1.56E-87
PM20D1	0.068062	0.165133	1.278706	1.29E-37	1.36E-36
FHL5	0.511451	1.157478	1.178317	9.15E-48	1.42E-46
SRPX2	5.797462	12.16319	1.069029	7.18E-85	4.72E-83
CRHBP	0.114369	0.237641	1.055093	2.52E-42	3.17E-41
GABRB2	0.102839	0.222602	1.114077	9.42E-37	9.68E-36
GIMAP6	3.706445	7.52299	1.02127	4.48E-71	1.70E-69
CLDN11	0.956155	1.950133	1.028256	1.34E-33	1.23E-32
MSRB3	4.230526	10.05328	1.248757	9.96E-107	1.83E-104
WISP1	3.023915	8.367162	1.468321	1.72E-119	7.33E-117
IL9R	0.126891	0.266589	1.071033	1.58E-37	1.66E-36
TWIST2	1.399721	3.046965	1.122234	5.47E-69	1.93E-67
FBLN2	20.87396	45.16378	1.113462	7.09E-98	8.53E-96
CD52	16.33177	47.5384	1.541412	4.47E-34	4.15E-33
KLK4	0.90518	2.739022	1.597384	1.16E-74	5.18E-73
LY9	0.230218	0.519904	1.175243	2.52E-38	2.73E-37
CYP2C8	0.56937	0.28254	-1.01091	0.024605598	0.031932129
ANTXR2	2.572935	5.160287	1.004036	9.04E-112	2.32E-109
CAMK4	0.249476	0.500981	1.005857	1.22E-68	4.27E-67
TMEM130	0.379373	0.816214	1.10533	2.64E-52	5.01E-51
LRFN5	0.108615	0.231417	1.09127	2.86E-59	6.92E-58
VCAN	16.38733	46.35644	1.500189	5.44E-112	1.45E-109
TPSAB1	5.855386	13.62819	1.218758	5.27E-35	5.08E-34
NR5A1	0.179008	0.083538	-1.09951	0.030130026	0.038651765

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SLC9A9	1.160101	2.335385	1.00941	1.06E-83	6.64E-82
NOX4	1.081425	2.567157	1.247238	2.92E-95	3.03E-93
SLC28A1	0.221297	0.10432	-1.08496	1.80E-07	3.92E-07
NETO1	0.112819	0.301558	1.418424	9.31E-20	4.64E-19
FGF7	0.812506	2.263324	1.477993	8.98E-94	8.60E-92
IL33	2.327581	5.628825	1.274002	1.03E-35	1.01E-34
CD5	1.761189	3.711782	1.075563	2.66E-35	2.58E-34
KLK2	0.044092	0.229363	2.379033	2.61E-57	5.81E-56
KCNIP2	0.749495	1.833838	1.290876	2.09E-11	6.20E-11
RTBDN	1.388851	0.380226	-1.86896	1.50E-07	3.29E-07
TSHZ2	0.953989	1.914612	1.005008	1.90E-75	8.77E-74
C1orf105	0.403477	0.064845	-2.63742	0.00104144	0.001591339
HPGDS	0.951947	1.920097	1.012227	1.94E-58	4.53E-57
SLC38A3	1.951338	0.957438	-1.02721	0.003402351	0.004903176
ADAM12	5.700672	17.34209	1.605074	1.75E-110	3.90E-108
CD96	1.048765	2.169694	1.0488	4.94E-37	5.13E-36
TFR2	1.065222	0.525786	-1.01861	3.87E-12	1.21E-11
P4HA3	1.497286	3.782842	1.337121	1.61E-97	1.90E-95
TMEM255A	0.481097	0.978981	1.024953	5.48E-58	1.26E-56
CSDC2	0.445488	1.131046	1.344198	1.06E-58	2.50E-57
GNG2	1.78358	3.883056	1.122417	1.54E-109	3.17E-107
COL3A1	323.5202	1083.454	1.74371	8.31E-122	4.52E-119
ZEB1	2.56072	6.148752	1.263744	2.57E-115	8.75E-113
ADAMTS6	0.306866	0.671304	1.129357	2.37E-72	9.59E-71
IGDCC4	0.410673	0.846618	1.043722	8.50E-62	2.29E-60
CTGF	93.67212	226.3096	1.272606	3.55E-79	1.85E-77
TLL1	0.388504	0.990321	1.349966	2.18E-94	2.13E-92
CLEC4G	0.066849	0.146864	1.135493	3.06E-15	1.16E-14
HSPB6	3.695889	8.793816	1.250568	7.63E-41	8.98E-40
AL845331.2	0.050982	0.108621	1.091242	1.15E-12	3.72E-12
ASPHD1	3.345412	1.443672	-1.21244	8.08E-09	1.97E-08
GNG3	1.311725	0.440552	-1.57408	1.71E-06	3.41E-06
ANTXR1	18.07282	44.39325	1.296519	3.78E-87	2.75E-85
PRSS35	0.155375	0.424908	1.4514	2.11E-34	1.99E-33
HBQ1	0.194411	0.048747	-1.99572	1.80E-12	5.73E-12
LAX1	0.645345	1.485941	1.203233	3.81E-40	4.37E-39
CAMK2B	1.456361	0.704871	-1.04694	0.023579077	0.030681888
SLFN12L	0.220666	0.50025	1.180786	1.97E-38	2.14E-37
C7	2.640374	7.648845	1.5345	2.35E-35	2.29E-34
CLEC2B	2.947153	6.03214	1.033348	2.47E-106	4.47E-104
TEX11	0.067909	0.144251	1.086907	2.34E-47	3.58E-46
TPSD1	1.148653	3.294213	1.51999	8.28E-15	3.05E-14

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
AQP7	0.372455	1.197404	1.684771	1.68E-21	9.21E-21
AKR1B15	1.266191	4.492802	1.827121	5.01E-08	1.14E-07
PGC	0.727679	1.865194	1.357951	0.018921448	0.02493841
BRINP2	3.333084	0.833074	-2.00034	1.53E-05	2.81E-05
TNFSF8	0.69126	1.527324	1.143706	5.41E-71	2.03E-69
FCAMR	0.070303	0.215714	1.617454	0.000154369	0.000258905
KLHL6	0.614977	1.302045	1.082175	9.59E-59	2.28E-57
TCF4	2.221721	4.908811	1.143696	1.69E-121	8.84E-119
PTPRC	4.352418	10.34417	1.248929	5.13E-56	1.10E-54
NID1	15.10688	30.86231	1.03064	2.17E-94	2.13E-92
MMP11	40.57909	84.75469	1.062557	5.71E-35	5.51E-34
AOC3	4.371049	11.56055	1.403158	1.89E-66	6.00E-65
FLRT2	0.25401	0.630463	1.311523	4.55E-99	5.78E-97
ABCA8	0.325096	1.158882	1.833797	1.39E-58	3.27E-57
ZCCHC24	5.184296	11.17964	1.108653	8.93E-92	7.79E-90
AKAP12	2.16732	6.105127	1.494109	1.45E-100	2.01E-98
CA9	5.704306	2.290349	-1.31648	0.000337743	0.000544446
MPEG1	5.628759	12.09719	1.103783	1.71E-63	4.92E-62
EVI2B	5.719385	12.27725	1.102055	2.47E-68	8.59E-67
APLP1	6.612317	2.129753	-1.63447	5.21E-11	1.50E-10
FCRLB	4.80399	1.582998	-1.60157	5.50E-08	1.25E-07
PDGFRA	3.236679	7.363006	1.185781	3.37E-111	8.18E-109
SIGLEC6	0.16053	0.398475	1.311649	2.26E-52	4.29E-51
COL5A1	25.75171	69.29407	1.428063	2.46E-100	3.32E-98
TIMP2	48.62659	106.6482	1.133042	7.18E-114	2.13E-111
ITK	0.489057	1.149129	1.232465	1.44E-39	1.61E-38
FNDC1	7.511947	16.86392	1.166681	6.19E-77	3.01E-75
CYS1	1.207093	3.057541	1.340835	3.40E-90	2.80E-88
IL6	0.863728	2.067188	1.25902	1.80E-19	8.83E-19
TUBB4A	0.825233	0.357197	-1.20808	0.002082591	0.003076519
SLAMF1	0.548368	1.188871	1.116377	1.44E-37	1.52E-36
CD200R1	0.289807	0.617624	1.091636	6.13E-49	1.00E-47
PDIA2	0.627987	0.132763	-2.24188	4.82E-08	1.10E-07
MS4A6E	0.026146	0.150725	2.527258	4.57E-11	1.32E-10
COL12A1	28.15552	73.88848	1.391932	8.50E-77	4.10E-75
TLR10	0.392725	0.815278	1.053771	1.66E-33	1.50E-32
DIRC1	0.112266	0.266436	1.246869	2.91E-55	6.13E-54
TRAT1	0.468075	1.019597	1.123187	8.46E-34	7.77E-33
HTR2B	0.461867	1.186825	1.361556	2.06E-74	9.08E-73
RPL3L	0.494354	0.106217	-2.21853	4.09E-12	1.27E-11
DOCK2	1.302006	2.769112	1.088688	1.07E-62	2.99E-61
ECM2	2.314453	7.290659	1.655378	1.12E-130	1.27E-127

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
RUNX2	1.833327	3.868193	1.077195	9.26E-90	7.45E-88
JAM2	1.817581	3.959234	1.123201	1.97E-86	1.40E-84
ARMH4	0.54487	1.235126	1.180674	1.59E-101	2.28E-99
BRSK2	0.618765	0.245114	-1.33594	0.000143706	0.000241827
AOAH	1.832563	3.702445	1.014616	2.76E-51	4.98E-50
PODN	5.751664	18.20064	1.661938	1.61E-116	5.78E-114
ALPK2	0.156965	0.341008	1.119361	2.78E-48	4.45E-47
HTRA3	18.64694	48.48069	1.378471	2.02E-76	9.63E-75
SH3GL3	0.169217	0.061866	-1.45165	2.14E-05	3.88E-05
ITIH5	0.884258	2.172281	1.296671	4.73E-43	6.12E-42
CASQ2	0.44189	0.914475	1.049257	9.38E-32	7.99E-31
CDK15	0.120904	0.301413	1.317876	3.29E-77	1.63E-75
SLURP1	1.75456	0.694204	-1.33768	0.003060284	0.004438897
FREM1	0.201174	0.546029	1.440531	1.27E-53	2.54E-52
DOCK11	1.95399	4.164363	1.091673	1.54E-86	1.10E-84
VGLL3	0.853127	2.005884	1.233405	1.98E-89	1.56E-87
GZMK	2.384973	5.847128	1.293755	7.02E-36	6.96E-35
MS4A4E	0.153584	0.317802	1.049098	2.05E-34	1.93E-33
IL16	1.108937	2.469009	1.154755	2.65E-94	2.58E-92
DDN	0.257258	0.082448	-1.64166	5.16E-08	1.17E-07
TMEM179	0.504323	0.165407	-1.60833	0.037479264	0.047559483
GXYLT2	2.871213	8.892444	1.63092	2.65E-102	4.06E-100
EEF1A2	75.8926	35.88525	-1.08057	0.000645202	0.001008068
COL8A1	6.73658	18.19668	1.433587	3.24E-91	2.77E-89
PTGER4	1.716715	3.447834	1.006039	1.05E-70	3.92E-69
ABCB5	0.029901	0.081528	1.447096	1.10E-35	1.08E-34
TCEAL7	0.986602	2.096214	1.087246	1.48E-71	5.77E-70
IGF1	0.175739	0.571351	1.700943	1.90E-75	8.77E-74
FST	4.650148	9.353755	1.008269	1.30E-58	3.08E-57
ANGPTL2	10.32445	27.16243	1.395547	1.54E-118	6.00E-116
TFF2	0.721248	0.306779	-1.2333	0.011754135	0.01589846
XCR1	0.158382	0.395927	1.321827	7.41E-33	6.58E-32
RASGRF2	0.716847	1.952952	1.44592	3.35E-127	3.04E-124
DCN	22.08507	76.50543	1.792491	2.40E-145	1.63E-141
CST7	4.681054	9.445094	1.012732	4.40E-48	6.98E-47
TNN	1.136619	3.60731	1.666174	1.58E-60	4.00E-59
FABP4	17.54774	66.38834	1.919645	2.05E-25	1.35E-24
LVRN	0.060611	0.141297	1.221076	3.03E-23	1.81E-22
CCDC36	0.093701	0.243129	1.375582	2.21E-97	2.55E-95
NRTN	1.9742	0.823537	-1.26136	1.23E-10	3.46E-10
PYHIN1	0.452032	0.9662	1.095896	1.23E-34	1.16E-33
CA4	0.117445	0.401257	1.772534	4.15E-17	1.77E-16

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SFRP4	14.02719	52.07969	1.892495	3.67E-102	5.48E-100
PHGDH	23.29832	10.07963	-1.20878	1.46E-08	3.49E-08
PAH	0.462175	0.189488	-1.28633	0.000788541	0.001220668
LOXL1	10.89372	22.93358	1.073965	6.46E-81	3.57E-79
ADAM33	0.444618	1.3105	1.559481	1.16E-66	3.67E-65
CMA1	0.35103	1.036535	1.562102	2.93E-33	2.63E-32
ACSM5	0.287722	0.614269	1.094196	3.06E-51	5.50E-50
PLIN1	3.603054	13.06485	1.858398	3.74E-22	2.12E-21
BHLHE22	0.357631	0.937879	1.390929	2.63E-85	1.77E-83
ABCC9	0.714953	1.433622	1.003743	5.96E-70	2.19E-68
INHBA	6.823756	15.69425	1.201598	1.16E-70	4.30E-69
ADH1B	2.517512	10.31472	2.034634	1.83E-30	1.50E-29
RUNDC3A	1.790276	0.353958	-2.33853	1.42E-05	2.62E-05
MAB21L1	0.265578	0.637684	1.263707	6.36E-67	2.06E-65
CCL14	0.305743	0.842191	1.461825	1.20E-38	1.31E-37
GSTM5	0.677276	1.719286	1.343993	1.61E-49	2.71E-48
SCN7A	0.169701	0.591407	1.801156	1.16E-52	2.24E-51
WNT2	2.08759	5.219593	1.322099	3.11E-79	1.62E-77
FGF16	0.083529	0.355585	2.089845	6.82E-66	2.11E-64
CLDN18	0.052894	0.147395	1.478517	3.71E-18	1.69E-17
MRC2	15.24852	30.91815	1.019785	1.01E-77	5.01E-76
SERPING1	52.07141	108.5458	1.059741	2.76E-102	4.18E-100
TEX19	0.343354	0.093135	-1.8823	2.14E-06	4.24E-06
VXN	1.211027	0.48132	-1.33116	0.018172641	0.024014288
PRDM1	2.221413	4.572045	1.041362	4.65E-92	4.22E-90
COL1A2	226.2341	718.3252	1.666821	3.28E-115	1.09E-112
GEM	7.274045	16.98512	1.223442	2.28E-60	5.71E-59
ATOH8	0.264283	0.625948	1.243957	1.52E-32	1.33E-31
CEL	2.862412	1.144692	-1.32227	4.80E-09	1.19E-08
MT1G	20.30477	9.559389	-1.08683	0.000762359	0.001182156
CD3E	4.617012	9.414181	1.027876	1.42E-33	1.29E-32
CSAG1	1.861663	0.72086	-1.3688	0.000720514	0.001120589
SLC18A2	0.232129	0.485847	1.065574	9.59E-42	1.17E-40
SULT4A1	0.864419	0.376759	-1.19809	1.80E-06	3.60E-06
SAMD3	0.138743	0.310555	1.162433	1.18E-41	1.44E-40
LAMA4	6.068924	12.50985	1.043551	5.38E-114	1.63E-111
FAM110D	0.960742	1.924691	1.002405	1.43E-25	9.52E-25
MMP19	1.688712	4.273564	1.339516	2.53E-122	1.50E-119
C2CD4B	0.695659	1.498514	1.107081	2.98E-20	1.53E-19
FPR1	1.579053	3.29853	1.062763	1.14E-57	2.59E-56
CACNA1G	0.10027	0.214555	1.097449	5.95E-45	8.26E-44
LILRB5	0.312219	0.677222	1.117069	1.63E-39	1.82E-38

