

Table S3. The risk scores of the brain metastasis immune gene model.

Id	Futime	Fustat	TNFRSF11A	MS4A2	IL11	CAMP	MS4A1	F2RL1	riskScore
TCGA-05-4244	0	0	1.917151563	0.449588556	0.087692569	1.206175112	0.22099899	2.396360034	1.26976541
TCGA-05-4249	4.17260274	0	1.353797938	2.209355218	0.155911911	0.113478388	1.471859899	5.231638276	1.034724308
TCGA-05-4250	0.331506849	1	0.816258927	0.339983147	0.622550632	0.217741285	0.331656257	3.739350659	1.637703986
TCGA-05-4382	1.663013699	0	0.622815139	0.393170994	0.935813848	1.785565368	0.828292873	2.850523842	0.883165708
TCGA-05-4384	1.167123288	0	1.511679282	0.682168239	0.219498701	0.518080953	0.317591552	2.42556916	1.233505819
TCGA-05-4389	3.750684932	0	1.127345671	1.505180694	0.049397187	0.297427654	0.99725142	2.321856154	0.721270354
TCGA-05-4390	3.084931507	0	0.914289269	0.10320793	0.394743876	0.164644737	0.541994836	2.600364528	1.375332187
TCGA-05-4395	0	1	0.800615531	0.179829873	0.755026692	0.020298301	0.131370211	1.983615305	1.415656473
TCGA-05-4396	0.830136986	1	2.343617702	0.455886466	0.037542897	0	0.631565737	3.654626902	2.281356453
TCGA-05-4397	2.002739726	1	1.053257408	0.041896362	0.150021967	5.330382525	0.139486387	3.040970964	0.453400131
TCGA-05-4398	3.920547945	0	0.565521559	0.458511983	1.13273475	0.335191129	1.638621551	1.881391274	0.939115635
TCGA-05-4402	0.668493151	1	0.927714214	0.82493443	0.512059028	0.566488563	1.334961547	4.128501546	1.174340117
TCGA-05-4403	1.583561644	0	1.930913277	0.643508426	0.629465092	0.970835449	0.69850923	5.493632739	2.369916518
TCGA-05-4405	1.671232877	0	1.518823706	1.403327479	1.207964621	0.2333867	1.572167416	1.908030811	1.026311341
TCGA-05-4410	0	0	1.120673223	1.030667741	0.135085971	0.380337195	2.723409986	1.696521488	0.571400459
TCGA-05-4415	0.249315068	1	0.241772883	0.533804307	3.661710715	0.223131646	0.168158252	1.147089398	1.922360902
TCGA-05-4417	1.246575342	0	0.703412313	0.756856219	0.418272103	0.159230164	2.261463455	1.790330886	0.675981651
TCGA-05-4418	0.750684932	1	0.674728567	0.449394185	0.932776535	0.170358291	1.785664403	4.077497449	1.388937967
TCGA-05-4420	2.498630137	0	0.26532384	0.096003901	0.826411879	0.970603874	0.146848061	2.012451351	0.975980549
TCGA-05-4422	1	0	0.848381682	0.059593625	0.183872383	0.047691125	2.231189135	4.12527343	1.313745292
TCGA-05-4424	2.501369863	0	1.441204818	1.241808354	0.131642454	0.583260541	0.761459943	3.337061932	1.04765908
TCGA-05-4425	1.832876712	0	0.486625874	1.031546012	0.389738955	0.193433291	0.41045699	4.684698322	1.270091437
TCGA-05-4426	2.167123288	0	1.049706346	0.376483712	0.356615367	0.296888783	0.238001331	4.164968914	1.752046804

TCGA-05-4427	2.167123288	0	1.046962172	0.42090479	0.582818741	0.185586732	0.608620654	1.288955326	1.067218058
TCGA-05-4430	2.084931507	0	1.005179879	1.670062659	1.040379775	0.538428768	0.912272015	3.911924531	1.099311304
TCGA-05-4432	2.084931507	0	0.891708669	0.362223903	0.541796661	0.604787954	1.650330606	2.575640455	0.974205945
TCGA-05-4433	2	0	1.846167244	0.987217666	0.065976144	0.323826237	1.246386316	5.63200106	1.914531651
TCGA-05-4434	1.252054795	1	1.204761923	1.290253285	1.103920518	0.554427374	2.569922482	4.538931174	1.159252907
TCGA-05-5420	1.252054795	0	0.485236875	0.807163845	0.168160869	0.479207872	2.912468315	3.143873101	0.605626614
TCGA-05-5423	0.41369863	0	0.742301031	1.293474562	0.10699065	0.96069611	2.165025707	3.878086967	0.635575894
TCGA-05-5425	2.416438356	0	0.348279789	0.511014027	0.375021696	0.270224378	1.523176702	3.286790708	0.91401369
TCGA-05-5428	1.835616438	0	1.502228051	1.464801451	0.245604786	0	0.304848942	2.128492861	1.028490472
TCGA-05-5429	0.753424658	1	2.963393142	0.628070566	0.605407587	0.061394333	0.456570008	7.038727161	5.849637719
TCGA-05-5715	0.169863014	0	1.424291226	1.270131478	0.296056302	1.647261088	0.536999372	5.270314453	1.220964113
TCGA-35-3615	0.038356164	0	1.069396882	0.885857749	0.098522517	0.139281674	1.102267821	3.514504704	1.111871167
TCGA-35-4122	0.616438356	0	0.721876995	0.312407444	0.932550743	0.502228407	1.078893387	3.504835952	1.382911012
TCGA-35-4123	0.498630137	0	1.045799101	1.014279181	2.242530236	0.139050158	1.776195639	1.453765994	1.208850896
TCGA-35-5375	0.723287671	0	0.288491795	0.376327748	0.94982177	2.207415203	1.601460823	2.642411172	0.606373355
TCGA-38-4625	8.145205479	0	1.159962458	1.146861674	0.460969456	0.708003869	1.711285328	3.05341862	0.848190116
TCGA-38-4626	7.109589041	0	0.864360893	1.420000839	1.685749395	0.247177048	0.276758941	2.63651619	1.296141847
TCGA-38-4627	3.142465753	1	0.733800192	1.554920523	0.361340251	1.275359773	0.559964404	4.122089205	0.785167824
TCGA-38-4628	4.087671233	1	0.880419876	0.667179987	0.21634516	2.48702965	0.1397848	4.51866029	0.914171921
TCGA-38-4629	2.367123288	1	1.163114375	0.202146004	2.069811003	0.161872453	0.686657276	4.378326092	3.143119112
TCGA-38-4630	2.939726027	1	0.698201083	0.010210362	0.338505211	0.406501063	0.093667743	2.149160273	1.2098467
TCGA-38-4631	0.969863014	1	0.874884434	0.186225367	1.981087961	0.830093582	0.0975609	5.035308543	2.92268667
TCGA-38-4632	3.717808219	1	0.99009172	0.622731412	0.685620512	0.240948672	1.330466108	2.015923315	1.004469222
TCGA-38-6178	1.22739726	0	0.890183548	1.42661014	0.86802993	0.338161967	1.346508974	3.929493953	1.068542557
TCGA-38-7271	2.191780822	1	1.258333374	2.290018828	0.566967421	1.063555908	5.19576246	3.61815244	0.35509122

TCGA-38-A44F	0.364383562	0	1.446275368	2.123156616	0.450612019	1.273926566	3.719839642	3.612295439	0.469288016
TCGA-44-2655	1.575342466	0	1.36904524	0.633298156	0.335616524	0.472526433	2.858820429	3.860171066	1.060686043
TCGA-44-2656	1.594520548	0	2.369714764	2.723138906	0.063980446	0	2.557050488	3.411811279	0.761996105
TCGA-44-2657	1.095890411	0	0.749499845	2.136093394	0.317465025	0.527303693	5.097295983	2.894402855	0.295227631
TCGA-44-2659	1.449315068	0	1.290747328	1.824380437	0.282551729	0.226833547	1.629676038	1.341553178	0.566442769
TCGA-44-2661	1.221917808	0	0.9905062	2.969732768	0.314379128	0.94430999	3.441736808	3.46747675	0.319374588
TCGA-44-2662	1.315068493	0	2.688043204	1.251879136	3.162596173	0	1.274358408	1.632819413	3.032531207
TCGA-44-2665	1.095890411	0	0.953370995	1.139740336	0.659825169	2.277220055	0.19681917	3.267658765	0.759325347
TCGA-44-2666	0.265753425	1	3.050171473	4.217355896	0.351790147	0.092210865	1.0282533	4.107773107	0.911312992
TCGA-44-2668	0.673972603	0	0.548308964	0.469360328	0.643879961	0.30393865	0.827474763	2.44089043	1.027922119
TCGA-44-3396	1.126027397	0	1.399765545	0.916908922	0.912814131	0.574436689	1.689791066	3.205439849	1.208958295
TCGA-44-3398	0.693150685	0	0.660836189	1.220053104	0.715420601	1.045400873	1.898881763	3.852189538	0.766219943
TCGA-44-3917	1.073972603	0	0.754537992	0.204636662	0.341919304	0.310002984	2.226564734	1.299264147	0.719611151
TCGA-44-3918	0.539726027	0	0.783741526	1.528794857	0.803340671	1.145530108	1.872027393	3.128647543	0.638574005
TCGA-44-3919	0.520547945	0	1.028791491	1.757856336	0.384106127	0.968621187	2.399596087	2.933647001	0.530313946
TCGA-44-4112	1.01369863	0	2.176516434	3.04104633	1.618355231	0	2.490642255	3.331372249	0.992427173
TCGA-44-5643	1.142465753	0	0.45249029	0.321965203	0.057509623	0.629252824	1.989457564	3.512314336	0.81607823
TCGA-44-5644	1.364383562	0	0.092783033	0.31859539	0.410977499	0.276208344	0.107606033	1.044664516	0.759025065
TCGA-44-5645	1.049315068	0	1.348110425	1.738727077	0.132110189	0.087477102	2.656523157	3.988952168	0.797947317
TCGA-44-6145	0.898630137	0	0.62413848	1.477119207	0.355602951	0.486310996	2.812601654	3.054761207	0.536421723
TCGA-44-6146	0.82739726	0	1.59168529	0.443914519	0.120143459	0.036954834	0.088793477	4.889243411	2.414544245
TCGA-44-6147	1.208219178	0	1.028689855	1.686700566	0.701129243	0.704668715	3.030055762	3.078084494	0.586558317
TCGA-44-6148	0.991780822	0	0.732780153	2.803940261	0.118148293	0.226486107	1.818233283	3.298115169	0.438173288
TCGA-44-6774	0.989041096	0	0.493322322	0.758685378	1.067076004	0.073618941	0.485713444	2.205662632	1.107284266
TCGA-44-6775	1.01369863	0	1.79727863	1.055258891	0.5241697	0.786549442	0.498378682	4.224221846	1.648008601

