

Supplementary Data 6-1: 29 immune microenvironment signatures
signature

aDCs: CD83 LAMP3 CCL1

APC_co_inhibition: C10orf54 CD274 LGALS9 PDCD1LG2 PVRL3

APC_co_stimulation: CD40 CD58 CD70 ICOSLG SLAMF1TNFSF14
TNFSF15 TNFSF18 TNFSF4 TNFSF8 TNFSF9

B_cells: BACH2 BANK1 BLK BTLA CD79A CD79B FCRL1 FCRL3 HVCN1
RALGPS2

CCR: CCL16TPOTGFB2 CXCL2 CCL14 TGFBR3 IL11RA CCL11 IL4I1 IL33
CXCL12 CXCL10 BMPER BMP8A CXCL11 IL21R IL17B TNFRSF9 ILF2
CX3CR1 CCR8 TNFSF12 CSF3 TNFSF4 BMP3 CX3CL1 BMP5 CXCR2
TNFRSF10D BMP2 CXCL14 CCL28 CXCL3 BMP6 CCL21 CXCL9 CCL23
IL6 TNFRSF18 IL17RD IL17D IL27CCL7 IL1R1 CXCR4 CXCR2P1
TGFB1I1IFNGR1 IL9R IL1RAPL1 IL11CSF1 IL20RA IL25TNFRSF4
IL18ILF3CCL20 TNFRSF12A IL6ST CXCL13 IL12B TNFRSF8 IL6R
BMPR2 IFNE IL1RAPL2 IL3RA BMP4 CCL24 TNFSF13B CCR4
IL2RA IL32TNFRSF10C IL22RA1BMPR1A CXCR5 CXCR3 IFNA8
IL17REL IFNB1 IFNAR1 TNFRSF1B CCL17 IFNL1 IL16IL1RL1 ILK CCL25
ILDR2 CXCR1 IL36RN IL34TGFB1 IFNG IL19ILKAP BMP2K CCR10
ILDR1 EPOCCR7 IL17C IL23A CCR5 IL7 EPOR CCL13 IL2RG
IL31RA TNFAIP6 IFNL2 BMP1 IL12RB1TNFAIP8 IL4R TNFRSF6B
TNFAIP8L1 TNFRSF10B IFNL3 CCL5 CXCL6 CXCL1 CCR3 TNFSF11
CSF1R IL21IL1RAP IL12RB2CCL1 IL17RA CCR1 IL1RN TNFRSF11B
TNFRSF14 IL13IL2RB BMP8B CCL2 IL24IL18RAPTGFB1 TNFSF10
TNFRSF11A CXCL5 IL5RA TNFSF9 IL1RL2 TNFRSF13C IL36G IL15RA
TNFRSF21 CXCL8 IL22RA2TNFAIP8L2 IL18R1 IFNLR1 CXCR6 CCL3L3
TNFRSF1A IL17RE IFNGR2 IL17RC TNFAIP8L3 ILVBL TGFBRAP1 CCL4L1
CSF2RA CCRN4LCCL26 TNFAIP1 CCRL2 IFNA10 TNFRSF17 IFNA13
IL20IL18BP CCL3L1 TNFSF12-TNFSF13 IL5 IL23R IL26TNFTGFA CSF2
IL1F10 CXCL17 TNFSF13 IFNA4 IL37IL12A IL7R IFNA1 IL1A IL4
IL2 CCL22 CSF3R IL10IFNK TGFB2 IL1R2 IL1B IL17F IL27RA
IL15TNFSF8 IL36B XCL1 CXCL16 TNFRSF19 IL3 CCL3 IFNA2
BMPR1B IFNA21 TNFSF18 CCL8 IL17RB TNFRSF25 IL22IL10RB
IFNAR2 CCL18 IFNA16 CSF2RB IL36A TNFAIP3 IL13RA2IL13RA1CCR9
TNFRSF10A IFNA7 IFNW1 XCL2 TNFSF14 CCR2 BMP15 BMP10
CCL15-CCL14 TGFBR1 IFNA5 BMP7 IFNA14 IL20RB IL10RA IFNA17
CCR6 TGFB3 CCL15 CCL4 CCL27 TNFRSF13B TNFAIP2 IL31IL17A
TNFSF15 CCL19 IFNA6 IL9

CD8+_T_cells: CD8A

Check-point: IDO1 LAG3 CTLA4 TNFRSF9 ICOS CD80 PDCD1LG2
TIGIT CD70 TNFSF9 ICOSLG KIR3DL1 CD86 PDCD1 LAIR1
TNFRSF8 TNFSF15 TNFRSF14 IDO2 CD276 CD40 TNFRSF4
TNFSF14 HHLA2 CD244 CD274 HAVCR2 CD27 BTLA LGALS9
TMIGD2CD28 CD48 TNFRSF25 CD40LGADORA2A VTCN1 CD160

