Supplementary Table 3 The risk score for patients in the TCGA-COAD dataset

id	futime	fustat	TRAF2	RBCK1	MLKL	RIPK3	CAMK2B	JMJD7.PLA2G4B	CDKN2A	CXCL1	Risk score	Risk
TCGA-4N-A93T	0.4	0	30.89639	186.2297	22.64742	19.23654	0.05294274	3.838142	0.7697531	158.0329	1.212367257	High
TCGA-AA-3511	0.580821918	0	21.02108	137.5922	14.86988	21.9826	4.58643	2.105247	2.007599	90.63695	1.792175992	High
TCGA-AA-A00K	1.421917808	0	35.10773	268.1555	16.18851	24.01217	0.05703869	1.262793	2.257554	338.9794	0.463985649	Low
TCGA-G4-6307	4.58630137	0	38.7626	198.8355	9.989766	25.22104	0.02046756	1.131071	2.546006	73.80115	0.23680671	Low
TCGA-A6-2683	1.380821918	1	35.23276	296.0059	12.63726	18.32572	0.09164436	4.260765	5.147204	18.00082	1.409220566	High
TCGA-DM-A285	0.490410959	1	42.56942	107.8301	9.083529	7.316841	0.4782628	1.325724	3.913958	138.3437	0.912754088	High
TCGA-CM-5864	1.252054795	0	22.81581	140.1303	12.57063	35.70263	0.04753229	0.505611	1.030234	226.6	-0.560365958	Low
TCGA-G4-632	2.202739726	0	31.83898	91.52854	16.27972	17.67784	0.07188162	1.928867	5.36104	88.69637	0.623992963	High

0												
TCGA-A6-5666	2.726027397	0	21.11381	41.74434	13.92976	22.89449	0.04152941	0.5171791	2.035066	43.92349	-0.116919859	Low
TCGA-AA-3662	0.504109589	0	20.9342	167.0946	16.07856	35.8375	0.04248849	7.963296	38.66232	97.47238	1.324203943	High
TCGA-AA-3846	1.419178082	0	17.23782	181.25	21.28752	23.07354	0.05374274	1.208414	6.989052	574.2736	0.21758996	Low
TCGA-CK-5913	4.276712329	0	27.31683	120.1837	24.41641	26.45668	0.2036918	0.4051577	2.143466	827.5413	-0.14310313	Low
TCGA-NH-A6GB	1.304109589	0	34.39711	151.8985	13.27839	10.55366	0.02127087	2.991083	8.81977	538.7921	0.91182281	High
TCGA-A6-6648	2.098630137	0	29.06548	48.18793	21.99713	23.48941	0.07559583	1.750074	1.391899	109.1311	0.381536857	Low
TCGA-AA-3947	2.750684932	0	1.817491	41.67614	16.82023	8.373438	0	0.1612935	0.4393932	342.9517	0.116862862	Low
TCGA-A6-2686	3.084931507	1	37.10448	111.711	12.96602	18.44342	0.08955983	1.326552	106.403	42.18446	1.28080445	High
TCGA-	1.989041	0	30.1258	332.0237	22.5711	11.3441	0.2624402	0.962967	1.254238	189.294	1.32704891	High

A6-6654	096				5	5				8	4	
TCGA-AA-3864	4.416438356	0	25.75142	155.298	20.40699	15.70858	0.05858693	0.2229339	3.533458	301.0927	0.448568361	Low
TCGA-CM-6161	1.252054795	0	23.47663	130.5665	17.77724	17.83733	0.1375963	1.875365	3.094696	88.93408	0.662869789	High
TCGA-AA-3675	3.920547945	0	21.7585	211.3978	16.08363	27.43094	0.01520393	1.088701	1.561714	562.6705	-0.080733426	Low
TCGA-CM-5863	1.252054795	0	25.38097	85.53193	12.88905	18.14221	0.06201273	0.8848861	8.035313	118.8288	0.242766453	Low
TCGA-AA-3506	4.835616438	0	35.45077	277.1741	11.46337	30.10902	0	0.7767868	3.11848	233.8772	0.060903913	Low
TCGA-AA-3861	2.504109589	0	14.8421	111.0097	14.86868	15.95143	0.04579649	0.2613959	5.739886	267.9869	0.127432648	Low
TCGA-CM-6170	1.252054795	0	28.96859	58.82619	17.17536	22.26782	0.04264099	0.8761866	1.848437	75.38007	0.155425524	Low
TCGA-NH-A50U	0.915068493	1	49.8411	160.1126	19.01732	25.41253	0.05831707	6.530119	10.29876	32.38146	1.614344265	High

TCGA-A6-2681	3.8	0	36.04534	191.418	15.15689	36.87205	0.3794093	0.4622189	19.21401	153.1807	-0.035794088	Low
TCGA-AU-3779	1.208219178	0	23.42912	157.8705	30.5929	10.41781	0.09259291	1.470188	2.163957	377.2081	1.137970183	High
TCGA-DM-A28E	9.994520548	0	30.39034	101.1977	16.7343	21.47537	0.8261385	3.264848	0.3617387	125.5589	0.912966875	High
TCGA-NH-A6GC	1.065753425	0	33.91485	119.3509	10.58962	27.67435	0.025043	2.287035	2.902757	5.360399	0.212676824	Low
TCGA-A6-2676	3.575342466	1	52.96562	239.4575	22.59999	9.216949	0.01988213	0.8872281	8.468777	165.5978	1.401105097	High
TCGA-D5-6534	3.605479452	0	46.64692	80.81407	15.4565	23.48411	0.4132309	2.823881	26.45081	73.97112	0.91662018	High
TCGA-F4-6807	3.58630137	0	29.3194	178.3045	15.2152	23.59039	0.09477364	1.114677	3.751078	139.5497	0.32791437	Low
TCGA-G4-6310	5.301369863	0	24.31509	146.2973	9.340661	11.09531	0.2645534	0.9970406	0.918496	19.37243	0.611393685	High
TCGA-CM-47	1.084931507	0	27.24355	145.5427	10.31304	24.17711	0.07379214	0.8423774	3.164031	340.871	-0.103038564	Low

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TCGA-AZ-6603	2.463013699	1	33.47	189.5113	21.49779	19.19709	0.172966	2.513002	4.210761	116.6497	1.048786127	High
TCGA-CM-6167	1.249315068	0	30.47699	77.07934	17.82694	16.23017	0.1645686	2.073824	2.193328	75.55738	0.7248569	High
TCGA-AA-3534	2.416438356	0	34.88299	114.6914	9.484828	19.12789	0.2489133	3.336586	1.211931	91.01887	0.716249439	High
TCGA-AA-3821	0.084931507	0	29.02682	123.0546	24.07963	18.93451	0.04380387	3.273022	8.916319	37.64239	1.146958069	High
TCGA-CM-6676	0.923287671	0	31.85704	73.41473	11.24544	20.30961	0.01791144	1.775161	1.822945	63.31579	0.273725959	Low
TCGA-AA-A02Y	3.331506849	0	22.62027	289.8926	11.16001	18.79942	0.01287941	0.4143446	1.225848	307.6277	0.293729879	Low
TCGA-CM-5860	2.668493151	0	25.08036	87.9767	16.21173	23.54937	0.06248544	0.5965827	14.32062	171.6705	0.097617057	Low
TCGA-AA-A024	3.254794521	1	17.2941	85.24135	10.60053	18.61544	0.03353877	1.026769	2.338827	185.7012	0.020799334	Low
TCGA-	1.610958	0	32.0995	132.1894	19.7426	30.3597	0.0394645	4.081891	0.508264	21.5737	0.70320448	High

AY-A71X	904		2		3	6	8		1	6	3	
TCGA-AZ-6606	0.978082192	1	26.90768	74.10716	33.17644	27.88935	0.09748696	1.534407	11.48354	259.3016	0.539297437	Low
TCGA-G4-6297	6.865753425	0	21.79715	233.1083	22.51504	27.67163	3.625554	2.113045	2.232046	93.91508	1.708049135	High
TCGA-AA-3526	1.589041096	0	27.93455	116.9879	20.92934	29.57408	0.01661096	0.8446847	5.306569	420.2332	-0.092632553	Low
TCGA-AA-3678	3.917808219	0	33.1656	75.74954	26.35794	22.34401	0.01422135	0.9888254	3.43084	492.6886	0.287968803	Low
TCGA-G4-6625	7.649315068	0	45.55482	95.90758	17.27344	21.30583	0.1194944	1.564415	3.343574	123.7211	0.548895011	Low
TCGA-AD-A5EK	1.369863014	0	47.31858	284.517	11.23091	16.90495	0.08375682	2.417981	24.49686	63.9942	1.282434087	High
TCGA-AD-6899	0.482191781	1	47.77299	206.2791	19.67819	32.66948	0.064263	2.984407	9.356404	86.88127	0.730277023	High
TCGA-CA-5256	1.038356164	0	18.99543	99.62631	13.84046	13.53026	0	0.1318465	10.32627	200.257	0.240223552	Low