TCGA-44-6776	5.309589041	0	1.172305956	1.188906758	0.112009116	0.114631269	0.396317807	2.520660351	0.990565095
TCGA-44-6777	2.704109589	1	1.596305478	1.260053808	0.326387466	0.612110066	1.339697502	2.682656397	0.936061852
TCGA-44-6778	3.04109589	0	1.40322792	1.432585169	0.016654223	0.222196897	3.8924985	1.725313946	0.461411815
TCGA-44-6779	1.369863014	1	1.796577963	1.597933336	0.492275708	0.070767306	0.420361985	3.867824307	1.541157849
TCGA-44-7659	1.216438356	0	0.385630251	1.006113015	0.480116629	0.449249496	2.655379854	4.016312338	0.733143441
TCGA-44-7660	0.890410959	0	2.086691612	0.057432863	0.353437887	3.440363029	0.655677374	2.734502909	0.953837843
TCGA-44-7661	1.002739726	0	1.727059475	0.991988763	1.199469357	0.447270791	1.161787341	3.822044648	1.8048766
TCGA-44-7662	0.597260274	0	1.125284755	0.89106157	1.486728374	0.150356789	0.291552312	4.10029449	2.124944313
TCGA-44-7667	1.526027397	0	0.352860896	0.081530146	0.361462568	0.091068043	0.106198474	0.427204979	0.833611584
TCGA-44-7669	1.57260274	1	2.245017312	0.824069	0.512206154	0.291752249	2.055249397	1.187630692	1.062173963
TCGA-44-7670	1.454794521	0	1.343713617	0.346902873	1.352179429	0.083305281	1.506989914	5.112710486	2.645324804
TCGA-44-7671	1.465753425	0	0.544668888	0.901684206	0.852242304	0.07699734	0.368047502	3.076008544	1.202547001
TCGA-44-7672	1.145205479	0	1.05599443	0.573581601	0.469027803	1.052329587	2.907697572	3.885768772	0.86963015
TCGA-44-8117	1.054794521	0	0.523943294	0.773299901	0.727507725	0.048686506	0.777190569	4.356173627	1.42150522
TCGA-44-8119	0.780821918	0	0.956567357	0.227311606	3.072765601	0.505897085	0.540188947	1.341328646	2.11582003
TCGA-44-8120	0.712328767	0	1.761212083	1.135163314	1.505085585	0.269499932	1.286299992	2.990200642	1.67726717
TCGA-44-A479	1.073972603	0	0.704261953	0.342428857	0.872563616	0.376181455	3.499079869	2.809770721	0.820877004
TCGA-44-A47A	1.276712329	0	1.826289976	0.981111582	0.188630521	1.130520664	1.119424864	2.892329697	1.017685241
TCGA-44-A47B	0.78630137	0	0.851355467	1.439939174	0.218100044	0.074768573	0.458546753	3.137013093	0.933246532
TCGA-44-A47G	0.961643836	0	1.131129565	1.011914282	0.572315822	0.825482983	3.620440457	3.350379658	0.679861808
TCGA-44-A4SS	1.136986301	0	1.098931902	0.7747568	1.974644761	0.181207765	0.914648789	2.125080641	1.587206166
TCGA-44-A4SU	1.120547945	1	0.92567309	0.652536105	0.749381387	0.396157274	3.345929457	3.126710953	0.835297785
TCGA-49-4486	6.350684932	1	1.039445487	0.026109535	0.049346586	0.044307505	0.192918097	2.897800482	1.537167293
TCGA-49-4487	2.342465753	1	0.493733531	0.228598397	1.120091719	0.329484883	4.398284071	2.793261523	0.738681922
TCGA-49-4488	2.380821918	1	2.643582388	0.241043515	0.203620548	0.5389245	1.228674008	1.408131905	1.527919558

TCGA-49-4490	1.054794521	1	0.367842834	0.650761128	0.633092623	1.026378135	0.760973892	4.29399957	1.065960387
TCGA-49-4494	2.961643836	1	1.48716833	0.142305389	0.107445468	1.603256945	0.1727011	3.47287049	1.343581149
TCGA-49-4501	3.893150685	1	1.283589892	1.556108461	0.488331738	0.432586412	2.689586298	5.277914866	1.05475656
TCGA-49-4505	1.17260274	1	1.162755677	2.321315302	0.798766978	1.345782161	0.975671181	3.522007606	0.663388108
TCGA-49-4506	2.736986301	1	0.232428442	0.043793395	0.515763284	0.070721858	1.586229104	2.703299031	0.998887035
TCGA-49-4507	0.734246575	1	0.422993128	0.398139772	0.548895502	0.373044026	0.581444508	1.814577554	0.897090357
TCGA-49-4510	2.454794521	1	0.490330233	0.264300314	1.405711754	0.288502455	0.29547053	3.071658352	1.640318788
TCGA-49-4512	2.479452055	1	1.140125926	0.997978665	0.255293417	2.530200644	1.471414367	2.892651854	0.541963634
TCGA-49-4514	4.657534247	0	0.654761121	0.170207001	0.106900974	0.351344757	2.065762303	3.051764028	0.911373764
TCGA-49-6742	1.219178082	0	0.990553816	0.470694389	0.478234604	1.588299796	0.193647374	5.462858537	1.595289114
TCGA-49-6743	1.010958904	0	0.927753602	0.688126756	1.760006794	0.491504721	1.363132346	3.097050242	1.480444757
TCGA-49-6744	2.438356164	0	1.066355817	1.658686398	0.305324816	1.908492756	1.580580661	3.224596004	0.520509212
TCGA-49-6745	1.430136986	0	1.383362633	1.053887431	0.549460463	1.29069741	0.68021365	4.97731995	1.405506866
TCGA-49-6761	0.969863014	0	0.172697768	0.321780447	1.546407218	0.27194531	2.095413037	3.01885466	1.107959689
TCGA-49-6767	1.854794521	0	0.219845108	0.018329209	1.317381532	0.34196584	0.204042603	3.26794395	1.634758256
TCGA-49-AAQV	1.854794521	1	1.462348058	0.308750686	0.302199271	0.669862717	2.632362482	2.432467057	0.929160213
TCGA-49-AAR0	12.75342466	0	0.605852139	0.706968587	0.3283537	1.001599017	2.544500655	2.299624623	0.551082428
TCGA-49-AAR2	6.093150685	0	0.529892395	0.015045345	0.188803411	0.129599594	1.908705142	0.589771566	0.656792735
TCGA-49-AAR3	5.18630137	0	0.426359663	0.124567821	1.761504453	0.344276763	2.62289028	4.868430668	1.725325892
TCGA-49-AAR4	2.408219178	1	1.235514512	0.693993214	0.549936212	0.216988441	2.161767917	2.518944597	0.989542983
TCGA-49-AAR9	0.712328767	1	2.1548218	0.026848887	0.500749208	0.078799885	0.018458616	3.415648815	2.917192605
TCGA-49-AARE	3.367123288	1	0.173292823	0.20428595	0.883888114	0.683606483	2.357458533	3.034623372	0.829571308
TCGA-49-AARN	3.109589041	1	1.18970638	0.60941852	0.46821524	0.527896604	3.301305806	4.123669202	1.001414352
TCGA-49-AARO	10.29863014	0	1.717180671	0.510291157	0.632484172	0.508655619	3.224876407	2.557926497	1.009587749
TCGA-49-AARQ	18.44383562	0	0.932399227	0.234514612	0.391885992	4.599483885	1.195753851	1.662674422	0.343171179