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PCSK5	0.502481	1.170818	1.220377	1.80E-98	2.22E-96
LIPE	2.491479	5.630245	1.176195	1.99E-13	6.70E-13
AADAC	0.216683	0.594483	1.456053	4.65E-15	1.74E-14
CCR2	0.980888	2.205771	1.169123	2.42E-47	3.69E-46
EPYC	1.033386	3.706323	1.84261	1.03E-31	8.79E-31
BLK	0.248334	0.520665	1.068071	1.76E-17	7.72E-17
CNR2	0.084332	0.195151	1.210437	9.40E-20	4.68E-19
CAVIN2	1.742025	4.548669	1.384679	1.16E-43	1.55E-42
VGF	0.985507	0.347733	-1.50289	1.46E-15	5.66E-15
ONECUT2	0.353889	0.171942	-1.04137	4.39E-05	7.74E-05
DLGAP1	0.93254	0.395225	-1.23849	0.023625256	0.030739038
FSTL1	24.86914	62.07765	1.319717	1.20E-136	3.27E-133
LMO1	0.399867	0.145659	-1.45692	0.000468019	0.000742317
ADAMTS14	0.902465	1.921759	1.090484	9.14E-55	1.90E-53
CILP2	2.367954	5.82397	1.298362	5.72E-56	1.22E-54
ST6GAL2	0.898278	2.453637	1.449687	3.22E-72	1.29E-70
ACTL6B	0.412158	0.027191	-3.92202	3.96E-06	7.68E-06
COL5A3	5.16901	10.90291	1.076753	6.84E-58	1.56E-56
CYR61	48.90063	114.2537	1.224316	1.70E-54	3.49E-53
ARL9	2.301354	1.033598	-1.15481	3.51E-06	6.84E-06
TFEC	0.724558	1.504824	1.054422	3.29E-48	5.23E-47
SLC27A2	11.5402	4.987947	-1.21015	0.001859214	0.002761224
CLMP	4.244493	8.601882	1.01906	1.97E-90	1.65E-88
TGFBR2	13.55915	32.92261	1.279812	3.30E-121	1.60E-118
CIDEC	1.852647	6.997951	1.917345	5.88E-18	2.65E-17
ANGPT4	0.052722	0.128786	1.288504	8.80E-43	1.12E-41
PGPEP1L	0.140393	0.064784	-1.11575	2.75E-07	5.90E-07
CLEC9A	0.124177	0.261588	1.074895	2.89E-28	2.16E-27
CTHRC1	36.41541	76.80803	1.076708	2.10E-85	1.45E-83
DAB2	6.94493	14.22125	1.034016	1.72E-125	1.38E-122
MFAP4	12.62364	41.00961	1.699834	1.51E-78	7.75E-77
EGFL6	1.418883	2.951298	1.056594	1.21E-29	9.57E-29
PLIN4	4.521226	14.96286	1.7266	3.01E-15	1.14E-14
MATN4	0.472251	0.171626	-1.46029	0.000146202	0.000245813
ADAMTS16	0.999533	2.824352	1.498594	8.50E-65	2.52E-63
C1QL4	0.584618	0.23669	-1.3045	0.00238771	0.003507457
PDGFRL	5.908689	15.36716	1.378941	1.72E-100	2.36E-98
PLN	1.394304	3.114189	1.159312	4.19E-63	1.19E-61
FOXI3	0.421244	0.18143	-1.21525	0.00838329	0.011524695
GLDC	2.726753	0.931845	-1.54902	7.59E-06	1.43E-05
COL1A1	368.289	1119.015	1.603319	9.10E-105	1.57E-102
SOHLH1	0.174655	0.072557	-1.26731	0.006028259	0.008423343

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TLX1	0.897316	0.383159	-1.22767	5.31E-08	1.20E-07
C11orf86	0.63777	0.144763	-2.13934	0.002645933	0.003867985
CYP2A13	0.425204	0.063968	-2.73273	1.08E-05	2.02E-05
SELE	1.501335	3.021533	1.009034	5.84E-28	4.32E-27
FAM189A1	0.212708	0.431954	1.022002	1.57E-23	9.50E-23
NR2F1	3.521436	7.762799	1.140413	1.16E-52	2.23E-51
SCN2B	0.097813	0.266357	1.445265	1.98E-62	5.48E-61
MT3	0.202767	0.082097	-1.30443	1.08E-05	2.01E-05
INMT	0.76475	1.746272	1.191218	2.26E-42	2.84E-41
STAB2	0.057588	0.121842	1.081166	1.02E-16	4.25E-16
CLEC4D	0.067023	0.232641	1.795369	4.98E-10	1.33E-09
GLIS3	0.570327	1.185265	1.055349	3.01E-71	1.15E-69
AP3B2	0.967393	0.416522	-1.21571	4.81E-07	1.01E-06
CNRIP1	1.469268	3.425156	1.221072	4.80E-140	2.18E-136
DHH	0.155387	0.310863	1.000413	1.17E-35	1.15E-34
PGM5	0.630376	1.498453	1.24919	3.22E-54	6.54E-53
CYBB	9.889828	19.99619	1.015707	1.29E-51	2.34E-50
BICC1	1.820694	4.617104	1.3425	1.57E-117	5.78E-115
CNTN1	1.185344	2.714486	1.195374	1.18E-62	3.27E-61
CFH	3.588411	9.327826	1.378196	1.36E-131	1.85E-128
MMP2	49.07799	154.6103	1.655488	4.01E-131	4.96E-128
ITGBL1	2.241135	6.582105	1.554319	3.60E-99	4.62E-97
CD226	0.177876	0.368816	1.05203	6.46E-45	8.95E-44
TNFSF4	1.394779	2.859057	1.035503	8.44E-59	2.01E-57
GPIHBP1	0.866225	2.330757	1.427984	1.42E-34	1.34E-33
TMEM82	0.176952	0.05961	-1.56973	0.004501656	0.006395952
WISP2	2.844927	9.047208	1.669081	2.74E-61	7.23E-60
UBASH3A	0.485068	0.972901	1.004106	8.67E-32	7.39E-31
THSD7B	0.170207	0.378183	1.151797	2.98E-42	3.72E-41
NCAN	1.455371	0.363723	-2.00048	0.0211123	0.027654512
TCL1A	0.621605	1.244251	1.001208	1.01E-11	3.06E-11
CD209	0.569308	1.262595	1.149112	9.44E-37	9.70E-36
RFX8	0.294137	0.619781	1.07527	4.04E-67	1.32E-65
SBSN	5.475512	0.87821	-2.64036	0.002891725	0.00420876
GAS7	2.592191	6.961687	1.425265	8.93E-124	6.75E-121
ACKR4	0.381711	1.035803	1.440195	2.62E-78	1.32E-76
KL	0.270776	0.548446	1.018251	2.03E-47	3.12E-46
NMU	3.464222	1.029932	-1.74998	1.16E-06	2.36E-06
MYOG	0.125669	0.046874	-1.42276	3.83E-06	7.42E-06
ADAMTS12	2.901195	6.788183	1.226378	3.88E-76	1.83E-74
PPP1R16B	1.30209	2.618363	1.007836	3.65E-43	4.75E-42
FBN1	9.708461	31.12972	1.680978	3.42E-122	1.94E-119

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CLDN6	2.494945	0.417582	-2.57888	0.033733825	0.043019321
RGS18	0.42491	0.868989	1.032179	3.48E-46	5.07E-45
LEP	0.509573	2.728144	2.420558	1.66E-18	7.76E-18
NID2	3.35112	8.164395	1.284703	2.00E-89	1.56E-87
GLRA3	0.713602	1.773445	1.313363	0.00077772	0.001204602
TENM4	0.666298	1.417226	1.088831	2.91E-85	1.95E-83
GYPE	0.093444	0.190149	1.024964	2.32E-58	5.39E-57
AICDA	0.030415	0.231272	2.926725	7.90E-19	3.76E-18
SLC38A4	0.166782	0.431321	1.370803	1.02E-80	5.54E-79
TREML2	0.089356	0.186616	1.062436	1.25E-27	9.08E-27
BHMT2	0.778829	1.586482	1.026453	1.68E-81	9.50E-80
GZMM	1.307191	2.639437	1.01376	1.76E-21	9.61E-21
ABCD2	0.15145	0.346964	1.195941	7.66E-45	1.05E-43
GLYAT	0.061072	0.233808	1.936749	6.37E-15	2.37E-14
CCDC69	3.089055	6.285219	1.024798	6.39E-45	8.87E-44
GIMAP7	6.704325	13.4454	1.003949	4.85E-45	6.77E-44
ABCB1	0.536773	1.168816	1.122664	8.13E-46	1.17E-44
DPYSL5	0.580468	0.095173	-2.6086	8.85E-05	0.000152131
SPN	1.22719	2.605913	1.08643	4.05E-55	8.49E-54
ZEB2	1.104462	2.641516	1.258022	2.37E-122	1.47E-119
TLR7	1.222782	2.794947	1.192654	2.01E-67	6.66E-66
GPR34	2.604936	5.865366	1.170973	3.97E-82	2.34E-80
GREM1	2.154606	5.522	1.357767	1.82E-65	5.58E-64
GAPT	0.943378	1.989809	1.076722	8.31E-61	2.13E-59
FHL1	3.585038	10.09388	1.49342	2.28E-85	1.56E-83
ASPN	18.63238	82.75899	2.151104	5.23E-95	5.27E-93
MMP13	5.615603	17.57689	1.646167	6.20E-36	6.16E-35
FCRL3	0.298083	0.604608	1.020287	1.79E-23	1.09E-22
GLIS1	0.233295	0.470902	1.013271	2.73E-52	5.17E-51
GAS1	6.156056	14.35206	1.221179	5.49E-93	5.15E-91
TRARG1	1.233954	3.893155	1.657651	1.13E-22	6.54E-22
SH2D1A	0.955894	2.095952	1.132683	7.12E-34	6.57E-33
LGALS12	0.735079	1.719644	1.226139	2.68E-17	1.16E-16
MEOX1	1.304268	2.823749	1.114371	7.33E-24	4.52E-23
MYOM2	0.317077	0.927609	1.548682	2.36E-09	6.01E-09
TMEM273	1.083815	2.348699	1.115743	1.71E-71	6.59E-70
FCRL6	0.332159	0.671702	1.015947	6.71E-30	5.36E-29
SVEP1	0.962158	2.781492	1.531513	5.06E-89	3.83E-87
CD300LG	0.275647	0.93126	1.756361	9.12E-25	5.82E-24
PLPP4	2.674305	6.952018	1.378268	2.82E-69	1.00E-67
KCNK7	0.362313	0.165876	-1.12713	0.012856565	0.017296745
KCNA5	0.147138	0.314816	1.097342	1.25E-28	9.51E-28

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
METTL24	0.135037	0.345559	1.355579	8.81E-72	3.46E-70
ADAMTS2	6.652906	17.85299	1.42411	2.84E-110	6.14E-108
FOLR2	4.283695	10.11357	1.239365	8.68E-48	1.36E-46
JCHAIN	64.51482	164.8194	1.353183	9.31E-33	8.24E-32
COMP	25.80341	66.52678	1.366374	5.06E-54	1.02E-52
CD1E	0.706462	1.501716	1.087929	9.21E-28	6.73E-27
ITGA11	4.247094	11.65115	1.455925	3.69E-68	1.27E-66
EMX2	0.236981	0.533062	1.16953	3.65E-70	1.35E-68
JAML	0.737223	1.599117	1.117102	2.17E-47	3.33E-46
LEPR	0.727178	1.46111	1.006684	1.11E-39	1.24E-38
ADH1A	0.024782	0.062432	1.332972	4.49E-20	2.29E-19
CD40LG	0.552583	1.231953	1.156685	3.92E-36	3.93E-35
SALL1	0.227294	0.473497	1.058792	1.21E-71	4.73E-70
FAT4	0.468926	1.077001	1.199588	7.74E-87	5.60E-85
GPR1	0.3256	1.127263	1.791651	9.06E-82	5.24E-80
IFFO1	1.315919	2.63354	1.000932	1.20E-92	1.12E-90
DBX2	0.050813	0.137277	1.433821	4.94E-45	6.89E-44
SIT1	1.476449	2.97478	1.010652	4.75E-32	4.10E-31
EMILIN1	13.21609	31.97722	1.274749	1.28E-75	5.97E-74
TH	0.314227	0.155956	-1.01067	0.003155591	0.004569345
ANGPTL1	0.474073	1.663547	1.811081	3.02E-82	1.78E-80
CLEC10A	1.102251	2.721491	1.303945	5.13E-31	4.29E-30
IL21R	0.671572	1.378851	1.037853	7.79E-52	1.43E-50
ACVR1C	0.152213	0.359026	1.238002	2.89E-21	1.56E-20
MRVI1	1.623625	3.496862	1.106843	2.00E-96	2.16E-94
TNXB	0.580297	1.753556	1.59542	5.04E-45	7.03E-44
FBN3	0.496456	0.240363	-1.04645	0.001103889	0.001683548
3-Sep	5.258872	2.33447	-1.17166	2.80E-17	1.22E-16
MCTP1	0.651973	1.323839	1.021842	2.22E-69	7.92E-68
P2RY12	0.481577	0.996268	1.048767	5.56E-45	7.74E-44
KCNH2	1.506782	0.553018	-1.44607	6.21E-08	1.40E-07
ABCA6	0.232507	0.736731	1.663862	5.67E-94	5.47E-92
APOA1	1.27782	0.284688	-2.16623	0.021832024	0.028536826
CD248	12.30018	26.21395	1.091655	1.44E-78	7.38E-77
HSD11B1	1.251101	3.254204	1.379107	7.25E-40	8.22E-39
SLC19A3	0.471713	1.383196	1.552025	3.24E-17	1.39E-16
SGIP1	0.47994	1.006364	1.068226	9.82E-67	3.15E-65
ROPN1B	1.967686	0.721074	-1.44828	0.036005496	0.045813239
SPIN2A	0.058612	0.147843	1.334791	8.07E-37	8.31E-36
CPXM1	8.004237	23.13446	1.531208	1.09E-80	5.89E-79
F2RL2	5.646246	13.93021	1.302853	6.92E-53	1.34E-51
CLDN5	1.992881	4.476605	1.167549	1.09E-28	8.32E-28

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ARSI	1.024252	2.198125	1.101703	3.47E-65	1.05E-63
GFPT2	2.907697	5.942321	1.03115	7.09E-97	8.04E-95
MGARP	0.172875	0.466779	1.433011	9.49E-28	6.92E-27
C2orf70	0.649772	0.309073	-1.07198	4.26E-08	9.75E-08
CCDC80	7.634024	27.18417	1.832251	6.03E-139	2.05E-135
PI16	1.880419	6.304699	1.745373	1.81E-22	1.04E-21
CCL23	0.192142	0.418531	1.123163	2.15E-32	1.87E-31
SLITRK1	0.370406	0.094974	-1.96351	0.001036652	0.0015842
NEXN	1.842856	3.756721	1.02753	5.63E-92	5.07E-90
ANK2	0.482254	1.144863	1.247309	4.92E-76	2.32E-74
CPA1	0.022127	0.071157	1.6852	8.40E-18	3.76E-17
NLRP3	0.576432	1.226724	1.089588	1.34E-72	5.49E-71
LRRC17	3.351968	9.322823	1.475759	1.05E-66	3.37E-65
CORIN	0.356903	1.048974	1.555375	3.26E-62	8.88E-61
PEX5L	0.788032	0.363802	-1.1151	8.55E-05	0.00014714
ARHGAP20	0.210816	0.54964	1.3825	7.88E-97	8.86E-95
PLA2G2D	1.467224	3.166657	1.109871	2.97E-14	1.05E-13
HSPB7	0.65552	1.528017	1.22095	6.45E-46	9.30E-45
GALNT15	0.880987	3.091316	1.811028	3.11E-103	5.04E-101
HIC1	0.866363	1.85743	1.100264	2.25E-78	1.14E-76
CD84	1.550968	3.670711	1.242891	5.77E-64	1.69E-62
PSORS1C2	1.33125	0.613749	-1.11706	0.006045044	0.008444197
RBMS3	0.895212	2.149176	1.263483	1.04E-98	1.31E-96
VCAM1	4.571069	9.984068	1.127096	1.18E-57	2.68E-56
ABCA10	0.173832	0.372451	1.099355	2.43E-25	1.60E-24
PLA2G5	0.270247	0.587568	1.120477	3.89E-53	7.64E-52
XPNPEP2	0.168084	0.507249	1.593512	5.80E-58	1.33E-56
B3GALT2	0.107928	0.258943	1.262566	6.98E-42	8.59E-41
PDK4	7.395936	15.79381	1.094554	5.35E-25	3.46E-24
COL6A3	36.37068	100.2132	1.462224	3.13E-119	1.25E-116
MS4A2	0.484983	1.203817	1.31161	1.59E-49	2.68E-48
SEMA3D	0.360257	0.90468	1.328382	1.17E-76	5.61E-75
CRTAM	0.380608	0.869182	1.191351	4.33E-54	8.76E-53
JCAD	3.246038	6.915707	1.091197	3.71E-121	1.74E-118
PTH1R	0.404766	1.163598	1.523433	4.04E-83	2.44E-81
TAGLN3	0.321949	0.071314	-2.17456	0.022843559	0.029796042
GPR141	0.403549	0.902912	1.16184	1.50E-74	6.62E-73
COL5A2	39.62302	117.727	1.571034	1.76E-114	5.56E-112
TNFRSF17	1.088005	2.204634	1.018854	5.81E-25	3.75E-24
TMEM119	7.818352	22.08482	1.498119	5.87E-111	1.38E-108
GPX3	15.1274	31.54309	1.06016	4.79E-32	4.13E-31
FILIP1L	4.279196	10.09839	1.238714	3.77E-106	6.75E-104

