

Supplementary Table 1 Results of gastric cancer prognostic model constructed using subgroups analysis of disulfidptosis-related genes

Gene	Coef
<i>PLS3</i>	0.164102182
<i>GRP</i>	0.079055019
<i>APOD</i>	0.064996712
<i>SGCE</i>	0.092021914
<i>COL8A1</i>	0.107438278
<i>VAMP7</i>	-0.072364309

risk.all

id	futime	fustat	PLS3 GRP	APOD	SGCE	COL8A1	VAMP7	riskScore	risk
TCGA-BR-65642	1.17534246575342	1	8.904285	8.328912	11.615144	9.010114	9.065679	0	3.26765979865963 high
TCGA-CD-85301	0.03287671232877	0	9.683478	5.236078	11.666171	8.688737	9.457866	0	2.95446045735552 high
TCGA-MX-A5UJ	1.64383561643836	0	9.391702	6.587037	8.823479	7.108749	7.773073	0	1.87961063585998 high
TCGA-BR-43670	0.00273972602739726	0	9.877328	8.741068	7.003012	7.669356	8.759202	0	2.50993198641509 high
TCGA-VQ-A8PX	5.38082191780822	0	8.266041	5.02148	6.081387	5.734897	5.213482	0	0.773311433599876 low
TCGA-HU-A4G8	1.89041095890411	0	8.956279	5.213748	5.834617	5.945369	6.779076	0	1.0438642070845 high
TCGA-VQ-A923	0.00273972602739726	1	9.474692	5.23635	8.94596	6.560918	7.212463	0	1.54530659258245 high
TCGA-BR-67100	0.747945205479452	0	7.330225	7.369912	9.299819	6.671698	5.376009	0	1.09184377906462 high
TCGA-D7-85731	1.62465753424658	0	8.99178	5.099411	5.662742	5.744946	6.130312	0	0.942140922787776 low
TCGA-VQ-A91E	1.81917808219178	0	10.036905	5.02148	6.243045	5.923561	5.324831	0	1.07611876198861 high
TCGA-HU-A4GC	0.271232876712329	0	7.915723	8.434371	9.47364	7.72265	7.428088	0	1.81589847994744 high
TCGA-CG-57190	0.0849315068493151	0	8.972264	9.389396	11.978876	7.982944	8.969545	0	3.31300926251493 high
TCGA-CD-85320	0.96986301369863	1	8.438149	7.026429	10.150567	7.28876	7.832139	0	1.85611932737249 high
TCGA-BR-42800	0.550684931506849	1	7.853324	5.02148	5.211636	5.745096	6.035834	0	0.746737528499992 low
TCGA-VQ-A8PE	1.84931506849315	1	9.095207	5.71201	10.203159	7.978284	7.374417	0	1.89665900314233 high
TCGA-D7-68151	1.33150684931507	0	8.717911	5.919927	11.104101	7.317208	8.210181	0	1.97809357269697 high
TCGA-F1-6874	1.20547945205479	0	9.242152	5.331961	5.240246	7.18009	7.648779	0	1.3068448839899 high
TCGA-HU-8244	2.03287671232877	0	7.193186	5.02148	5.396169	5.263755	4.905967	0	0.574610731729641 low
TCGA-BR-43660	0.00273972602739726	0	8.973808	6.74561	10.634165	8.401263	8.489156	0	2.43168952764809 high
TCGA-D7-65191	1.71232876712329	0	9.270992	7.456509	8.717636	8.916167	7.813046	0	2.3250214036804 high
TCGA-F1-A72C0	0.947945205479452	0	8.708915	7.5921	8.131513	6.282271	7.639786	0	1.58902934835316 high
TCGA-BR-8365	1.46027397260274	1	9.373379	10.303969	11.229842	9.181907			

	9.170602 0	4.13393481097026 high					
TCGA-VQ-A91A	3.28767123287671 0	10.426987	5.15927	6.488632	7.334143		
	9.417952 0	2.08296384057443 high					
TCGA-CG-44601.83287671232877 1	8.906564	5.02148	8.573613	7.396678	7.191217 0		
	1.45561574959268 high						
TCGA-VQ-A94P	0.221917808219178	1	9.845141	5.816993	11.891801	10.217483	
	8.601487 0	3.38415756017279 high					
TCGA-BR-83800.0575342465753425	0	9.200179	10.76424	11.164893	9.242793		
	9.402876 0	4.27819170019885 high					
TCGA-D7-65201.56986301369863 0	9.358727	9.383502	12.540388	9.198774	8.716568 0		
	3.98290086508547 high						
TCGA-R5-A7O7	3.80547945205479 0	8.029111	5.336687	7.725605	5.981908	6.916943 0	
	1.04245723185465 high						
TCGA-CD-58040.00273972602739726	0	8.443626	8.023576	11.765983	7.14711		
	8.024349 0	2.24977165376473 high					
TCGA-IN-8663 0.282191780821918	1	11.753348	10.071246	6.447572	5.91804		
	7.637258 0	2.76066314786149 high					
TCGA-BR-83810.613698630136986	0	8.847984	6.326712	9.134556	6.489407	8.629552 0	
	1.77980518925997 high						
TCGA-BR-77232.39452054794521 1	7.151852	5.124596	10.462447	6.899593	8.219537 0		
	1.32728432488543 high						
TCGA-R5-A7ZE 1.51780821917808 1	9.957235	5.02148	9.515935	6.68359	5.902598 0		
	1.49934375028111 high						
TCGA-BR-86830.821917808219178	1	10.209555	7.150314	9.902431	8.484634	9.45099	
	0	3.27663964626197 high					
TCGA-MX-A663	0.821917808219178	1	9.596502	6.4171	12.029065	8.680287	
	8.701387 0	3.01603587103724 high					
TCGA-D7-A6EX	0.942465753424658	0	7.375571	8.461335	9.565036	9.925229	7.69323
	0	2.11104749640315 high					
TCGA-BR-83722.60547945205479 0	10.131165	5.178724	7.864026	6.493972	6.769863 0		
	1.51340264896869 high						
TCGA-CD-A489	0.942465753424658	1	9.539792	9.547477	11.970762	9.420581	
	9.082003 0	4.2517710649082 high					
TCGA-BR-85892.26027397260274 0	9.518264	5.02148	6.835603	6.230697	5.669377 0		
	1.09641493040782 high						
TCGA-VQ-A91V	3.55342465753425 0	9.869486	5.608908	8.063534	5.687788	5.787978 0	
	1.26961711508884 high						
TCGA-CD-A48C	0.967123287671233	1	8.475668	9.419329	10.236194	6.306682	
	8.664967 0	2.26706492973206 high					
TCGA-CD-58011.0986301369863	1	8.308528	5.63008	7.531523	5.454507	7.258545 0	
	1.09000443720065 high						
TCGA-VQ-A8E7	3.11780821917808 0	9.119904	6.353332	7.845408	6.029822	7.429454 0	
	1.44514879470603 high						
TCGA-VQ-A8DU	0.454794520547945	1	9.058469	5.268254	9.470615	7.739889	

7.678114 0 1.7542863938692 high
 TCGA-BR-64540.00273972602739726 0 9.078596 6.352401 9.820905 12.310582
 7.583983 0 2.95745958328147 high
 TCGA-VQ-A94T 0.936986301369863 1 10.422474 5.02148 5.290792 6.112764
 7.29075 0 1.35441009270439 high
 TCGA-HJ-7597 2.20547945205479 1 9.279929 5.639562 6.506531 6.092195 6.688507 0
 1.19381808894479 high
 TCGA-KB-A93H 3.13698630136986 0 8.480966 5.373489 5.689266 6.421834 5.339518 0
 0.867007276136837 low
 TCGA-BR-41911.52876712328767 1 10.120459 5.364745 10.291125 7.870957
 7.397013 0 2.17963124259808 high
 TCGA-VQ-A8PC 3.85479452054795 1 9.341776 5.167393 8.731997 7.102263 7.296899 0
 1.57292902124787 high
 TCGA-BR-85881.06575342465753 0 8.505065 6.514277 9.708434 7.207618 8.712138 0
 1.91041853128411 high
 TCGA-VQ-AA6A 3.24383561643836 0 9.949657 5.02148 10.084398 6.696288
 6.672748 0 1.68985758538185 high
 TCGA-BR-43710.00273972602739726 0 9.098764 5.276228 6.332892 6.26384 6.019773 0
 1.05270728114093 high
 TCGA-CD-85351.06849315068493 0 9.502914 7.692034 7.429944 8.809506 7.291874 0
 2.11891224801651 high
 TCGA-VQ-A8DZ 1.08493150684932 1 8.15847 5.150099 9.863213 9.194148 7.212029 0
 1.67245987531438 high
 TCGA-BR-79010.287671232876712 1 9.349539 8.969458 11.099694 8.673675
 8.907856 0 3.40880248562332 high
 TCGA-D7-68181.03013698630137 1 8.619484 7.445188 10.4865 7.714191 8.371208 0
 2.22609861959538 high
 TCGA-SW-A7EB 0.482191780821918 0 6.911706 5.02148 10.455561 7.020799
 5.891894 0 0.996209959116124 high
 TCGA-BR-79582.46301369863014 0 8.959307 6.543389 7.556924 6.653539 8.117011 0
 1.59903127195304 high
 TCGA-BR-A4J6 0.0547945205479452 0 8.877748 8.265075 10.642987 7.067827
 8.182471 0 2.31142064508206 high
 TCGA-FP-8209 4.96164383561644 1 9.229959 7.115578 11.324839 9.753358 9.401753 0
 3.41176863793078 high
 TCGA-VQ-A924 4.61917808219178 1 9.498684 5.480587 9.090271 6.243586 6.924262 0
 1.50332911074152 high
 TCGA-BR-80800.8 1 9.170692 5.02148 10.858574 8.308037 9.386222 0
 2.42778786045503 high
 TCGA-CD-85270.597260273972603 1 7.688697 6.609597 9.953079 10.875627
 7.658838 0 2.14076595922309 high
 TCGA-BR-43690.00273972602739726 0 9.40565 5.253797 9.735955 8.653716 7.935668 0
 2.11045152513084 high
 TCGA-B7-A5TK0.789041095890411 0 10.963503 6.319051 10.347576 8.092656

8.098767 0 2.98144858072618 high
 TCGA-BR-65633.26027397260274 0 8.217034 5.940937 11.22149 8.058093 8.796922 0
 2.09686940700813 high
 TCGA-IN-AB1X 1.12602739726027 0 9.82765 5.295334 7.525261 6.114785 6.682627 0
 1.36000319289432 high
 TCGA-BR-43700.00273972602739726 0 10.172835 5.83387 8.138636 9.198529
 8.704656 0 2.57948387392407 high
 TCGA-HU-A4GX 1.68767123287671 0 7.677433 5.847535 7.279218 5.917349 6.563452 0
 0.952487425297818 low
 TCGA-IN-7806 3.03013698630137 0 7.582554 6.20151 9.591164 6.233807 7.459867 0
 1.27053048659265 high
 TCGA-VQ-A8P5 0.643835616438356 1 9.955936 7.234841 7.634376 7.545445
 8.308333 0 2.21504797782221 high
 TCGA-MX-A666 1.16986301369863 0 8.080172 5.09852 9.098461 7.428595 6.558804 0
 1.23987648948813 high
 TCGA-B7-A5TN 0.786301369863014 0 9.911672 10.232124 7.494793 7.907712
 9.460491 0 3.23170689307444 high
 TCGA-BR-42530.33972602739726 1 11.574243 5.109475 5.936251 6.326932 7.155158 0
 1.72706484560978 high
 TCGA-ZQ-A9CR 0.0657534246575342 1 9.159995 7.528785 6.595453 7.597929
 8.054663 0 1.81837889778371 high
 TCGA-VQ-A91Q 1.73424657534247 1 9.186508 8.497951 7.53153 10.273946
 8.743154 0 2.88630774170788 high
 TCGA-BR-80770.0575342465753425 0 7.749579 5.227622 9.562167 6.156673 6.938127 0
 1.13293926659956 high
 TCGA-RD-A8MV 10.1917808219178 0 7.535988 5.02148 8.770297 6.176153 7.018021 0
 1.03290516653372 high
 TCGA-D7-A6EY0.953424657534247 1 9.080116 8.71099 10.297014 7.120869
 8.209521 0 2.43908582380338 high
 TCGA-RD-A8N1 9.64109589041096 0 8.168354 5.02148 11.283993 6.742474 8.12867
 0 1.60154719030888 high
 TCGA-FP-8210 0.419178082191781 1 9.264421 6.66926 11.741843 8.698156
 9.337669 0 3.0670602732137 high
 TCGA-CD-A487 1.02465753424658 0 9.249843 6.689813 8.377778 7.171872 8.168895 0
 1.88754353705438 high
 TCGA-CD-57981.11780821917808 0 8.975604 7.469571 10.011724 8.83718 9.069062 0
 2.74032129100178 high
 TCGA-VQ-A8PF 0.208219178082192 1 9.435788 5.02148 9.380248 6.512875
 7.425108 0 1.58170605356384 high
 TCGA-R5-A7ZI 6.21095890410959 0 7.048105 5.307855 5.579642 6.335847 5.416783 0
 0.677213365657601 low
 TCGA-HU-A4H4 1.98630136986301 0 8.77964 5.02148 5.596446 5.919559 6.157477 0
 0.917689548287604 low
 TCGA-BR-83641.84931506849315 0 10.100235 8.081936 12.741424 9.270122