TCGA-F4-6808	2.805479452	0	20.25115	113.2455	12.02874	11.14417	0.1084704	0.9005445	1.412478	61.45904	0.503313701	Low
TCGA-A6-5659	2.536986301	0	34.05007	107.9364	14.47525	19.70281	0.1012374	0.858005	2.305564	28.78664	0.362614065	Low
TCGA-AA-3554	1.495890411	0	27.41819	126.1368	16.57519	24.09477	0.08289192	1.03228	3.71044	554.3333	-0.027343034	Low
TCGA-AA-3667	1.167123288	0	45.59541	284.2477	7.237225	16.15856	0.05487976	1.9364	7.757518	256.5314	0.839349742	High
TCGA-CA-5797	1.049315068	0	35.25063	216.935	23.91221	22.81284	0.02542985	0.6157784	6.789858	14.24839	0.731310412	High
TCGA-AZ-6601	8.334246575	1	45.33155	157.1393	28.07357	17.95221	0.1277685	1.505903	4.833386	126.8032	1.131004671	High
TCGA-AA-A02E	0.246575342	1	32.90575	182.5806	21.56353	20.75966	0.09655625	1.84375	6.369389	155.98	0.817303198	High
TCGA-CK-4947	1.463013699	0	25.74788	118.221	26.12357	30.85498	0.05448342	0.9140895	4.021892	191.2234	0.141749146	Low
TCGA-AA-38	2.589041096	0	33.66327	190.1241	15.3672	24.01928	0.0186123	0.6180934	1.508405	527.8698	0.024118677	Low

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TCGA-AA-3692	3	1	26.118	164.2758	14.66939	24.00232	0.02788521	1.085198	2.759196	451.0811	0.029220987	Low
TCGA-CM-5341	2.421917808	0	9.565012	156.8507	8.920896	19.29897	0.04667643	0.1453191	6.891182	134.1927	-0.072920213	Low
TCGA-AD-6548	1.780821918	0	36.68915	260.5189	18.59048	21.80502	0.0415951	1.545359	2.32051	158.6367	0.772002893	High
TCGA-D5-6929	1.117808219	0	51.52191	227.6795	18.8542	32.49014	0.03750951	1.790619	5.042936	42.58429	0.550281423	High
TCGA-NH-A8F7	1.487671233	0	34.67424	87.86139	13.05024	20.62888	0.01709727	2.838904	2.996809	28.73889	0.59477203	High
TCGA-AA-3930	0.167123288	1	29.82867	119.7476	26.4317	6.226445	0	0.5428726	3.746509	80.3555	1.13542672	High
TCGA-A6-6782	1.690410959	0	23.44219	255.2809	12.01815	22.4265	0.04255975	2.252544	3.334598	123.4802	0.584033494	High
TCGA-AA-3561	1.161643836	0	14.55199	95.88104	14.59315	21.53009	0.04863383	0.8748319	8.6162	163.906	0.061825412	Low
TCGA-	0.753424	0	54.3189	251.4285	18.5245	37.3918	0.0517762	4.072894	3.220278	158.220	0.76714732	High

D5-6926	658		1		1	2				1	7	
TCGA-AA-3538	2.167123288	0	23.1603	61.74432	13.63923	26.18805	0	2.015234	5.955679	277.955	-0.034628167	Low
TCGA-AA-3860	2.589041096	0	42.18371	198.7025	12.60666	20.04755	0.1108593	1.553137	3.65645	746.4229	0.281977719	Low
TCGA-AA-A01I	2.583561644	0	10.62797	90.84493	16.38095	11.63173	0.01178136	0.99034	0.8437784	112.0706	0.441720109	Low
TCGA-AA-3544	1.167123288	0	50.15419	233.6782	10.49254	31.30207	0.05967357	0.1444983	5.398492	205.7454	-0.043164709	Low
TCGA-AA-A00R	0.082191781	0	52.36204	164.7219	30.52164	9.551185	0.0798236	1.284006	1.203568	582.6854	1.269616113	High
TCGA-AA-A00N	0.334246575	1	28.78872	93.58707	15.77101	17.06483	0.1636045	1.29461	14.49247	347.2309	0.445171997	Low
TCGA-AA-3715	1.58630137	1	63.80598	254.2718	17.01886	26.10858	0	1.676389	119.9545	490.0042	1.507633016	High
TCGA-AA-3815	2.753424658	0	39.65666	133.6719	19.28211	22.43733	0.06246998	1.383038	35.59646	207.7836	0.741633433	High

TCGA-AA-3663	0.580821918	0	29.75412	135.7171	23.21709	18.1077	0.02064633	1.135593	18.58084	186.3905	0.772424984	High
TCGA-DM-A1HB	11.30410959	0	23.0544	84.56593	10.87398	9.825981	0.06879368	0.57763	7.850174	927.4866	-0.026800394	Low
TCGA-QG-A5Z2	2.608219178	0	41.78444	139.9166	32.15358	28.00126	0.5782462	4.185047	1.01907	210.7628	1.349509303	High
TCGA-AA-3986	1.589041096	0	25.23091	151.0677	9.020537	25.85338	0.0662425	1.237408	5.649432	228.2204	-0.060190934	Low
TCGA-CM-5868	1.419178082	0	46.66881	88.68699	24.97388	20.94302	0.02720162	0.980965	3.050431	65.93067	0.684848646	High
TCGA-AA-A00L	3.169863014	0	37.92831	379.221	8.074294	9.857454	0.01846854	2.165783	1.496754	412.1741	1.13485336	High
TCGA-A6-6649	2.01369863	0	33.41448	139.4698	21.42429	39.2505	0.2827869	7.000325	21.39709	117.3256	1.151901774	High
TCGA-A6-A567	5.153424658	1	22.2374	174.2323	14.90898	16.14739	0.2178224	2.8068	0.3763254	51.99539	0.917906665	High
TCGA-F4-680	2.868493151	0	34.29512	97.66412	16.43745	20.37477	0.1112133	1.231089	5.147021	438.6028	0.23853305	Low

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TCGA-AA-3681	0.498630137	0	28.76522	135.1694	17.04623	24.80167	0.0249309	1.966325	14.94219	701.8943	0.147612456	Low
TCGA-AA-3543	0.082191781	0	29.53394	235.9635	20.25288	27.75265	0	0.541583	5.318627	406.177	0.160635556	Low
TCGA-D5-6533	2.123287671	0	47.22922	159.6338	23.40041	17.57072	0.06913162	0.860918	4.020515	216.926	0.831442693	High
TCGA-A6-2675	3.619178082	0	30.37212	125.3909	18.22748	37.40005	0.07849454	1.105526	2.557268	124.6706	-0.231346945	Low
TCGA-A6-2674	3.646575342	0	32.22984	85.54173	24.70622	33.77024	0.07092967	5.329301	1.951777	319.5437	0.708267427	High
TCGA-AA-3819	2.084931507	0	27.07291	63.3434	19.25528	24.58823	0.01346006	1.606382	2.663703	101.6011	0.237622434	Low
TCGA-AA-3552	1.084931507	1	31.96628	167.6188	18.49147	28.64014	0.2782805	1.299569	9.815342	106.9924	0.384232613	Low
TCGA-AA-A03J	3.41369863	0	28.72889	136.357	16.95125	22.06226	1.933059	2.225236	3.184058	50.82605	1.161770835	High
TCGA-	1.252054	0	25.5148	77.21792	19.8605	16.4558	0.0124375	0.1936105	8.767077	129.822	0.36021138	Low

CM-5861	795		8		4	5	2			6	4	
TCGA-G4-6295	0.695890411	0	35.59131	163.4014	15.11157	18.93486	0.04558857	1.218252	5.026447	96.28983	0.570475999	High
TCGA-AA-A017	1.252054795	0	36.172	86.31544	13.92808	15.2178	0.01499492	1.369402	5.341404	204.6611	0.489599397	Low
TCGA-CM-5349	2.506849315	0	39.96535	76.24604	10.25734	19.73663	0.03842083	1.69457	1.701703	21.40631	0.355845215	Low
TCGA-D5-5538	4.550684932	1	34.8325	130.9065	16.95602	23.72935	0.07406418	0.669798	1.316144	104.1787	0.238538855	Low
TCGA-CK-6747	2.246575342	0	33.91352	122.0673	16.51917	17.20893	0.04278841	0.5846633	2.163965	134.2837	0.420792306	Low
TCGA-D5-6530	1.701369863	0	35.52619	130.0277	18.76189	30.60907	0.08278317	1.58457	2.149664	518.4998	-0.030115186	Low
TCGA-A6-5664	1.84109589	0	25.94947	87.15644	13.48544	14.44751	0.5307966	0.8547643	4.17412	692.8724	0.196500701	Low
TCGA-AA-3518	0.084931507	0	26.16495	150.332	15.23313	19.82978	0.0569312	1.851232	0.9299335	197.9628	0.463079219	Low