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CPN2	0.103962	0.212813	1.03353	1.31E-46	1.94E-45
ZFPM2	0.518185	1.328084	1.357807	5.33E-111	1.27E-108
MYT1	1.092954	0.285551	-1.93641	7.38E-06	1.39E-05
MAP1LC3C	0.213667	0.667785	1.644022	2.26E-58	5.26E-57
FIBIN	6.071702	16.70131	1.459789	1.92E-110	4.21E-108
KCNA3	0.293175	0.755368	1.365419	6.73E-47	1.01E-45
HMCN1	1.180521	3.639145	1.624176	1.01E-100	1.42E-98
FCER1A	1.548099	3.801758	1.296169	1.61E-40	1.86E-39
OLFML2B	12.74606	31.52271	1.30634	1.31E-112	3.56E-110
POU5F1B	0.36584	0.155032	-1.23865	0.00063158	0.000988487
PDE1A	0.449143	0.962719	1.099938	1.37E-72	5.61E-71
HSPG2	11.74674	23.97271	1.029132	2.81E-74	1.23E-72
OMD	2.127916	8.824745	2.052114	3.07E-103	5.04E-101
CR2	0.652143	1.645998	1.335701	4.51E-08	1.03E-07
ERG	1.394249	2.795577	1.003658	1.17E-81	6.74E-80
HEPACAM	0.031394	0.107057	1.769824	4.08E-19	1.96E-18
CASS4	0.31397	0.645599	1.040012	4.41E-59	1.06E-57
SYNDIG1	1.356353	4.344002	1.679292	9.01E-81	4.95E-79
OLFML1	2.07629	5.547427	1.417811	2.32E-151	3.16E-147
C7orf61	0.390505	0.18215	-1.10022	0.000152999	0.000256735
CSF2RB	2.290159	5.0456	1.139578	5.88E-60	1.46E-58
SERPINF1	32.42892	85.94985	1.406214	1.03E-127	1.00E-124
DDR2	3.208797	6.559042	1.031452	6.71E-97	7.67E-95
GLI1	0.235779	0.552821	1.229377	7.64E-41	8.99E-40
HGF	0.432188	1.082531	1.324678	3.78E-90	3.10E-88
THY1	17.40804	37.17553	1.094599	1.48E-93	1.41E-91
METTL11B	0.106059	0.269253	1.344092	1.33E-31	1.13E-30
G0S2	9.534128	22.48835	1.238005	5.89E-20	2.97E-19
GPR15	0.151655	0.405314	1.418249	5.34E-24	3.31E-23
LPO	0.190159	0.051782	-1.87668	0.0052259	0.007356592
TMEM132C	0.205961	0.731781	1.829041	6.45E-35	6.20E-34
REEP2	2.253005	1.109192	-1.02234	1.24E-08	2.98E-08
COL14A1	5.724734	21.02912	1.877108	1.06E-85	7.36E-84
TMEM145	2.707647	0.913457	-1.56763	5.47E-11	1.57E-10
LYZ	64.80755	130.3403	1.00805	3.41E-35	3.31E-34
TNFAIP6	5.202276	10.47825	1.010183	2.13E-80	1.14E-78
ASPA	0.142016	0.319913	1.171631	3.40E-46	4.96E-45
MSLNL	0.249464	0.105867	-1.23657	1.90E-09	4.88E-09
MRO	0.233923	0.746971	1.675019	5.93E-34	5.49E-33
TMEM151A	0.294442	0.102064	-1.52851	3.71E-06	7.21E-06
FCER2	0.331626	0.691725	1.060639	1.49E-22	8.61E-22
USH1C	0.284488	0.049699	-2.51707	0.00011915	0.000202356

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ABI3BP	1.470486	3.55055	1.271749	3.02E-72	1.21E-70
CD3G	0.800306	1.795654	1.165886	5.20E-39	5.75E-38
LRP1B	0.59527	1.319451	1.148321	1.51E-10	4.20E-10
DMBT1	0.165723	1.25341	2.919013	3.60E-15	1.36E-14
BMX	0.278902	0.657028	1.236197	5.77E-42	7.13E-41
OMG	0.115351	0.249758	1.114496	3.53E-21	1.89E-20
LRRC70	0.183883	0.378364	1.040986	4.19E-43	5.45E-42
THBS4	8.839271	20.83456	1.236979	1.39E-46	2.05E-45
VMO1	2.474678	7.568237	1.612716	0.000194006	0.000322246
BNC2	0.516974	1.565981	1.598905	7.36E-126	6.26E-123
FGL2	5.236208	12.11778	1.210532	9.01E-73	3.73E-71
S1PR1	5.034631	10.9527	1.121329	6.41E-64	1.86E-62
C1QTNF6	4.527487	9.21705	1.025595	1.00E-80	5.46E-79
EGR1	52.06311	113.6361	1.126088	2.34E-32	2.04E-31
SLC38A5	1.526549	3.238216	1.084925	6.45E-65	1.92E-63
FBLN1	22.08322	45.05221	1.028647	4.59E-72	1.82E-70
ABCA9	0.277193	0.912496	1.718926	9.36E-72	3.67E-70
SLC24A2	0.253302	0.922327	1.864418	4.11E-77	2.03E-75
PNOC	0.249963	0.5417	1.11578	5.87E-36	5.85E-35
HAS1	0.296332	0.661177	1.157819	5.03E-29	3.88E-28
MS4A1	1.499212	3.220684	1.103163	1.87E-20	9.68E-20
MAST1	0.490363	0.182088	-1.42921	1.16E-15	4.51E-15
EBF1	1.231513	2.692459	1.128493	3.61E-89	2.76E-87
COL6A2	101.9679	240.1029	1.235537	2.21E-83	1.37E-81
CRISPLD2	5.947034	17.32157	1.542328	1.22E-131	1.84E-128
CAV1	12.67735	26.71003	1.075128	1.73E-79	9.09E-78
SPON1	6.15901	17.44062	1.501681	4.66E-110	9.92E-108
GNG13	1.577726	0.745787	-1.08101	1.11E-07	2.46E-07
THEMIS	0.330627	0.749054	1.179864	1.18E-41	1.43E-40
BACH2	0.406501	0.827469	1.025445	1.13E-68	3.97E-67
PRKCB	0.588465	1.412375	1.263093	3.15E-43	4.12E-42
FCRL5	0.266374	0.556447	1.062792	3.01E-22	1.71E-21
PDE2A	0.809476	1.653018	1.030041	9.49E-49	1.54E-47
FCGR3B	0.367833	0.879234	1.257197	4.65E-09	1.15E-08
GIMAP5	0.161278	0.363153	1.171033	3.00E-43	3.92E-42
ELAVL3	0.232079	0.021051	-3.46268	3.33E-09	8.39E-09
GRP	3.859387	8.147288	1.077948	1.88E-41	2.27E-40
BARX2	10.32219	5.143943	-1.0048	1.61E-09	4.16E-09
PRND	0.574521	1.445409	1.331046	2.12E-38	2.30E-37
PODNL1	1.816463	3.907965	1.105286	1.57E-71	6.09E-70
DLL3	0.410981	0.150802	-1.44641	2.02E-08	4.75E-08
MAT1A	1.286743	0.474846	-1.43819	7.75E-08	1.73E-07

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CLEC4C	0.07399	0.198278	1.422124	3.27E-16	1.32E-15
COL2A1	17.27541	7.473683	-1.20883	5.69E-05	9.94E-05
CORO2B	0.572435	1.280664	1.161708	6.12E-75	2.74E-73
SPARCL1	46.60231	112.5836	1.272524	1.62E-90	1.37E-88
RASL10B	1.909806	0.912027	-1.06628	0.000212377	0.000350791
CPZ	0.137841	0.376989	1.451518	1.74E-72	7.07E-71
KCNJ15	0.206047	0.417911	1.020222	1.32E-65	4.07E-64
CHSY3	0.851307	2.016012	1.243752	2.20E-109	4.47E-107
SLIT3	2.185583	5.30701	1.279881	3.95E-103	6.18E-101
LAMP5	5.173644	10.89779	1.074783	2.21E-57	4.93E-56
NR4A3	0.718384	1.670414	1.217378	6.23E-27	4.40E-26
F13A1	5.276401	18.92928	1.842993	1.19E-110	2.70E-108
ACKR1	5.990046	17.65809	1.55969	5.08E-30	4.08E-29
CD1C	1.042491	2.349374	1.172242	5.09E-33	4.54E-32
FYB1	3.25908	6.798301	1.060709	8.22E-54	1.65E-52
LTBP2	13.87084	28.8785	1.057941	1.02E-85	7.10E-84
NAP1L3	0.834115	1.947558	1.223348	9.79E-100	1.29E-97
SSC5D	2.700384	5.610315	1.054917	3.80E-67	1.25E-65
DMP1	0.074992	0.258167	1.783503	0.000370973	0.000595473
CDH11	6.087292	15.94942	1.389631	2.30E-109	4.61E-107
PLAU	21.88393	44.82204	1.034336	1.87E-52	3.56E-51
MMP8	0.082706	0.178079	1.106456	1.13E-11	3.41E-11
FGF18	0.510552	1.068401	1.065323	2.21E-57	4.93E-56
CBLN4	0.236478	0.492712	1.059037	1.99E-29	1.56E-28
C14orf180	0.125691	0.402144	1.677826	3.29E-18	1.51E-17
HSD17B13	0.072986	0.174421	1.256884	1.53E-33	1.39E-32
LGI2	0.5517	1.159668	1.071756	1.46E-64	4.32E-63
IL12B	0.085986	0.17675	1.039535	8.84E-17	3.71E-16
C6	0.236763	0.695229	1.554042	1.67E-25	1.11E-24
LRRC32	7.038867	15.98535	1.183335	8.33E-107	1.55E-104
FCN1	0.478968	1.031544	1.106805	2.32E-26	1.59E-25
TSPAN11	0.538718	1.096751	1.025632	3.18E-65	9.65E-64
PRSS1	0.732806	0.309397	-1.24397	0.009122935	0.012487252
LILRA4	0.505793	1.063859	1.072689	5.20E-35	5.02E-34
MSLN	16.62659	5.237529	-1.66653	1.57E-05	2.88E-05
LYVE1	0.545518	1.494404	1.453872	2.34E-44	3.17E-43
P2RY13	1.133197	2.323198	1.035714	2.12E-50	3.72E-49
CCR4	0.772858	1.995223	1.368275	7.19E-57	1.58E-55
NTSR2	0.270847	0.023473	-3.52843	7.99E-16	3.15E-15
ADH1C	0.571921	1.213476	1.085257	3.82E-26	2.60E-25
ALDH1A1	5.660941	11.76752	1.055696	2.32E-79	1.22E-77
TBX15	1.166643	2.477731	1.086656	1.44E-98	1.80E-96

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
VWF	11.78163	23.69121	1.007813	8.31E-64	2.41E-62
MRAP	0.136899	0.513173	1.906337	2.06E-20	1.06E-19
PTGDS	6.343909	15.81215	1.317589	2.75E-34	2.58E-33
FLNC	0.975933	2.133898	1.128637	2.91E-84	1.87E-82
F2R	12.72295	26.57116	1.062428	5.30E-89	3.98E-87
TFCP2L1	6.572677	3.266403	-1.00878	6.94E-10	1.84E-09
SGCD	1.068576	2.866268	1.423484	9.85E-97	1.10E-94
COL11A1	13.26381	41.50512	1.645795	3.57E-45	5.01E-44
GRID1	0.352457	0.713098	1.016651	5.97E-84	3.80E-82
ELN	12.21209	29.49115	1.271971	2.59E-55	5.48E-54
SFRP2	126.7616	383.8459	1.59841	1.70E-105	3.00E-103
LRRN4CL	0.446377	1.352934	1.599756	5.22E-76	2.45E-74
NPR1	1.351818	2.746195	1.022533	2.37E-38	2.56E-37
CCNE1	5.022873	2.420482	-1.05322	2.78E-12	8.75E-12
ENHO	7.990382	3.038556	-1.39488	6.07E-13	1.99E-12
DIO2	2.865629	7.019647	1.292547	8.24E-58	1.88E-56
DPYSL3	14.4471	34.06656	1.237576	1.02E-115	3.57E-113
CDK5R2	0.617012	0.062069	-3.31336	0.001203444	0.001826306
COX6A2	0.385174	0.172913	-1.15546	0.010509867	0.014293629
FMR1NB	0.440038	0.044019	-3.32142	0.020123718	0.026448704
FLI1	1.627208	3.34997	1.04175	2.82E-99	3.69E-97
DACT1	2.197908	5.745184	1.386222	7.17E-113	1.99E-110
AXL	7.535407	15.73355	1.062087	1.51E-128	1.58E-125
CILP	12.32775	47.88523	1.957671	1.15E-84	7.50E-83
SLIT2	1.1739	2.82469	1.266784	4.30E-95	4.37E-93
EOMES	0.486819	1.110422	1.189651	2.11E-32	1.84E-31
GLI2	0.388807	0.90961	1.226194	2.77E-91	2.38E-89
MAGEL2	0.142641	0.401591	1.493336	2.99E-100	3.99E-98
ASCL1	3.863548	1.429858	-1.43405	0.005424172	0.007619937
ZNF831	0.147089	0.357387	1.280798	3.87E-38	4.16E-37
PLAC9	2.325955	5.824868	1.324402	3.72E-50	6.46E-49
IL7R	2.708594	7.041039	1.378244	1.21E-48	1.97E-47
MSR1	4.111582	8.482946	1.044872	4.09E-61	1.07E-59
EVI2A	3.081755	6.940376	1.171262	1.36E-95	1.43E-93
SOX17	0.999276	2.064305	1.046702	1.13E-41	1.38E-40
RGS13	0.073889	0.168256	1.187219	2.63E-48	4.21E-47
ENPP2	3.254802	6.590492	1.017816	1.63E-48	2.64E-47
ROS1	0.073575	0.280519	1.930809	1.52E-10	4.23E-10
SPOCK1	4.680589	11.48984	1.295597	7.38E-78	3.72E-76
SELP	1.370387	3.781494	1.464373	1.90E-40	2.18E-39
CHRDL1	2.201697	6.761083	1.618638	7.06E-34	6.52E-33
MMP9	35.39459	96.06222	1.44044	2.25E-08	5.28E-08