9.959549 0 4.73023160699499 high
 TCGA-IN-8462 1.56712328767123 0 9.087404 6.092097 10.678182 7.122141 7.583441 0
 1.90295779326476 high
 TCGA-HU-A4GU 0.547945205479452 0 8.393905 5.268254 4.413771 5.515878
 6.611055 0 0.82285670583443 low
 TCGA-CD-85311.04931506849315 0 6.10121 5.291925 7.711626 7.972646 7.219804 0
 0.938465696396891 low
 TCGA-VQ-A8E0 1.53972602739726 1 8.98694 5.02148 10.182111 7.750811 5.6246
 0 1.42966382416554 high
 TCGA-BR-83660.0794520547945206 0 9.643126 6.26336 11.051929 7.031844
 8.540531 0 2.37965358907218 high
 TCGA-VQ-AA6D 1.42739726027397 0 9.52103 5.65149 11.674876 8.707419
 6.495236 0 2.16730284102273 high
 TCGA-D7-A6EV 0.936986301369863 0 8.927065 5.245841 5.43208 5.7139
 7.177648 0 1.03668749630872 high
 TCGA-F1-6177 0.00273972602739726 0 7.907219 5.02148 5.093563 5.648258 6.471998 0
 0.776528369671768 low
 TCGA-BR-A4J7 2.70958904109589 0 9.168086 6.379309 11.317713 8.922326 9.005022 0
 2.82726877267345 high
 TCGA-BR-77152.8027397260274 0 8.997099 5.274239 9.862366 7.174434 8.237075 0
 1.79669063656713 high
 TCGA-D7-85751.51780821917808 1 9.121032 5.583965 10.859073 6.37574 6.762885 0
 1.58989885371384 high
 TCGA-BR-43630.00273972602739726 0 9.889343 8.047358 9.377888 8.464185 8.967198 0
 3.05638741721261 high
 TCGA-IN-A7NU 0.975342465753425 0 8.454931 9.527406 8.653267 6.58414
 7.504191 0 1.86183478601102 high
 TCGA-CG-44400.334246575342466 1 9.812301 6.649258 8.08539 8.668019 6.866882 0
 2.02012379329585 high
 TCGA-HU-A4G3 0.465753424657534 0 7.847315 5.02148 7.801651 5.984858
 6.005059 0 0.899489221430774 low
 TCGA-HU-A4HD 2.78356164383562 0 7.743653 5.35784 8.664734 6.982583 7.535191 0
 1.24104832536247 high
 TCGA-FP-A9TM 0.517808219178082 0 8.494902 5.104303 7.650282 5.973975
 5.537502 0 0.947258101878183 low
 TCGA-D7-65281.26849315068493 0 9.624686 7.055189 4.887897 5.847535 6.822265 0
 1.26149207109923 high
 TCGA-CG-44370.671232876712329 0 8.403079 6.438776 8.739331 6.349944 7.728876 0
 1.4579979073948 high
 TCGA-VQ-A8DT 4.06575342465753 0 8.364525 5.179852 6.917019 6.835545 6.124171 0
 1.02536438283892 high
 TCGA-CG-44360.665753424657534 0 9.375384 5.02148 9.749386 5.704317 6.148659 0
 1.29827938270549 high
 TCGA-VQ-A8PD 1.35890410958904 1 9.42535 5.87686 7.009889 7.280647 8.066649 0

1.6651672960116 high
 TCGA-CG-44432.4986301369863 0 7.880975 5.492635 6.336674 6.42304 7.194337 0
 1.00976767216589 high
 TCGA-VQ-AA68 3.63835616438356 0 9.746311 5.092716 7.233173 5.704012 6.632393 0
 1.24102697005296 high
 TCGA-D7-85761.22191780821918 1 6.629324 5.245571 6.912968 6.510455 8.356427 0
 0.956135372900999 low
 TCGA-BR-86772.22739726027397 0 9.724272 7.294644 10.269797 8.080361 9.001263 0
 2.87758132482317 high
 TCGA-VQ-A925 0.378082191780822 1 10.033907 5.181825 7.680788 7.204253
 6.220816 0 1.48157885115446 high
 TCGA-BR-83840.30958904109589 0 9.43143 8.628779 10.973141 9.608638 9.028497 0
 3.68267789505872 high
 TCGA-BR-77171.51232876712329 1 7.60161 9.075989 9.097402 6.610639 7.506622 0
 1.6118954978748 high
 TCGA-BR-42670.515068493150685 1 9.284738 5.455971 5.968307 6.082991 7.254141 0
 1.20728375950201 high
 TCGA-BR-43680.00273972602739726 0 8.452734 6.149885 8.510867 7.849274 8.152214 0
 1.70059624480057 high
 TCGA-CG-57200.0821917808219178 1 7.753653 5.02148 10.958089 6.69822 7.57959
 0 1.37529682584635 high
 TCGA-CD-58001.0958904109589 0 7.774043 5.204892 10.774988 7.2255 6.562673 0
 1.30197169523379 high
 TCGA-VQ-A8PJ0.224657534246575 1 9.697103 5.144339 13.228979 7.845345
 6.378192 0 2.16277360774638 high
 TCGA-D7-55772.14246575342466 1 9.229498 6.551784 6.569005 6.260654 6.570153 0
 1.28125916071349 high
 TCGA-RD-A8MW 3.15890410958904 1 7.022779 5.833128 8.66533 7.063994 8.048663 0
 1.21887735420334 high
 TCGA-D7-A6F01.85753424657534 0 7.877665 5.497359 12.36727 9.774413 6.823827 0
 1.95445673168402 high
 TCGA-D7-A4YX 3.03561643835616 0 9.623552 5.02148 5.602721 5.89735 7.041925 0
 1.15717232904825 high
 TCGA-IN-A7NT0.884931506849315 0 12.026265 5.02148 6.290515 7.528303
 7.917069 0 2.29121342329701 high
 TCGA-CD-85241.06301369863014 0 9.957868 10.737774 11.159387 9.401148
 8.729158 0 4.56130024558733 high
 TCGA-HU-A4GD 1.8958904109589 0 7.545983 5.669214 8.808108 6.39902 5.702142 0
 0.96735732908177 low
 TCGA-IN-A6RS 1.04931506849315 0 8.553469 5.02148 6.885191 5.533924 6.676486 0
 0.981206313235338 high
 TCGA-BR-42940.00273972602739726 0 7.168575 5.02148 6.771346 8.241454 6.100731 0
 0.935810534988265 low
 TCGA-BR-65662.73150684931507 0 7.37162 6.607452 7.045697 6.07709 7.807502 0

1.09899097549172 high
 TCGA-VQ-A91X 0.791780821917808 1 8.372433 5.02148 6.757641 5.338974
 5.008482 0 0.77559953648398 low
 TCGA-BR-65650.764383561643836 1 8.522991 5.339872 10.937801 6.924276
 7.754313 0 1.66253825139984 high
 TCGA-HU-A4GY 0.0219178082191781 0 8.557956 5.14015 11.270534 7.798504
 8.531315 0 1.98148933172068 high
 TCGA-KB-A6F75.3013698630137 0 5.3 5.02148 10.646617 6.774222 5.437591 0
 0.720821518467661 low
 TCGA-BR-77072.98630136986301 0 8.826979 5.137544 6.064724 6.08504 7.248767 0
 1.09851412795906 high
 TCGA-D7-68221.02739726027397 0 9.432993 5.02148 7.501368 8.851407 7.19212 0
 1.69230028353048 high
 TCGA-VQ-A8P3 3.1013698630137 0 8.295597 5.142318 7.563685 6.353228 7.750969 0
 1.20105143020788 high
 TCGA-VQ-A927 0.547945205479452 1 8.670228 5.155551 7.409562 6.725185 6.93189
 0 1.19953206365754 high
 TCGA-D7-65211.54520547945205 0 9.282209 5.885049 8.448441 6.826551 9.038293 0
 1.90253908242683 high
 TCGA-BR-84842.0986301369863 1 9.452497 5.092716 9.105697 6.861409 8.636582 0
 1.84275940691766 high
 TCGA-BR-71961.82465753424658 0 9.826583 5.542493 11.422838 8.421828 9.251344 0
 2.91088699529495 high
 TCGA-VQ-A91Z 4.63013698630137 0 9.750724 5.246652 5.745736 7.83998 5.901283 0
 1.28423214116121 high
 TCGA-CG-43051.32876712328767 0 8.979385 10.032241 11.080162 6.998287 8.29843
 0 2.79747912050728 high
 TCGA-D7-85741.43287671232877 0 8.418101 5.102822 9.414645 7.764519 9.338723 0
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 TCGA-BR-83672.19452054794521 1 9.399484 5.119181 13.819725 8.170954 8.932264 0
 2.89599136056818 high
 TCGA-BR-82961.2986301369863 1 8.311184 6.535659 7.928902 6.877297 7.786936 0
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 TCGA-CG-57241.0027397260274 1 8.913126 8.608362 7.501337 6.701982 7.197068 0
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 TCGA-CG-44772.58082191780822 0 9.86493 5.461043 8.440238 7.653477 7.567411 0
 1.86419337697903 high
 TCGA-CG-44661.58082191780822 0 5.58003 5.103267 9.804521 5.843678 6.192804 0
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 TCGA-VQ-A8PQ 1.3041095890411 1 9.780659 6.993428 10.443707 8.298477
 8.368691 0 2.7341026960409 high
 TCGA-RD-A8N6 0.745205479452055 1 9.09986 7.276019 12.364474 8.082304
 7.937982 0 2.65143019132405 high
 TCGA-BR-84830.449315068493151 0 8.829958 10.237316 11.614767 7.860001

7.630317 0 2.89409610907411 high
 TCGA-D7-A6F21.3041095890411 0 8.826241 5.327862 8.750426 5.956531 7.357124 0
 1.32745132235387 high
 TCGA-BR-A4CS0.123287671232877 1 8.274909 6.277522 12.675357 5.684406 7.52921
 0 1.67601035572038 high
 TCGA-BR-82970.616438356164384 0 9.50258 7.153224 10.444621 9.321748
 8.556592 0 2.96599669145238 high
 TCGA-BR-64581.61095890410959 1 9.751254 6.871335 9.250348 12.420276 9.215496 0
 3.99097875797217 high
 TCGA-CG-57210.501369863013699 0 9.350342 5.02148 7.953945 6.196311 7.222753 0
 1.35108188358765 high
 TCGA-FP-8211 1.13150684931507 0 8.221557 7.133345 6.803993 5.993418 6.441354 0
 1.11099637641542 high
 TCGA-VQ-A92D 5.56712328767123 0 10.493763 7.909589 6.988501 6.024696
 7.165377 0 1.88166242355095 high
 TCGA-ZA-A8F6 1.43835616438356 0 8.887055 5.097034 11.901779 8.301345 7.869344 0
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 TCGA-D7-A74A 1.66301369863014 0 9.9425 6.472524 6.286587 5.437339 5.860978 0
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 TCGA-FP-7998 1.85753424657534 0 9.67107 5.231447 8.893415 7.157377 8.805448 0
 1.99307843541294 high
 TCGA-BR-86782.06575342465753 0 8.400626 8.010387 5.922839 8.719506 8.594115 0
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 9.372472 0 2.94262511566728 high
 TCGA-IN-7808 0.287671232876712 1 7.240082 5.02148 8.752602 7.32562 5.008404 0
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TCGA-HU-A4G2 2.02465753424658 0 9.16236 5.166114 6.011328 6.910131 6.199584 0
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0 2.31382737169861 high
TCGA-BR-A4J9 0.0383561643835616 0 9.067245 6.601679 11.177347 9.08336 7.87935
0 2.52211403121546 high
TCGA-CG-57160.00273972602739726 0 7.960247 5.320663 8.413432 5.912643 5.54931 0
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GSM2235942 3.45205479452055 0 7.499712 4.949032 7.28966 6.495158 5.620273
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 GSM644666 1.06027397260274 1 10.018121 7.125939 9.67951 7.897318 7.842912
 10.820127 1.13789660684244 high
 GSM644667 1.54520547945205 1 10.18951 8.414783 10.134482 8.132732 9.178347
 11.233553 1.52804761703289 high
 GSM644668 4.87397260273973 0 9.638309 7.004937 9.685145 7.904663 8.180156
 10.958981 1.08818882045797 high
 GSM644670 0.542465753424658 1 7.639799 6.160473 10.304244 6.831891
 6.593059 10.297658 0.611804674408512 low
 GSM644671 0.6 1 8.898803 3.644175 10.768856 8.240305 7.354119 10.718914
 0.761415095500073 low
 GSM644674 3.13150684931507 1 10.069757 6.975071 10.147061 4.837836
 9.680291 7.681906 1.34861494991218 high
 GSM644676 9.22191780821918 0 9.562456 4.315117 9.376843 8.304363 7.434823
 10.420836 0.84791999526717 low
 GSM644677 3.02465753424658 0 9.119745 6.885637 9.535897 7.305378 8.663035
 7.970095 1.2132543692566 high
 GSM644679 9.75616438356164 0 7.980704 5.161832 9.728736 8.678585 8.071967
 10.719386 0.776123925526584 low
 GSM644690 10.7424657534247 0 7.852407 7.014225 7.437601 4.825226 6.354035
 10.665505 0.443863483022295 low
 GSM644693 9.58356164383562 0 9.305219 7.743383 6.064934 5.379758 9.196848
 9.936878 0.821830393460665 low
 GSM644694 10.3315068493151 0 10.111723 7.662703 9.969184 5.063456 8.057208
 8.5784 1.13913673799737 high
 GSM644695 6.4027397260274 0 9.568164 7.330838 8.109491 7.614083 6.096317
 7.234184 1.01539131845191 high
 GSM644697 9.58356164383562 0 7.925208 6.423406 9.716727 5.318188 9.438774
 9.439948 0.791841523767091 low
 GSM644699 1.32328767123288 1 8.853896 7.827265 5.333629 7.526904 7.270531
 7.446766 0.869040179315525 low
 GSM644700 5.40821917808219 0 9.585365 6.883125 7.459588 5.147809 6.612106
 10.635773 0.620500957057423 low
 GSM644703 4.07671232876712 1 8.634492 8.021672 7.708469 6.937921 8.165263
 10.302205 0.842528575197841 low
 GSM644704 9.44383561643836 0 10.194685 7.602292 8.994439 4.744721 6.099479
 10.790828 0.723241201397163 low
 GSM644705 0.50958904109589 1 9.436741 7.01242 4.130499 5.380348 6.968391
 11.489643 0.491699039919948 low
 GSM644706 6.94520547945205 0 8.678672 4.081164 9.483458 5.24914 7.239671 7.70208

0.652503501758428 low
GSM644709 6.15616438356164 0 9.437391 7.465592 10.073186 5.153004 8.748052
9.755018 1.00813981939616 high
GSM644710 5.86027397260274 0 7.4872749 7.3700953 4.1689399 5.0174406
7.8247828 8.9119542 0.470537772546306 low
GSM644712 1.30684931506849 1 9.388655 7.166286 9.117605 7.950942 6.957512
10.009118 0.961798052962925 low
GSM644713 1.59452054794521 0 8.378966 4.7489 8.407126 5.130746 7.408046
9.102897 0.55573405516968 low
GSM644717 2.0958904109589 1 10.174245 7.637563 9.057747 7.841137 9.477367
9.934487 1.47603218880635 high
GSM644718 5.81917808219178 0 8.374093 5.149306 5.145847 5.308802 7.424815 8.74192
0.484675900378557 low
GSM644720 5.00547945205479 0 9.328016 3.618764 8.61635 4.909615 6.570539
6.975557 0.62885535346747 low
GSM644721 5.0958904109589 0 7.776563 6.163814 4.086465 4.82334 5.121461 7.46496
0.363956678221413 low
GSM644722 3.61643835616438 0 9.972057 7.267428 9.289094 5.319018 8.340476
10.034075 0.980700037158518 high
GSM644723 5.62191780821918 0 9.530338 7.189292 8.176747 6.415945 6.983727
9.553969 0.834823840004927 low
GSM644724 5.35068493150685 0 9.872941 7.120353 9.078067 7.318622 7.105289
8.785558 1.08388545012099 high
GSM644726 0.468493150684932 1 10.60753 7.506295 8.272802 5.406461 8.62687
10.810486 1.02046026779507 high
GSM644727 1.01917808219178 1 7.374043 7.274224 7.687741 8.017606 6.216809
7.524065 0.706400741741282 low
GSM644728 5.02191780821918 0 9.566161 7.55479 9.934838 7.605068 10.017184
9.599298 1.49266519184731 high
GSM644730 1.04383561643836 1 9.780052 5.39911 10.117299 7.124155 8.314095
8.409899 1.14561752562536 high
GSM644731 4.42191780821918 0 9.534386 6.739392 7.537243 7.900194 6.97612 9.04429
0.919105787351022 low
GSM644734 0.410958904109589 1 9.748144 7.298287 10.610308 7.56749
7.039059 9.694875 1.13169164390686 high
GSM644736 8.76164383561644 0 9.90762 7.955403 8.21991 7.820237 6.917325
11.072731 0.957850070270697 low
GSM644739 9.46027397260274 0 9.908359 7.438982 9.490159 7.689884 7.963866
10.352235 1.16343288423013 high
GSM644743 4.66027397260274 0 9.7083749 3.6400409 9.5736168 4.7371751
6.2993264 7.4020734 0.661393388483832 low
GSM644746 0.789041095890411 1 7.72432125 3.67238967 4.69144757
8.54065906 8.09820788 7.09534217 0.613673269650784 low
GSM644748 3.7972602739726 1 7.8084604 3.5218735 9.2076302 8.2864173