TCGA-49-AARR	13.67671233	0	0.689582813	1.57486724	0.295411832	1.88938657	3.227537324	2.621598585	0.321589572
TCGA-4B-A93V	0.695890411	0	1.845036771	0.045146212	0.570005971	0.112939003	0.583102732	1.339886331	1.655108313
TCGA-50-5044	1.709589041	1	0.527788569	0.309113333	1.125524935	0.067098233	0.03116879	4.253195712	2.05516303
TCGA-50-5045	5.956164384	1	0.862127126	0.613889437	1.458573603	1.169191625	3.602838982	2.082734509	0.668389222
TCGA-50-5049	5.879452055	0	0.829505078	0.416868062	0.575264979	0.43436717	3.246107144	2.384222696	0.733161403
TCGA-50-5051	1.309589041	1	0.846566708	0.596433868	2.032532	0.540909438	2.134034122	1.853691003	1.119265078
TCGA-50-5055	5.01369863	1	1.149983536	0.989006881	0.580519259	2.15402251	5.262220844	3.519459418	0.394628591
TCGA-50-5066	2.58630137	0	0.381849366	0.376648054	1.368111376	0.349735213	2.380961934	3.528132744	1.142707777
TCGA-50-5068	4.106849315	1	0.709011881	0.741701507	0.073299274	0.843312989	3.619867788	3.064429271	0.52494129
TCGA-50-5072	0.684931507	1	0.744231692	0.40958006	0.416276473	0.925535415	0.396965158	3.751189386	1.227587747
TCGA-50-5930	0.77260274	1	0.136676743	0.170470726	1.002670541	0.104295288	1.871694109	3.69931531	1.201067125
TCGA-50-5931	1.189041096	1	1.208288874	0.084070685	1.341367089	0.213383405	0.118111463	3.659092084	2.574844995
TCGA-50-5932	3.383561644	1	1.905458447	0.308910723	0.087942845	0.263402835	0.156864767	3.659332709	2.107158876
TCGA-50-5933	6.556164384	1	0.885191167	1.070149026	1.768655554	0.136963083	0.085307509	1.743886988	1.358784756
TCGA-50-5935	1.789041096	1	1.237005053	0.666133026	0.166444915	0.309347681	0.729656374	4.902609663	1.69034736
TCGA-50-5936	0.704109589	1	0.543316623	0.384249365	0.954001491	0.365153692	1.060999501	4.364429213	1.539086281
TCGA-50-5939	1.260273973	1	0.707884033	0.757425311	1.815726379	0.283583119	1.919697208	2.904638713	1.260658039
TCGA-50-5941	1.553424658	0	0.973915614	1.848245956	0.312773317	0.259741043	2.637956568	3.352077447	0.60840038
TCGA-50-5942	2.419178082	0	0.649561629	2.75072803	0.308129093	0.099143494	0.864956358	4.030828299	0.627290496
TCGA-50-5944	2.093150685	0	0.80683297	2.50682664	0.25032835	0.685101242	0.225874211	2.884499669	0.556214682
TCGA-50-5946	1.879452055	0	0.647313106	0.940498003	0.830489058	1.51613136	0.584435857	1.178813309	0.594729151
TCGA-50-6590	3.528767123	1	0.544732482	0.193396116	2.784353771	0.099569023	1.785543099	2.207029071	1.785746652
TCGA-50-6591	0.326027397	1	0.273588456	0	0.685811793	0.293634154	0	1.931346354	1.155504557
TCGA-50-6592	2.128767123	1	0.289436403	0.29716989	1.105231665	0.275405154	1.203268138	4.251299765	1.477995142
TCGA-50-6593	0.920547945	1	1.571727675	1.044889396	0.397591964	0.835573592	0.841420099	2.995537711	1.104990458

TCGA-50-6594	1.01369863	1	0.775603295	0.173721837	0.233508127	0.3447755	0.0391663	1.91696181	1.123526466
TCGA-50-6595	0.517808219	1	0.783463514	0.220050857	2.634230422	0.055744742	0.124807525	4.813380041	3.891108499
TCGA-50-6597	3.473972603	1	0.872021812	0.259731164	0.219622535	0.258826902	1.292688928	4.583551144	1.504192134
TCGA-50-6673	0.060273973	1	1.709723031	0.706995241	0.215954315	0.562428962	0.464809197	5.582403833	2.220183957
TCGA-50-7109	0.843835616	1	0.490881267	0.50592383	0.384318563	0.174724983	1.633038305	1.244904024	0.675789891
TCGA-50-8457	2.134246575	0	0.484700929	2.131086059	0.28719727	0.218332724	3.280275337	3.705258072	0.446576945
TCGA-50-8459	1.61369863	0	0.745807187	0.642090336	1.26417095	0.693535216	2.7802816	5.12351099	1.323889533
TCGA-50-8460	2.271232877	0	1.215590197	2.257463259	0.158024835	1.015491454	2.099437685	2.656898628	0.444960306
TCGA-53-7624	2.857534247	1	0.130282654	0.04740014	0.900794779	0.118441541	0.586441462	3.09584025	1.339366216
TCGA-53-7626	2.545205479	1	1.126296908	2.229919057	0.153972564	0.50807961	2.829881602	1.657280971	0.365148489
TCGA-53-7813	1.161643836	0	0.819959427	0.251958911	0.380980739	0.227848858	1.53225139	2.392741997	1.017525809
TCGA-53-A4EZ	2.934246575	0	0.776462143	0.259501171	0.561738825	0.132451049	2.137557588	2.421998898	0.980454788
TCGA-55-1592	1.920547945	1	1.355036603	1.101316859	0.32355405	2.240859793	0.585889782	3.919509872	0.857995531
TCGA-55-1594	3.22739726	0	0.481299297	0.304167056	0.15825778	0.272421876	1.16825501	2.891183914	0.953289118
TCGA-55-1596	5.657534247	0	0.492524321	0.422044603	0.444167104	1.928557254	0.543424983	2.50079932	0.690018133
TCGA-55-5899	2.547945205	0	1.373160933	0.348165968	0.212549877	0.578426737	0.301076285	0.572727456	0.930942888
TCGA-55-6543	1.191780822	0	0.47756118	1.120624323	0.31859829	0.834912563	0.080409307	3.656719044	0.906116138
TCGA-55-6642	6.709589041	0	1.212664995	0.995405258	0.605902908	0.057525469	0.431189923	1.702213582	1.07577348
TCGA-55-6712	0.468493151	1	1.371060062	1.400284869	0.201350625	0.740901516	2.432907463	3.88920729	0.798704681
TCGA-55-6968	3.542465753	1	1.210652769	0.0764932	0.26814157	2.075190797	1.066892103	2.58749849	0.857234273
TCGA-55-6970	1.271232877	1	1.053562697	0.99223891	0.079533323	0.112738776	1.989309472	3.056294817	0.851851397
TCGA-55-6971	3.835616438	0	1.050443813	1.281279229	0.970705388	0.701021258	3.410200372	1.969077363	0.564451994
TCGA-55-6972	4.471232877	1	0.764326482	0	0.067639869	0	0.132893982	1.315061117	1.088234996
TCGA-55-6975	0.323287671	1	1.077820943	0.642330487	1.01627255	0.210561843	1.148907844	3.134787616	1.432487937
TCGA-55-6978	0.482191781	1	0.946832658	1.229475688	4.480478502	0.118984581	0.590841646	5.33867167	4.996597012

TCGA-55-6979	0.649315068	1	1.122194332	0.855864201	0.219135588	0.346456747	2.138654729	2.951173442	0.860463661
TCGA-55-6980	5.778082192	0	0.940465417	0.873797538	0.878721538	0.446706882	0.279837896	4.047805229	1.55348238
TCGA-55-6981	3.778082192	1	1.694358636	1.520620155	0.200503291	0.761218999	2.07185216	2.889185669	0.761295829
TCGA-55-6982	2.726027397	1	1.148397331	0.484057604	0.599741097	0.749181017	1.50047773	4.088181037	1.349804798
TCGA-55-6983	7.734246575	0	0.721257568	0.970491858	0.3169353	1.620508872	4.277228661	3.402423913	0.413561748
TCGA-55-6984	2.082191781	1	3.109108488	0.385243239	0.617848953	0.231724437	2.525032028	5.895532092	3.746760673
TCGA-55-6985	3.378082192	0	1.251886562	1.46618337	0.961472246	0.606446443	1.703603291	2.813844471	0.893918959
TCGA-55-6986	8.934246575	0	1.185606004	0.658359192	0.219837471	0.464014256	1.614778528	4.484250964	1.307171202
TCGA-55-6987	5.854794521	0	0.703549498	1.382265997	0.382640253	0.321833237	3.90091052	1.206855083	0.360202118
TCGA-55-7227	2.608219178	1	2.011237374	1.38356309	0.407811628	0.050314698	0.901748731	3.593954748	1.544407344
TCGA-55-7281	2.389041096	0	0.874233047	0.402070151	0.243903122	0.623215386	0.29807311	2.998743536	1.174646971
TCGA-55-7283	1.668493151	0	0.543918834	1.632491493	0.208916669	0.121954431	0.188247884	3.875550861	0.920979823
TCGA-55-7284	0.665753425	1	1.965230369	1.265054631	0.6827281	0.452143625	0.641428401	5.587893697	2.305134339
TCGA-55-7570	2.257534247	0	0.757723064	0.546312362	0.637869008	0.418922527	0.285657435	2.21689618	1.100860614
TCGA-55-7573	1.334246575	0	0.533773528	1.949373734	0.409994876	0.314762266	3.599596916	3.438993724	0.442272487
TCGA-55-7574	2.726027397	1	0.694703719	1.618719645	0.410159134	0.372657214	4.878908247	2.860013192	0.377697548
TCGA-55-7576	1.835616438	0	1.256346896	1.142252052	0.420405217	0.167133127	1.431569428	3.282059207	1.080617129
TCGA-55-7724	1.931506849	0	0.685914142	1.946816655	0.357248547	0.500602226	2.57886451	3.644649471	0.539399868
TCGA-55-7725	1.210958904	0	0.887523405	2.460714948	0.022632544	0.294841361	3.103241586	3.648010272	0.428812769
TCGA-55-7726	1.78630137	0	0.292765139	0.945518412	2.609387426	0.072095092	0.358491362	4.515723629	2.313332068
TCGA-55-7727	0.326027397	0	1.214825057	1.231857365	0.134563407	0.23296434	4.034824048	3.781966683	0.669609621
TCGA-55-7728	1.928767123	0	1.761770212	0.518936099	0.131075098	0.987577704	3.12941544	3.582884148	0.961894746
TCGA-55-7815	2.117808219	0	1.776744218	0.832987777	0.13289846	0	2.135705288	2.515927419	1.077771342
TCGA-55-7816	1.282191781	1	0.729265095	0.761382433	0.207288264	0.157576383	0.860243173	1.501441442	0.766434733
TCGA-55-7903	1.553424658	0	2.494635024	1.235071842	0.611915661	0.156771857	0.961893699	3.286882232	1.8692284