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ADGRA2	3.29402	7.255749	1.139275	1.76E-97	2.05E-95
GAB3	0.594114	1.22047	1.038624	5.75E-82	3.35E-80
CAMK2N2	1.089958	0.481	-1.18016	2.88E-08	6.67E-08
DPEP1	0.412066	0.827402	1.005715	3.35E-42	4.19E-41
SPARC	312.91	841.2864	1.426849	2.86E-121	1.44E-118
SCML4	0.146115	0.332047	1.184287	1.64E-32	1.44E-31
CCL11	0.854299	1.950447	1.190992	1.52E-39	1.70E-38
PLPP7	0.566111	1.226677	1.115598	1.46E-94	1.46E-92
CD300LB	0.272145	0.638461	1.230224	3.36E-49	5.54E-48
VSTM4	1.336686	3.230667	1.273172	6.45E-109	1.27E-106
LMOD1	4.136328	8.583664	1.053243	5.39E-71	2.03E-69
CD28	0.608587	1.327559	1.12524	2.90E-48	4.62E-47
KLRB1	1.118274	2.545909	1.186907	3.37E-42	4.20E-41
HMCN2	0.106526	0.307318	1.528521	3.98E-54	8.07E-53
GPR174	0.465436	1.204738	1.372065	7.78E-36	7.70E-35
ATP6V0D2	0.364091	0.893185	1.29466	8.40E-25	5.37E-24
TBX5	0.511746	1.148968	1.166839	4.09E-95	4.19E-93
TLR8	0.504618	1.08394	1.103022	5.39E-51	9.64E-50
SLC22A3	0.392684	0.789484	1.00754	5.54E-48	8.71E-47
NCKAP1L	2.287054	4.826606	1.077518	2.19E-67	7.24E-66
RFTN2	0.489764	0.980096	1.000836	4.74E-104	7.97E-102
KRTDAP	8.07128	0.84693	-3.25248	7.93E-05	0.000136989
DLGAP3	0.395612	0.180915	-1.12877	9.95E-05	0.000170243
SYT13	18.45142	8.303717	-1.1519	0.000151055	0.000253632
MMRN1	0.580575	1.76835	1.606849	1.61E-43	2.13E-42
COL6A1	91.82498	221.1245	1.2679	9.93E-87	7.15E-85
ARHGAP28	0.422085	0.975142	1.208081	1.83E-96	2.01E-94
C16orf54	1.062089	2.292409	1.10996	3.56E-42	4.44E-41
CYP19A1	0.051638	0.92074	4.156302	1.04E-22	6.06E-22
MYL3	0.196028	0.441893	1.17264	7.49E-92	6.58E-90
CEMIP	1.852437	4.299808	1.214848	7.16E-31	5.93E-30
TMSB15A	6.610548	2.429219	-1.44428	8.24E-08	1.84E-07
ADAMTS5	1.064608	2.198705	1.046331	5.15E-74	2.22E-72
RECK	1.557915	3.853149	1.306421	1.01E-123	7.26E-121
PRSS3	0.444472	0.140418	-1.66236	0.014386857	0.019231945
CLEC17A	0.17535	0.35498	1.017499	1.39E-21	7.64E-21
SLCO2B1	3.186958	6.596754	1.049577	2.80E-75	1.28E-73
PENK	0.201243	0.727917	1.854837	1.68E-28	1.27E-27
HPDL	2.273143	1.037774	-1.1312	3.38E-05	6.01E-05
TMPRSS6	3.14985	1.518859	-1.0523	0.009639446	0.013162463
MUC7	0.175424	0.628501	1.841068	3.56E-07	7.56E-07
FADS6	0.188302	0.032112	-2.55186	2.95E-06	5.78E-06

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PRDM8	0.223851	0.491611	1.134978	9.05E-91	7.70E-89
PECAM1	14.72296	29.78364	1.016452	3.86E-95	3.98E-93
MYH11	2.938914	6.544446	1.154988	1.22E-40	1.42E-39
PCDHGA12	0.331355	0.694535	1.067668	7.07E-80	3.73E-78
GPR158	0.525924	0.236632	-1.15221	0.018693571	0.024652396
MFAP5	6.90962	19.1193	1.468351	4.79E-85	3.18E-83
TBX18	0.486931	1.142214	1.230043	1.40E-101	2.03E-99
LCN6	0.071742	0.178961	1.318748	2.30E-21	1.25E-20
ELAVL2	1.002201	0.467524	-1.10006	0.000775418	0.001201584
EGR2	3.993135	8.249238	1.046739	1.04E-43	1.39E-42
POSTN	122.6003	337.7909	1.462168	2.00E-93	1.89E-91
CST9L	0.587715	0.276837	-1.08608	0.010900049	0.014788809
TEK	1.800491	3.768683	1.06567	3.00E-71	1.15E-69
PARP15	0.366861	0.795425	1.116493	9.18E-42	1.13E-40
NEURL1	4.340861	2.108994	-1.04143	4.35E-05	7.68E-05
CHIT1	1.206048	4.210135	1.803579	2.40E-15	9.19E-15
PCOLCE	16.8827	40.69438	1.269284	5.99E-90	4.85E-88
VEGFD	0.341527	0.76017	1.15432	5.31E-15	1.98E-14
TMEM252	0.043554	0.108498	1.316797	5.88E-36	5.85E-35
AGXT	0.081498	0.249698	1.615345	4.01E-09	1.00E-08
KLHL4	0.089896	0.250704	1.479657	4.74E-63	1.34E-61
GPD1	2.213281	7.81726	1.820476	4.19E-18	1.91E-17
PRTN3	0.421844	0.16451	-1.35853	0.000541722	0.000852262
CR1	0.093652	0.221032	1.23887	2.86E-31	2.40E-30
TPSB2	7.727632	16.96091	1.134115	4.58E-29	3.54E-28
CRYBA2	0.40755	0.063212	-2.6887	8.65E-08	1.93E-07
LAMA2	2.038473	5.980339	1.552739	3.82E-89	2.90E-87
TSHZ3	1.611	3.625759	1.170327	7.24E-118	2.74E-115
LRRC15	11.04221	39.86284	1.852015	6.73E-98	8.18E-96
HTRA1	69.19381	179.5765	1.375884	6.66E-111	1.53E-108
CD48	3.62074	7.265684	1.004814	2.75E-44	3.72E-43
PDGFRB	18.18703	40.37043	1.150389	4.02E-114	1.24E-111
PCDH7	1.252097	2.845589	1.18438	5.32E-81	2.96E-79
RUNX1T1	0.299432	0.728818	1.283333	5.35E-113	1.52E-110
TMEM213	0.900241	0.385613	-1.22316	0.024354653	0.031621542
SORCS2	1.064212	3.00887	1.499436	1.64E-80	8.84E-79
MXRA8	25.43406	52.00347	1.031846	1.46E-69	5.27E-68
C3orf80	1.21724	2.469936	1.02086	8.12E-81	4.48E-79
MSI1	2.912179	1.276551	-1.18985	5.14E-09	1.27E-08
CIDEA	0.749215	2.306358	1.622165	8.22E-19	3.90E-18
TSPAN7	2.235329	4.564347	1.029921	4.33E-38	4.64E-37
LRTM2	0.739518	0.197325	-1.90601	0.000371613	0.00059636

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
DPT	9.459844	34.01147	1.846133	3.33E-103	5.33E-101
ERVFRD-1	0.059934	0.240765	2.006176	3.90E-28	2.91E-27
FMO1	1.385284	3.174777	1.196474	3.37E-56	7.32E-55
CPED1	1.025133	2.194414	1.098025	2.56E-85	1.74E-83
PRRX1	7.845041	19.97272	1.348178	2.37E-119	9.77E-117
PRSS33	1.41159	0.375432	-1.9107	0.006724023	0.009338005
TERT	0.167503	0.068617	-1.28754	1.55E-15	6.02E-15
CYP1A1	0.05025	0.162623	1.694343	0.02631852	0.033996212
NUGGC	0.189962	0.420819	1.147489	2.73E-41	3.27E-40
GFRA3	1.518352	0.259942	-2.54624	0.008608932	0.011826526
C1QTNF3	3.154058	8.273563	1.391299	3.22E-52	6.06E-51
TESPA1	0.470854	1.029836	1.129064	9.47E-46	1.35E-44
COL6A6	0.167515	0.4444	1.407567	4.71E-54	9.52E-53
DKK3	7.776233	16.0715	1.047361	9.37E-74	4.01E-72
CD36	5.6039	12.19	1.121195	1.43E-24	9.08E-24
ACTL8	4.374555	1.762887	-1.3112	2.33E-07	5.03E-07
FAM131C	0.431519	0.167295	-1.36703	2.34E-11	6.92E-11
NDN	4.547895	9.947947	1.1292	1.43E-102	2.21E-100
SLC1A7	0.118054	0.314545	1.413826	3.92E-79	2.03E-77
PIK3CG	0.606742	1.512947	1.318207	5.14E-67	1.67E-65
SLC1A2	2.565454	1.127468	-1.18613	9.11E-06	1.71E-05
LOX	6.353005	16.39884	1.368083	1.52E-103	2.53E-101
LHFPL6	10.18344	22.02517	1.112928	1.13E-96	1.26E-94
FOS	50.57364	107.135	1.082972	3.67E-27	2.61E-26
C9orf84	0.080297	0.185415	1.20733	6.66E-09	1.63E-08
DACT3	0.722325	1.531938	1.084639	2.45E-86	1.74E-84
PLXNC1	2.83257	6.642928	1.229708	9.42E-110	1.97E-107
PDPN	3.906365	9.276355	1.247731	1.75E-100	2.38E-98
DCSTAMP	0.233543	0.520125	1.15517	3.74E-23	2.23E-22
C8orf86	0.299091	0.097334	-1.61957	4.18E-07	8.82E-07
GRIN2C	0.566263	0.245184	-1.20761	8.11E-05	0.00013978
TEX14	1.388928	0.507279	-1.45312	0.004787185	0.006777569
CTSK	57.55395	177.0593	1.621246	3.94E-135	8.93E-132
SPOCK3	0.042665	0.138093	1.694514	8.79E-13	2.85E-12
PDE1B	0.53296	1.15211	1.112181	3.22E-84	2.06E-82
COL15A1	13.42067	28.48256	1.085622	1.87E-98	2.29E-96
C1S	36.92673	75.49182	1.031655	1.28E-111	3.23E-109
AVPR2	0.306345	0.646522	1.07754	2.43E-25	1.59E-24
LUM	116.3737	369.4877	1.666761	2.99E-133	5.81E-130
OGDHL	0.402885	0.117155	-1.78195	8.42E-05	0.000145057
KCNA1	0.043804	0.111382	1.346375	5.45E-50	9.38E-49
SULT1B1	0.099635	0.325443	1.707679	3.02E-30	2.45E-29

Table S2 *(continued)*

Table S2 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PREX2	0.512404	1.114959	1.121638	4.81E-65	1.44E-63
GIMAP1	1.0652	2.13265	1.001522	1.18E-54	2.43E-53
RARRES2	14.82585	32.12196	1.115445	3.84E-69	1.36E-67
HEG1	5.625239	12.77524	1.183365	1.60E-120	7.26E-118
THBS2	32.38425	91.6077	1.500177	1.27E-101	1.85E-99
WDFY4	0.697652	1.505824	1.109973	1.37E-58	3.23E-57
CYTL1	0.729683	1.569356	1.104832	9.73E-43	1.24E-41
FOSB	6.456207	17.06021	1.401876	1.62E-19	7.95E-19

Table S3 DEGs based upon immune scores

Gene	conMean	treatMean	logFC	P value	fdr
NSG2	2.728889	0.325978	-3.06547	0.00077113	0.001358121
CPLX2	2.414082	0.314533	-2.94019	0.013903927	0.020225331
CNMD	1.051576	0.163392	-2.68615	0.017872377	0.025522893
KCNC1	0.330574	0.056977	-2.53652	1.39E-05	3.11E-05
LMOD2	0.200502	0.03494	-2.52066	0.002133283	0.003507262
TRH	21.80203	4.152237	-2.3925	1.65E-08	5.39E-08
CGA	18.60144	3.687994	-2.33451	0.001563637	0.002628173
CSMD3	0.210856	0.042826	-2.2997	2.94E-05	6.30E-05
RTL9	0.366743	0.075721	-2.276	0.004543666	0.007112594
NELL1	0.932896	0.197731	-2.23818	0.013314072	0.019419519
CYP2A6	38.51201	8.240002	-2.22459	3.16E-07	8.73E-07
UGT2B4	5.81663	1.318364	-2.14143	7.59E-05	0.000153386
ZDHHC22	0.314074	0.076728	-2.03328	0.000270025	0.000506252
SLC5A7	0.204297	0.051331	-1.99276	3.76E-05	7.93E-05
CYP17A1	0.376669	0.099247	-1.9242	0.000894484	0.001560714
RPL3L	0.473993	0.126541	-1.90527	0.00163843	0.002744085
ASCL1	4.174378	1.119588	-1.89859	0.020482352	0.028964839
RUNDC3A	1.689786	0.454267	-1.89523	0.009426403	0.014103006
MYT1	1.082448	0.296037	-1.87045	6.89E-14	3.86E-13
KCNH6	0.232574	0.064325	-1.85424	0.004525178	0.007086809
PRR4	2.118757	0.592475	-1.83839	0.011363716	0.016771319
FAM135B	0.39912	0.114336	-1.80355	1.81E-08	5.88E-08
CELF3	0.348343	0.102576	-1.76381	1.27E-05	2.85E-05
CST9	15.23604	4.584421	-1.73268	5.31E-10	2.05E-09
INSYN2	5.310157	1.738563	-1.61086	2.89E-09	1.03E-08
SYNPO2L	2.336806	0.774807	-1.59263	2.56E-08	8.16E-08
SEZ6L	2.447436	0.812118	-1.59151	0.007724211	0.011704485
GDAP1L1	0.161179	0.05356	-1.58944	3.04E-05	6.50E-05
CHRNB2	1.050718	0.350755	-1.58284	4.74E-05	9.85E-05
LRTM2	0.700936	0.235837	-1.57149	0.013114704	0.01915256
INHA	2.76851	0.932215	-1.57038	4.98E-05	0.00010329
FCRLB	4.754776	1.632123	-1.54263	0.000604089	0.001082773
SERPINC1	0.418512	0.145265	-1.52659	0.004919878	0.007670778
MYOG	0.127913	0.044634	-1.51896	2.12E-07	5.99E-07
CPB1	446.7315	156.7354	-1.51108	5.40E-09	1.86E-08
C8orf86	0.292849	0.103565	-1.49962	1.01E-14	6.09E-14
ATRNL1	1.670195	0.593519	-1.49265	5.80E-06	1.36E-05
WDR72	1.021145	0.363768	-1.4891	0.002015285	0.003330003
SCGN	3.385736	1.206497	-1.48864	0.00020948	0.000398531
RLN2	3.068419	1.111423	-1.46509	2.90E-07	8.06E-07
SLC8A2	0.510237	0.187064	-1.44764	0.002344165	0.003827569
KCNC2	2.280864	0.846008	-1.43084	9.03E-06	2.07E-05

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
PHF21B	0.504652	0.189302	-1.4146	1.58E-07	4.55E-07
NXPH1	3.391889	1.291178	-1.3934	0.010493857	0.015567567
SYT13	19.34318	7.413561	-1.38359	9.56E-08	2.82E-07
KCNJ3	17.78859	6.847611	-1.37728	5.05E-08	1.54E-07
RTBDN	1.272728	0.496139	-1.35911	0.008663226	0.013027721
SMCO3	1.458359	0.569081	-1.35764	0.015459605	0.022342719
PHGR1	3.529591	1.394687	-1.33956	7.00E-08	2.11E-07
PAH	0.463776	0.18789	-1.30354	0.000123769	0.000243232
CYP2A7	12.73642	5.236363	-1.28232	0.000136376	0.000266074
PXDNL	2.750532	1.134218	-1.27801	0.009846075	0.014663813
TMEM145	2.561657	1.059184	-1.27412	3.74E-13	1.97E-12
PEX5L	0.81471	0.337172	-1.2728	1.17E-10	4.86E-10
CDH7	0.213111	0.088206	-1.27266	4.99E-07	1.35E-06
NOVA1	3.879278	1.610373	-1.26839	5.23E-05	0.000107921
SYP	2.272178	0.949057	-1.25951	0.016342399	0.023514663
BRINP2	2.924498	1.240924	-1.23677	2.42E-06	5.99E-06
NTSR2	0.205699	0.088503	-1.21674	0.032645845	0.044748446
COL2A1	17.27513	7.473957	-1.20875	2.28E-09	8.22E-09
CST9L	0.601475	0.263101	-1.19289	4.13E-10	1.61E-09
SLC27A2	11.49557	5.032495	-1.19173	3.24E-08	1.02E-07
VSTM2A	6.427241	2.828086	-1.18437	0.024388033	0.034059943
KRT24	0.601491	0.265788	-1.17827	0.000485485	0.000882329
RP1	0.185142	0.081868	-1.17727	0.000264173	0.000495874
CACNB2	1.009616	0.44651	-1.17704	0.017650787	0.025221815
HEPACAM2	2.522725	1.126542	-1.16308	7.12E-06	1.65E-05
NRCAM	2.640977	1.18083	-1.16127	4.40E-05	9.21E-05
FAM234B	23.35576	10.47959	-1.1562	4.00E-21	3.62E-20
CADM2	0.430231	0.195544	-1.13762	3.91E-12	1.89E-11
ELOVL2	16.22456	7.384002	-1.1357	5.24E-09	1.81E-08
RIMS4	9.093853	4.141138	-1.13486	5.70E-10	2.19E-09
NPC1L1	0.527981	0.241455	-1.12873	1.29E-12	6.51E-12
KRT33A	0.259284	0.118925	-1.12448	9.22E-05	0.000184027
STC2	126.7623	58.14373	-1.12443	8.97E-11	3.78E-10
APLP1	5.987257	2.753686	-1.12053	0.008000043	0.012091189
KLHL41	0.566586	0.261596	-1.11495	0.00027436	0.000514106
PYY	1.42129	0.657762	-1.11156	6.92E-09	2.36E-08
SLC1A2	2.520135	1.172705	-1.10366	4.73E-12	2.26E-11
EEF1A2	76.26907	35.50946	-1.10289	2.31E-14	1.35E-13
RBM24	5.20993	2.435521	-1.09703	4.26E-05	8.91E-05
DCDC1	0.486767	0.229865	-1.08244	2.00E-09	7.25E-09
AFF3	15.63104	7.398875	-1.07904	7.51E-18	5.73E-17
BMPR1B	45.21727	21.41082	-1.07853	2.38E-06	5.90E-06

