

	OS.time	OS	PANX1	AURKA	EIF2S1	ACSL3	riskScore
TCGA.44.3917.01A	3.241096	0	3.25579	4.832026	5.148854	4.361796	3.660902
TCGA.35.4123.01A	0.49863	0	3.766681	3.800792	5.130297	2.773623	3.138563
TCGA.49.AARO.01A	10.29863	0	3.729478	2.625677	3.319299	3.080039	2.68983
TCGA.L9.A5IP.01A	0.158904	1	3.597703	3.291555	3.811925	4.619583	3.321287
TCGA.53.7624.01A	2.857534	1	3.952315	4.414554	4.245862	6.075604	4.069007
TCGA.05.4420.01A	2.49863	0	3.267709	4.44584	4.054135	4.178991	3.327737
TCGA.49.AARQ.01A	18.44384	0	2.436349	3.95609	3.46189	2.581127	2.495999
TCGA.73.A9RS.01A	0.931507	1	2.832565	4.654969	3.750409	5.03471	3.467031
TCGA.55.8512.01A	1.663014	1	2.445818	1.088209	2.992017	4.43932	2.582849
TCGA.38.4632.01A	3.717808	1	3.903271	4.267308	3.902922	3.747272	3.26402
TCGA.50.5051.01A	1.309589	1	2.623528	3.105578	3.535854	3.856494	2.820933
TCGA.95.7948.01A	1.30411	0	2.516243	1.536685	3.1565	3.114222	2.289187
TCGA.86.8076.01A	2.720548	0	3.125038	1.672642	3.728736	3.757682	2.738543
TCGA.69.7973.01A	0.630137	0	3.679359	4.312521	4.060328	4.073985	3.358753
TCGA.44.2666.01A	0.265753	1	2.606081	2.073272	4.196411	4.009407	2.865789
TCGA.86.8358.01A	1.789041	0	4.336318	4.71454	4.847478	3.100608	3.408385
TCGA.97.A4M6.01A	1.556164	0	3.050955	2.052855	3.533906	3.458396	2.6432
TCGA.73.4676.01A	0.769863	1	3.613376	3.613899	4.306266	4.699077	3.494393
TCGA.78.7535.01A	2.6	1	3.420587	3.031401	2.916726	3.243717	2.649305
TCGA.49.4490.01A	1.054795	1	3.395769	1.340691	3.602211	3.22228	2.558275
TCGA.49.6767.01A	1.854795	0	3.995341	4.533427	4.606419	3.488922	3.385962
TCGA.86.8279.01A	2.6	0	4.13135	2.795022	3.149412	3.377495	2.843824
TCGA.05.4398.01A	3.920548	0	3.277098	3.062952	3.728218	3.708393	2.936339
TCGA.44.7670.01A	2.416438	0	3.839105	5.045209	3.510196	3.836675	3.299255
TCGA.50.5930.01A	0.772603	1	3.261925	2.46488	3.489221	3.864887	2.851756
TCGA.71.6725.01A	0.70137	0	3.648988	2.976703	3.670008	3.54101	2.933581
TCGA.86.A4D0.01A	0.317808	1	2.477898	4.413505	3.724877	4.027507	3.056974
TCGA.L4.A4E5.01A	1.583562	0	3.099598	4.538878	3.818147	2.432746	2.730078
TCGA.93.A4JQ.01A	1.441096	0	3.628832	2.911118	3.755803	3.762874	3.006122
TCGA.44.7667.01A	3.005479	0	3.468398	4.534969	4.179983	4.470499	3.492591
TCGA.50.6593.01A	0.920548	1	3.962194	2.802972	3.431619	3.645755	2.952598
TCGA.55.7816.01A	1.282192	1	3.06551	1.531633	3.490949	3.32358	2.527391
TCGA.NJ.A7XG.01A	1.690411	0	3.07131	0.900081	2.974013	3.621436	2.426998
TCGA.99.8028.01A	3.063014	0	3.140143	2.335189	3.012182	3.565504	2.620808
TCGA.55.7910.01A	2.849315	0	3.400424	4.674321	3.089094	4.9308	3.408822
TCGA.44.6779.01A	1.369863	1	4.502681	2.560552	4.16787	3.828584	3.233854
TCGA.86.8674.01A	2.208219	0	3.142478	2.398595	3.423397	4.236352	2.918644
TCGA.NJ.A4YF.01A	5.920548	0	3.63047	5.365763	3.482705	3.758351	3.272053
TCGA.44.5644.01A	2.364384	0	2.482114	3.87366	3.534513	3.682818	2.842375
TCGA.49.4510.01A	2.454795	1	2.11332	1.527517	2.842903	4.018962	2.418606
TCGA.53.7813.01A	1.161644	0	3.298361	3.398885	3.686964	3.974864	3.05676
TCGA.44.2668.01A	2.084932	1	5.035347	4.002037	4.730542	4.4937	3.845536
TCGA.05.4417.01A	1.246575	0	3.619649	2.377487	3.816781	4.314111	3.113404
TCGA.55.8094.01A	1.482192	0	2.878454	4.29873	3.611592	4.265637	3.167097
TCGA.49.AAR4.01A	2.408219	1	3.33541	3.043973	3.819872	3.327623	2.849038
TCGA.49.AARE.01A	3.367123	1	3.191223	2.62148	3.183393	4.335022	2.937051
TCGA.NJ.A4YP.01A	0.136986	0	3.280813	2.450756	3.697294	4.050055	2.95309
TCGA.67.6215.01A	0.476712	0	4.417734	2.488378	3.662747	3.795935	3.092388
TCGA.97.A4M1.01A	1.646575	0	2.500115	2.0415	3.508824	3.390808	2.510173
TCGA.86.8359.01A	1.216438	1	3.659748	3.454426	3.092035	4.510619	3.171059
TCGA.86.6562.01A	1.030137	1	3.514027	3.02171	3.876406	4.068035	3.116228
TCGA.91.6836.01A	1.142466	0	3.760002	5.058828	4.004975	4.584755	3.615725
TCGA.73.4666.01A	2.191781	0	4.222841	4.396913	4.663821	3.880663	3.542163
TCGA.44.7672.01A	1.969863	0	3.165205	3.437831	3.411342	3.275968	2.767205
TCGA.78.7145.01A	2.263014	1	3.238677	3.62174	4.424949	3.953231	3.22266
TCGA.4B.A93V.01A	0.821918	1	1.879761	4.030841	3.248817	4.46369	2.923816
TCGA.78.8662.01A	9.208219	1	3.139876	3.250573	3.002635	3.542315	2.732626