TCGA-55-7907	0.939726027	1	0.355335677	0.930256057	0.27727426	0.307327285	1.173841498	3.659474109	0.868705184
TCGA-55-7910	2.849315068	0	1.072217049	0.479772508	1.739251367	0.607892346	1.264422478	2.068315785	1.367304725
TCGA-55-7911	1.471232877	0	0.735347115	0.643405593	0.220127893	0	1.983184825	2.987862124	0.903087233
TCGA-55-7913	1.536986301	1	1.222214837	0.021230311	0.129503116	0.437692069	0.345955073	1.586916679	1.181297251
TCGA-55-7914	0.512328767	1	4.210171298	1.412581684	0.65268144	0.132437075	1.900927988	3.914260453	3.181831207
TCGA-55-7994	1.652054795	0	0.57807668	0.443702695	0.140049523	0.757338086	2.2109058	0.274618101	0.441465247
TCGA-55-7995	2.435616438	0	1.902863406	0.29120935	0.240332438	1.366404849	3.197607547	2.908753765	0.901188442
TCGA-55-8085	2.476712329	0	0.649672301	0.104926267	0.095724404	0.167328188	2.690768376	2.481295066	0.790738476
TCGA-55-8087	1.265753425	0	0.892265694	1.529662609	0.191674556	0.678422601	0.180834375	3.785925661	0.925159877
TCGA-55-8089	1.923287671	1	0.901026755	0.535733752	0.10879315	0.62440467	2.320939335	2.706365054	0.744457441
TCGA-55-8090	1.638356164	1	0.999299705	0.408441883	0.464182886	0.404000805	1.17558983	4.378224637	1.52415547
TCGA-55-8091	1.643835616	0	0.815290589	1.233051367	0.538830645	1.90388161	0.138338613	3.026722465	0.71673023
TCGA-55-8092	0.421917808	1	0.36007057	0.181210588	0.925010344	0.031707115	1.996447982	2.930989142	1.103419325
TCGA-55-8094	1.482191781	0	0.055226631	0.044775717	0.609317591	0.757760825	0.265055822	0.657517192	0.702720563
TCGA-55-8096	1.969863014	1	0.986416686	0.871814477	0.78821501	3.434806228	1.471333016	3.687926157	0.575722312
TCGA-55-8097	1.304109589	0	0.50945852	2.261774705	0.333661279	0.623946313	1.952413551	2.948578458	0.430154431
TCGA-55-8203	1.498630137	0	1.135513047	0.397865016	0.42840339	0.183426965	3.288297114	1.413284406	0.701487102
TCGA-55-8204	1.410958904	0	0.430340333	1.085569333	0.65212341	0.068716275	0.588349606	3.680277327	1.103470258
TCGA-55-8205	1.64109589	0	1.293691476	0.915398127	0.189204861	0.274220636	2.672354497	3.285734996	0.880444388
TCGA-55-8206	2.432876712	0	0.756892995	2.856145182	0.102863012	1.36222934	1.503243112	3.421464081	0.353224692
TCGA-55-8207	2.676712329	0	1.465060909	1.794906103	0.477062596	1.763228555	0.945610067	3.476122907	0.724182704
TCGA-55-8208	1.846575342	0	0.603046584	1.212397297	0.672556581	1.299107836	3.778300916	2.420222532	0.398672011
TCGA-55-8299	1.284931507	1	0.670566312	1.662840866	1.106850642	0.107121349	2.618875194	2.701924948	0.675044897
TCGA-55-8301	1.463013699	0	0.859556457	0.656400776	0.488798831	0.366440134	3.204220084	2.4530466	0.691740555
TCGA-55-8302	1.309589041	0	0.950304487	0.733949939	0.409194982	1.269577914	1.24269944	4.185920282	1.024688403

TCGA-55-8505	1.205479452	0	0.95485803	0.679534303	1.172331315	0.050968407	0.220286167	4.360698	2.12878744
TCGA-55-8506	0.030136986	0	1.65990092	1.233715429	0.528906512	0.473108036	0.249538876	0.380866084	0.840426421
TCGA-55-8507	1.145205479	0	1.063761468	1.177338938	1.096049489	0.461568705	0.353651519	2.023127066	1.072733083
TCGA-55-8508	1.690410959	0	0.347697065	0.4729792	1.375441978	0.281810237	1.193127731	2.802483516	1.18852949
TCGA-55-8510	1.476712329	0	1.528020174	1.737173499	0.254008915	0.284470225	1.900349743	2.728321203	0.760202847
TCGA-55-8511	1.512328767	0	1.821718427	0.550776041	0.718833698	0.192186581	3.095929815	1.066673126	0.896869567
TCGA-55-8512	1.663013699	1	0.898579215	0.872127591	0.255784828	0.649873707	0.720509995	2.788224954	0.908023675
TCGA-55-8513	2.167123288	0	1.641036161	1.048179026	0.170412278	0.855296397	2.770212372	3.952352513	0.913035317
TCGA-55-8514	1.424657534	0	1.015141147	0.213638686	0.388101581	0.34155734	0.814418553	3.344738252	1.434693239
TCGA-55-8614	1.468493151	0	0.45009492	0.875801537	1.573670538	0.156137981	0.764793652	2.896934045	1.282615981
TCGA-55-8615	1.221917808	0	1.016608418	0.097302419	0.373258126	0.132562398	0.264384489	0.464396034	1.025267474
TCGA-55-8616	0.131506849	0	2.184427369	0.691226265	0.313477812	0.293477314	2.7739332	2.841715214	1.224169406
TCGA-55-8619	1.139726027	0	1.385281468	1.864164353	0.116286969	1.810615121	3.523902401	4.484887812	0.481594183
TCGA-55-8620	1.02739726	1	2.087680794	0.260818549	0.103797121	0.506176356	2.015755748	0.823611213	0.965590127
TCGA-55-8621	1.410958904	0	0.964787095	2.30902796	0.368848225	2.036228226	0.647317923	2.791344447	0.430138629
TCGA-55-A48X	1.887671233	0	1.361137915	1.350065861	0.875025747	0.658786963	5.081638527	3.217307348	0.576009785
TCGA-55-A48Y	1.726027397	0	0.752627964	0.545288951	0.341099946	0.318203496	0.767934057	3.397871711	1.179989639
TCGA-55-A48Z	1.783561644	0	0.920632938	0.981491187	0.603332536	1.118335676	0.31421451	4.103518875	1.173830668
TCGA-55-A490	0.271232877	1	0.946793141	0.278697305	1.18419606	0.04211431	0.256735509	1.264580031	1.39917176
TCGA-55-A491	1.715068493	0	2.132365736	0.600303594	0.222552503	0.618290892	1.876216777	3.451598879	1.439189203
TCGA-55-A492	1.632876712	0	0.666082612	0.43341068	0.05441093	0.287445897	0.275858237	1.550726077	0.860508395
TCGA-55-A493	0.076712329	0	0.555851249	0.28981274	1.500720985	0.082842615	2.552571573	1.610800014	0.959590591
TCGA-55-A494	1.317808219	0	1.632830775	0.026691205	0.247061383	0.355052131	0.024415027	4.914460835	2.743669843
TCGA-55-A4DF	1.205479452	1	1.28876496	0.447515873	0.445848319	0.734854368	2.784730685	3.346342221	0.98078137
TCGA-55-A4DG	1.665753425	0	1.059947523	1.499602278	0.339086955	0.139833662	4.105328463	2.439914623	0.489236924