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
GRIA2	3.915184	1.857686	-1.07557	5.64E-07	1.51E-06
C10orf113	0.342183	0.162657	-1.07294	0.000262464	0.00049293
FAM57B	0.701035	0.334833	-1.06605	9.33E-12	4.32E-11
PRTN3	0.396688	0.18962	-1.06489	1.29E-07	3.75E-07
STH	0.289018	0.138206	-1.06434	2.16E-08	6.95E-08
WDR17	0.523047	0.251158	-1.05835	0.000444123	0.00081135
TMPRSS6	3.153326	1.515389	-1.05719	2.29E-09	8.24E-09
ADAMTS19	0.63702	0.307087	-1.05269	2.65E-07	7.39E-07
MPPED1	0.213485	0.103044	-1.05088	0.003742782	0.00593754
NEURL1	4.34863	2.101239	-1.04932	6.43E-07	1.71E-06
SCUBE1	1.38817	0.671386	-1.04797	0.020885545	0.029499416
SERPINA6	35.01784	16.97602	-1.04459	0.000517383	0.000935828
MS4A8	1.170655	0.568422	-1.04228	9.63E-10	3.60E-09
BSN	0.363356	0.176512	-1.04162	7.22E-12	3.39E-11
LRP2	11.1319	5.408756	-1.04133	1.89E-06	4.74E-06
TMEM82	0.158981	0.077549	-1.03569	0.010797409	0.015989215
DNAJC12	30.90977	15.14134	-1.02957	4.17E-16	2.78E-15
TMPRSS11E	1.379565	0.678235	-1.02436	0.020208214	0.028611691
IGDCC3	0.908454	0.451056	-1.01011	5.46E-06	1.29E-05
VNN3	0.089672	0.179444	1.00081	2.32E-16	1.59E-15
CTSG	1.023617	2.060403	1.00925	2.02E-16	1.38E-15
SAMHD1	15.4686	31.15543	1.01014	1.34E-99	6.60E-98
SLC12A3	0.070932	0.142893	1.010416	1.40E-73	4.00E-72
CD300LG	0.400417	0.806715	1.010555	2.03E-15	1.29E-14
GYPC	4.163223	8.389582	1.010898	1.21E-73	3.45E-72
LIPG	0.312924	0.630775	1.011315	7.85E-33	1.02E-31
TLR4	2.391856	4.827445	1.013129	3.59E-71	9.70E-70
C11orf16	0.144779	0.292254	1.01337	3.41E-07	9.38E-07
GIMAP8	2.210054	4.46849	1.015706	1.27E-75	3.78E-74
IL12RB2	0.460834	0.932988	1.01761	3.10E-45	5.24E-44
DOCK8	2.121543	4.300225	1.019298	6.78E-67	1.73E-65
ACSL5	3.970288	8.051108	1.019944	4.45E-60	9.74E-59
CSAG3	0.249791	0.506849	1.020835	4.53E-12	2.17E-11
C5AR1	3.272868	6.641662	1.020989	1.42E-71	3.88E-70
BATF3	0.44015	0.894802	1.023574	5.72E-72	1.57E-70
NRROS	1.504625	3.062123	1.025128	6.69E-89	2.60E-87
P2RY6	0.994139	2.026326	1.027347	1.92E-71	5.24E-70
S100A7A	1.494377	3.046007	1.027375	3.82E-08	1.19E-07
EPHB6	1.135144	2.31385	1.027419	3.53E-40	5.33E-39
WARS	17.05904	34.77832	1.027651	2.38E-50	4.44E-49
MAL	0.750744	1.53073	1.027826	3.39E-79	1.08E-77
LILRA1	0.182739	0.372617	1.027909	2.17E-65	5.34E-64

Table S3 *(continued)*

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Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
IFI16	11.19982	22.86692	1.029786	1.13E-85	4.11E-84
TDRD12	0.475181	0.973268	1.034359	0.001548303	0.002603334
TPSD1	1.456181	2.98724	1.036624	0.008429851	0.012701216
GLYAT	0.096603	0.19834	1.037832	3.72E-08	1.16E-07
BMP3	0.070599	0.144998	1.03832	6.33E-05	0.000129345
PRDM1	2.223254	4.570207	1.039587	1.06E-78	3.34E-77
HAPLN3	5.432724	11.17957	1.041117	5.69E-71	1.52E-69
GAPT	0.957449	1.975764	1.045143	2.55E-47	4.45E-46
RGS13	0.079034	0.16312	1.045395	2.99E-29	3.51E-28
BIRC7	0.155378	0.320903	1.04635	1.49E-22	1.42E-21
SLC1A3	1.905253	3.940747	1.048487	6.54E-70	1.72E-68
KLRF1	0.246053	0.509008	1.048717	1.02E-44	1.71E-43
APOBEC3C	6.87736	14.23285	1.049298	2.39E-82	8.31E-81
SOWAHD	0.427735	0.885446	1.049689	2.54E-61	5.74E-60
IFI44L	4.684015	9.705149	1.051005	5.17E-39	7.62E-38
CAMK4	0.244063	0.506384	1.052976	7.90E-60	1.72E-58
RUBCNL	0.698612	1.450203	1.053692	6.61E-67	1.69E-65
C14orf180	0.171605	0.356312	1.054049	1.28E-09	4.74E-09
TF	1.838286	3.818779	1.05475	3.27E-08	1.03E-07
LGI2	0.555935	1.155441	1.055457	1.42E-50	2.65E-49
P2RY14	0.466392	0.970441	1.057099	1.58E-65	3.91E-64
LAT2	1.96848	4.099775	1.058463	1.09E-104	6.03E-103
MIXL1	0.159139	0.33164	1.059335	2.62E-40	3.97E-39
ICAM1	9.274419	19.355	1.061378	1.01E-58	2.16E-57
LCP1	23.18574	48.41775	1.062298	1.59E-73	4.52E-72
MEFV	0.086515	0.181458	1.068613	2.61E-50	4.85E-49
FLI1	1.606163	3.370977	1.069549	1.35E-99	6.63E-98
ALOX5AP	7.175782	15.07118	1.070585	1.50E-79	4.85E-78
MZB1	8.023471	16.85415	1.070805	4.07E-29	4.78E-28
TREML1	0.225493	0.473937	1.071615	1.47E-60	3.25E-59
CYSLTR2	0.206646	0.434417	1.071917	3.83E-63	9.00E-62
HEPHL1	0.132491	0.278611	1.072355	0.003603536	0.005731509
SERPINB9	2.617045	5.506606	1.073225	9.66E-89	3.74E-87
SAMD9L	5.069203	10.66718	1.073348	2.59E-54	5.16E-53
GIMAP6	3.615793	7.613478	1.074244	6.79E-80	2.23E-78
EPYC	1.526004	3.214592	1.074877	4.63E-14	2.63E-13
SLC22A3	0.380521	0.801625	1.07495	3.53E-44	5.86E-43
CPNE5	1.010179	2.1313	1.077122	6.58E-59	1.41E-57
HLA-B	356.8178	752.8702	1.077214	3.33E-74	9.62E-73
IL7	0.300135	0.634984	1.081107	2.51E-51	4.75E-50
MAP1LC3C	0.282915	0.598661	1.081371	4.69E-31	5.80E-30
C2	3.044141	6.453943	1.084146	3.31E-83	1.17E-81

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
S100A9	205.7698	436.4039	1.084633	1.67E-31	2.09E-30
MEOX1	1.319936	2.808109	1.089132	1.22E-28	1.40E-27
OSCAR	1.725058	3.671157	1.08959	3.75E-78	1.17E-76
CMA1	0.443238	0.944494	1.091462	7.70E-16	5.03E-15
TAP2	3.888744	8.289627	1.092003	8.70E-63	2.03E-61
DPT	13.87647	29.6028	1.093093	7.31E-40	1.10E-38
COL4A4	0.241102	0.515337	1.095871	9.31E-46	1.59E-44
HLA-E	123.7002	264.4688	1.09625	1.32E-108	8.13E-107
LYN	3.838819	8.21086	1.096871	1.48E-92	6.25E-91
AGAP2	0.589864	1.262327	1.097631	2.56E-88	9.82E-87
DOK3	1.353008	2.902501	1.101126	3.21E-106	1.86E-104
GPBAR1	0.16178	0.347267	1.102017	1.05E-65	2.61E-64
LGALS9	6.814745	14.64762	1.103935	3.86E-87	1.45E-85
LY86	3.959979	8.516019	1.104687	2.44E-99	1.19E-97
CD300A	2.438561	5.248581	1.105897	7.95E-102	4.11E-100
CELF2	2.134897	4.597909	1.106812	2.95E-79	9.44E-78
ADGRE5	4.433888	9.549683	1.106881	3.40E-86	1.25E-84
CLIC2	2.868779	6.18097	1.107396	1.32E-90	5.36E-89
IL15	0.321184	0.692573	1.108565	1.23E-81	4.22E-80
TSHR	0.071301	0.153827	1.109319	4.94E-48	8.76E-47
CD14	23.43428	50.58969	1.110223	2.23E-73	6.29E-72
LY6D	4.348987	9.391013	1.110601	6.68E-11	2.85E-10
LYL1	0.906892	1.958813	1.110977	2.38E-64	5.73E-63
TEX11	0.066981	0.145177	1.115984	5.54E-45	9.35E-44
MCOLN2	0.812659	1.762798	1.117145	1.22E-64	2.95E-63
CASP1	3.315466	7.19423	1.117629	4.46E-94	1.95E-92
CHRDL1	2.8247	6.139203	1.119954	3.47E-25	3.63E-24
ABI3	2.848489	6.192482	1.120321	4.88E-116	4.18E-114
SLC15A3	3.878231	8.431998	1.120476	2.72E-110	1.82E-108
CCDC69	2.952072	6.421956	1.121285	1.35E-70	3.60E-69
CPA1	0.029329	0.063968	1.125004	7.27E-07	1.92E-06
CLEC7A	2.123307	4.639366	1.127615	1.93E-92	8.06E-91
MILR1	1.523007	3.329235	1.128269	1.99E-109	1.26E-107
PLD4	0.771792	1.687527	1.128626	1.07E-38	1.56E-37
WNT10A	0.389571	0.852652	1.130071	7.71E-75	2.26E-73
LY96	6.261711	13.70789	1.130377	3.49E-110	2.31E-108
SELE	1.417646	3.105072	1.13113	7.09E-39	1.04E-37
CXCR2	0.09745	0.213591	1.132123	1.12E-41	1.74E-40
IFI30	0.276989	0.607863	1.133916	1.23E-79	3.99E-78
PILRA	2.468964	5.420289	1.134464	1.47E-103	7.89E-102
SIGLEC9	0.791121	1.739745	1.136907	3.18E-97	1.46E-95
GLT1D1	0.070043	0.154084	1.137407	1.77E-60	3.91E-59

Table S3 *(continued)*

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Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
APOBEC3D	1.180195	2.596265	1.137412	1.89E-64	4.55E-63
PRAM1	0.425113	0.935906	1.138518	1.99E-79	6.45E-78
MATK	0.723905	1.594247	1.139003	1.13E-54	2.26E-53
G0S2	9.999633	22.02369	1.139109	8.63E-32	1.09E-30
SEL1L3	3.164518	6.975114	1.140231	3.46E-51	6.52E-50
CARMIL2	0.452781	1.001728	1.145608	2.88E-52	5.51E-51
C4BPA	0.724631	1.60384	1.146211	7.28E-07	1.92E-06
IRF1	5.738171	12.70845	1.147125	1.86E-87	7.02E-86
TRIM22	6.310583	13.97701	1.14721	1.90E-80	6.35E-79
ADGRE2	0.437833	0.970074	1.147714	2.79E-67	7.15E-66
TNFSF18	0.165361	0.366385	1.147741	1.03E-33	1.35E-32
CARD16	1.941866	4.304895	1.148535	1.41E-104	7.74E-103
KRT81	28.19567	62.60873	1.15089	2.11E-08	6.78E-08
VSIR	3.776617	8.391591	1.15185	1.24E-98	5.97E-97
CAPN6	2.858231	6.351328	1.151936	4.02E-15	2.49E-14
GPA33	0.075935	0.168825	1.152689	3.86E-68	9.99E-67
PRSS12	0.616447	1.372842	1.155117	2.54E-10	1.02E-09
PIGR	9.302722	20.73798	1.15655	2.29E-11	1.02E-10
OR52N4	0.06517	0.145285	1.156614	7.48E-41	1.14E-39
CEACAM21	0.508402	1.133444	1.156672	2.36E-82	8.21E-81
HLA-G	1.797553	4.015942	1.159704	9.85E-27	1.07E-25
GSDMA	0.283409	0.633376	1.160174	5.78E-39	8.51E-38
CD68	0.409871	0.916508	1.160977	1.80E-63	4.27E-62
IL18R1	0.45456	1.017294	1.162196	1.37E-74	3.97E-73
TRARG1	1.581955	3.545781	1.164395	7.13E-11	3.03E-10
CH25H	1.009343	2.264275	1.165633	5.97E-44	9.78E-43
ACHE	0.383356	0.861208	1.167678	9.08E-32	1.14E-30
IVL	0.381178	0.85673	1.168374	7.19E-06	1.67E-05
MGAM2	0.311779	0.701028	1.168947	3.75E-06	9.02E-06
LPXN	5.117802	11.5093	1.169204	1.56E-128	2.20E-126
CCL20	0.699452	1.57345	1.169634	1.10E-33	1.44E-32
C1S	34.56428	77.85001	1.171415	6.69E-78	2.09E-76
APOL3	4.216521	9.511335	1.173595	4.07E-82	1.40E-80
CMKLR1	1.929114	4.353126	1.174113	4.64E-89	1.81E-87
FCGR2B	0.838801	1.892858	1.174166	3.68E-87	1.38E-85
IL1B	0.988997	2.232195	1.174425	9.13E-45	1.53E-43
CD1A	0.569387	1.286093	1.175513	1.73E-32	2.23E-31
KBTBD8	0.301596	0.681535	1.176168	2.99E-75	8.81E-74
CDX1	0.16117	0.364334	1.176674	8.15E-40	1.22E-38
ADGRE1	0.232721	0.526101	1.176739	1.81E-76	5.50E-75
RGS1	9.73868	22.03374	1.177917	1.90E-58	4.05E-57
SLC9A9	1.071041	2.424285	1.178546	5.25E-103	2.75E-101