TCGA-AZ-5407	7.350684932	0	21.64395	83.59475	15.74679	20.97756	0	0.6066533	0.644424	286.151	-0.041113352	Low
TCGA-CA-5796	1.032876712	0	33.31808	83.11802	16.67016	24.71841	0	0.1818043	2.717629	157.6284	-0.051516735	Low
TCGA-AD-6895	2.090410959	0	49.88503	254.5419	22.99515	19.98095	0.01051948	2.47813	7.514204	463.7785	1.10861966	High
TCGA-D5-6538	1.42739726	0	17.54342	137.7922	14.34399	15.7683	0.06632551	5.996908	16.15699	8.612048	1.493608572	High
TCGA-AU-6004	2.257534247	0	24.65256	131.3436	18.60712	27.2983	0.1106782	1.80493	1.519789	267.1642	0.19213584	Low
TCGA-AA-A00E	2.501369863	0	33.49097	183.6195	22.04807	15.30191	0	0.777203	4.994528	33.00355	0.886154338	High
TCGA-AA-A00D	1.583561644	0	32.14919	65.84633	15.8946	26.8719	0.0405434	1.0098	9.437056	191.6868	-0.00639717	Low
TCGA-AA-3812	2.920547945	0	37.47041	153.2786	5.121453	22.7558	0.4168386	0.4634843	59.8761	47.79823	0.538161351	Low
TCGA-A6-267	3.646575342	1	52.97583	204.7774	13.16481	14.45613	0.09230378	1.085628	6.784745	82.41945	0.932312754	High

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TCGA-AA-3713	1.58630137	0	27.40735	227.0935	27.0938	25.66194	0.0518088	3.010893	0.5695996	107.8514	1.019460224	High
TCGA-D5-6531	1.479452055	0	35.21531	295.1998	12.53921	8.036079	0.01728812	1.067502	41.15291	27.3727	1.468358639	High
TCGA-AA-3548	2.832876712	0	27.51579	146.5377	17.13616	36.35655	0.09056649	0.6391169	3.550425	36.2624	-0.229772723	Low
TCGA-CK-6748	0.167123288	0	27.19303	63.51422	9.745319	17.12794	0.08041437	0.1972506	5.855708	187.6349	-0.019066897	Low
TCGA-G4-6294	2.350684932	1	24.77466	314.3474	12.10579	13.3157	0.0649023	0.993473	1.330267	134.9893	0.828451733	High
TCGA-CM-6172	0.917808219	0	22.03471	84.02704	16.04097	16.46719	0.05031805	2.600501	0.7966223	118.6019	0.630998887	High
TCGA-AA-3496	0.084931507	0	30.91532	61.53049	15.2529	16.30914	0.0313661	2.555254	0.6798416	205.809	0.579430921	High
TCGA-A6-6142	2.090410959	0	27.63197	323.3178	9.92944	15.96843	0.2829706	0.7752633	5.823893	320.3757	0.656400571	High
TCGA-	2.084931	0	40.8710	209.2691	9.35464	21.8978	0.0670492	0.8813731	3.496228	87.0953	0.35557356	Low

CM-4747	507		3		1	5				3	3	
TCGA-AA-A02W	3.416438356	0	20.84139	195	5.360015	23.82816	0.1184403	1.738364	5.038578	79.78392	0.148804835	Low
TCGA-AD-6901	1.868493151	1	59.68067	304.9417	19.12253	41.81471	0.3492877	3.566362	2.696962	51.9236	0.81818954	High
TCGA-DM-A28A	2.205479452	1	56.7989	130.7769	17.18906	23.5578	1.055042	2.815452	32.95179	39.02199	1.41826068	High
TCGA-G4-6304	4.468493151	0	46.12794	172.3896	22.11913	19.16537	0.0840472	3.331889	5.544222	38.52002	1.321946087	High
TCGA-AA-3870	2.498630137	0	22.43549	119.6715	12.07496	16.75096	2.373187	0.2444038	69.24336	126.8228	1.370248575	High
TCGA-AA-3710	2.249315068	0	36.96433	167.9566	28.14335	24.24808	0.07012062	1.140056	3.083698	1392.468	0.018829116	Low
TCGA-CM-6677	0.923287671	0	33.4328	300.1771	18.17591	29.81686	0.02789911	1.216028	2.865736	131.9931	0.450231585	Low
TCGA-AA-3966	0.167123288	0	34.16103	107.5615	8.936169	36.96434	0.1024396	0.7745401	50.36397	938.9903	-0.644596278	Low

TCGA-G4-6299	6.21369863	0	38.13206	130.8218	24.78719	13.22897	0.2237839	1.667889	46.79758	128.9086	1.485266074	High
TCGA-CM-6162	1	0	27.9827	78.56751	16.28086	16.10152	0.1441643	0.5022635	1.475002	133.2212	0.329016866	Low
TCGA-A6-6137	2.257534247	0	34.94486	156.0218	15.39795	25.02372	0.0373315	2.808778	1.284067	318.2191	0.456258835	Low
TCGA-AA-3697	7.087671233	0	34.98956	93.85497	18.57566	24.71436	0.3825542	2.133906	0.9012646	512.5333	0.305514974	Low
TCGA-CA-6716	1.016438356	0	25.08103	111.352	17.87267	24.72928	0.06408232	2.137601	0.9144614	28.87419	0.412245615	Low
TCGA-DM-A1D0	10.88767123	0	28.42536	78.85285	9.146355	15.07941	0.1646037	2.763295	0.3193581	19.50619	0.639245071	High
TCGA-AA-3856	0.082191781	0	42.8671	277.6546	14.14491	27.22077	0.04088939	1.499337	5.394588	115.2385	0.551567285	High
TCGA-DM-A0XD	2.035616438	1	21.17626	120.778	11.57594	9.794019	0.08450777	0.9811458	4.190908	31.42247	0.612233686	High
TCGA-AZ-660	0.265753425	1	30.40581	139.4838	10.0321	15.54258	11.92996	0.4664394	41.79892	316.5096	4.095017376	High

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TCGA-AD-6890	2.043835616	0	57.33942	197.3082	16.57745	21.25406	0.09905783	1.619099	2.870472	168.7674	0.811391309	High
TCGA-AA-3489	0.58630137	1	34.08035	220.1143	23.02907	16.33437	0.01646094	3.091983	2.559516	121.4028	1.319481291	High
TCGA-3L-AA1B	1.301369863	0	28.68978	233.2988	19.21674	31.17378	0.1721203	3.46329	5.06425	54.96197	0.773083662	High
TCGA-RU-A8FL	3.224657534	0	35.79089	116.391	12.82931	18.32338	0.007762508	3.987595	0.3803861	845.386	0.473516151	Low
TCGA-CK-5912	4.090410959	1	41.39945	153.5669	27.30211	14.17352	0.01180836	1.298971	3.338338	161.3175	1.110947458	High
TCGA-A6-5667	2.430136986	0	26.97335	79.99878	23.0086	16.5393	0.1650078	0.7610723	1.796862	141.9131	0.561069348	High
TCGA-AZ-6605	0.435616438	1	29.00029	90.12013	25.97848	19.36165	0.1799092	0.9728342	4.6222	373.527	0.511751529	Low
TCGA-G4-6322	2.169863014	0	47.04026	133.7347	13.54302	17.2435	0.08945738	1.014063	2.801405	174.8028	0.541542958	Low
TCGA-	1.191780	0	50.7347	144.8664	23.5721	25.4242	0.0510705	2.755994	1.989256	153.899	0.89301891	High

D5-6924	822		7		3	7	9			1	7	
TCGA-AA-A01C	1.252054795	0	48.87768	291.8225	15.38818	19.60579	0.07278187	0.9441419	8.779153	62.77342	0.932259652	High
TCGA-A6-2678	3.523287671	0	33.63401	158.1743	35.61936	14.66667	0.1038995	0.6828881	6.723241	83.50701	1.26950086	High
TCGA-G4-6323	1.147945205	0	25.34492	102.469	15.42421	21.75995	0.5602393	2.095057	3.331547	161.8772	0.526034944	Low
TCGA-DM-A28M	7.931506849	0	23.53353	135.4472	12.31022	19.68931	0.01739642	0.5055008	0.6011054	369.3731	-0.033672762	Low
TCGA-CM-5344	1.835616438	0	23.04376	113.6396	10.6617	19.57025	0.1774971	1.122757	5.384408	34.37449	0.262829342	Low
TCGA-AZ-4313	6.328767123	0	48.38814	101.4066	6.00995	17.0295	0.02303708	0.35861	12.76509	185.9291	0.197407133	Low
TCGA-AA-3494	0.084931507	0	29.71012	233.5744	6.189105	28.87888	0.04815313	0.9827869	4.326022	362.3645	-0.198173596	Low
TCGA-CM-6164	2.419178082	0	46.80865	138.4339	18.19657	23.03384	0.04588392	1.404709	4.770751	101.3429	0.577363358	High