7.5236601 10.3686828 0.597593504152031 low
 GSM644749 11.9835616438356 0 8.425682 3.966337 9.897835 4.850446 7.387166
 8.841598 0.574702995679109 low
 GSM644755 2.13698630136986 0 8.66202925 4.15534506 6.06167565 8.67707949
 5.63657263 7.87309646 0.597277072113999 low
 GSM644760 9.16438356164384 0 9.000664 6.543493 9.605337 8.521148 8.27228
 7.021155 1.33615335511716 high
 GSM644765 5.13698630136986 0 8.13603296 3.89101671 4.35636895 5.85339965
 6.44258544 8.34192443 0.39039457411318 low
 GSM644766 3.81369863013699 0 8.953887 3.6546561 8.5447598 7.6381683
 7.6691754 10.0415492 0.683990547836225 low
 GSM644768 1.91506849315068 1 7.67803 3.610405 10.555346 8.282861 7.968202
 7.150123 0.851028161880759 low
 GSM644769 4.73424657534247 0 7.812734 3.707453 4.173296 5.472007 3.466414
 9.836603 0.226938832471526 low
 GSM644773 7.96438356164384 0 7.125164 5.462352 9.570568 8.592289 8.591694
 9.742127 0.769706722478505 low
 GSM644774 5.68767123287671 0 7.64598 6.259397 8.545334 8.341787 6.510128
 10.572508 0.61465964078312 low
 GSM644775 4.92328767123288 0 7.475756 6.602526 9.437581 8.329913 7.977907
 7.162688 0.974189647508419 high
 GSM644776 2.49041095890411 1 7.239237 6.91095 8.878297 8.089841 7.927272
 9.682561 0.750652376848485 low
 GSM644778 7.17534246575342 0 8.695663 3.73662119 7.29133529 8.3706901
 7.00061019 6.97086777 0.756245878514063 low
 GSM644786 6.04109589041096 1 9.319119 7.004504 9.531367 7.911559 8.581419
 8.260838 1.29835808383622 high
 GSM644788 5.97534246575342 0 7.420894 6.079658 7.586074 8.43793 7.036546
 10.002413 0.610472228223168 low
 GSM644791 6.57534246575342 0 7.920502 5.588428 9.538003 7.409229 7.917798
 9.164972 0.768831890193486 low
 GSM644792 5.62191780821918 0 9.311398 6.380984 3.74371 8.290586 6.23642
 10.066745 0.598466506637566 low
 GSM644793 1.16712328767123 1 7.244168 6.577766 9.313306 8.013262 7.752609
 7.993852 0.828880471833245 low
 GSM644794 6.04109589041096 0 9.482366 6.978603 9.35222 8.337957 7.863627
 10.956459 1.04211358598968 high
 GSM644795 0.772602739726027 1 9.371774 7.262306 10.280372 8.260128
 8.485634 9.376974 1.32289333616221 high
 GSM644796 5.95890410958904 0 8.935622 4.925094 9.157262 8.20343 7.619859
 9.488011 0.855739748262319 low
 GSM644797 5.16164383561644 0 7.913962 3.683777 4.466684 4.769571 5.583683
 7.923189 0.317281349337485 low
 GSM644799 5.45753424657534 0 7.639799 5.558555 9.019369 7.936238 7.623378

9.031949 0.727219068036545 low
 GSM644801 0.526027397260274 1 7.43981 4.4123191 8.8873574 8.7511286
 6.2993264 7.2545689 0.677605976274721 low
 GSM644802 0.156164383561644 1 8.610195 4.251199 10.4953 8.269851 8.885202
 9.538785 0.96356557131808 low
 GSM644803 5.0958904109589 0 9.998623 6.835534 10.189105 7.744944 9.338342
 10.428713 1.36494607126097 high
 GSM644804 5.087671232876710 7.197431 3.6259666 4.2218048 6.0450214
 4.1520064 7.4206139 0.276341961640765 low
 GSM644807 0.378082191780822 1 8.22191 3.889884 4.317888 8.95177 8.172218
 7.95055 0.65062155082434 low
 GSM644811 3.6 0 7.8121 3.845023 4.116364 4.69291 6.01938 7.730721
 0.325946955818962 low
 GSM644813 1.627397260273971 9.305937 7.091236 10.335361 8.35554 9.752914
 7.724007 1.68812360073945 high
 GSM644816 10.7342465753425 0 7.245483 6.57627 9.660412 7.751429 7.843789
 7.441888 0.869900276079887 low
 GSM644819 0.805479452054795 1 8.392868 3.941535 9.726312 8.534784 5.991263
 8.91683 0.67788772938413 low
 GSM644820 10.2657534246575 0 9.968677 4.962924 5.138755 8.91899 9.741541
 7.244818 1.23573097698668 high
 GSM644824 2.05479452054795 1 7.664236 6.631277 8.404884 8.127572 8.784041
 7.014108 1.0188488665174 high
 GSM644825 8.42465753424658 0 9.279746 6.262349 8.670602 5.34205 6.788916
 7.408443 0.796657594278767 low
 GSM644826 4.27397260273973 0 7.072719 3.687895 4.234948 9.465632 6.212045
 8.772153 0.422089989189455 low
 GSM644828 1.43835616438356 1 8.2183388 3.9062871 4.1645861 5.7517048
 5.9788926 7.2140938 0.400152065858468 low
 GSM644830 1.33150684931507 1 7.760682 6.971188 9.766735 8.063603 7.999293
 8.283805 0.968321290745743 low
 GSM644833 8.0958904109589 0 9.388995 5.573533 4.604049 8.721633 5.583683
 10.407578 0.56910402404549 low
 GSM644834 1.17534246575342 1 7.225881 7.437292 10.003064 8.187271 7.875756
 7.392075 0.994905134781218 high
 GSM644837 5.087671232876710 8.163982 6.376847 9.946021 8.431386 7.573097
 9.510488 0.902979615478892 low
 GSM644840 2.31780821917808 0 7.407369 3.744016 10.090206 8.730371 5.434918
 8.733936 0.564961016835639 low
 GSM644842 7.01917808219178 0 7.1622697 3.7366212 4.1836531 8.4136883
 6.2164223 7.7168323 0.420089600085213 low
 GSM644846 4.73424657534247 1 7.01504549 3.59794085 10.45722034 8.01717633
 7.15418424 8.40683395 0.6185872936664 low
 GSM644851 1.47945205479452 1 7.337393 3.56423 9.598407 8.50966 8.230946

7.760445	0.757203016343658	low		
GSM644852	2.95890410958904 0	7.358305	5.552601	8.930845 8.291101 7.228724
8.119138	0.730054132261454	low		
GSM644853	6.53424657534247 0	7.110692	3.914143	9.108008 8.662037 6.71601
7.097074	0.656867039191618	low		
GSM644854	1.89041095890411 1	9.174541	6.425703	9.780294 8.627101 7.958661 8.30613
1.22563266747269	high			
GSM644855	4.9972602739726 0	7.543337	5.357274	6.408064 8.409573 6.698596
8.133016	0.600048508008161	low		
GSM644859	5.08767123287671 0	9.126701	6.737821	9.484937 8.243836 7.86627
8.785558	1.12884524295345	high		
GSM644861	5.54794520547945 1	7.887262	6.174099	8.806772 8.812554 7.794435
7.503311	0.967115467320634	low		
GSM644864	4.91506849315068 0	8.312807	3.8112122	4.3805068 5.4668409
8.0982079	9.8983603 0.412032339276669	low		
GSM644865	5.17808219178082 0	7.299367	3.637361	9.002497 8.595768 8.107811
6.948902	0.768055191261231	low		
GSM644866	0.879452054794521	1	7.108061	6.815203 9.82518 7.836742 8.091999
7.50644	0.902593441109351	low		
GSM644867	5.02191780821918 0	7.255537	5.609663	9.399613 8.408987 7.913593
8.733495	0.773716378280193	low		
GSM644868	0.986301369863014	1	8.108381	5.225565 7.629924 7.817109 6.431831
9.14666	0.603175371296538	low		
GSM644871	4.21643835616438 0	8.529452	4.459655	9.20243 8.765752 6.978712
9.883228	0.739309031530346	low		
GSM644873	3.26301369863014 0	7.167489	5.026004	9.716727 8.852506 6.852926
7.415406	0.760112558849283	low		
GSM644874	1.91506849315068 1	8.608823	7.218004	10.179335 7.417493 8.224782
9.972143	0.995922932733674	high		
GSM644875	12.6986301369863 0	9.61411063	6.4831178	7.94360686 7.2385302
8.45199761	8.85546103 1.04730913347911	high		
GSM644878	2.12876712328767 1	9.022702	5.268993	4.998905 7.341274 7.835924
10.486946	0.598695361205496	low		
GSM644879	1.59452054794521 0	9.4350439	3.7005811	4.4337798 7.6962366
6.2331247	10.0434298 0.489925856691873	low		
GSM644881	11.8191780821918 0	7.566358	7.314784	8.245537 5.006279 7.061651
10.231836	0.517452485971929	low		
GSM644885	2.07123287671233 1	7.135568	6.951971	9.180735 6.072074 7.416549
7.695358	0.685455333438317	low		
GSM644886	7.87397260273973 0	6.979151	6.876401	7.80573 7.11333 6.205613
9.218281	0.525621932893674	low		
GSM644887	2.4986301369863 1	9.814297	6.772833	7.867222 7.871777 8.482212
9.169062	1.14549755412924	high		
GSM644888	0.517808219178082	1	9.500089	7.011067 9.835312 7.947081 8.917163

9.674162 1.28163759884889 high
 GSM644890 1.45479452054795 1 7.69333148 7.2119804 10.06926653 7.43843716
 8.88435858 10.68288396 0.868844573934712 low
 GSM644891 7.15890410958904 1 9.424968 4.5176765 4.1847856 4.7610619
 5.8353199 7.9704953 0.436234042477099 low
 GSM644895 9.53424657534247 1 9.487328 6.90208 9.694676 8.386416 7.408046
 11.492704 0.975292024793045 high
 GSM644897 4.25753424657534 0 9.146845 6.686959 9.090133 5.152264 7.136667 8.38618
 0.787288959467006 low
 GSM644898 2.76164383561644 0 8.501851 6.478201 8.939329 5.24378 6.378543
 10.519294 0.549524804070291 low
 GSM644899 1.07671232876712 1 7.614151 5.507533 9.750436 4.921491 7.527876
 9.943578 0.531046461261058 low
 GSM644904 1.33972602739726 1 8.820221 7.972102 8.614085 6.911921 7.451788
 10.180053 0.855444971348388 low
 GSM644905 2.35068493150685 1 9.93372 7.673591 9.429701 7.775376 8.444967
 10.727421 1.22453353747985 high
 GSM644908 5.8027397260274 1 7.581863 5.951441 8.65238 4.723245 8.810518
 9.538785 0.591184733721976 low
 GSM644909 0.542465753424658 1 9.8286193 7.1580918 9.9138198
 6.2787376 8.8877571 11.1642392 1.05576443926401 high
 GSM644914 6.15616438356164 0 9.831485 7.623234 10.44077 8.147347 7.929835
 10.147372 1.30784091331374 high
 GSM644915 6.77260273972603 0 9.51378 7.878953 9.649463 7.696608 9.049518
 8.010672 1.51962686384697 high
 GSM644916 6.86301369863014 0 9.418043 7.228203 8.730787 7.715974 6.79964
 10.891319 0.854876081148943 low
 GSM644918 1.43835616438356 1 9.989104 7.22103 10.032854 7.88224 9.182507
 10.89857 1.33878587897893 high
 GSM644920 4.58630136986301 0 9.6298347 7.2423106 8.641492 5.9574909
 7.9144597 10.5969372 0.862885032106304 low
 GSM644921 0.558904109589041 1 9.79928 7.732784 7.513088 7.520848 7.891045
 10.675312 0.981611471517793 high
 GSM644923 7.03561643835616 0 9.741653 7.030456 9.307704 7.106715 7.40299
 8.947202 1.06995175279313 high
 GSM644925 2.04657534246575 1 10.205415 7.462587 10.481312 7.826168
 9.693237 10.563137 1.56751304369124 high
 GSM644926 6.77260273972603 0 8.519591 7.272643 9.585335 5.794621 7.164185
 9.721479 0.742177754874031 low
 GSM644929 1.18356164383562 1 9.376353 4.514252 9.112399 8.003705 8.025919 8.33497
 0.989878761137947 high
 GSM644931 2.48219178082192 1 9.376353 8.263857 9.482744 8.446324 8.290385
 10.172968 1.27949114896324 high
 GSM644932 6.07397260273973 0 9.5624563 8.0324226 7.0454086 4.7614704

