

The Discovery set

id	age	grade	stage	M	T	MIR324	XIST	MIR210	MIR25	GABPB1.AS1	LINC00894	SNHG7	FGD5.AS1	MIR22HG	
TCGA-3Z-A93Z-01A-11R-A37O-07	1		2	1	1	0	0.612994625	0.017067153	3.225795816	2.570791284	0.743989965	0.135492261	3.899170055	4.145603507	3.200293686
TCGA-A3-3306-01A-01R-0864-07	1		3	1	1	0	0.88577595	0.005145434	0.281897603	2.60562447	0.977179296	0.391317923	1.441174126	4.360450706	2.776280333
TCGA-A3-3307-01A-01R-0864-07	1		3	1	1	2	0.484714312	0.004847677	1.011797781	2.466104779	1.182134566	0.580251633	2.640142256	4.704912301	4.30062154
TCGA-A3-3311-01A-02R-1325-07	0		2	1	1	0	0.181635462	0.003259461	0.348477879	1.281629773	0.506645685	0.337764557	2.349022868	4.28629044	2.498248126
TCGA-A3-3316-01A-01R-0864-07	0		3	1	1	1	0.318189979	0.003995546	1.173933342	2.569322713	2.13836557	0.600056476	1.418402138	4.331072939	4.034135136
TCGA-A3-3322-01A-02R-1325-07	0		2	1	1	0	1.436572454	0.016813401	2.882044796	3.506785875	2.038529096	0.642447871	4.203742106	4.108666845	2.77547061
TCGA-A3-3324-01A-02R-1325-07	0		3	1	1	0	1.070503483	0.005563705	1.872002034	2.994166784	1.757966131	0.407530454	2.236170111	4.159969709	2.709265411
TCGA-A3-3325-01A-01R-0864-07	0		2	1	1	0	1.564626783	0.003337968	2.986442091	3.427029174	2.192708363	0.780208414	2.899234695	4.544274306	3.884063664
TCGA-A3-3326-01A-01R-0864-07	0		0	1	1	0	0.811778007	0.003058685	2.489194856	3.401639195	2.050318401	0.744755886	3.096730379	4.010027102	2.35283203
TCGA-A3-3328-01A-01R-0864-07	1		2	1	1	0	0.162490348	0.001931713	1.556875941	1.888406987	1.081957349	1.142674252	2.90086614	6.051657241	5.001901716
TCGA-A3-3329-01A-01R-0864-07	1		2	1	1	0	0.715568508	0	4.221315867	3.049190828	0.795570848	0.628501044	3.795103959	4.493731857	3.973617836
TCGA-A3-3331-01A-02R-1325-07	1		2	1	1	0	0.839902193	4.276446755	1.524404398	2.173381601	1.431317191	0.651998986	2.413291504	4.423857058	3.901148586
TCGA-A3-3335-01A-01R-0864-07	0		4	1	1	1	1.074695993	0.01005463	1.349812207	1.074695993	1.661221394	0.664864528	2.900347554	3.597536036	1.900514427
TCGA-A3-3343-01A-01R-0864-07	1		3	1	1	1	0.372642314	0.002387353	2.498569602	2.514892678	1.300531513	0.54020439	3.63085585	4.336509501	2.818106371
TCGA-A3-3346-01A-01R-1766-07	1		3	1	1	0	0.374345468	0.003598101	2.384858827	1.834918089	1.139656113	0.44858756	1.70672591	3.948594154	1.870165575
TCGA-A3-3347-01A-02R-1325-07	1		2	1	1	0	1.147750238	4.422461737	2.289887409	3.222819834	1.44294522	0.592229977	1.512641097	4.88114337	3.498082763
TCGA-A3-3349-01A-01R-1188-07	0		2	1	1	0	0.761124026	2.296947881	2.002391016	3.223071373	1.347489107	0.683590811	3.515640566	4.618519963	2.590553847
TCGA-A3-3351-01A-02R-1325-07	0		2	1	1	1	0.632657476	0.022140609	3.56497564	3.219932327	2.162229568	1.356109531	3.033614183	4.461891409	2.748192051
TCGA-A3-3352-01A-01R-0864-07	1		3	1	1	2	1.201110179	0.004852942	2.370684618	2.721679819	1.01271579	0.745199779	3.101184112	4.270679917	2.302202596
TCGA-A3-3359-01A-01R-0864-07	1		2	1	1	0	1.111658238	3.904797427	2.868736082	2.034158266	1.008416597	0.846844204	2.585563961	4.410656634	3.691176217
TCGA-A3-3362-01A-02R-1325-07	0		2	1	1	0	0.827033403	3.339759142	2.65986119	1.732095958	1.026468089	0.773591872	2.80026231	4.375406672	3.19277564
TCGA-A3-3363-01A-01R-0864-07	0		2	1	1	1	0.484500009	0.10701751	0.858151766	3.01705373	0.862262497	0.889887091	2.354737178	5.431375747	2.647157491
TCGA-A3-3365-01A-01R-0864-07	0		2	1	1	0	0.230286292	0.008393958	0.234151056	2.758926466	1.724728195	0.505873413	2.491012747	5.237677123	4.749241757
TCGA-A3-3367-01A-02R-1420-07	1		3	1	1	0	0.548657118	0.002810756	0.436537679	2.531437994	0.878063741	0.594756831	3.816034373	4.201271172	1.949998431
TCGA-A3-3370-01A-02R-1420-07	0		2	1	1	0	0.629053046	4.546922515	2.291428992	2.708930724	1.028402557	0.90254606	2.981932338	4.372988402	3.003469631
TCGA-A3-3372-01A-02R-1325-07	0		2	1	1	2	0.884609178	0.018180215	1.782972359	2.511333662	2.348491201	0.775702778	2.57859596	4.62067451	2.735664437
TCGA-A3-3373-01A-02R-1420-07	0		3	1	1	0	0.742059926	2.927208034	1.312498555	0.67611675	0.925156268	0.254105705	1.655224791	4.558682345	3.400664357
TCGA-A3-3374-01A-02R-1325-07	0		2	1	1	0	0.508855161	0.126832068	0	1.617115936	0.305919126	0.402856725	2.687029058	5.361132257	3.76615494
TCGA-A3-3378-01A-02R-1325-07	0		3	1	1	0	0.511484573	0.010312119	1.107916357	2.138857283	1.450944361	0.740549762	1.37725409	4.354650317	2.58262656
TCGA-A3-3380-01A-01R-0864-07	0		2	1	1	0	1.061215601	0.010970501	2.796421778	2.910758375	1.711536749	0.866219181	4.074754043	4.476725339	2.876421668
TCGA-A3-3382-01A-02R-1325-07	1		3	1	1	0	0.712210919	0.005165583	2.193630532	2.206988983	0.936181763	0.768781454	3.302832174	4.475608227	2.003859915
TCGA-A3-3383-01A-02R-1325-07	0		2	1	1	0	1.149579478	0.001645461	1.961564829	3.007227286	0.626830268	0.388862309	4.127562061	3.180763726	2.228591483
TCGA-A3-3385-01A-02R-1420-07	0		2	1	1	0	0.90433916	4.279462467	1.536979135	2.410592353	1.528644054	0.484645215	3.517049678	4.730541686	1.171061287
TCGA-A3-3387-01A-01R-1541-07	0		2	1	1	0	0.615831135	0.002156652	2.088388553	2.850360742	2.169902981	0.629481015	3.102031087	4.644681465	2.953302186
TCGA-A3-A6NI-01A-11R-A33J-07	0		3	1	1	0	1.210963064	0.004730081	4.105569525	2.774859591	1.349823322	0.42396146	3.815907235	3.950723858	2.844287077
TCGA-A3-A6NJ-01A-12R-A33J-07	0		0	1	1	0	1.21795398	3.547577122	2.383944423	1.778756997	0.721113738	0.32483724	2.829070612	4.403901691	3.901135882
TCGA-A3-A6NL-01A-11R-A33J-07	0		2	1	1	0	1.50357892	3.929955013	3.175675357	3.102076308	0.865595169	0.649801673	3.529893052	4.360605598	3.000273959
TCGA-A3-A6NN-01A-12R-A33J-07	1		2	1	1	0	0.981925585	0	2.450942053	2.681948747	1.465168943	0.464652728	4.295234184	4.669329602	2.459078033
TCGA-A3-A8CQ-01A-11R-A37O-07	0		2	1	1	0	0.95113009	3.876517783	4.526587607	2.164993148	0.794009572	0.548859763	3.047193208		

TCGA-AK-3455-01A-01R-0864-07	1	3	1	1	2	0.239181111	1.028320044	1.303815105	1.423852472	1.126102092	0.955355464	3.162362947	4.149272586	2.597510204
TCGA-AK-3456-01A-02R-1325-07	0	3	1	1	1	0	0.001524229	0	1.002351855	0.832869067	0.337119156	1.629813577	5.139685931	1.633486492
TCGA-AK-3458-01A-01R-1503-07	0	3	1	1	0	0.26267265	0.055579584	2.742704936	1.872889883	1.330085026	0.864455168	4.449753522	4.290539994	1.868527923
TCGA-AK-3465-01A-02R-1325-07	1	1	1	1	0	0.49516194	1.410903263	0.874874112	2.156339112	1.210052124	0.828701961	3.747043489	5.685847879	3.973491545
TCGA-AS-3778-01A-01R-A32Z-07	0	0	1	1	0	1.676032457	0.003555393	3.691770793	2.404189837	1.482318566	0.646331805	4.087508707	4.201578997	3.125043269
TCGA-B0-4691-01A-01R-1277-07	0	3	1	2	1	1.066457636	0.049823588	2.60724704	2.116019731	0.60289818	0.638374526	2.592864693	3.918399011	3.298125705
TCGA-B0-4693-01A-01R-1277-07	1	4	1	1	2	1.622325633	4.049374919	1.958338539	1.592501564	1.235114774	0.750907614	2.268722514	4.148516032	4.025199305
TCGA-B0-4697-01A-01R-1277-07	0	4	1	2	2	2.586790188	3.692786743	2.191896546	2.323682719	1.928915014	1.415523562	3.164178955	4.174945746	2.354286995
TCGA-B0-4698-01A-01R-1503-07	1	4	1	1	3	1.006196411	0.012213433	1.107898882	1.422778864	0.952628053	0.969412088	3.84822797	5.374507206	2.541883068
TCGA-B0-4699-01A-01R-1277-07	1	4	1	2	3	0.999814464	0.011741149	1.463740342	1.72353147	1.229260155	1.023990302	2.95931446	5.465216616	3.606612567
TCGA-B0-4700-11A-01R-1541-07	0	4	1	2	3	1.173711779	0.002906147	0.242057741	1.419296926	0.949420613	0.670035038	1.169083084	5.040116929	3.575573458
TCGA-B0-4700-01A-02R-1541-07	0	4	1	2	3	0.866784453	0.436786838	1.59099184	1.069100728	0.657875384	0.23988225	1.558085998	4.143126492	2.752678245
TCGA-B0-4701-01A-01R-1277-07	1	3	1	2	2	1.964330139	4.229498098	2.991524391	1.899790611	1.150498432	0.908411313	3.615539194	4.157683445	3.291623428
TCGA-B0-4706-01A-01R-1503-07	0	4	1	1	2	2.010914841	0.007002252	3.358456001	2.675214597	1.635704744	1.24336188	4.610597719	4.199402512	2.041823042
TCGA-B0-4707-01A-01R-1277-07	0	4	1	1	2	0.774127771	0.401173266	2.54113108	2.806709948	1.102105564	0.765734008	3.553266347	3.852998454	1.841477441
TCGA-B0-4710-01A-01R-1503-07	1	3	1	1	2	2.820169397	4.251437685	2.493009276	2.497709632	1.426374544	0.810960414	2.770824401	3.920260793	3.283561272
TCGA-B0-4712-01A-01R-1503-07	1	3	1	2	2	0	0.001169909	1.304456842	1.548376689	0.361976545	0.224994942	2.247117269	4.672651177	2.620492079
TCGA-B0-4712-11A-02R-1503-07	1	3	1	2	2	0	0	0.155386172	0.200276643	0.565462146	0.069645782	2.030783144	5.828314292	3.324135643
TCGA-B0-4714-01A-01R-1277-07	1	3	1	2	2	1.605440365	0.040089504	3.277732686	4.272327069	1.541935909	1.486824642	3.135656557	4.156690426	2.395927886
TCGA-B0-4718-01A-01R-1277-07	0	2	1	1	2	1.132686837	0.152188829	4.089959659	2.679594458	1.201694561	1.358009421	3.088728869	3.899446619	3.159627533
TCGA-B0-4810-01A-01R-1503-07	0	3	1	1	2	1.160532164	0.007768842	3.071659823	1.973924375	1.426437214	0.753313251	3.087660596	4.338214081	2.802725819
TCGA-B0-4811-01A-01R-1503-07	0	3	1	1	2	2.555608744	0.093468	3.714513598	3.95808118	1.66601883	0.986358532	3.925370587	3.764393403	2.998561301
TCGA-B0-4813-01A-01R-1277-07	1	3	1	1	2	1.514656257	0.163530525	3.386174026	3.775219207	1.347031779	1.488163146	3.540314221	3.963474787	3.644244326
TCGA-B0-4814-01A-01R-1277-07	0	3	1	2	3	2.079346457	0.024567721	2.099232808	2.406412322	1.305222341	1.081228361	3.189572486	3.994275818	1.535014538
TCGA-B0-4815-01A-01R-1503-07	0	4	1	1	2	1.590689608	0.005813579	3.004227154	3.237404132	1.172236495	0.795485755	2.840031683	4.378521916	3.118788402
TCGA-B0-4816-01A-01R-1503-07	0	3	1	1	1	0.673997429	0.02203803	2.095620425	3.081245031	1.451753548	0.430908223	2.816543832	4.496634122	3.377117995
TCGA-B0-4818-01A-01R-1503-07	1	3	1	1	1	0.637534696	4.007703015	3.329460262	1.917753546	0.844135898	0.791451036	2.912239481	4.432852367	2.744235979
TCGA-B0-4819-01A-01R-1277-07	0	4	1	2	2	1.667493521	2.703846543	1.016396636	2.813025752	1.565307337	1.025061946	2.210901026	4.509835894	3.705454856
TCGA-B0-4823-01A-02R-1420-07	1	2	1	1	0	0	0.009382424	0.198839404	0.255215985	0.214015523	0.058154248	3.765151232	4.380066043	2.825007553
TCGA-B0-4824-01A-01R-1277-07	0	3	1	1	0	0.866943928	3.775280105	2.906985806	1.795511935	1.647799395	1.061501465	2.833139472	4.223823421	2.707295408
TCGA-B0-4827-01A-02R-1420-07	1	4	1	1	2	0	0.980520136	0.321651408	0	0.156198365	0.009372324	2.529545933	3.7993921	2.080482308
TCGA-B0-4828-01A-01R-1277-07	1	3	1	2	1	1.429162885	0.120095612	2.980891194	3.107364601	1.063439052	1.051038566	3.306139144	3.924602526	3.489430937
TCGA-B0-4833-01A-01R-1305-07	1	2	1	1	0	0.964749564	3.314317576	2.355685093	3.106649416	1.893215831	1.141005909	3.399903842	4.166896407	2.601474387
TCGA-B0-4834-01A-01R-1305-07	0	3	1	1	0	0.204113129	0.00491998	0	1.009480808	0.35548443	0.779110675	3.143869334	5.22106084	4.276789894
TCGA-B0-4837-01A-01R-1305-07	0	3	1	1	0	0.210872842	0.017753695	2.228278602	1.814842099	1.167160674	0.357913745	2.903620134	3.954306724	2.078351224
TCGA-B0-4838-01A-01R-1305-07	1	3	1	1	0	1.925287422	4.150307033	1.003983148	2.025897369	2.105338733	0.732762823	1.870248475	4.409084208	3.478917962
TCGA-B0-4841-01A-01R-1277-07	0	3	1	2	1	0	0.561436229	1.319916238	0.477101901	0.334159127	0.260462869	2.437644324	3.947744438	2.678679046
TCGA-B0-4842-01A-02R-1420-07	1	4	1	1	2	0	0.190241779	0.694119889	0	0.343739691	0.035739346	2.56489162	3.491095607	1.728653156
TCGA-B0-4843-01A-01R-1277-07	0	3	1	1	2	1.161884757	0.054149442	2.948596243	2.357547747	0.8779195	0.560647507	3.133009378	3.897895812	3.200457551
TCGA-B0-4844-01A-01R-1277-07	0	3	1	2	2	0.474012747	0.045014427	1.915435541	2.211125136	0.91070181	0.753208614	2.064660713	3.790513124	2.471093783
TCGA-B0-4845-01A-01R-1277-07	1	2	1	2	2	2.991031437	0.032853642	3.656862347	3.885772828	2.494066199	1.054122445	2.08516735	4.336954142	2.981578158
TCGA-B0-4846-01A-01R-1277-07	0	2	1	2	2	1.015944124	3.722828599	1.130600896	1.897602728	1.047727287	0.621084223	2.088243891	4.525813924	4.114595975
TCGA-B0-4847-01A-01R-1277-07	0	3	1	2	2	1.390787625	0.014719997	3.075995979	3.529123405	0.837220168	1.029719037	2.888110188	3.593357749	3.01725437
TCGA-B0-4849-01A-01R-1277-07	0	3	1	1	2	1.082399564	0.10481931	2.882074943	2.859633476	2.2450794	1.095083694	3.39713198	4.387835844	4.33136322
TCGA-B0-4852-01A-01R-1503-07	1	2	1	1	1	1.187315577	4.217898982	2.087895181	1.829675971	1.253102554	0.919957865	2.487846681	4.283844185	3.343007288
TCGA-B0-4945-01A-01R-1420-07	1	2	1	1	0	0.452854969	3.435050932	2.460849543	1.568833002	1.824199822	1.261694175	1.918476338	4.470468546	4.482982985
TCGA-B0-5075-01A-01R-1334-07	1	2	1	1	2	0.995866441	3.611439872	1.930585598	1.389734573	0.571600265	0.744262075	2.117810219	3.933866943	2.868418675
TCGA-B0-5077-01A-01R-1334-07	1	3	1	1	0	1.049965504	0.002889921	2.742421877	0.964611614	1.12294792	0.891711585	3.4519181	4.067125841	3.00318358
TCGA-B0-5083-01A-02R-1420-07	0	3	1	1	0	0	0.223745518	0	0.957646665	0.122580383	0.040066709	3.074975679	5.082187587	3.113185335
TCGA-B0-5085-01A-01R-1334-07	1	3	1	1	2	2.22750294	2.473830991	4.34879937	2.835663702	0.980048281	1.06730275	3.408814092	3.348912989	3.901840044
TCGA-B0-5094-01A-01R-1420-07	0	2	1	2	2	1.336093536	0.010077917	2.133244734	3.131251138	0.966622207	0.618447181	2.371015199	3.86935751	2.487027791
TCGA-B0-5096-01A-01R-1420-07	1	1	1	1	2	0.232294218	1.723822514	1.37901155	1.517770928	0.502704704	0.164381832	1.707139869	4.06439021	2.156999135
TCGA-B0-5097-01A-01R-1420-07	0	2	1	1	2	0.837234847	2.651902187	1.287864999	2.255738816	0.523004172	0.338837529	1.824842214	4.379294993	3.814015398
TCGA-B0-5099-01A-01R-1420-07	1	3	1	1	2	1.980424072	4.053738549	2.961381596	1.516362556	0.811594351	0.825199673	3.203762044	4.050432156	4.896987289
TCGA-B0-5100-01A-01R-1420-07	1	3	1	1	2	0.567206223	0.010375346	3.247991372	1.321045799	0.730692685	0.265332826	3.57097047	4.723462256	3.195315299
TCGA-B0-5104-01A-01R-1420-07	1	2	1	1	0	1.392016492	2.172302712	1.718147766	1.736625307	0.760520889	0.679912748	2.326709321	4.197511262	3.916771212
TCGA-B0-5107-01A-01R-1420-07	0	4	1	2	1	1.294209433	3.0736529	2.823677757	3.752759547	1.04597469	0.864259239	3.061860616	4.082354755	1.654829317
TCGA-B0-5108-01A-01R-1420-07	0	2	1	1	2	1.183350637	0.001144476	3.223430427	1.862440685	0.658300825	0.403486662	2.104940811	4.316039647	2.681157727