TCGA-CK-6751	1.419178082	0	32.17226	131.1356	14.67705	10.24522	0.008926951	0.3335107	0.5720468	215.8074	0.527795821	Low
TCGA-CM-4743	1.920547945	0	23.01003	136.0504	23.16596	19.32203	0.008702949	0.5238396	0.4756786	1394.779	-0.276043541	Low
TCGA-QG-A5YX	2.747945205	0	26.09927	127.7316	17.08214	21.50622	0	1.10835	0.897841	221.687	0.237631564	Low
TCGA-AA-3664	4.501369863	0	27.05723	97.1925	20.63955	23.09195	0.3926961	3.694948	8.289418	460.6584	0.749630986	High
TCGA-A6-6653	2.032876712	0	29.62337	136.7955	12.60066	12.07399	0.04127067	0.2891007	8.0701	311.0051	0.388226193	Low
TCGA-AY-A54L	1.438356164	0	23.11367	134.2138	18.82324	26.66457	0.02854726	1.555348	1.573764	267.7378	0.145092647	Low
TCGA-AA-A01R	2.917808219	0	54.54755	196.1367	12.22041	10.08581	0.1528454	1.357077	1.504378	199.6118	1.033567683	High
TCGA-CM-6680	1.002739726	0	41.23194	101.7444	18.6814	25.16787	0.0576672	2.094599	3.912738	352.1539	0.368350737	Low
TCGA-A6-566	2.794520548	0	28.22262	142.9365	27.24335	33.72922	0.07178811	0.5401252	3.416357	702.4337	-0.224907136	Low

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TCGA-AA-3685	3.087671233	0	19.70939	115.1736	9.747337	24.31511	0.06160887	0.4795217	2.670671	421.216	-0.372105528	Low
TCGA-CK-4952	1.301369863	0	42.72362	133.8431	17.18226	12.09805	0	1.902659	2.813736	131.5263	0.979689237	High
TCGA-A6-3809	2.728767123	0	17.35987	55.20304	25.97266	17.18	0	0.7136618	2.042337	473.7334	0.247411135	Low
TCGA-AA-3530	1.589041096	0	20.5753	175.5732	23.72935	14.7899	0.02021296	2.265466	0.8000158	79.02299	1.053687975	High
TCGA-D5-6928	0.969863014	0	78.67773	226.6044	35.65476	28.30097	0.1461334	6.22864	7.869203	190.8315	2.247221706	High
TCGA-5M-AAT4	0.134246575	1	35.57538	204.0729	16.85204	21.14502	2.372511	3.418225	2.458581	217.8838	1.64568436	High
TCGA-F4-6459	0.717808219	1	27.66722	157.2273	25.91739	14.83733	0.6630893	1.337509	3.203572	44.50835	1.203205722	High
TCGA-AA-A00A	3.169863014	0	33.04006	128.3289	23.27069	28.78815	0	1.690224	0.7591623	317.3073	0.250757973	Low
TCGA-	5.084931	0	34.3397	165.3228	26.4638	30.0445	0.0402005	1.919084	9.717152	332.678	0.49904132	Low

AA-3655	507		9		8	2	8			5	2	
TCGA-A6-5660	2.432876712	0	32.96735	98.28662	11.59788	29.55823	0.1076419	0.6143955	4.818307	221.1438	-0.274523841	Low
TCGA-CM-6674	1.079452055	0	39.66177	86.27005	20.83109	24.42634	0.01049277	0.3157854	0.8108179	80.98648	0.203167513	Low
TCGA-AA-A00J	1.504109589	0	26.57465	78.38475	18.27586	14.32354	0.1424566	1.108786	0.7719157	67.26294	0.590817834	High
TCGA-CM-6166	1.832876712	0	23.54994	282.1591	16.36624	9.587325	0.0120694	0.701419	2.524981	43.31043	1.019262767	High
TCGA-DM-A1D8	1.049315068	1	36.49467	197.6644	11.92194	14.9341	0.01960437	3.921491	3.260746	86.42472	1.194442047	High
TCGA-F4-6570	0.515068493	1	43.67504	155.7024	17.11936	12.32828	0.02673819	1.489157	1.511829	61.27245	0.982436191	High
TCGA-AA-A01X	2.167123288	0	24.1698	168.2502	17.05253	15.20041	0.1030632	2.612796	15.20671	32.07107	1.079412187	High
TCGA-AD-6963	2.284931507	0	40.85336	325.2575	21.19688	15.8762	0.1252634	1.484685	3.417059	511.4686	1.074203157	High

TCGA-AA-3811	0.838356164	1	32.2173	213.0907	17.55659	9.338755	2.074922	2.571424	43.51094	60.1139	2.281046133	High
TCGA-AA-3939	1.082191781	0	12.79379	124.1326	13.99096	20.13077	0.09702362	0.5034444	3.181824	442.1077	-0.112769016	Low
TCGA-T9-A92H	0.991780822	0	27.65573	167.0698	16.74326	19.58512	0.01564725	1.120446	0.825744	200.1183	0.414962918	Low
TCGA-A6-5662	1.967123288	0	31.73007	103.7972	18.12205	23.38807	0.1225603	1.046874	8.013687	29.85427	0.384183872	Low
TCGA-DM-A0XF	3.183561644	1	28.22932	104.9863	20.90027	12.76427	0.07921007	1.593461	2.147475	276.9148	0.762123385	High
TCGA-A6-4105	1.210958904	1	50.6685	99.19817	15.48431	15.13127	0.0404584	1.931392	8.273469	423.7048	0.700881357	High
TCGA-A6-2672	3.887671233	0	26.27071	195.0936	24.09409	20.35645	0.02005831	2.081605	21.47297	176.031	1.004313793	High
TCGA-A6-2684	3.087671233	0	32.43007	78.39516	20.92928	35.06463	0.01381361	3.784558	2.52539	74.78898	0.369729424	Low
TCGA-AA-A0	2.668493151	0	17.93395	67.68301	19.9864	21.28994	0.8893161	2.125992	1.646191	297.2316	0.56438398	High

1F												
TCGA-D5-6535	1.260273973	0	29.57939	128.9923	15.3838	25.65543	0.1840371	2.271769	1.150116	449.0527	0.199977198	Low
TCGA-A6-A56B	4.687671233	1	38.47996	115.4197	13.63329	26.08043	0.188805	2.35125	0.4448084	33.87587	0.425182079	Low
TCGA-A6-6780	1.676712329	0	24.16456	82.71203	44.26975	29.15441	0.05419847	0.6936998	1.583318	74.66764	0.677426612	High
TCGA-AA-3977	2.084931507	0	24.33761	135.102	21.10262	16.62003	0	0.8753054	13.87342	394.6235	0.510586714	Low
TCGA-D5-6536	1.487671233	0	35.69131	122.8851	15.6937	12.11098	0.05380083	1.10736	3.751805	267.633	0.650720234	High
TCGA-D5-6529	1.682191781	0	27.99258	130.273	15.36332	22.92361	0.05753519	1.108875	4.972672	411.4753	0.092761989	Low
TCGA-D5-6931	1	0	34.52785	162.6441	20.54028	26.72196	0.09674906	2.922869	6.301065	67.20249	0.774743945	High
TCGA-DM-A1HA	7.123287671	0	60.35295	185.0244	7.13311	14.16455	0.3346014	1.263368	67.81322	43.16064	1.385456086	High
TCGA-	3.249315	0	33.4764	240.5851	11.1159	31.4701	0.2058809	0.8546336	9.830097	136.957	0.08949698	Low

AA-3837	068		3		2	3				6		
TCGA-AA-3955	1.747945205	0	13.59058	112.9226	21.03666	18.99388	1.908404	0.2231547	2.684957	105.9298	0.814959843	High
TCGA-G4-6314	2.994520548	0	32.34961	171.5846	12.86985	17.13845	0.1927888	1.457666	3.270196	52.42056	0.662906061	High
TCGA-D5-5540	4.673972603	0	18.32386	70.70042	13.38516	11.11405	0	1.552237	0.5677265	110.5776	0.496086667	Low
TCGA-DM-A288	1.169863014	1	38.18775	179.5958	16.83126	15.30559	0.052655	5.748562	1.766481	36.53031	1.671489663	High
TCGA-AA-3971	1.339726027	0	25.29311	211.2433	20.67696	26.99682	0.04012506	1.478251	1.058749	65.04665	0.463062191	Low
TCGA-AD-5900	1.01369863	0	35.4654	183.8171	26.90722	18.58325	0.09257132	0.6724783	2.810938	112.4127	0.867720164	High
TCGA-AA-3818	0.082191781	1	19.75999	196.8758	12.08359	18.39596	0.07355959	1.05347	1.303216	53.07083	0.406159643	Low
TCGA-AA-A01V	0.084931507	0	30.13241	172.9217	12.45455	17.79597	0.03142396	2.087106	4.471538	414.1577	0.480004373	Low