	8.153145	10.9658712	0.732770719028682	low				
GSM644934	6.0986301369863	0	8.731518	6.762061	8.00181	8.372931	7.095393	
	10.045287	0.818535244450672	low					
GSM644935	1.45479452054795	1	10.020025	7.275741	9.246003	7.565003	9.209603	
	10.086149	1.32647954404932	high					
GSM644938	5.06301369863014	0	9.267808	5.534124	6.927335	6.789055	6.252735	
	9.887892	0.604085439670382	low					
GSM644941	5.02191780821918	0	9.300439	7.854176	9.391005	7.831686	7.669999	
	10.671082	1.03706612120828	high					
GSM644942	3.62465753424658	1	9.619179	5.751437	8.568012	7.294702	8.444967	
	9.209965	1.00859408088282	high					
GSM644944	5.17808219178082	0	7.907396	6.044595	9.126121	4.699005	5.880175	
	7.364415	0.552244170330096	low					
GSM644945	0.435616438356164	1	8.122477	4.23286	9.507885	7.095731	5.250052	
	7.785169	0.574371625709419	low					
GSM644948	4.47123287671233	0	7.71965	6.605557	4.514685	8.326703	5.611025	
	7.873096	0.542343623683316	low					
TCGA-BR-A4J4	0.0438356164383562	0	10.378046	6.156234	7.8356	6.091557		
	8.342571	0	1.93913452500917	high				
TCGA-RD-A7C1	1.38904109589041	1	8.508188	5.548072	6.01325	6.967192	7.06059	0
	1.14078056698931	high						
TCGA-BR-68523	7.4520547945205	0	8.459383	5.516115	8.156629	6.487493	8.147964	0
	1.39538829726655	high						
TCGA-BR-78511	1.03561643835616	0	7.662307	5.254603	9.296951	6.69358	8.285227	0
	1.33579414562295	high						
TCGA-BR-84870	0.0931506849315069	0	7.917616	7.726558	6.562743	5.945505	7.11035	0
	1.16656392128836	high						
TCGA-D7-65261	4.3287671232877	0	8.447452	5.474761	11.594171	6.712848	7.457695	0
	1.64534616211272	high						
TCGA-FP-7735	0.29041095890411	1	8.00199	5.02148	9.938707	6.870616	6.390369	0
	1.1987293244817	high						
TCGA-D7-55781	0.05479452054795	0	7.521261	5.195845	8.252979	6.713519	8.152397	0
	1.19894734629241	high						
TCGA-BR-82950	0.183561643835616	1	7.869093	5.558838	8.335984	7.184265	6.171969	0
	1.10866944113432	high						
TCGA-D7-85791	7.4246575342466	0	8.784263	5.090776	10.246758	8.338423	8.78967	0
	2.07089831487669	high						
TCGA-3M-AB46	4.83561643835616	0	7.681721	7.199406	7.582596	6.185461	7.221426	0
	1.19003156197615	high						
TCGA-D7-85721	4	0	7.996892	6.994707	10.137291	7.756102	8.759725	0
	1.98450588167782	high						
TCGA-BR-68022	5.7534246575342	0	9.685451	5.982294	7.206433	6.103266	7.373317	0
	1.4782859716398	high						
TCGA-VQ-A91N	1.56164383561644	1	8.58824	5.090477	7.785283	6.844411	6.355462	0

1.14659227074061 high
 TCGA-HF-A5NB 2.54246575342466 0 8.478275 5.708697 4.789349 5.55313 6.075875 0
 0.838644687999994 low
 TCGA-VQ-A8PP 1.95068493150685 1 8.590248 7.411433 7.430538 6.42534 8.297805 0
 1.59626743634652 high
 TCGA-MX-A5UG 0.30958904109589 1 9.568879 5.640192 10.367822 8.136175 9.30833
 0 2.57321276810194 high
 TCGA-CG-57325.75342465753425 1 6.938145 5.02148 10.091617 5.987001 5.801407 0
 0.879881935099159 low
 TCGA-HU-A4GT 0.542465753424658 0 8.243122 5.331577 6.694905 5.831201
 6.536926 0 0.95562234568282 low
 TCGA-CG-44690.589041095890411 1 7.401702 5.258362 5.794781 6.151093 6.025524 0
 0.760886158126159 low
 TCGA-BR-86900.89041095890411 0 7.245044 7.48233 10.276664 6.492911 7.822555 0
 1.48092768824005 high
 TCGA-CD-58030.934246575342466 1 9.175441 7.496968 11.411609 8.578685
 9.823335 0 3.29126911993726 high
 TCGA-CD-85281.02739726027397 0 9.519701 5.281786 6.232667 6.286942 7.629951 0
 1.3357429090294 high
 TCGA-RD-A7BS 0.920547945205479 1 9.661562 7.203306 10.16743 7.303506
 7.892097 0 2.32130716646379 high
 TCGA-VQ-A8PB 2.85753424657534 1 11.594792 5.811264 5.489225 6.225303
 7.108495 0 1.75392251592497 high
 TCGA-BR-A4CR 0.00273972602739726 0 8.071057 13.500545 7.230259 8.752177
 7.546793 0 2.67582467431241 high
 TCGA-HU-A4H3 2.41643835616438 0 8.568964 7.963043 5.565111 5.745245 6.565877 0
 1.14783460169653 high
 TCGA-VQ-A8E3 1.81095890410959 1 9.434345 5.105635 5.675261 6.308184 6.440866 0
 1.10464810141159 high
 TCGA-BR-68013.35068493150685 0 8.998852 5.542269 7.629855 6.572406 7.580957 0
 1.39993442119773 high
 TCGA-HU-A4H5 1.98356164383562 0 8.763474 5.02148 6.321781 6.624367 6.313453 0
 1.04103036687709 high
 TCGA-CD-85261.04383561643836 0 8.620899 5.844038 10.728846 8.408404 8.079044 0
 2.05885236115798 high
 TCGA-VQ-A8PM 0.156164383561644 1 9.033786 5.593081 8.139819 7.224742
 7.350613 0 1.5137689139715 high
 TCGA-BR-71970.767123287671233 0 7.612285 6.153289 8.968637 6.528172 7.400361 0
 1.24699159862537 high
 TCGA-SW-A7EA 1.58630136986301 0 6.727999 8.924552 6.652851 6.073233 7.702425 0
 1.14427736940398 high
 TCGA-BR-86760.627397260273973 0 6.865462 5.02148 7.222799 5.598895 5.807431 0
 0.696682308497063 low
 TCGA-HF-71344.35068493150685 0 9.04692 5.191233 6.24642 6.667491 5.795087 0

1.04448368186116 high
 TCGA-RD-A7BW 0.427397260273973 1 9.703298 9.796436 12.900595 9.643168
 8.936871 0 4.75489685798859 high
 TCGA-BR-43570.00273972602739726 0 9.219019 5.285349 9.77391 6.690966 7.949581 0
 1.71964080493696 high
 TCGA-BR-67071.65753424657534 1 7.805856 5.272113 9.982249 6.490894 7.142087 0
 1.24301578058112 high
 TCGA-VQ-A94U 2.24383561643836 0 8.863768 5.02148 11.907778 6.980888
 8.538538 0 1.99692382555398 high
 TCGA-BR-80812.68767123287671 0 8.555879 5.366873 10.262135 6.636023 7.937145 0
 1.59213925089118 high
 TCGA-BR-A44T2.84383561643836 0 7.700663 9.503881 10.991315 8.17375 7.391051 0
 2.18587121115956 high
 TCGA-BR-86802.66301369863014 0 10.420291 7.290382 8.539447 6.915642 7.62311 0
 2.23249168568866 high
 TCGA-BR-83612.59178082191781 0 6.136397 5.158556 5.410341 5.830769 7.534019 0
 0.68304464081749 low
 TCGA-CG-57220.0821917808219178 0 8.44544 5.228579 7.64282 6.660133 7.285659 0
 1.21896201386812 high
 TCGA-VQ-AA6F 4.50958904109589 0 9.877454 5.343431 5.909821 7.490054 6.54093 0
 1.3851316882939 high
 TCGA-HU-A4HB 1.30684931506849 1 8.28264 5.773743 8.176649 7.435625 6.35107 0
 1.24611480946419 high
 TCGA-BR-64551.15616438356164 1 7.8873 5.468679 9.957135 6.742569 8.25553 0
 1.47343861264597 high
 TCGA-VQ-A91K 5.1013698630137 0 9.153165 6.034455 8.072753 6.260891 7.88035 0
 1.54179179411167 high
 TCGA-VQ-A8PH 1.06575342465753 1 8.126308 5.02148 8.033716 6.480567 5.713353 0
 0.969683367528644 low
 TCGA-B7-A5TI 1.63013698630137 0 9.367585 8.031876 9.713296 7.777024 8.300218 0
 2.50251304300015 high
 TCGA-BR-83822.08767123287671 1 8.307362 7.542779 7.052147 6.686893 8.017043 0
 1.49322655720465 high
 TCGA-D7-65221.55068493150685 0 8.042777 5.718114 11.047247 7.7599 8.647295 0
 1.89533018524866 high
 TCGA-BR-A4IV 2.38082191780822 1 10.314136 7.552614 10.693073 9.773144
 9.150558 0 3.94901663035954 high
 TCGA-BR-68032.6 0 8.786278 7.801593 11.278832 8.609033 8.687719 0
 2.78332669170602 high
 TCGA-IN-A7NR0.542465753424658 0 8.765568 6.360363 9.682448 6.512454 6.723668 0
 1.48974752834068 high
 TCGA-FP-7916 1.17260273972603 1 9.692505 8.399388 11.273671 7.065952 8.759608 0
 2.95947030730327 high
 TCGA-HU-8604 1.9013698630137 0 9.578628 5.02148 10.447725 6.975369

	7.845661 0	1.89471791396289 high						
TCGA-IN-A6RJ	1.03835616438356 0	9.805186 5.516911 7.869035 5.122237 5.90962 0						
	1.18444570071549 high							
TCGA-CD-85291	0.2465753424658 0	8.650844 6.855174 8.640959 7.570617 8.721797 0						
	1.94109812910879 high							
TCGA-BR-85900	0.778082191780822 1	9.480524 7.904503 11.207866 8.047574						
	9.704134 0	3.31557972638825 high						
TCGA-F1-6875	6.01917808219178 1	7.976223 8.351879 5.959375 9.789535 7.056357 0						
	1.68511204173559 high							
TCGA-HU-8249	2.41369863013699 0	8.936622 5.107113 6.901139 5.806322 6.463534 0						
	1.05537630005451 high							
TCGA-CD-A486	0.526027397260274 1	7.647783 7.068826 12.100739 7.334287						
	8.051242 0	1.90908321520241 high						
TCGA-CD-85341	0.00547945205479 0	8.309268 5.02148 11.108463 7.758417 7.100123 0						
	1.5930800464312 high							
TCGA-HU-A4GQ	0.00821917808219178 1	9.38917 7.472495 9.437148 7.579588						
	7.235695 0	2.06706152448632 high						
TCGA-D7-A4Z01	0.23013698630137 0	8.374856 5.02148 8.48228 7.218669 7.294558 0						
	1.3191139609126 high							
TCGA-D7-A6EZ1	0.69315068493151 1	9.116048 5.02148 6.372222 6.377643 7.662664 0						
	1.25057133358258 high							
TCGA-D7-A4YU	1.36986301369863 0	9.777879 5.16027 8.167475 7.211892 8.169977 0						
	1.80604620367469 high							
TCGA-CG-57251	0.25205479452055 1	7.964707 7.685705 8.606012 9.081036 6.913323 0						
	1.74846069650365 high							
TCGA-VQ-A91Y	0.810958904109589 1	9.638719 9.819317 12.109728 8.957177						
	9.120414 0	4.28695157581802 high						
TCGA-VQ-A8P8	2.58082191780822 0	9.142931 5.446252 9.477384 6.987492 7.607548 0						
	1.67132321334679 high							
TCGA-VQ-A8PK	1.48767123287671 1	9.708409 8.177462 9.859519 8.543487 7.620609 0						
	2.69595929809543 high							
TCGA-FP-8631	0.0465753424657534 0	8.98623 5.968999 10.454442 7.422028						
	8.556849 0	2.08487752169315 high						
TCGA-HU-A4H2	1.07945205479452 0	7.998927 5.02148 7.813087 7.119358 6.821157 0						
	1.11826008191864 high							
TCGA-HU-A4GJ	1.78082191780822 0	6.845985 5.02148 8.935674 6.711504 6.462578 0						
	0.922637862149406 low							
TCGA-BR-84860	0.00273972602739726 0	8.846388 5.196264 8.585817 6.82828 7.509725 0						
	1.43631333314907 high							
TCGA-HU-8238	0.126027397260274 0	7.470115 5.168246 8.456382 5.902367						
	6.605583 0	0.944838453031695 low						
TCGA-IN-A6RL	1.11232876712329 1	8.420477 5.274504 11.228388 7.721323 6.50598 0						
	1.55966226980251 high							
TCGA-BR-79570	0.756164383561644 1	10.127531 6.408203 11.044912 8.855424						

TCGA-D7-85781.76164383561644	0	9.994488	3.60189928697876	high					
TCGA-BR-86870.684931506849315	1	2.65318376828481	8.012251	7.615582	8.722713	6.732707	8.055921	0	
TCGA-BR-64531.32876712328767	0	1.60840099035369	7.32145	5.253662	11.460786	6.946443	6.926815	0	
TCGA-VQ-A91U	0	1.28592957846753	high						
TCGA-CG-44420.00273972602739726	0	0.142465753424658	1	8.948578	5.02148	10.036721	5.751222		
TCGA-D7-A748	0	6.091542	1.23103540305867	high					
TCGA-BR-42570.805479452054795	1	1.45286925895673	high						
TCGA-BR-83710.983561643835616	1	9.159438	6.679706	12.157728	7.434249				
TCGA-RD-A8N5	1	9.364043	2.76730798238048	high					
TCGA-BR-82862.45205479452055	0	8.936876	5.727574	6.773156	7.834316	7.556439	0		
TCGA-BR-80591.2027397260274	1	1.48990278134881	high						
TCGA-D7-65251.11232876712329	1	2.54962079481848	high						
TCGA-CG-57170.580821917808219	1	8.894922	6.835529	11.54719	9.23883	7.714544	0		
TCGA-BR-84850.767123287671233	0	1.72860942127395	high						
TCGA-CD-A4MG	0	8.907154	5.469499	8.684739	7.302189	7.982311	0		
TCGA-VQ-AA69	0	1.63962166106838	high						
TCGA-HU-A4GH	0	2.24148070955992	high						
TCGA-VQ-AA6J	0	9.015982	7.340874	8.701457	7.881017	8.843449	0		
TCGA-BR-64561.44109589041096	1	2.868584	3.92070684781453	high					
TCGA-BR-64561.44109589041096	1	10.657678	9.721603	7.139114	10.058406				
TCGA-BR-64561.44109589041096	1	8.868584	3.92070684781453	high					
TCGA-BR-64561.44109589041096	1	10.39464	5.02148	9.362819	5.973302	6.711156	0		
TCGA-BR-64561.44109589041096	1	1.6296456666642	high						
TCGA-BR-64561.44109589041096	1	9.024788	5.268254	9.267336	6.93088	8.768872	0		
TCGA-BR-64561.44109589041096	1	1.79690398135396	high						
TCGA-BR-64561.44109589041096	1	0.547945205479452	1	7.602825	5.02148	6.169515	6.380886		
TCGA-BR-64561.44109589041096	1	7.481885	0.944573167995023	low					
TCGA-BR-64561.44109589041096	1	8.466041	5.295988	8.412471	5.564214	6.113636	0		
TCGA-BR-64561.44109589041096	1	1.03041894750119	high						
TCGA-BR-64561.44109589041096	1	9.965637	9.185607	10.27938	8.215644	9.353825	0		
TCGA-BR-64561.44109589041096	1	3.65830264178913	high						
TCGA-BR-64561.44109589041096	1	0.980821917808219	0	7.81077	5.146789	7.294773	6.47137		
TCGA-BR-64561.44109589041096	1	5.305755	0.847616765278626	low					
TCGA-BR-64561.44109589041096	1	3.61369863013699	0	9.542149	6.921056	10.889412	9.263537		
TCGA-BR-64561.44109589041096	1	9.068289	3.17047541984808	high					
TCGA-BR-64561.44109589041096	1	1.67945205479452	0	10.029705	5.20267	7.226335	8.556188		
TCGA-BR-64561.44109589041096	1	9.857944	2.4101840647572	high					
TCGA-BR-64561.44109589041096	1	7.956583	6.042508	5.668163	7.568482	5.953407	0		
TCGA-BR-64561.44109589041096	1	0.994245919162506	high						
TCGA-BR-64561.44109589041096	1	2.2958904109589	0	9.204247	5.514409	8.350743	8.615524	6.989386	0