TCGA-B0-5109-01A-02R-1420-07	1	4	1	1	2	1.126253749	0.010918508	0.229046276	1.598293051	0.567014969	0.357686519	4.12751317	4.167942179	2.256319646
TCGA-B0-5110-01A-01R-1420-07	1	2	1	1	0	1.087699369	4.897164907	2.348282304	2.215363423	0.831713403	0.825140986	2.655385034	4.556577166	4.289414322
TCGA-B0-5113-01A-01R-1420-07	1	2	1	1	2	0.184049813	4.732747994	2.245083814	1.293604278	0.698442138	0.880613822	2.283526751	4.719077674	2.635983988
TCGA-B0-5115-01A-01R-1420-07	0	3	1	2	1	1.285593068	0.016227514	2.391079643	2.435447844	2.073382767	0.982171273	3.402848146	4.349762606	2.143780698
TCGA-B0-5116-01A-02R-1420-07	0	3	1	1	2	0	0.00116876	1.386981768	1.547443745	0.212765518	0.061332671	3.048180659	4.277815102	2.190593753
TCGA-B0-5117-01A-01R-1420-07	0	2	1	1	0	0	0	0.22969739	2.341464509	0.379167938	0.92656804	3.5311565	4.831691087	3.997557181
TCGA-B0-5399-01A-01R-1503-07	0	2	1	1	0	0.366771262	0.002344794	2.587450225	2.33699544	0.954517024	0.74791824	3.800965328	4.297998901	2.72772217
TCGA-B0-5400-01A-01R-1503-07	0	4	1	1	2	0.375835156	1.29220883	0.540525126	1.131169307	0.33562342	0.34050336	1.852776848	3.635310465	2.802673689
TCGA-B0-5402-11A-01R-1503-07	0	4	1	1	3	0.310316062	0.005824807	0.315383732	0.400507797	0.268983079	0.097796685	2.015589261	4.994093785	3.830134868
TCGA-B0-5402-01A-01R-1503-07	0	4	1	1	3	0.291462585	0.002719953	1.662448926	0.922594905	0.297670903	0.204987435	2.715658042	4.176100796	2.688338633
TCGA-B0-5690-11A-01R-1541-07	0	0	1	1	0	0	1.766623315	0	0.608736138	0.394897945	0.049446138	2.639152484	5.536044469	3.131323955
TCGA-B0-5690-01A-11R-1541-07	0	0	1	1	0	0.712200913	3.696337271	1.781213364	1.543448668	0.66798021	0.290777709	3.374368804	4.521160859	2.779407797
TCGA-B0-5691-11A-01R-1541-07	1	3	1	1	0	0.149044085	2.866792363	0	1.011344571	0.568030406	0.17278789	2.175675564	5.371073438	3.730660959
TCGA-B0-5692-01A-11R-1541-07	1	3	1	1	2	0.411826669	0.566402454	1.81673048	1.345806763	0.25301446	0.272311401	2.746285803	3.919397973	1.895286556
TCGA-B0-5694-11A-01R-1541-07	1	3	1	1	2	0	0.02463905	0	0.980474355	0.402346877	0.17539887	2.259693193	5.236556414	3.885627707
TCGA-B0-5694-01A-11R-1541-07	1	3	1	1	2	0.510255188	0.015396843	0.518048308	1.936847355	0.372515629	0.154110901	2.671323161	4.024779873	2.128938335
TCGA-B0-5695-01A-11R-1541-07	0	2	1	1	0	0.168086925	2.727947656	1.253358274	0.866934864	0.312296837	0.169616801	3.360650089	4.358387827	2.912738122
TCGA-B0-5696-01A-11R-1541-07	1	4	1	1	2	0.344576318	0.402882872	0.867144681	0.622514396	0.207615599	0.037427692	2.546823468	3.860024528	2.505892785
TCGA-B0-5696-11A-01R-1541-07	1	4	1	1	2	0	0.002470746	0.208249861	0.68710689	0.32258459	0.094285996	2.510427372	5.302345123	3.315073257
TCGA-B0-5697-01A-11R-1541-07	0	2	1	1	0	0.16843633	1.900800995	1.400094079	0.993288847	0.381581341	0.195066281	1.413122487	5.003658098	2.694176432
TCGA-B0-5698-01A-11R-1672-07	1	3	1	1	0	0.733887441	0.002148763	0.744308426	1.043332673	0.497302479	0.126467285	2.955150818	4.221794151	4.013217205
TCGA-B0-5699-11A-01R-1541-07	0	2	1	1	0	0	0.00140504	0.436263407	0.944688526	0.36036027	0.102608085	2.433631652	5.248253766	3.636174136
TCGA-B0-5701-01A-11R-1541-07	0	4	1	1	2	0.540155248	0.126800242	2.001985298	1.493911641	0.390532382	0.095417197	2.019793911	3.573380837	1.829868176
TCGA-B0-5702-01A-11R-1541-07	1	2	1	1	0	0	0.033291259	0	0	0.233941786	0.021077074	3.418311197	1.586879907	1.456886466
TCGA-B0-5703-01A-11R-1541-07	1	3	1	1	0	0.244938877	0	0.810342652	0.57864588	0.422453858	0.143897186	3.370726727	4.126936939	2.261991988
TCGA-B0-5703-11A-01R-1541-07	1	3	1	1	0	0	0.002900631	0.241634289	0.967219125	0.560882627	0.184464637	3.143709452	5.707230767	3.854047135
TCGA-B0-5705-11A-01R-1541-07	0	2	1	1	0	0	2.321333063	0	0.752040441	0.560760044	0.161124879	2.146998463	5.534367844	3.35524009
TCGA-B0-5706-11A-01R-1541-07	0	2	1	1	1	0.227997089	0.002773317	0.231826438	0.752604119	0.836576903	0.382127483	2.350453694	5.703982168	3.716275951
TCGA-B0-5709-11A-01R-1541-07	0	3	1	1	2	0.46182652	3.439061579	0.328946837	0.740476758	0.497327571	0.282237918	1.997151491	5.321041271	4.004283415
TCGA-B0-5709-01A-11R-1541-07	0	3	1	1	2	0	1.707775932	1.680090184	0.886795438	0.304492449	0.103592812	1.812059787	4.68839724	2.631671003
TCGA-B0-5710-01A-11R-1672-07	0	2	1	1	0	0	0.002502948	0.39464905	1.021490764	0.964127398	0.397758239	2.580674556	4.538427534	2.117028525
TCGA-B0-5711-01A-11R-1672-07	0	3	1	1	2	0.194733741	0.00234125	0.527492034	0.470269017	0.641218423	0.157289267	2.904070502	4.223472927	2.258057565
TCGA-B0-5712-11A-01R-1672-07	1	3	1	2	1	0	1.950557121	0	0.449646034	0.319229042	0.146503124	2.357652207	5.389088031	3.839707375
TCGA-B0-5713-01A-11R-1672-07	1	3	1	1	2	0.765427095	3.251340887	0.776186647	1.317919183	0.776291473	0.209392635	2.40916542	4.366729353	3.343569063
TCGA-B2-3923-01A-02R-A277-07	0	2	1	1	1	0	0.03450683	0	1.103478011	1.548529776	1.663116888	3.791518849	5.686715353	3.785409852
TCGA-B2-3924-01A-02R-A277-07	1	2	1	1	0	0.520124397	0.014008189	2.315491213	2.161123794	1.616315969	0.835331144	3.78897386	4.572716092	2.903052538
TCGA-B2-3924-01A-02R-1325-07	1	2	1	1	0	0.212423538	0.001285474	2.285819798	1.537840141	1.003791424	0.189658993	3.595680318	4.360834076	2.765812727
TCGA-B2-4098-01A-02R-1325-07	1	2	1	1	0	1.340409408	1.072679309	1.356194777	2.346517606	1.433532307	1.686062956	2.257109506	4.759818072	2.844444536
TCGA-B2-4101-01A-02R-1277-07	0	3	1	1	1	1.228412531	0.022954511	2.251159394	3.029125624	2.004393476	1.06650539	3.317117596	4.362411902	3.013995774
TCGA-B2-4102-01A-02R-1325-07	0	2	1	1	0	1.338998047	0.059523927	2.914907262	3.458697447	0.927965131	1.072337008	1.919877337	4.541779693	3.026690157
TCGA-B2-5633-01A-01R-1541-07	0	2	1	1	0	0.988024857	0.149811368	1.849401667	1.2086984	1.257832174	0.179376089	2.772020539	4.309064862	2.280514851
TCGA-B2-5633-01A-01R-A277-07	0	2	1	1	0	0	0.01353137	0.250614823	1.453673058	1.460322682	0.467643077	3.258994089	4.962467879	2.325262163
TCGA-B2-5635-01A-01R-1541-07	1	2	1	1	0	0.207629894	0.147772895	3.071656472	2.172667352	1.003693677	0.442732564	2.266163544	4.438385844	2.450152531
TCGA-B2-5635-01B-04R-A277-07	1	2	1	1	0	1.264865578	0.042036337	2.301158848	3.002745887	3.063724921	3.022618298	1.977642566	4.990697313	2.720610799
TCGA-B2-5636-01A-02R-1541-07	1	2	1	1	0	0.85384624	0.006530134	3.152364497	2.152032394	0.780663287	0.103477648	3.210602417	5.003052415	2.627151382
TCGA-B2-5636-11A-01R-1541-07	1	2	1	1	0	0	0.002257374	0.511564001	1.201902691	0.83138616	0.220770476	2.287599476	5.082231838	3.663926819
TCGA-B2-5639-01A-01R-1541-07	0	3	1	2	2	0	0	1.253794074	0.44641885	0.168806931	0.041112243	2.263026976	3.991131381	1.777390019
TCGA-B2-5641-11A-01R-1541-07	1	3	1	1	0	0	0.001435104	0.783505951	1.273131878	1.321876167	0.158431832	2.033946793	5.793452778	3.443359759
TCGA-B4-5377-01A-01R-1503-07	1	3	1	2	2	0.287122498	3.71530934	3.411553207	0.666493898	0.450808523	0.314732763	2.376244498	4.370721579	3.471054322
TCGA-B4-5378-01A-01R-1503-07	0	2	1	1	0	0.590822868	0.074950717	3.267745505	1.426006232	0.63629536	0.297015217	4.105667828	5.021696197	2.703680617
TCGA-B4-5832-01A-11R-1672-07	0	2	1	1	2	0	0	0	0	0.357274976	0.034914484	0.672766198	5.033712897	2.70964867
TCGA-B4-5834-01A-11R-1672-07	0	0	1	1	0	0	0	1.664450066	0.222991612	0.497666937	0.080978242	3.95656133	4.477941897	1.762735663
TCGA-B4-5835-01A-11R-1672-07	0	2	1	1	0	0	2.061574025	0.15549787	0.674574783	0.273114125	0.24623391	1.758184395	4.531025405	1.169507961
TCGA-B4-5843-01A-11R-1672-07	0	2	1	1	0	0.436155529	0.001430163	0.238427459	1.122107417	0.481130129	0.209535194	2.774330579	4.351432561	1.772452665
TCGA-B8-4146-01B-11R-1672-07	0	2	1	1	0	0	3.421056033	0.229619793	0.293872811	1.0468732	0.246209558	1.935810705	4.32032937	2.357493003
TCGA-B8-4148-01A-02R-1325-07	0	3	1	1	0	1.78011977	4.880701907	4.144916221	2.579492942	1.354191405	0.861137283	2.51896454	4.670320464	4.114973396
TCGA-B8-4151-01A-01R-1188-07	0	2	1	1	2	0.941433002	1.819359429	2.408978644	0.986809298	0.657440913	0.249898756	3.597374454	4.280944297	2.702664711
TCGA-B8-4153-01B-11R-1672-07	1	3	1	1	2	0.639155971	0.003009539	1.790519613	1.576246278	0.994303524	0.337192785	3.301664617	3.996185927	3.097891567

TCGA-B8-4154-01A-01R-1188-07	1	2	1	1	0	1.558557481	1.965057271	1.767849206	1.415569424	0.618675872	0.151563059	3.680472539	4.606307067	2.880596962
TCGA-B8-4619-11A-01R-1758-07	0	2	1	1	0	0	0.001855183	0.552172271	1.15136562	0.52497076	0.165660927	1.808438432	5.199575224	3.93386676
TCGA-B8-4619-01A-02R-1325-07	0	2	1	1	0	0.398207704	0.003860314	0.404520735	1.908763147	0.769440809	0.922383031	2.298852087	5.567695118	4.413892374
TCGA-B8-4620-01A-02R-1325-07	1	2	1	1	2	0.923083911	3.287119889	2.761051476	2.67287455	0.786165618	0.921609401	2.667108147	4.251628537	3.57652723
TCGA-B8-4620-11A-01R-1758-07	1	2	1	1	2	0.308114949	1.478947416	0.78847981	0.965215947	0.534657147	0.26595314	2.161446781	5.45072223	4.126603345
TCGA-B8-4622-01A-02R-1277-07	0	3	1	2	2	1.135221551	0.02200343	1.852236783	2.588325057	0.615012506	0.450333318	2.338563866	4.337372704	2.098495071
TCGA-B8-4622-11A-01R-1758-07	0	3	1	2	2	0	0.001506862	0	0	0.191378663	0.074101159	2.375633603	5.300164621	3.323677014
TCGA-B8-5158-01A-01R-1420-07	0	4	1	1	2	0.443933337	0	0.688343085	0.400837119	0.501600723	0.15413179	1.505351866	4.043616928	1.842289812
TCGA-B8-5162-01A-01R-1420-07	0	2	1	1	1	0	0.002406927	0.931780408	0.481492327	0.432607232	0.08478233	2.17859168	4.672659975	2.436566821
TCGA-B8-5163-01A-01R-1420-07	0	3	1	1	2	0	2.252780903	0.865428188	0	0.226974385	0.113985847	1.540548645	4.615247061	2.621675145
TCGA-B8-5164-01A-01R-1420-07	0	3	1	1	2	0.162276034	0	2.174808097	0.84291819	0.437981139	0.206568194	1.447689287	4.77855451	2.902906953
TCGA-B8-5165-01A-01R-1420-07	0	2	1	1	0	0	0.003964336	1.319456365	1.205259703	0.673188838	0.117119797	3.436470444	4.658652719	2.707741291
TCGA-B8-5546-01A-01R-1541-07	0	2	1	1	0	0.261020451	1.35188694	0	0.338492507	0.466168862	0.135355163	3.204032203	4.969850287	1.744457313
TCGA-B8-5549-11A-01R-1541-07	0	3	1	1	0	0	0	0.50937489	0.63644689	0.635158203	0.17650086	2.266842394	6.049265957	3.085317077
TCGA-B8-5551-01A-01R-1541-07	0	3	1	1	0	0.229459304	3.017062323	0.908927925	1.103868992	0.56113525	0.177990977	2.106410014	4.596220443	2.641009927
TCGA-B8-5552-11A-01R-1672-07	0	2	1	1	0	0	2.282286599	0	1.30539839	0.510477199	0.108618891	1.326397746	5.649833218	3.727134916
TCGA-B8-5552-01B-11R-1672-07	0	2	1	1	0	0.48214988	2.806114934	1.230692058	0.612681047	0.767939542	0.147668415	2.558950434	4.826964179	3.13005326
TCGA-B8-A54D-01A-21R-A266-07	1	2	1	1	2	1.663081866	0.005843942	3.29649956	2.127887254	1.372583118	1.701238416	2.910072974	4.988093946	2.859649099
TCGA-B8-A54E-01A-11R-A266-07	0	3	1	1	0	0.475248531	0.734925416	0	0.832132819	0.550131624	0.177990762	3.076755867	4.334473869	3.164836271
TCGA-B8-A54F-01A-11R-A266-07	0	2	1	1	0	1.474649154	4.635912694	3.04370067	2.933987862	1.664067052	0.878360318	3.69196466	4.267576701	2.353543021
TCGA-B8-A54G-01A-11R-A266-07	0	3	1	1	0	1.006566239	0.024336654	2.568484961	3.047135101	1.468394594	1.363437454	3.007918518	4.488369283	2.515051906
TCGA-B8-A54H-01A-11R-A33J-07	1	3	1	1	1	1.505125611	3.962906614	3.26466202	2.392032577	1.311675239	0.761055018	3.109336356	4.304693752	2.089111876
TCGA-B8-A54I-01A-21R-A33J-07	0	3	1	1	0	1.502987633	0.001651356	4.313530881	2.264372595	0.829706034	0.63780215	1.673888923	3.530691496	2.703044131
TCGA-B8-A54K-01A-11R-A33J-07	0	0	1	1	0	1.04354973	0.002865143	4.059056434	3.055044805	1.328746838	0.89897835	4.641013371	4.969033338	1.918341227
TCGA-B8-A7U6-01A-12R-A37O-07	0	3	1	1	0	1.693930437	2.17582785	2.586699285	2.097119176	0.690240277	0.583905442	3.284928989	4.183918697	4.804230177
TCGA-BP-4159-01A-02R-1289-07	1	2	1	1	0	0.456625155	0.089245589	1.095784199	1.578092594	0.539956105	0.157579245	3.760072353	4.454941147	2.469562625
TCGA-BP-4162-01A-02R-1325-07	0	2	1	1	0	1.594995891	4.252383842	2.505013725	0.575238757	0.528055115	0.700281365	1.803640963	4.279119216	3.945727451
TCGA-BP-4165-01A-02R-1289-07	0	0	1	1	0	0.632064944	3.776825033	3.586039376	2.365666116	1.394233976	0.763763875	3.779344647	4.470746255	2.513125903
TCGA-BP-4166-01A-02R-1289-07	1	3	1	1	2	0	0.032274348	1.134591836	0.53338394	0.299544265	0.218372903	3.321651252	4.381419614	2.007225704
TCGA-BP-4167-01A-02R-1325-07	0	2	1	1	2	1.063023392	0.017554892	0.944303092	1.668396381	0.519251182	0.153875482	2.486692847	4.722806331	2.805811924
TCGA-BP-4169-01A-02R-1289-07	1	2	1	1	1	0.529696368	3.907922685	2.937804994	2.276423089	1.581129555	0.874164587	2.21033401	4.504204716	3.953170954
TCGA-BP-4170-01A-02R-1289-07	1	2	1	1	0	0.169239733	2.461468332	2.059431211	1.318223775	0.349677029	0.201530932	2.590009385	4.372876097	2.754231943
TCGA-BP-4173-01A-02R-1289-07	0	3	1	1	1	1.494378997	0.034713924	2.473789406	1.694583858	1.068594475	0.736503773	2.586276067	4.589543341	3.235148496
TCGA-BP-4174-01A-02R-1289-07	0	3	1	1	1	0	0.034725502	1.484581306	0.892477805	0.467949235	0.251638407	2.787034497	4.255709275	1.919324219
TCGA-BP-4177-01A-02R-1420-07	0	2	1	1	0	0.339422208	0.014974786	1.389806285	0.436872193	0.42574916	0.069472835	4.329119048	4.989349327	2.728183641
TCGA-BP-4325-01A-02R-1289-07	0	2	1	1	0	1.154921892	4.361654844	2.198793296	3.027840952	1.328589638	0.714582014	2.969762653	4.337893754	2.463351443
TCGA-BP-4327-01A-01R-1289-07	1	2	1	1	1	1.191885828	3.979374518	4.421924331	2.51345947	2.036958381	1.637059652	3.610234401	3.883265643	2.241206567
TCGA-BP-4331-01A-01R-1289-07	0	2	1	1	0	2.108353649	0.006697058	3.725114215	3.242445965	1.343969125	0.874632461	3.056084221	4.295717061	4.107915795
TCGA-BP-4332-01A-01R-1289-07	0	2	1	1	2	0.812244636	0.069394143	3.145806924	3.595400945	1.075813364	0.580562967	3.936431448	4.517472001	3.24370162
TCGA-BP-4337-01A-01R-1289-07	1	4	1	1	2	0.967685578	2.747783947	3.379400755	3.310321645	2.737687803	1.017330557	2.764112224	4.066701403	2.557559724
TCGA-BP-4338-01A-01R-1289-07	0	3	1	1	0	0	0.01046168	1.143255359	0.6559138	0.286333141	0.069984014	1.563529894	3.515267977	2.187231902
TCGA-BP-4341-01A-01R-1289-07	1	2	1	1	2	2.368558732	0.087328969	3.63964943	2.518475965	1.704613506	1.215522566	4.157733879	3.999222785	3.102638369
TCGA-BP-4342-01A-01R-1289-07	1	3	1	1	1	1.414946384	0.024729128	3.184664692	2.489265017	1.960411653	0.648622402	3.114842258	4.13809932	2.657260621
TCGA-BP-4343-01A-02R-1289-07	0	3	1	1	2	0	0.198708836	0.228377484	0	0.262891895	0.177967597	1.965295919	5.090792021	2.231519013
TCGA-BP-4345-01A-01R-1289-07	0	3	1	1	2	0.773530637	0.03858973	1.727489633	1.329691558	0.682564724	0.421475275	1.983758991	4.744802087	3.23890445
TCGA-BP-4346-01A-01R-1289-07	0	3	1	1	2	1.296871983	0.024722623	3.208106259	3.585937374	1.976018603	1.188332063	2.273469233	4.394763031	2.363782088
TCGA-BP-4347-01A-01R-1289-07	1	2	1	1	2	1.117860659	0.021402462	3.11948254	2.432237808	1.414309261	0.737331077	2.706743381	4.446259039	3.981151693
TCGA-BP-4349-01A-01R-1289-07	1	2	1	1	0	1.639258486	4.13449907	4.09419885	3.183362207	2.369105405	1.088429769	2.717102191	4.112209129	3.338087969
TCGA-BP-4351-01A-01R-1289-07	0	2	1	1	2	2.463891578	5.165860246	3.531197639	2.119670729	1.639179611	1.541695824	3.239344058	4.013574226	2.469068748
TCGA-BP-4352-01A-01R-1289-07	1	4	1	2	2	2.553850548	1.950380238	3.212199911	3.825015118	2.934298209	1.774478496	4.157788609	4.299851788	1.438641406
TCGA-BP-4353-01A-02R-1289-07	0	2	1	1	0	0.386819642	0.104562441	0.701502807	0.691548245	1.217969873	0.264879975	2.60898385	4.875096962	2.42375684
TCGA-BP-4354-01A-02R-1289-07	0	4	1	2	3	1.168262508	0.013421137	2.653527133	2.647737408	0.631290451	0.585761605	2.628114937	4.791925914	4.117719843
TCGA-BP-4355-01A-01R-1289-07	0	4	1	1	2	1.60534841	4.087421347	3.530963098	2.64100778	1.359714697	1.415312607	3.547049652	4.376645068	3.783011064
TCGA-BP-4761-01A-01R-1289-07	0	4	1	1	2	0.689924426	0.101950285	2.506553866	1.787765117	0.381652961	0.244458759	3.806608924	3.16576675	2.148206704
TCGA-BP-4762-01A-02R-1289-07	0	3	1	1	0	0	0.012933018	1.312235007	0.979060833	0.270345938	0.033121414	3.748929079	5.29592489	2.445671469
TCGA-BP-4763-01A-01R-1289-07	1	2	1	1	0	0.704087991	2.353242488	0.214296715	0.505291026	0.55242947	0.108363899	1.406009733	4.646473213	2.871471675
TCGA-BP-4766-01A-01R-1289-07	0	3	1	1	0	1.684957542	3.711660132	3.269993547	2.351182986	2.082433666	0.369740225	2.383859954	4.333211613	2.960008105
TCGA-BP-4768-01A-01R-1289-07	1	2	1	1	0	0.596292672	0.009306092	3.950601644	2.936165971	2.094008417	0.831617487	3.294220552	3.904621583	2.314389387