TCGA.78.7220.01A	2.210959	1	2.822674	5.135812	4.170938	5.312095	3.700568
TCGA.55.6981.01A	3.778082	1	3.800084	2.914983	3.653724	4.292196	3.178289
TCGA.55.8507.01A	1.145205	0	3.131745	3.551777	3.689583	3.90576	3.024582
TCGA.MP.A4SW.01A	4.871233	1	3.539426	1.922839	3.337349	3.745321	2.765531
TCGA.44.5643.01A	2.775342	0	2.720292	3.965019	3.78629	4.637652	3.241747
TCGA.69.7974.01A	0.50411	0	4.135811	3.255897	3.401371	4.461785	3.286288
TCGA.86.8280.01A	1.920548	0	3.114729	2.396002	3.63203	3.595412	2.762756
TCGA.44.8117.01A	1.054795	0	3.605162	3.238868	3.379847	3.069037	2.756268
TCGA.MP.A4T9.01A	3.465753	1	3.500661	2.591125	4.105744	3.319973	2.878513
TCGA.55.8302.01A	1.309589	0	2.423703	3.431195	4.185966	4.024925	3.01258
TCGA.55.7576.01A	1.835616	0	3.8706	3.070185	4.08302	4.158669	3.261804
TCGA.62.A46R.01A	4.726027	1	3.222616	3.006153	4.005396	3.884903	3.029788
TCGA.55.A493.01A	0.076712	0	3.600642	4.513196	3.524474	4.221036	3.302443
TCGA.95.7039.01A	3.484932	0	3.721628	2.975266	3.861564	3.43107	2.954188
TCGA.55.1596.01A	5.657534	0	4.031351	4.060311	4.350645	4.697147	3.642356
TCGA.50.5941.01A	4.038356	0	3.217347	3.585207	4.170575	3.743984	3.097192
TCGA.44.2665.01A	3.564384	0	3.815333	1.801933	4.020257	3.07194	2.741826
TCGA.62.8398.01A	1.216438	1	2.72579	3.551666	3.580912	4.863605	3.213577
TCGA.97.8175.01A	1.509589	0	3.820267	2.855491	3.592356	3.524773	2.929315
TCGA.97.8552.01A	1.715068	0	2.352209	1.831513	2.995512	3.353991	2.335437
TCGA.64.5781.01A	4.271233	0	3.692549	3.646722	3.688456	3.845976	3.126546
TCGA.55.8510.01A	1.476712	0	3.416311	2.918879	3.278989	3.244579	2.709717
TCGA.MP.A4TK.01A	1.594521	1	3.530672	3.18055	3.163795	3.161468	2.71699
TCGA.78.7542.01A	0.879452	1	3.968905	4.219598	4.478446	4.672194	3.670597
TCGA.55.8089.01A	1.923288	1	3.846373	3.845141	4.031279	4.400114	3.421695
TCGA.44.6774.01A	1.80274	0	4.136919	2.66485	3.679896	3.726793	3.044414
TCGA.86.A4JF.01A	2.019178	1	2.913639	3.554346	3.92038	3.983357	3.054804
TCGA.L9.A743.01A	1.819178	0	3.636801	3.037716	3.43104	3.38399	2.841774
TCGA.55.6980.01A	5.778082	0	3.182161	1.398233	3.718066	3.275817	2.565281
TCGA.49.AARN.01A	3.109589	1	3.199915	2.775206	3.741412	3.27555	2.755336
TCGA.NJ.A55O.01A	0.035616	0	2.790211	3.199207	3.41735	4.348521	2.989356
TCGA.MP.A4TE.01A	2.454795	1	2.770626	3.582963	3.592769	3.291326	2.753184
TCGA.69.7765.01A	0.452055	0	4.128767	2.450384	3.665685	3.903643	3.06505
TCGA.55.8206.01A	2.432877	0	2.838154	2.660161	3.73315	4.192173	2.946193
TCGA.35.3615.01A	0.038356	0	3.031494	1.274055	3.878703	4.088712	2.799466
TCGA.05.4415.01A	0.249315	1	3.790067	4.800578	4.713573	4.608592	3.742939
TCGA.05.4402.01A	0.668493	1	3.795532	2.41984	4.118577	4.325274	3.219341
TCGA.38.4626.01A	10.06575	0	3.26676	1.940043	3.634255	3.924506	2.831772
TCGA.86.8585.01A	0.967123	0	2.782556	3.873454	3.611954	3.516275	2.865902
TCGA.50.5045.01A	5.956164	1	2.843446	2.798668	3.786039	3.100478	2.646329
TCGA.MN.A4N4.01A	3.219178	0	3.174028	2.482327	3.212916	3.834617	2.770177
TCGA.67.6216.01A	0.386301	0	2.801464	1.261112	3.672259	3.048642	2.39572
TCGA.05.5428.01A	1.835616	0	2.769389	3.318012	4.419577	3.36141	2.912234
TCGA.49.AAR0.01A	13.05479	0	2.432718	3.172234	2.906294	3.644575	2.597183
TCGA.86.8073.01A	2.027397	0	3.561471	2.751575	4.157366	3.74649	3.051214
TCGA.55.5899.01A	2.547945	0	3.194718	4.658181	4.826293	4.340745	3.552321
TCGA.55.8301.01A	1.463014	0	3.044326	3.15587	4.038191	3.336252	2.8562
TCGA.05.4390.01A	3.084932	0	3.454655	3.541354	4.951711	4.222851	3.445368
TCGA.50.5936.01A	0.70411	1	3.35171	2.486623	4.004426	4.525776	3.179647
TCGA.64.1676.01A	4.734247	0	2.959069	3.065449	4.384707	3.117128	2.834129
TCGA.MP.A4TF.01A	0.920548	1	2.812254	3.384717	4.233051	5.219342	3.452266
TCGA.44.8120.01A	0.712329	0	3.448464	2.327464	3.011197	3.979929	2.804185
TCGA.78.8648.01A	3.312329	1	3.511104	2.449713	3.164444	3.403753	2.690146
TCGA.73.7498.01A	3.257534	0	3.464556	1.235753	3.27694	4.520759	2.88234
TCGA.97.7553.01A	5.123288	0	3.259897	2.857793	3.782874	3.881979	2.969893
TCGA.64.1679.01A	6.816438	0	3.855663	2.736576	3.756083	4.04518	3.11211
TCGA.55.8616.01A	0.131507	0	3.247522	2.119542	3.593093	3.364845	2.673863
TCGA.55.6985.01A	3.378082	0	3.278615	2.996328	3.88807	3.978903	3.043125