CD44 TNFSF18 TNFRSF18 BTNL2 C10orf54 CD200R1 TNFSF4
 CD200 NRP1
 Cytolytic_activity: PRF1 GZMA
 DCs: CCL17CCL22 CD209 CCL13
 HLA: HLA-E HLA-DPB2 HLA-C HLA-J HLA-DQB1 HLA-DQB2 HLA-DQA2
 HLA-DQA1 HLA-A HLA-DMA HLA-DOB HLA-DRB1 HLA-H HLA-B
 HLA-DRB5 HLA-DOA HLA-DPB1 HLA-DRA HLA-DRB6 HLA-L HLA-F
 HLA-G HLA-DMB HLA-DPA1
 iDCs: CD1ACD1E
 Inflammation-promoting: CCL5 CD19 CD8B CXCL10 CXCL13 CXCL9 GNL1
 GZMB IFNG IL12A IL12B IRF1 PRF1 STAT1 TBX21
 Macrophages: C11orf45CD68 CLEC5A CYBB FUCA1 GPNMB HS3ST2 LGMN
 MMP9 TM4SF19
 Mast_cells: CMA1 MS4A2 TPSAB1
 MHC_class_I: B2M HLA-A TAP1
 Neutrophils: EVI2B HSD17B11 KDM6B MEGF9 MNDA NLRP12 PADI4 SELL
 TRANK1VNN3
 NK_cells: KLRC1 KLRF1
 Parainflammation: CXCL10 PLAT CCND1 LGMN PLAUR AIM2 MMP7
 ICAM1 MX2 CXCL9 ANXA1 TLR2 PLA2G2D ITGA2 MX1
 HMOX1CD276 TIRAP IL33PTGES TNFRSF12A SCARB1CD14 BLNK
 IFIT3 RETNLB IFIT2 ISG15 OAS2 REL OAS3 CD44 PPARG BST2
 OAS1 NOX1 PLA2G2A IFIT1 IFITM3 IL1RN
 pDCs: CLEC4C CXCR3 GZMB IL3RA IRF7 IRF8 LILRA4 PHEX PLD4
 PTCRA
 T_cell_co-inhibition: BTLA C10orf54 CD160 CD244 CD274 CTLA4
 HAVCR2 LAG3 LAIR1 TIGIT
 T_cell_co-stimulation: CD2 CD226 CD27 CD28 CD40LG ICOS SLAMF1
 TNFRSF18 TNFRSF25 TNFRSF4 TNFRSF8 TNFRSF9 TNFSF14
 T_helper_cells: CD4
 Tfh: PDCD1CXCL13 CXCR5
 Th1_cells: IFNG TBX21 CTLA4 STAT4 CD38 IL12RB2LTA CSF2
 Th2_cells: PMCH LAIR2 SMAD2 CXCR6 GATA3 IL26
 TIL: ITM2C CD38 THEMIS2 GLYR1 ICOS F5 TIGIT KLRD1 IRF4
 PRKCQ FCRL5 SIRPG LPXN IL2RG CCL5 LCKTRAF3IP3 CD86
 MAL LILRB1 DOK2 CD6PAG1 LAX1 PLEK PIK3CD SLAMF1XCL1
 GPR171XCL2 TBX21 CD2CD53 KLHL6 SLAMF6CD40 SIT1
 TNFRSF4 CD79A CD247 LCP2 CD3D CD27 SH2D1AFYB ARHGAP30
 ACAP1 CST7 CD3G IL2RB CD3E FCRL3 CORO1A ITK TCL1A
 CYBB CSF2RB IKZF1 NCF4 DOCK2 CCR2 PTPRC PLAC8 NCKAP1L
 IL7R 6-Sep CD28 STAT4 CD8A LY9 CD48 HCST PTPRCAP
 SASH3 ARHGAP25 LATTRAT1 IL10RA PAX5 CCR7 DOCK11PARVG
 SPNS1 CD52 HCLS1 ARHGAP9 GIMAP6PRKCB MS4A1 GPR18
 TBC1D10C GVINP1 P2RY8 EVI2B VAMP5 KLRK1 SELL MPEP1

MS4A6A ARHGAP15 MFNG GZMK SELPLG TARP GIMAP7FAM65B
 INPP5D ITGA4 MZB1 GPSM3 STK10 CLEC2D IL16NLRC3 GIMAP5
 GIMAP4IFFO1 CFHPVRIG CFHR1

Treg: IL12RB2 TMPRSS6 CTSC LAPTM4B TFRC RNF145 NETO2 ADAT2
 CHST2 CTLA4 NFE2L3 LIMA1 IL1R2 ICOS HSDL2 HTATIP2
 FKBP1A TIGIT CCR8 LTA SLC35F2 IL21R AHCYL1 SOCS2 ETV7
 BCL2L1 RRAGB ACSL4 CHRNA6 BATF LAX1 ADPRH TNFRSF4
 ANKRD10 CD274 CASP1 LY75 NPTN SSTR3 GRSF1 CSF2RB
 TMEM184C NDFIP2 ZBTB38 ERI1 TRAF3 NAB1 HS3ST3B1 LAYN
 JAK1 VDR LEPROT GCNT1 PTPRJ IKZF2 CSF1 ENTPD1 TNFRSF18
 METTL7A KSR1 SSH1 CADM1 IL1R1 ACP5 CHST7 THADA CD177
 NFAT5 ZNF282 MAGEH1