TCGA-BP-4769-01A-01R-1289-07	0	2	1	1	0	0.214467826	0.02703185	2.477500791	1.438084657	0.804984216	0.233908903	3.465114017	5.008822179	3.921961839
TCGA-BP-4770-01A-01R-1503-07	1	4	1	1	3	0	0.115498451	0.763004799	0.685725612	0.473312675	0.043085295	1.93373767	5.484153485	1.841911236
TCGA-BP-4771-01A-01R-1289-07	0	4	1	2	2	0.877373557	0.022443967	3.953096878	3.559291108	2.104850452	1.063322131	2.992445061	4.499744605	2.899611034
TCGA-BP-4774-01A-01R-1289-07	0	2	1	1	0	2.131427574	3.511517179	2.782780713	3.024805395	1.210697535	0.791808165	2.881715174	4.159891395	5.906239554
TCGA-BP-4777-01A-01R-1289-07	0	3	1	1	0	0.997867369	0.021774719	2.16369065	1.219954871	1.238479344	0.452440925	2.409806333	4.284873633	3.399500069
TCGA-BP-4781-01A-01R-1305-07	1	3	1	1	0	0.381001026	0.009768136	1.725982615	0.682115006	0.596776349	0.093453716	2.753986866	4.366488488	3.318849579
TCGA-BP-4784-01A-01R-1305-07	1	2	1	1	0	0.216212791	1.436291613	1.490989375	0.719595486	0.584613726	0.08425615	4.091294575	5.058474976	2.594424298
TCGA-BP-4787-01A-01R-1305-07	0	4	1	2	2	0.215811305	2.906080166	2.043176883	2.079680694	1.122451154	0.336795332	1.772530668	4.367322472	2.002867832
TCGA-BP-4789-01A-01R-1305-07	0	2	1	1	0	0.345854707	0.018548232	1.617636588	1.578517102	0.895403344	0.169620048	4.035408788	4.839155687	2.548917994
TCGA-BP-4790-01A-01R-1305-07	1	2	1	1	0	0.62494637	0.079796989	1.910753445	1.868105228	1.373273918	0.222131765	2.955911866	4.956381501	2.513745928
TCGA-BP-4795-01A-02R-1420-07	1	2	1	1	0	0	1.378547364	1.045384294	0.762656419	0.345730371	0.099929876	2.690250176	5.02445717	3.029019819
TCGA-BP-4797-01A-01R-1305-07	0	3	1	1	2	0	0.002830028	1.128244096	0.551785924	0.477773797	0.128083384	1.829846913	4.194867801	2.707276508
TCGA-BP-4799-01A-01R-1305-07	1	3	1	1	2	0	0.016889951	0.21925386	0.280877853	0.153744084	0.103315533	1.512596069	4.546268309	2.158520539
TCGA-BP-4804-01A-02R-1305-07	0	2	1	1	0	0.522286465	0.038386699	2.038832196	2.070051813	0.509707602	0.413876018	2.995894216	4.547302794	3.036956483
TCGA-BP-4807-01A-01R-1305-07	0	3	1	1	0	0	0.018248614	1.725276818	0.323882332	0.279938506	0.12026787	2.982712393	4.594876709	2.691322779
TCGA-BP-4959-01A-01R-1334-07	0	3	1	1	0	0	0.004551918	0.938202643	0.535943413	0.472905803	0.157754901	1.843567457	4.159166594	2.500139361
TCGA-BP-4960-01A-01R-1334-07	0	3	1	1	1	2.323957111	0.006482473	2.344797882	2.072321789	0.844721638	0.969521284	2.347728306	3.970290673	2.810835309
TCGA-BP-4961-01A-01R-1334-07	0	2	1	1	0	0	0.00174658	2.064397644	2.153518598	0.6173566	0.401353566	3.268714573	4.672239782	3.517876691
TCGA-BP-4962-01A-01R-1334-07	0	2	1	1	1	0	0.002959709	1.163707391	0.857676029	0.295301303	0.172882101	2.689555348	4.348832003	2.318719422
TCGA-BP-4963-01A-01R-1334-07	0	3	1	1	0	1.939517774	0.001149033	2.11117615	3.097958683	0.958891971	0.678300069	2.432100977	4.365907312	3.300842541
TCGA-BP-4964-01A-01R-1334-07	0	2	1	1	0	0.649716407	3.604388996	2.124121486	1.899379413	0.63399768	0.549431327	3.04534336	3.997076358	2.341084278
TCGA-BP-4965-01A-01R-1334-07	0	2	1	1	0	0.35074225	0.000743541	0.951638719	1.303238084	0.51242405	0.270675457	2.606181267	4.475367959	2.156454783
TCGA-BP-4967-01A-01R-1334-07	1	2	1	1	2	1.092015578	0.000917198	2.781715376	1.893796925	0.959344043	0.98714967	2.828383377	4.468971664	2.485801529
TCGA-BP-4969-01A-01R-1334-07	0	2	1	1	0	1.304671035	3.864633631	2.345607613	3.22898889	2.53447539	1.117411182	3.840974107	3.607149309	2.500155499
TCGA-BP-4970-01A-01R-1334-07	0	3	1	1	0	0	0.00232406	1.116680309	0.173142878	0.356086417	0.217381806	2.407115225	4.680613728	2.972934923
TCGA-BP-4972-01A-01R-1334-07	0	3	1	1	2	0.344986407	3.09722207	2.041677728	1.546456704	1.106738763	0.413334288	3.25599348	4.52259402	2.593554555
TCGA-BP-4973-01A-01R-1334-07	0	3	1	1	2	1.42443531	0.004260284	2.593825273	2.172656994	1.870685576	0.987352635	3.191253009	4.188726773	1.78068882
TCGA-BP-4974-01A-01R-1334-07	0	4	1	2	2	1.841982435	4.60782408	2.715397492	2.495640201	1.913236651	1.057498907	3.841408617	4.614925532	4.640054345
TCGA-BP-4977-01A-01R-1334-07	0	3	1	1	0	0.93019234	0.005495412	1.507915587	2.208554746	1.460824202	0.81054052	3.13590707	4.58749811	2.15984592
TCGA-BP-4983-01A-01R-1334-07	1	4	1	1	2	1.415052274	4.47551773	2.218803341	2.655175976	0.548994354	0.908110607	3.672623234	4.732338543	3.260595907
TCGA-BP-4986-01A-01R-1334-07	1	3	1	1	0	0	0.004707224	3.528616454	2.498926689	1.627591588	0.662725934	1.93973361	4.685920132	4.122451741
TCGA-BP-4987-01A-01R-1334-07	0	2	1	1	0	0.719155168	4.173861106	3.333416105	2.454292512	1.022446188	0.742485524	3.449932158	4.622503033	2.341198164
TCGA-BP-4989-01A-01R-1334-07	0	3	1	1	2	1.315170636	0.009021148	3.035279928	3.449180653	1.636372921	1.190922276	2.194541859	4.282500851	3.783438297
TCGA-BP-4992-01A-01R-1334-07	1	4	1	1	0	2.289295912	0.017707483	4.145359517	4.009158742	3.140370176	1.755985646	2.932108326	3.606548314	5.114552317
TCGA-BP-4993-01A-02R-1420-07	0	3	1	1	0	0.395124999	0.002551925	2.229288736	0.704972322	0.740404338	0.198980384	3.351822202	4.327969362	3.040236118
TCGA-BP-4995-01A-01R-1334-07	1	3	1	1	0	0.378417578	0.002429385	0.38445687	1.519108773	0.908149518	0.785978668	2.406244173	5.476011561	3.90126985
TCGA-BP-4998-01A-01R-1334-07	0	3	1	1	0	1.300317592	0.001823349	1.559596236	1.485636671	1.069171825	0.923665792	2.958427615	4.656961234	2.334390802
TCGA-BP-5000-01A-01R-1334-07	0	3	1	1	0	0.475893795	0.730124735	1.92036674	2.161435076	0.613462009	0.460575985	1.994570468	3.951902136	2.840168812
TCGA-BP-5001-01A-01R-1334-07	0	2	1	1	0	1.170515049	2.679336648	3.188972238	2.939522901	0.923798323	1.273869306	2.579607573	3.583391284	4.472996844
TCGA-BP-5004-01A-01R-1334-07	0	3	1	1	0	1.41897958	0.000847933	2.241343681	1.562160349	1.608022347	0.751745096	2.331064899	4.499813873	4.010784033
TCGA-BP-5006-01A-01R-1334-07	0	2	1	1	0	0.56808617	0.002931101	1.981113136	1.291407103	0.51226895	0.394100133	3.189426362	4.20686195	4.192975615
TCGA-BP-5008-01A-01R-1334-07	0	2	1	1	0	0.938700242	0.00278452	2.243022735	0.818850949	0.768765149	0.536692595	2.787041199	4.468270009	4.150884765
TCGA-BP-5009-01A-01R-1334-07	0	3	1	1	0	0.434590484	0.003794808	2.232197674	2.693364281	1.660462635	0.41143913	1.995370597	4.064586112	3.291977101
TCGA-BP-5169-01A-01R-1426-07	1	4	1	1	0	1.423012411	0.006799752	1.136463114	2.771678687	0.397049283	0.328996854	2.285342966	3.239039028	2.126923932
TCGA-BP-5170-01A-01R-1426-07	0	2	1	1	0	0	0.005462005	0.426148819	0	0.442189495	0.025645186	4.278960276	4.023340581	2.283154683
TCGA-BP-5173-01A-01R-1426-07	1	2	1	1	0	0	0.002210704	1.078225797	0.788875422	0.849215314	0.14894973	3.829256142	4.614869338	1.982973892
TCGA-BP-5174-01A-01R-1426-07	0	2	1	1	0	0.359684594	2.684916401	1.725238367	1.432356583	0.667163772	0.290642178	2.285561913	3.430376571	1.969114783
TCGA-BP-5175-01A-01R-1426-07	0	3	1	1	0	0.362087683	0.002310967	2.255841723	1.872889766	0.189571883	0.362340882	1.868296216	2.977252317	3.041519064
TCGA-BP-5176-01A-01R-1426-07	1	2	1	1	0	0	1.764780991	1.501791204	0.970550463	0.310431536	0.045261114	2.770198283	4.025501557	2.240385465
TCGA-BP-5180-01A-01R-1426-07	0	2	1	1	0	0	0.003118112	1.432323919	1.610467501	0.677272864	0.113489177	2.651534328	3.680276631	1.671541768
TCGA-BP-5181-01A-01R-1426-07	0	2	1	1	0	0	1.951297136	0.92254578	0.475991853	0.190845884	0.080138707	3.309323096	4.126634697	1.523452567
TCGA-BP-5183-01A-01R-1426-07	0	3	1	1	2	0.882595135	0.008184544	2.092311826	1.364508391	1.369686956	0.519427397	2.368065044	4.073321975	2.167888187
TCGA-BP-5184-01A-01R-1426-07	0	3	1	1	0	0	0.001484972	0.246829484	0.983612369	0.763639596	0.103883282	3.290803513	4.619756983	2.827248971
TCGA-BP-5185-01A-01R-1426-07	0	3	1	1	0	0.283902525	0.007035434	1.581564354	1.85192094	0.981195342	0.304500701	2.5329517	3.105193185	2.156643771
TCGA-BP-5186-01A-01R-1426-07	0	2	1	1	0	0.192915556	3.408322392	1.458420177	1.539838253	0.603645167	0.194656556	2.38172673	4.561920524	2.568445607
TCGA-BP-5187-01A-01R-1426-07	0	2	1	1	0	0.322469237	0.03609489	0.327713727	0.415713896	0.505554871	0.163225338	2.972712809	4.571471405	2.380955991
TCGA-BP-5189-01A-02R-1426-07	0	4	1	1	0	0	0.003643754	1.131808144	0.879738592	0.509608628	0.294411767	1.711910306	4.202151051	2.704043319
TCGA-BP-5191-01A-01R-1426-07	1	2	1	1	2	0.230884464	0.002811288	1.72125295	0.760618473	0.789676811	0.302919149	2.373752799	3.605478972	1.8676839

TCGA-BP-5194-01A-02R-1426-07	0	2	1	1	0	0.147432125	0.00435487	1.140829978	1.003049543	0.411097782	0.108545151	3.515938305	4.386233303	1.981904443
TCGA-BP-5195-01A-02R-1426-07	1	2	1	1	0	0.326541301	0.00308553	1.27644857	0.884932423	0.821079082	0.103311851	2.351044878	4.644757672	2.889832309
TCGA-BP-5196-01A-01R-1426-07	0	2	1	1	0	0	0.001244441	2.508625321	2.66075938	1.163162569	0.572314339	2.018624582	4.114193301	3.317361774
TCGA-BP-5199-01A-01R-1426-07	0	4	1	1	1	1.177767518	0.001022962	2.789100543	3.042115879	1.238483639	0.644721485	4.058888209	4.330480497	3.384799079
TCGA-BP-5200-01A-01R-1426-07	0	4	1	1	1	0.595027832	0.001654519	0.699320897	0.347402133	0.092972184	0.129669134	1.840689241	4.501102538	4.297318167
TCGA-BP-5202-01A-02R-1426-07	1	2	1	1	2	0.157284726	0.001866437	2.175817584	0.822043676	0.435312373	0.195173495	2.447233503	4.486669752	3.889582576
TCGA-CJ-4634-01A-02R-1325-07	0	2	1	1	0	1.359990555	4.09631153	2.914722156	1.893691223	1.00078	0.490776939	2.823419659	4.410348852	2.933751193
TCGA-CJ-4635-01A-02R-1305-07	0	3	1	1	0	0.496057878	0.050664794	4.180341777	3.57806773	2.165420375	0.706970775	2.940067289	4.418945894	2.650618375
TCGA-CJ-4636-01A-02R-1325-07	0	3	1	1	2	0.474855485	0.038968472	1.131324538	2.292130912	1.80180541	0.934595166	2.673623308	4.424289	2.446728043
TCGA-CJ-4638-01A-02R-1325-07	0	4	1	2	2	1.090106981	2.489462699	1.721961996	2.296755121	1.077161382	2.035422062	2.99497793	3.357621955	2.014439957
TCGA-CJ-4639-01A-02R-1325-07	0	2	1	1	1	0.562177255	4.366455987	0.78888533	0.709579795	1.768090217	0.669766622	3.894633596	4.443632876	2.097482295
TCGA-CJ-4641-01A-02R-1325-07	0	4	1	2	2	0.584515657	3.844626093	1.236532118	1.783319797	1.572210526	0.847434868	2.290709263	4.42500146	3.270549694
TCGA-CJ-4643-01A-02R-1325-07	1	3	1	1	1	1.783270945	4.73008894	2.50599034	1.803202384	1.533842331	1.078571963	2.47557793	4.816414542	2.963432184
TCGA-CJ-4644-01A-02R-1325-07	0	3	1	2	2	0	1.63859914	0.998378817	0.284234252	0.260690895	0.037082186	2.459541008	4.697158229	1.92350801
TCGA-CJ-4868-01A-01R-1305-07	0	3	1	2	2	0.455111029	0.00899236	1.707432186	1.689446699	0.557304781	0.17390381	2.778305735	4.128216924	2.672824156
TCGA-CJ-4869-01A-02R-1426-07	0	2	1	1	1	0.168019241	0	0.70381218	0.730093044	0.419438058	0.103512838	2.183830702	4.465071028	2.484339154
TCGA-CJ-4870-01A-01R-1305-07	0	2	1	1	2	0	1.577000613	2.465108623	0.286059898	0.2363493	0.089627875	4.618751221	4.399793679	2.567864455
TCGA-CJ-4871-01A-01R-1305-07	0	4	1	2	2	0	0.010240575	0.895669418	1.210770035	0.509272817	0.110813862	1.873783547	4.426735492	2.398905269
TCGA-CJ-4872-01A-01R-1305-07	0	4	1	1	0	0.78055106	0.01735265	0.36998012	1.721118017	0.739959895	0.375749198	2.556940717	4.562211029	2.214122317
TCGA-CJ-4873-01A-01R-1305-07	1	3	1	1	2	1.755922222	2.814782799	2.795265916	2.931297821	0.889465324	0.968702897	2.494457481	3.705865477	2.817124867
TCGA-CJ-4878-01A-01R-1305-07	1	2	1	1	2	2.775154283	4.201457606	4.082553709	2.941211982	1.427852641	1.040966796	3.511234102	4.218929958	3.358352509
TCGA-CJ-4882-01A-02R-1426-07	0	3	1	1	2	1.200809525	0.101620766	1.679798096	1.2886448	1.020575587	0.55736336	3.75225168	4.777912878	2.9429324
TCGA-CJ-4884-01A-01R-1305-07	1	3	1	1	2	0.7168189	3.731630407	3.036996515	2.355790393	1.441506974	0.769331224	2.555101519	4.308543477	3.10171201
TCGA-CJ-4886-01A-01R-1305-07	0	3	1	1	0	0.207326596	2.641810498	2.516191893	0.497867467	1.194526017	0.236263294	2.857277022	4.638912323	3.010869141
TCGA-CJ-4887-01A-01R-1305-07	0	3	1	2	2	1.749845531	0.005099992	2.690202095	3.167109116	1.729094641	0.472907128	2.74016315	3.925630942	2.880569047
TCGA-CJ-4888-01A-01R-1305-07	0	4	1	2	2	0.325479556	0.007163285	1.614219335	1.51395889	1.119779804	0.363902641	2.092567366	4.611958093	2.928205906
TCGA-CJ-4890-01A-01R-1305-07	1	4	1	2	2	0	0.009280381	1.117228287	1.239451618	1.2570863	0.275246907	2.177182835	4.659262273	2.95034074
TCGA-CJ-4891-01A-01R-1305-07	0	4	1	1	2	1.17201262	1.83645358	2.138416662	1.313444979	1.075592462	0.323761818	1.929991215	3.468205289	3.110385879
TCGA-CJ-4894-01A-01R-1305-07	0	3	1	1	2	0.186517586	0.005583598	2.1284737	2.108465033	1.710953451	0.868916474	3.111891005	4.394003897	2.255133461
TCGA-CJ-4900-01A-01R-1334-07	1	4	1	2	3	1.187883384	2.433469406	1.84913641	2.361453116	1.205351977	0.966533204	2.676709713	3.778475411	2.964923847
TCGA-CJ-4901-01A-01R-1426-07	0	3	1	1	2	0.377815782	0.007262797	0	1.675997888	0.527174872	0.636121748	2.639703671	3.920718391	2.629425996
TCGA-CJ-4903-01A-01R-1426-07	0	3	1	1	0	0.663101592	0	0.672734912	1.595857788	0.722899648	0.573206117	3.412762458	4.413932354	2.153531624
TCGA-CJ-4905-01A-02R-1426-07	0	2	1	1	0	0	2.672973968	1.816657901	0.958913689	0.59157728	0.135168212	3.627103775	4.529894838	2.327152745
TCGA-CJ-4912-01A-01R-1426-07	0	3	1	1	1	1.851041868	0.001509211	3.46612286	3.921776832	1.475187154	1.418295236	2.6521489	3.865846646	3.460906571
TCGA-CJ-4916-01A-01R-1426-07	1	3	1	1	2	0.988595558	3.485472331	1.249720428	1.857850886	1.547286784	0.739015378	3.334272157	3.998435461	2.832631718
TCGA-CJ-4918-01A-01R-1426-07	0	4	1	2	2	0	0.008965075	0.19052747	0.636579743	0.683999216	0.148046719	3.748653119	4.619996612	2.701006743
TCGA-CJ-5671-01A-11R-1541-07	0	3	1	1	0	0.208254172	0.002515685	0.396406669	1.025214544	0.26601824	0.06213623	2.581002556	4.229471527	2.31732142
TCGA-CJ-5672-11A-01R-1541-07	1	3	1	1	0	0.165953145	0.001975263	0.581586629	0.722615441	0.48273662	0.113774383	2.307415857	5.719964928	3.302486478
TCGA-CJ-5672-01A-11R-1541-07	1	3	1	1	0	0	0.028167088	1.478277944	0.664259508	0.359597276	0.218019458	2.503065193	3.841979622	2.381608296
TCGA-CJ-5676-01A-11R-1541-07	0	3	1	1	2	0.246040768	0	1.33034676	1.798799912	0.354824508	0.114157694	2.738783705	4.061057122	2.688665644
TCGA-CJ-5677-01A-11R-1541-07	0	4	1	2	2	0.454457648	1.273803053	0.646623124	1.310962635	0.371057006	0.143964704	1.962250668	4.085644488	2.339787113
TCGA-CJ-5677-11A-01R-1541-07	0	4	1	2	2	0.188897329	2.567955199	0.192112893	0.950553756	0.557311308	0.190604408	1.770782959	5.269796676	4.066250641
TCGA-CJ-5678-01A-11R-1541-07	0	3	1	2	1	0	0.001516625	0.96560343	2.390278496	0.447469651	0.1367983	3.894901677	3.863958622	2.655469905
TCGA-CJ-5679-01A-11R-1541-07	1	4	1	1	2	0.242025565	0.193702217	1.314860775	0.981227062	0.506254469	0.099197368	1.811247882	4.033656474	2.21559166
TCGA-CJ-5680-01A-11R-1541-07	0	4	1	2	2	0.374023423	2.34850174	1.410008471	0.670771472	0.543301289	0.177675712	2.623159375	4.336973886	1.701998666
TCGA-CJ-5680-11A-01R-1541-07	0	4	1	2	2	0.549103257	3.231726769	0.557382955	1.020967848	0.69514026	0.301534728	2.134459193	5.489360106	3.512505462
TCGA-CJ-5681-01A-11R-1541-07	0	3	1	2	2	0	0.357373008	2.453061061	1.38783765	0.374592454	0.394120248	1.144862654	5.022030678	2.686026279
TCGA-CJ-5681-11A-01R-1541-07	0	3	1	2	2	0.788588567	1.652071506	0.63733817	1.555663939	1.083498695	0.29712689	1.525891714	5.080083619	3.607155228
TCGA-CJ-5682-01A-11R-1541-07	0	4	1	2	2	0.25865236	0	1.137231381	0.607511076	0.236273989	0.049326277	3.136646177	4.904635809	2.229572327
TCGA-CJ-5686-01A-11R-1672-07	0	3	1	1	0	0.454345727	3.195917412	0.587386105	0.990662128	0.723153376	0.240500267	2.643361252	4.150377044	2.07128558
TCGA-CJ-5689-11A-01R-1541-07	1	4	1	1	0	0	0.001564971	0.478515337	0	0.494921262	0.081557425	1.955174598	5.335156968	3.913489643
TCGA-CJ-5689-01A-11R-1541-07	1	4	1	1	0	0	0.001223054	0.206231681	1.142357149	0.289692259	0.056723255	2.510861922	4.376426592	2.65894131
TCGA-CJ-6027-01A-11R-1672-07	1	4	1	1	0	0	0.004582638	0.365388813	0.81137638	0.723767028	0.13787752	2.081523819	4.234243633	2.331939233
TCGA-CJ-6030-11A-01R-1672-07	0	3	1	1	0	0.414700889	0.006285895	0.15448696	0	0.398829699	0.145585497	1.964018157	5.122001564	3.311356284
TCGA-CJ-6030-01A-11R-1672-07	0	3	1	1	0	0.336535254	0.00212832	0.849992444	0.766033497	0.621697623	0.149726971	1.972890603	4.377249316	1.699001258
TCGA-CJ-6031-01A-11R-1672-07	0	3	1	1	0	0	0.002161361	0.346705071	0.439076371	0.315440161	0.066618208	2.886722042	4.160058883	2.000790893
TCGA-CJ-6032-01A-11R-1672-07	0	3	1	1	1	0.311640506	2.851288931	2.10911951	0.71631653	0.560461944	0.098245346	1.74789661	4.034927941	4.053182177
TCGA-CJ-6033-01A-11R-1672-07	0	4	1	2	2	0	1.63766024	1.366111813	0.755913034	0.494830203	0.089558962	2.575213288	3.944922927	2.500661789