TCGA.55.6971.01A	3.835616	0	3.064288	2.830988	3.97546	4.160575	3.053362
TCGA.05.4430.01A	2.084932	0	3.586187	2.591272	3.877744	3.44983	2.886519
TCGA.69.8253.01A	1.167123	0	3.572703	2.358464	3.628384	4.713869	3.183364
TCGA.73.4675.01A	2.526027	1	2.657477	1.262398	3.225973	3.862866	2.521112
TCGA.50.5068.01A	4.106849	1	2.935256	2.260548	3.990776	3.661878	2.805589
TCGA.83.5908.01A	2.257534	0	3.837387	4.668115	4.613471	4.291212	3.617574
TCGA.55.6979.01A	0.649315	1	3.818521	3.447664	3.97939	3.8672	3.191783
TCGA.78.8640.01A	19.34795	0	3.138558	3.530208	3.799667	4.290987	3.16262
TCGA.69.7978.01A	0.367123	0	4.140327	3.530831	4.081047	4.552627	3.493219
TCGA.44.2656.01A	3.915068	0	4.30985	3.080905	4.425485	3.842395	3.323626
TCGA.78.7158.01A	0.490411	1	2.875395	1.98525	3.826067	3.230394	2.592729
TCGA.86.A4P8.01A	2.205479	0	2.408455	1.005999	3.037365	3.570581	2.311509
TCGA.97.8177.01A	1.367123	0	3.45816	2.132676	3.316692	3.764939	2.779238
TCGA.91.6840.01A	1.019178	0	3.873956	2.826305	4.381653	3.624247	3.131091
TCGA.55.8087.01A	1.265753	0	3.078982	1.187548	3.398658	4.260143	2.748536
TCGA.91.6848.01A	0.613699	0	5.523617	3.709346	4.143228	4.414782	3.75388
TCGA.44.7669.01A	1.572603	1	3.669067	4.474737	3.8226	3.969931	3.296957
TCGA.91.A4BC.01A	0.120548	0	3.268807	3.67642	3.287571	2.797764	2.648049
TCGA.86.8672.01A	0.052055	1	3.499778	3.386561	3.55959	4.197525	3.134523
TCGA.78.7150.01A	1.824658	1	3.766063	4.741691	3.865601	4.71964	3.586637
TCGA.44.6778.01A	5.106849	0	3.607459	3.274191	4.080228	3.656286	3.08563
TCGA.64.5774.01A	7.331507	0	3.442991	4.325817	4.469212	4.084728	3.403937
TCGA.55.8097.01A	1.30411	0	2.520761	2.078426	3.077812	3.651413	2.507627
TCGA.05.5429.01A	0.753425	1	3.548734	2.82227	4.208393	4.054968	3.1621
TCGA.55.7570.01A	2.257534	0	3.428627	4.653119	5.130617	4.331636	3.657542
TCGA.44.6776.01A	7.167123	0	2.84732	1.197908	3.607153	4.958195	2.960204
TCGA.44.6148.01A	1.928767	0	2.87192	0.951739	3.151158	3.984504	2.542423
TCGA.L9.A444.01A	0.841096	0	3.10612	2.561072	2.993858	2.94856	2.453636
TCGA.55.8620.01A	1.027397	1	3.396335	4.311769	3.522585	4.408422	3.29288
TCGA.55.8508.01A	1.690411	0	3.14091	2.713117	3.28573	3.724023	2.776078
TCGA.55.6543.01A	1.191781	0	3.631806	1.375921	4.212445	4.06617	2.991297
TCGA.50.7109.01A	0.843836	1	3.215309	4.211482	4.310087	4.574321	3.459889
TCGA.78.7163.01A	19.85753	0	4.270842	1.661648	3.826548	4.07285	3.073047
TCGA.44.3918.01A	2.838356	0	3.82658	3.546546	4.58974	3.742798	3.296522
TCGA.MN.A4N1.01A	2.265753	0	2.475381	3.108855	2.754155	3.758754	2.599703
TCGA.44.4112.01A	2.213699	1	2.920232	2.965295	4.119079	3.768156	2.954776
TCGA.55.A48Z.01A	1.783562	0	3.325286	3.143738	3.453537	3.44489	2.819056
TCGA.97.A4M0.01A	1.786301	0	3.158856	1.486772	2.979135	3.560167	2.503832
TCGA.64.5778.01A	3.575342	0	2.252047	3.086501	3.376649	3.343521	2.558538
TCGA.78.7159.01A	5.408219	0	3.135919	3.27889	4.52977	4.876072	3.458748
TCGA.71.8520.01A	0.575342	1	3.453348	2.761178	3.248913	4.187532	2.97496
TCGA.69.A59K.01A	1.619178	0	3.71836	2.534332	4.220793	3.557948	3.008911
TCGA.55.8299.01A	1.284932	1	3.539961	2.834276	3.751111	4.516997	3.206043
TCGA.55.6975.01A	0.323288	1	3.615898	4.388043	4.602007	4.764118	3.678691
TCGA.86.8673.01A	2.361644	0	3.638246	2.900664	3.11387	3.771899	2.874905
TCGA.55.A494.01A	1.317808	0	3.096329	2.567346	3.315774	4.072404	2.859939
TCGA.49.AAR9.01A	0.712329	1	3.871013	4.154802	3.9695	4.642493	3.52771
TCGA.MP.A4SY.01A	4.112329	1	3.576126	2.802068	4.499339	3.152784	2.952684
TCGA.J2.A4AD.01A	1.506849	1	3.658925	2.850281	3.492476	3.93807	3.001745
TCGA.99.8032.01A	0.120548	0	3.573362	3.467675	3.210626	3.909238	2.999116
TCGA.86.8668.01A	1.158904	0	3.271541	1.518993	3.675458	3.509105	2.660052
TCGA.86.8054.01A	3.145205	0	2.907381	4.616225	3.907123	4.229775	3.265597
TCGA.55.6968.01A	3.542466	1	4.191615	4.738921	4.427662	4.542823	3.7322
TCGA.35.5375.01A	0.723288	0	2.473324	3.665119	4.788351	4.68566	3.378977
TCGA.49.4505.01A	1.172603	1	3.369732	1.517658	3.885988	3.228267	2.637856
TCGA.64.5779.01A	2.367123	0	3.543328	3.81446	3.542252	3.859067	3.093383
TCGA.44.5645.01A	2.334247	0	3.596956	1.636371	3.688405	4.131783	2.929147
TCGA.95.7567.01A	1.556164	0	3.333468	3.915403	4.087667	4.140881	3.265814