Type_I_IFN_Reponse: DDX4 IFIT1 IFIT2 IFIT3 IRF7 ISG20 MX1
 MX2 RSAD2 TNFSF10

Type_II_IFN_Reponse: GPR146 SELP AHR

Supplementary Data 6-2:stromal score, immune score, estimate score, tumor purtiy of TCGA samples					
	ID	StromalScore	ImmuneScore	ESTIMATEScore	TumorPurity
	TCGA-KK-A6E5	-550.919	-252.873	-803.793	0.883741
	TCGA-EJ-A65E	-1180.92	-694.705	-1875.62	0.94615
	TCGA-EJ-7785	-55.1382	197.5854	142.4472	0.810438
	TCGA-SU-A7E7	-586.069	91.52555	-494.543	0.861594
	TCGA-VN-A88Q	-1194.96	-646.745	-1841.7	0.944526
	TCGA-EJ-8472	-727.43	-794.506	-1521.94	0.928076
	TCGA-HC-8262	-1083.66	-736.556	-1820.22	0.943486
	TCGA-HC-7747	-518.929	402.9644	-115.964	0.832071
	TCGA-QU-A6IM	-839.45	558.0319	-281.418	0.845296
	TCGA-HC-7819	-1349.71	-930.08	-2279.79	0.96368
	TCGA-EJ-5510	-513.076	69.56141	-443.514	0.857768
	TCGA-HC-A76X	-1318.14	-1159.26	-2477.4	0.97102
	TCGA-J4-A67N	-867.235	185.5835	-681.652	0.875209
	TCGA-EJ-A7NH	-647.578	-536.732	-1184.31	0.908488
	TCGA-G9-6365	5.6383	-228.961	-223.323	0.840708
	TCGA-XA-A8JR	-593.903	-386.188	-980.09	0.895554
	TCGA-KC-A4BL	-436.235	71.14078	-365.094	0.851794
	TCGA-CH-5737	-1201.39	-726.694	-1928.09	0.948615
	TCGA-XK-AAK1	-1037.84	-346.009	-1383.85	0.920337
	TCGA-XK-AAIR	-482.949	-1.34205	-484.291	0.860829
	TCGA-HC-7210	155.8637	247.7469	403.6107	0.78739
	TCGA-G9-6361	-191.049	-624.053	-815.102	0.884517
	TCGA-YL-A8HO	430.1321	994.4227	1424.555	0.686526
	TCGA-CH-5765	-1080.24	-954.542	-2034.78	0.953454

TCGA-EJ-A65G	-1039.41	-891.546	-1930.96	0.948748
TCGA-HC-7742	-429.711	-673.735	-1103.45	0.903464
TCGA-CH-5763	-64.211	-120.983	-185.194	0.837665
TCGA-J4-A6G3	-375.692	716.244	340.5515	0.793062
TCGA-HC-8216	-481.47	165.0773	-316.393	0.848027
TCGA-2A-A8W1	-1670.59	-884.165	-2554.76	0.973671
TCGA-G9-6362	-567.704	-343.178	-910.881	0.890988
TCGA-EJ-7782	-483.682	-358.448	-842.13	0.88636
TCGA-CH-5743	-688.072	794.6426	106.5705	0.813512
TCGA-EJ-5501	-877.725	-482.554	-1360.28	0.918979
TCGA-EJ-A7NG	-433.525	-324.051	-757.576	0.880546
TCGA-VP-A876	-1328.38	-967.589	-2295.97	0.964311
TCGA-J4-A83L	-503.126	-602.716	-1105.84	0.903614
TCGA-VN-A943	-1925.26	-1339.23	-3264.49	0.992098
TCGA-YL-A8SH	-666.68	-474.493	-1141.17	0.905824
TCGA-EJ-7315	210.2827	922.3812	1132.664	0.717041
TCGA-EJ-5508	-405.102	298.4548	-106.648	0.831312
TCGA-KK-A7AV	-282.044	1065.023	782.9797	0.751859
TCGA-V1-A8MU	1.836886	455.7875	457.6244	0.782478
TCGA-QU-A6IL	-1059.14	-225.058	-1284.2	0.914518
TCGA-J4-A67O	-112.713	161.6042	48.89076	0.818407
TCGA-EJ-7781	-529.027	-56.4493	-585.477	0.868293
TCGA-G9-6348	-124.904	66.18476	-58.7193	0.827381
TCGA-XK-AAJU	-884.257	-149.079	-1033.34	0.899004
TCGA-J4-A83J	-887.83	139.9681	-747.862	0.879869
TCGA-WW-A8ZI	-936.194	-405.62	-1341.81	0.917907
TCGA-EJ-5503	-472.702	32.4511	-440.25	0.857522
TCGA-HC-7211	-915.959	-92.594	-1008.55	0.897405
TCGA-CH-5750	-777.322	358.3619	-418.96	0.85591
TCGA-HI-7170	253.5063	346.1311	599.6374	0.769328
TCGA-KK-A6E3	-176.616	580.5962	403.9799	0.787357
TCGA-CH-5746	-1240.23	-902.968	-2143.19	0.958132
TCGA-EJ-7123	-817.021	-687.724	-1504.74	0.927133
TCGA-J4-A67L	-471.71	499.0426	27.33273	0.820221
TCGA-EJ-A7NJ	-1051.78	-107.68	-1159.46	0.906958
TCGA-KC-A7F6	-842.022	-382.215	-1224.24	0.910922
TCGA-V1-A9ZR	272.7534	707.4098	980.1633	0.732463
TCGA-KK-A6DY	-808.604	-17.5541	-826.158	0.885272
TCGA-4L-AA1F	1771.63	1646.975	3418.604	0.447527
TCGA-XK-AAJT	-100.447	15.52334	-84.9236	0.829535
TCGA-HC-8260	-579.914	-350.13	-930.045	0.892261
TCGA-V1-A8MK	-622.472	-405.778	-1028.25	0.898677
TCGA-HI-7169	-221.315	-436.674	-657.989	0.873523