1.71470027265954 high
TCGA-BR-77163.31506849315068 0 9.764377 5.820083 10.284281 7.054998 8.312599 0
2.1805053588428 high
TCGA-HU-A4GP 0.747945205479452 0 8.961629 5.134208 6.232974 5.980834
6.335204 0 1.01916730951801 high
TCGA-HU-8610 0.063013698630137 0 9.479897 5.02148 12.146927 6.433207
7.918293 0 1.99615576279404 high
TCGA-HF-71335.25479452054795 0 8.78788 5.206972 7.884343 8.127281 6.962229 0
1.44548644222721 high
TCGA-CD-A4MH 1.01643835616438 0 8.315341 5.88442 8.700336 6.350057 7.258724 0
1.30448080020121 high
TCGA-BR-64522.89041095890411 0 10.641387 6.133744 7.215215 6.432334 8.139452 0
1.95989685818669 high
TCGA-IN-A6RI 1.53150684931507 0 8.207334 5.02148 7.780768 6.074262 5.599627 0
0.919856664671714 low
TCGA-BR-77221.27671232876712 1 7.433566 8.064687 8.091336 6.861677 6.973406 0
1.31036815835703 high
TCGA-BR-64571.13972602739726 0 8.966041 7.362233 12.758653 8.78155 9.264637 0
3.29515982448441 high
TCGA-CG-43010.252054794520548 0 9.947735 8.568109 9.607249 7.372304 8.621149 0
2.84406877315842 high
TCGA-BR-86861.73972602739726 1 9.498157 5.02148 11.632769 7.472265 7.940595 0
2.13574030348943 high
TCGA-RD-A7BT 0.717808219178082 1 9.239981 5.099411 10.360613 5.6733
5.697861 0 1.26291341477667 high
TCGA-D7-65241.48767123287671 0 9.842446 5.18267 8.227272 8.308728 9.173274 0
2.26170400702661 high
TCGA-BR-85920.523287671232877 1 9.369639 9.513767 11.055125 9.163417
9.311268 0 3.88919390166419 high
TCGA-VQ-A91D 0.975342465753425 1 9.131733 6.954385 6.005463 5.97074
7.978496 0 1.42138339933449 high
TCGA-IN-A6RR0.561643835616438 1 8.175983 5.182811 8.620603 7.104107 5.890497 0
1.11035216536271 high
TCGA-BR-83731.23287671232877 0 10.64963 5.892837 11.47343 7.476591 9.196287 0
3.13180235286139 high
TCGA-CD-85331.28219178082192 0 8.365573 8.540783 10.585746 10.198022
8.838754 0 3.09703552991973 high
TCGA-IN-AB1V1.31232876712329 0 10.239954 5.02148 7.902539 7.06375 6.110785 0
1.49766493535782 high
TCGA-VQ-A8DV 1.1041095890411 1 8.540954 5.070792 7.035364 8.40858 5.659216 0
1.15936269230039 high
TCGA-RD-A8N2 9.6986301369863 0 9.450777 6.271158 10.899293 9.88691
8.273198 0 2.88663801737215 high
TCGA-CG-57183 1 7.36012 5.329144 9.976603 5.710406 6.691547 0

1.02871312921821 high
 TCGA-VQ-A922 0.753424657534247 1 9.310803 5.489516 9.566597 8.9311
 8.784007 0 2.35286530176014 high
 TCGA-CD-57991.08493150684932 0 8.529919 5.337324 9.731525 6.432334 8.049516 0
 1.51789370436485 high
 TCGA-VQ-A94R 3.54520547945205 1 8.849298 5.644282 10.980898 7.029275
 9.085896 0 2.09904963486418 high
 TCGA-FP-8099 1.42191780821918 0 9.269659 9.018578 8.264839 8.361206 8.852367 0
 2.71329526233431 high
 TCGA-D7-A747 0.698630136986301 1 9.575449 5.846984 11.721782 9.005838
 8.42175 0 2.81611899128168 high
 TCGA-VQ-AA6K 1.03561643835616 1 9.441413 6.100172 8.712156 6.91573 8.32754 0
 1.88760075620573 high
 TCGA-R5-A8050.76986301369863 1 8.475183 6.69356 8.916956 6.534636 7.60347 0
 1.5282234601494 high
 TCGA-RD-A8N0 3.38630136986301 0 7.837193 5.02148 10.325346 7.386567
 7.908171 0 1.47682962970714 high
 TCGA-CG-44443.92054794520548 0 7.679646 5.02148 8.192808 6.579658 7.991693 0
 1.17369399098303 high
 TCGA-BR-42790.797260273972603 1 10.290694 6.517572 13.22021 9.634568
 8.793669 0 4.05907239368513 high
 TCGA-BR-A4J5 2.36164383561644 0 9.280218 5.531162 9.496352 9.036322 9.480295 0
 2.54424041170016 high
 TCGA-HU-8602 1.86027397260274 0 9.546928 5.208495 4.768182 6.164708 7.41892 0
 1.1724011233623 high
 TCGA-BR-41870.386301369863014 1 9.330163 6.053101 12.178488 9.398162
 9.058215 0 3.14423244889216 high
 TCGA-F1-A448 1.77260273972603 0 8.297968 5.02148 6.903402 6.749842 8.284274 0
 1.25221242532966 high
 TCGA-HU-A4H0 0.175342465753425 0 9.949124 5.02148 6.786521 5.759115
 6.269385 0 1.19797010882597 high
 TCGA-CG-44384.50684931506849 0 9.060697 6.582394 10.220225 7.06481 7.627373 0
 1.91069249941369 high
 TCGA-RD-A8N4 5.94794520547945 0 8.233456 8.611087 10.549216 9.867866
 7.635671 0 2.59168822207128 high
 TCGA-D7-65270.854794520547945 1 7.444725 5.02148 8.432122 8.37671 7.031576 0
 1.22063895368354 high
 TCGA-CD-85251.04931506849315 0 7.530722 8.241875 12.69703 6.70968 7.358413 0
 1.87197055433179 high
 TCGA-HU-A4H6 1.76438356164384 0 8.071559 5.314725 7.475051 6.0218 6.462219 0
 0.985448157265351 high
 TCGA-BR-A4QL 1.34520547945205 1 6.071634 5.849648 7.871471 5.535573 6.748943 0
 0.749210812565728 low
 TCGA-CG-44411.16712328767123 1 9.10045 9.260755 7.850376 6.996351 8.653073 0

2.26051914170558 high
 TCGA-BR-80583.1041095890411 0 9.091842 5.379084 9.563707 7.364142 9.799669 0
 2.17213453962969 high
 TCGA-HF-71326.44109589041096 0 8.741621 5.269586 10.610722 6.881561 8.504982 0
 1.81144978283873 high
 TCGA-CG-44620.00273972602739726 1 9.515449 5.118594 12.110375 9.187821
 10.008931 0 3.25586622526247 high
 TCGA-VQ-A91S 2.73972602739726 0 10.609671 5.154118 7.722963 6.059808
 6.732484 0 1.54929812755319 high
 TCGA-BR-A4J8 1.12602739726027 0 7.481474 9.148224 9.598072 7.472332 8.001134 0
 1.87455788083798 high
 TCGA-BR-83691.16986301369863 0 8.956808 6.270037 10.150003 7.65217 7.727359 0
 1.94634266926734 high
 TCGA-VQ-A8P2 3.17808219178082 0 8.880588 5.36048 5.604229 5.798014 5.796614 0
 0.912123279396916 low
 TCGA-HU-A4GF 2.15068493150685 0 6.93606 5.02148 6.80812 6.291253 5.891145 0
 0.737796631045052 low
 TCGA-BR-67091.01369863013699 1 7.601865 5.234309 6.003608 10.100184 10.2024 0
 1.79213293283227 high
 TCGA-BR-82840.671232876712329 1 8.771965 6.390321 8.666393 7.140579 9.208648 0
 1.93627835347037 high
 TCGA-CG-44650.750684931506849 1 8.795018 5.740723 7.324123 6.654919 7.67988 0
 1.37302195936307 high
 TCGA-BR-77042.93698630136986 0 8.468036 6.942489 7.313834 6.934262 7.007388 0
 1.36498963967091 high
 TCGA-CG-44751.91506849315068 0 9.847427 6.382836 10.600388 9.230039 9.243479 0
 3.18478026777121 high
 TCGA-B7-A5TJ 0.917808219178082 0 7.736224 6.912112 9.480089 5.975053 7.487604 0
 1.34014554466235 high
 TCGA-BR-86822.71506849315068 0 8.417674 6.12176 11.760839 8.131982 8.385131 0
 2.19301893610612 high
 TCGA-HU-A4G9 2.01643835616438 0 7.682278 5.096439 4.489568 5.23084 5.10034 0
 0.601127998340344 low
 TCGA-CG-57236.83835616438356 0 8.409176 5.127806 9.041516 7.744909 6.868488 0
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 TCGA-BR-42560.778082191780822 1 9.436951 6.03633 9.795206 8.583563 8.666554 0
 2.43469692174262 high
 TCGA-FP-A8CX0.0191780821917808 0 7.166653 5.02148 10.083656 6.294743
 5.908615 0 0.950137021200492 low
 TCGA-CG-57262.41369863013699 1 8.286478 5.02148 7.407974 6.826369 5.468996 0
 0.96116946260721 low
 TCGA-HU-8608 1.75616438356164 0 9.38122 5.02148 5.256384 6.322117 6.66436 0
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 TCGA-HU-A4H8 0.73972602739726 0 8.43092 5.02148 6.09014 5.448514 5.423782 0

0.791989817381562 low
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 8.300781 0 2.55915779992475 high
 TCGA-IP-7968 0.210958904109589 0 8.428468 5.307465 6.85116 6.712848 9.120211 0
 1.42183405514172 high
 TCGA-FP-7829 1.62739726027397 0 8.984403 6.39324 7.216474 6.762628 8.055729 0
 1.55732979141411 high
 TCGA-CD-58131.03287671232877 1 8.691271 5.129992 12.949125 8.435648 8.507856 0
 2.38723717361117 high
 TCGA-VQ-A940 1.75342465753425 1 9.175455 5.112422 9.536494 6.506135 6.544773 0
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 TCGA-RD-A8NB 1.40547945205479 1 9.846122 6.995324 9.566791 7.856715 8.33727 0
 2.49845252410456 high
 TCGA-BR-85912.34520547945205 0 9.418232 7.01006 8.08154 6.353114 7.851053 0
 1.74976209216704 high
 TCGA-VQ-AA6G 2.16986301369863 1 9.83345 5.097629 7.385526 5.684098 6.867386 0
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 TCGA-BR-42012.57534246575342 1 9.883141 6.613542 9.944038 8.890191 8.504265 0
 2.79862597829813 high
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 3.45170515514636 high
 GSM2235695 9.94520547945205 0 11.248906 5.199434 5.132278 7.575804 6.068453
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GSM2235934 3.86301369863014 0 8.536564 5.050241 8.525309 7.34931 6.944937
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GSM2235935 1.56164383561644 1 8.376021 6.217957 9.790219 7.877715 8.098848

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GSM2235943	10.4383561643836 0	8.168438 5.173427 10.138271	8.616565	7.880886			
10.908553	0.790550298794381	low					
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10.442958	1.07794818937635	high					
GSM2235946	10.7671232876712 0	7.333284 5.411761 7.573344	6.860255	6.999098			
9.891185	0.495254963463371	low					
GSM2235947	10.6027397260274 0	7.325444 5.03937	6.989819	5.168502	6.856819		
10.09236	0.384097763610902	low					
GSM2235949	10.8493150684932 0	9.641487 5.727802 6.789231	6.586523	7.792957			
10.963459	0.692550285629099	low					
GSM2235950	10.5205479452055 0	9.101755 11.165237	12.561699	8.765656			
7.505041	10.632667	1.72053392704386	high				
GSM2235953	0.821917808219178	1	9.694077 6.877766	11.973301	7.936095		
8.014772	10.763174	1.2606516149403	high				
GSM2235954	12.2465753424658 0	7.776076 5.618735 7.660173	6.352764	8.358027			
10.362098	0.581124592468936	low					
GSM2235955	12.2465753424658 0	9.684583 10.864642	12.523271	7.261388			
8.046597	10.605435	1.70530780135289	high				
GSM2235957	12.1643835616438 0	8.776802 5.916754 7.660173	6.192692	6.970102			
10.694469	0.58105661398108	low					
GSM2235958	12.4931506849315 0	8.711903 5.595642 9.936742	7.619321	8.930644			
9.984032	0.963055249085611	low					
GSM2235959	11.8356164383562 0	8.321099 5.156465 5.450708	5.108295	6.162065			
9.914061	0.386149658380753	low					
GSM2235964	1.80821917808219 1	8.653591 5.054138 9.99065	6.925032	8.042562			
10.516926	0.752477111639835	low					
GSM2235966	2.71232876712329 0	7.82933 5.05226	10.402557	7.881345	6.181785		
10.355253	0.610643987522647	low					
GSM2235967	0.821917808219178	1	5.701312 5.725136 7.557334	7.263795	6.293098		
10.664224	0.352954261331223	low					
GSM2235969	5.26027397260274 0	7.264014 5.445757 5.772647	3.965413	8.095411			
9.141602	0.397419999557049	low					
GSM2235974	0.986301369863014	1	6.482377 5.525667 7.8269	6.548949	7.298847		
9.176853	0.466926493657982	low					
GSM2235976	4.52054794520548 0	7.157986 5.205525 5.092711	3.600076	7.171933			
9.271856	0.318030548322753	low					
GSM2235977	0.575342465753425	1	8.901802 6.503401 10.703172	6.9884			
9.762013	10.285855	1.13260213680455	high				
GSM2235979	3.45205479452055 0	8.171945 4.911429 9.255718	7.491431	7.294377			