TCGA.78.7160.01A	1.909589	1	3.364665	2.50821	4.068308	5.725549	3.561296
TCGA.64.1681.01A	3.19726	1	2.472525	2.498674	3.514529	3.829995	2.699295
TCGA.86.7714.01A	1.712329	1	2.598032	1.913291	3.575345	3.687743	2.615804
TCGA.44.7662.01A	0.59726	0	4.153502	4.076802	4.240043	3.778567	3.366975
TCGA.62.8399.01A	7.386301	0	3.952902	2.878886	3.609552	3.391022	2.921027
TCGA.50.5946.01A	4.430137	0	2.983359	4.221715	3.525705	3.266056	2.856725
TCGA.MP.A4TJ.01A	0.928767	1	3.409238	3.132906	3.756517	4.18415	3.120808
TCGA.78.7143.01A	13.59178	1	3.301965	2.886686	3.918053	3.601408	2.925215
TCGA.91.6847.01A	2.306849	0	3.400771	4.078647	4.436587	4.871461	3.594346
TCGA.91.7771.01A	1.347945	0	3.209888	3.181933	3.452254	4.31076	3.06359
TCGA.95.A4VN.01A	1.515068	0	3.025451	3.484092	3.520184	3.865855	2.947691
TCGA.55.8506.01A	0.030137	0	4.888494	3.370873	3.672871	4.087733	3.389764
TCGA.55.8505.01A	1.205479	0	3.26756	3.634454	3.561238	4.608636	3.247351
TCGA.86.8074.01A	0.065753	0	3.452839	3.337735	4.284762	4.24713	3.285863
TCGA.86.7955.01A	2.936986	0	3.544807	4.134156	3.465188	5.120732	3.501412
TCGA.44.6145.01A	1.630137	0	3.876398	2.973431	3.54928	3.815566	3.034623
TCGA.78.7156.01A	2.673973	1	3.312173	1.208217	3.505283	4.997641	3.041485
TCGA.50.8457.01A	3.082192	0	2.85352	1.113721	3.061575	3.639636	2.437202
TCGA.86.8056.01A	0.380822	0	3.32454	2.546953	3.15502	4.047694	2.859966
TCGA.MN.A4N5.01A	0.230137	0	2.7673	3.598654	3.41648	3.323669	2.727499
TCGA.49.AAQV.01A	1.854795	1	3.159134	2.976295	4.128583	3.40899	2.895469
TCGA.95.7043.01A	1.378082	1	3.710761	3.117854	4.228019	3.772974	3.151068
TCGA.86.A4P7.01A	1.136986	0	2.606598	2.954046	3.583076	3.968016	2.84129
TCGA.L9.A443.01A	0.528767	1	3.365433	3.292898	3.498585	3.490648	2.869739
TCGA.50.6591.01A	0.326027	1	3.435388	5.541429	4.790945	3.426469	3.431227
TCGA.55.6642.01A	6.709589	0	3.838833	2.688029	3.85249	4.056461	3.126059
TCGA.64.1680.01A	3.084932	0	2.845522	1.654699	3.345923	3.397004	2.49323
TCGA.55.A48X.01A	1.887671	0	3.488672	2.216837	3.649243	4.233682	3.007624
TCGA.97.8176.01A	1.282192	1	2.854603	3.51524	3.244097	4.35325	3.008625
TCGA.53.A4EZ.01A	2.934247	0	3.109654	4.69589	3.875581	4.036977	3.250054
TCGA.86.8278.01A	2.586301	0	4.062878	1.788013	3.979315	3.555004	2.925107
TCGA.91.8496.01A	1.383562	0	2.686382	1.895657	3.668918	3.27527	2.525262
TCGA.55.7903.01A	1.553425	0	2.813555	3.556163	3.683205	3.391878	2.807242
TCGA.86.8669.01A	2.569863	0	2.288365	4.264482	3.291038	3.78391	2.836375
TCGA.93.A4JP.01A	1.583562	0	2.851066	2.749495	3.918172	3.866627	2.900722
TCGA.49.AAR2.01A	6.093151	0	1.685679	2.964907	2.832966	2.670054	2.11613
TCGA.44.7671.01A	2.435616	0	3.240532	1.888054	3.365115	4.983862	3.083988
TCGA.55.8085.01A	2.476712	0	3.297001	3.476071	3.653513	3.36766	2.876007
TCGA.55.7728.01A	1.928767	0	2.369111	1.760643	2.763102	3.260034	2.252253
TCGA.38.4627.01A	3.142466	1	3.500762	1.786066	4.13553	3.722109	2.900102
TCGA.49.6744.01A	4.610959	0	3.515141	2.203944	3.424041	3.619545	2.778086
TCGA.44.6146.01A	1.994521	0	3.187531	1.747044	3.078245	5.225828	3.068329
TCGA.55.7574.01A	2.726027	1	3.479	2.422787	3.865311	3.729313	2.925618
TCGA.L9.A8F4.01A	1.30411	0	2.90461	2.865964	3.700471	3.762941	2.849453
TCGA.62.A471.01A	3.413699	0	2.490334	4.711898	3.519608	4.265224	3.12771
TCGA.62.A46O.01A	3.983562	1	3.313466	4.10315	3.826798	5.752997	3.71983
TCGA.97.7937.01A	1.545205	0	3.361702	3.086395	3.769739	4.788198	3.291028
TCGA.44.2655.01A	3.627397	0	3.585464	1.694913	4.053149	3.752772	2.896369
TCGA.91.6830.01A	0.164384	0	3.937986	2.665762	3.480277	3.688216	2.952858
TCGA.38.4628.01A	4.087671	1	3.394393	2.594461	3.692073	3.478778	2.819982
TCGA.44.2662.01A	3.506849	0	4.60118	3.971782	3.927205	4.905032	3.714393
TCGA.44.2659.01A	3.745205	0	2.923412	1.774507	3.289343	3.256069	2.469539
TCGA.55.1592.01A	1.920548	1	3.584599	2.620912	3.711518	4.228488	3.09088
TCGA.78.7152.01A	3.328767	1	3.388621	2.129461	3.701197	4.373525	3.030042
TCGA.05.4397.01A	2.00274	1	3.515501	6.00961	4.575572	3.652191	3.531644
TCGA.62.8394.01A	0.380822	1	3.79195	3.622905	4.061165	3.391743	3.08311
TCGA.05.5423.01A	0.413699	0	2.986762	3.768719	3.918138	3.40641	2.922163
TCGA.J2.8192.01A	2.024658	0	3.427926	1.447195	4.235295	3.898523	2.915608