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
GNGT2	0.506531	1.147449	1.179707	1.60E-131	3.12E-129
SNAI3	0.470624	1.067272	1.181282	2.59E-78	8.13E-77
GLYATL2	10.18764	23.11888	1.182252	5.68E-06	1.34E-05
KIF21B	0.517089	1.173734	1.182622	1.39E-68	3.61E-67
APOL1	16.29846	37.06103	1.185167	2.16E-90	8.67E-89
CTSC	5.559414	12.64762	1.185862	4.35E-84	1.56E-82
TMEM273	1.047839	2.38461	1.186337	5.65E-92	2.36E-90
PTGER4	1.574191	3.590101	1.189414	5.35E-90	2.13E-88
C3AR1	5.29832	12.09034	1.190248	1.26E-104	6.93E-103
RUNX3	2.840457	6.498944	1.194083	1.30E-92	5.48E-91
KIF19	0.140739	0.32256	1.196549	1.10E-40	1.68E-39
CPVL	4.057838	9.305414	1.197359	6.38E-105	3.55E-103
SPNS3	0.194281	0.445622	1.197675	1.76E-54	3.52E-53
HVCN1	0.978827	2.249782	1.200659	2.10E-110	1.42E-108
TLR7	1.217115	2.800604	1.202272	2.02E-69	5.27E-68
FXYD7	0.096488	0.222023	1.202296	4.28E-43	6.86E-42
WIPF1	4.604925	10.60962	1.204123	4.17E-115	3.45E-113
FCGR1B	0.174368	0.401882	1.204634	1.49E-81	5.11E-80
SCARA5	0.501713	1.156425	1.204737	3.57E-30	4.29E-29
SLCO2B1	2.957001	6.826296	1.206968	1.99E-93	8.53E-92
HAVCR2	3.17254	7.333054	1.208776	5.53E-118	5.12E-116
EMILIN2	1.56566	3.620029	1.20923	1.23E-94	5.41E-93
LILRA6	0.265357	0.613796	1.209823	7.62E-65	1.85E-63
AKNA	2.229258	5.156894	1.209939	3.94E-103	2.08E-101
KCNAB2	1.391016	3.220194	1.211008	9.54E-115	7.62E-113
GBP6	0.178546	0.414709	1.215804	3.53E-40	5.33E-39
CCL22	1.663371	3.865684	1.216614	1.28E-69	3.37E-68
IL1A	0.105146	0.244458	1.2172	1.72E-19	1.43E-18
GPR150	0.0743	0.172824	1.217871	1.03E-66	2.61E-65
PRDM8	0.214734	0.500711	1.221427	4.73E-82	1.63E-80
PPBP	0.064947	0.151507	1.222042	4.40E-05	9.21E-05
TRAF1	1.643852	3.835383	1.22229	9.08E-85	3.28E-83
CD33	0.37316	0.871272	1.22333	7.80E-115	6.27E-113
CASS4	0.287637	0.671884	1.223963	5.23E-103	2.75E-101
OSM	0.83442	1.952434	1.226427	1.77E-45	3.01E-44
ABI3BP	1.502638	3.518456	1.227445	5.12E-48	9.06E-47
CCL3	2.204605	5.169713	1.229564	4.11E-63	9.63E-62
GPSM3	8.004102	18.79422	1.231478	6.06E-109	3.79E-107
LRRC25	1.663194	3.907079	1.232134	8.93E-121	9.11E-119
SLC26A9	0.146952	0.345284	1.232439	4.11E-20	3.55E-19
FAM20A	1.342258	3.154476	1.232739	2.58E-75	7.61E-74
TNFRSF4	1.404835	3.301915	1.232902	7.85E-60	1.71E-58

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
NFAM1	1.312583	3.085737	1.233207	9.16E-98	4.35E-96
LSP1	7.781112	18.30887	1.234495	2.88E-100	1.43E-98
FCGR1A	1.163663	2.746591	1.238969	9.15E-87	3.40E-85
TRPV2	2.348036	5.549271	1.240844	1.78E-130	3.09E-128
NLRC3	0.69509	1.643526	1.241523	1.75E-82	6.11E-81
TNFAIP3	4.925116	11.65614	1.242861	2.48E-93	1.06E-91
CSF2RA	1.491727	3.530939	1.243068	1.80E-103	9.55E-102
STX11	1.153815	2.731748	1.243412	2.31E-97	1.07E-95
FCGR3A	16.77016	39.75154	1.245115	2.01E-77	6.22E-76
AGXT	0.098203	0.233023	1.246626	6.64E-08	2.00E-07
RAB33A	0.457933	1.086727	1.246781	3.82E-94	1.68E-92
PLA1A	1.119757	2.659386	1.247907	8.69E-46	1.48E-44
LEP	0.95839	2.280136	1.250435	1.90E-11	8.55E-11
RCSD1	2.000945	4.762531	1.251047	7.76E-104	4.22E-102
CD40	3.508589	8.352104	1.251249	3.22E-112	2.32E-110
FMO3	1.27826	3.043196	1.251406	2.38E-24	2.44E-23
KRT86	1.90644	4.539927	1.251788	8.45E-14	4.68E-13
RNASE6	7.770187	18.50439	1.251847	3.08E-115	2.58E-113
CCL4L2	1.877723	4.480599	1.254707	2.39E-63	5.62E-62
MFNG	2.113132	5.042502	1.254756	6.62E-106	3.81E-104
KLRG1	0.420363	1.004718	1.257084	6.55E-66	1.64E-64
TRPM8	0.126489	0.302477	1.257814	7.43E-17	5.26E-16
FABP4	24.73791	59.21112	1.259144	4.84E-14	2.74E-13
SELP	1.5165	3.635645	1.261466	2.42E-34	3.24E-33
FABP7	9.636444	23.13858	1.263727	3.39E-09	1.19E-08
FCER1G	21.9509	52.96642	1.270798	4.02E-123	4.63E-121
HLA-F	9.874743	23.83534	1.271287	1.99E-76	6.01E-75
SIRPB2	0.442301	1.069047	1.273223	4.71E-99	2.28E-97
CSF1R	7.188162	17.39719	1.27516	1.33E-109	8.60E-108
SLC7A7	2.357376	5.706983	1.275547	1.02E-121	1.10E-119
1-Sep	1.490387	3.610018	1.27632	4.46E-64	1.07E-62
PIK3AP1	2.433871	5.89929	1.277288	5.14E-99	2.48E-97
VSIG4	4.678339	11.33972	1.277317	1.90E-63	4.49E-62
FAM92B	0.121409	0.294539	1.27858	1.12E-27	1.26E-26
APOE	77.32314	187.7546	1.279876	1.68E-62	3.90E-61
PNMA5	0.112779	0.273868	1.27998	1.89E-15	1.21E-14
CADM3	0.5659	1.374739	1.280538	3.56E-31	4.40E-30
FPR1	1.422014	3.455287	1.28087	6.13E-80	2.01E-78
CD300C	0.788746	1.917222	1.281385	2.30E-101	1.17E-99
FATE1	0.172696	0.420556	1.284065	9.53E-13	4.87E-12
MMP1	10.75846	26.20053	1.284124	1.09E-10	4.57E-10
NLRP7	0.094597	0.230544	1.28517	6.03E-50	1.11E-48

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
ADA2	6.725749	16.41883	1.287585	2.99E-97	1.38E-95
XPNPEP2	0.196074	0.47931	1.289563	2.39E-50	4.45E-49
TM4SF19	0.194752	0.476834	1.29185	2.24E-11	1.00E-10
GIMAP1	0.927241	2.27036	1.291905	1.84E-91	7.62E-90
BCL11B	0.570256	1.396339	1.291967	1.35E-73	3.87E-72
IL15RA	1.84549	4.519897	1.292286	1.53E-106	8.89E-105
APOC1	27.83079	68.17604	1.292583	1.65E-65	4.07E-64
S100A7	69.09969	169.3087	1.292905	5.95E-11	2.55E-10
SLC2A5	0.522276	1.280369	1.293674	7.98E-67	2.03E-65
PI3	10.94128	26.848	1.295033	6.98E-13	3.60E-12
PI16	2.368824	5.817173	1.296147	2.35E-24	2.40E-23
VAV1	1.733235	4.258705	1.296948	1.39E-110	9.43E-109
FMNL1	2.443226	6.010995	1.298816	6.85E-133	1.48E-130
P2RY13	0.997803	2.458348	1.300862	7.67E-72	2.10E-70
HCK	3.718612	9.163342	1.30111	1.99E-119	1.93E-117
CD180	0.919881	2.267965	1.301879	3.50E-93	1.49E-91
MCEMP1	0.126424	0.312218	1.304279	7.57E-21	6.78E-20
TAP1	19.20395	47.43313	1.304492	3.31E-61	7.47E-60
CCL7	0.417146	1.031011	1.305436	6.19E-23	6.00E-22
SH2D2A	1.103972	2.729954	1.306174	4.05E-80	1.34E-78
CD80	0.267203	0.66089	1.306473	3.33E-73	9.37E-72
EVI2A	2.885238	7.136539	1.306534	1.87E-116	1.61E-114
CD1D	0.543835	1.345643	1.307056	2.98E-86	1.10E-84
PIM2	6.78147	16.8183	1.310362	7.25E-60	1.58E-58
NCF2	3.537107	8.778621	1.311424	1.97E-105	1.11E-103
ADGRG3	0.106191	0.263614	1.31177	8.04E-39	1.18E-37
BATF2	1.691455	4.199822	1.312064	8.24E-43	1.31E-41
NLRP3	0.517485	1.285565	1.312815	4.04E-100	2.00E-98
PLCB2	1.251155	3.111213	1.314216	3.86E-121	4.15E-119
TYROBP	30.90247	76.99359	1.317016	7.99E-123	9.06E-121
RASSF4	1.97494	4.939821	1.32265	2.45E-107	1.46E-105
JCHAIN	65.48074	163.8552	1.323279	5.41E-48	9.56E-47
C1orf162	3.025395	7.577808	1.324657	3.13E-133	7.46E-131
DNASE1L3	0.238878	0.599716	1.328008	1.71E-44	2.86E-43
GIMAP4	8.114773	20.40162	1.330061	4.29E-124	5.06E-122
DERL3	2.99144	7.521325	1.330147	1.93E-47	3.38E-46
IGSF6	2.396136	6.025605	1.330396	1.78E-109	1.14E-107
SIGLEC7	0.49027	1.233203	1.330761	1.02E-108	6.32E-107
GAB3	0.515411	1.299031	1.333641	2.26E-126	2.86E-124
THEMIS2	2.69226	6.786633	1.333878	5.96E-115	4.84E-113
SIGLEC1	1.680399	4.243965	1.336609	1.17E-73	3.35E-72
IL22RA2	0.1812	0.457888	1.337416	3.90E-37	5.55E-36

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CCL2	7.654475	19.34746	1.337769	2.31E-76	6.95E-75
CCL11	0.793844	2.010792	1.340836	1.46E-49	2.65E-48
CCDC88B	0.929632	2.361138	1.344751	2.52E-70	6.65E-69
AIF1	9.663958	24.62497	1.349436	7.37E-138	2.53E-135
PIK3R5	0.80019	2.041878	1.351482	9.08E-131	1.66E-128
CD8B2	0.219893	0.561248	1.351839	1.57E-19	1.32E-18
SHISAL2A	0.186883	0.477902	1.354583	2.67E-66	6.72E-65
GPR65	0.835928	2.142667	1.357957	2.14E-115	1.80E-113
IL18BP	1.938808	4.980065	1.360995	7.47E-116	6.37E-114
NLRC5	1.987358	5.110503	1.362613	5.80E-91	2.39E-89
IL6	0.819796	2.111042	1.364619	1.40E-36	1.96E-35
ETV7	1.771908	4.56511	1.365346	4.22E-55	8.57E-54
ACKR1	6.609754	17.0395	1.366214	4.25E-29	4.99E-28
LAPTM5	38.71369	99.87358	1.367259	5.84E-145	3.74E-142
MS4A6A	4.002798	10.33631	1.368641	1.19E-129	1.88E-127
ERVFRD-1	0.083913	0.216829	1.369594	2.82E-07	7.86E-07
ITGAX	1.884083	4.869604	1.369942	1.44E-117	1.29E-115
CCL24	0.174072	0.450018	1.370296	3.27E-35	4.48E-34
ITGAL	2.820233	7.310689	1.374193	3.31E-85	1.20E-83
CLEC4A	1.371277	3.555589	1.374568	1.15E-129	1.84E-127
LILRB3	0.247313	0.642121	1.376509	3.74E-112	2.67E-110
SELL	4.668111	12.13138	1.377833	1.72E-98	8.24E-97
INPP5D	1.855621	4.833975	1.381308	1.01E-122	1.12E-120
LIMD2	2.603699	6.797279	1.384394	1.00E-85	3.66E-84
RARRES1	15.82678	41.33833	1.385112	3.57E-42	5.61E-41
TNFAIP8L2	2.373102	6.201352	1.385809	1.41E-131	2.79E-129
C3	36.39676	95.12733	1.38605	1.11E-89	4.36E-88
MMP8	0.072087	0.188679	1.388129	2.55E-12	1.26E-11
TRABD2A	0.1404	0.368019	1.390237	1.70E-92	7.15E-91
PTAFR	2.320355	6.083163	1.390476	4.19E-118	3.93E-116
APBB1IP	2.399474	6.297181	1.391988	7.87E-132	1.58E-129
LAIR1	2.014008	5.291486	1.393603	9.28E-141	4.35E-138
CD274	0.732226	1.929698	1.398014	1.98E-77	6.13E-76
AC119396.1	0.181649	0.479319	1.399837	1.93E-32	2.48E-31
CD70	0.30109	0.794844	1.400479	1.34E-66	3.39E-65
IL10	0.228009	0.601979	1.400621	4.08E-90	1.62E-88
BHLHE22	0.355835	0.939673	1.40095	1.13E-60	2.50E-59
CCR1	2.97572	7.87595	1.404215	2.05E-95	9.16E-94
DPEP2	0.413625	1.096114	1.406001	4.79E-111	3.31E-109
MYO1F	1.458462	3.867157	1.406826	1.79E-143	9.34E-141
PLA2G7	2.520955	6.68632	1.407242	9.90E-62	2.26E-60
SOCS1	1.702924	4.528598	1.411051	6.19E-79	1.97E-77

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
HLA-DMA	15.76589	41.99059	1.413259	8.07E-131	1.49E-128
CD300E	0.346579	0.923108	1.413314	5.95E-62	1.37E-60
PPP1R16B	1.068852	2.851181	1.415497	3.99E-73	1.12E-71
TSPAN32	0.170758	0.456326	1.418109	3.13E-74	9.07E-73
S100A8	42.36826	113.5952	1.422847	5.58E-35	7.57E-34
GPR84	0.563762	1.511664	1.42298	6.48E-70	1.71E-68
LST1	2.223523	5.971214	1.425177	4.67E-132	9.51E-130
GNG8	0.241501	0.648599	1.425297	9.74E-45	1.63E-43
SPI1	6.379661	17.15413	1.427005	1.03E-135	3.00E-133
EPSTI1	2.629633	7.074613	1.42779	1.31E-96	5.95E-95
TNFSF8	0.600634	1.617787	1.429464	2.04E-101	1.04E-99
CD300LF	0.768277	2.07313	1.432111	2.61E-124	3.14E-122
SIGLEC14	0.82717	2.234006	1.433378	1.04E-73	3.00E-72
MS4A4A	2.481477	6.70899	1.434897	1.45E-110	9.83E-109
SELPLG	6.437585	17.46849	1.440164	2.23E-140	1.01E-137
FOLR2	3.87263	10.5239	1.442283	2.65E-69	6.92E-68
CLEC4G	0.057474	0.156222	1.442621	2.92E-33	3.81E-32
TRIM55	0.198054	0.53876	1.443753	3.50E-12	1.70E-11
IL32	7.826902	21.30714	1.444824	8.78E-87	3.28E-85
IL16	0.961029	2.616651	1.44507	3.37E-107	2.00E-105
PIK3CD	1.703144	4.644648	1.447369	8.72E-119	8.35E-117
CLEC9A	0.103395	0.282333	1.449237	4.29E-56	8.89E-55
MNDA	3.141132	8.580019	1.449696	2.64E-122	2.92E-120
CXCL1	1.066856	2.915685	1.450469	2.77E-25	2.90E-24
ASB2	0.209757	0.573961	1.452235	1.21E-90	4.94E-89
GMFG	5.408415	14.82527	1.454781	9.65E-135	2.56E-132
SIGLEC10	1.231834	3.386419	1.458953	1.14E-113	8.61E-112
FAM78A	1.019279	2.802502	1.459167	1.11E-143	6.01E-141
GIMAP7	5.372128	14.7752	1.459612	6.74E-94	2.93E-92
BTK	1.17079	3.221649	1.460317	4.33E-138	1.56E-135
EGFL6	1.163364	3.206357	1.462633	2.18E-36	3.06E-35
ARHGAP30	3.438403	9.487228	1.464248	3.75E-134	9.10E-132
CD86	2.158199	5.955658	1.464433	4.81E-135	1.30E-132
PARVG	0.822132	2.276955	1.469664	6.31E-138	2.22E-135
RAC2	8.727129	24.18842	1.470738	4.83E-107	2.85E-105
IPCEF1	0.203351	0.563767	1.471127	1.24E-93	5.34E-92
P2RX5	0.215504	0.597997	1.472427	1.01E-52	1.94E-51
CYTH4	1.529391	4.244253	1.472553	2.45E-139	1.01E-136
CXorf21	0.976862	2.717795	1.47621	2.15E-114	1.68E-112
CCR8	0.339464	0.946427	1.479232	2.28E-71	6.21E-70
ITGAD	0.10497	0.292965	1.480753	3.27E-51	6.16E-50
NCF4	2.617373	7.309393	1.481632	2.60E-143	1.31E-140