TCGA-CA-5255	1.030136986	0	27.45756	227.6102	17.33218	14.40116	0	1.091536	7.897743	79.30087	0.871265304	High
TCGA-G4-6627	5.95890411	0	21.71528	147.7893	17.25803	26.95532	0.1740914	1.207623	1.58877	186.8963	0.127673473	Low
TCGA-AA-A00O	2.252054795	0	34.31075	68.21602	12.99979	14.38441	0.03396667	2.97861	4.6093	79.97542	0.810931829	High
TCGA-AZ-4323	0.117808219	1	31.21689	121.129	16.69612	17.53337	13.84805	3.538685	20.22344	51.59942	5.324371548	High
TCGA-AA-3524	3.002739726	0	28.98816	117.6076	15.37107	17.95474	0.04874268	0.101168	6.063211	223.7015	0.197059578	Low
TCGA-AA-3989	0.663013699	1	28.25383	328.0627	18.61588	33.68039	0.01890405	1.353654	6.73389	132.5782	0.375718214	Low
TCGA-AA-3542	1.082191781	0	25.12287	70.13712	6.546676	20.10272	0.3574319	0.2885047	30.46453	66.13153	0.12304433	Low
TCGA-D5-5541	4.660273973	0	39.61352	65.38022	16.12203	24.23653	0.06300999	1.226068	2.553273	67.43576	0.231577486	Low
TCGA-AA-36	0.167123288	1	26.03755	215.8053	12.2291	25.88489	0.02193173	0.8193684	4.753573	698.5051	-0.190771122	Low

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TCGA-DM-A0X9	9.975342466	0	29.6914	211.2531	15.2362	19.43274	0.04084263	2.177557	1.145039	27.67316	0.786446217	High
TCGA-AA-A01Z	3.084931507	0	23.57408	83.5019	9.6946	9.710568	0	2.352241	10.40429	298.0493	0.629061189	High
TCGA-AA-3519	0.756164384	0	37.75337	112.1494	15.3468	23.53901	0.05834581	0.847699	2.199323	430.4961	0.034507718	Low
TCGA-D5-6539	1.04109589	0	33.65203	114.9902	12.53633	41.88177	0.239337	1.862838	2.311815	33.08576	-0.333491919	Low
TCGA-D5-6920	1.032876712	0	37.43381	183.8781	20.61826	46.43334	0.0164201	1.687	0.9593718	597.2901	-0.52740018	Low
TCGA-AA-3994	2.252054795	0	30.41594	153.6552	10.52573	11.42108	0.05425946	0.863408	9.68104	95.0764	0.637592435	High
TCGA-CM-6678	0.917808219	0	18.52766	149.4898	15.82734	17.2995	0.2590632	0.9010102	2.784427	74.00939	0.483513649	Low
TCGA-D5-6923	1.035616438	0	47.39968	95.23023	17.22033	16.98068	0.1131925	2.811413	5.902334	549.1342	0.740221049	High
TCGA-	2	0	17.1906	203.1518	10.0815	24.8711	0.1197879	1.79366	36.21962	42.8775	0.50808061	Low

AA-3941			2		8	2				3	7	
TCGA-AD-6888	1.293150685	1	44.31019	161.6998	13.80209	19.88773	0.05172808	1.142664	27.17284	120.353	0.710031035	High
TCGA-AA-3855	2.671232877	0	29.83343	87.86631	16.5633	29.40475	0.04484524	1.272076	5.465705	323.92	-0.116941086	Low
TCGA-AY-5543	2.750684932	0	25.27563	116.4961	29.81266	14.48984	0.04610145	0.5604469	1.861904	1300.575	0.177217098	Low
TCGA-D5-7000	0.854794521	0	33.35692	208.6724	23.96773	26.30011	0.05033834	3.003797	2.688103	155.3897	0.901194275	High
TCGA-AA-A00W	1.249315068	0	35.22763	130.9579	23.00564	17.54322	0.03900248	1.720225	6.06451	967.5549	0.400060883	Low
TCGA-AA-3560	1.665753425	0	16.86357	67.46351	10.97739	26.68041	0.1963644	0.3396372	3.001873	106.7267	-0.353515428	Low
TCGA-CK-4948	12.33424658	0	38.52579	76.88077	13.00584	13.71546	0.0191825	0.7432004	6.290773	362.171	0.32523691	Low
TCGA-AZ-6598	4.117808219	1	33.28646	130.8235	11.34208	13.77821	0.02753814	0.3905719	1.245648	11.90454	0.433736032	Low

TCGA-CM-4746	3.084931507	0	26.60431	102.5857	12.30414	20.35229	0.03185083	0.2479053	1.650831	213.3508	-0.047159751	Low
TCGA-G4-6321	1.84109589	0	20.53835	121.6649	13.21714	81.11557	0.04671093	0.3490235	0.9331975	104.5712	-2.349139899	Low
TCGA-AA-3866	1.419178082	0	34.33492	299.3784	26.52061	17.37954	0.04009036	0.2496289	2.115666	197.7474	0.980135049	High
TCGA-AY-6197	1.78630137	0	36.23352	141.9947	29.26811	39.49152	0.05918388	2.018075	0.8764305	535.0443	0.02128156	Low
TCGA-AA-A01T	2.753424658	0	64.39737	287.7686	14.59511	21.55155	0.1421578	0.6454352	1.105208	147.3324	0.814904338	High
TCGA-AZ-6608	0.161643836	1	23.71754	129.4962	22.42797	15.01643	0.1400136	2.092362	0.7124977	190.3511	0.879502728	High
TCGA-AA-A00Z	1.832876712	0	39.20723	125.0645	19.42697	15.01159	0.05546902	1.976379	7.248393	179.4921	0.922292811	High
TCGA-AA-A02J	0.419178082	1	50.09627	268.4938	10.69141	20.78521	0	1.701199	0.6488138	126.5243	0.726302506	High
TCGA-AA-35	1.084931507	1	20.42463	108.6044	18.2643	13.3806	0	0.3630634	53.26999	212.2488	0.778158672	High

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TCGA-CK-5914	1.832876712	0	40.16872	90.12971	22.28237	19.92354	0.05096705	0.9785095	4.194584	383.4328	0.426630953	Low
TCGA-A6-6651	1.81369863	0	24.76336	72.23511	11.70649	11.33341	0.7255842	1.539455	3.540384	43.39536	0.774587355	High
TCGA-DM-A1DA	0.624657534	1	48.07989	213.6825	12.86813	12.34941	0.04342079	1.487016	19.25204	18.6566	1.174556254	High
TCGA-CK-5916	1.761643836	1	25.85456	93.13939	27.41783	15.36313	0.01148117	0.3931913	0.5626116	155.1851	0.625653698	High
TCGA-AZ-6599	0.564383562	1	33.25748	127.4761	21.55136	15.179	0.02835004	3.285346	1.549534	59.4333	1.19220544	High
TCGA-CA-5254	1.057534247	0	35.60134	151.8207	27.69293	30.96112	0.01533906	1.321237	1.517774	37.51643	0.468940891	Low
TCGA-DM-A282	11.59726027	0	20.65597	184.1214	10.76126	15.87159	0.01725845	1.355222	1.72396	20.75235	0.507945682	Low
TCGA-AA-3949	2.167123288	0	18.72192	119.1356	16.14005	17.81673	0.2114527	0.2194407	5.180908	250.7659	0.190110817	Low
TCGA-	2.704109	0	28.5634	125.0047	20.8024	27.3400	0.0298918	0.6669536	3.239444	121.003	0.13798266	Low

A6-4107	589		4		5	1	9				3	
TCGA-G4-6293	11.09863014	0	21.74065	133.4519	13.26983	27.14888	0.06771417	1.465676	3.15411	605.8886	-0.2391754	Low
TCGA-DM-A280	0.646575342	1	23.44631	113.7105	9.00771	13.63756	0.03333735	0.2248787	2.591817	147.1756	0.154488498	Low
TCGA-QG-A5YW	2.454794521	0	20.99201	130.279	11.06528	21.28141	0.05070293	1.881105	9.436686	511.7202	0.086511952	Low
TCGA-AA-3522	3.087671233	0	14.50413	126.7404	18.22467	19.36754	0.135257	0.862252	2.512814	153.2725	0.301835139	Low
TCGA-CM-4748	2.169863014	0	24.77166	134.1687	18.73117	26.47471	3.89245	2.885353	16.76851	213.5438	1.734732385	High
TCGA-AA-A029	4.331506849	0	38.40115	234.2937	10.62902	14.86496	0.06179311	0.9619118	2.329268	293.3211	0.58835837	High
TCGA-AA-3869	2.252054795	1	29.57258	51.49684	16.00714	28.19277	0.1171963	0.4691196	2.808377	234.8352	-0.25889005	Low
TCGA-AY-6386	1.484931507	0	31.38092	155.3731	17.47003	26.15077	0.02795344	0.49316	0.6322164	198.6832	0.073003877	Low