TCGA.62.A46P.01A	1.627397	1	2.233309	2.533799	3.175816	4.282393	2.723923
TCGA.NJ.A4YG.01A	6.194521	0	3.38821	1.689995	3.228951	3.402866	2.579444
TCGA.78.7153.01A	9.958904	0	2.922024	3.368067	3.846942	3.868597	2.981727
TCGA.05.4427.01A	2.167123	0	3.477505	3.220627	3.865741	3.590558	2.988807
TCGA.73.4662.01A	6.890411	0	3.1258	2.677978	3.371881	4.13881	2.912044
TCGA.86.7701.01A	2.594521	0	3.99682	3.579066	4.121239	4.538508	3.476159
TCGA.97.A4M2.01A	1.709589	0	2.449723	1.407203	3.238396	3.891083	2.511455
TCGA.78.7540.01A	3.279452	1	3.185078	1.990975	3.258434	4.394788	2.886396
TCGA.91.6831.01A	0.849315	0	3.582833	4.028894	4.44974	4.225896	3.430222
TCGA.73.4659.01A	1.947945	1	3.146296	3.338698	4.294569	4.076828	3.17763
TCGA.73.4668.01A	1.279452	0	3.725219	3.061566	4.108361	3.901529	3.160253
TCGA.05.4432.01A	2.084932	0	4.622354	3.557495	3.800429	4.60654	3.546918
TCGA.J2.A4AG.01A	2.706849	0	3.885167	1.706678	3.228113	4.438839	2.990338
TCGA.86.8075.01A	1.90137	1	4.020163	2.765647	4.052848	4.390384	3.314102
TCGA.38.4625.01A	8.145205	0	3.180618	4.746545	4.289722	3.50659	3.196625
TCGA.95.A4VP.01A	1.657534	0	2.62604	3.102628	2.960757	3.786381	2.679431
TCGA.05.4384.01A	1.167123	0	3.107553	1.699809	3.795262	4.174386	2.878752
TCGA.MP.A4SV.01A	7.178082	1	3.209997	3.636907	3.987022	3.720717	3.057145
TCGA.55.6970.01A	1.271233	1	3.532039	3.291961	4.432628	4.795236	3.491792
TCGA.55.8615.01A	1.221918	0	2.678755	2.333528	2.971385	3.894097	2.622804
TCGA.44.A4SU.01A	1.120548	1	3.262235	1.950563	4.037858	3.519084	2.794135
TCGA.95.8494.01A	0.230137	0	3.363031	4.059933	3.161573	3.724231	2.970683
TCGA.NJ.A55R.01A	1.652055	0	3.207204	4.276412	3.633799	4.29323	3.240307
TCGA.49.4501.01A	3.893151	1	3.48501	2.446819	3.929387	3.580664	2.898392
TCGA.05.4249.01A	4.172603	0	3.449469	2.250451	3.779874	3.684882	2.865861
TCGA.78.7633.01A	4.186301	1	2.950608	1.66032	3.511699	5.318845	3.13023
TCGA.95.7947.01A	1.306849	0	4.066311	3.879192	4.287386	4.458964	3.539861
TCGA.L4.A4E6.01A	1.191781	0	2.71952	1.649035	3.278016	3.658148	2.533056
TCGA.78.7147.01A	1.605479	1	3.712819	2.768251	3.728986	3.724845	2.986274
TCGA.97.8174.01A	0.449315	1	3.044741	1.025632	3.152684	4.968196	2.883275
TCGA.05.5420.01A	1.252055	0	2.780256	3.951652	4.522537	4.321807	3.310076
TCGA.50.5942.01A	5.060274	0	2.468861	1.085568	3.22302	3.755956	2.428563
TCGA.55.8096.01A	1.969863	1	3.805253	2.019693	3.551207	3.701445	2.860888
TCGA.05.4434.01A	1.252055	1	3.680877	3.427011	4.548727	4.323302	3.419763
TCGA.44.6147.01A	2.315068	0	3.410105	2.318987	4.221629	4.164454	3.104894
TCGA.97.7547.01A	5.383562	0	2.919284	0.807178	2.969815	4.610357	2.683795
TCGA.05.4422.01A	1	0	3.737541	4.590062	3.892488	3.802023	3.289179
TCGA.S2.AA1A.01A	1.405479	0	3.228354	1.387359	2.923697	3.478761	2.467826
TCGA.05.4382.01A	1.663014	0	3.970636	2.692862	3.974745	4.186494	3.216948
TCGA.MP.A4T8.01A	0.441096	1	3.206326	3.279958	4.031273	4.024853	3.110568
TCGA.49.AARR.01A	13.67671	0	2.666372	1.002367	3.182192	3.688641	2.426613
TCGA.86.7954.01A	1.657534	0	4.08711	3.100828	3.467242	3.318588	2.924419
TCGA.50.8459.01A	3.065753	0	3.20545	1.700911	3.151459	3.404313	2.529989
TCGA.55.1594.01A	3.227397	0	3.571674	4.756178	3.727297	4.513364	3.459852
TCGA.38.4629.01A	2.367123	1	4.390334	4.023748	4.879198	3.238414	3.375866
TCGA.05.5425.01A	2.416438	0	3.101604	4.397416	3.94297	4.447047	3.347247
TCGA.49.4506.01A	2.736986	1	2.411734	4.087529	4.616833	4.715758	3.396127
TCGA.MP.A4T4.01A	7.169863	1	3.318894	3.260905	3.868177	3.782	3.022075
TCGA.55.7725.01A	1.210959	0	2.486982	1.892053	3.706486	3.513245	2.566328
TCGA.49.6761.01A	0.969863	0	3.358025	3.445053	4.379226	3.458058	3.062894
TCGA.78.7155.01A	3.208219	1	4.114919	5.143135	4.778117	3.819695	3.625455
TCGA.55.A48Y.01A	1.726027	0	3.360429	3.07197	3.386143	4.172542	3.022341
TCGA.49.AAR3.01A	5.186301	0	4.073548	4.028543	3.938605	3.474704	3.190221
TCGA.49.4512.01A	2.479452	1	2.83371	2.687744	3.192701	2.901804	2.445507
TCGA.78.8660.01A	0.879452	1	3.456319	4.217957	4.027975	3.498401	3.122523
TCGA.55.8203.01A	1.49863	0	2.8409	3.060536	4.041872	3.621564	2.891605
TCGA.44.7661.01A	1.526027	1	4.254423	3.698038	4.203118	4.225276	3.463749
TCGA.73.4670.01A	0.358904	0	3.229206	4.073646	4.355191	4.275781	3.363488