10.794296 0.62449736961348 low
 GSM2235984 0.657534246575342 1 8.271285 5.587423 9.327254 8.490937 6.950647
 11.058202 0.697350861386064 low
 GSM2235986 2.87671232876712 0 7.452369 5.400734 9.349525 6.75109 6.483993
 10.96624 0.490784839379059 low
 GSM2235993 10.3561643835616 0 8.086897 5.186358 9.245455 7.313575 7.547638
 10.191484 0.664160184017984 low
 GSM2235994 10.1095890410959 0 8.744636 4.9723 7.55018 8.050076 7.314983
 10.195831 0.679810251321077 low
 GSM2235995 0.821917808219178 1 8.432374 6.709848 5.569932 5.259018 7.143267
 10.468513 0.485026392815599 low
 GSM2235996 0.493150684931507 1 8.22624 4.997018 5.265541 5.700144 8.453842
 8.582068 0.551749707605261 low
 GSM2235999 7.80821917808219 1 8.135035 4.964899 5.990537 5.807842 7.86111
 10.276158 0.476442756338119 low
 GSM2236000 10.027397260274 0 7.942528 6.183013 11.897677 6.648073 8.982903
 9.354837 0.97215319293948 high
 GSM2236001 10.1917808219178 0 8.687584 5.712202 10.987652 7.317381 9.141098
 10.517665 0.992125949274232 high
 GSM2236003 10.3561643835616 0 8.209185 8.871431 12.819799 7.548928 8.485548
 9.951412 1.31558001902757 high
 GSM2236004 3.78082191780822 1 8.747352 6.75978 8.436417 5.651595 7.18432
 10.551979 0.639475143328415 low
 GSM2236005 0.73972602739726 1 8.273794 9.172423 7.672162 7.098693 8.707999
 10.199677 0.940445400179416 low
 GSM2236006 1.97260273972603 1 8.170783 4.969182 7.993526 5.991391 6.582133
 10.170819 0.487769240789886 low
 GSM2236010 3.12328767123288 1 8.052174 5.473224 9.849593 5.914619 6.765877
 9.826186 0.583170324265146 low
 GSM2236012 0.246575342465753 1 9.240525 6.440572 6.9429 8.692395 7.224867
 10.892862 0.795347081943637 low
 GSM2236015 9.04109589041096 0 9.011088 5.69656 10.491235 8.52157 7.571052
 10.656522 0.94531307764269 low
 GSM2236017 1.3972602739726 1 9.161605 6.983424 7.960915 7.892329 6.493126
 10.79516 0.757285250453487 low
 GSM2236018 9.53424657534247 0 9.033886 5.351346 6.606782 6.710289 6.485417
 10.377702 0.551339139314936 low
 GSM2236019 7.56164383561644 1 9.104871 6.335612 10.118582 6.565183 7.440913
 11.007536 0.791390830988004 low
 GSM2236020 8.95890410958904 0 7.785955 6.423652 5.776411 6.141391 6.20553
 10.726969 0.415991812787829 low
 GSM2236021 4.19178082191781 1 10.620012 6.860144 10.728548 8.790085
 9.470867 10.940977 1.68782088214728 high
 GSM2236024 8.46575342465753 0 8.419723 7.482133 8.132967 6.59831 7.722286

10.981335 0.704939590762811 low
 GSM2236026 5.26027397260274 1 9.748908 5.049095 12.508754 9.019388 8.383652
 10.89893 1.29739489977164 high
 GSM2236027 10.1917808219178 0 9.979171 6.337625 11.703053 7.750177 7.863981
 10.810974 1.19886938234662 high
 GSM2236028 7.80821917808219 1 9.566708 5.218521 9.587278 6.390186 6.528024
 10.957185 0.67600236398063 low
 GSM2236029 11.3424657534247 0 7.54969 5.076619 6.964037 5.752513 5.381929
 10.195831 0.356651782432919 low
 GSM2236034 10.027397260274 0 10.328988 5.490517 8.784784 6.044365 8.057833
 11.069797 0.841359811653846 low
 GSM2236040 3.04109589041096 0 9.12664 4.890065 6.567753 5.768446 5.717884
 10.61521 0.446861272811863 low
 GSM2236041 3.36986301369863 0 8.684854 6.754968 11.312931 8.507067 7.857873
 10.660386 1.05813352382801 high
 GSM2236042 3.04109589041096 0 5.67685 5.417415 7.487614 6.009592 6.508238
 10.565455 0.31366113349651 low
 GSM2236044 11.5890410958904 0 8.125822 5.809067 6.498578 7.141885 6.400429
 10.297491 0.507185498583947 low
 GSM2236047 4.02739726027397 1 8.157766 4.965202 11.29239 6.406819 7.748104
 10.113043 0.713003479249177 low
 GSM2236049 2.71232876712329 1 7.770552 5.044535 9.413535 7.180784 7.642608
 10.873422 0.598818797095022 low
 GSM2236051 3.12328767123288 1 9.53421 5.074725 9.803229 8.109686 8.437569
 10.374267 1.0114136208861 high
 GSM2236055 10.9315068493151 0 6.754295 5.06895 8.786382 10.080125 5.194917
 10.527108 0.501821396619536 low
 GSM2236056 10.5205479452055 0 8.897557 5.192413 9.795885 6.477669 6.64429
 10.639569 0.639961532575615 low
 GSM2236057 3.04109589041096 1 9.746947 5.381847 11.051443 8.492713 8.354183
 10.917367 1.14872875153411 high
 GSM2236058 11.1780821917808 0 10.012338 7.64083 10.56198 7.408921 8.395365
 11.18145 1.23931563875221 high
 GSM2236059 11.2602739726027 0 9.092632 5.303621 6.985121 8.749476 9.37641
 10.427472 0.932118529012264 low
 GSM2236061 10.6027397260274 0 8.841725 5.212835 11.790027 8.012956 8.691854
 10.571483 1.04280225698092 high
 GSM2236065 9.78082191780822 0 10.092412 6.251747 9.118657 7.537054 6.610765
 10.510445 0.898245299889738 low
 GSM2236066 10.4383561643836 0 11.222376 5.534163 8.670022 7.69568 8.896598
 10.874353 1.25367361592144 high
 GSM2236067 1.3972602739726 1 10.945107 6.228132 9.277458 6.911208 6.575821
 11.22651 0.930445536442949 low
 GSM2236068 3.45205479452055 1 10.712564 6.197034 12.217033 9.083118

8.341607 11.001004 1.62295184185587 high
 GSM2236070 10.19178082191780 11.173861 5.331482 4.951968 5.303636 6.352542
 11.314606 0.568430862751018 low
 GSM2236071 9.36986301369863 0 10.231819 5.555177 6.823779 5.866217 5.769556
 11.604554 0.542282563253145 low
 GSM2236073 1.80821917808219 1 8.346148 4.939453 8.068297 8.181059 6.889054
 10.894603 0.603789859889749 low
 GSM2236074 11.7534246575342 0 10.49618 5.418599 4.894606 8.454915 6.826499
 11.352853 0.715491405987053 low
 GSM2236082 10.7671232876712 0 8.379717 5.126125 8.194467 6.457402 6.229218
 10.315385 0.514966481290226 low
 GSM2236083 0.575342465753425 1 8.732437 5.089834 8.649629 6.797879 4.593822
 10.538015 0.47733365451627 low
 GSM2236084 10.5205479452055 0 8.552523 5.54947 8.44917 6.70929 7.492321
 10.927369 0.624581039298402 low
 GSM2236087 12.7397260273973 0 8.336123 5.661037 8.213577 7.167592 7.086715
 10.681926 0.608766066534028 low
 GSM2236088 2.79452054794521 1 7.642399 5.073953 7.009552 8.66237 8.468093
 10.518343 0.645952272057244 low
 GSM2236092 12.2465753424658 0 8.53264 5.653685 10.074911 8.637439 7.265506
 11.436089 0.783659770360313 low
 GSM2236095 12.3287671232877 0 8.455454 5.47352 9.439007 7.987506 7.540713
 11.510208 0.706363564943756 low
 GSM644520 1.8986301369863 1 10.046573 7.765043 11.49144 7.202762 9.082466
 11.84741 1.34590538290321 high
 GSM644522 10.241095890411 0 9.432355 7.355781 9.608441 7.176291 7.868807
 11.199287 0.956572293750366 low
 GSM644523 12.7643835616438 0 9.463116 3.619198 10.34944 7.802669 8.230946
 11.13477 0.830799088222237 low
 GSM644525 12.5013698630137 0 7.292158 3.545894 9.792065 8.062273 5.941848
 10.304491 0.474443023866153 low
 GSM644529 0.246575342465753 1 9.932977 6.373095 11.626217 8.472557
 8.770285 10.908413 1.38874965668191 high
 GSM644530 3.4027397260274 1 8.64549 5.111133 10.567172 7.447955 7.276329
 10.782223 0.742942423883632 low
 GSM644531 1.26575342465753 1 9.737167 6.255363 10.861602 8.161154 8.042531
 11.537157 1.08863328030258 high
 GSM644533 10.8328767123288 0 9.540157 4.967255 10.869637 8.466968 7.100383
 11.824999 0.867077824613499 low
 GSM644538 2.88493150684931 1 10.4461801 7.2226144 11.1488024 5.3355202
 10.092726 11.5571858 1.29072827609847 high
 GSM644539 4.76712328767123 0 9.546784 7.585553 11.550521 8.899603 7.074235
 12.067044 1.13790968201825 high
 GSM644540 0.756164383561644 1 10.02866 6.346184 10.811593 7.811609

8.578023 11.516802 1.17765670957181 high
 GSM644541 8.9013698630137 0 7.409728 6.878091 10.555346 8.396873 7.338093
 10.235055 0.796556498265707 low
 GSM644543 1.2986301369863 1 8.44627 6.486099 9.984166 8.35058 7.973534
 11.477145 0.859551583061798 low
 GSM644544 2.75342465753425 0 9.46573 6.4579 10.136584 7.603649 6.967542
 10.719386 0.906329097648167 low
 GSM644549 8.61369863013699 0 9.9993631 6.1942057 9.1800878 7.7032938
 6.3581045 11.4877593 0.814070652515345 low
 GSM644552 7.77534246575342 0 8.509116 5.980452 10.572396 7.530438 7.394609
 9.865928 0.848871609982158 low
 GSM644553 7.91506849315068 0 10.218403 5.1553668 8.8518881 7.9144419
 8.1016084 11.9785589 0.903040758567452 low
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 GSM644556 0.986301369863014 1 10.094981 7.128341 10.782395 7.894484
 7.966489 11.602406 1.18539397756763 high
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 9.717257 11.953954 1.51311646001914 high
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 10.640364 0.897989026366698 low
 GSM644568 6.99452054794521 0 10.096214 7.536292 10.296229 7.685797
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 GSM644570 5.02191780821918 0 9.743028 5.056572 10.190132 8.093509 8.823446
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 GSM644576 5.24383561643836 0 9.118714 6.634328 9.971003 8.09989 7.882653
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 9.255609 11.486489 1.31705473784884 high
 GSM644585 5.30958904109589 0 9.63426 7.684426 9.835312 7.707807 6.525827
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 7.697973 11.666461 1.06388083890178 high
 GSM644588 2.6958904109589 1 10.017751 7.730522 11.437548 8.258157

8.700904 11.435195 1.45072013321845 high
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 11.049968 1.0247708732181 high
 GSM644590 3.09041095890411 1 10.269013 6.96464 10.33191 8.056436 10.48104
 11.674893 1.54686373171137 high
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 7.2813211 11.5027961 0.684135194043973 low
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 9.771438 0.769635447955734 low
 GSM644599 1.21643835616438 1 9.774393 8.082423 10.596683 4.823627 8.899554
 11.420171 1.01173671017905 high
 GSM644600 12.4767123287671 0 9.196592 7.123651 9.728736 7.196897 6.469587
 9.381934 0.8953482896178 low
 GSM644602 0.649315068493151 1 9.086534 7.860952 9.306333 7.568195 7.435715
 10.644106 0.950145423449914 low
 GSM644605 7.09315068493151 0 8.936614 7.657786 10.021324 5.131698 5.855001
 7.858752 0.788351087647605 low
 GSM644606 3.44383561643836 0 9.091425 7.382793 10.181552 8.01239 6.94492
 11.675575 0.888919895761137 low
 GSM644607 12.2712328767123 0 7.841577 6.071319 10.633815 4.833797 6.281956
 10.307208 0.515900727529639 low
 GSM644608 2.18630136986301 1 9.352064 5.758723 10.485064 8.439701 7.734785
 10.697776 1.01136523197219 high
 GSM644609 9.63287671232877 0 8.9349358 7.3345412 10.8696373 5.1398781
 7.3215023 11.6977375 0.720364388140463 low
 GSM644610 0.50958904109589 1 8.425355 7.475763 10.411458 7.87299 8.302622
 11.286654 0.957362180941675 low
 GSM644613 8.72876712328767 0 9.9932778 7.6584727 10.7658596 7.7328841
 7.3380931 11.8357407 1.09960463003311 high
 GSM644614 9.94520547945205 0 9.793242 6.964203 10.776316 8.314382 7.444874
 11.357083 1.113534447564 high
 GSM644615 1.62739726027397 0 9.897524 7.574308 9.82518 6.373397 6.052751
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 GSM644618 10.0109589041096 0 9.147864 7.507516 10.655938 4.772541 8.560108
 10.799506 0.878973225883033 low
 GSM644619 6.01643835616438 0 9.8257742 7.2154923 7.2587445 5.6528125
 7.2995344 11.4207853 0.696954826179843 low
 GSM644620 9.53424657534247 0 9.426956 6.956389 10.736543 7.678364 8.404869
 11.184107 1.10667261206435 high
 GSM644622 7.71780821917808 0 9.722065 6.550144 10.657356 7.932146 8.508884
 11.371242 1.1428328079206 high
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8.096465 11.286654 1.26000529603587 high
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 11.164239 1.08036931616832 high
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 11.370637 1.08963329299906 high
 GSM644628 8.441095890410960 9.717266 7.291957 10.050312 7.669638 7.75519
 11.270169 1.05558250634041 high
 GSM644631 1.117808219178081 9.736138 7.458389 11.62936 7.538962 8.545698
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 10.346288 0.846968440458007 low
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 7.1507688 10.625203 0.77743319317349 low
 GSM644638 3.994520547945211 9.385696 6.88436 10.49658 7.164214 8.602138
 11.202544 1.04690997502797 high
 GSM644639 5.071232876712330 10.076416 6.879765 10.665836 5.992787
 6.144596 11.756889 0.78496480281949 low
 GSM644640 7.561643835616440 8.889882 7.897108 10.027066 7.349013 6.229796
 10.466336 0.843179960726729 low
 GSM644642 2.293150684931511 9.731346 7.405831 10.755436 7.804596 8.120817
 10.715648 1.22515249584599 high
 GSM644643 1.684931506849321 7.846201 3.516737 5.516999 8.109924 6.391795
 9.782727 0.429823438685751 low
 GSM644645 0.567123287671233 1 9.382382 6.825409 10.044532 4.730412
 7.860174 11.311786 0.740576330477831 low
 GSM644646 1.684931506849321 10.130773 5.902754 9.777786 7.391864 9.092424
 11.282161 1.11812639285492 high
 GSM644653 6.484931506849310 9.449115 7.52995 9.941343 5.859108 6.857993
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 GSM644654 6.394520547945210 7.461696 6.13042 11.146814 4.842964 7.557288
 10.841288 0.556020545284111 low
 GSM644655 0.789041095890411 1 8.878963 5.595396 10.639354 6.857914
 6.699436 10.54406 0.729868514286954 low
 GSM644656 1.726027397260271 9.376679 3.597649 10.482542 7.704017 7.542862
 10.553863 0.79170065355033 low
 GSM644658 1.660273972602741 8.562402 4.035391 10.429636 6.950987 7.371163
 11.184107 0.625390486705871 low
 GSM644659 5.021917808219180 9.618495 6.627068 8.802627 7.670009 6.627805
 10.051406 0.879264743620345 low
 GSM644660 0.953424657534247 1 9.555166 6.989506 8.941113 5.330423 7.887653