TCGA-CW-5583-01A-02R-1541-07	0	2	1	1	0	0.591676772	4.052905985	2.592899459	0.883617215	0.861111345	0.135909752	3.639381295	4.348544954	2.210209391
TCGA-CW-5584-01A-01R-1541-07	1	3	1	1	2	0.192034205	0	1.375501747	1.219597744	0.361725853	0.077900938	2.434982268	4.577493658	1.951469577
TCGA-CW-5584-11A-01R-1541-07	1	3	1	1	2	0.404722189	0	0	0.898059128	0.520970687	0.088273477	2.073673197	5.414428857	3.512936146
TCGA-CW-5585-01A-01R-1541-07	0	2	1	2	2	0.453036218	0	1.809073543	1.400339192	0.618761727	0.182756145	3.421634393	4.123308616	1.844879256
TCGA-CW-5587-11A-01R-1541-07	0	2	1	1	2	0	1.571991569	0	0.436951964	0.317859889	0.091925232	1.78300603	5.228986222	3.159641473
TCGA-CW-5587-01A-01R-1541-07	0	2	1	1	2	0.346023631	2.30351143	1.250903187	0.928660909	0.25092362	0.109988351	2.115276136	4.243064165	1.899086387
TCGA-CW-5588-01A-01R-1541-07	1	2	1	1	0	0	0.60992489	0.214415295	1.035024553	0.240744691	0.043572797	2.745788295	4.563847738	2.114089387
TCGA-CW-5589-11A-01R-1541-07	0	2	1	1	0	0.185941935	0.002228683	0	0.793812968	0.460241542	0.085309265	2.448138683	5.364664822	3.761130076
TCGA-CW-6087-11A-01R-1672-07	0	4	1	2	2	0	0.000957692	0	1.072392398	0.505766837	0.194626227	2.164018877	5.095042539	2.741296913
TCGA-CW-6087-01A-11R-1672-07	0	4	1	2	2	0.151007964	0.001788038	0	0.667670967	0.22534881	0.098101355	1.861500567	5.08952751	2.048674182
TCGA-CW-6088-01A-11R-1672-07	0	2	1	1	0	0.785253152	0	0.576310789	1.468999335	0.842466868	0.87074812	2.368613269	4.817564485	2.879362729
TCGA-CW-6088-11A-01R-1672-07	0	2	1	1	0	0.269066057	0.000830845	0.143233572	1.157150409	0.705685939	0.494224498	2.294421697	5.988953808	3.072029182
TCGA-CW-6093-01A-11R-1672-07	1	0	1	1	0	0.503878394	0	0.511590369	1.201952621	0.86850692	0.226881117	3.228409258	4.575059324	3.505734741
TCGA-CZ-4853-01A-01R-1426-07	1	2	1	1	0	0.898532584	0.00349869	2.518374178	1.287047587	1.192359564	0.469460273	3.170765857	3.809445526	1.583753112
TCGA-CZ-4854-01A-01R-1305-07	1	2	1	1	0	1.594589478	0.018442175	2.634731898	2.633973303	1.581207125	0.748339311	3.298398402	4.74470267	2.415231672
TCGA-CZ-4857-01A-01R-1305-07	0	3	1	2	2	0.915744436	0.004305919	2.365200269	2.686491416	1.41954548	0.556897921	2.062278362	4.203827139	2.46006717
TCGA-CZ-4858-01A-01R-1305-07	0	4	1	1	1	0.232962292	0.011321278	2.300270673	2.171498991	1.216019437	0.250176776	2.898241063	4.28278253	1.206682195
TCGA-CZ-4859-01A-02R-1426-07	0	2	1	1	0	0	2.206786583	1.923571825	0.525062627	0.183897405	0.049619526	3.406971091	4.046244417	2.410942269
TCGA-CZ-4860-01A-01R-1305-07	0	4	1	2	3	0.180669593	0.016132883	2.222667623	0.236192257	0.610780223	0.148872591	3.364873356	4.058671087	1.245551544
TCGA-CZ-4862-01A-01R-1305-07	0	2	1	1	0	0.841980037	0.676150593	2.079863236	1.510550172	1.58723527	0.652637972	2.646228844	5.207394631	2.708499148
TCGA-CZ-4863-01A-01R-1503-07	0	3	1	1	2	1.503437913	2.714654927	2.964737192	2.377036624	1.039452476	0.673020442	2.464927848	4.440680713	3.170640021
TCGA-CZ-4864-11A-01R-1503-07	1	3	1	1	1	0	0.003741124	0.304782526	0.944204305	0.339247896	0.198271018	1.916532843	5.086555085	3.91968712
TCGA-CZ-4865-01A-02R-1503-07	1	2	1	1	0	0	2.315539959	0.657458522	1.176312296	0.304197288	0.142452343	2.111062371	4.739300152	3.082064034
TCGA-CZ-5451-11A-01R-1503-07	1	3	1	1	1	0.154701058	0	0.546952013	0.380554893	0.275386258	0.156115581	2.254769203	5.25286714	3.903814253
TCGA-CZ-5451-01A-01R-1503-07	1	3	1	1	1	0	0.001461921	1.680046432	0.783811062	0.275661702	0.045383808	3.329132263	4.247439906	2.205918419
TCGA-CZ-5452-11A-01R-1503-07	1	2	1	1	1	0.187568304	0.085229357	0.771323437	0.945320792	0.486458936	0.128893418	2.897084834	5.953733253	3.43239732
TCGA-CZ-5452-01A-01R-1503-07	1	2	1	1	1	0.660294164	0.001175865	2.989820652	1.645310182	0.543856179	0.278967331	2.574299118	3.840758491	2.127274639
TCGA-CZ-5453-11A-01R-1503-07	1	2	1	1	1	0	0	0	0.543440759	0.720641992	0.096091088	1.985372512	6.093916086	3.539701754
TCGA-CZ-5454-01A-01R-1503-07	0	2	1	2	1	0	0	0.397994749	0.978689202	0.384930728	0.090143715	4.465488569	3.870178363	1.802720373
TCGA-CZ-5455-01A-01R-1503-07	0	4	1	2	2	0	0.001566229	1.188579217	1.194499176	0.540960388	0.195997822	2.094599107	4.496149454	2.732916062
TCGA-CZ-5455-11A-01R-1503-07	0	4	1	2	2	0	0.001878297	0.669146058	0.207340955	0.306317378	0.029322559	2.128775247	5.659366625	3.316300066
TCGA-CZ-5456-11A-02R-1503-07	0	3	1	1	1	0	0	1.005660863	0.611576806	0.702463982	0.097791982	1.773520112	5.667111996	3.770393492
TCGA-CZ-5456-01A-01R-1503-07	0	3	1	1	1	0.361545236	0.004610428	0.659887096	1.097074827	0.443836482	0.095051688	1.960679845	4.715898655	1.844180698
TCGA-CZ-5457-01A-01R-1503-07	0	4	1	1	2	0	0.001871947	1.041693854	0.823893606	0.264356898	0.037877467	4.655942687	4.651795441	1.997924637
TCGA-CZ-5457-11A-01R-1503-07	0	4	1	1	2	0	0	0.31974806	0.217174446	0.363744629	0.081709038	2.552876602	5.48312087	3.434549933
TCGA-CZ-5460-01A-01R-1503-07	0	2	1	2	2	0.178766139	0	2.544806623	1.791781101	0.515164411	0.278143617	2.785803433	4.099486278	2.034710673
TCGA-CZ-5461-11A-01R-1503-07	0	4	1	2	0	0	0.000817982	0	0	0.425262001	0.085128661	1.611277761	5.752895775	3.413729761
TCGA-CZ-5462-11A-01R-1503-07	1	3	1	2	0	0	0	0.547457101	0.884478234	0.334157005	0.013833121	2.560753271	6.030425309	2.962310236
TCGA-CZ-5462-01A-01R-1503-07	1	3	1	2	0	0.315643611	0	1.750875506	0.72436913	0.396711	0.167952718	1.596280675	4.407304996	3.291693254
TCGA-CZ-5463-11A-01R-1503-07	1	2	1	1	1	0	0.000925821	0.1587416	1.149595715	0.849694236	0.188552531	2.476169375	5.876228719	3.321652839
TCGA-CZ-5464-01A-01R-1503-07	1	2	1	2	2	0.566704864	0.016483052	1.37413546	1.288896144	0.33383074	0.258236527	2.676229565	4.202021302	2.157188131
TCGA-CZ-5465-01A-01R-1503-07	1	2	1	1	2	0.461977223	3.388320266	1.593366116	2.216757051	0.558821235	0.257673029	3.170245748	4.328608574	2.850251646
TCGA-CZ-5466-11A-01R-1503-07	1	2	1	1	2	0	0.001559612	0.13486527	0.174177041	0.300449807	0.036427042	2.21467347	5.395426139	3.449826987
TCGA-CZ-5467-01A-01R-1503-07	1	4	1	1	2	0.178257311	0.749659159	1.454595473	0.609816436	0.37671964	0.257835206	3.737301347	4.349519417	3.155825151
TCGA-CZ-5468-11A-01R-1503-07	1	4	1	2	2	0	0	0.773305846	0.63896746	0.400195844	0.129302776	2.79625606	5.610525597	3.50140077
TCGA-CZ-5469-11A-01R-1503-07	0	2	1	1	1	0	0	0.654969411	1.038015656	0.506799464	0.110987507	2.196679904	5.846802125	3.878492246
TCGA-CZ-5469-01A-01R-1503-07	0	2	1	1	1	0.521021815	0.007035494	1.749330713	0.826422139	0.627121161	0.3790476	3.453700149	4.143176883	1.705913959
TCGA-CZ-5470-11A-01R-1503-07	1	3	1	1	1	0	1.221150853	0.528076107	0.658843039	0.456464923	0.067720227	2.799392332	6.216355119	3.417958673
TCGA-CZ-5470-01A-01R-1503-07	1	3	1	1	1	0.30949645	2.268615535	1.972143542	1.692977938	0.689809159	0.188861825	2.778071494	4.038588237	2.158427511
TCGA-CZ-5982-11A-01R-1672-07	0	2	1	1	0	0	1.671329809	0.365416943	0.462026477	0.519791828	0.042767844	1.814616257	4.943770301	2.986137701
TCGA-CZ-5984-01A-11R-1672-07	0	3	1	1	0	0.463924825	0	0.471120035	2.012322802	0.480084185	0.272942945	2.371478305	4.01551022	2.154551114
TCGA-CZ-5985-11A-01R-1672-07	0	2	1	1	1	0.52320955	0	0	0.662538404	0.301327179	0.070844373	2.134796699	5.136875757	3.321006503
TCGA-CZ-5986-01A-11R-1672-07	0	3	1	1	0	1.094442525	0.003676907	0	1.641193184	1.059086952	0.353340393	2.754362991	4.305208785	3.492378521
TCGA-CZ-5986-11A-01R-1672-07	0	3	1	1	0	0	0	0.459845018	0.987811928	0.742471077	0.21412618	2.481688939	5.57071948	3.481714558
TCGA-CZ-5987-01A-11R-1672-07	0	2	1	2	2	0.827376009	0.002091335	0	0.755660551	0.878258566	0.108002988	1.9466186	3.897926274	1.822488073
TCGA-CZ-5987-11A-01R-1672-07	0	2	1	2	2	0	0.003697299	0	0.686037588	0.542990534	0.073924141	1.76106075	5.331192056	3.731265438
TCGA-CZ-5988-11A-01R-1672-07	0	2	1	1	0	0	0.00155854	0	0.597344649	0.722106729	0.149294359	2.444263157	5.471700303	3.546578527
TCGA-CZ-5988-01A-11R-1672-07	0	2	1	1	0	0.742847084	0.051836566	0	1.135724676	0.586896841	0.152300904	2.620617865	4.342156296	2.427221448

TCGA-CZ-5989-01A-11R-1672-07	0	2	1	1	1	0	0.001686318	0	0	1.580426325	0.225994342	1.180215377	5.077234774	2.806409725
TCGA-CZ-5989-11A-01R-1672-07	0	2	1	1	1	0	0.002388011	0.201736332	1.469271187	0.923423934	0.156890299	2.368570516	6.139048816	3.728117759
TCGA-DV-5565-01A-01R-1541-07	0	2	1	1	0	0.21598221	0.147948048	2.044108262	1.841534628	0.607181025	0.060612624	2.808781041	4.425221152	2.971746497
TCGA-DV-5566-01A-01R-1541-07	1	2	1	1	0	0.271369153	1.754775718	1.730257525	1.800509629	0.612498376	0.102074253	2.447411353	4.050232603	3.254967035
TCGA-DV-5568-01A-01R-1541-07	0	2	1	1	0	0	0	1.600216917	1.60728277	0.772792002	0.156011391	2.16035127	3.99952996	3.606646288
TCGA-DV-5569-01A-01R-1541-07	0	2	1	1	0	0.523540319	2.800421846	1.22422417	0.473911282	0.315376887	0.191647175	3.055040966	3.980531511	3.330246532
TCGA-DV-5574-01A-01R-1541-07	0	2	1	1	0	0	0	0.878411293	0.449900802	0.286989734	0.075158674	3.062489874	4.640030219	3.004685205
TCGA-DV-5575-01A-01R-1541-07	0	2	1	1	0	0.220976496	2.618437649	1.59568528	1.072779063	0.699321487	0.152394636	3.245848233	4.401346242	2.697837489
TCGA-DV-A4VX-01A-11R-A266-07	0	4	1	2	2	0.723864189	0.008777511	1.469465246	3.092477785	0.483272735	1.247004729	3.540021065	3.975491039	3.086626045
TCGA-DV-A4VZ-01A-11R-A266-07	0	2	1	3	0	2.088380126	0.001464249	4.134156494	4.09955147	0.827987646	1.635135047	3.712173224	4.500507705	5.2101618
TCGA-DV-A4W0-05A-11R-A266-07	0	3	1	1	0	0.692429347	0	3.312902543	2.839964437	1.547301342	0.736033706	3.426720316	5.064179235	3.023919801
TCGA-DV-A4W0-01A-11R-A266-07	0	3	1	1	0	1.437035702	0	1.110446794	1.712310845	1.85154233	0.620807155	2.682355712	4.167041085	3.971679566
TCGA-EU-5905-01A-11R-1672-07	1	3	1	1	0	0.304367909	1.71517762	2.19762	0.393053666	0.27840269	0.126350511	2.914321416	4.178191829	3.044485859
TCGA-EU-5906-01A-11R-1672-07	0	2	1	1	0	0.390061435	0.003351878	0.88199081	0.975147355	0.454588804	0.126510846	2.307575658	4.456642534	3.014323549
TCGA-EU-5907-01A-11R-1672-07	1	3	1	1	2	0.73041789	0	0.533466065	0.909831566	0.211091419	0.108134633	2.136845268	4.145196454	2.673842428
TCGA-G6-A5PC-01A-11R-A33J-07	0	4	1	2	0	1.063409676	0.253753693	2.500969914	2.42208753	0.431000315	0.401042021	3.540532969	2.376218773	2.849086739
TCGA-MW-A4EC-01A-11R-A266-07	1	2	1	3	0	1.252735135	3.115738581	4.203583951	2.079576474	0.802259196	0.729729965	3.156027609	4.137104392	4.341750671
TCGA-T7-A92I-01A-11R-A37O-07	0	0	1	3	0	0.601757592	3.431673819	0	1.697230435	1.175438996	0.795522389	1.189507153	5.907387812	3.619255126

MIR126	MALAT1	MIR4645	HOXA13	TRG.AS1	HOXA10	NEAT1	HOXA3	MIR570	SNHG1	MIR4668	HOXA9	MIR4701	SNHG5	MIR4768
3.968059001	3.747917597	1.726936923	0.057700495	0.601095375	2.598044821	4.385219424	1.781316517	2.558368131	3.493339112	0.509487556	2.397147302	0	5.547738685	4.250147372
1.41984578	4.401119755	2.23244844	0.013404145	0.562712392	1.875857936	5.096628277	1.195314169	3.925372324	3.821597708	0.746920277	1.449905101	0.461299521	5.915725461	3.75597297
2.870616418	4.697585329	1.112116554	0.092139141	0.831607512	2.672351106	4.70915583	1.304297378	3.868014716	2.951101252	0	2.586228437	1.472334667	5.081580443	1.143209465
0.913750017	4.763012775	2.350001864	0.149674128	0.614679468	2.666023931	3.930992519	2.08355336	3.227355734	2.520275991	1.051964341	3.000892874	1.132650651	4.665911172	2.945081595
3.083799185	6.491135786	0.442472668	0.169904218	0.605941323	2.236603884	5.114242111	1.973354101	3.983321776	2.995602952	1.127285762	2.501452831	0.908726808	4.806064638	0.457838749
3.614074236	5.787539827	2.436552739	0.035703844	0.533488123	2.932615546	5.905134481	2.737160207	2.484991103	4.168001138	0.933782216	3.647081638	0.743540489	5.695407577	0.896134874
2.840147078	5.908209079	3.000190686	0.233453563	0.958681117	1.828277025	4.349100753	2.379318949	2.878033703	3.564380248	1.214248801	2.233227498	1.563573534	5.192928041	1.717883665
3.105025885	5.87361583	2.29198141	0.009788688	0.849653327	2.784029492	5.264307684	2.664962082	4.180660614	3.554105153	0.220187569	3.44317842	2.103564963	4.360040717	0.9529552
2.316511444	6.020108717	1.404950831	0.058781465	1.143130555	1.848689531	5.989973403	2.26651707	3.405178475	3.708529864	0.681942846	1.949679808	0	5.826810209	0.652265262
0.836273631	6.018668711	0.604281598	0	0.094767535	0.03084678	8.077310853	0.013358797	4.516446831	3.016514968	0.466231185	0.037661994	0.710019606	3.429338593	0
3.479387271	4.602312339	1.116038271	0.064823024	0.791918566	2.432724311	4.776336716	1.923491707	5.071370605	3.764429091	0	2.903410891	0.892331633	5.438580346	2.665688361
2.633253736	5.808869049	1.543485433	0.198945765	0.955304469	2.705104041	5.650090683	2.048488342	4.365257102	2.570139216	1.981512021	2.830717064	1.635279267	4.463179618	2.317659004
0.629129572	5.347168604	0.681156393	0.627691867	0.41549747	2.183631054	5.513769844	1.993406777	3.783825541	3.573699007	1.779811059	2.051239973	0.317118332	5.13690264	1.527902503
1.73553827	5.025577248	1.050826398	0.027819922	0.720181484	2.323949393	5.356507981	2.364858488	2.9645743	3.762992846	0.557341598	3.222908303	0.836671679	5.28825331	3.174595301
0.66496703	3.572383149	0	0.721696467	0.647445644	2.906542267	3.304376969	2.117815046	3.402964279	3.291920715	0	3.592600673	0	5.310717513	0.291827718
1.613299092	5.076717826	2.870902513	0.919214324	1.26512407	2.507321645	5.63138298	2.840243312	3.985393759	3.411075305	0.637600901	2.946829554	0.945782377	4.641664944	2.380064296
2.797189021	5.091543926	2.471929031	0.17150128	0.615694592	2.599119126	5.131860838	2.235516859	4.003808242	3.787560827	1.256781898	3.200929178	1.660669848	5.578683274	2.869798591
2.419954674	5.935096591	1.976570439	0.112107499	1.379688286	2.440708494	5.713900611	2.33126972	4.165717952	3.9473798	1.465367732	3.045959275	1.715109897	5.294410684	3.221978343
1.572987384	5.838408607	1.85459443	0.098180621	0.74400662	0.480821006	5.773018017	2.045100475	4.459493242	3.609368292	1.286334348	0.445865612	0.438641244	5.303554544	3.098067208
3.580495836	6.888385951	2.460227632	0.140466171	1.179237559	0.637251549	6.24428017	1.814081157	5.154967577	3.054877016	0.947666956	0.557968127	1.90760408	5.175969874	3.795494255
3.726704648	5.735453557	2.034263171	0.117995367	0.723089364	2.325010152	5.38849661	2.185360204	4.168390335	3.61561611	0.94773379	2.665596408	1.768969697	5.584478516	3.634851908
0.23301847	3.997712295	0.471974998	0.012624013	0.37788826	1.353601218	4.492766533	3.5669726	3.573618705	3.402743287	1.434471041	2.176971008	0.960524272	4.521408268	4.257111581
1.987156434	4.99612224	1.004997069	0.100859443	0.596053923	2.53348489	4.696429671	1.633298228	3.458321372	3.19438712	1.075623921	2.418229905	0	4.857638392	3.453350613
0.937012467	6.00521743	1.817192048	0.239847645	0.565575374	1.894981357	4.922503906	1.904620189	3.352802016	3.981065724	1.310756184	2.428769483	1.61190372	6.227122762	3.121632409
2.201883789	5.836435951	2.267808283	0.051173121	1.166729147	2.032533373	5.731967322	1.551154481	4.317016402	3.25594591	1.262533475	2.39508779	1.649668785	5.138215093	1.408396784
1.772308782	5.436140856	1.157645276	0.246539273	0.726013296	2.878473764	5.187336992	2.501508969	4.190822687	3.180577432	1.89065918	2.782991584	1.587825847	4.807505474	2.80265209
1.471135113	4.876757588	0.407179562	0.049014789	0.241705691	2.251756462	4.745908112	1.033295359	2.533271362	1.224662058	0	1.997299976	0.845679395	4.510226832	3.686598502
0	3.510325795	0.269095896	0.035392061	0.604004413	1.728038985	4.288729592	0.242861749	2.246040748	3.456746359	0.293438355	1.659023056	0.32264305	2.654214293	0
1.084989947	5.625907959	3.763939265	0.285275024	0.931885879	2.092703938	5.064570934	1.963384037	2.97791176	2.61198596	2.96500135	2.241511438	0.589107328	4.073372245	0.515359044
3.261716658	6.054403844	0.480430209	0.123981815	0.509568694	2.679200811	6.115562879	1.850978572	2.766201488	4.456092642	0.520724562	2.908692104	0.78614411	6.202481474	4.175041842
1.728114494	4.372828022	0.301135488	1.822602526	1.009093115	2.243836532	5.663941936	1.678005249	4.811754843	3.556261125	0.595169746	2.677846869	0.648363499	5.436157932	1.427963633
3.515514061	3.854519853	0.91546441	0.025579491	0.453111621	2.592470597	4.693439342	2.017150133	1.741947858	3.387507318	0.405917503	3.287349265	0	6.303266965	3.168570224
0.409433844	5.31797979	0.626101982	0.015738655	0.229251688	1.749641096	5.467803518	2.799696173	3.887837937	3.403801466	0.84556707	2.198965514	0.914964945	5.288254567	1.936248894
1.928379821	4.432907099	3.612311903	0.167502434	0.922366948	1.58630474	3.925422725	2.187674006	2.565161869	3.475790942	0.889010036	1.322602856	0.559032149	5.476525716	2.078413108
3.300932195	4.349882669	3.803564235	0.153944602	0.388513171	2.044484416	4.39337235	2.704390331	1.749206857	3.433279198	0	2.429385627	0.603572966	5.905759531	1.869292873
3.818200148	4.520744496	1.664523628	0.020913774	1.220739398	2.473184413	5.525111951	1.519532038	3.081477687	2.965619186	0.339403291	2.376455175	0	4.756067334	1.002583709
4.397349195	4.776544913	1.520459576	0.275219767	0.74583083	2.551732403	5.70639904	2.035046552	4.149125458	3.708597692	0.666615503	2.554069799	0.98470449	5.865443763	1.807430667
3.086594428	4.364791381	2.837152844	0.151785226	0.881101609	2.747472268	4.847700263	2.336156361	2.883627601	3.253072683	0.333454219	2.664978346	0.900532917	4.970469023	0.988328055
3.86082518	5.340758921	2.179478603	0.035152582	0.388254087	2.534581271	5.034586286	2.710393394	3.557930367	2.911492992	0.675696152	2.833795724	2.110599653	4.750288688	0.646233865
5.244659635	5.051183221	3.368508647	0.299149227	0.548186436	2.945814032	5.667778183	2.911306994	1.898436256	2.722702137	0.622977423	3.06733444	1.765629505	5.039018517	1.929685304
3.905929985	5.055449372	1.764010142	0.225657198	0.302550298	2.960932301	6.025853104	3.08732919	2.875979185	3.906498498	0	3.795036726	0	5.682815261	1.412713096
4.422820041	4.854911975	2.078866888	0.124502743	0.566552217	0.619050422	5.668669623	1.670116343	3.464996097	3.394326434	0.628285891	0.469529296	1.145825795	5.448630691	0
2.796341499	3.921306145	1.157603026	2.361777052	1.020662142	2.552435517	4.570205475	1.855683625	1.480942351	2.436064881	0.745861691	2.51326432	1.002109699	5.739307421	0.714032097
0.30732446	2.227532816	1.208132624	0.072559414	0.730865078	2.545839246	2.868830357	1.965546974	2.042856199	2.780808995	0.365451193	2.381430997	0	5.897863661	1.669757997
1.22312295	4.782336738	1.073734255	0.152528348	1.931775831	1.97731265	4.831261479	2.149840309	1.461597045	3.327336155	0.856182049	2.348042834	1.887838913	3.636773849	2.670185804
0.266700929	1.778515212	0.534360643	0.05758545	0.053266548	2.886990351	2.379100364	0.984053235	2.008942453	2.865172196	0	3.077537601	0	5.948036564	0
1.088715855	2.795809746	0	0.062042156	0.065411709	2.280509178	2.790922978	1.073667417	1.403670142	3.132464977	1.713925617	2.089846863	0	6.138607842	0
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1.684468554	4.485846214	1.995462559	1.116179128	0.926982582	2.234591573	4.64131882	1.797765623	4.046348307	3.06					