TCGA.05.5715.01A	0.169863	0	3.832318	2.296717	3.798436	4.193544	3.103285
TCGA.05.4418.01A	0.750685	1	2.693278	3.977032	4.189903	3.849322	3.084157
TCGA.97.A4M3.01A	1.479452	0	3.375359	2.142499	3.453184	4.21729	2.930037
TCGA.78.7536.01A	0.668493	1	4.042019	4.6605	4.40346	4.856794	3.783014
TCGA.50.5944.01A	4.794521	0	2.715834	2.991002	3.587414	3.95173	2.863139
TCGA.J2.8194.01A	1.983562	0	3.721196	1.115989	3.939766	4.187737	2.953841
TCGA.35.4122.01A	0.616438	0	3.048849	3.613154	4.80248	2.718704	2.890633
TCGA.NJ.A4YQ.01A	3.923288	0	3.916844	3.220558	3.117776	4.840509	3.294753
TCGA.86.7953.01A	2.731507	0	3.094614	3.155401	3.376979	5.750905	3.457833
TCGA.69.7763.01A	1.890411	0	2.774239	2.260262	3.740325	4.476556	2.968633
TCGA.78.7161.01A	0.79726	1	2.733394	2.541314	3.738876	4.174898	2.906344
TCGA.L9.A7SV.01A	1.547945	0	2.699212	3.186843	3.605287	2.690942	2.508155
TCGA.44.2661.01A	3.175342	0	3.23155	1.994711	3.862192	2.869637	2.560837
TCGA.62.A46Y.01A	1.134247	1	2.96061	2.389208	3.622005	3.461044	2.689503
TCGA.55.8514.01A	1.424658	0	3.805046	1.395724	2.877546	3.488168	2.572915
TCGA.86.7711.01A	2.865753	1	4.366432	2.919688	3.60228	4.411819	3.313139
TCGA.64.1678.01A	3.257534	0	1.862173	4.20614	4.581961	3.116192	2.815028
TCGA.86.7713.01A	3.169863	0	2.47936	4.038554	3.939022	5.665477	3.548061
TCGA.91.6828.01A	0.884932	0	3.419293	4.000488	4.06574	4.349445	3.352041
TCGA.38.6178.01A	1.227397	0	3.617231	2.083886	4.120596	3.688049	2.948378
TCGA.97.7552.01A	5.293151	0	3.30758	1.749636	3.706319	4.410537	2.976582
TCGA.50.5049.01A	8.476712	0	3.411597	3.537359	3.968069	3.724144	3.079802
TCGA.55.7727.01A	0.326027	0	3.802257	3.544961	4.037874	4.238539	3.326082
TCGA.05.4424.01A	2.50137	0	3.899598	2.918452	3.965977	4.8162	3.421744
TCGA.44.7659.01A	1.893151	0	2.91623	1.995001	2.962927	3.658808	2.550779
TCGA.55.7911.01A	1.471233	0	3.529122	3.252694	4.063302	3.635692	3.057968
TCGA.55.7281.01A	2.389041	0	2.955993	1.921317	2.985013	3.251714	2.430163
TCGA.62.A472.01A	2.493151	0	3.130678	2.952595	4.327205	3.767372	3.036862
TCGA.05.4389.01A	3.750685	0	2.909338	3.364504	4.237512	3.644486	2.992782
TCGA.49.6742.01A	1.336986	1	2.894077	4.587625	3.629613	4.144361	3.175335
TCGA.69.7980.01A	1.126027	0	3.040598	2.445786	2.995663	3.825135	2.69137
TCGA.05.4425.01A	1.832877	0	3.784279	2.747048	4.398722	4.028067	3.229125
TCGA.93.A4JO.01A	0.090411	1	3.037402	2.497156	2.976087	3.745665	2.669401
TCGA.99.AA5R.01A	1.80274	0	2.625788	1.555864	3.086902	3.318055	2.359857
TCGA.67.3770.01A	1.671233	0	3.151373	1.070797	3.892665	3.404248	2.591525
TCGA.62.8397.01A	3.531507	0	1.958066	1.694903	2.980059	2.746103	2.054547
TCGA.55.A492.01A	1.632877	0	2.516852	1.289558	3.21982	4.403687	2.659993
TCGA.MP.A4TH.01A	2.030137	0	2.888559	1.246842	3.252621	4.490469	2.758886
TCGA.95.7562.01A	0.238356	1	4.103633	3.851278	3.797414	4.272153	3.384269
TCGA.69.8255.01A	0.353425	0	3.029055	6.933157	3.837245	4.058898	3.528621
TCGA.64.5775.01A	0.169863	1	4.954286	3.490222	5.189208	4.047523	3.723415
TCGA.95.7944.01A	1.032877	0	2.605259	3.824173	3.717762	3.263852	2.77112
TCGA.50.6592.01A	2.128767	1	4.120185	4.276237	3.943092	5.174588	3.747053
TCGA.78.7148.01A	1.715068	1	2.432264	2.714104	3.796422	5.233608	3.203617
TCGA.93.A4JN.01A	1.967123	0	3.125462	3.496043	4.067828	3.986212	3.11953
TCGA.55.6984.01A	2.082192	1	3.136451	2.415097	3.673666	3.871804	2.861777
TCGA.55.6712.01A	0.468493	1	4.158275	2.873899	4.489026	4.390897	3.446393
TCGA.MP.A4TD.01A	0.841096	1	3.052438	2.957973	3.253509	3.503171	2.717861
TCGA.78.7146.01A	0.473973	1	4.151766	3.735162	4.365335	4.699629	3.626379
TCGA.55.A4DG.01A	1.665753	0	3.471883	1.833394	3.486848	3.269592	2.628126
TCGA.69.7979.01A	1.117808	0	3.525972	3.146444	3.909264	3.675314	3.023073
TCGA.55.7914.01A	0.512329	1	3.050678	2.679487	4.199876	3.719041	2.944152
TCGA.44.3919.01A	2.810959	1	3.65919	2.895321	3.98299	3.735211	3.049057
TCGA.78.7149.01A	10.79452	0	2.772391	1.712072	3.039856	4.129503	2.644271
TCGA.05.4426.01A	2.167123	0	3.778788	1.953077	3.942876	3.282323	2.802208
TCGA.97.8179.01A	1.191781	0	3.03453	2.912892	3.834687	3.964932	2.96981
TCGA.55.8619.01A	1.139726	0	3.14782	1.636929	3.029999	3.092317	2.390662
TCGA.97.7941.01A	1.326027	0	2.522877	1.444851	3.299599	3.415224	2.399344

TCGA.50.5044.01A	1.709589	1	3.15637	3.503947	3.763175	3.052983	2.780433
TCGA.44.6775.01A	1.931507	0	4.272814	2.887567	3.985862	4.447077	3.381872
TCGA.78.7537.01A	4.443836	1	2.667197	2.105897	3.047268	4.286024	2.724967
TCGA.50.5933.01A	6.556164	1	4.404359	3.650151	4.29469	4.51335	3.592544
TCGA.38.7271.01A	2.191781	1	3.132916	1.786598	3.628201	3.567676	2.676583
TCGA.55.7573.01A	1.334247	0	3.094839	1.374182	3.408154	4.08549	2.725384
TCGA.38.4631.01A	0.969863	1	2.673422	4.752764	4.644942	3.740196	3.245025
TCGA.49.4487.01A	2.342466	1	2.98741	4.400496	3.543668	3.649951	3.001003
TCGA.95.8039.01A	2.273973	0	2.950525	2.193063	3.591243	3.235233	2.586915
TCGA.50.5066.01A	3.950685	0	2.915383	3.762941	4.500754	2.913582	2.880563
TCGA.44.7660.01A	1.621918	0	3.097025	3.461013	4.139846	4.765024	3.360111
TCGA.99.8025.01A	2.90411	0	2.802296	2.221431	3.384058	3.671485	2.65078
TCGA.55.7726.01A	1.786301	0	3.891601	4.361564	4.348716	4.397375	3.564202
TCGA.55.6972.01A	4.471233	1	2.817649	2.761279	3.763066	3.75828	2.830614
TCGA.49.4486.01A	6.350685	1	2.623063	1.222287	3.949199	4.483114	2.848223
TCGA.MP.A4TI.01A	1.175342	1	3.672968	3.330462	3.964094	3.388384	3.000295
TCGA.86.8671.01A	2.29863	0	2.78399	2.244995	3.403198	3.585341	2.628322
TCGA.50.6590.01A	3.528767	1	4.248944	4.658377	5.136904	3.488013	3.561959
TCGA.78.7154.01A	1.624658	1	3.698003	4.32172	4.123358	5.602086	3.839001
TCGA.44.A47G.01A	0.961644	0	3.751086	1.923397	3.66797	3.448145	2.785582
TCGA.67.3774.01A	1.054795	0	2.834163	2.195685	3.558501	4.052792	2.805366
TCGA.55.8207.01A	2.676712	0	3.127045	1.350995	3.267618	3.727352	2.590753
TCGA.44.8119.01A	0.780822	0	3.597716	4.071781	3.762489	4.179086	3.280723
TCGA.55.8511.01A	1.512329	0	3.764903	2.894423	3.907798	4.157054	3.181119
TCGA.67.6217.01A	1.156164	0	3.422123	1.187024	3.857862	4.000283	2.83191
TCGA.44.A4SS.01A	1.136986	0	3.614994	2.705977	3.305691	4.309792	3.047597
TCGA.69.7760.01A	0.553425	0	2.664062	3.226851	3.228088	3.370453	2.633281
TCGA.62.8402.01A	4.10411	1	3.426226	3.804366	3.842144	5.246429	3.552011
TCGA.55.7995.01A	2.435616	0	3.125709	3.583639	3.658501	4.468421	3.191332
TCGA.55.8208.01A	1.846575	0	3.365399	2.827418	3.776845	4.102904	3.051721
TCGA.49.4507.01A	0.734247	1	3.568253	3.215219	3.787491	4.248523	3.188186
TCGA.62.A46S.01A	4.528767	1	2.331503	4.130175	3.319694	5.829539	3.451738
TCGA.44.A479.01A	1.331507	0	3.432747	3.882437	4.181737	4.227844	3.326534
TCGA.86.6851.01A	0.490411	0	3.321422	2.943282	3.692093	3.408504	2.830772
TCGA.44.3396.01A	3.09589	0	4.190137	2.875662	4.118396	3.668922	3.156763
TCGA.44.2657.01A	3.70137	0	2.827326	2.575354	3.647111	3.425615	2.683015
TCGA.55.6986.01A	8.934247	0	2.730439	1.880229	4.280868	4.189513	2.936351
TCGA.49.4488.01A	2.380822	1	3.525523	2.950395	4.365109	2.965069	2.877666
TCGA.64.5815.01A	2.372603	0	3.177831	2.48682	3.652154	3.60747	2.794733
TCGA.50.6595.01A	0.517808	1	4.418365	4.318678	5.218043	4.596694	3.902016
TCGA.55.8091.01A	1.643836	0	3.667908	1.864009	3.963961	4.160331	3.039158
TCGA.50.5072.01A	0.684932	1	2.927291	4.638674	4.36282	4.388176	3.415695
TCGA.05.4405.01A	1.671233	0	3.53827	1.425768	3.443458	3.895408	2.767281
TCGA.50.8460.01A	2.271233	0	2.818747	2.078884	3.062982	2.500352	2.213633
TCGA.97.A4M7.01A	1.723288	0	2.966685	1.871408	3.195724	3.553046	2.560889
TCGA.99.8033.01A	1.79726	1	4.113385	4.019017	3.691958	4.781667	3.540349
TCGA.95.A4VK.01A	1.783562	0	2.734257	2.52346	3.544658	5.184846	3.16901
TCGA.99.7458.01A	2.046575	0	3.759065	1.549085	3.918476	3.515167	2.810398
TCGA.73.4677.01A	0.10411	1	3.914646	1.51097	3.972446	4.938858	3.277226
TCGA.O1.A52J.01A	4.926027	1	3.091426	2.459829	3.878895	3.27003	2.719954
TCGA.55.8092.01A	0.421918	1	3.301621	3.331829	3.490393	4.248775	3.090242
TCGA.MP.A4TA.01A	2.60274	1	4.103893	4.264132	3.921195	4.991489	3.682352
TCGA.78.7162.01A	8.682192	1	3.13955	1.65499	3.476745	5.001135	3.062402
TCGA.97.8172.01A	1.493151	0	2.970744	1.598449	3.372133	3.975108	2.690226
TCGA.50.5932.01A	3.383562	1	4.043878	2.516197	3.846851	4.67371	3.328303
TCGA.50.5931.01A	1.189041	1	3.127836	3.655329	3.588282	3.891403	3.011958
TCGA.MP.A4T7.01A	0.457534	1	2.50575	3.744608	3.092385	4.477764	2.977799
TCGA.69.7764.01A	1.134247	0	2.504894	4.163853	3.320617	4.901221	3.208871