9.3765 0.875897534947455 low
 GSM644661 5.52328767123288 0 9.644714 7.090307 10.223625 7.236431 8.31756
 10.808098 1.0958201936898 high
 GSM644669 3.99452054794521 0 7.25727 5.53007 9.43389 5.160434 8.012424
 10.594059 0.504953913663509 low
 GSM644672 3.97808219178082 0 10.287469 7.318976 10.058194 7.718979
 7.556418 11.468611 1.12652448345104 high
 GSM644673 1.32328767123288 1 9.887712 8.66442 10.614466 8.65107 9.498448
 11.506516 1.62862216358957 high
 GSM644675 4.70958904109589 0 7.416614 4.559055 4.175471 7.472929 7.233706
 9.810528 0.410718506901585 low
 GSM644678 7.59452054794521 0 8.145331 6.553157 4.157507 4.737434 7.744939
 8.293882 0.49617061497074 low
 GSM644680 1.77534246575342 1 7.14285 8.229495 10.547535 7.24694 9.302976
 10.402523 0.930755183755768 low
 GSM644681 12.0904109589041 0 9.407633 7.84561 9.170257 8.171789 8.425823
 10.276601 1.19722823637801 high
 GSM644682 11.7698630136986 0 9.896795 7.641097 9.758609 7.949657 9.362705
 10.18282 1.44680427260645 high
 GSM644683 0.641095890410959 1 10.099828 7.084299 8.90114 5.250208
 9.104945 10.156752 1.02912572271879 high
 GSM644684 8.15342465753425 0 8.892593 7.145096 9.385313 7.375119 8.751436
 11.106749 0.95665523861706 low
 GSM644685 10.6849315068493 0 8.106447 6.8928 4.973058 4.674236 7.828061
 10.238176 0.465361679852089 low
 GSM644686 3.26301369863014 1 9.623872 8.345806 10.010712 4.699656 8.127005
 7.395765 1.18118371118064 high
 GSM644687 2.24383561643836 1 7.276644 5.891912 4.626622 8.403783 6.610454
 7.005782 0.573233087111799 low
 GSM644688 10.5041095890411 0 7.069757 6.435349 4.401897 4.909268 6.442585
 10.410823 0.317248662927056 low
 GSM644689 9.55068493150685 0 7.312932 6.800236 7.819857 7.447955 7.222951
 9.029713 0.644189435780744 low
 GSM644691 9.18082191780822 0 8.813414 6.457166 9.494594 8.207446 6.336087
 8.067574 0.934664273388548 low
 GSM644692 7.23287671232877 0 9.767753 5.676866 8.389797 7.976038 9.559018
 9.629437 1.18233919064434 high
 GSM644696 9.38630136986301 0 9.51043 7.008883 8.993844 7.785042 8.151372
 9.812396 1.09174866676643 high
 GSM644698 9.01643835616438 0 9.6120755 7.0146498 4.8824994 7.7085212
 9.0890496 9.941154 0.925035046593259 low
 GSM644701 8.01369863013699 0 9.205963 6.375328 9.687508 4.737717 6.52927 8.06292
 0.744323346721748 low
 GSM644702 1.8 1 9.788032 7.713085 5.603005 8.450555 8.094742 9.870739

1.01974102851951 high
GSM644707 1.01095890410959 1 8.898128 6.841731 9.364931 7.424407 8.013249 9.2973
0.987532742820777 high
GSM644708 5.4986301369863 0 7.315678 7.698355 4.487766 5.354892 5.594872
7.080402 0.444257430698681 low
GSM644711 2.11232876712329 1 9.610357 6.983373 10.150104 5.012639 7.806642
7.796657 1.031510123433 high
GSM644714 1.2986301369863 0 9.79856 4.78822 4.983581 5.608633 5.865571
10.72461 0.443518132594757 low
GSM644715 6.16438356164384 0 7.716197 6.717846 8.074448 8.27926 6.261645
9.600652 0.649436684878088 low
GSM644716 5.11232876712329 1 9.82059 8.149389 8.485901 7.251793 6.496156
9.662418 0.979978768002269 high
GSM644719 5.76164383561644 0 8.424353 6.741771 10.157351 6.175643 8.89435
10.175835 0.877643294137321 low
GSM644725 0.904109589041096 1 9.451798 7.68805 8.42282 7.560643 8.62182
10.606729 1.06945488945576 high
GSM644729 4.81643835616438 0 9.861754 5.967028 9.612411 5.044517 8.610789
9.965044 0.895295927721721 low
GSM644732 4.05205479452055 0 10.149021 7.457187 8.252253 6.927761 8.07116
11.031994 1.00406095217375 high
GSM644733 3.73972602739726 0 8.959379 7.192211 7.494747 7.353885 7.721005
8.696096 0.913268952828604 low
GSM644735 7.40547945205479 0 9.200384 6.8966 5.845893 5.305431 7.07758
9.174026 0.622550056304939 low
GSM644737 3.4027397260274 0 7.805647 6.505829 7.092027 7.289123 7.679338
9.320991 0.659582338180411 low
GSM644738 10.158904109589 0 9.336814 7.186818 10.140737 4.653268 8.373488
10.294903 0.859552386811263 low
GSM644740 0.682191780821918 1 10.020414 7.9325581 8.5963573
8.0193106 7.9367804 10.6879293 1.16625893419042 high
GSM644741 0.312328767123288 1 9.0434641 7.9192518 10.1460037
8.1862925 9.1715406 9.9787488 1.33976922075948 high
GSM644742 2.55616438356164 1 8.092631 6.398715 9.787927 8.257623 6.153603
10.627557 0.689599081786973 low
GSM644744 4.23287671232877 1 7.563865 6.074398 9.074228 8.360646 8.671573
9.343384 0.854269557644926 low
GSM644745 2.62191780821918 0 7.3872578 3.7688742 8.6643109 8.0492799
7.0324025 7.79818 0.613643491071547 low
GSM644747 2.05479452054795 1 7.4425004 7.6670818 3.98521 8.6650056
9.6756874 7.7444048 0.877492053636134 low
GSM644750 3.02465753424658 1 7.996575 3.686312 4.523403 4.728305 7.963866
7.194326 0.437861170718147 low
GSM644751 9.62465753424657 0 8.57668 3.864361 9.176118 8.348351 7.462053

10.812893 0.672458080178247 low
 GSM644752 1.35616438356164 1 9.419349 3.811016 10.442041 9.006809 8.201311
 10.368683 0.991728480845136 high
 GSM644753 2.41643835616438 1 7.087771 4.003811 4.143514 9.061178 7.558129
 10.711859 0.417279920799643 low
 GSM644754 1.28219178082192 1 7.3095692 5.421416 9.7239428 8.9284892
 6.1706054 7.2079361 0.762962352258045 low
 GSM644756 6.11506849315068 0 8.37993408 5.98552798 9.92114131 4.76294868
 8.47705365 7.1608017 0.844007772688651 low
 GSM644757 6.13150684931507 1 7.587332 3.917638 10.088166 7.921008 8.578907
 10.359126 0.682376822590499 low
 GSM644758 10.0438356164384 0 7.870761 7.98895 3.893763 8.539341 8.304378
 10.62616 0.664753768506479 low
 GSM644759 1.21643835616438 0 7.881353 5.925098 9.287726 8.839272 7.512646 8.00823
 0.916506782991847 low
 GSM644761 6.61643835616438 0 9.671627 6.850814 8.699424 8.118268 8.85179
 9.700503 1.21727389908743 high
 GSM644762 9.25479452054794 0 7.321586 6.995196 9.93858 8.064062 6.758227
 9.736481 0.719212594313768 low
 GSM644763 9.28767123287671 0 8.0548056 7.0403968 4.2591393 8.6342642
 7.9770313 10.8966403 0.621646445290886 low
 GSM644764 1.66849315068493 1 7.815466 6.73381 7.317808 8.327749 8.059871
 8.483059 0.83131828077782 low
 GSM644767 8.36712328767123 0 7.802974 6.28061 8.744867 7.417821 7.870561
 10.594059 0.679295113021561 low
 GSM644770 1.75068493150685 1 9.04044 6.824565 6.12496 7.824971 7.258812
 10.24687 0.730485308199991 low
 GSM644771 8.0958904109589 0 8.562039 3.743144 9.742879 8.096179 5.81991 7.41193
 0.722173861674756 low
 GSM644772 6.42739726027397 1 9.098629 5.124856 7.07982 7.224963 8.28702
 10.364134 0.718898067844694 low
 GSM644777 2.13698630136986 1 7.485288 3.74886 9.51991 8.592978 5.995304
 7.249914 0.64407356705507 low
 GSM644779 6.18082191780822 0 8.858931 7.014225 9.639935 8.382439 8.166994
 8.555486 1.18636241022136 high
 GSM644780 7.25753424657534 0 7.9651392 3.65542 10.0193608 8.2119422
 6.9373807 7.0322807 0.775519928622226 low
 GSM644781 5.4986301369863 0 8.100017 6.323236 8.451774 5.269835 6.569733
 10.207965 0.515243552561338 low
 GSM644782 1.51232876712329 1 9.683855 8.072168 9.642248 8.51153 8.977756
 10.337081 1.4334897841757 high
 GSM644783 1.12602739726027 0 9.560798 8.315249 10.950212 8.09989 9.051194
 10.474921 1.4980788875725 high
 GSM644784 4.33972602739726 1 9.365756 4.816365 9.058393 7.780382 8.088552

	9.122841	0.939531784075411	low				
GSM644785	6.92054794520548	0	9.161724	6.692356	9.140391	8.146873	9.227304
	10.030364	1.1597203064966	high				
GSM644787	3.01643835616438	0	7.319455	3.628557	9.317561	8.182433	7.534428
	8.982842	0.61407457587907	low				
GSM644789	1.66849315068493	1	8.644155	6.338429	6.39078	8.000193	7.021557
	9.750748	0.68818613207834	low				
GSM644790	6.57534246575342	0	7.192838	6.458638	10.400631	8.356654	7.760292
	9.148039	0.830319505075158	low				
GSM644798	0.665753424657534	1	9.585365	7.317925	10.296229	8.652502	9.23982
	10.822098	1.39495153702923	high				
GSM644800	4.86575342465753	0	7.230747	3.650303	4.964365	7.931315	5.705392
	7.351605	0.412716702603188	low				
GSM644805	2.4	0	8.171674	5.511249	8.223212	8.207969	6.84869
	0.771215243436481	low					
GSM644806	1.22465753424658	1	7.378139	3.548851	4.088039	7.580022	6.547455
	7.490469	0.415741845870902	low				
GSM644808	4.02739726027397	0	8.61054	5.671971	7.803987	7.784662	7.506053
	10.092177	0.717105215047124	low				
GSM644809	4.23287671232877	0	9.858582	6.518549	5.092106	5.270392	6.395812
	7.481453	0.671131301793759	low				
GSM644810	1.03561643835616	0	7.12001	3.658915	8.614085	7.708521	6.345099
	0.515233660750702	low					
GSM644812	3.01643835616438	0	8.37508	3.677213	9.130628	7.395306	7.204531
	8.366823	0.6797632028448	low				
GSM644814	10.027397260274	0	8.7239418	4.6105257	4.9051916	8.8489033	
	7.1549662	6.9243463	0.743195064911231	low			
GSM644815	1.9972602739726	1	7.9939914	3.8352632	8.9650809	5.4638199	
	7.6996805	10.1416371	0.496690674112062	low			
GSM644817	0.978082191780822	1	10.174245	7.365575	9.790455	8.88492	
	10.025186	10.998052	1.63791259254199	high			
GSM644818	10.4630136986301	0	8.00773	4.011712	9.150711	8.590899	6.762437
	7.232246	0.76039386498541	low				
GSM644821	6.14794520547945	0	6.9089692	3.8170376	5.9432348	8.6687659	
	8.1208174	7.9065269	0.563392049363537	low			
GSM644822	1.07671232876712	1	7.898257	3.866976	10.705968	6.050752	6.910602
	8.864289	0.583814916365781	low				
GSM644823	0.501369863013699	1	7.1006389	6.5291179	8.402036	5.0804143	
	5.587709	7.8860841	0.463481400156274	low			
GSM644827	7.46301369863014	1	9.7764738	3.5053106	9.379612	8.7864678	
	7.5756615	6.8074834	1.13574171059544	high			
GSM644829	6.46027397260274	0	7.734005	4.460652	4.532541	7.553543	6.83695
	7.438507	0.503640588675525	low				
GSM644831	8.54794520547945	0	8.97274	6.331374	4.679214	8.429567	7.377914