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SAMSN1	1.609922	4.499169	1.482668	2.99E-129	4.63E-127
PDE6G	0.325891	0.915147	1.489616	4.56E-99	2.22E-97
FPR3	6.13306	17.228	1.490076	8.23E-91	3.37E-89
C1QC	44.10048	123.8825	1.490106	5.73E-121	6.06E-119
SLA	1.54323	4.344529	1.493247	3.87E-133	8.92E-131
FGR	1.489968	4.216522	1.500772	2.63E-130	4.46E-128
CFP	0.206596	0.585845	1.503704	4.44E-61	9.98E-60
RGS18	0.337057	0.956685	1.505053	1.48E-101	7.61E-100
PSMB9	6.784775	19.27521	1.506373	5.49E-90	2.18E-88
HCRTR2	0.057519	0.163529	1.507445	3.07E-05	6.56E-05
LILRA5	0.384453	1.093482	1.508049	3.16E-90	1.27E-88
GP1BA	0.307578	0.876228	1.510352	5.31E-40	7.98E-39
ARHGAP15	0.553357	1.576585	1.510522	6.40E-133	1.41E-130
CD300LB	0.236346	0.674196	1.512269	1.50E-67	3.85E-66
APOBEC3G	1.416778	4.043881	1.513127	2.09E-108	1.28E-106
AQP9	0.685554	1.957944	1.513998	1.51E-27	1.68E-26
HTRA4	0.190965	0.545555	1.514418	2.42E-73	6.82E-72
PIK3CG	0.549393	1.570192	1.515029	2.51E-80	8.36E-79
MYO1G	0.666113	1.908759	1.518795	5.58E-110	3.64E-108
ARHGAP25	1.512422	4.336038	1.519517	2.69E-145	1.89E-142
ABCD2	0.128654	0.369719	1.522933	2.12E-76	6.40E-75
VNN1	0.4791	1.377289	1.523433	8.77E-73	2.45E-71
CD72	0.758925	2.182865	1.524193	1.85E-109	1.18E-107
VCAM1	3.737038	10.8166	1.53328	4.44E-74	1.28E-72
TNFRSF1B	5.870949	16.99466	1.533416	5.31E-147	3.93E-144
LILRB5	0.253963	0.735374	1.533858	2.30E-68	5.96E-67
POU2F2	0.553728	1.606914	1.537042	3.52E-115	2.93E-113
PDCD1LG2	1.011863	2.939686	1.538648	5.76E-107	3.39E-105
IL2RB	2.648194	7.701101	1.540056	8.75E-111	5.97E-109
FCGR3B	0.319027	0.927953	1.540375	2.01E-21	1.83E-20
MMP12	2.05997	6.001652	1.542737	9.24E-19	7.45E-18
CD74	328.7308	959.866	1.545926	1.32E-134	3.44E-132
LCP2	2.082452	6.084416	1.546836	4.63E-152	9.30E-149
ARRDC5	0.087941	0.257063	1.547513	4.55E-84	1.63E-82
CLDN16	0.064098	0.187681	1.549938	4.79E-18	3.70E-17
CTSS	12.71293	37.39482	1.556541	7.97E-121	8.24E-119
CSF3	0.051423	0.151291	1.556836	6.95E-11	2.96E-10
TNFSF13B	2.555604	7.521146	1.557288	2.25E-108	1.37E-106
SRGN	27.32365	80.57723	1.560222	9.49E-138	3.18E-135
CD163	4.596869	13.59259	1.564097	3.46E-88	1.32E-86
VNN2	0.470984	1.39515	1.566669	4.24E-95	1.88E-93
HLA-DMB	5.017561	14.90156	1.570405	4.03E-145	2.70E-142

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
HCLS1	4.465497	13.27215	1.571509	6.48E-153	1.52E-149
TBX10	0.432545	1.287687	1.573861	0.000803925	0.001411813
CD84	1.311611	3.909636	1.575695	2.22E-105	1.25E-103
FGL2	4.350769	13.00163	1.57935	1.83E-112	1.34E-110
HLA-DPA1	26.46526	79.27484	1.582763	6.87E-129	1.01E-126
CD4	7.498467	22.49005	1.584619	2.09E-154	5.87E-151
HLA-DPB1	43.50944	130.5614	1.585328	1.52E-136	4.85E-134
PHKG1	0.633816	1.902184	1.585521	3.07E-08	9.69E-08
HLA-DQB2	4.906605	14.73766	1.58671	3.01E-71	8.16E-70
TOX	0.512217	1.548202	1.595766	1.44E-90	5.83E-89
JSRP1	0.381592	1.154004	1.596544	3.05E-32	3.90E-31
KLRC1	0.08953	0.27097	1.597688	7.80E-76	2.33E-74
CLEC12A	0.227977	0.692821	1.603596	1.51E-90	6.10E-89
CD200R1	0.224479	0.682834	1.604955	4.18E-101	2.11E-99
GPR55	0.12664	0.38572	1.606823	1.89E-75	5.62E-74
DCSTAMP	0.186223	0.567359	1.607229	1.28E-39	1.91E-38
TFEC	0.550628	1.678441	1.607972	3.81E-110	2.51E-108
CD209	0.452233	1.37946	1.608966	7.28E-71	1.94E-69
FGD2	0.385128	1.17502	1.609275	1.68E-130	2.96E-128
LILRB1	0.713254	2.17747	1.610164	6.06E-139	2.30E-136
SIRPB1	0.16986	0.520434	1.615367	5.82E-62	1.34E-60
CCL23	0.150212	0.460385	1.615835	1.08E-67	2.79E-66
HLA-DRB1	155.2191	475.9225	1.61642	4.67E-133	1.06E-130
FPR2	0.0609	0.187207	1.62011	3.18E-67	8.14E-66
IKZF3	1.101902	3.393023	1.622575	4.19E-81	1.42E-79
MPEG1	4.339699	13.38393	1.624835	8.61E-123	9.69E-121
CYTIP	1.983161	6.130623	1.628232	1.40E-119	1.37E-117
FOXP3	1.213175	3.757957	1.631161	8.13E-101	4.08E-99
SCIMP	0.549126	1.700994	1.63117	1.73E-127	2.29E-125
GPR18	0.347792	1.078382	1.632573	2.71E-95	1.21E-93
HLA-DOA	4.162829	12.91502	1.633414	1.56E-120	1.58E-118
ITGB2	7.117906	22.13959	1.637104	1.20E-135	3.37E-133
BIN2	1.372589	4.272628	1.638224	2.51E-147	2.21E-144
ITGB7	0.428389	1.333549	1.638277	1.54E-88	5.93E-87
PATL2	0.157316	0.489734	1.63833	1.38E-82	4.83E-81
FERMT3	4.033852	12.56807	1.639533	9.33E-149	1.01E-145
GIMAP5	0.12731	0.397059	1.641003	8.19E-90	3.22E-88
CTSE	0.150036	0.468097	1.641499	1.95E-15	1.24E-14
C1QB	37.84303	118.2799	1.644105	2.27E-123	2.64E-121
KRT2	0.056583	0.176892	1.644428	1.83E-17	1.36E-16
P2RY10	0.821348	2.569825	1.645604	9.54E-91	3.90E-89
HLA-DRA	285.763	894.1829	1.645751	7.99E-145	4.89E-142

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TXK	0.113666	0.355856	1.646499	2.99E-63	7.04E-62
BIRC3	2.57086	8.049611	1.646668	3.13E-82	1.08E-80
PTPN22	0.61479	1.931845	1.651814	1.18E-115	9.98E-114
TAGAP	1.290242	4.070469	1.657553	1.99E-117	1.79E-115
DOCK2	0.979411	3.091126	1.658146	2.57E-134	6.33E-132
LILRB4	1.829003	5.782417	1.660615	1.67E-129	2.61E-127
WAS	2.408691	7.620902	1.661712	9.85E-155	3.46E-151
NCKAP1L	1.707635	5.404981	1.66229	2.24E-144	1.31E-141
CLECL1	0.214109	0.679014	1.665097	1.17E-97	5.52E-96
P2RX1	0.198162	0.629497	1.667519	1.20E-64	2.91E-63
RIPOR2	0.61865	1.966485	1.668424	1.65E-78	5.20E-77
SULT1B1	0.10171	0.323372	1.668732	3.99E-14	2.28E-13
IL9R	0.094105	0.299315	1.669322	2.27E-80	7.58E-79
CD226	0.130251	0.416356	1.676521	1.70E-109	1.09E-107
C1QA	39.33399	125.844	1.677789	8.23E-126	1.03E-123
CXorf65	0.136229	0.437042	1.681738	3.20E-65	7.83E-64
CYBB	7.08854	22.79243	1.684994	2.56E-112	1.86E-110
CCL8	1.823721	5.880063	1.688947	5.81E-60	1.27E-58
TNFRSF8	0.195198	0.632428	1.695963	7.26E-113	5.34E-111
LILRB2	0.791109	2.577837	1.704213	1.51E-142	7.30E-140
HLA-DQB1	14.06281	45.85692	1.705254	8.43E-106	4.84E-104
EBI3	1.021709	3.333353	1.70599	7.06E-110	4.58E-108
GRAP2	0.308035	1.005684	1.707011	9.67E-104	5.19E-102
PSORS1C2	0.455297	1.488122	1.708612	0.006514528	0.009990932
WDFY4	0.515299	1.687849	1.711705	5.11E-122	5.62E-120
HLA-DRB5	50.62613	166.0396	1.713573	6.82E-90	2.69E-88
STAT4	0.470021	1.547382	1.719032	5.22E-112	3.71E-110
GPR183	3.391108	11.25802	1.731124	9.20E-114	6.99E-112
P2RY8	0.844293	2.805906	1.732651	3.57E-114	2.76E-112
CIITA	0.982035	3.267814	1.734479	1.28E-117	1.16E-115
RUFY4	0.148619	0.498734	1.746656	3.46E-55	7.06E-54
PRKCQ	0.389876	1.30971	1.748159	2.94E-102	1.52E-100
TRAF3IP3	0.579291	1.947248	1.749076	2.76E-120	2.77E-118
TMEM150B	0.300469	1.01032	1.749525	4.27E-100	2.11E-98
KLRK1	0.05591	0.188005	1.7496	3.33E-66	8.34E-65
KLHL6	0.438752	1.477953	1.752123	1.06E-124	1.29E-122
EVI2B	4.115023	13.87872	1.753902	8.95E-144	5.03E-141
RASAL3	1.106488	3.73569	1.755387	2.18E-131	4.09E-129
CEACAM4	0.070216	0.237468	1.757858	9.22E-84	3.27E-82
HTR3A	0.109756	0.37143	1.758795	3.50E-18	2.71E-17
CD53	9.80268	33.33192	1.765656	2.46E-161	3.46E-157
FYB1	2.284396	7.771229	1.76633	6.09E-124	7.14E-122

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
MEI1	0.276629	0.943238	1.769669	1.73E-105	9.80E-104
XCL1	0.229175	0.781693	1.770154	4.88E-91	2.01E-89
LAMP3	1.865129	6.379882	1.774254	6.65E-81	2.24E-79
UTS2	0.074851	0.256122	1.774741	2.46E-53	4.79E-52
ADGRG5	0.204986	0.703689	1.779412	2.93E-82	1.01E-80
SPOCK2	2.430739	8.363947	1.782789	1.41E-116	1.23E-114
IRF8	1.831791	6.308502	1.784042	2.07E-134	5.30E-132
IL10RA	1.919089	6.621414	1.786717	1.42E-147	1.33E-144
KLRD1	0.09091	0.314366	1.789943	2.02E-97	9.39E-96
AOAH	1.23863	4.295308	1.794016	3.55E-136	1.08E-133
CCL4	1.572836	5.464184	1.796638	5.05E-117	4.50E-115
MAP4K1	1.055384	3.668859	1.797563	1.91E-124	2.31E-122
HCST	2.770915	9.643491	1.799193	1.72E-111	1.21E-109
FCRL6	0.22393	0.779736	1.799938	2.65E-95	1.18E-93
HLA-DQA2	9.061418	31.55652	1.800129	1.98E-53	3.86E-52
CARD17	0.170896	0.595701	1.801468	1.20E-61	2.75E-60
GBP1	7.768416	27.07945	1.801506	1.12E-94	4.95E-93
IL4I1	2.100103	7.325673	1.802501	1.22E-95	5.49E-94
APOBEC3H	0.300332	1.058619	1.817556	6.28E-112	4.44E-110
CD28	0.426534	1.509284	1.823132	3.88E-110	2.54E-108
IL2RA	0.617433	2.190411	1.826848	8.66E-104	4.67E-102
CARD11	0.806924	2.862746	1.826895	1.05E-135	3.00E-133
HLA-DQA1	9.804146	35.00756	1.836203	1.14E-128	1.66E-126
LILRA4	0.342844	1.226514	1.83894	1.16E-74	3.37E-73
CASP5	0.058804	0.210558	1.840225	5.01E-63	1.17E-61
ACY3	0.76692	2.749067	1.841793	4.85E-38	7.02E-37
GFI1	0.250216	0.899995	1.846743	2.46E-108	1.49E-106
CD37	2.513035	9.043413	1.847437	1.21E-151	2.13E-148
CALHM6	2.619007	9.435149	1.849025	1.41E-114	1.12E-112
JAK3	1.017678	3.666297	1.849043	3.78E-120	3.74E-118
CORO1A	4.947004	17.83368	1.849977	8.99E-133	1.92E-130
PTCRA	0.08714	0.315484	1.856164	2.54E-86	9.36E-85
ZC3H12D	0.155456	0.563357	1.857538	1.29E-113	9.68E-112
ACAP1	0.717599	2.603969	1.859462	7.87E-111	5.40E-109
CCL21	6.302648	22.87745	1.859896	1.02E-40	1.56E-39
TNFRSF13C	0.392336	1.425986	1.8618	5.22E-39	7.69E-38
HK3	0.636577	2.31461	1.862363	2.49E-79	8.03E-78
RASGRP2	0.387618	1.411249	1.864264	3.15E-80	1.04E-78
CD244	0.138569	0.504528	1.864327	5.59E-114	4.27E-112
PLEK	3.981504	14.53125	1.867774	3.05E-147	2.53E-144
TBC1D10C	0.81057	2.966032	1.871526	3.54E-104	1.93E-102
NCF1	0.392232	1.437563	1.873845	1.52E-128	2.16E-126