TCGA.93.7348.01A	1.454795	0	3.906611	1.668491	3.465583	4.008779	2.90903
TCGA.L9.A50W.01A	1.210959	1	2.778708	1.545631	2.833281	4.054667	2.557625
TCGA.91.8497.01A	1.189041	1	2.654021	1.305278	2.710353	3.819728	2.405126
TCGA.78.7539.01A	2.167123	0	4.118621	1.847449	3.304029	3.427509	2.76374
TCGA.55.8621.01A	1.410959	0	3.096471	2.049874	3.449776	3.57887	2.670384
TCGA.38.4630.01A	2.939726	1	3.101661	4.097873	4.446573	3.106448	3.007583
TCGA.91.6849.01A	0.09589	0	3.621892	1.451753	3.549555	4.420643	2.967874
TCGA.05.4396.01A	0.830137	1	3.338723	2.126653	3.044832	4.524545	2.928372
TCGA.97.7546.01A	3.520548	0	4.126291	2.60972	3.80113	4.384283	3.259363
TCGA.53.7626.01A	2.545205	1	3.339288	2.182682	3.593702	4.246296	2.966602
TCGA.MP.A5C7.01A	6.158904	0	3.285463	3.106322	3.297231	4.318582	3.038041
TCGA.97.7938.01A	0.049315	1	3.286833	1.907673	3.761673	4.136633	2.922195
TCGA.05.4403.01A	1.583562	0	2.939423	1.784943	3.64871	3.904196	2.745281
TCGA.93.7347.01A	1.871233	0	2.944728	1.560854	2.93147	3.759098	2.522675
TCGA.55.8205.01A	1.641096	0	3.760692	4.167099	4.272835	4.841891	3.631955
TCGA.MP.A4T6.01A	4.90411	1	3.836258	1.757887	3.372405	3.396758	2.702674
TCGA.55.7724.01A	1.931507	0	3.467309	2.982858	4.392273	4.484426	3.336067
TCGA.55.8614.01A	1.468493	0	3.067053	2.535709	4.158819	3.862101	2.962993
TCGA.NJ.A55A.01A	0.041096	0	2.9238	1.541681	3.530868	3.722169	2.630423
TCGA.55.7283.01A	1.668493	0	3.481982	2.305271	3.506556	3.471216	2.757499
TCGA.55.7815.01A	2.117808	0	3.608873	3.023257	4.174548	4.552313	3.343561
TCGA.91.8499.01A	0.09863	0	3.881074	3.913904	5.288207	4.400295	3.70061
TCGA.69.8453.01A	2.227397	0	2.426024	2.131567	3.541538	3.749617	2.623221
TCGA.78.8655.01A	6.465753	0	2.649129	1.992545	3.424796	3.55734	2.565125
TCGA.49.4494.01A	2.961644	1	3.867063	2.905569	3.826884	2.912742	2.80887
TCGA.J2.A4AE.01A	2.956164	0	2.794582	1.982921	3.734769	3.707029	2.701968
TCGA.55.7907.01A	0.939726	1	3.231634	3.01431	4.008883	4.39254	3.18689
TCGA.78.7167.01A	7.345205	1	3.996983	1.204554	3.381207	4.542861	3.009027
TCGA.MP.A4TC.01A	0.20274	1	3.870682	3.15204	3.662156	4.667481	3.338448
TCGA.55.7227.01A	2.608219	1	2.984285	2.025132	3.767061	3.536733	2.699233
TCGA.44.3398.01A	3.186301	0	2.844131	2.062358	3.951949	3.224893	2.621592
TCGA.55.8513.01A	2.167123	0	2.891818	1.483203	3.205639	3.849872	2.587107
TCGA.67.3771.01A	1.671233	0	3.867633	3.682258	4.629378	5.831556	3.962488
TCGA.55.6987.01A	5.854795	0	3.193093	2.883937	3.912362	3.956467	3.01015
TCGA.64.1677.01A	1.720548	1	3.53894	3.628433	4.46185	3.661603	3.200739
TCGA.93.8067.01A	0.509589	0	2.6941	4.193047	3.944518	5.310856	3.503596
TCGA.55.A490.01A	0.271233	1	3.313539	3.582714	3.29254	3.477409	2.850905
TCGA.44.A47A.01A	1.276712	0	3.536324	3.761172	3.776202	3.34525	2.978541
TCGA.97.8547.01A	1.8	0	3.315184	2.114631	3.381191	2.824174	2.478301
TCGA.91.A4BD.01A	1.652055	0	2.111306	1.42587	3.522744	3.62957	2.429314
TCGA.91.6829.01A	3.446575	1	4.542819	3.329163	3.630686	3.435559	3.111725
TCGA.86.A456.01A	2.454795	0	2.898109	2.08081	3.548684	3.984585	2.779794
TCGA.62.A46V.01A	6.024658	0	2.554318	2.661305	3.922728	2.613151	2.453833
TCGA.55.6982.01A	2.726027	1	3.501246	3.080891	4.058007	3.886701	3.104747
TCGA.49.4514.01A	4.657534	0	2.374749	4.2126	2.953481	3.259616	2.616859
TCGA.50.6594.01A	1.013699	1	3.738473	3.759881	3.84496	3.683932	3.134054
TCGA.86.8055.01A	0.339726	1	4.279346	2.685646	3.731795	4.273391	3.250737
TCGA.50.5055.01A	5.013699	1	3.008082	2.14034	3.571835	3.207869	2.57867
TCGA.50.6597.01A	3.473973	1	3.512904	1.862922	3.151935	3.211812	2.552321
TCGA.05.4250.01A	0.331507	1	3.20022	5.015118	4.328075	4.298734	3.483514
TCGA.44.A47B.01A	0.786301	0	3.832398	2.849083	3.862779	4.579005	3.306317
TCGA.38.A44F.01A	0.364384	0	3.214549	1.478514	3.44567	3.532022	2.602588
TCGA.73.4658.01A	4.383562	1	3.539398	2.479038	4.000166	3.397481	2.872499
TCGA.55.A57B.01A	1.49589	0	3.646711	1.710604	3.631275	3.501189	2.745793
TCGA.55.8090.01A	1.638356	1	3.447271	2.362242	3.756227	3.813915	2.914285
TCGA.62.8395.01A	3.331507	0	2.21834	4.201324	3.483997	4.794098	3.16056
TCGA.73.7499.01A	4.194521	1	2.817175	3.881467	4.53655	2.957533	2.898134
TCGA.55.6983.01A	7.734247	0	3.331803	1.722876	3.829069	3.90189	2.849529