TCGA-55-A57B	1.495890411	0	1.264474416	0.946077789	0.565254521	0.316915742	0.348464971	2.975978068	1.31428096
TCGA-62-8394	0.380821918	1	0.666953734	0.484044192	0.164582817	0.649510838	0.644431159	3.954733411	1.154343518
TCGA-62-8395	3.331506849	0	0.83000258	1.033544504	0.289618715	0.235266674	1.313335857	2.573315374	0.819062389
TCGA-62-8397	3.531506849	0	0.749434053	1.560581257	0.056422121	0.837101546	0.245930847	3.12515351	0.708628812
TCGA-62-8398	1.216438356	1	0.871163531	0.322834174	0.315482877	0.032892693	0.199260466	4.303703504	1.818407056
TCGA-62-8399	7.38630137	0	0.215131691	1.190269373	2.084562337	0.268233738	0.625634485	0.727836729	0.831561992
TCGA-62-8402	4.104109589	1	1.675349732	0.045004353	0.121736688	0.211422104	0.698366259	3.337833632	1.872850355
TCGA-62-A46O	3.983561644	1	0.247790227	0.136158992	0.670920562	0.188019097	0.382189207	2.975022722	1.263976097
TCGA-62-A46P	1.62739726	1	0.530738213	0.45482141	0.09935325	0.278582046	0.535537062	2.959942011	1.017092231
TCGA-62-A46R	4.726027397	1	1.691427983	2.475474306	0.098722028	0.622541621	1.95356512	3.562670599	0.638588766
TCGA-62-A46S	4.528767123	1	1.170255172	0.627812807	0.794478506	0.108642442	0.403723977	4.104245599	1.921063794
TCGA-62-A46V	6.024657534	0	1.294560252	1.994620841	0.456041047	0.570159465	0.006667477	2.73907049	0.865583248
TCGA-62-A46Y	1.134246575	1	1.461233011	1.284807768	0.141999319	1.483937402	1.716190029	3.388062856	0.723829765
TCGA-62-A470	3.271232877	1	1.360048564	0.555550191	0.114278107	0.971231744	0.408872444	2.813370896	1.118109152
TCGA-62-A471	3.41369863	0	0.401971683	0.340964826	0.986369424	0	1.122339051	3.985017515	1.514937291
TCGA-62-A472	2.493150685	0	1.760808101	1.939177016	1.247862669	0.517341299	1.353119412	3.968056801	1.320868668
TCGA-64-1676	4.734246575	0	2.259723786	0.074864819	0.306603373	3.413713118	0.491268984	3.579922696	1.196216169
TCGA-64-1677	1.720547945	1	0.724440056	0.197063239	0.3705131	0.081779077	2.815106632	3.672563134	1.053066475
TCGA-64-1678	3.257534247	0	0.128083872	0.019899179	0.73110259	0.169312179	0.465530876	1.061582047	0.903258091
TCGA-64-1679	4.619178082	0	1.127114627	0.611413676	0.530628926	0.136999124	0.064466243	1.493020965	1.164567894
TCGA-64-1680	3.084931507	0	0.706507411	1.207014743	0.076244048	0.951539341	0.146797579	4.325734903	0.96596416
TCGA-64-1681	3.197260274	1	0.835002762	0.537318496	0.193209112	1.034895151	1.400553772	3.56854355	0.912609514
TCGA-64-5774	6.98630137	0	0.650882162	0.116524678	0.497700922	0.39424075	0.30505115	3.337685991	1.437663288
TCGA-64-5775	0.169863014	1	0.952729313	0.033842908	0.769231574	0.117857985	0.049227339	6.822509346	3.684693905
TCGA-64-5778	2.536986301	0	0.273013418	0.123540101	0.265028026	0.617663873	3.299323199	3.309563132	0.67740249

TCGA-64-5779	1.389041096	0	0.265964687	0.580453347	0.692478409	0.129596485	2.989451318	3.003359722	0.735052787
TCGA-64-5781	3.293150685	0	0.168261333	0.578447691	2.056968326	0.298340978	0.571386628	2.950653325	1.478825814
TCGA-64-5815	0.61369863	0	1.013676909	0.647040769	0.412348762	0.525392417	0.248658464	3.418564472	1.328074412
TCGA-67-3770	1.671232877	0	0.500502306	0.940224211	0.076181831	0.868867596	0.123246265	4.470964475	1.030560934
TCGA-67-3771	1.671232877	0	0.459578319	0.263182402	0.41536756	0.279295553	1.507001508	3.165561402	1.023314877
TCGA-67-3772	1.569863014	0	0.23205411	1.362143508	0.334718262	0.579290406	1.613498671	4.612832403	0.754964041
TCGA-67-3773	1.169863014	0	0.318576865	2.324044277	0.155035789	1.512447661	0.500440548	3.026474814	0.387320144
TCGA-67-3774	1.054794521	0	1.284060335	0.663872915	0.744308261	0.186909523	1.825164557	4.022391749	1.494343961
TCGA-67-4679	1.22739726	0	0.848451704	3.563049614	0.10278913	0.613080182	0.781252638	3.244431361	0.377145386
TCGA-67-6215	0.476712329	0	1.454000118	0.913741291	0.059315149	1.106783139	0.047170691	4.167875071	1.319225823
TCGA-67-6216	0.38630137	0	1.168102593	1.445833034	0.141867927	0.138864062	2.795593018	3.855850348	0.779810026
TCGA-67-6217	1.156164384	0	0.355065047	1.226410494	0.2414134	0.228794845	2.317284503	2.952997262	0.581010669
TCGA-69-7760	0.553424658	0	0.229364157	0.24126948	0.731627349	0.173773108	0.034873853	4.414050834	1.69167736
TCGA-69-7761	0.509589041	0	2.824686859	2.079560943	0.604645607	0.408662639	1.875335842	4.757720619	1.667391725
TCGA-69-7763	1.890410959	0	0.497136598	0.653167845	0.685585314	0.852259991	1.117621379	3.304835729	0.934946417
TCGA-69-7764	1.134246575	0	0.962588447	0.574426705	0.277656278	0.111154034	1.786363655	2.528734218	0.944201709
TCGA-69-7765	0.452054795	0	1.553682774	0.687944661	0.41818161	0.319840714	2.246843945	1.676614121	0.886578017
TCGA-69-7973	0.630136986	0	0.38045971	0.617595362	0.434563711	0.292101209	1.29854771	2.035645431	0.749909221
TCGA-69-7974	0.504109589	0	1.355764731	1.041791043	0.184178564	0.124867515	1.765516892	3.835869878	1.142789859
TCGA-69-7978	0.367123288	0	1.097186046	1.35289814	0.797957122	0.118260633	2.115792149	2.099782131	0.777159889
TCGA-69-7979	0.243835616	0	0.521486993	0.244638973	3.004004378	0.156092245	0.065701975	1.826564146	2.262785372
TCGA-69-7980	1.126027397	0	1.531966836	0.303938399	0.584547716	0.412465984	1.091698237	3.579402158	1.735748989
TCGA-69-8253	1.167123288	0	0.478702552	0.259061403	0.413923056	0.674183595	1.965433173	3.215249661	0.877168418
TCGA-69-8254	1.120547945	0	1.807895894	0.932077591	0.158915938	0.083576758	1.958477463	4.700192749	1.579508837
TCGA-69-8255	0.353424658	0	1.259737961	0.136714389	0.061294025	0.243541288	1.539953332	2.931734486	1.237577062