TCGA-KC-A4BN	-1475.86	-742.934	-2218.79	0.96125
TCGA-V1-A8ML	-387.152	-653.661	-1040.81	0.899485
TCGA-EJ-A7NK	-843.467	-534.119	-1377.59	0.919977
TCGA-G9-6384	-342.08	-240.536	-582.616	0.868084
TCGA-J4-A83I	-525.209	-199.495	-724.704	0.878249
TCGA-VP-A87C	514.4221	2018.131	2532.553	0.55973
TCGA-EJ-A65M	-566.609	102.4297	-464.179	0.859323
TCGA-EJ-7797	-924.779	-279.896	-1204.67	0.909733
TCGA-EJ-AB27	-938.185	283.6279	-654.557	0.873278
TCGA-KK-A8I6	-1001.77	-455.576	-1457.35	0.924504
TCGA-2A-A8VV	-922.085	-996.459	-1918.54	0.948171
TCGA-VN-A88I	670.0433	333.7929	1003.836	0.730093
TCGA-2A-A8VX	-1072.42	-1325.51	-2397.93	0.968166
TCGA-EJ-A8FN	-417.349	131.6857	-285.663	0.845628
TCGA-G9-6379	-304.06	1045.94	741.8798	0.755823
TCGA-EJ-7788	-111.931	-291.294	-403.225	0.854713
TCGA-HC-7740	-189.717	1.474221	-188.243	0.837909
TCGA-KC-A7F3	-914.035	-428.331	-1342.37	0.917939
TCGA-EJ-7792	397.2586	586.6029	983.8614	0.732093
TCGA-EJ-7317	-742.128	-884.632	-1626.76	0.933696
TCGA-EJ-5498	152.096	180.6568	332.7528	0.793759
TCGA-G9-6369	-747.353	-778.112	-1525.46	0.928268
TCGA-QU-A6IO	-886.222	257.8784	-628.343	0.871397
TCGA-EJ-7125	-407.43	-154.75	-562.18	0.866591
TCGA-J4-A6G1	104.5695	1996.209	2100.779	0.611092
TCGA-KK-A6E4	-1099.23	-370.478	-1469.71	0.925194
TCGA-EJ-7314	-1273.26	-696.916	-1970.18	0.950552
TCGA-YL-A8SA	-1408.14	-812.249	-2220.39	0.961315
TCGA-EJ-7330	-317.347	-430.128	-747.475	0.879842
TCGA-EJ-7325	-867.187	-491.675	-1358.86	0.918897
TCGA-EJ-7791	225.2806	-82.7696	142.511	0.810433
TCGA-VN-A88R	-334.065	-328.302	-662.367	0.873836
TCGA-XK-AAJP	-682.404	-268.546	-950.951	0.893643
TCGA-2A-A8VL	-1095.46	-795.652	-1891.11	0.946883
TCGA-KK-A8IG	173.8688	-95.9687	77.90019	0.815952
TCGA-QU-A6IN	-1388.39	-814.06	-2202.45	0.960586
TCGA-EJ-8468	164.2736	345.3649	509.6384	0.777701
TCGA-G9-7510	-98.1399	-54.8702	-153.01	0.835075
TCGA-EJ-5522	-439.508	-24.1621	-463.67	0.859285
TCGA-EJ-A46H	86.66863	415.293	501.9616	0.778409
TCGA-HC-7230	-1262.98	-893.243	-2156.23	0.958678
TCGA-KK-A8IF	-950.925	-937.141	-1888.07	0.94674
TCGA-HC-7737	-10.6869	510.894	500.2071	0.77857