0.560913343	4.956451949	1.957974061	0.10493718	1.770118724	3.147569458	5.113360767	1.962941626	3.538361731	3.299422374	2.489608751	3.390664417	0	5.356601455	3.817642343
0.319461844	4.602271725	0	0.640835007	0.292144286	2.88522097	4.674512235	3.009966978	2.58391118	1.734594173	1.768853898	3.694074673	0	4.426970278	1.832844652
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1.203042764	4.559148684	1.544350615	0.517678811	1.209941908	2.239564993	3.290640285	1.737679105	2.524757931	2.45275272	0.337482793	2.118942064	0	5.03531436	3.550909982
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1.868298548	5.773047445	2.485092822	2.58424068	1.447030301	2.412657712	5.612191031	2.570833003	3.963665488	4.178117092	0.756857242	2.264437936	1.605905937	5.91051955	2.091731588
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1.905218514	5.947019279	2.011108887	0.118566446	1.085858892	3.315660595	5.851424505	2.238190596	3.917921139	3.012009516	2.445024318	2.860267255	0.991212648	4.18598237	1.177291317
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3.99190243	4.935969428	1.488792468	0.055898042	0.869525412	2.473262297	4.920417228	2.102680973	3.694933378	3.505045794	1.21710399	2.777756616	1.154883071	5.321309436	2.941792628
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3.807998722	6.934585949	0.742446101	0.048185499	0.550174561	2.520806697	6.488786948	2.119578456	4.163318456	3.375373761	1.793980535	2.499150253	2.569346946	5.410757077	5.338064522
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0.289200308	3.314016973	0	0.451273545	0.717317294	2.287856498	1.734926302	0.694028455	1.650552208	2.369937817	0	2.007531285	0	5.036134729	2.608606843
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1.4364400528	6.387308614	2.253227495	0.060432916	2.207087368	1.807070755	5.828997107	2.121568441	4.515344036	3.466007728	2.362955207	2.528743231	1.591945699	4.916247538	3.465394403
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4.412112623	7.141038259	0.296960069	0.213091189	0.38133007	1.516508077	6.71230981	2.420251814	5.429329644	4.112759124	2.91391672	1.888173828	2.21146		

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0.524873721	5.170019753	1.294661398	0.188196121	1.640530537	1.750389927	4.796659981	1.746772321	3.795090755	3.322921611	2.158157967	1.866899105	1.473073125	4.767224162	3.097701295
2.73950597	5.56186813	0.702070714	0.155595028	0.989566206	2.734478467	5.986588152	2.01085247	3.748442872	2.8849312	1.250381891	2.66527283	0.595271625	4.608924949	2.531860578
0.281195918	2.800568436	1.129482292	0.16180618	0.465610922	0.639322325	2.051269267	1.064711707	1.3269004	1.473834762	0	0.670679679	0	4.139361721	1.574116094
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0.462906592	5.167925727	1.417102233	0.777751062	0.892568147	2.657382398	3.773933807	2.076789061	2.93173578	3.468916961	0.940179691	2.599003386	0.820190681	5.883930416	3.176197185
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0.162788759	1.868777984	0.611112868	0.008614369	0.048818586	2.554655325	1.554684342	1.582455891	0.504556425	1.438886828	0	3.054966341	0	3.233466039	0.631169089
0.215524945	3.570645378	3.566799379	0.322428076	0.699052249	2.932011496	3.460739178	1.729221839	1.880752261	2.172423784	0.257799238	2.904658807	0	3.836821484	0.799344453
0	3.925193826	0.735215172	0.014444523	0.164553414	2.466827766	3.660645748	1.890196434	1.440802051	2.056977851	0.242178796	3.056610296	1.011088371	3.859766051	0
0.708380124	4.330381561	0.765394966	0.067196089	0.989216877	0.806230723	3.005028325	1.642102221	2.96446465	2.855462863	0.469791614	0.682461656	0	5.044043404	1.586197519
1.165618209	4.434976296	0	0.092872465	0.386325713	2.040224822	3.919040888	1.747830964	3.490717379	3.647019729	1.238017551	2.378700557	0.588073186	5.646497231	1.192381275
0	4.850272649	1.262950844	0.15906509	0.30743067	2.3438705	1.925263401	1.250526549	0.530562158	1.152203127	0	3.209818282	0	5.082065348	1.603718656
0.230562115	4.33292078	0.654333905	0.041189008	0.309127689	2.794193679	3.757753986	1.582222092	3.271376046	2.953318382	0.506756307	2.278413642	0.30311636	5.888480291	0.844953238
0.632881274	3.419270588	0.266184896	0.008824286	0.058738971	2.222142879	3.464692436	1.631290592	1.193306742	1.853115341	0.290289569	2.907958689	0	3.288747536	0.507592362
0	2.922117426	0	0.010717179	0.056291485	2.546506685	4.134187854	1.526939122	1.797443114	1.984871535	0	3.061623766	0	4.273620279	0
0.466854048	4.388268181	0	1.360475603	0.323824713	2.455687814	3.963723239	3.29474862	3.093141368	3.230743725	0	2.64723395	0.330857499	6.392454753	2.17348539
0.192827421	2.541463235	0	0.006879425	0.125964595	2.998924718	2.541015086	1.882580749	0.17032336	1.980001312	0	3.405297064	0	4.397021891	0.21941153
0.960393306	4.278402891	0.231454818	1.169145367	0.927475806	2.173062839	3.71749893	2.303466625	1.911792711	3.225188397	0.820224098	2.192172193	0	5.395577768	2.558015765
0	3.537265171	1.021108815	0.099894484	0.038255131	2.005442579	2.524747428	1.189841723	1.566238007	1.380712072	0	3.304067577	0	3.147126004	0
0.584740405	3.285641918	0.633843301	0.312920681	0.693451972	2.062847664	3.002266816	2.068016621	3.15103983	2.718826672	0	1.821207894	0	4.760244595	1.226182491
0	3.847073609	0.710043071	0.094081874	0.017002402	1.800344592	3.644708032	1.099442676	1.594069327	1.419560006	0	2.784874251	0	3.161389543	0
0.377608439	4.33712831	1.406729048	0.130935025	0.618906069	2.515973021	4.562374485	1.969940294	2.223555733	2.660333134	0.787930176	2.561482719	0.853858666	5.870515418	0.426168187
0.789692626	4.13304049	0.851531855	0.074195277	0.220297036	2.142149465	3.394358205	1.81446931	2.799059205	2.000488073	0	3.317636115	1.399786253	4.335634228	1.081364438
0.748723635	4.542553772	1.524799247	0.220156253	0.43299806	0.218831828	3.749871593	1.961247176	2.194359564	2.14584927	1.162937028	0.2520			

0	5.522699353	2.689111489	0.360825151	1.262882206	4.320321537	4.053075182	2.714800027	3.078897298	2.421349184	0.414681417	4.866230064	0.454180906	3.826829034	0.959779173
0.25607269	4.202591533	1.441068695	0.004675355	0.147864117	3.341139152	3.858889249	2.162658606	1.961003635	1.988001245	0.305495063	3.339681409	0.607952613	4.226529677	0
1.315884081	4.036495012	0.769520304	0.045452417	0.404994317	2.873495332	3.34043279	1.596765027	1.994030903	2.801435467	0	2.297848506	0.36412546	4.590064841	2.06264384
0.34788177	3.666668255	2.612912991	0.089230956	0.337741934	2.668698075	3.217771682	2.463685412	0.77977839	2.179471925	0	2.847662805	0	4.864089623	2.510553327
0.855254578	4.182654346	0.920779583	0.212731903	0.7292205	2.696453525	4.023293684	1.718900865	2.441260761	2.330029705	0.576498824	2.088279087	0.348122801	4.141710521	3.488361955
1.546696418	4.334803845	0.277521534	0.0590043	0.311771692	2.556231852	3.928154436	1.287666474	2.011058497	2.831507522	1.736915828	2.197146766	0	5.827271535	0.28772032
0.625234595	3.124180219	1.26138015	0.176252251	0.934904886	1.367192034	2.940472723	1.553165551	2.113524078	2.283029456	0	1.457081596	0	3.984147149	0.501208336
0.726220502	3.733628288	2.859919678	0.020882647	0.765741049	2.606669094	3.774749384	1.944891407	2.431816515	2.92018202	1.640937515	2.490788608	0	5.17577045	1.323727809
0.894199717	4.233051054	2.671466024	0.358618672	0.613640208	2.35460825	4.938803268	2.385642172	3.003971308	3.470430685	1.625326375	0.224848393	0	5.020851138	2.982480035
4.021373792	6.110725635	1.633550963	0.089050373	0.23440051	2.706021727	6.933021827	1.519027316	3.124335858	4.366305237	1.108702852	3.778425691	2.074692521	5.753212334	5.079807611
4.189671775	5.164486227	2.511978631	0.099250697	0.317768253	1.676330218	5.508614937	1.553212843	3.082061368	4.525635085	0.798426241	2.334270972	2.004166009	4.745051299	0.552046472
3.357590338	5.519639638	1.551823626	0.45173789	0.393823884	0.395382222	5.565281639	2.264529625	3.350681368	3.942116961	0.382479529	0.583149674	1.008583378	5.14881718	1.284427122
0.695077356	2.445455997	0.423997575	0.220965527	0.446854201	2.013373032	3.011371377	0.682404511	2.908576551	3.659960826	0	1.775286961	0	5.45849074	1.942579028
0.966784178	3.387732749	1.409107991	0.032507492	0.415706906	2.17747667	3.144753191	1.386794575	2.920618829	2.177578079	0.581803129	2.337985717	0	5.141490625	0.955861904
0.366806926	3.39346931	0	0.145926002	0.215206258	0.293597204	3.591261901	1.728756011	3.747431096	2.078370189	0	0.155404517	0	4.813831051	0
2.484236953	3.942468994	1.181551939	0.006908418	0.675386258	0.203476521	4.000322056	2.203457323	2.007253523	3.057483548	0	0.143754813	0	5.685621307	5.444857568
2.142950786	4.242449026	0.323590721	0.053899864	0.608850592	0.855620454	5.10772876	2.193627794	2.376166403	3.836289381	0.352290195	0.831722139	0.691207623	4.922463767	1.033186741
1.241189762	5.892934771	1.325179977	0.292898013	0.31686831	3.132856658	7.536871571	3.224932428	2.639000476	2.974541937	1.164885492	3.693959674	0.941192128	3.542703634	0.4768174

The test set

id	age	grade	stage	M	T	MIR324	XIST	MIR210	MIR25	GABPB1.AS1	LINC00894	SNHG7	FGD5.AS1	MIR22HG	MIR126
TCGA-CJ-6033-11A-01R-1858-07	0	4	1	2	2	0.423758576	1.774511129	0.605435533	0.541240885	0.578250392	0.210684135	2.766387983	5.10113994	2.869272594	0.925799049
TCGA-CZ-5984-11A-01R-1672-07	0	3	1	1	0	0.184250443	0.001103974	0.187391932	0.932194695	0.548654848	0.213201265	2.348907139	5.203332882	3.741524511	0.621520036
TCGA-CZ-4865-11A-01R-1503-07	1	2	1	1	0	0	2.328843557	0.547993771	1.493237877	0.591588621	0.260960168	2.585594648	6.118883206	3.535878892	0.676220939
TCGA-CJ-5678-11A-01R-1541-07	0	3	1	2	1	0	0.003427006	0	0.645512292	0.294260866	0.035607773	2.332400781	5.261142852	3.362677958	0
TCGA-CZ-5458-11A-01R-1503-07	0	3	1	1	2	0.123968392	0	0.630552675	0.163031905	0.505320481	0.084603019	2.417820495	5.861753631	4.651786329	0.161217145
TCGA-CZ-5454-11A-01R-1503-07	0	2	1	2	1	0.24105013	0	0.45451078	0.97810819	0.750956274	0.247111086	2.083761756	5.751243723	3.57660018	0
TCGA-CW-6090-11A-01R-1672-07	1	3	1	1	0	0	0.002200799	0	1.061220927	0.703789363	0.265571536	2.11665476	5.436677986	3.273014934	0.237545779
TCGA-A3-3387-11A-01R-1541-07	0	2	1	1	0	0.40325	0	0.219306143	1.053073685	0.498897888	0.129943891	2.192274703	4.988400416	3.94430098	0.510880692
TCGA-CJ-5679-11A-01R-1541-07	1	4	1	1	2	0	0.002166821	0.347484005	0.919598345	0.566013457	0.191733525	2.25232309	5.446084945	4.155398913	0.234157759
TCGA-CW-5580-11A-02R-1672-07	1	3	1	2	2	0	2.062755009	0.159639041	1.250366488	0.709588861	0.274604674	2.45621765	5.798934457	3.72323509	0.540290102
TCGA-B0-5701-11A-01R-1541-07	0	4	1	1	2	0	0.001137543	0.514771648	0.458719273	0.591676841	0.133523426	2.420296189	5.390304842	3.077164498	0.244836818
TCGA-A3-3358-11A-01R-1541-07	0	2	1	1	0	0.617148764	2.619590617	0.446112932	1.6486326	0.535032156	0.280167165	2.605699634	5.867546222	3.768518254	0.768428925
TCGA-CZ-5465-11A-01R-1503-07	1	2	1	1	2	0	1.71248891	0	0.667027567	0.546544127	0.08742266	2.343893448	6.062220341	3.566486167	0.52171633
TCGA-CW-5581-11A-01R-1541-07	0	3	1	1	0	0	0	0	1.13344063	0.280737195	0.126953999	2.468011887	5.162362558	3.041573084	0.557686815
TCGA-CW-5591-11A-01R-1541-07	0	2	1	2	2	0.356504127	0	0.651529711	0.247173854	0.358800679	0.10696826	1.754311687	3.946357119	1.768833503	0.453504367
TCGA-CZ-5467-11A-01R-1503-07	1	4	1	1	2	0	0.91865786	0.466111847	0.414624977	0.24065099	0.059383701	1.540283685	5.309006702	4.653360075	0
TCGA-CZ-4863-11A-01R-1503-07	0	3	1	1	2	0	1.469485604	0.61773031	0.765438914	0.450146277	0.138050512	2.448819075	5.899575892	2.984530673	0
TCGA-CW-5585-11A-01R-1541-07	0	2	1	2	2	0.166912829	0	0	0.575907052	0.252314587	0.055343358	2.445829264	5.235789152	3.824903846	0.40406197
TCGA-B0-5697-11A-01R-1541-07	0	2	1	1	0	0	0.001510918	0.464372586	0.320339512	0.341932448	0.144951991	1.648054333	5.379947805	3.887466888	0.31695593
TCGA-CJ-5676-11A-01R-1541-07	0	3	1	1	2	0	0	0	0.718323148	0.400810218	0.066464774	2.231318537	5.252813564	4.17967765	0.213402414
TCGA-B0-5711-11A-01R-1672-07	0	3	1	1	2	0	0.000983712	0	0.720162788	0.804260014	0.12756973	2.450175869	5.73739922	3.388798765	0.214047635
TCGA-BP-4163-01A-02R-1325-07	0	3	1	1	2	0.272726949	2.040929114	1.640956868	2.01862511	1.411722627	1.022938632	1.338396533	4.299806039	2.354249151	0.630756013
TCGA-A3-3320-01A-02R-1325-07	0	0	1	1	0	0.933075831	5.156265877	2.369170925	1.688331196	1.506302809	1.258989153	2.571875303	4.427215191	3.773057894	3.167991903
TCGA-B0-4703-01A-01R-1277-07	0	4	1	2	2	0.672809855	0.006008735	2.008949369	1.755613718	0.75414063	1.196547269	2.535482013	4.617255319	2.648641346	1.74361757
TCGA-CW-6097-01A-11R-1672-07	0	4	1	1	2	0	0.004021632	1.124444102	1.217036168	0.854860515	0.12942451	1.873182166	4.499160698	2.654861391	0.726439739
TCGA-MM-A564-01A-11R-A266-07	1	2	1	3	1	1.058869154	0.012243211	3.29630378	3.229203939	1.149919031	0.602258795	5.481691476	4.067585269	1.945764409	4.011717959
TCGA-BP-5192-01A-01R-1426-07	0	2	1	1	0	0	0.001044814	2.341785786	0.894907459	0.542413651	0.10175281	3.932624126	4.095907131	2.27631581	0.887040873
TCGA-CJ-4920-01A-01R-1426-07	0	2	1	1	0	1.193708723	3.881392462	1.39972301	2.07673017	1.504410628	0.490332421	2.950143258	4.267720346	3.694358016	2.268063817
TCGA-B2-5641-01A-01R-1541-07	1	3	1	1	0	0.190502781	0.002286993	0.193743883	1.527146045	0.734261965	0.084077544	1.502786509	3.979546049	1.975733501	0.802402783
TCGA-CZ-5459-01A-01R-1503-07	0	3	1	1	2	0.23768756	0	1.186819468	0.967320952	0.638747371	0.196521715	4.331374831	3.710171403	1.921392484	1.846358521
TCGA-A3-3323-01A-02R-1325-07	0	0	1	1	0	0.662914344	0.015676745	1.755114512	3.294837527	2.408991321	0.723248165	2.624576036	4.32224568	2.603038567	3.733014442
TCGA-BP-4161-01A-02R-1325-07	1	3	1	1	0	0.916059426	0.003590823	2.423548561	2.305100494	1.962033232	0.827869509	2.284346644	4.481253905	2.488821332	1.651960099
TCGA-B8-4143-01A-01R-1188-07	1	3	1	2	2	1.21249948	4.165786343	4.837604519	4.544291224	3.604429472	1.849408169	4.649642183	4.757716997	3.650259039	1.798999734
TCGA-CZ-4866-01A-01R-1503-07	1	3	1	1	0	1.11195523	1.544592065	2.770096937	1.706291533	1.430546515	1.143383027	2.0403374	4.391367971	3.194201099	0.436316162
TCGA-B8-A54J-01A-11R-A33J-07	0	2	1	1	1	1.436364766	0	2.480377157	2.360836301	1.268324615	0.558379256	3.469957864	4.257956734	3.382110947	4.449486696
TCGA-B2-3923-01B-10R-A277-07	0	2	1	1	1	0	0.41290208	0	0	3.444476789	3.01015859	2.544793738	6.184994672	3.185586281	0
TCGA-CW-5580-01A-01R-1672-07	1	3	1	2	2	0.822706371	3.988939231	0.740611277	1.608772472	0.413818238	0.261122709	2.610379222	4.687847665	2.851133733	0.194970048
TCGA-AK-3460-01A-02R-1277-07	0	2	1	1	0	0.552959005	0.137164071	3.257088509	1.520229434	0.910790853	0.486736863	4.019050271	4.476588074	3.180766873	0.943503489
TCGA-BP-5177-01A-01R-1426-07	0	3	1	1	0	0.560384087	3.85755208	1.384587678	1.179998043	0.497312606	0.314782773	3.593211966	4.269564724	2.504992065	0.502796775
TCGA-B8-5549-01A-01R-1541-07	0	3	1	1	0	0.204826956	0.088731557	1.864124271	0.85884822	0.210562193	0.06106227	2.420331412	4.339122449	2.621845476	0.487495714
TCGA-B2-3923-01A-02R-1325-07	0	2	1	1	1	0.456180805	0.010514297	0	1.31476661	1.267547891	1.03844722	3.1676088	5.533900654	4.05696761	1.153869862
TCGA-CZ-5982-01A-11R-1672-07	0	2	1	1	0	1.018843031	3.525357146	1.133716224	1.464333681	1.226578577	0.218607138	1.815877469	4.372073961	3.597941036	0.825979739
TCGA-BP-4982-01A-01R-1334-07	0	3	1	1	0	0.528269473	0.004474216	2.09228421	1.98111767	1.385315008	0.810564826	2.815815321	4.673657725	3.033148678	2.25921154
TCGA-A3-3358-01A-01R-1541-07	0	2	1	1	0	1.698426199	3.862673901	0.972802975	2.477605536	0.621599718	0.65213548	3.02244565	4.585153714	2.693791487	2.290739969
TCGA-CZ-5461-01A-01R-1503-07	0	4	1	2	0	0.411042563	0	0.834435981	1.384936326	0.273179689	0.105554461	2.775875414	4.701756389	2.178875006	0.785700531
TCGA-6D-AA2E-01A-11R-A37O-07	1	2	1	3	0	0.511810328	1.731167988	1.663528531	1.829861529	0.718514977	0.903969374	2.649458624	4.794021197	4.41771234	1.92809458
TCGA-AK-3461-01A-02R-1277-07	1	2	1	1	0	1.680807472	0.095918725	2.913483639	2.073420641	1.7762912	0.838857617	3.092023539	4.435968858	3.433181986	2.45742822
TCGA-B0-5095-01A-01R-1420-07	1	3	1	1	2	0.220065499	0.001335316	2.066216352	1.947216828	0.98769993	0.636531713	2.780366091	4.455359959	2.511883868	1.665076198
TCGA-B0-4821-01A-01R-1503-07	1	3	1	1	2	2.035045434	1.651470185	2.839789693	2.119109671	1.064718889	0.944967701	4.005091109	3.791807438	2.791062943	1.35346636
TCGA-B0-5092-01A-01R-1420-07	0	3	1	2	0	0.632245508	3.586473321	3.833167944	3.100547408	1.299675714	1.423352529	3.051631539	4.145583717	3.430017446	1.552113052
TCGA-CJ-4908-01A-01R-1426-07	0	2	1	1	0	0.452316615	0.00099476	2.832660928	1.398680042	1.027664994	0.76006718	2.701618271	4.598213085	3.140376942	1.706768167
TCGA-CJ-4907-01A-01R-1426-07	0	3	1	1	2	0.313447316	0	2.540566054	1.296334715	0.521932354	0.702729728	2.755268175	4.557640846	2.379969509	1.083487871
TCGA-B2-5635-01A-01R-A277-07	1	2	1	1	0	0	0.028037144	1.521759206	2.065521397	0.991748208	0.688908263	2.46337974	5.07251543	2.196885234	1.668864302
TCGA-BP-5182-01A-01R-1426-07	0	3	1	1	0	0	0.002915758	1.151785301	0.214135977	0.332246848	0.128993428	2.529344188	4.37165686	2.935149893	0.211792875
TCGA-DV-5576-01A-01R-1541-07	0	2	1	1	0	0.191779535	3.057082851	3.669626322	1.711383492	1.068636834	0.249594272	3.325178096	4.873254782	3.360847648	1.522719244
TCGA-BP-4776-01A-01R-1289-07	0	2	1	1	0	2.221334608	0.011830624	2.453075246	2.909281129	1.513441117	0.615489174	4.081222001	4.022962159	4.121500115	4.410940447