TCGA-69-8453	1.506849315	0	1.097466856	1.504771679	0.385587127	0.951373069	2.039744017	4.35301451	0.810782921
TCGA-69-A59K	1.619178082	0	0.35273972	0.363463576	0.820300738	1.098746084	0.995263713	2.390859371	0.830007729
TCGA-71-6725	0.701369863	0	1.278074746	0.113319019	0.118725001	0.887689669	0.133321133	1.403119335	1.046762895
TCGA-71-8520	0.575342466	1	1.907558806	0.862836874	0.562778484	0.44150826	0.034683387	3.871443377	2.036292748
TCGA-73-4658	4.383561644	1	1.628690551	0.600943281	0.447545533	0.141365508	0.371678181	3.668993734	1.910607322
TCGA-73-4659	1.947945205	1	0.726270893	0.691438689	0.441405218	0.546929809	0.723822475	3.087371346	1.0329541
TCGA-73-4662	2.498630137	0	0.990020555	0.769594445	0.127284219	0.588055038	2.608443751	3.67658953	0.817382145
TCGA-73-4666	2.191780822	0	0.819334975	0.370082595	0.641938832	0.134894369	0.508072409	3.735749762	1.616965717
TCGA-73-4668	1.279452055	0	1.464383097	0.854224256	2.427026176	0.12104432	0.342176094	4.187403632	3.221905605
TCGA-73-4670	0.35890411	0	0.623470153	0.130840827	1.185262653	0.328078942	0.596389008	1.969153809	1.309605182
TCGA-73-4675	0.109589041	0	1.926108691	0.593171013	1.072223078	0.180001655	0.642786952	3.504632596	2.344051852
TCGA-73-4676	0.449315068	0	2.153780809	1.099955064	0.350352528	0.843777115	0.0949867	4.120798748	1.816041588
TCGA-73-4677	0.104109589	1	0.844055556	0.742893117	0.089556179	0.146851504	1.184813766	4.382296388	1.232611277
TCGA-73-7498	3.257534247	0	0.827737005	1.548317814	0.149912623	0.309139695	1.524405984	2.718120009	0.644987556
TCGA-73-7499	1.95890411	0	0.832074894	0.319855989	0.256238758	3.240598911	1.985314459	3.732363548	0.546625579
TCGA-73-A9RS	0.931506849	1	0.448321553	0.556851709	0.15643151	0.233856184	0.516563855	1.756401838	0.794368683
TCGA-78-7143	13.59178082	1	1.27748007	0.925080334	0.240484244	1.802479029	1.962305502	4.719830691	0.885058793
TCGA-78-7145	2.263013699	1	1.670708233	1.399207634	0.536561039	0.255588284	0.083079315	4.111721716	1.681664594
TCGA-78-7146	0.473972603	1	0.577367163	0.39328438	0.237720234	0.111401232	0.034991857	2.975914739	1.244589615
TCGA-78-7147	1.605479452	1	0.352660927	1.030005667	0.10270169	1.007205091	0.243503419	4.193130922	0.862519344
TCGA-78-7148	1.715068493	1	1.046878896	0.288134874	0.045509195	0.080587648	0.270757905	4.487731084	1.831380319
TCGA-78-7149	2.994520548	0	0.872948958	0.821763326	0.291533071	0.119054213	0.751904461	2.920655911	1.070984072
TCGA-78-7150	1.824657534	1	0.933870035	0.255239824	1.65335621	0.194841712	0.151282369	5.402537464	3.28039046
TCGA-78-7152	3.293150685	0	0.558757876	0.419155134	0.149639754	0.47699242	2.374537303	4.480961746	0.975191691
TCGA-78-7153	2.082191781	0	0.476649962	0.373912437	0.083424926	0.043330569	1.309160131	4.280790636	1.203669023

TCGA-78-7154	1.624657534	1	2.704456549	0.758443386	0.31144533	0.693360085	0.548279461	4.230431862	2.408395923
TCGA-78-7155	3.208219178	1	0.026597953	0.209859483	0.514098314	0.053021243	0.200170562	4.6457601	1.560387314
TCGA-78-7156	2.673972603	1	0.47126584	0.914565435	0.054956066	0.049353908	0.239930584	2.586127751	0.87565868
TCGA-78-7158	0.490410959	1	0.944653876	1.213639707	0.286805299	0.28897477	0.119906396	3.859052531	1.210427182
TCGA-78-7159	3.345205479	0	0.701997311	0.403758606	0.24167562	0.128825391	1.399307701	2.266325038	0.912146337
TCGA-78-7160	1.857534247	0	1.232080419	0.75462937	0.747853934	0.051510794	2.369827024	3.622411687	1.254398563
TCGA-78-7161	0.589041096	0	0.434643157	0.263041809	0.606342461	0.056374186	0.118106039	2.423798844	1.243308524
TCGA-78-7162	8.682191781	1	0.880032563	1.777037104	0.059306051	0.25512458	2.289266878	2.814712189	0.539839921
TCGA-78-7163	18.6630137	0	0.329043828	0.075727457	0.008615718	1.624367285	0.574625681	3.391989757	0.809543008
TCGA-78-7166	0.706849315	1	0.605038595	0.080933613	0.510363081	0.29062337	1.452759372	3.340719261	1.221756496
TCGA-78-7167	7.345205479	1	0.988194098	0.709227223	0.271427495	0	0.631684224	2.595149428	1.141603174
TCGA-78-7220	2.210958904	1	0.629553884	0.639146663	1.44669363	0.083376945	0.252235367	5.065494202	2.322398913
TCGA-78-7535	2.6	1	1.530596431	0.065450082	0.342821788	0.703803901	0.016228109	2.256265751	1.53948392
TCGA-78-7536	0.668493151	1	0.978761397	0.060904804	0.150855916	0.185813865	0.207915504	2.489920361	1.371950932
TCGA-78-7537	4.443835616	1	1.186883876	0.76720717	0.060125558	0.027255811	0.29911935	2.784295865	1.228107414
TCGA-78-7539	0.895890411	0	0.615875063	0.633940217	0.163780987	1.232206881	1.088258706	2.657582729	0.691157564
TCGA-78-7540	2.41369863	0	2.435673994	0.11406064	0.210984343	0.125735215	0.891413237	5.963524505	3.889820218
TCGA-78-7542	0.879452055	1	0.289409621	0.217695813	1.564593592	0.024432473	0.669249856	4.654670296	2.155211241
TCGA-78-7633	2.723287671	0	1.3782085	0.38219808	0.025374263	0.022763815	0.055071809	3.209668769	1.663765912
TCGA-78-8640	17.88493151	0	0.952650603	0.404930255	0.373601344	0.560767034	0.533096114	2.268879859	1.074907866
TCGA-78-8648	3.312328767	1	0.933896815	1.2138131	2.489548782	0.828435818	1.713798752	1.659951263	1.03337298
TCGA-78-8655	6.465753425	0	0.924913441	0.829236671	0.270561547	0.578247945	1.112564825	3.462990589	1.004706038
TCGA-78-8660	0.879452055	1	0.95139802	1.11705513	0.134797482	0.189607334	1.887828484	1.201641276	0.57441267
TCGA-78-8662	9.208219178	1	0.307887627	0.21145758	0.599228809	0.453346045	0.592752624	4.854387744	1.56099776
TCGA-83-5908	2.257534247	0	1.040280778	0.758338578	0.291597423	0.066591618	1.276827454	4.066826774	1.323638182

TCGA-86-6562	1.030136986	1	1.471650805	1.327415898	0.520289051	1.469448913	0.795636582	2.365357524	0.775951655
TCGA-86-6851	0.490410959	0	0.499590984	0.971179724	0.202592016	0.026642537	2.748511156	2.30546092	0.57494458
TCGA-86-7701	1.298630137	0	0.848693926	0.940710429	0.491919417	0	3.35104396	2.288571012	0.650143703
TCGA-86-7711	1.726027397	0	0.921289734	0.499122748	2.466350553	1.655693222	0.646483568	0.866884196	1.096961435
TCGA-86-7713	1.156164384	0	0.823547477	0.131238221	0.183227615	0.070699661	0.328846878	2.720549463	1.343783847
TCGA-86-7714	1.712328767	1	1.364688485	1.000053822	0.15205707	0.155567351	0.049382049	3.690989858	1.474821779
TCGA-86-7953	1.619178082	0	1.643486268	0.203250705	0.304989646	0.215071917	1.42599437	2.747185594	1.478230137
TCGA-86-7954	1.657534247	0	1.202193284	0.839415518	0.101431942	0.606234764	1.420699371	3.414664157	0.986966717
TCGA-86-7955	1.391780822	0	1.283658147	0.245456687	0.139196489	0.252335405	0.656061271	3.390027615	1.539294536
TCGA-86-8054	2.04109589	0	0.30384086	0.668265294	0.974301178	0.0592485	0.379952711	2.383549143	1.094169542
TCGA-86-8055	0.339726027	1	1.215059642	0.851442294	0.940953251	0.638061013	0.883222681	4.183600396	1.55796311
TCGA-86-8056	0.380821918	0	2.578199541	1.952891671	0.340879573	0.243380218	1.874479859	5.503697209	1.755356404
TCGA-86-8073	2.02739726	0	1.175619321	1.735750121	0.303209261	0.406152287	0.920169778	3.436555604	0.878310387
TCGA-86-8074	0.065753425	0	1.456111	0.259241978	0.864297262	1.009482429	0.565389969	3.651392114	1.772938385
TCGA-86-8075	1.312328767	0	0.87907604	0.981883621	2.992517627	0.581487771	1.00059749	5.186027413	2.819680969
TCGA-86-8076	1.339726027	0	1.100269999	1.265686789	0.147787499	0.495168576	2.838006385	2.647429527	0.594878851
TCGA-86-8278	1.304109589	0	0.75484626	1.528622359	0.253132789	0.321978593	0.699297585	2.983969622	0.778937583
TCGA-86-8279	1.320547945	0	0.997241095	0.119904658	0.947711601	0.944859432	0.121276264	4.353255328	1.995970802
TCGA-86-8280	1.920547945	0	0.677349832	1.935877844	0.450811117	0.516828935	2.533977038	2.940312214	0.49076654
TCGA-86-8281	0	0	1.442636821	0.704793692	0.06764923	0.060780189	1.757838664	1.859204388	0.913442974
TCGA-86-8358	1.789041096	0	1.383993657	0.275017748	0.732345087	0.065560144	0.970661742	3.186309176	1.793695295
TCGA-86-8359	1.216438356	1	0.465742488	0.21286517	0.49926336	0.251033799	0.573623192	2.980579761	1.212143912
TCGA-86-8585	0.967123288	0	0.329658781	0.514585359	0.45289522	0.802172957	2.743937411	1.972392445	0.52854986
TCGA-86-8668	1.15890411	0	1.281821472	1.729345272	0.283718597	0.185868165	2.252066178	4.386315436	0.913558806
TCGA-86-8669	2.569863014	0	0.626705712	0.196116982	0.122043685	0.260393077	1.386923826	3.421521409	1.09576042