TCGA-EJ-8474	-253.088	-458.511	-711.599	0.877327
TCGA-G9-6370	-324.237	-126.386	-450.623	0.858304
TCGA-HC-7744	-1095.9	-790.393	-1886.29	0.946656
TCGA-EJ-5527	43.44897	129.4965	172.9455	0.807807
TCGA-EJ-5509	-180.462	390.5378	210.0759	0.804583
TCGA-TP-A8TV	-1128.93	-899.914	-2028.84	0.953191
TCGA-G9-6364	-123.666	-530.704	-654.37	0.873265
TCGA-G9-A9S7	-1360.39	-495.443	-1855.83	0.945206
TCGA-CH-5767	-915.409	-841.629	-1757.04	0.940372
TCGA-EJ-5502	-391.004	230.4506	-160.554	0.835684
TCGA-V1-A8WL	-424.239	295.8255	-128.413	0.833083
TCGA-CH-5791	-597.718	-313.266	-910.984	0.890995
TCGA-FC-A66V	-858.991	-36.6675	-895.658	0.889971
TCGA-EJ-5497	-500.087	-234.355	-734.442	0.878931
TCGA-HC-7078	-528.631	-14.8158	-543.447	0.865216
TCGA-KK-A7AQ	-491.99	-334.082	-826.072	0.885267
TCGA-G9-6332	-1316.66	-930.309	-2246.97	0.962382
TCGA-CH-5740	-854.275	-264.437	-1118.71	0.904422
TCGA-G9-6338	-205.782	-440.907	-646.689	0.872715
TCGA-EJ-5496	-1266.12	-791.693	-2057.82	0.954468
TCGA-KK-A59Z	165.8213	37.56932	203.3906	0.805165
TCGA-J4-A83M	-835.576	-285.64	-1121.22	0.904579
TCGA-XK-AAJR	-513.191	-552.966	-1066.16	0.901104
TCGA-KK-A6E2	-1168.55	-532.419	-1700.97	0.93754
TCGA-VN-A88L	-326.818	-684.691	-1011.51	0.897597
TCGA-G9-7522	-404.052	-253.725	-657.777	0.873508
TCGA-EJ-5516	238.4179	187.9474	426.3653	0.785327
TCGA-G9-6363	-478.376	-169.923	-648.299	0.87283
TCGA-QU-A6IP	-827.574	-577.998	-1405.57	0.92158
TCGA-J4-A67R	-470.042	522.2483	52.20659	0.818127
TCGA-EJ-7784	-996.316	-572.426	-1568.74	0.930612
TCGA-CH-5794	-1123.11	-590.107	-1713.22	0.938165
TCGA-HC-A8D1	-247.154	-33.856	-281.01	0.845264
TCGA-HC-A76W	-27.798	-121.011	-148.809	0.834736
TCGA-KK-A8I5	-489.28	-546.721	-1036	0.899176
TCGA-J4-AAU2	-798.852	-434.392	-1233.24	0.911467
TCGA-CH-5739	-35.177	80.75691	45.57989	0.818686
TCGA-CH-5762	-308.602	304.3937	-4.20853	0.822861
TCGA-CH-5752	-506.991	-784.822	-1291.81	0.914969
TCGA-HC-A8D0	-264.762	205.2909	-59.4714	0.827443
TCGA-EJ-5515	-673.702	-643.194	-1316.9	0.916449
TCGA-J4-8200	-330.938	-433.097	-764.035	0.880995
TCGA-EJ-5517	-358.117	102.5553	-255.562	0.843262

TCGA-TP-A8TT	-164.259	878.0789	713.8199	0.758513
TCGA-VP-A87E	42.31693	866.7521	909.069	0.739528
TCGA-EJ-7331	29.88053	14.69873	44.57926	0.81877
TCGA-G9-6339	-968.153	-412.129	-1380.28	0.920132
TCGA-EJ-5505	-1129.83	-670.282	-1800.12	0.942504
TCGA-CH-5768	-1110.67	-619.797	-1730.47	0.939038
TCGA-CH-5789	-562.14	-32.7285	-594.868	0.868976
TCGA-VN-A88P	-233.898	-254.898	-488.796	0.861166
TCGA-EJ-7794	-227.951	96.94341	-131.008	0.833294
TCGA-Y6-A8TL	-651.237	-664.689	-1315.93	0.916392
TCGA-EJ-5511	-518.191	-752.631	-1270.82	0.913722
TCGA-KC-A7FE	29.0553	-227.909	-198.853	0.838758
TCGA-EJ-5499	-589.764	147.3465	-442.417	0.857685
TCGA-EJ-A8FS	-1426.04	-775.629	-2201.67	0.960554
TCGA-J4-A67M	-93.548	753.3234	659.7754	0.763659
TCGA-CH-5744	-868.189	-249.409	-1117.6	0.904352
TCGA-XK-AAJA	-1137.96	-642.598	-1780.56	0.941541
TCGA-HC-8258	-924.061	-157.559	-1081.62	0.902086
TCGA-EJ-7783	-534.363	-239.466	-773.829	0.881674
TCGA-G9-7525	-285.851	-461.831	-747.682	0.879857
TCGA-EJ-A7NF	-1449.35	-742.86	-2192.21	0.960167
TCGA-EJ-A46I	-873.349	-578.281	-1451.63	0.924183
TCGA-J4-A67S	-1042.32	34.03379	-1008.29	0.897388
TCGA-J4-AATV	-414.197	221.2137	-192.983	0.838289
TCGA-EJ-7786	-463.729	-531.096	-994.825	0.896514
TCGA-KC-A7FA	-681.824	-218.643	-900.467	0.890293
TCGA-EJ-7115	-317.455	-468.905	-786.36	0.88254
TCGA-VP-A875	-1328.58	-1189.14	-2517.72	0.972418
TCGA-EJ-5542	-243.566	-427.758	-671.324	0.874475
TCGA-KK-A8I9	-63.6453	409.6281	345.9828	0.792577
TCGA-CH-5745	-248.241	294.5147	46.2735	0.818627
TCGA-G9-6377	-660.693	-102.755	-763.448	0.880954
TCGA-KK-A7B1	-130.15	-405.108	-535.258	0.864613
TCGA-XK-AAJ3	-475.806	-715.781	-1191.59	0.908934
TCGA-VP-A87J	-864.736	-740.693	-1605.43	0.93257
TCGA-CH-5790	-1077.92	-421.609	-1499.53	0.926846
TCGA-VN-A88O	-890.906	-182.484	-1073.39	0.901564
TCGA-V1-A9OX	-673.83	65.78081	-608.049	0.869932
TCGA-HC-7212	-541.107	-640.05	-1181.16	0.908295
TCGA-EJ-5531	-307.639	411.2104	103.5716	0.813768
TCGA-V1-A8X3	-457.34	-464.052	-921.392	0.891687
TCGA-HC-8265	-722.799	-173.087	-895.886	0.889986
TCGA-EJ-5512	-893.804	-673.594	-1567.4	0.93054