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
SASH3	3.153664	11.61662	1.881089	7.77E-160	5.46E-156
SLAMF8	2.522517	9.292544	1.88121	6.60E-122	7.20E-120
GPR15	0.118853	0.438056	1.881936	1.09E-34	1.48E-33
CD69	1.001709	3.692566	1.88216	6.15E-103	3.21E-101
CD1C	0.720947	2.670339	1.889058	2.02E-62	4.69E-61
MMP9	27.9422	103.5012	1.88913	2.69E-31	3.34E-30
TNFSF14	0.178452	0.661049	1.889222	5.00E-109	3.16E-107
CSF2RB	1.557112	5.777326	1.89153	8.39E-119	8.08E-117
CCR7	1.512651	5.636606	1.897748	9.17E-106	5.24E-104
TMC8	1.194898	4.471193	1.903772	2.54E-134	6.33E-132
KLRB1	0.772492	2.891068	1.904011	1.56E-105	8.88E-104
ZBP1	0.387241	1.450676	1.905423	3.91E-90	1.56E-88
CXCL5	0.35897	1.346109	1.906859	1.55E-16	1.07E-15
CCL17	0.735642	2.764512	1.909949	2.30E-65	5.66E-64
IKZF1	0.873493	3.284498	1.910804	1.62E-136	5.06E-134
SPN	0.804732	3.027609	1.911598	1.14E-138	4.24E-136
XIRP1	0.150752	0.569775	1.918217	1.73E-63	4.10E-62
ARHGAP9	0.808487	3.080628	1.929928	2.31E-151	3.61E-148
CD8B	0.793738	3.03439	1.934671	1.63E-98	7.82E-97
HLA-DOB	1.027149	3.952845	1.944246	7.92E-80	2.59E-78
SIGLEC12	0.109856	0.422963	1.944913	6.28E-28	7.10E-27
CCL25	0.072468	0.27968	1.948369	1.62E-22	1.54E-21
KCNJ10	0.1093	0.421938	1.948735	1.09E-53	2.15E-52
DOK2	1.344184	5.18939	1.948834	7.31E-136	2.19E-133
CD1E	0.454002	1.753721	1.949648	2.49E-65	6.11E-64
GBP4	4.079801	15.91592	1.9639	1.19E-96	5.41E-95
CLLU1OS	0.102689	0.404284	1.97709	1.46E-26	1.58E-25
LGALS2	1.13529	4.476765	1.979396	1.45E-87	5.50E-86
BCL2A1	2.193047	8.685402	1.985656	1.06E-97	5.00E-96
C16orf54	0.666152	2.687633	2.012413	2.69E-130	4.51E-128
TIMD4	0.164707	0.667094	2.017985	1.57E-64	3.78E-63
IL12RB1	0.370429	1.511853	2.029048	3.16E-151	4.04E-148
VMO1	1.961646	8.080345	2.042352	1.93E-24	1.97E-23
JAML	0.454647	1.881184	2.048823	4.73E-128	6.52E-126
SLFN12L	0.139308	0.581462	2.061409	8.66E-104	4.67E-102
PSTPIP1	0.485927	2.034006	2.065511	3.25E-139	1.31E-136
IL21R	0.394556	1.655368	2.06885	6.25E-120	6.15E-118
TESPA1	0.288674	1.211688	2.069505	2.04E-112	1.49E-110
STAP1	0.317869	1.346143	2.082328	2.08E-81	7.10E-80
SNX20	0.602676	2.562436	2.088062	2.92E-155	1.37E-151
TLR10	0.229803	0.977907	2.089302	4.64E-84	1.66E-82
XCR1	0.105406	0.448808	2.090136	1.72E-90	6.92E-89

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
APOBEC3A	0.241446	1.029593	2.092299	1.83E-53	3.58E-52
CST7	2.672764	11.44977	2.098914	4.07E-132	8.41E-130
CCR5	1.365963	5.869168	2.103237	7.01E-148	7.04E-145
CR1	0.05936	0.255262	2.104409	4.32E-73	1.21E-71
CCR4	0.52214	2.245489	2.10452	6.90E-107	4.05E-105
SP140	0.357501	1.539744	2.106671	3.61E-133	8.46E-131
C11orf21	0.109233	0.472142	2.111816	4.89E-108	2.95E-106
CXCR6	0.482678	2.0904	2.114646	4.31E-121	4.59E-119
LAG3	0.789612	3.422886	2.115997	2.39E-79	7.71E-78
THEMIS	0.202011	0.877439	2.118867	3.39E-110	2.25E-108
KCNA3	0.196154	0.852214	2.119227	1.70E-89	6.65E-88
PTPRC	2.738553	11.95513	2.126144	2.00E-131	3.80E-129
PTPN7	0.686195	3.019085	2.137422	3.10E-151	4.04E-148
TLR8	0.293878	1.2943	2.138881	2.15E-113	1.61E-111
SAMD3	0.083015	0.366182	2.14112	7.44E-123	8.51E-121
CD48	1.99152	8.891968	2.158633	4.00E-150	4.69E-147
CCR2	0.582173	2.603768	2.16108	3.49E-112	2.51E-110
TNFRSF9	0.213978	0.964232	2.171917	1.14E-116	9.98E-115
CD6	0.699663	3.170452	2.179956	3.98E-129	6.03E-127
IL18RAP	0.096591	0.439605	2.186252	1.44E-107	8.64E-106
KLK14	2.916702	13.30816	2.189902	0.000984031	0.001706004
GPR25	0.040325	0.184934	2.19727	1.10E-48	1.97E-47
ICAM3	0.246301	1.131999	2.200376	6.29E-121	6.60E-119
NCR3	0.18823	0.873579	2.214438	1.48E-101	7.61E-100
PTGDS	3.925659	18.22604	2.214994	1.08E-63	2.58E-62
CLEC4E	0.299555	1.393186	2.217496	1.16E-93	5.01E-92
NUGGC	0.107989	0.502644	2.218652	1.72E-87	6.51E-86
CD8A	1.460698	6.803574	2.219635	1.43E-114	1.13E-112
LYZ	34.45826	160.6349	2.220864	4.64E-105	2.59E-103
PARP15	0.205176	0.956818	2.221386	4.00E-111	2.77E-109
CD7	0.777276	3.626996	2.222277	6.69E-115	5.40E-113
CLEC10A	0.674511	3.14846	2.222734	2.29E-85	8.32E-84
TNIP3	0.081258	0.379624	2.223992	1.98E-97	9.22E-96
TMIGD2	0.086992	0.407824	2.228994	1.68E-86	6.23E-85
CXCL10	17.85152	83.84436	2.231667	3.90E-88	1.48E-86
LAIR2	0.119289	0.566434	2.247446	7.73E-90	3.04E-88
CRTAM	0.216757	1.032738	2.252325	1.21E-139	5.33E-137
KLHDC7B	2.556513	12.23784	2.2591	1.06E-41	1.64E-40
GZMH	0.85945	4.137055	2.267119	7.69E-109	4.78E-107
CTSW	1.110158	5.358009	2.270932	1.26E-111	8.83E-110
FCN1	0.258971	1.251144	2.272388	1.36E-97	6.37E-96
CD79B	1.143646	5.534794	2.274889	1.16E-79	3.78E-78

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CD96	0.547952	2.669604	2.284503	5.76E-129	8.52E-127
IRF4	0.442578	2.157243	2.285186	1.48E-97	6.90E-96
CLEC17A	0.090223	0.439953	2.285786	9.00E-62	2.06E-60
PLAC8	0.242532	1.192623	2.297889	1.47E-93	6.28E-92
CD247	0.536154	2.650495	2.305542	1.60E-130	2.85E-128
ZNF683	0.438206	2.16758	2.306404	2.71E-105	1.52E-103
CCL18	2.100773	10.41627	2.309848	7.13E-52	1.36E-50
VPREB3	0.591471	2.94	2.313438	1.70E-43	2.75E-42
IL7R	1.630233	8.117458	2.31595	8.95E-107	5.22E-105
SLA2	0.41529	2.075603	2.32134	2.39E-135	6.60E-133
TNFRSF17	0.546996	2.744668	2.32703	5.60E-61	1.25E-59
XCL2	0.344063	1.728255	2.328571	5.48E-101	2.76E-99
CXCL11	2.786998	14.0878	2.337663	2.34E-83	8.28E-82
FUT7	0.100588	0.510666	2.34392	2.28E-111	1.59E-109
CD40LG	0.292571	1.491496	2.349901	2.83E-110	1.88E-108
PRKCB	0.327929	1.672442	2.350501	9.94E-126	1.24E-123
PENK	0.150912	0.778157	2.366358	1.13E-09	4.20E-09
MARCO	1.059976	5.47911	2.36991	5.69E-44	9.35E-43
LCK	1.069391	5.531834	2.370969	1.69E-128	2.35E-126
UBASH3A	0.23506	1.22246	2.378689	2.35E-127	3.06E-125
FASLG	0.229015	1.19407	2.38237	1.49E-108	9.15E-107
CD5	0.87347	4.597901	2.396145	1.84E-131	3.54E-129
SLAMF7	1.419632	7.481632	2.397836	7.08E-118	6.51E-116
PNOC	0.125856	0.665583	2.402839	2.58E-76	7.72E-75
PRF1	0.84572	4.479172	2.404979	3.26E-129	4.99E-127
LAX1	0.338	1.792732	2.407064	5.63E-94	2.45E-92
CCL5	9.755549	51.86385	2.410435	7.14E-128	9.65E-126
CD27	1.371251	7.305437	2.413478	4.73E-118	4.41E-116
IL12B	0.04145	0.221206	2.415933	2.06E-88	7.92E-87
S1PR4	0.466799	2.491182	2.415956	2.83E-120	2.82E-118
UBD	3.139272	16.78631	2.418783	2.03E-72	5.61E-71
GPR171	0.329591	1.776984	2.430682	4.73E-115	3.89E-113
GNLY	0.632314	3.425065	2.437418	1.09E-102	5.66E-101
GZMA	2.481537	13.46392	2.439793	8.34E-130	1.35E-127
IL2RG	3.681922	20.05697	2.445573	3.53E-147	2.76E-144
PAX5	0.124347	0.679575	2.450261	7.49E-59	1.61E-57
ZAP70	0.391871	2.148626	2.454963	3.12E-118	2.94E-116
GZMM	0.603181	3.342179	2.470125	1.40E-104	7.69E-103
SIT1	0.680083	3.769711	2.470672	1.94E-132	4.08E-130
CD2	3.263507	18.17974	2.477836	2.27E-139	9.69E-137
ADAMDEC1	1.289364	7.193976	2.48013	6.21E-77	1.90E-75
CTLA4	0.362666	2.027524	2.483006	3.14E-114	2.44E-112

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
CD3G	0.38948	2.20574	2.501641	1.24E-128	1.78E-126
AIM2	0.382315	2.166142	2.502294	5.20E-109	3.26E-107
EOMES	0.239469	1.357327	2.502857	2.05E-114	1.61E-112
CCL13	0.576998	3.273173	2.504051	5.82E-84	2.07E-82
TREML2	0.041321	0.234564	2.505021	1.53E-88	5.90E-87
LTA	0.201381	1.143801	2.505833	5.65E-117	5.00E-115
SCML4	0.071172	0.406856	2.51514	1.08E-116	9.49E-115
TBX21	0.165363	0.946595	2.517109	7.61E-130	1.25E-127
POU2AF1	0.403348	2.310413	2.518053	4.61E-72	1.27E-70
MS4A6E	0.026163	0.150708	2.526186	4.15E-12	2.00E-11
BANK1	0.205982	1.186854	2.526554	2.26E-76	6.81E-75
LY9	0.110426	0.63948	2.533821	9.25E-125	1.14E-122
SLAMF1	0.255608	1.481103	2.534665	2.04E-130	3.50E-128
ZNF831	0.073937	0.430407	2.54133	5.93E-115	4.84E-113
PYHIN1	0.207402	1.210389	2.54497	3.56E-130	5.89E-128
AC136428.1	0.234799	1.380948	2.556159	4.24E-44	7.02E-43
CXCR3	0.813501	4.790686	2.558016	5.78E-133	1.29E-130
CD3E	2.017282	12.00923	2.573659	4.89E-137	1.60E-134
CD1B	0.112801	0.673503	2.577901	6.19E-69	1.61E-67
PDCD1	0.313487	1.873529	2.57928	1.04E-117	9.47E-116
ITK	0.234743	1.402985	2.579344	1.59E-126	2.03E-124
OR2I1P	1.440637	8.613051	2.579818	2.44E-81	8.32E-80
GPR174	0.238965	1.430801	2.581953	1.21E-97	5.67E-96
IGLL5	6.649046	39.979	2.588023	2.25E-58	4.79E-57
NKG7	2.440551	14.76835	2.59723	3.12E-124	3.72E-122
KIR2DL4	0.043435	0.263735	2.602148	1.05E-65	2.61E-64
FAM129C	0.074225	0.454484	2.614248	6.45E-61	1.44E-59
ROS1	0.049541	0.30451	2.6198	0.000283684	0.000530658
TNFRSF13B	0.059102	0.365627	2.629106	1.97E-73	5.59E-72
CD3D	2.123914	13.20874	2.636695	5.07E-139	1.98E-136
TIGIT	0.359398	2.240623	2.640246	7.14E-128	9.65E-126
ICOS	0.257932	1.608969	2.641077	5.20E-114	3.99E-112
SH2D1A	0.418491	2.632386	2.653103	2.17E-127	2.85E-125
CCL19	7.899773	49.98754	2.661686	2.93E-69	7.63E-68
SLAMF6	0.644465	4.082037	2.663115	1.11E-130	1.99E-128
ZBED2	0.157458	0.999064	2.665614	1.19E-93	5.14E-92
CD38	0.269294	1.732079	2.685249	2.71E-100	1.35E-98
CD52	8.482918	55.37312	2.706553	4.24E-127	5.47E-125
LTB	2.020641	13.35687	2.724697	5.29E-98	2.52E-96
GZMK	1.074322	7.155418	2.735609	7.11E-121	7.41E-119
SIRPG	0.326951	2.178715	2.736331	4.61E-129	6.89E-127
BTLA	0.114988	0.77777	2.757867	3.11E-113	2.30E-111

Table S3 *(continued)*

Table S3 *(continued)*

Gene	conMean	treatMean	logFC	P value	fdr
TIFAB	0.043913	0.299204	2.768418	2.16E-113	1.61E-111
FCRL5	0.103987	0.718541	2.788673	1.68E-70	4.45E-69
SPIB	0.403624	2.868219	2.82907	2.26E-84	8.14E-83
CHIT1	0.666338	4.748873	2.83326	2.75E-37	3.93E-36
FCRLA	0.166665	1.204025	2.852839	1.65E-86	6.13E-85
CR2	0.275467	2.021995	2.875826	7.24E-42	1.13E-40
TRAT1	0.178223	1.308927	2.876628	8.69E-121	8.92E-119
CLEC4C	0.03222	0.239973	2.896829	3.24E-77	9.98E-76
IDO1	1.499219	11.19081	2.900031	4.36E-94	1.91E-92
GBP5	0.918153	6.89248	2.908216	8.92E-119	8.47E-117
CNR2	0.031987	0.247403	2.951326	7.27E-78	2.26E-76
CD79A	2.146012	17.02748	2.988135	1.50E-78	4.74E-77
CLEC4D	0.032602	0.267	3.033801	2.06E-60	4.54E-59
BLK	0.082816	0.685885	3.049989	1.09E-72	3.03E-71
FCRL2	0.046213	0.383003	3.050996	1.47E-72	4.08E-71
CXCL9	9.174485	76.14552	3.05306	1.20E-100	6.02E-99
FCRL3	0.095955	0.806371	3.071017	1.71E-103	9.12E-102
GZMB	0.665798	5.59977	3.072211	5.47E-108	3.29E-106
IFNG	0.070838	0.699267	3.303254	6.92E-96	3.13E-94
CD19	0.161633	1.660855	3.361128	5.15E-81	1.74E-79
IGLL1	0.034445	0.378258	3.457023	1.76E-32	2.26E-31
FCAMR	0.023444	0.262488	3.484953	3.42E-28	3.91E-27
MS4A1	0.362738	4.35511	3.585709	2.37E-80	7.91E-79
FCRL1	0.045721	0.586412	3.680998	1.58E-73	4.50E-72
DMBT1	0.098058	1.320953	3.751802	0.0010808	0.001863609
PLA2G2D	0.315815	4.315992	3.772539	1.43E-95	6.43E-94
FCER2	0.063118	0.95975	3.926535	3.84E-72	1.06E-70
KRT1	0.897951	14.29212	3.99244	6.96E-07	1.84E-06
TCL1A	0.108973	1.755959	4.010215	2.22E-82	7.75E-81
AICDA	0.01164	0.250014	4.424884	4.41E-43	7.05E-42
LOR	0.053887	2.216532	5.362215	7.23E-18	5.53E-17