TCGA-A6-2680	2.926027397	0	34.31049	309.8433	20.2228	28.40836	0.1439604	1.363264	10.31041	141.3838	0.70955156	High
TCGA-AA-3862	2.504109589	0	18.07548	155.4609	17.64885	14.25781	0.06995707	0.1935995	2.065654	736.5234	0.096880843	Low
TCGA-AA-A00U	1.419178082	0	40.36969	162.1484	16.34139	9.459687	0.05634423	1.422836	1.734497	779.1939	0.648301278	High
TCGA-AA-A02H	0.167123288	1	31.86372	126.3237	22.80139	15.22447	0.05523279	1.891536	8.744311	299.734	0.88300812	High
TCGA-G4-6317	3	0	41.41193	81.52609	9.674979	20.36851	0.0111196	0.9000936	0.6077663	184.4598	0.079957316	Low
TCGA-AA-3679	1.252054795	0	22.3287	125.155	28.80718	22.78167	0.5263471	0.4469158	2.074229	146.101	0.593355532	High
TCGA-D5-5539	1.632876712	0	22.70074	69.96615	24.84975	17.14157	0.05208627	0.9369342	6.315511	61.10062	0.614911056	High
TCGA-AA-3562	1.665753425	0	33.87012	195.513	15.07847	27.1425	0.08679259	0.6845422	3.827789	110.1552	0.192728072	Low
TCGA-CM-47	1.668493151	0	28.0151	165.8487	17.1334	15.57436	0.01224678	0.3240902	5.493487	245.4475	0.447155047	Low

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TCGA-NH-A8F8	1.4	1	18.19943	79.27811	26.04621	15.27263	0.1232236	4.416728	1.911541	56.15286	1.340708423	High
TCGA-G4-6303	5.487671233	1	34.72204	135.3875	18.57753	20.06625	1.49479	1.312604	2.801799	403.9791	0.833241824	High
TCGA-G4-6586	2.983561644	0	34.33101	166.6563	19.7269	43.42496	0.02415828	1.169975	11.65615	240.7062	-0.305981984	Low
TCGA-CA-6719	1.191780822	0	33.43467	205.757	19.9467	19.05293	0.6198445	2.262131	3.894132	128.1887	1.120793434	High
TCGA-QG-A5YV	3.564383562	0	55.99575	281.3093	19.30709	31.00578	0.02453423	2.053858	1.294732	139.1647	0.730787313	High
TCGA-AA-3495	3.087671233	0	21.97716	96.23291	13.23908	18.9638	0.0203437	0.8656007	16.67894	422.2608	0.092036923	Low
TCGA-AA-3842	3.084931507	0	26.33228	198.8758	16.15141	16.5091	0	0.2875435	36.38096	97.48933	0.74530382	High
TCGA-AA-3844	1.243835616	0	25.11823	158.89	14.97874	20.22055	0	1.769448	2.354472	575.7095	0.212791482	Low
TCGA-	2.252054	0	26.3383	161.136	11.3276	21.4567	0.1164992	0.7657013	2.671431	85.0771	0.19868561	Low

AA-3982	795		8		1					7	7	
TCGA-A6-6140	2.010958904	0	46.24504	69.51014	16.8537	16.71316	0.04764067	1.483212	0.7901508	507.4699	0.395482986	Low
TCGA-CA-6718	0.838356164	1	44.46455	255.6233	21.02531	9.644582	0.07366219	1.901567	24.52145	373.0225	1.507570859	High
TCGA-AA-A01K	2.583561644	0	24.45411	85.12567	20.60685	8.781974	0.1430453	0.705133	12.40169	108.5157	0.867018373	High
TCGA-AA-3509	5.246575342	0	16.96701	53.1913	31.01838	27.3479	0.06831728	1.010297	1.416356	196.6601	0.219460199	Low
TCGA-DM-A28K	8.18630137	0	45.67004	89.45936	17.13415	18.56885	0.03403095	1.333199	0.4650091	59.77374	0.585613126	High
TCGA-QL-A97D	1.824657534	0	29.46441	98.63522	18.21066	30.35343	0.01689414	3.629193	0.9711472	740.9923	0.071529165	Low
TCGA-F4-6461	0.926027397	1	23.25357	130.9869	10.76896	14.3105	0.1430101	2.196506	1.365647	5.822092	0.684162759	High
TCGA-F4-6855	3.950684932	0	34.05137	112.0753	22.56707	19.63881	0.04146682	1.836087	3.334562	62.91434	0.769686371	High

TCGA-D5-6541	1.298630137	0	21.4611	64.14755	23.20439	22.93799	0.02864152	1.224608	2.008114	128.0225	0.289250436	Low
TCGA-AA-3841	3.079452055	0	58.38773	175.8087	11.73167	32.40777	0.1930287	1.442309	13.3881	168.9151	0.26770618	Low
TCGA-4T-AA8H	1.054794521	0	18.1198	66.22415	14.45676	20.49587	0.022166	3.024942	4.198585	46.95743	0.491682514	Low
TCGA-AA-3696	0.419178082	1	24.86609	250.4031	25.3368	23.89476	0.1162884	6.275431	5.479305	73.20961	1.744128797	High
TCGA-AZ-6600	1.008219178	1	37.83097	185.657	29.59413	22.22761	0.1633105	2.006998	18.90518	40.31335	1.263433382	High
TCGA-AA-3520	2.002739726	0	30.3152	197.815	12.37356	20.73996	0.1777803	1.086478	10.1265	162.7844	0.458741101	Low
TCGA-AA-3854	3.002739726	0	30.42346	80.93725	11.47105	15.0569	0	0.5348927	7.260173	203.9133	0.217501264	Low
TCGA-G4-6588	2.180821918	0	37.71005	104.7682	17.28222	18.76193	0.01013166	1.345843	9.853254	429.7773	0.403206398	Low
TCGA-CM-53	1.915068493	0	47.946	143.3963	7.814561	25.84589	0.5715501	3.002207	21.24605	213.5674	0.692739154	High

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TCGA-AA-3875	1.504109589	0	29.60521	128.2076	20.4718	23.14671	0.04607046	2.29492	1.780023	129.7918	0.599287628	High
TCGA-AA-3549	1.750684932	0	30.67445	152.8916	17.85777	31.55568	0.0336708	1.327826	3.712434	383.4636	-0.063884819	Low
TCGA-A6-2685	3.104109589	0	25.968	140.2374	13.61473	31.22721	2.588769	1.185794	13.02224	172.3056	0.697897185	High
TCGA-AA-3510	5.331506849	0	34.38978	200.198	16.41978	21.48927	0.124511	0.9691094	0.7333427	176.8588	0.472599928	Low
TCGA-D5-6540	1.345205479	0	48.2121	129.1044	14.62327	32.14765	0.01924849	2.427039	2.702727	473.8716	0.057573962	Low
TCGA-AA-3555	2.495890411	0	35.61593	98.27095	16.65526	12.5101	0.3197969	1.143134	3.549417	178.8472	0.749792114	High
TCGA-CA-6715	1.049315068	0	37.70394	339.9458	18.38059	13.14966	0.02467531	1.34866	0.7906073	49.39942	1.285214261	High
TCGA-DM-A1D6	1.561643836	1	30.40658	61.77264	19.65478	15.68084	0.0654281	1.993342	0.2906695	89.76569	0.70219775	High
TCGA-	0.698630	0	32.8653	119.6058	14.3086	14.4280	0.0101548	1.190842	2.277551	45.6459	0.60328527	High

A6-6141	137				1	4	1				7	
TCGA-AA-A02R	1.835616438	1	48.31799	182.2433	20.52595	18.01093	0.0740989	0.7113073	0.8728531	13.29501	0.847345922	High
TCGA-AY-A8YK	1.569863014	0	32.63197	192.1494	15.51507	26.90388	0.08735956	2.574736	0.5433427	164.1673	0.492555478	Low
TCGA-A6-6138	1.876712329	0	45.80986	249.1057	18.98516	13.85093	0.1350516	0.4605039	6.581571	370.1498	0.892878138	High
TCGA-AA-3848	0.838356164	1	60.63905	296.329	11.50014	25.06878	0.1467603	2.233798	4.287357	45.11872	0.94638057	High
TCGA-F4-6463	2.978082192	0	27.54402	96.91045	13.25042	10.42244	0.7118554	1.456387	11.28907	45.64731	0.970053518	High
TCGA-DM-A1D7	1.109589041	1	39.13139	113.5294	9.707138	17.34142	0.005935175	2.11267	1.118621	432.351	0.332366054	Low
TCGA-D5-6927	0.78630137	0	53.96912	271.2747	39.57055	30.82211	0.07944112	3.228984	2.645144	375.5094	1.423309602	High
TCGA-AA-3867	2.002739726	0	26.24619	106.18	11.11613	22.13173	0.06462495	0.9389275	6.861436	47.05875	0.123667138	Low