TCGA-V1-A8MF	-243.85	509.9005	266.0503	0.799676
TCGA-G9-6333	-455.719	-191.257	-646.975	0.872735
TCGA-EJ-7327	63.62152	-321.117	-257.496	0.843414
TCGA-EJ-7218	-971.767	-469.078	-1440.84	0.923577
TCGA-KK-A8IH	-929.22	-23.0246	-952.245	0.893728
TCGA-KK-A8IM	-416.234	-82.4621	-498.696	0.861904
TCGA-KK-A7AY	-894.268	-422.359	-1316.63	0.916433
TCGA-G9-6496	-387.881	-520.066	-907.947	0.890792
TCGA-KC-A7FD	-1526.01	-722.66	-2248.67	0.96245
TCGA-HC-7748	12.49442	13.38872	25.88314	0.820343
TCGA-EJ-5532	-488.733	-589.556	-1078.29	0.901875
TCGA-HC-7752	-765.134	-364.914	-1130.05	0.905131
TCGA-CH-5771	303.745	614.0178	917.7628	0.738668
TCGA-EJ-7312	-890.892	-524.03	-1414.92	0.922112
TCGA-FC-A800	-973.133	-915.275	-1888.41	0.946756
TCGA-EJ-7321	-907.166	-3.32055	-910.487	0.890961
TCGA-HC-7080	-1168.71	-738.124	-1906.83	0.947623
TCGA-G9-6494	-512.895	-700.909	-1213.8	0.910289
TCGA-EJ-5530	-473.18	-684.254	-1157.43	0.906832
TCGA-2A-AAYU	-884.522	-930.915	-1815.44	0.943253
TCGA-V1-A8MM	-103.711	305.6675	201.9562	0.80529
TCGA-HC-7079	609.7865	3013.203	3622.99	0.4205
TCGA-EJ-AB20	363.9109	509.7001	873.611	0.743021
TCGA-HC-7818	-678.046	-48.3999	-726.446	0.878371
TCGA-VP-A87B	-670.511	-523.647	-1194.16	0.909091
TCGA-V1-A9ZK	-538.006	-453.305	-991.31	0.896286
TCGA-HC-8257	-610.551	-325.494	-936.044	0.892659
TCGA-HC-7209	-796.057	-358.964	-1155.02	0.906683
TCGA-V1-A9O9	-274.946	1224.201	949.2552	0.735544
TCGA-EJ-A46B	-951.24	-834.374	-1785.61	0.94179
TCGA-VN-A88N	-1107.56	-743.424	-1850.98	0.944973
TCGA-HC-7749	-343.466	-229.022	-572.488	0.867345
TCGA-CH-5764	-708.846	-213.772	-922.618	0.891769
TCGA-EJ-5521	-643.83	-173.828	-817.659	0.884692
TCGA-KC-A7F5	-1393.48	-1323.73	-2717.21	0.97883
TCGA-HC-7736	-328.308	-66.1508	-394.459	0.854044
TCGA-EJ-A46D	-853.177	-469.828	-1323.01	0.916808
TCGA-EJ-A7NN	-478.919	138.9296	-339.989	0.849858
TCGA-EJ-A6RA	-830.585	-240.752	-1071.34	0.901433
TCGA-HI-7168	111.623	-703.039	-591.416	0.868725
TCGA-V1-A9O7	189.0522	113.215	302.2672	0.796473
TCGA-V1-A9OA	-28.8096	-154.854	-183.664	0.837542
TCGA-KK-A8IJ	-857.301	-713.399	-1570.7	0.930718