TCGA-B0-4817-01A-01R-1277-07	1	3	1	1	2	1.156776115	0.060197827	3.405750898	0.628990834	0.592354292	1.045149546	3.794793508	3.592975639	2.559830443	0
TCGA-B0-5691-01A-11R-1541-07	1	3	1	1	0	0	3.062984332	1.528468384	1.346312615	0.660658354	0.288451212	3.074822307	4.808230859	2.742764568	0.686869226
TCGA-BP-4760-01A-02R-1420-07	1	2	1	1	0	0	0.00588699	1.222535254	0.661851209	0.554537904	0.040338753	3.024115857	4.921743925	3.379207547	0.253086894
TCGA-B2-3924-01B-03R-A277-07	1	2	1	1	0	1.097213651	0.015313894	2.033396024	2.184227652	3.823327066	2.79081453	3.072296226	4.511198259	3.693542127	3.955402839
TCGA-CW-6090-01A-11R-1672-07	1	3	1	1	0	0.168283241	0	0.324165337	1.652825431	0.495445675	0.070944209	3.126049389	4.105988676	2.305816289	0.217875847
TCGA-B0-5106-01A-01R-1420-07	0	2	1	1	0	1.194474761	0.015585828	3.660425916	1.74951743	1.779557553	1.504591441	3.504751716	4.513801753	2.192403498	2.204178876
TCGA-CW-5591-01A-01R-1541-07	0	2	1	2	2	0	0	0	0.884364853	0.392099127	0.032067906	2.134041237	5.219441694	3.04480513	0.503857221
TCGA-BP-5190-01A-01R-1426-07	0	3	1	1	0	0	0.003541026	1.47564669	1.969182875	0.899056922	0.490969565	2.063121368	3.658786395	2.700555056	0.253478099
TCGA-CJ-5675-01A-11R-1541-07	1	3	1	1	1	0	0	0.893478033	0.642984286	0.363431422	0.063173038	2.337147437	4.191249777	1.801340786	0
TCGA-CJ-4640-01A-02R-1325-07	0	4	1	1	2	0	0.018330484	1.109978636	0.649725057	0.46094429	0.141803605	2.671416576	4.706583405	2.615016021	0.459205386
TCGA-B0-4690-01A-01R-1277-07	0	3	1	2	3	0.365625446	0.012804219	0.911540759	1.807278267	1.532902412	0.548318233	2.001355464	4.749818674	2.648192309	0.250999292
TCGA-BP-4765-01A-01R-1289-07	0	2	1	1	0	1.263292048	0.007206836	3.09057134	2.294025257	1.311744508	0.700136823	2.914011683	4.47524501	4.156459067	2.670853963
TCGA-CZ-4861-01A-01R-1305-07	0	2	1	1	1	0.18156754	0.02265413	2.270083419	1.383710193	0.974117005	0.388275838	3.46412585	4.262608165	1.984737502	0.436624234
TCGA-CZ-5468-01A-01R-1503-07	1	4	1	2	2	0.625284222	0.002197426	2.509751062	1.961034886	0.305787164	0.285247041	2.628696003	4.493134653	2.532831913	0.921096256
TCGA-B0-4848-01A-01R-1277-07	0	3	1	1	2	0	0.073960556	1.372123032	0	0.463505958	0.101034098	1.694651527	4.390187144	2.480025901	0.598298851
TCGA-CZ-5458-01A-01R-1503-07	0	3	1	1	2	0.327750176	0.001033501	1.846762064	0.594652956	0.474157905	0.180498532	2.718467794	4.457792939	1.959450688	0.588908157
TCGA-B0-5080-01A-01R-1503-07	0	3	1	2	2	0	0.003680425	0.69340529	0.854475947	0.35006731	0.324562023	2.519459576	4.8743529	3.070315748	1.136120598
TCGA-CZ-5985-01A-11R-1672-07	0	2	1	1	1	0.33669118	0	0.739062021	1.036628265	0.398235237	0.263285153	2.036757893	3.875924427	1.782486306	0
TCGA-BP-4758-01A-01R-1289-07	0	2	1	1	0	0.462534235	0.044255057	2.865046386	2.511848753	0.764682245	0.372476825	3.418712799	3.890982574	3.003994059	1.659047133
TCGA-B2-4099-01A-02R-1188-07	1	3	1	1	0	0.868000586	0	2.067814097	3.121219248	0.784928829	0.503865243	2.615918938	4.745853828	3.691722725	2.686200618
TCGA-BP-4981-01A-01R-1334-07	1	3	1	1	2	1.416512174	0.84452771	2.608629334	2.499289149	1.212833494	1.268203691	3.399047115	3.554553492	3.055666983	2.137337245
TCGA-B0-5705-01A-11R-1541-07	0	2	1	1	0	0.445895804	2.393621444	1.156492346	0.975086512	0.35013321	0.195859165	2.442085657	4.386715511	2.35500436	0.966723703
TCGA-A3-3317-01A-02R-1325-07	1	2	1	1	1	1.640225841	0.003673285	1.585763232	2.495070482	2.056542943	0.983831665	2.207087238	4.538444684	3.696920623	2.80277735
TCGA-BP-4971-01A-01R-1334-07	0	3	1	1	2	2.097661534	0.0068779	2.964079774	2.510328897	2.734654826	2.166153715	2.773404452	4.516199142	3.139941046	2.227054814
TCGA-CJ-4895-01A-01R-1305-07	0	4	1	2	2	0.991849889	0.009321497	1.421075484	2.027175101	1.311233693	0.289053284	1.353135052	4.393023033	2.7820093	1.45263174
TCGA-BP-4330-01A-01R-1289-07	0	2	1	1	2	0.948895612	4.316219755	3.820385136	2.393205136	1.709439634	1.015619649	3.500282175	4.29042405	2.621728591	1.36524321
TCGA-DV-5573-01A-01R-1541-07	0	2	1	1	0	0.223219143	0.076612038	1.830120624	2.507259657	1.022933168	0.622418353	2.555427057	4.557507492	3.010965717	1.4667117
TCGA-CJ-4874-01A-01R-1305-07	1	3	1	1	0	0	1.24902199	0.921540306	0.475393816	0.28059879	0.06222236	2.826386899	4.596019199	1.923834264	0.47062114
TCGA-CJ-4881-01A-01R-1305-07	0	3	1	1	2	1.093173017	0.101368341	3.985281373	3.022261414	1.223660105	0.611385633	2.56172394	4.320197108	2.880647518	2.141961325
TCGA-A3-3319-01A-02R-1325-07	1	2	1	1	0	0.974497516	0.000977539	0.576522796	1.550858016	1.001341697	0.348774216	1.306700897	4.482213286	2.40299052	0.843718763
TCGA-B0-4694-01A-01R-1277-07	1	4	1	1	2	0.188850764	0.023615792	1.648913011	1.083276594	0.338477806	0.165283477	1.717730574	4.336641985	2.310496842	0.796697417
TCGA-BP-4985-01A-01R-1334-07	1	4	1	1	2	0.160443754	0.005710527	0.969496276	0.210190763	0.199138483	0.13204505	0.75297463	4.255263309	2.649042763	0.948582679
TCGA-B0-4696-01A-01R-1277-07	0	3	1	1	2	1.14954938	0.364651538	0.696260721	1.23500939	1.754400894	0.431801109	2.697297349	4.676164408	3.499960743	0.34207712
TCGA-AK-3447-01A-01R-1766-07	1	2	1	1	1	0	0.00313833	0	0.600944524	0.074584236	0.029407916	4.388786231	4.314522524	3.847459769	0
TCGA-A3-3376-01A-02R-1420-07	0	2	1	1	0	0.923606159	0.015268437	1.498921875	2.111588714	0.817804429	0.480663541	3.123281006	5.218212342	2.652799216	2.674336161
TCGA-B8-5550-01A-01R-1541-07	1	3	1	1	2	0	0.004787694	1.002756061	1.036767425	0.325673768	0.116130523	2.641596271	4.306497426	2.898520747	0
TCGA-MM-A84U-01A-11R-A37O-07	0	2	1	3	0	0.487097311	0.59997913	2.875450832	2.326600583	0.998277942	0.623550466	3.163672833	3.898042345	2.870245227	2.234002208
TCGA-EU-5904-01A-11R-1672-07	0	0	1	1	0	0.193897005	2.84783604	1.803186019	0.468424999	0.394158282	0.24920671	3.256707417	4.330726326	2.735508225	0.961781181
TCGA-CJ-4899-01A-01R-1334-07	0	2	1	1	0	0.153845163	0.004554271	2.111941066	1.632534992	0.813823821	0.674449284	3.255242971	4.665149795	3.399413068	2.140890703
TCGA-B0-5102-01A-01R-1420-07	1	3	1	1	0	0.736980449	3.327357583	2.773516618	2.130227377	1.366616069	0.876629198	2.600774505	4.037361957	2.447872557	1.930189577
TCGA-BP-4158-01A-02R-1289-07	1	2	1	1	0	1.23017343	0.02969941	2.770681265	3.500670079	1.070507555	0.636267901	4.159825055	4.324928568	2.375793075	2.608521259
TCGA-CJ-4893-01A-01R-1305-07	1	3	1	1	0	0.454979252	2.463142712	1.591371095	1.10667339	0.397761235	0.230130058	2.090501398	4.29321846	2.171364883	0.573893044
TCGA-CJ-4904-01A-02R-1426-07	0	3	1	2	2	0	2.163520944	0.811388504	0.770713695	0.370484621	0.042669443	2.81876429	4.580475687	3.303226661	0
TCGA-BP-4759-01A-01R-1289-07	0	2	1	1	0	0	0.032024534	1.758772724	1.071690962	0.321513333	0.095334387	3.79022332	3.851620168	1.523743956	1.062765564
TCGA-BP-5178-01A-01R-1426-07	1	4	1	2	2	0.45285216	0.000996131	0.701102424	0.987914644	0.167882245	0.085372381	1.897151379	3.996905937	2.66209925	0.216557859
TCGA-B0-4839-01A-01R-1305-07	1	2	1	1	0	0.204097449	0.290284781	1.731585962	0.490817783	0.494856541	0.185588538	3.311393329	4.070625323	1.703628226	0
TCGA-B0-5707-01A-11R-1541-07	0	3	1	1	0	0	2.386758209	0.463068468	2.077757577	0.539211128	0.144499162	1.375915388	5.293813185	2.780250469	0.316021424
TCGA-CJ-6028-01A-11R-1672-07	0	4	1	2	2	0.24444596	0.010440219	0.248528516	0.577602676	0.645761027	0.139319881	2.406662697	4.370439501	2.535889893	0
TCGA-AK-3429-01A-02R-1325-07	0	2	1	1	1	0	1.37052591	1.411818109	0.346922263	0.411046965	0.081043062	2.987673808	4.004610054	2.204623129	0
TCGA-B8-5545-01A-01R-1672-07	0	2	1	1	0	0	0	0.808684665	0.669529033	0.347551452	0.048231668	2.622143457	5.109047476	2.393123889	1.115840229
TCGA-CZ-4864-01A-01R-1503-07	1	3	1	1	1	0.661971017	0.003771289	3.390291389	2.786609019	1.247408608	0.877699121	2.754500707	4.699120213	2.72807753	2.273800125
TCGA-BP-4999-01A-01R-1334-07	0	2	1	1	0	0.494765274	0.002485255	2.368850759	1.844350576	1.427398503	0.520826485	3.169249137	4.772724534	4.173119978	2.445479084
TCGA-B0-5119-01A-02R-1420-07	0	2	1	1	0	0.375571978	3.12401375	2.509134294	0.842330016	0.453446911	0.181815044	2.690085549	4.56451069	2.425479954	0.258101203
TCGA-CJ-4637-01A-02R-1325-07	0	4	1	2	1	0.604940773	4.186130684	1.936867221	2.084491928	1.633828691	0.860014016	2.712490675	4.554273714	3.487840314	1.100286792
TCGA-CZ-5463-01A-01R-1503-07	1	2	1	1	1	0.444213183	0.001460849	1.006909287	1.42366895	1.884033433	0.398072068	3.563560548	4.306346515	2.275289576	0.672545826
TCGA-B0-5120-01A-01R-1420-07	1	2	1	1	0	0.378126887	3.655756605	2.018283809	2.534672683	0.621263102	0.258685768	3.051640465	4.325549648	4.168553756	1.127311112
TCGA-B4-5836-01A-11R-1672-07	0	2	1	1	0	0	2.797372416	0.360282701	0.245789118	0.281250048	0.106339945	2.110346			

TCGA-A3-3313-01A-02R-1325-07	0	3	1	1	0	0.987779147	0.007948359	0	1.99863069	1.318135834	0.874520062	3.010695444	4.889012013	3.390607882	1.198756996
TCGA-B0-5081-01A-01R-1334-07	1	2	1	1	2	1.04987197	4.005470142	1.612835707	1.687050435	1.217283824	0.893265366	2.550633332	4.254249835	2.590441138	1.602720761
TCGA-B0-4713-01A-01R-1277-07	1	2	1	1	2	0.502127999	2.675524335	2.389209401	1.255603638	1.047291173	1.190977496	3.568643516	3.461854276	2.626742446	1.245705431
TCGA-B0-4836-01A-01R-1305-07	0	3	1	2	2	0	0.008864138	1.922855771	0.98177187	1.06708596	0.240396651	2.128832306	4.165551808	2.241774467	0
TCGA-BP-4994-01A-01R-1334-07	0	3	1	1	0	0.13477323	0.006336825	0.997838605	1.031735634	0.880811313	0.890143229	2.413119725	5.78789405	4.237612391	0.82712455
TCGA-BP-5168-01A-01R-1420-07	1	2	1	1	0	0	0.011355485	1.654287811	0.768170568	0.376244431	0.048583798	3.602430183	4.094591834	2.222116015	0.300548177
TCGA-B8-5553-01A-01R-1541-07	1	2	1	1	0	0	2.116423967	1.723562085	1.141482266	0.452683535	0.132425601	2.730904226	4.501866417	3.021358902	0.482637163
TCGA-B4-5844-01A-11R-1672-07	0	0	1	1	1	0	2.898008565	0.847098802	0.702827096	0.571394559	0.144861451	2.590683851	4.51153514	2.872134848	0.499310449
TCGA-B0-4688-01A-01R-1277-07	0	4	1	2	3	0.925948109	0.037210968	0.818506227	1.847918673	2.008471766	0.802313012	1.873351619	5.40474421	3.126893745	0.840385786
TCGA-BP-4803-01A-01R-1305-07	1	3	1	1	2	0	0.004551218	0.363170445	1.209126784	1.105664292	0.107269123	2.728390016	4.411341133	2.018913316	0.945683443
TCGA-BP-5007-01A-01R-1334-07	0	2	1	1	1	0.32075337	0.011059347	3.126318945	2.410259218	0.875913141	0.94737362	3.200965534	4.483824715	2.977851994	2.717475752
TCGA-G6-A8L6-01A-11R-A37O-07	0	3	1	2	1	1.481941	0.016519834	2.960088764	3.253876081	0.776662809	0.507927776	5.200227897	3.914595981	2.918922822	4.498461631
TCGA-CJ-4902-01A-01R-1426-07	0	3	1	1	2	1.12369286	0.003471657	1.398905554	2.652559225	1.039275831	0.90415806	2.465414823	4.394683715	3.104079456	2.134083945
TCGA-CJ-4889-01A-01R-1305-07	0	4	1	1	0	0.367327	2.323154565	1.616653295	1.812700232	1.252112635	0.241634837	2.616138408	4.93331862	3.555363974	1.338146501
TCGA-B0-5693-01A-11R-1541-07	0	2	1	1	0	0.875919544	4.526547416	1.757456372	0.531496703	0.812102015	0.3030369	2.516841961	4.258457687	2.851020849	2.029033495
TCGA-DV-5567-01A-01R-1541-07	0	2	1	1	0	0	2.357826876	2.401260811	1.264270276	0.51101124	0.084791955	3.638307082	5.10685079	2.602452718	0.899930638
TCGA-B0-5812-01A-11R-1672-07	0	3	1	1	0	0.342964449	0.002173973	0.184749638	0.921842888	0.717080322	0.137271825	3.083684383	4.523128077	2.754362589	0.913806534
TCGA-CJ-4876-01A-01R-1305-07	0	3	1	1	1	1.400301001	0.022421378	2.4169423	1.941825686	1.292468898	0.663336091	2.563384187	4.180752145	3.591092378	1.056711821
TCGA-BP-5010-01A-02R-1420-07	0	4	1	1	2	1.772986453	0.004515929	3.034803637	2.797227249	0.522538536	0.428550653	2.325479763	4.047822572	3.744408925	1.304659999
TCGA-B0-5121-01A-02R-1420-07	0	2	1	1	0	0.171959627	0.004099188	1.194649992	1.332881137	0.92316851	0.393873789	2.847944458	3.93096702	2.104312684	1.223041463
TCGA-B8-4621-01A-01R-1503-07	0	3	1	1	0	0.768161899	0	1.351106988	1.988644053	0.860713713	0.356387693	1.576044831	4.834563061	2.976350289	0.693876131
TCGA-B8-A8YJ-01A-13R-A39I-07	0	2	1	1	0	1.104362402	3.225563671	1.900031074	2.418079109	1.872517748	0.43263663	2.383874548	5.042666321	4.843367544	3.370809504
TCGA-CW-5589-01A-01R-1541-07	0	2	1	1	0	0.2040582	0.077920395	1.662548108	0.856240963	0.405883121	0.057094467	3.755836224	4.291943127	2.341685254	1.000705075
TCGA-B2-5633-01B-04R-A277-07	0	2	1	1	0	1.54508067	0.178243446	2.507767423	2.935417009	4.126210098	2.822761049	2.758152896	4.488937427	3.457657352	3.65839112
TCGA-B0-4822-01A-01R-1277-07	1	4	1	1	1	3.076824132	0.014592708	2.612763415	3.133000326	1.413089117	0.757668574	3.055940642	3.85021919	3.28370832	4.766690434
TCGA-CJ-5683-01A-11R-1541-07	1	3	1	1	0	0.586661473	0.282346453	0.226874517	1.477191449	0.97215391	0.206713603	3.510820929	4.241447935	2.521744646	1.346355065
TCGA-CZ-5453-01A-01R-1503-07	1	2	1	1	1	0	0.001003817	1.3296304	0.580582273	0.949415387	0.206118243	3.244894969	4.131787891	2.822158906	0.574948064
TCGA-B0-5088-01A-01R-1334-07	0	3	1	1	0	1.195602736	0.010423646	2.761501125	1.532363856	0.960223261	0.994215896	2.846687649	3.824289249	3.384468947	2.245086839
TCGA-A3-3357-01A-02R-1420-07	0	3	1	1	1	1.413480914	0.004809281	1.062831042	1.45576471	1.535189799	0.60002327	2.410418088	3.74022403	2.592781291	1.171678753
TCGA-CZ-4856-01A-02R-1426-07	0	2	1	1	0	0.152129637	1.3080524	0.930430335	0.374684743	0.231442459	0.016951377	2.697476959	4.099521683	2.330394926	0.910120088
TCGA-BP-4176-01A-02R-1289-07	0	2	1	1	0	0.195488223	0.038308994	1.617533623	1.349284425	0.971740344	0.467786903	2.56073048	4.297642229	2.986114054	0.467187416
TCGA-BP-4801-01A-02R-1420-07	0	2	1	1	0	0	0.01046695	1.119522927	0.970736573	0.298626589	0.06122944	2.617381476	4.386714279	2.598053298	0
TCGA-CJ-4892-01A-01R-1305-07	0	2	1	1	0	0.911737782	3.040697332	2.864203675	1.977353501	1.607584936	0.813213694	2.91433517	4.374393255	2.32822633	1.553570095
TCGA-B0-5700-01A-11R-1541-07	1	2	1	1	0	0.854956787	0.135982935	2.031317948	1.055385018	0.233038857	0.055741044	3.372192064	3.616156164	3.549375543	1.377612885
TCGA-BP-4775-01A-01R-1289-07	0	2	1	1	0	1.721440439	4.304943953	3.489929284	3.015147131	1.506690608	1.080060423	2.815792832	4.080172981	4.427012653	1.329840675
TCGA-CW-5581-01A-02R-1541-07	0	3	1	1	0	0.741028813	0.001088153	1.791133214	0.620205243	0.254097753	0.109009083	2.094496772	4.037608884	1.933713199	0.614262327
TCGA-BP-4164-01A-02R-1325-07	0	2	1	1	2	0.548110951	4.081125468	2.87828104	1.158629834	1.669035501	1.126275396	1.674476999	4.450059426	2.701313693	0.936187664
TCGA-CJ-4642-01B-01R-1305-07	0	2	1	1	1	0	2.64850482	2.380352438	0	2.963713167	0.664898446	3.982136609	3.046098555	2.717824047	0
TCGA-BP-4976-01A-01R-1334-07	1	3	1	1	0	0	0.011339441	1.505004428	1.139875215	0.221687842	0.099047597	3.35583597	4.73469191	2.100345296	0.48180159
TCGA-CJ-4897-01A-03R-1426-07	1	3	1	1	2	0.258546795	1.737410289	1.377808802	1.206947858	0.333152135	0.187849182	3.165253004	4.310812906	2.174821858	0.175440727
TCGA-BP-4160-01A-02R-1289-07	1	2	1	1	2	0.32539169	0.012254549	1.194101761	0	0.546172391	0.111921992	2.787031526	4.733207814	3.244031925	0.415077978
TCGA-B8-5159-01A-01R-1420-07	0	3	1	1	0	0.298049584	2.301930715	1.398117499	0.205376766	0.365136571	0.147590456	3.138357441	4.203536776	1.610170893	0.381145051
TCGA-CJ-4885-01A-01R-1305-07	0	3	1	2	2	0	0.038138888	2.203417147	0.240748128	0.468440668	0.116951346	2.918071791	4.136175303	1.796038364	0
TCGA-BP-5201-01A-01R-1426-07	0	4	1	2	2	0.937977022	0.018967039	1.301788894	1.151287273	1.485762986	0.445225798	2.345985867	3.801150408	3.768882782	1.534224679
TCGA-BP-4991-01A-01R-1334-07	0	2	1	1	0	0.804677975	0.00259224	2.090369402	2.316927102	1.712413489	0.707546081	2.768328463	4.62361426	3.586377194	2.081685116
TCGA-BP-4968-01A-01R-1334-07	0	3	1	1	0	0.862207701	0.002838677	2.694199428	1.867173874	1.698763554	0.634631576	1.979023774	4.182919473	3.14184344	1.509597731
TCGA-BP-4975-01A-01R-1334-07	0	3	1	1	0	0.245965541	0.001506204	0.888847773	1.080873911	1.303824172	0.230034106	3.701814801	4.277904972	2.059668436	1.230896544
TCGA-BP-4340-01A-01R-1289-07	1	2	1	1	0	2.482020319	1.472482245	2.79335538	2.263535089	1.252203499	1.547727531	3.109493976	3.969599208	2.931803184	0.861341025
TCGA-B0-5084-01A-01R-1334-07	0	3	1	2	2	0.177638624	1.201841781	1.137976602	2.720423182	1.300629013	2.210287279	4.288813721	4.512418261	1.941381898	1.025678471
TCGA-CW-5590-01A-01R-1541-07	0	3	1	2	2	0.974035364	0.004460448	2.079331441	2.166698276	0.835180967	0.312174314	2.101585332	4.635640266	2.668658978	1.397082236
TCGA-BP-5198-01A-01R-1426-07	1	3	1	1	2	0.181895677	0.003264425	1.157916486	0.779603004	0.259559819	0.053921452	1.222513375	4.697449465	3.09253789	0
TCGA-A3-3308-01A-02R-1325-07	1	2	1	1	2	0.93247729	3.766980855	0.636953271	2.285840653	0.95476395	0.536660807	2.718789971	4.445188058	2.730431727	2.533213243
TCGA-B0-5706-01A-11R-1541-07	0	2	1	1	1	0	0.003603007	1.491749017	0.672028396	0.231514256	0.140734929	2.184058897	3.987422638	2.760210747	0
TCGA-CZ-5466-01A-01R-1503-07	1	2	1	1	2	0.451446413	0.007427396	1.85544554	0.316076603	0.597038272	0.064270171	2.558657276	3.973837158	2.632807072	0.569605191
TCGA-AK-3434-01A-02R-1277-07	1	2	1	1	0	0.517865997	0.176100462	1.67736684	1.286557374	0.986348153	0.372386542	3.466907837	4.511728837	2.220523438	0
TCGA-BP-4335-01A-01R-1289-07	0	3	1	2	2	0.594702026	4.012269323	2.041459496	1.895634858	1.279096794	1.449162986	3.069880142	4.121271707	2.668546406	3.010461654
TCGA-B0-5699-01A-11R-1541-07	0	2	1	1	0	0.364597072	0.002329077	1.300854882							