TCGA-86-8671	2.298630137	0	0.580057324	1.595233142	0.189564441	1.164663882	4.410544688	2.395149967	0.28133499
TCGA-86-8672	0.052054795	1	0.151046838	0.073150403	1.328412097	0.062690514	0.669783407	2.484715792	1.355657939
TCGA-86-8673	1.246575342	0	0.5691007	0.119738876	2.036285421	0.151651333	0.402757896	1.827686955	1.725939481
TCGA-86-8674	1.109589041	0	1.492613926	0.016550934	0.418604818	1.000009887	0.453237626	1.448002298	1.183936433
TCGA-86-A456	1.109589041	0	1.034786456	0.909607984	0.137922395	1.675354819	0.964565535	2.587221371	0.658195449
TCGA-86-A4D0	0.317808219	1	0.347806483	0.098401383	0.180618939	0.357577063	0.360499366	1.917229019	0.920793509
TCGA-86-A4JF	1.468493151	0	1.44130124	0.85039103	1.056478701	1.417155201	0.847042019	3.717546299	1.33880736
TCGA-86-A4P7	1.136986301	0	0.755282302	1.973176867	0.725362296	2.099393034	3.048767422	4.018623399	0.408689764
TCGA-86-A4P8	1.180821918	0	0.497814829	2.462855682	0.116171085	2.380987774	1.652584974	1.857030984	0.212599385
TCGA-91-6828	0.884931507	0	1.003248003	0.694045206	0.186954159	0.825074247	1.773513215	1.32945989	0.610893725
TCGA-91-6829	3.446575342	1	1.054852154	1.838244716	1.012941187	0.092695663	0.343589449	3.26917179	1.145161755
TCGA-91-6830	0.164383562	0	0.631718023	1.932977346	0.375233358	1.377116792	1.577171649	4.369187136	0.578386691
TCGA-91-6831	0.849315068	0	0.911888276	0.336463555	0.810772625	0.231971989	0.246979684	2.383407704	1.421801985
TCGA-91-6835	0.216438356	0	1.800829357	1.536496785	0.093896632	0.413070424	4.269527869	4.045041273	0.712273741
TCGA-91-6836	1.142465753	0	0.412461282	0.491571919	0.773865808	0.042073566	0.646754647	4.055655178	1.474587513
TCGA-91-6840	1.019178082	0	0.322962962	0.643501274	0.453729695	0.41278641	1.884355646	4.279032439	0.962638754
TCGA-91-6847	2.306849315	0	0.637886689	0.088430623	1.422225003	0.574308394	0.01948058	4.778401611	2.435214541
TCGA-91-6848	0.61369863	0	0.421538565	0.507021058	3.124776995	0.31819687	0.986307864	5.286763636	3.16648925
TCGA-91-6849	0.095890411	0	0.966472166	0.212885379	1.489964618	0.223690367	2.844138246	3.398688801	1.439700617
TCGA-91-7771	1.347945205	0	0.719815797	0.780084125	0.103201661	0.180059798	2.456070259	4.843630594	1.022556051
TCGA-91-8496	1.383561644	0	0.452106624	1.691440298	0.061933037	1.248554592	0.100496605	3.251800931	0.578795566
TCGA-91-8497	1.189041096	1	0.782645891	2.627194572	0.173304098	0.414470134	3.929493845	3.175739571	0.31828234
TCGA-91-8499	0.098630137	0	0.160592721	0.067030944	0.294591148	1.251399312	0.238889185	2.609686595	0.834516254
TCGA-91-A4BC	0.120547945	0	0.207007031	0.692801413	0.945633982	0.165385065	1.088692725	2.182214472	0.870760944
TCGA-91-A4BD	1.652054795	0	0.441159198	1.612438748	0.034680257	0.870791326	0.821269178	3.160574703	0.563060351



TCGA-93-7347	0.81369863	0	1.776473452	1.819751361	0.276477009	0.904632392	2.368905425	3.4555475	0.737804145
TCGA-93-7348	0.347945205	0	1.799665636	1.351930623	0.89487322	0.237742809	2.490222206	2.608460342	1.028463927
TCGA-93-8067	0.509589041	0	1.085892625	0.252159986	0.316876435	0.155953235	0.461065948	3.981750569	1.766730558
TCGA-93-A4JN	1.967123288	0	0.975598044	1.570692125	1.696869099	0.416748596	3.449246448	3.812127269	0.906412466
TCGA-93-A4JO	0.090410959	1	0.616575405	1.035782381	0.665934634	0.46715306	3.588755197	1.129461247	0.425666126
TCGA-93-A4JP	1.583561644	0	0.860546709	2.620015957	0.039775582	3.635200956	0.329639025	2.727394416	0.240217903
TCGA-93-A4JQ	1.44109589	0	0.445914348	0.573006256	0.846735533	0.392073345	5.092036555	2.716124122	0.51945671
TCGA-95-7039	0.093150685	0	0.757786518	0.617214617	0.82491895	0.226757213	0.78971852	3.747537601	1.436217213
TCGA-95-7043	0.005479452	0	1.330380719	0.193316808	0.179903001	1.222316926	0.447895549	4.576349338	1.626276811
TCGA-95-7562	0.238356164	1	1.378372604	0.240439008	0.417852827	1.204631473	0.159167717	3.246189161	1.448858487
TCGA-95-7567	0.446575342	0	0.228298761	0.14970649	0.216658825	0.101137184	0.672731155	3.246557377	1.122071121
TCGA-95-7944	0.057534247	0	0.738620655	0.173056299	1.806517692	0.029400673	1.069514698	3.191520018	1.986533425
TCGA-95-7947	0.109589041	0	1.685821593	0.544400545	0.093903874	0.502314092	1.992716177	5.142755733	1.641134519
TCGA-95-7948	0.364383562	0	1.886959144	0.485906915	0.533095475	0.222205243	0.338195882	3.289961464	2.057156572
TCGA-95-8039	0.073972603	0	0.970778029	1.385396501	0.215480646	0.405851572	1.446209874	2.768478323	0.729083109
TCGA-95-8494	0.230136986	0	1.22738555	0.558661592	0.182889773	0.719038832	0.03520013	3.27276617	1.331660376
TCGA-95-A4VK	1.783561644	0	0.64725318	0.451762907	0.352899902	0.275906825	3.638603887	4.413776891	0.89057725
TCGA-95-A4VN	1.515068493	0	1.148817483	0.967751401	0.879966286	0	2.159720977	1.298851967	0.816646031
TCGA-95-A4VP	1.657534247	0	0.552670346	0.325025805	0.351002209	0.606740889	3.164779839	1.89580751	0.572161191
TCGA-97-7546	3.520547945	0	0.570537001	2.763514395	0.350379448	0.158271075	2.466146165	4.000924693	0.46389001
TCGA-97-7547	5.383561644	0	2.157252362	1.089501981	0.05582393	0.066466616	1.503289328	4.989765249	1.878615158
TCGA-97-7552	5.293150685	0	1.845052942	2.1790001	0.021625401	0.435040637	4.506269715	5.151491977	0.666527207
TCGA-97-7553	5.123287671	0	0.809243401	2.55619828	1.878454668	1.022854062	2.72716902	2.849032553	0.529903765
TCGA-97-7554	2.123287671	0	0.296352177	1.082101467	0.314122137	1.553375056	1.270703024	3.588649205	0.586854368
TCGA-97-7937	1.545205479	0	1.059298143	1.142564189	0.776617878	0.104599804	0.696815933	2.444750441	1.099320583