TCGA-ZG-A9L1	-411.759	-1117.71	-1529.47	0.928487
TCGA-KK-A7AW	-790.743	728.4756	-62.2679	0.827673
TCGA-X4-A8KQ	-159.986	4.579331	-155.407	0.835269
TCGA-HI-7171	-631.959	-473.448	-1105.41	0.903587
TCGA-CH-5769	-516.159	-248.283	-764.442	0.881023
TCGA-ZG-A9MC	294.2652	1818.975	2113.24	0.609643
TCGA-YL-A9WL	-958.817	-1001.96	-1960.77	0.950122
TCGA-ZG-A9ND	-1126.79	-637.264	-1764.06	0.940722
TCGA-V1-A8WV	-450.235	375.2891	-74.9463	0.828716
TCGA-KK-A59Y	-1202.66	-695.985	-1898.64	0.947239
TCGA-ZG-A9N3	-1013.41	451.7637	-561.643	0.866552
TCGA-J4-AATZ	-1170.34	-682.806	-1853.15	0.945077
TCGA-ZG-A9LZ	-535.999	96.67161	-439.328	0.857452
TCGA-EJ-5507	-522.297	-2.45506	-524.753	0.863837
TCGA-XK-AAIV	223.2745	1488.146	1711.421	0.65531
TCGA-EJ-5518	209.1274	-191.63	17.4977	0.821046
TCGA-J9-A52E	417.9517	231.9451	649.8968	0.764594
TCGA-KK-A8I7	-84.6253	299.913	215.2876	0.804128
TCGA-VP-A87H	-760.316	-488.145	-1248.46	0.912383
TCGA-YL-A9WX	-398.578	235.239	-163.339	0.835908
TCGA-V1-A9Z7	372.646	132.8969	505.5429	0.778079
TCGA-ZG-A9LM	-85.181	-11.7191	-96.9001	0.830516
TCGA-KK-A6E8	-1037.9	-839.724	-1877.62	0.946245
TCGA-YL-A8SJ	58.11583	-729.445	-671.329	0.874475
TCGA-CH-5766	-972.874	-65.3754	-1038.25	0.89932
TCGA-MG-AAMC	-1251.49	-735.083	-1986.57	0.951296
TCGA-YL-A8HM	-563.704	428.3018	-135.402	0.83365
TCGA-KK-A5A1	-130.755	7.540743	-123.214	0.832661
TCGA-YL-A9WJ	-170.593	203.5399	32.94697	0.819749
TCGA-KK-A8I8	-797.556	-450.745	-1248.3	0.912374
TCGA-KK-A8IC	-44.338	34.33792	-10	0.823343
TCGA-KK-A7B2	-50.0052	1071.798	1021.793	0.728289
TCGA-YL-A9WI	-717.255	-730.335	-1447.59	0.923957
TCGA-EJ-8469	-770.723	-603.305	-1374.03	0.919773
TCGA-FC-A5OB	-1165.01	-1011.15	-2176.15	0.959506
TCGA-V1-A9ZI	16.48266	232.3742	248.8568	0.801189
TCGA-YL-A8SQ	-464.403	-183.992	-648.396	0.872837
TCGA-CH-5741	-1280.85	-864.663	-2145.52	0.958229
TCGA-ZG-A9LB	-333.571	371.3482	37.77696	0.819343
TCGA-YL-A9WH	-798.966	-563.447	-1362.41	0.919102
TCGA-2A-A8VT	-984.114	-551.621	-1535.74	0.928828
TCGA-KK-A7B3	-72.8797	473.2738	400.3941	0.787681
TCGA-G9-6499	-1049.69	-291.811	-1341.5	0.917888

TCGA-YL-A8HL	-1072.73	-1044.01	-2116.74	0.957013
TCGA-ZG-A9LY	-272.769	-4.50468	-277.274	0.84497
TCGA-CH-5751	126.565	1667.054	1793.619	0.646148
TCGA-KK-A8IA	-975.477	-791.685	-1767.16	0.940876
TCGA-V1-A9ZG	-122.958	-236.958	-359.917	0.851396
TCGA-EJ-A65F	-204.53	-156.581	-361.111	0.851488
TCGA-VP-A878	-184.708	10.46158	-174.247	0.836786
TCGA-2A-A8W3	-675.956	-541.137	-1217.09	0.910489
TCGA-HC-A8CY	-885.825	223.0378	-662.787	0.873866
TCGA-ZG-A9L6	173.6327	147.5899	321.2226	0.794788
TCGA-ZG-A8QZ	2.620654	308.4008	311.0214	0.795695
TCGA-HC-A9TE	132.8602	1014.122	1146.982	0.715574
TCGA-G9-7521	-8.38238	741.3864	733.004	0.756675
TCGA-YL-A9WK	94.10289	140.8383	234.9412	0.80241
TCGA-YL-A8SI	-109.942	32.3944	-77.5478	0.82893
TCGA-G9-A9S0	-867.014	21.73835	-845.276	0.886574
TCGA-EJ-5506	-963.392	-499.633	-1463.02	0.924821
TCGA-KK-A7B0	-233.056	1050.009	816.9534	0.748561
TCGA-KK-A7AU	-1810.53	-1132.44	-2942.97	0.985074
TCGA-HC-7821	323.8894	376.2993	700.1887	0.759816
TCGA-V1-A9Z9	-262.427	-374.169	-636.596	0.871991
TCGA-V1-A9OY	-452.325	-12.7916	-465.117	0.859394
TCGA-EJ-5514	136.2114	228.6841	364.8955	0.790881
TCGA-EJ-5519	-535.088	-590.941	-1126.03	0.90488
TCGA-CH-5761	-221.268	-553.137	-774.405	0.881714
TCGA-J9-A52B	-410.783	-67.7338	-478.517	0.860398
TCGA-VN-A88K	-250.553	-430.683	-681.236	0.875179
TCGA-HC-7213	-437.301	-37.0515	-474.353	0.860086
TCGA-EJ-5495	300.2322	339.6244	639.8566	0.765543
TCGA-KC-A4BR	-35.7771	-287.658	-323.435	0.848575
TCGA-KK-A8IL	-399.126	795.3983	396.2719	0.788054
TCGA-KK-A7B4	-521.874	3.090221	-518.784	0.863395
TCGA-G9-6356	-208.621	325.5268	116.9057	0.812629
TCGA-ZG-A9M4	-694.415	841.383	146.9678	0.810049
TCGA-G9-6367	-604.466	-394.021	-998.487	0.896752
TCGA-CH-5753	-1065.35	-215.396	-1280.75	0.914313
TCGA-XK-AAIW	-1308.02	92.92525	-1215.09	0.910367
TCGA-V1-A9Z8	119.7725	98.52777	218.3002	0.803865
TCGA-G9-A9S4	-1325.09	-898.829	-2223.92	0.961458
TCGA-YL-A8SB	-27.4132	-159.413	-186.826	0.837796
TCGA-V1-A9O5	-502.42	699.3811	196.9608	0.805724
TCGA-YL-A8HK	-191.767	-70.6606	-262.427	0.843803
TCGA-EJ-A65J	-564.289	-440.039	-1004.33	0.897132