TCGA-BP-4344-01A-01R-1289-07	1	2	1	1	0	0.713101778	3.402369845	2.743257149	2.886208428	0.776315443	0.428029996	3.294625219	4.796162281	3.735494339	4.256384
TCGA-G6-A8L7-01A-11R-A37O-07	1	3	1	3	0	0.393687716	1.006100032	3.680292125	3.350957124	0.586066351	0.328425433	2.84373514	2.780135881	1.908331249	3.50273828
TCGA-BP-4782-01A-02R-1420-07	0	2	1	1	0	0	2.563890811	1.029880959	0.474887646	0.596242968	0.083456362	2.338610011	4.17431464	2.901079953	0.254124746
TCGA-G6-A8L8-01A-21R-A37O-07	0	3	1	3	0	1.102199924	3.837963124	5.387790745	3.484645787	1.897351458	2.09440775	3.926396063	3.894563479	3.230814663	4.453094111
TCGA-BP-4756-01A-01R-1289-07	0	2	1	1	0	0.357379008	3.022040668	1.100862536	2.55393479	1.000445249	0.845313076	1.814714028	4.536201825	2.561378034	1.199342752
TCGA-AK-3436-01A-02R-1325-07	0	2	1	2	1	0.568514898	0.024588573	0.988089051	0.894262814	0.303425306	0.279630717	3.533882675	4.302150045	1.730704882	0
TCGA-B0-5712-01A-11R-1672-07	1	3	1	2	1	0.36282406	2.540329815	0.368644963	0.465978851	0.32707265	0.348804076	2.912014752	4.41830843	2.02980125	0.249001606
TCGA-CJ-4875-01A-01R-1305-07	1	3	1	2	2	1.160195672	0.061593962	3.643346622	3.961930142	2.532199699	1.207447107	3.02811952	4.321332492	2.399037591	2.717811324

MALAT1	MIR4645	HOXA13	TRG.AS1	HOXA10	NEAT1	HOXA3	MIR570	SNHG1	MIR4668	HOXA9	MIR4701	SNHG5	MIR4768
4.086426021	1.16447674	0.068835685	0.210886751	2.457412918	3.629246175	2.329766159	2.567467221	1.825858919	0	3.179601717	0	3.917460738	2.035779462
4.178425832	0	0.132242554	0.102840251	2.247780943	3.588971738	1.457771513	1.814213679	1.686130223	0.90446447	3.2483253	0.787884826	4.025442636	1.796667351
4.739927055	1.464770091	0.042615937	0.108277987	3.570118999	4.132151495	1.88100518	2.376235954	2.221141003	0	3.312139236	0.620902879	4.748120426	0.754316954
3.84509945	0.496100407	0.112062236	0.116585646	2.003302004	2.684315539	1.019644923	0.983557371	2.693469179	0	2.927722907	0	3.049294121	1.546784388
3.29034579	0.33459985	0.005690083	0.048328708	2.293898827	3.473791533	1.491118558	1.465328586	2.247477606	0	2.790547609	0.213523805	3.92807592	0.747623278
3.745247653	0	0.011508861	0.089648313	2.337659094	4.541666492	1.929652988	2.517129126	1.811754334	0.788610926	2.875954323	0.570404934	3.568237767	0.350764701
4.394545444	0.260123503	0.095991791	0.092622753	2.155625976	3.845935898	1.633303623	2.153981084	1.699568831	0	3.40234883	0.3120705	3.693901473	0.693117855
3.34782931	0.554900469	0.02034642	0.155346657	1.661292949	3.403867301	1.092452943	1.516903635	1.486984193	0.600245017	2.880004021	0.363622155	4.567595861	2.22052387
4.272535786	0.256441179	0.168248519	0.355313662	2.416747272	3.916261066	1.57665776	1.347209064	1.830363683	1.049565468	3.296749876	0	4.354769537	2.335795972
4.526248779	0.416091199	0.050228591	0.128943693	2.234091366	5.007769223	2.218968754	2.354271886	2.148476828	0.451792178	2.56677317	1.015422765	3.870040634	1.626281718
3.995749154	0	0.039587882	0.223413773	2.1938307	3.605684572	1.927524481	1.845283635	1.763080453	0.535242273	2.519435166	0.321405742	4.418226787	1.18568618
3.37715603	0.601852253	0.055454057	0.145566538	2.036377673	4.035307204	1.96251298	2.029264726	2.425540458	0.361448462	3.302014937	0.396543256	5.349090989	2.170318079
3.452638275	0	0.010466241	0.063271079	2.974436727	3.325699588	2.287304973	1.718348496	1.803681701	0	4.000438496	0	4.327451933	0
3.731545467	0.604960045	0.082907995	0.101438744	2.211113601	3.072166901	1.593011649	1.163872914	1.346636196	0	3.262208904	0	3.880179503	0.858445389
2.332304559	0.688499681	1.274879989	0.60836498	2.188122014	1.693314439	1.470800292	2.992562684	1.551340008	0.291905006	1.821408414	0.320973392	4.91669732	1.043112943
3.198173297	0	0.003961255	0.033795354	1.677739362	3.182218391	0.908306413	1.52313182	1.253986718	0	2.055828699	0	3.585684933	0
4.2624701	0.38449777	0.013279909	0.072100268	2.674156584	3.466336412	1.074441114	1.826017042	1.993983165	0.224006799	2.919927079	0.457618569	4.491339674	1.183420621
3.138763504	0.777047956	0.072200058	0.070242282	2.338507783	2.330036106	1.357957772	1.354918692	1.189091205	0	3.089216001	0	4.37060955	0.455518684
4.294828658	1.89229997	0.05235517	0.02889028	2.041062048	3.506954689	1.546280494	2.15213702	1.55335097	0.675091876	3.107485218	0	3.959151992	0
3.316815856	0.233866407	0.034185734	0.243349197	2.138550993	2.446314279	1.203404913	1.75482535	1.967699701	0	2.852563525	0	4.309419246	1.301549112
3.014488882	0.23456862	0.041807431	0.14877293	2.603887957	3.111563775	2.409439543	2.418110659	1.993653552	0.256057004	3.359468199	0	3.991722385	0.451461736
4.955727203	1.14450368	0.231592718	0.559756181	1.013281748	5.097685284	1.947767457	3.43975402	2.681891502	3.413504404	0.977814644	1.310191906	4.053705409	2.928628287
6.163650285	0.732347283	0.04736352	0.685521531	0.525652963	7.061506343	2.055739821	4.181848748	3.259661329	2.053940884	0.631512195	1.529093026	4.264523511	3.060095345
4.97951314	1.329092026	0.418918462	0.728237085	2.358657888	3.734137837	1.861960207	4.182011971	3.116323587	1.536729044	2.216313525	1.638130207	4.712121774	1.886696419
2.796189524	2.128270056	0.041483036	1.183201245	1.725226172	3.256095208	1.943687392	2.432268056	2.65150589	0.339065875	1.788767729	0	5.938044442	0.3226393
5.321728557	0.705121906	0.060656167	0.837797054	4.015563119	5.023347623	2.743590791	0.585277242	4.875871933	0.429380646	3.857865892	0.470065743	5.988818755	2.787121
3.719006435	0.643926054	0.132942555	0.236716551	2.169243259	4.073532681	1.888610617	3.312028148	2.915895029	0	2.186330665	0	5.578518113	0.257164655
4.882448571	3.085820244	0.168682928	0.752884452	2.633954318	5.106655058	3.196337968	4.631320907	3.2241627	1.193708723	3.24477208	1.441766806	5.612445936	2.612306662
3.018660551	1.95403184	0.099627249	0.696129959	1.767831347	2.263844044	1.824064376	2.247556798	1.971311067	0.293792046	1.864374855	0	4.143244383	0.513287796
3.793615212	2.216346806	0.03929032	0.680113464	2.790742402	3.584664778	1.671211146	1.291356554	3.561863395	1.587813117	2.592886477	0	6.240616693	0
5.204992041	1.271429626	0.373423712	0.954953334	2.501852818	5.521143911	2.185884413	4.632042935	3.511803491	0.951024006	2.606409916	1.773794848	5.711915661	2.179891541
5.862565997	1.65543979	0.205391653	1.255232473	0.65640428	5.105199052	2.529936787	4.228916893	3.247720943	1.274486368	0.512325099	0.609379117	3.743797051	1.966641103
6.241292439	2.427575779	0.011908803	1.348467839	1.521408589	6.929076902	1.837866915	3.64581198	5.478202171	2.004023859	3.08300073	2.226607612	6.123639622	4.464550948
6.323006994	1.995931551	2.213979906	0.454885179	1.071251412	5.842295314	1.450731183	4.103908995	3.084576961	1.000415979	1.376015463	1.280597294	5.003482005	3.029681324
5.59394842	1.089623942	0.067397479	0.982565505	2.416839541	5.324906444	1.829467664	4.035958467	2.971107956	0.994799306	2.393976754	1.072527577	5.066766407	2.018705129
12.32690828	0	0.043588239	0.30945359	0.913631857	9.425610076	0.83591934	8.362384011	3.196718868	2.94224795	1.547376726	0	2.349000601	1.636090177
3.716750488	1.082797551	0.956594419	0.304825864	1.975645692	3.732483069	1.932205517	2.508827853	3.037513821	0.767934828	1.911194041	0.2572891	5.3321548	0.872670846
4.686162105	0	0.086397379	0.510294474	2.295459968	5.353676185	1.297425463	2.901468946	3.488423525	0.458038955	2.188354598	0.500998391	6.186165581	3.536580506
4.539445189	1.723073734	0.218791082	0.471099518	2.689205909	4.152283764	2.166657127	1.830915517	3.787074895	0	2.930282142	0.643913516	6.38034004	0.309722186
3.035462971	0.289112217	0.042971606	0.271240249	1.907484718	3.159016554	1.484095639	0.769392639	2.222295438	0	1.929419993	0	4.321442933	0.299694344
5.704915752	0	0.023439358	0.203243105	0.18248504	6.935587299	0.219644614	4.462143954	3.125000234	0.375761411	0.237282111	1.215572766	2.448250319	0
3.711424357	1.188739265	0.107669871	0.304021881	2.098408365	4.157430858	1.213783922	2.719494816	2.574751923	1.524390025	2.363784276	0	3.488797913	0
5.687111558	1.700968302	0.178185121	0.860322039	1.637336214	5.35716213	1.988205308	4.455080929	2.927162729	1.469257151	1.828105768	1.363036678	5.198752574	0.41644686
4.879622974	0.754979145	0.108458523	1.360206913	2.692228679	4.213508612	2.132386489	4.228014929	3.954999421	0.960111241	3.177119363	0.880026257	6.10934538	2.249835655
2.792979579	0.565095634	1.020334645	0.533043069	2.906314534	1.916141801	1.945735637	1.599311631	2.785456233	0.233656645	2.779671029	0.257428248	5.461127893	0.221948903
5.615079876	1.663528531	0.60449872	0.465806444	2.830113633	6.337944187	2.23248661	2.564840353	2.881287385	1.240425708	3.07452637	0.813151778	3.805480026	1.552640614
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5.410583602	2.473552822	0.964025932	0.9144264	2.499551376	5.163765617	3.040264472	3.932644057	3.371682381	1.636574407	2.670850679	1.118901135	4.402389388	3.206395666
6.193407064	0.515217447	0.969722527	0.799256925	2.72415771	5.435798427	2.294736627	5.207314746	4.54151038	1.124544014	2.951864613	1.035045922	5.97930218	4.688563694
6.525903114	2.662911123	0.308227809	2.103035963	2.490410877	6.044471842	2.912236296	2.835632944	3.821876011	2.176272937	3.028253819	1.563386998	5.284057679	2.937186944
5.756322383	1.807164576	0.11248665	0.979641559	0.946452721	5.565997639	1.262055139	4.027370892	3.352788949	2.117252508	0.945515685	1.669995752	5.376386624	2.632673453
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5.648887311	0.438531197	0.097493908	0.674509123	2.48840856	5.647913131	1.51660614	2.957462253	2.978516593	1.901194705	2.306309832	0.520208516	6.106246013	5.659060542

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3.879144316	1.423767435	0.014628209	0.434457218	2.343634506	3.525674595	1.682039067	2.990325963	3.054321407	0.454415367	2.448277465	0.497089918	4.889616392	0
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3.91984101	1.887274279	0.127807922	0.5977316	2.565398091	3.378131276	2.468363847	1.836467766	4.334079612	0	3.233225634	0	6.886558522	2.726303607
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5.251639689	2.122207862	0.197456541	0.675778131	2.76494067	5.143755991	2.076676062	3.542076587	4.674477492	0.495576546	3.035451552	0.541442233	6.782522909	1.351013537
5.796820495	2.095596759	0.053480766	1.067525329	1.149025785	5.583974952	1.573681677	3.616147153	3.269872544	1.346798589	1.255287913	1.440935017	5.663765266	1.559110008
4.139282347	1.636359827	0.156959898	0.955810424	2.973644068	4.445185967	2.760673353	1.741401862	2.341443483	0.762055728	3.257185793	1.022169652	3.64601528	1.861223197
4.060054442	0.789839498	0.046986818	0.6924714	2.397659404	4.387434366	1.167941463	3.877102808	3.354659	0	2.443805686	0.375125054	6.082578969	0.325168165
3.233043185	2.270167496	0.089063832	0.151210806	2.435132299	3.431426788	1.089649112	2.433307234	3.411689303	0.275374854	2.648114499	0	4.167212767	1.480505266
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4.902224137	0.345398042	0.080431142	0.61784786	2.057742107	4.732588533	2.683113608	4.947067065	2.457277392	0.920411337	2.62712319	0.412090932	4.225932056	3.648485864
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5.616979651	0.664273938	0.4135883	1.037094954	1.951061851	5.004325684	2.403962889	3.854173114	3.445750825	1.383009642	2.450764137	1.051079194	5.447918346	3.615514268
4.208468546	0.790641632	0.243862805	0.246062416	2.917270316	4.189431898	1.624719859	1.811701914	2.806292711	0.850261758	2.230236103	0	5.456459291	2.33637006
4.0293531	1.486274756	0.069148296	0.288883077	3.243752613	3.679139465	2.501263776	2.441891221	3.309763787	0	3.557854566	0	4.918379838	0.247889348
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6.518638814	2.457961043	0.408311377	0.789405242	0.090353039	4.779407125	1.347980806	3.310237173	2.927052891	0.964019829	0.09802705	1.040103561	5.080959046	3.396854491
2.285075029	1.906846266	0.075706364	0.514245762	2.208527749	1.649587805	1.43030656	1.191599147	1.680424389	0.236258365	1.757394328	0	4.987088936	0
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4.544593918	0.481536215	0.079959264	0.217257149	3.409434744	4.002012564	2.600757945	1.363263008	1.574310107	1.206366738	3.010930274	0	5.692403503	1.022000169
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5.720780786	1.259959759	0.167600487	0.438741326	2.927151114	5.385286667	2.259197153	2.667182317	2.961910366	1.188179169	2.879520636	2.044599828	5.056234406	2.865834568
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2.643366346	0.303552792	0.145823154	0.399141462	2.449043061	2.233726401	1.264746638	2.347580555	3.616205944	0	2.17766883	0	6.558233077	1.879867014
4.01177385	0.501733308	0.1467139	0.435971689	1.8464197	2.835935479	0.690268456	1.575772011	1.992766578	0.937351986	1.822729767	0.326732302	4.98647784	0.721733611
5.845050576	0.597598668	0.08171026	1.421799063	2.956740072	5.416383616	3.551871524	3.25625991	3.531427641	1.429506761	3.862767024	0	5.271573578	1.977098779