TCGA.97.A4LX.01A	1.682192	0	3.357836	2.663253	4.092471	3.680897	2.967
TCGA.97.8171.01A	1.556164	0	2.655042	2.859893	3.35078	3.109696	2.529892
TCGA.55.6978.01A	0.482192	1	3.636005	3.924099	4.377944	4.106556	3.375469
TCGA.49.6743.01A	4.441096	0	4.485177	3.785497	4.260609	5.233045	3.836522
TCGA.91.6835.01A	0.216438	0	3.74744	3.312308	3.892457	4.179897	3.236647
TCGA.55.7994.01A	1.652055	0	3.549372	3.778173	3.978238	4.248412	3.298795
TCGA.55.A491.01A	1.715068	0	3.359527	1.948201	3.065815	3.137296	2.493546
TCGA.67.3772.01A	1.569863	0	3.086394	1.640357	3.926407	3.953581	2.827494
TCGA.05.4433.01A	2	0	2.390356	2.66351	3.634359	4.278159	2.865931
TCGA.49.6745.01A	1.430137	0	3.89588	3.391036	4.309028	4.055027	3.32499
TCGA.97.A4M5.01A	1.736986	0	2.843668	2.07232	3.585921	4.639334	2.974073
TCGA.97.7554.01A	2.123288	0	3.838092	2.509607	3.945274	3.523542	2.960567
TCGA.78.7166.01A	0.706849	1	2.495626	3.044873	3.196681	4.72135	2.978967
TCGA.62.A470.01A	3.271233	1	2.553445	3.30079	3.597463	4.340426	2.992535
TCGA.50.6673.01A	0.060274	1	3.536134	2.881374	3.311734	3.709934	2.875413
TCGA.69.7761.01A	0.509589	0	3.649632	3.439375	3.815628	4.44537	3.298859
TCGA.67.3773.01A	1.169863	0	1.896734	1.111969	3.615982	3.121204	2.21237
TCGA.44.6777.01A	2.70411	1	3.631232	1.802272	3.518388	3.592247	2.758839
TCGA.69.8254.01A	1.120548	0	2.892719	1.540171	3.362345	3.962655	2.661723
TCGA.50.5939.01A	1.260274	1	5.341745	3.297459	4.232693	4.772651	3.791529
TCGA.50.5935.01A	1.789041	1	3.330786	2.65858	3.403166	4.130966	2.953042
TCGA.55.8204.01A	1.410959	0	4.184339	2.855433	4.528893	4.690581	3.547963
TCGA.NJ.A4YI.01A	0.010959	1	3.858504	1.68226	3.514488	3.570373	2.779223
TCGA.55.A4DF.01A	1.205479	1	2.905055	4.416677	5.116782	4.682422	3.628944

risk
high
high
low
high
high
high
low
high
low
high
low
low
low
high
low
high
low
high
low
low
low
high
low
high
low
low
low
high
low
low
high
low
high
low
low
low
low
high
high
high
high
low
low
low
high
low
high
high
high
high
low
high
low
low

high
high
high
low
high
high
low
low
low
high
high
high
high
low
high
high
low
high
low
low
high
low
low
high
high
high
high
low
low
low
high
low
high
low
low
high
high
low
low
low
low
low
low
low
low
high
high
low
high
high
low
high
low
low
low
low
high
low
high

high
low
high
low
low
high
high
high
high
high
low
low
low
high
low
high
high
low
high
high
high
high
low
high
high
low
low
low
low
high
low
high
high
high
high
low
low
low
low
low
high
high
high
high
high
low
low
high
low
high
high
low
high
high
high
low
high
low
high

high
low
low
high
low
low
high
low
high
high
low
high
high
high
high
high
high
low
low
low
low
low
high
low
low
high
high
low
high
high
high
low
low
low
low
low
low
high
low
low
low
low
high
low
low
high
high
high
low
low
low
high
low
high
high
high
high
low
low

low
low
high
high
low
high
low
low
low
high
high
high
high
high
high
high
low
low
high
high
low
low
low
low
high
low
low
high
low
low
high
high
low
high
low
low
low
high
high
high
high
high
low
high
high
high
high
low
high
low
high
low
high
high

high
high
low
high
low
low
low
high
high
low
low
low
low
low
low
high
low
high
high
low
high
high
high
high
low
high
low
high
high
high
low
high
low
low
low
low
low
low
low
high
high
high
low
high
high
high
low
high
low
high
low
high
low
low
low
low
low

low
high
low
high
low
low
high
high
low
low
high
low
high
low
low
low
high
low
high
high
low
low
low
high
high
high
low
low
low
low
low
high
high
high
low
low
low
low
low
high
high
high
low
low
high
low
high
high
high
low
high
high
high
high

low
low
low
low
low
high
low
low
high
low
high
low
low
low
high
low
high
low
low
low
high
high
high
low
low
low
high
high
high
high
high
low
high
low
low
high
low
low
high
low
high
high
low
low
low
low
low
high
low
low
low
low
low
high
low
low

low
low
high
high
high
high
low
low
low
high
low
low
high
high
low
high
low
low
low
low
high
low
high
low
high