TCGA-XQ-A8TB	-95.51	-501.953	-597.463	0.869164
TCGA-CH-5788	-908.11	-737.799	-1645.91	0.934698
TCGA-V1-A9OL	-513.219	9.30917	-503.91	0.862291
TCGA-KK-A6E7	-932.665	-605.561	-1538.23	0.928964
TCGA-VP-AA1N	-204.536	230.6854	26.14966	0.82032
TCGA-YL-A8S9	-1543.39	-1281.12	-2824.5	0.981932
TCGA-VP-A87D	-1159.76	-984.941	-2144.7	0.958195
TCGA-KK-A8ID	-1247.63	-671.34	-1918.97	0.948191
TCGA-VP-A879	-609.341	-856.985	-1466.33	0.925005
TCGA-KC-A4BV	-8.77689	88.28375	79.50686	0.815816
TCGA-EJ-5526	-116.03	-82.8376	-198.867	0.838759
TCGA-KK-A6E6	-185.747	-105.29	-291.037	0.846049
TCGA-YL-A8SC	-362.898	269.5427	-93.3558	0.830226
TCGA-YL-A8SK	-392.397	-18.743	-411.14	0.855316
TCGA-HC-A9TH	-122.229	41.73185	-80.4974	0.829172
TCGA-ZG-A9L2	616.2952	745.8949	1362.19	0.693154
TCGA-EJ-5524	150.6974	217.3615	368.0589	0.790596
TCGA-EJ-A65B	-266.644	-139.133	-405.777	0.854907
TCGA-ZG-A9L4	229.5499	6.052289	235.6022	0.802352
TCGA-YL-A9WY	366.2278	1172.915	1539.143	0.6742
TCGA-ZG-A9LU	-776.405	417.0171	-359.388	0.851355
TCGA-V1-A8WW	-546.086	-216.108	-762.194	0.880867
TCGA-ZG-A9NI	183.923	-306.352	-122.429	0.832597
TCGA-KK-A59V	-300.598	2169.161	1868.563	0.637713
TCGA-ZG-A9LS	507.2379	1149.801	1657.039	0.661318
TCGA-CH-5772	-463.46	-312.047	-775.507	0.88179
TCGA-YL-A8S8	-307.824	-558.718	-866.542	0.888014
TCGA-CH-5754	-217.37	724.1154	506.7453	0.777968
TCGA-M7-A723	-21.513	803.6423	782.1294	0.751941
TCGA-J9-A8CM	154.7002	-50.0273	104.6729	0.813674
TCGA-YL-A8SR	-522.119	-587.241	-1109.36	0.903836
TCGA-YL-A8SL	-1278.71	-955.839	-2234.54	0.961885
TCGA-EJ-A46F	-1361.12	-871.469	-2232.59	0.961807
TCGA-EJ-5504	67.94905	-301.129	-233.18	0.841491
TCGA-ZG-A9LN	315.3209	1689.52	2004.841	0.622178
TCGA-EJ-5525	405.4222	-470.714	-65.2922	0.827923
TCGA-KK-A8IK	-1414.26	-857	-2271.26	0.963345
TCGA-G9-7523	1047.437	783.2521	1830.689	0.641986
TCGA-KK-A6E0	-1077.65	-608.816	-1686.47	0.936798
TCGA-KK-A8I4	436.5492	1186.119	1622.669	0.665094
TCGA-CH-5792	196.9577	770.8947	967.8524	0.733692
TCGA-KK-A6E1	-1136.02	-613.302	-1749.32	0.939986