The validation set

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE151419>

	age	grade	stage	M	T	MIR324	XIST	MIR210	MIR25	GABPB1.AS1	LINC00894	SNHG7	FGD5.AS1	MIR22HG	MIR126	MALAT1
001C	-	-	-	-	-	20.03255	0	10.993069	14.395685	2.023725	2.988192	4.974711	7.011268	9.213046	1.778291	92.194867
004C	-	-	-	-	-	22.21272431	0.03694517	23.46471422	21.94828711	0.75124238	2.27431879	3.56426039	15.19911397	6.23607729	4.33801439	88.31860374
005C	-	-	-	-	-	13.345747	6.836745	7.55248	20.439647	2.350286	1.716816	3.836787	5.710112	8.23539	3.909519	77.032704
006C	-	-	-	-	-	14.8269868	0.01896991	8.60587346	12.39655581	0.47941213	2.69486469	4.61884854	8.61593684	18.0389022	10.02331144	80.60818422
009C	-	-	-	-	-	30.80111507	0	18.26066108	8.69555289	2.52985467	1.41510737	6.38807936	5.33833397	20.30321325	15.03819147	96.7992325
011C	-	-	-	-	-	49.63599324	16.63643284	32.9129024	34.18294051	4.10592902	4.71884365	9.51040654	5.62044671	4.93347661	30.84332842	223.1328725
012C	-	-	-	-	-	11.05212447	0.01378678	8.33933028	10.92055156	0.58203953	0.75440407	4.56024137	7.77698215	7.8338317	4.31682979	38.19137039
016C	-	-	-	-	-	1.12476713	0.49107487	4.24343961	5.55688521	0.29345167	0.47246267	10.50654162	22.28818896	6.75312292	2.19660403	16.34657274
019C	-	-	-	-	-	35.20949023	0	14.68185203	22.88837476	2.14433121	0.63246194	5.00899834	11.73583461	19.93450199	6.33334793	75.73665171
024C	-	-	-	-	-	39.58230937	0	20.18017001	7.39939567	0.59956684	0.91278327	3.86233127	11.90594634	18.22838398	5.22310283	67.15997459
028C	-	-	-	-	-	4.1274048	0	9.3429436	1.0195673	0.7129077	0.7720525	6.3271833	13.9039485	8.8052915	11.0832958	36.5465076
030C	-	-	-	-	-	5.8094445	0	5.0097028	0	0.6696275	0.42487	4.8511679	23.1580369	14.9485772	0.8103931	27.5848368
034C	-	-	-	-	-	0	0	8.78528018	5.75226678	0.39377529	0.76417904	19.90588799	8.94622664	13.99731093	5.68459305	180.002915
035C	-	-	-	-	-	8.818724654	0.007333842	6.654128603	12.19923577	3.740938008	1.273366378	15.16130568	11.29814235	5.49088174	3.4444901	85.04211966
045C	-	-	-	-	-	8.87340631	0.01229886	13.39077679	14.61295086	0.50016969	0.15530449	6.21512847	7.94242786	6.90616084	5.77641352	58.7736055
050C	-	-	-	-	-	2.9083383	7.9633628	12.069604	4.3105728	0.5269342	0.4199451	5.5278508	23.0524496	8.9733827	0	27.4064793
058C	-	-	-	-	-	10.4264813	18.7833105	11.8008811	0	1.2593835	0.5474604	9.5602075	11.9327431	10.5783741	0	42.5779745
059C	-	-	-	-	-	0.72539233	6.58147903	3.83139038	2.15027011	0.18224537	0.05713196	5.08542593	24.71197194	3.205962	1.41664855	6.80816534
062C	-	-	-	-	-	10.6706717	2.6067263	4.0257534	0	0.7411051	0.1925969	4.000274	17.5415674	10.2329098	0	35.8616231
065C	-	-	-	-	-	0.8875509	1.40609298	1.33939499	1.75396963	0.20583286	0.04660239	8.22286797	22.91406979	6.19234689	6.06667142	5.56181665
067C	-	-	-	-	-	6.18486499	8.06881496	1.75003566	6.11123565	0.51920068	0.25370858	7.01491088	23.87383803	6.68326859	0.75491734	9.93852349
068C	-	-	-	-	-	4.15497476	4.36412854	9.40535195	3.28440862	0.36937409	0.17453128	6.03212446	18.98056604	6.32903121	3.24576852	18.25350887
069C	-	-	-	-	-	4.38922121	6.61776082	8.61085398	3.46957486	0.69132981	0.2419868	7.83109797	37.47424857	13.8353074	5.1431345	31.24995156
073C	-	-	-	-	-	1.5187613	10.3474125	0.5729872	0.7503404	0.6824215	0.2990444	2.1468888	24.3835037	6.5012749	0.7415129	13.3832273
074C	-	-	-	-	-	0	0.008671391	4.720626369	0	0.231740006	0	8.285993963	23.00665174	6.666211606	9.163568833	7.018483141
075C	-	-	-	-	-	15.3697269	29.836368	16.5673679	8.6781451	2.7899992	0.4323289	7.5496867	21.843353	3.0515915	0	25.0204156
081C	-	-	-	-	-	3.55153046	10.89852448	4.8236241	0.70185007	0.72754794	0.32633864	1.75034461	19.11942996	11.15532627	0.69359301	17.82466693
082C	-	-	-	-	-	7.5910692	5.4038403	11.4556135	1.5001399	1.0782774	0.2790075	10.64357	19.3524182	10.5080125	0	24.9432735
083C	-	-	-	-	-	0.9179852	0	0.6926615	2.7211703	0.4923102	0.120501	2.8583248	20.046821	5.9453835	1.792771	8.8246109
084C	-	-	-	-	-	0	2.3381555	6.8990276	2.2586102	0.3092294	0.2400421	7.4230044	20.8174226	4.2570189	4.4640767	2.0586762
090C	-	-	-	-	-	1.015823	8.4055649	2.2994538	2.0074597	0.5398722	0.173347	4.4436703	16.4157072	5.8731306	1.9838425	10.9881763
091C	-	-	-	-	-	19.0309044	17.4179561	11.1686418	2.0893718	0.7662287	0.5551391	2.9082901	16.3159127	7.4058643	2.0647909	31.8539106
091N	-	-	-	-	-	2.950061825	0.391385953	0.127052448	1.687225468	0.405705865	0.195456583	5.121516065	25.79447826	12.42183865	0.262500615	26.47945337
096C	-	-	-	-	-	6.47879321	0.03591937	0	8.53555296	1.41903133	0.65201203	6.47680509	13.48454342	7.80377079	0	21.78394007
104C	-	-	-	-	-	7.33474131	20.68486137	6.14932857	4.02634609	1.90969602	0.24605095	4.85719118	30.40028622	14.88318741	5.57056824	27.50516356
106C	-	-	-	-	-	0	0.3805244	17.2628368	15.0707306	0.847449	0.8008486	17.7727096	14.618403	9.5390759	11.1700709	27.0756734
106N	-	-	-	-	-	4.75179216	0.8516447	0	1.87808928	0.85863631	1.06037937	4.12099038	19.75452709	13.94792629	5.56798234	47.10260787
107C	-	-	-	-	-	1.21265479	4.15741753	1.37250473	1.19821842	0.24021563	0.05571346	3.27779612	32.22929652	3.89320666	0.59206087	10.73182171
117C	-	-	-	-	-	13.61170968	0.005957786	7.027289354	12.74178839	1.713343686	0.639474013	4.666612794	20.29183399	16.54810964	12.591885	42.91021004
118C	-	-	-	-	-	9.64469499	5.39895878	1.81934019	5.95617325	0.27376415	0.15825354	1.03633302	15.65994145	9.34955635	0	9.82921657
119C	-	-	-	-	-	3.30722188	0.02062768	0	0	0.64714048	0.13023853	7.09149815	16.39720737	3.92995647	0	20.47379996
119N	-	-	-	-	-	3.385710432	0.009385434	1.703114944	2.23026957	0.256275227	0.029628759	5.454279506	21.56028673	11.85792354	1.102015552	9.85394489
123C	-	-	-	-	-	0	1.11748235	0	0	0.34355864	0.09608702	4.33470751	47.49905111	8.19689081	2.04221243	5.07579011
123N	-	-	-	-	-	0	1.57327764	0	1.3644506	0.4003045	0.07250599	5.38117963	26.35828173	12.82016948	4.04519472	7.48819217
124C	-	-	-	-	-	3.36429523	5.92671704	6.7693698	1.10808137	0.41178133	0.3091342	7.7976285	31.31047918	16.42751034	0	20.3274394
125C	-	-	-	-	-	3.7657034	3.4878646	1.4206972	0.9302184	0.3138451	0.1482936	1.02506	16.7363166	3.2186927	0	12.2004702
126C	-	-	-	-	-	3.60312413	0	16.8560698	4.27227576	2.27005839	0.80405	7.99785754	21.51874774	13.50073478	10.55503422	42.35677164
126N	-	-	-	-	-	3.9067147	0	5.8955876	5.7903092	2.3688395	1.589748	4.8507999	38.8021814	9.3389582	1.907396	75.147698
132C	-	-	-	-	-	8.22143495	0	8.75780664	4.77856513	0.77106831	0.49516304	10.56849241	14.82463453	3.18592347	0.94446934	14.27249062
132N	-	-	-	-	-	8.144506414	0.009675926	0	3.448949145	1.641458071	0.565097472	6.956637584	29.6995457	10.28447528	6.816746544	57.5783446
143C	-	-	-	-	-	14.19561765	0.00621336	7.32874232	5.16770292	0.71473672	0.56883145	4.05328689	11.92872215	6.04340877	1.45911612	24.2737424
143N	-	-	-	-	-	0	0	0	3.309232	0.63106374	0.63745763	3.96650869	21.53483851	19.92188694	1.63514993	50.26101625
147C	-	-	-	-	-	5.6583669	0.0156854	19.9243101	7.4546738	3.9367135	0.8170313	6.7014859	19.8316699	8.1262436	27.6261443	38.211696
147N	-	-	-	-	-	8.328579081	0.008657783	2.356609308	3.086035999	1.242390417	0.601296276	2.754349276	22.81898378	20.43026109	7.11603595	69.96119394
149C	-	-	-	-	-	4.25888697	0	8.35516189	13.46619499	0.40330388	0.54786947	2.94505219	20.25440651	11.00949381	1.66347115	28.90079238
152N	-	-	-	-	-	2.68825932	0	0	2.65625623	0.56628866	0.43757022	7.60013291	24.5694642	9.23587231	1.05000246	39.03868384

153C	-	-	-	-	-	10.3400987	0	4.255677	1.8576368	0.7720779	0.3948543	3.5015064	16.0116633	3.0832042	0	17.3508155
153N	-	-	-	-	-	2.7948925	0	0	2.76162	0.6211595	0.1834383	4.9651957	33.4408443	13.0256717	0	21.3384429
156N	-	-	-	-	-	2.94944024	0	0	0	0.14250162	0.01935818	3.95798589	21.98269948	15.98683533	0	15.57459415
158C	-	-	-	-	-	12.5784657	12.5944715	17.0838434	0	1.0574434	0.8255675	7.7850425	14.6499534	8.8108234	0	40.9734719
158N	-	-	-	-	-	3.36765524	1.56554381	0.50820979	1.33102564	0.29287368	0.14145963	3.96274976	23.18490507	11.43897524	0	29.96609258
162C	-	-	-	-	-	3.43721762	0	1.29676847	1.69814918	0.61860513	0.21431647	6.38535358	18.29275025	7.18955189	4.19542739	22.68789374
164C	-	-	-	-	-	11.98662294	0.34889174	13.15556633	11.84392505	0.65283895	0.67229043	11.71927824	12.95589965	6.5728267	1.06405316	31.2397743
171N	-	-	-	-	-	2.328844016	0.011303992	0.851557472	2.68617854	0.203420414	0.044033855	3.966329893	25.43007281	14.09628476	1.482544311	13.31080125
175C	-	-	-	-	-	8.3739947	0.7080062	12.6371192	3.6774686	0.512478	0.1465637	14.6455503	20.4543511	6.5950583	8.1769595	32.6196292
178C	-	-	-	-	-	6.5509892	0	8.6502834	0	0.5697176	0.3224728	15.86146	22.2801938	5.8270018	6.3968482	25.587393
179C	-	-	-	-	-	4.95127167	0.00823517	8.21911098	6.84925915	0.88989734	0.36396506	21.60235843	20.58381915	4.7068586	1.93390847	23.56364198
179N	-	-	-	-	-	11.0694538	0	2.08810151	1.36720932	0.57492987	0.94448368	4.41408801	23.85994771	15.73069107	4.05337353	54.12368662
180C	-	-	-	-	-	15.216511	0	9.3287587	2.8191304	0.5054381	0.574259	12.7350727	15.2456109	7.0846465	4.6432736	24.893356
180N	-	-	-	-	-	5.2240648	0	0	7.7428104	0.5552793	0.7886082	7.0852506	26.0699263	22.5075666	5.1011456	60.4956253
182C	-	-	-	-	-	12.6870418	0	13.0540224	10.2567319	1.5435748	1.4685689	5.3758337	21.2317615	16.5426727	2.2524588	37.7778885
182N	-	-	-	-	-	5.39648436	0	0	0	0.6518252	0.37780227	3.0582148	20.36872222	14.75027009	7.026011	59.90868121
183C	-	-	-	-	-	6.165981793	0.005697516	3.618621638	4.061718165	0.261497194	0.125904912	2.682884035	30.24400784	7.769770314	2.006966623	16.53636577
183N	-	-	-	-	-	1.2719776	0.01322255	0	3.14208751	0.1505656	0.05843895	2.47838028	29.29985889	16.33464597	1.86307307	16.7676576
185C	-	-	-	-	-	8.23556903	1.80353777	2.07137039	8.13752654	0.90190643	0.14414091	13.52945725	15.63115603	5.34144408	2.68059698	21.60092711

MIR4645	HOXA13	TRG.AS1	HOXA10	NEAT1	HOXA3	MIR570	SNHG1	MIR4668	HOXA9	MIR4701	SNHG5	MIR4768	y
7.852192	0	1.35417	0	50.464568	5.441007	42.073987	11.710867	0	0.19961	0	12.713441	20.42631	tumor
0	0.14499851	0.89281168	4.32689728	64.31377382	4.32441402	20.90744051	15.2165441	2.63379445	9.92129241	2.92643828	25.27273776	0	tumor
0	0	1.394679	2.898479	32.087063	3.562843	18.842269	10.21877	2.373636	5.924296	1.758249	5.292683	14.968878	tumor
0	0.03722556	0.38966061	0.89378508	41.56727221	1.86866969	5.85554276	7.66188521	1.35235154	0.71881346	0	45.70599722	23.02652628	tumor
0	0.03590378	2.12230443	0.09851989	154.5182218	1.5266693	30.12067806	19.05798494	2.60866587	0.48228884	0	30.3255073	7.40297071	tumor
0	0.07363864	0.84638674	0.26941903	209.7754302	9.13266227	48.90719234	28.11937404	0	1.77227068	0	12.24292053	26.99287429	tumor
0	0.27054453	0.35538066	1.163052	16.4068732	3.28073049	6.61988074	5.5684346	0	2.66506164	0	54.50113493	19.83408284	tumor
0	0.03671084	4.52085576	3.24868671	16.20510448	1.62602772	7.69943682	14.01826377	0	4.2840668	0	59.34132876	0	tumor
2.99629633	0.06048363	0.52138942	3.46456025	35.34310092	3.96490862	11.89251637	10.89281886	1.09864199	4.72245582	2.44142664	40.65447215	14.54958309	tumor
1.15315257	0.06983307	1.33296619	1.77250158	38.18162267	4.45407189	9.15389155	11.7728404	2.53693566	2.6969075	0	24.05730504	0	tumor
2.2245104	0	0.8087415	5.1289156	47.2776116	3.659645	16.7755602	8.9383148	0	5.1459703	1.359423	23.3573589	3.4720398	tumor
0.8945898	0.2708746	3.1022554	1.133501	18.722298	0.7358655	6.3912445	4.4565147	0.9840488	1.6828566	0	25.2950543	0	tumor
0	0.09500401	0.35098577	5.01829802	27.50537053	2.24426572	2.49067221	8.29759889	0	4.62612145	0	45.30990957	0	tumor
0	0	0.708914427	0.552865284	51.4075056	8.941195563	21.1285733	14.88852417	4.182595122	0.193319022	0	54.22852838	0	tumor
6.37656038	2.07557918	0.35665507	3.97352427	22.16993952	4.96012285	7.59270849	24.31445626	3.50710821	12.3194557	0	22.05436335	13.27013916	tumor
1.567481	0.5695448	1.1689689	5.4047862	14.3242719	3.5597764	3.7328672	8.6119645	0	6.3754924	1.9158102	32.225929	0	tumor
5.6194672	0.2552294	0.785773	4.7273559	20.3644289	9.3453332	8.9216284	12.1538184	3.090707	11.4281671	0	24.6238858	5.8472834	tumor
3.90958202	0.0473516	0.6122803	4.011672	7.45751869	2.72653851	4.96557222	3.17388113	0	4.88975257	0	14.91182309	0	tumor
0	0.2176725	0.8309818	2.6878176	11.3445898	2.4681814	3.4239655	5.6592061	0	5.2996672	0	11.0153489	0	tumor
0	0.11587373	0.24971771	3.81548721	2.89593351	2.30956985	3.03780307	3.35383649	0	3.64807153	0	34.01219558	0	tumor
1.66670063	0.08831613	0.63701863	2.40608266	2.76491337	3.50196794	1.32305102	5.43275182	0	2.24556133	2.03707855	32.95670835	0	tumor
1.79149561	0.05424505	0.36740842	3.31187467	14.89907117	3.31568144	11.37692057	4.38883037	0	3.09682107	0	26.36460862	0.93206191	tumor
1.89249538	0.02865162	0.5821829	4.02927429	14.21570178	2.82577776	8.26259581	5.43160282	1.04087246	4.54629998	0	27.2511884	0	tumor
0.8185532	0	2.6249196	0.9521449	11.657812	0.5415834	5.1982345	4.0441669	0	0.5202096	0	6.9480339	0	tumor
2.247917318	0.15314655	0.230506776	3.035021899	2.980240538	1.386807328	9.814360663	2.465467357	0	2.342910193	0	39.6792807	0	tumor
2.3667668	0.0716638	0.3971355	4.0803903	28.4964259	3.0895486	18.7877368	6.8413173	0	5.8360454	0	18.9154988	0	tumor
0	0.06955022	0.5995465	2.59232024	22.51062248	2.23170718	8.50902763	4.36357902	0	2.04368359	0.93580009	26.01718513	0	tumor
0	0.0991048	0.9763622	5.9487607	14.6064481	4.7408043	24.6827136	8.0854184	0	12.6885385	0	39.7338405	1.7028615	tumor
0	0.4194647	0.7194959	4.3779498	9.5680207	2.1764307	2.3564774	3.1036991	0	3.4713114	1.209409	7.82653	0	tumor
0	0.7460608	0.2296892	2.2007284	6.1999431	2.9079738	0	10.7085546	0	2.1296107	0	69.8051222	0	tumor
0	0	0.5920305	6.8233051	14.428104	2.2517488	3.4768374	3.5467259	0	8.183596	1.3383065	27.3701394	0	tumor
0	0.2760633	0.7649225	5.9654467	28.9467055	3.5460123	12.6654701	6.9623475	0	9.3287104	0	36.6844029	0	tumor
0.144886703	0.037815478	0.104875648	2.565561678	16.64023356	2.003103748	4.323002243	2.813306963	0	6.571072478	0.705768033	15.80036012	1.131525938	normal
4.65575616	0.21145884	0.69441787	4.40017311	32.01985205	11.57235443	31.41435471	9.68771626	0	1.53859753	2.84518432	35.09230381	0	tumor
0.87847551	0.09309837	1.26113349	3.26626058	15.82695157	3.11036638	5.57877231	5.54683845	1.93264612	3.61772978	1.07369229	13.33968521	0	tumor
0	0	0.3065233	0.6830005	22.6309191	1.5434724	6.525471	14.4086777	0	1.0448509	0	53.4649539	0	tumor
0	0.03101838	0.11459528	1.34055145	42.70531014	1.86849384	10.57151286	3.94818769	0	5.70309185	1.25205952	12.76078987	2.13188513	normal
0.65357368	0.18800202	0.87733959	6.92361439	6.49207339	3.44773019	2.07526489	2.6797217	0	9.81914084	0	21.30804594	0.68006991	tumor
4.633377596	0.303972406	1.454147601	1.090745666	21.72452441	2.306107854	17.16419604	7.994714582	0	2.061233513	1.887672354	22.32473208	0.803536205	tumor
0	0.01967434	0.31497052	1.61959068	7.65190495	1.13867204	11.34743109	10.09695056	0	1.65176148	0	58.19739788	0	tumor
0	0.08095736	0.61479893	0.81453833	11.47515348	2.05587695	1.41494544	4.12918451	0	0.67967832	0	24.19308561	0	tumor
0	0	0.18144566	2.147845256	10.08426275	2.240628463	0	2.34427696	0	9.030051505	0	16.72941648	1.265828675	normal
0	0.03413057	0.18913953	8.78008109	18.71826233	0.82641783	4.47391898	7.60256531	0	12.5506056	0	7.67291517	0	tumor
0	0.09014066	0	2.84447646	7.86343543	2.60848986	0	3.11251671	0	6.62179724	0	17.92636101	0	normal
0	0.03660198	0.18029798	8.63747481	17.70243573	4.77715338	8.63618054	3.96501958	0	8.02032877	0	12.7258822	0	tumor
2.0295674	1.3827076	1.2297802	1.6230517	7.9727401	0.9799049	4.8332997	3.2037553	1.1162621	2.2443169	0	5.4534636	0	tumor
1.55355482	0.04704039	1.18754784	2.96881099	27.40621644	2.6391671	6.1661712	10.5896931	3.41782061	5.1933045	1.89878923	49.34371463	0	tumor
0	0.1275098	0.353307	3.498865	58.280008	3.5769212	21.7285831	5.2229946	0	10.4374673	0	20.4836852	0	normal
1.04259603	0.09470691	0.38876462	0.24904742	8.22827484	2.74994993	7.86246387	6.90372892	1.14685563	0.50357147	0	36.9505884	0	tumor
0	0.037975059	0	3.178206171	48.21954182	5.068497489	15.92916718	6.427753997	0	7.874853841	6.131465146	16.86701543	0	normal
3.22142519	0.73156628	0.72072564	3.12822372	43.25916864	0.9072883	3.83582072	7.13242064	0.88589193	4.68829568	0	55.13202881	0	tumor
0	0	0.06730641	2.88698578	61.9269853	1.83982847	5.73145336	4.36649462	0	7.0663957	2.20615467	19.1021094	0	normal
0	0	1.7057305	3.2095116	31.8638438	2.2540607	0	11.5035382	0	4.6514802	2.4848913	57.3748413	0	tumor
1.122194909	0.016989581	0.115072529	2.109526631	64.27825181	2.217416484	7.126516121	4.290543127	0	5.505757193	2.057357333	18.1539326	2.335378594	normal
3.67259863	0.05560167	1.74604054	4.80598219	14.84315734	5.91061508	0.72884045	10.69121231	0	8.21575713	0	28.92171423	0.95537194	tumor
0.57954681	0.03509643	0.11885621	2.61225997	22.1684866	2.10378455	4.60052626	2.54253792	0	6.93906382	0.708335	18.09600703	3.01520978	normal

1.0132564	0	0.3211508	3.7463427	14.3862207	2.3917181	11.2607261	7.0002638	0	6.5425121	2.476849	31.6383335	0 tumor
0	0	0.1872285	3.4209223	18.1298707	3.070747	7.9716865	3.952734	0	6.6118415	1.2273867	15.858064	0 normal
0	0.07219924	0.05927446	1.46934955	3.05372712	0.83856299	1.26187392	1.31982739	0	4.88960521	0	19.82347921	0 normal
0	0	0.5055751	0.4506124	31.9068829	3.4428657	8.6104136	21.5139987	2.9828933	0.5514758	3.3143259	20.4019652	0 tumor
0	0.04396624	0.05414342	2.75971489	23.20884983	1.99932045	3.45792229	3.43812854	0	7.84377938	0.88735043	9.42389022	1.51089397 normal
1.85252638	0.05609301	0.69077255	2.27030681	12.05151121	2.2857577	13.97034068	4.74722215	1.01888951	3.57906384	0	24.35269913	0 tumor
4.69841655	0.03556607	0.41608858	3.83053397	21.96061398	0.92418923	8.39175945	22.70744967	0	8.39052813	0	42.40598399	0 tumor
0	0.010378895	0.212145875	2.704383793	8.588396755	1.972311767	1.3604915	2.704031625	0	8.558142388	0	17.55615765	0.632914338 normal
1.002946	0	0.8040567	3.2915675	12.9644214	1.9369481	1.592306	8.7795156	0	5.2011473	0	50.5816452	0 tumor
1.765364	0.267269	0.1974814	0.6600471	18.9626779	2.1466432	15.4150853	10.640125	0	0.9872983	2.1576671	44.1758006	0 tumor
2.13483402	0.06464106	0.61693085	4.83346694	13.33931351	4.90550748	9.32064132	16.49949328	0	4.66717428	0	40.03654274	0 tumor
0	0.04516146	0.11123059	2.26159363	54.70638863	2.66710597	11.83975085	3.69976453	0	6.82476229	0	9.08406367	0 normal
4.1005533	0	0.6498334	0.1703494	20.2097732	2.2547805	8.1376959	6.5149232	0	0.2345397	0	55.1758503	0 tumor
0	0	0	1.1111883	59.4489489	2.0139219	4.4700761	4.0981648	0	6.5132654	0	19.0882168	0 normal
13.6756425	0	0.7649088	5.6554518	29.4626692	4.7798054	10.8559224	15.1393295	0	14.632802	0	33.5087504	0 tumor
1.93899654	0.05871126	0	1.6513116	26.05436648	1.24823465	4.61761032	4.29304985	2.1328962	5.76705839	0	13.30579124	6.05281353 normal
0.738494212	0.279512654	1.748604091	3.144626688	10.7149292	2.443067823	4.103591548	7.539483239	0	2.853527981	0	24.91109609	0.768433166 tumor
0	0.02075779	0.24284609	3.26092233	7.09253076	1.70399507	2.720983	3.06378629	0	8.08623327	0	18.38289882	0 normal
0	0.08959919	0.49652704	5.90063969	18.57473446	3.28071205	9.39590694	8.79615489	3.25501062	6.16829348	0	38.41005728	0 tumor