TCGA-G4-6306	3.723287671	0	36.48169	127.2033	14.54548	27.12088	0.02502449	1.168642	17.99323	27.0185	0.288856921	Low
TCGA-AA-A01S	0.084931507	0	46.62835	152.4268	8.934533	12.91422	0.01520254	1.877444	3.438322	105.4701	0.789167583	High
TCGA-AA-3514	0.084931507	0	48.13974	278.9399	6.446313	21.0482	0.1672501	1.33069	5.568913	23.51538	0.670772801	High
TCGA-AA-3556	1.917808219	0	36.12622	165.2016	17.56615	14.62305	0.04024551	0.5638389	11.98461	150.4997	0.722911465	High
TCGA-A6-3810	3.043835616	0	28.45193	159.9822	22.18188	28.23038	0.6072673	2.759876	1.499736	167.8194	0.738383403	High
TCGA-AA-A01G	1	0	35.14357	202.7965	17.39701	12.2648	0.05968895	1.424707	20.36207	58.9964	1.16078642	High
TCGA-AA-A010	2.915068493	0	43.34916	223.3637	18.05515	7.244023	0.5678477	1.392889	5.643084	134.8712	1.48267924	High
TCGA-A6-5656	2.742465753	0	47.51481	126.6772	21.0434	32.38257	0.02812375	4.903277	2.120228	112.6947	0.893368186	High
TCGA-A6-665	2.057534247	0	32.61344	258.3749	22.47511	14.07538	0.07155464	4.548288	1.719481	374.4567	1.593751155	High

2												
TCGA-5M-AATE	3.287671233	0	25.60485	253.8575	19.86505	14.13491	0.1187536	3.019373	1.812931	93.00346	1.334446934	High
TCGA-A6-3808	2.778082192	0	21.54011	124.289	16.971	18.51417	0.3163239	0.5158584	5.961857	417.7726	0.22058175	Low
TCGA-AD-6964	0.906849315	1	42.71433	124.3377	20.7778	24.09747	0.141005	0.863357	4.252103	266.3989	0.380687965	Low
TCGA-AA-3833	1.328767123	0	25.32019	115.2434	17.86331	21.12333	0.1920194	0.7572385	4.342859	319.2609	0.208961334	Low
TCGA-CM-6679	0.838356164	0	32.98437	109.1613	17.13212	25.38708	0.1169304	1.794211	3.25851	139.393	0.335140093	Low
TCGA-5M-AAT6	0.794520548	1	41.37694	105.5184	24.41158	12.51046	0.2027423	1.867311	4.036088	248.1741	1.111217925	High
TCGA-AA-3532	2.416438356	0	25.83032	208.6063	21.54972	25.17062	0.03337145	1.194807	8.962706	224.9021	0.476539995	Low
TCGA-F4-6460	2.663013699	1	39.76946	343.9256	25.35019	22.47645	0.3011843	1.777696	6.971468	29.38976	1.37657512	High
TCGA-	2.835616	0	40.1076	136.8276	12.2508	20.3602	0	2.478592	7.193461	14.5937	0.69557732	High

AA-3531	438		5		4	4				9	2	
TCGA-AZ-4616	0.42739726	1	34.84886	220.3037	16.03417	11.15604	0.1044026	0.9286848	16.40225	193.0962	1.011356965	High
TCGA-DM-A28G	5.065753425	1	17.9765	91.15225	10.97103	14.68328	0	2.156558	3.711637	108.4626	0.458535359	Low
TCGA-AA-3956	2.835616438	0	20.84856	124.4181	14.39254	13.64633	0.07293508	0.9839745	1.695377	194.9919	0.434989627	Low
TCGA-A6-3807	2.887671233	0	23.22702	153.8149	18.06439	22.10557	0.1729733	0.7180307	161.2343	78.7161	1.572455733	High
TCGA-AA-3688	1.583561644	0	29.38221	260.4547	19.40846	18.07694	0.01585481	0.7897802	2.62962	406.0447	0.595135766	High
TCGA-CM-6168	1.082191781	0	32.65046	71.77731	23.14118	23.23125	0.1692449	1.629534	2.977157	325.7427	0.400481993	Low
TCGA-AZ-4614	0.471232877	1	34.30323	126.5451	10.69168	11.35492	0.2491486	1.195843	52.24055	71.36772	1.086864382	High
TCGA-DM-A28F	2.997260274	1	50.49951	182.1954	27.28641	22.82015	0.1766992	1.198986	2.13908	488.906	0.742366161	High

TCGA-DM-A28C	6.780821918	1	18.42104	118.8652	21.55028	20.92585	0.01344742	2.49802	0.1900858	19.21749	0.682701625	High
TCGA-AA-3673	4.169863014	0	37.63695	201.7328	18.93308	32.688	0.05949718	0.9570441	5.606807	78.09699	0.209546211	Low
TCGA-AA-3973	1.087671233	0	18.68002	190.9577	16.91124	19.28498	1.990002	1.454054	1.377778	69.79946	1.144304212	High
TCGA-DM-A1DB	3.693150685	1	39.54032	154.8635	14.85561	15.05796	0.05170401	4.024292	2.23048	18.9154	1.276559697	High
TCGA-CK-4951	5.846575342	1	39.04314	98.35997	34.29427	23.88825	0.1230071	0.2872212	1.159176	396.7801	0.502820268	Low
TCGA-AA-3979	2	0	28.93121	451.8303	11.35688	18.88727	0.01752864	0.6912509	17.37735	534.3246	0.727946696	High
TCGA-AY-4070	1.35890411	1	51.55116	108.9531	12.94819	22.54619	0.6414038	1.664085	127.234	171.5017	1.55501082	High
TCGA-AD-6965	2.205479452	0	58.72262	96.20257	19.33487	22.04234	0.5881317	2.826183	15.22942	9.900423	1.228569931	High
TCGA-AA-36	0.917808219	1	26.11949	101.4285	18.99037	28.88426	0.1995983	1.3464	4.185104	68.48338	0.168315769	Low

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TCGA-AZ-4615	2.745205479	0	19.73993	140.9134	18.96678	16.77123	0.03077182	0.4151456	2.870831	21.60031	0.462934155	Low
TCGA-AA-3952	0.167123288	1	25.72161	46.93061	14.95905	18.23589	0.7201562	0.8653658	2.714602	207.9962	0.33122476	Low
TCGA-AZ-5403	5.232876712	1	25.17317	90.59762	16.99138	29.91833	0.02856331	0.2569002	6.99844	152.9677	-0.243129755	Low
TCGA-AZ-4315	4.865753425	0	23.82951	131.0374	19.66772	22.52288	0.2585093	0.4952769	1.76149	512.3969	0.069778693	Low
TCGA-AA-3972	4.249315068	0	14.18968	116.919	15.65054	18.26873	0	1.891471	0.4907353	149.0572	0.381243562	Low
TCGA-AA-3517	3.249315068	0	24.16365	80.23798	17.67666	21.74728	1.261001	3.136882	0.5592114	194.2638	0.906016398	High
TCGA-AA-3877	2.583561644	0	18.30216	120.8506	21.10776	16.12953	0.1078791	1.026249	0.8132925	683.1176	0.245797923	Low
TCGA-NH-A50T	1.515068493	0	35.16439	225.428	13.96648	13.51908	0.01474054	2.202825	1.55579	184.8102	0.967779344	High
TCGA-	1.610958	0	21.6086	60.26553	21.8319	16.9410	0.0703498	4.103018	5.383177	754.506	0.69506650	High

NH-A50V	904		5		9	1	9			2	9	
TCGA-AA-3502	2.917808219	0	34.04948	92.23288	12.84714	21.91237	0.02180683	1.357837	1.233	24.71138	0.256999003	Low
TCGA-SS-A7HO	5.010958904	0	42.16814	88.9099	15.06553	17.52679	0.09325852	7.142474	10.12419	16.90881	1.727283814	High
TCGA-AA-A01Q	0.084931507	0	20.70205	80.94644	12.67004	21.04545	0.01468282	0.7313995	6.807601	129.3181	0.013976837	Low
TCGA-F4-6809	1.104109589	1	38.12564	68.86838	22.07359	17.1777	1.829898	2.717067	10.82413	62.60769	1.56484018	High
TCGA-AA-3553	2	0	21.15884	96.67822	18.79793	18.9587	0.4371363	0.5583383	5.006681	204.0715	0.357332146	Low
TCGA-G4-6309	7.123287671	0	41.25109	87.20059	28.41168	27.94005	0.336519	1.362003	1.120504	111.507	0.587394545	High
TCGA-AD-6889	6.936986301	1	36.14813	162.811	16.58756	13.83234	0.02616139	1.493232	0.2301002	244.1947	0.743969886	High
TCGA-CA-6717	1.063013699	0	26.16677	99.12778	25.37511	12.21984	0.2767515	0.7823893	2.356203	59.95903	0.923463446	High