TCGA-97-7938	0.049315068	1	1.496882849	1.694877174	0.315691448	0.101759563	1.82698568	4.561452633	1.136912001
TCGA-97-7941	1.326027397	0	0.707688219	1.591361807	0.184060616	0.029032767	1.732048522	4.814541308	0.923380271
TCGA-97-8171	1.556164384	0	0.925754854	0.196194684	0.092524906	0.130913269	0.343361929	4.228287339	1.708298062
TCGA-97-8172	1.493150685	0	0.804349488	2.970646716	0.241429056	0.470052632	4.654110788	2.339595051	0.220359867
TCGA-97-8174	0.449315068	1	0.686453824	0.976160309	0.2611085	0.105236909	1.517509451	2.266543917	0.743518181
TCGA-97-8175	1.509589041	0	1.889907045	0.365525563	0.161911253	1.528941137	1.077256666	3.642760773	1.325013365
TCGA-97-8176	1.282191781	1	0.50292567	0.189522551	0.166216121	0.369456166	0.841725275	4.705656028	1.422621459
TCGA-97-8177	1.367123288	0	0.993979925	2.148803342	1.607349125	1.007381019	1.976430522	4.096086815	0.850168088
TCGA-97-8179	1.191780822	0	1.100681123	0.58788141	0.305273727	0.231363771	0.25554885	0.907805355	0.930915828
TCGA-97-8547	1.8	0	1.034178916	0.721522907	0.400144952	3.488736517	0.028879969	5.983354012	1.035386618
TCGA-97-8552	1.715068493	0	0.671821507	1.108928896	0.314428249	1.739775816	2.888094711	3.369073901	0.46975191
TCGA-97-A4LX	1.682191781	0	0.907243855	1.444003973	0.268928324	0.992017455	3.965461188	1.734273184	0.339402179
TCGA-97-A4M0	1.78630137	0	1.162869925	1.402694786	0.250085282	0.837685459	1.692916986	2.281736412	0.622158091
TCGA-97-A4M1	1.646575342	0	0.526754873	2.17524436	0.045556127	0.655433034	0.178758219	2.630537445	0.514214814
TCGA-97-A4M2	1.709589041	0	1.208388392	2.41834576	0.241121242	0.724382395	2.691339056	2.101771436	0.380254942
TCGA-97-A4M3	1.479452055	0	0.583173209	0.330516278	0.380788789	0.227728032	0.87368657	2.259948869	0.990224551
TCGA-97-A4M5	1.736986301	0	1.184222704	2.003801638	0.364018034	1.124039705	2.073247755	3.87749712	0.616924542
TCGA-97-A4M6	1.556164384	0	0.536809992	1.163787393	0.528029797	1.33613035	3.016250165	4.345995211	0.600017702
TCGA-97-A4M7	1.723287671	0	1.30009155	2.071703603	0.069732549	0.411136252	2.381861523	3.380752825	0.598403508
TCGA-99-7458	1.073972603	0	2.804651568	1.13876577	0.169775348	0.513373867	2.034392612	3.664079874	1.565359997
TCGA-99-8025	2.904109589	0	1.50067747	0.316919896	0.483563289	0.140088189	1.668987211	1.559124856	1.127581665
TCGA-99-8028	3.063013699	0	0.538182918	0.272055352	0.556341359	0.456414864	2.491694191	1.99969841	0.72435851
TCGA-99-8032	0.120547945	0	0.341298983	1.243647869	1.579831527	0.180547299	1.83260356	2.945620895	0.920635176
TCGA-99-8033	1.797260274	1	0.991680344	0.50986371	1.416355527	0.100145341	0.780066406	2.63446085	1.623941749
TCGA-99-AA5R	1.802739726	0	0.813498377	1.636039955	0.260938842	0.294152387	4.584263264	1.04114382	0.290760977

TCGA-J2-8192	2.024657534	0	0.525820197	1.807882934	0.434464111	1.869537203	1.568069108	3.353183477	0.438025611
TCGA-J2-8194	1.983561644	0	0.763096152	0.164368271	0.917294235	0.18935315	0.627940425	2.83108184	1.512737046
TCGA-J2-A4AD	1.506849315	1	1.292682739	0.924753961	0.550476442	1.427847256	0.175361363	4.032521111	1.261785623
TCGA-J2-A4AE	1.838356164	0	0.422779257	1.336615782	0.157831473	1.120600989	3.15575669	3.368166029	0.423594867
TCGA-J2-A4AG	1.369863014	0	0.833879366	0.561594765	1.371172837	0.55982449	3.883908964	4.34649203	1.087286939
TCGA-L4-A4E5	1.583561644	0	1.592044832	0.521838076	0.83971701	0.359662464	0.497018034	1.698750659	1.417563992
TCGA-L4-A4E6	1.191780822	0	0.736055088	2.081409408	0.192433246	1.178804352	1.596794812	2.172848815	0.384095552
TCGA-L9-A443	0.528767123	1	2.226164053	0.858286184	0.26185221	0.307826006	1.00572402	3.504113684	1.732925644
TCGA-L9-A444	0.84109589	0	1.998917278	0.796813523	0.289733905	0.05931223	2.856862765	0.651494165	0.777230091
TCGA-L9-A50W	1.210958904	1	0.501777959	1.842595557	0.26535402	0.128841694	0.132801849	2.841993824	0.720641142
TCGA-L9-A5IP	0.15890411	1	0.963420892	0.288870619	1.374093995	0.140027813	0.092533059	0.732079026	1.351241091
TCGA-L9-A743	1.819178082	0	1.07084984	0.925253086	1.095223055	0.558173067	3.135550345	2.10240206	0.735521048
TCGA-L9-A7SV	1.547945205	0	2.837114497	0.109568739	0.18666065	0.098614977	1.262506127	2.54755864	2.307417793
TCGA-L9-A8F4	1.304109589	0	0.593851998	0.417351688	1.032093874	1.308889007	2.802214839	1.02146967	0.523705112
TCGA-MN-A4N1	2.265753425	0	1.067542443	0.084285784	1.465941796	0.646247155	0.175832634	2.372712345	1.799814056
TCGA-MN-A4N4	3.219178082	0	0.195087256	0.866818979	1.149755957	0.23239325	0.949334432	2.278518777	0.887887087
TCGA-MN-A4N5	0.230136986	0	1.058400441	0.23531822	1.080203472	0.418935117	1.587711062	3.078889023	1.453773883
TCGA-MP-A4SV	7.178082192	1	1.311633952	0.92449725	0.520706119	0.899754992	2.330253717	3.461479628	0.910062459
TCGA-MP-A4SW	4.871232877	1	1.123168934	1.102121323	0.32988571	0.98205604	2.856573166	3.575777721	0.696910899
TCGA-MP-A4SY	4.112328767	1	1.124427222	0.929172235	0.502944163	0.772605602	0.199669206	4.611394478	1.514514502
TCGA-MP-A4T4	7.169863014	1	1.030578127	1.351842153	1.119860334	0.207452401	1.852287738	2.684717109	0.943053255
TCGA-MP-A4T6	4.904109589	1	0.520437547	1.085166455	0.230985126	0.492659562	2.307581154	3.53921742	0.671740478
TCGA-MP-A4T7	0.457534247	1	0.440401466	0.515971928	0.438063597	0.603291066	1.078240221	3.012134464	0.907072178
TCGA-MP-A4T8	0.44109589	1	0.870251423	0.233906072	1.658474588	0.178248004	0.19508224	2.32224801	1.865271366
TCGA-MP-A4T9	3.465753425	1	0.664793681	1.843229927	1.172575985	1.638939996	1.738505455	4.169950108	0.667766535

TCGA-MP-A4TA	2.602739726	1	0.151932603	0.147509945	0.466126939	0.43141058	0.483044052	3.220238157	1.111506848
TCGA-MP-A4TC	0.202739726	1	1.639438791	0.709288012	1.401880073	0	0.195469258	2.953776125	2.277711735
TCGA-MP-A4TD	0.84109589	1	0.537829797	0.833544103	0.610267939	0.650148983	3.527837125	2.76148264	0.562498773
TCGA-MP-A4TE	2.454794521	1	0.550973471	0.042105668	0.04014011	0.41006553	0.138211827	1.084713904	0.856230261
TCGA-MP-A4TF	0.920547945	1	0.754181762	0.445477597	1.781409274	0.063570072	0.327547055	3.76609848	2.245555502
TCGA-MP-A4TH	1.221917808	0	0.879494844	1.05138744	0.252213806	0.468368186	4.903363138	3.15610913	0.478132315
TCGA-MP-A4TI	1.175342466	1	1.04718335	1.573827976	0.637003161	0.669775225	1.796025236	3.223561941	0.7621388
TCGA-MP-A4TJ	0.928767123	1	0.617453311	1.033700433	0.409461488	0.688719098	4.37393986	2.012424401	0.386211527
TCGA-MP-A4TK	1.594520548	1	1.75456359	0.465320253	0.765951892	1.273944065	2.679896833	4.173207842	1.304885027
TCGA-MP-A5C7	5.101369863	0	0.916989576	0.337112396	0.13790543	0.12420315	0.28277077	1.928958283	1.106699918
TCGA-NJ-A4YF	5.920547945	0	0.15878757	0.042818567	1.154081347	0.656440289	0.06219611	0.446569954	0.869807964
TCGA-NJ-A4YG	5.216438356	0	0.519928552	0.99709787	0.377876874	1.181869531	0.967238656	4.299297879	0.869139734
TCGA-NJ-A4YI	0.010958904	1	0.38767117	0.367973271	0.201540905	1.109517354	0.027108724	3.101186659	0.932460147
TCGA-NJ-A4YP	0.136986301	0	0.633549546	0.89224652	0.802403705	0.072169947	0.883771988	4.404215183	1.4306867
TCGA-NJ-A4YQ	2.42739726	0	1.203789229	1.272871578	0.380635461	1.348424133	4.270223703	1.293216102	0.332888445
TCGA-NJ-A55A	0.021917808	0	1.466764731	2.746287436	0.446737965	0.161304806	4.38657286	2.673082429	0.381508191
TCGA-NJ-A55O	0.035616438	0	0.597194076	0.741586162	0.319557741	0.41060305	1.133034548	4.055074238	1.075553847
TCGA-NJ-A55R	1.652054795	0	1.137792532	1.139424922	0.378784225	0.254847	2.893801316	1.134670226	0.539291183
TCGA-NJ-A7XG	1.690410959	0	1.178616115	0.646274942	0.131836112	0.074202177	0.138661008	4.185410097	1.693775772
TCGA-O1-A52J	4.926027397	1	0.78041316	0.476973749	0.181158845	0.293645392	0.213683913	3.247857572	1.249207739
TCGA-S2-AA1A	1.405479452	0	1.728163088	1.973458481	0.689547128	0.163284428	3.995723404	3.156646008	0.674529516