TCGA-D5-6930	1.112328767	0	44.64951	114.0911	26.82657	18.22205	0.2029353	0.7605055	2.592354	141.173	0.848721456	High
TCGA-AA-3968	1.832876712	0	38.0346	185.9472	11.06208	17.57578	0.03907488	0.7907443	3.314053	174.2887	0.429757647	Low
TCGA-CM-6675	1.087671233	0	64.74247	151.0383	15.24364	24.0011	0.05030505	2.391007	18.9623	45.921	0.954694213	High
TCGA-AA-3660	6.506849315	0	40.1802	111.2679	9.65997	35.26092	0.04634891	1.606533	4.05328	95.18211	-0.238911602	Low
TCGA-A6-A565	1.353424658	1	24.88259	95.30755	20.14945	42.54923	0.2048033	3.342676	1.181391	38.95384	0.006820557	Low
TCGA-CM-6165	1.336986301	0	23.34945	134.3786	11.0886	22.28571	0.07367417	0.7754959	1.210031	82.95711	0.057565203	Low
TCGA-CM-6163	1.169863014	0	22.53007	122.4472	25.69158	15.66864	0.08429102	1.773362	3.726128	175.4542	0.883486148	High
TCGA-A6-2677	2.02739726	1	26.70277	133.0188	21.3313	16.11935	0.0153893	0.7506208	0.9861592	71.01576	0.618662476	High
TCGA-AA-38	2.756164384	0	20.73828	116.4072	17.19899	19.89566	0.01780209	0.4064411	6.207148	58.95065	0.244261812	Low

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TCGA-AZ-4308	9.106849315	0	44.06442	113.114	8.063248	12.63021	0.05160736	1.231809	23.18172	149.9933	0.691033377	High
TCGA-AA-A02F	3.331506849	0	41.62237	60.86809	22.62436	26.61412	0.3128893	1.407074	2.162279	116.109	0.421273039	Low
TCGA-G4-6311	3.284931507	0	31.91899	245.123	19.06498	20.93788	0.3646882	1.647435	3.173888	253.157	0.818680872	High
TCGA-A6-2682	1.161643836	1	28.43648	201.0249	13.18953	26.37559	0	0.8104379	11.64686	244.5378	0.111716176	Low
TCGA-A6-6650	1.717808219	0	44.2499	119.7702	14.25362	19.84227	0.02154674	2.213709	0.8121963	181.7006	0.590789373	High
TCGA-NH-A6GA	0.82739726	1	32.24074	196.4058	26.54294	28.26582	1.26038	7.444862	19.36237	51.90025	2.246336119	High
TCGA-AY-A69D	1.487671233	0	44.43746	165.2808	15.88946	21.85098	0.1383036	2.497391	0.4170639	121.1135	0.774358475	High
TCGA-AA-3975	2.838356164	0	32.54791	130.091	12.47387	21.2157	0.09064794	2.314179	4.954562	168.9202	0.482440147	Low
TCGA-	0.802739	0	29.1591	171.0173	8.28508	61.5794	0.3062233	2.522469	15.18622	18.1939	-0.91270114	Low

A6-A5ZU	726		1		7	4				5	8	
TCGA-G4-6628	6.64109589	0	31.14823	112.7773	23.07427	14.64768	0.04496482	0.9519346	0.779669	352.2613	0.611688843	High
TCGA-WS-AB45	5.835616438	0	22.21597	68.58602	20.89427	10.84725	0.02650284	0.8801292	2.963743	351.8852	0.527625587	Low
TCGA-CM-5862	0.419178082	1	21.37665	107.4245	10.49727	18.11011	0.03202591	1.16325	6.941423	110.5549	0.220618014	Low
TCGA-D5-6898	0.62739726	0	29.34107	153.2602	19.27989	20.00336	0.09252876	1.117373	2.885392	110.3076	0.551159011	High
TCGA-AA-A00F	2.835616438	0	21.81981	78.47122	14.83964	21.47888	0.03710624	1.559574	3.776506	107.4575	0.216324205	Low
TCGA-CK-4950	7.120547945	0	23.98665	157.9768	14.08996	23.02348	0.02916808	0.3753475	1.297386	178.193	0.031401333	Low
TCGA-D5-6932	0.947945205	0	37.31876	120.5739	20.83735	24.23817	0.07153183	1.047525	4.374102	127.2433	0.415870479	Low
TCGA-F4-6806	3.452054795	0	26.98212	67.6658	19.80828	19.90951	0.03789471	1.848334	1.118934	168.1103	0.449441176	Low

TCGA-F4-6856	2.942465753	0	59.92562	128.0905	28.78033	30.67027	0.01660724	0.8789649	2.410114	50.08006	0.591772891	High
TCGA-F4-6569	2.978082192	0	33.41902	151.0918	11.62699	23.42349	0.2624772	0.3251139	4.787408	35.1275	0.177902879	Low
TCGA-A6-2679	3.742465753	0	44.96482	267.3748	10.14934	15.85513	1.004331	0	4.732234	323.7267	0.768061855	High
TCGA-A6-5657	2.635616438	0	45.95704	94.11005	11.37133	17.32776	0.2776562	1.461307	13.59353	159.9412	0.615011144	High
TCGA-AA-A00Q	3.501369863	0	27.52387	82.66258	25.55132	25.6499	0.05258253	2.128188	5.483752	47.88968	0.589858641	High
TCGA-CM-6169	1.084931507	0	26.75727	53.55735	16.63221	20.58105	0.1137569	1.770814	7.41828	102.1243	0.391305085	Low
TCGA-AA-3980	0.663013699	0	25.25952	215.9798	10.85187	13.87531	0.01564181	0.5356793	2.270007	1366.91	-0.217751864	Low
TCGA-A6-5665	1.838356164	0	29.13175	111.1815	11.61748	27.52764	0.09262576	1.316911	12.79632	628.3201	-0.244023185	Low
TCGA-A6-678	1.638356164	0	41.20314	72.25368	28.74542	24.62227	2.450012	1.008955	2.296591	114.7423	1.28260806	High

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TCGA-DM-A28H	9.756164384	0	38.1024	126.3614	17.57678	11.42725	0.02075988	2.815098	3.899636	43.21628	1.197214432	High
TCGA-F4-6703	3.989041096	0	34.39129	98.59139	21.33167	12.43037	0.08589732	1.181135	4.586979	348.8859	0.731803759	High
TCGA-D5-6922	0.843835616	0	55.56324	261.5581	21.98626	26.81858	0.153927	3.373372	3.617854	51.07468	1.284942713	High
TCGA-D5-5537	3.783561644	1	43.60262	184.8575	21.60332	23.45573	0.02010836	2.806744	4.661559	24.62228	1.025081805	High
TCGA-DM-A1D4	7.728767123	1	22.38367	71.02864	15.26566	16.45182	0.01566922	1.062395	1.161603	258.1236	0.212796177	Low
TCGA-AA-A004	1.161643836	0	99.80039	329.6356	6.944849	17.84785	0.2484599	2.707382	62.28125	422.0694	1.85012531	High
TCGA-AA-3950	2	0	14.50829	112.788	13.71968	6.665184	0.08377525	0.2608201	0.7105223	335.828	0.393728971	Low
TCGA-AA-A01P	3.17260274	1	46.113	155.5025	26.60287	17.33604	0.1219846	0.6872177	2.134861	537.46	0.707079708	High
TCGA-	0.4	1	40.2133	127.809	10.6879	17.8698	0.0270808	0.5527088	2.841229	987.409	-0.20472237	Low

D5-6537			7			1	1				6	
TCGA-D5-6532	1.520547945	0	39.07572	180.4227	32.87372	15.35452	0.05595895	1.229209	11.37292	24.48422	1.407357109	High
TCGA-AA-3831	1.498630137	0	23.70009	145.9702	16.16564	21.79411	0.01517861	0.9608724	1.573418	330.1506	0.136057298	Low
TCGA-CM-6171	1.169863014	0	26.6968	87.26215	9.447878	12.35888	0.05439752	2.088741	0.5126235	133.788	0.535945732	Low
TCGA-A6-A566	2.076712329	1	24.65669	122.0772	17.86979	16.9433	0.04695513	1.534961	2.9868	256.3653	0.507363382	Low
TCGA-AA-3970	3.002739726	0	26.48502	92.87748	13.08177	26.60718	0.0438764	1.593686	2.06738	330.227	-0.100816202	Low
TCGA-AA-A02K	1.167123288	1	50.32618	97.08024	16.94407	8.057284	0.1325942	7.251685	14.26954	81.93068	2.271272882	High
TCGA-DM-A1D9	11.69863014	0	24.40598	109.4903	10.63748	16.57692	0.01539642	1.784215	0.9769428	263.8071	0.292583088	Low
TCGA-CM-4751	2.252054795	0	28.41845	146.8837	13.41139	24.28973	0.02407268	1.090883	22.47354	31.47192	0.354428998	Low

TCGA-G4-6315	5.15890411	0	37.09771	116.0666	14.75826	14.63432	0.08651993	1.481508	0.7745675	82.9288	0.68222641	High
TCGA-F4-6704	0.128767123	0	37.29767	98.25835	18.25488	12.53606	0.1221478	0.7715955	4.79449	21.13035	0.781429355	High

TCGA, The Cancer Genome Atlas; COAD, colon adenocarcinoma.