	8.192263	0.785840504643384	low				
GSM644832	7.74246575342466	0	8.838636	7.394048	9.227089	8.030361	7.184281
	10.370511	0.906133839204068	low				
GSM644835	4.89041095890411	1	8.9474146	4.4292605	9.9174525	8.5979112	
	8.0399587	7.6412027	1.07405013561605	high			
GSM644836	0.978082191780822	1	7.467181	5.552972	4.040923	8.984342	7.311172
	9.213615	0.537342833226058	low				
GSM644838	1.33972602739726	1	8.528139	3.59518	9.501175	8.327238	8.362217
	7.950162	0.902122554563743	low				
GSM644839	6.76438356164384	0	7.056435	6.292222	9.003755	8.875814	6.961723
	8.070087	0.761629826398269	low				
GSM644841	7.30684931506849	0	7.237148	3.630004	4.069584	8.502032	6.941606
	8.629354	0.427058503910349	low				
GSM644843	7.01917808219178	0	8.97239	3.573912	7.954849	7.256618	7.451788
	8.333206	0.700231749396413	low				
GSM644844	1.56986301369863	1	7.080587	5.87343	8.052859	8.005037	7.245409
	8.664662	0.633863402959465	low				
GSM644845	7.22465753424658	0	7.165363	6.36039	9.094609	8.436697	8.32467
	7.117444	0.934107797336897	low				
GSM644847	0.747945205479452	0	9.059646	3.875616	4.165892	8.363415	7.23883
	9.340625	0.572138031643118	low				
GSM644848	5.57260273972603	0	7.1226723	7.2993854	6.9223826	9.1052382	
	3.7596352	7.2712111	0.558673177607042	low			
GSM644849	2.42465753424658	1	7.204228	3.886129	8.651817	8.440303	8.506242
	9.752653	0.633165245036303	low				
GSM644850	6.80547945205479	0	7.619188	3.893058	8.558919	8.761686	8.148004
	7.439115	0.789847880985767	low				
GSM644856	5.54794520547945	0	7.744405	6.888149	4.129653	7.48185	6.220027
	6.933869	0.574171592341908	low				
GSM644857	0.813698630136986	1	7.430413	3.578857	10.34944	8.997565	6.788916
	7.381625	0.744154727690055	low				
GSM644858	2.06301369863014	1	7.523975	3.756833	9.294045	8.905841	7.516037
	0.766277513550564	low					
GSM644860	5.71232876712329	0	7.29835	4.101798	7.56715	7.566093	6.670412
	6.985913	0.564113419179481	low				
GSM644862	5.05479452054795	0	7.250465	4.852622	9.546223	8.559359	7.310361
	8.029827	0.735096719423136	low				
GSM644863	5.02191780821918	0	10.117479	4.982467	6.728183	8.375695	7.288806
	9.135686	0.896362789804188	low				
GSM644869	3.22191780821918	0	8.788883	4.187432	7.965182	7.535393	6.506051
	7.675197	0.693764328752858	low				
GSM644870	0.912328767123288	0	10.4615945	3.6477408	4.0077513		
	8.2656979	6.1895008	9.7906725	0.599953508488841	low		
GSM644872	4.1013698630137	0	7.458458	5.572447	5.493259	8.612053	5.889127
						7.33496	

0.56118368179771 low

GSM644876	6.05753424657534 0	7.578889 4.535668 4.008379 4.94857 4.85126
	7.538392 0.301264248605424	low
GSM644877	7.7013698630137 0	7.411376 7.018228 9.518381 6.928124 6.812551
	9.833251 0.640150666567424	low
GSM644880	1.2986301369863 1	9.652485 6.602156 9.647894 5.274945 6.901613
	7.507706 0.925862938995688	low
GSM644882	0.641095890410959	1 9.434054 4.740245 9.467491 4.746475 7.930694
	8.151285 0.773806556142702	low
GSM644883	3.54246575342466 1	9.509287 7.241276 8.550487 8.085248 7.781607
	10.526494 1.01346141644228	high
GSM644884	9.78904109589041 0	9.51378 7.092642 9.025593 7.616693 7.71675
	10.758455 0.966927115762454	low
GSM644889	0.394520547945205	1 7.578363 7.266901 8.022881 7.692866 5.403561
	9.473249 0.576288049036246	low
GSM644892	9.43561643835617 0	7.783232 7.183331 10.159405 4.760135 9.185111
	9.34798 0.786789061399419	low
GSM644893	10.0109589041096 0	7.685798 5.327131 9.809718 4.640009 6.70107
	7.745907 0.555849855441079	low
GSM644894	8.30958904109589 0	9.886282 6.750137 4.396063 7.741941 6.186267 7.15113
	0.825018018950446	low
GSM644896	0.345205479452055	1 9.225147 7.176069 6.657981 6.952453 8.175787
	9.496399 0.861769180440757	low
GSM644900	2.25205479452055 1	9.7757865 4.7231337 9.3306044 6.4899894
	6.203239 7.5809742 0.823256600486203	low
GSM644901	0.526027397260274	1 7.224347 7.196574 9.267777 7.547164 6.936521
	10.707572 0.62380457769066	low
GSM644902	4.53698630136986 0	9.58 4.842561 8.648941 6.716074 8.71957 11.002677
	0.804177682918114	low
GSM644903	8.47397260273973 0	9.93186303 3.58093877 8.84305495 7.64071741
	9.17408704 10.15346635 0.94938410111365	low
GSM644906	5.21917808219178 1	9.930783 4.200895 10.032854 7.836742 9.131841
	10.284309 1.08139946322482	high
GSM644907	3.93698630136986 1	9.839654 6.977266 9.229834 8.04749 8.263403
	9.677006 1.22217364438173	high
GSM644910	0.452054794520548	1 9.792886 7.320051 8.628358 7.663787 7.057425
	10.588547 0.951344351156718	low
GSM644911	3.39452054794521 1	8.22256 6.28099 10.110197 8.04575 7.803247
	10.61454 0.83526720246312	low
GSM644912	7.48767123287671 0	9.597766 6.870143 9.37754 4.68506 8.114775
	9.603828 0.853831244406181	low
GSM644913	6.99452054794521 0	8.503189 7.326443 9.635859 8.154065 7.444874 9.03468
	1.0036626690866	high
GSM644917	7.21643835616438 0	7.635905 5.85011 9.834493 7.354579 7.579129

	9.888349	0.695315577483891	low					
GSM644919	1.04383561643836	1	8.5777	7.594238	9.398893	7.67577	7.299534	
	9.566492	0.926389056512006	low					
GSM644922	5.1041095890411	0	8.005543	5.668171	9.639142	7.822958	8.079039	
	9.845536	0.794610918357215	low					
GSM644924	6.94520547945205	0	9.654184	7.401417	9.20437	8.366723	6.532572	
	10.558867	0.981841660018109	high					
GSM644927	6.55890410958904	0	9.226164	7.244311	9.298842	7.972171	8.218571	
	10.297196	1.07135601543939	high					
GSM644928	1.52876712328767	1	9.569153	6.777684	10.170877	4.805496	7.607009	
	9.766776	0.840528355010882	low					
GSM644930	6.33698630136986	0	9.450436	7.627981	9.317561	8.088924	7.307906	
	10.731664	1.01891666086708	high					
GSM644933	6.10684931506849	0	7.944598	6.345825	4.392512	6.678462	6.4236	
	10.641293	0.419745675318245	low					
GSM644936	2.95068493150685	0	9.732023	5.275916	7.412612	6.986507	6.773212	
	10.487408	0.679752398644761	low					
GSM644937	1.47123287671233	1	9.430998	6.331374	8.730787	5.914257	7.389659	9.03468
	0.823967602067182		low					
GSM644939	2.57260273972603	1	9.503449	7.022732	9.986976	6.671119	8.310501	
	9.684029	1.07913592465658	high					
GSM644940	4.93150684931507	0	7.197806	6.442073	10.434583	7.806183	6.792197	
	9.468645	0.696213779559811	low					
GSM644943	1.77534246575342	1	9.419694	6.485343	9.242628	6.924537	7.849832	
	10.255982	0.908455244191993	low					
GSM644946	4.1013698630137	1	10.265335	7.109003	10.315823	7.883897		
	9.062249	10.717986	1.41471629781149	high				
GSM644947	4.10958904109589	0	9.033939	6.906742	9.696357	4.781892	7.517711	
	7.082646	0.905086437417486	low					
GSM644949	0.698630136986301		1	9.656554	4.96145	4.659486	5.522512	6.583047
	7.23321	0.593404860357686	low					
GSM644950	3.60821917808219	0	8.937974	6.564492	9.698026	7.153194	6.697001	
	7.350262	0.968747999750507	low					

risk.test

id	futime	fustat	PLS3 GRP	APOD	SGCE	COL8A1	VAMP7	riskScore	risk
TCGA-BR-A4J4	0.0438356164383562	0	10.378046	6.156234	7.8356	6.091557			
	8.342571	0	1.93913452500917	high					
TCGA-RD-A7C1	1.38904109589041	1	8.508188	5.548072	6.01325	6.967192	7.06059	0	
	1.14078056698931	high							
TCGA-BR-68523	7.4520547945205	0	8.459383	5.516115	8.156629	6.487493	8.147964	0	
	1.39538829726655	high							
TCGA-BR-78511	0.03561643835616	0	7.662307	5.254603	9.296951	6.69358	8.285227	0	
	1.33579414562295	high							
TCGA-BR-84870	0.0931506849315069	0	7.917616	7.726558	6.562743	5.945505	7.11035	0	
	1.16656392128836	high							
TCGA-D7-65261	4.3287671232877	0	8.447452	5.474761	11.594171	6.712848	7.457695	0	
	1.64534616211272	high							
TCGA-FP-7735	0.29041095890411	1	8.00199	5.02148	9.938707	6.870616	6.390369	0	
	1.1987293244817	high							
TCGA-D7-55781	0.05479452054795	0	7.521261	5.195845	8.252979	6.713519	8.152397	0	
	1.19894734629241	high							
TCGA-BR-82950	0.183561643835616	1	7.869093	5.558838	8.335984	7.184265	6.171969	0	
	1.10866944113432	high							
TCGA-D7-85791	7.4246575342466	0	8.784263	5.090776	10.246758	8.338423	8.78967	0	
	2.07089831487669	high							
TCGA-3M-AB46	4.83561643835616	0	7.681721	7.199406	7.582596	6.185461	7.221426	0	
	1.19003156197615	high							
TCGA-D7-85721	1.4	0	7.996892	6.994707	10.137291	7.756102	8.759725	0	
	1.98450588167782	high							
TCGA-BR-68022	2.57534246575342	0	9.685451	5.982294	7.206433	6.103266	7.373317	0	
	1.4782859716398	high							
TCGA-VQ-A91N	1.56164383561644	1	8.58824	5.090477	7.785283	6.844411	6.355462	0	
	1.14659227074061	high							
TCGA-HF-A5NB	2.54246575342466	0	8.478275	5.708697	4.789349	5.55313	6.075875	0	
	0.838644687999994	low							
TCGA-VQ-A8PP	1.95068493150685	1	8.590248	7.411433	7.430538	6.42534	8.297805	0	
	1.59626743634652	high							
TCGA-MX-A5UG	0.30958904109589	1	9.568879	5.640192	10.367822	8.136175	9.30833	0	
	2.57321276810194	high							
TCGA-CG-57325	7.5342465753425	1	6.938145	5.02148	10.091617	5.987001	5.801407	0	
	0.879881935099159	low							
TCGA-HU-A4GT	0.542465753424658	0	8.243122	5.331577	6.694905	5.831201			
	6.536926	0	0.95562234568282	low					
TCGA-CG-44690	0.589041095890411	1	7.401702	5.258362	5.794781	6.151093	6.025524	0	
	0.760886158126159	low							
TCGA-BR-86900	0.89041095890411	0	7.245044	7.48233	10.276664	6.492911	7.822555	0	
	1.48092768824005	high							
TCGA-CD-58030	0.934246575342466	1	9.175441	7.496968	11.411609	8.578685			

	9.823335 0	3.29126911993726 high						
TCGA-CD-85281.02739726027397 0	9.519701 5.281786 6.232667 6.286942 7.629951 0							
	1.3357429090294 high							
TCGA-RD-A7BS	0.920547945205479 1	9.661562 7.203306 10.16743 7.303506						
	7.892097 0	2.32130716646379 high						
TCGA-VQ-A8PB	2.85753424657534 1	11.594792 5.811264 5.489225 6.225303						
	7.108495 0	1.75392251592497 high						
TCGA-BR-A4CR	0.00273972602739726 0	8.071057 13.500545 7.230259 8.752177						
	7.546793 0	2.67582467431241 high						
TCGA-HU-A4H3	2.41643835616438 0	8.568964 7.963043 5.565111 5.745245 6.565877 0						
	1.14783460169653 high							
TCGA-VQ-A8E3	1.81095890410959 1	9.434345 5.105635 5.675261 6.308184 6.440866 0						
	1.10464810141159 high							
TCGA-BR-68013.35068493150685 0	8.998852 5.542269 7.629855 6.572406 7.580957 0							
	1.39993442119773 high							
TCGA-HU-A4H5	1.98356164383562 0	8.763474 5.02148 6.321781 6.624367 6.313453 0						
	1.04103036687709 high							
TCGA-CD-85261.04383561643836 0	8.620899 5.844038 10.728846 8.408404 8.079044 0							
	2.05885236115798 high							
TCGA-VQ-A8PM	0.156164383561644 1	9.033786 5.593081 8.139819 7.224742						
	7.350613 0	1.5137689139715 high						
TCGA-BR-71970.767123287671233 0	7.612285 6.153289 8.968637 6.528172 7.400361 0							
	1.24699159862537 high							
TCGA-SW-A7EA	1.58630136986301 0	6.727999 8.924552 6.652851 6.073233 7.702425 0						
	1.14427736940398 high							
TCGA-BR-86760.627397260273973 0	6.865462 5.02148 7.222799 5.598895 5.807431 0							
	0.696682308497063 low							
TCGA-HF-71344.35068493150685 0	9.04692 5.191233 6.24642 6.667491 5.795087 0							
	1.04448368186116 high							
TCGA-RD-A7BW	0.427397260273973 1	9.703298 9.796436 12.900595 9.643168						
	8.936871 0	4.75489685798859 high						
TCGA-BR-43570.00273972602739726 0	9.219019 5.285349 9.77391 6.690966 7.949581 0							
	1.71964080493696 high							
TCGA-BR-67071.65753424657534 1	7.805856 5.272113 9.982249 6.490894 7.142087 0							
	1.24301578058112 high							
TCGA-VQ-A94U	2.24383561643836 0	8.863768 5.02148 11.907778 6.980888						
	8.538538 0	1.99692382555398 high						
TCGA-BR-80812.68767123287671 0	8.555879 5.366873 10.262135 6.636023 7.937145 0							
	1.59213925089118 high							
TCGA-BR-A44T2.84383561643836 0	7.700663 9.503881 10.991315 8.17375 7.391051 0							
	2.18587121115956 high							
TCGA-BR-86802.66301369863014 0	10.420291 7.290382 8.539447 6.915642 7.62311 0							
	2.23249168568866 high							
TCGA-BR-83612.59178082191781 0	6.136397 5.158556 5.410341 5.830769 7.534019 0							

0.68304464081749 low
TCGA-CG-57220.0821917808219178 0 8.44544 5.228579 7.64282 6.660133 7.285659 0
1.21896201386812 high
TCGA-VQ-AA6F 4.50958904109589 0 9.877454 5.343431 5.909821 7.490054 6.54093 0
1.3851316882939 high
TCGA-HU-A4HB 1.30684931506849 1 8.28264 5.773743 8.176649 7.435625 6.35107 0
1.24611480946419 high
TCGA-BR-64551.15616438356164 1 7.8873 5.468679 9.957135 6.742569 8.25553 0
1.47343861264597 high
TCGA-VQ-A91K 5.1013698630137 0 9.153165 6.034455 8.072753 6.260891 7.88035 0
1.54179179411167 high
TCGA-VQ-A8PH 1.06575342465753 1 8.126308 5.02148 8.033716 6.480567 5.713353 0
0.969683367528644 low
TCGA-B7-A5TI 1.63013698630137 0 9.367585 8.031876 9.713296 7.777024 8.300218 0
2.50251304300015 high
TCGA-BR-83822.08767123287671 1 8.307362 7.542779 7.052147 6.686893 8.017043 0
1.49322655720465 high
TCGA-D7-65221.55068493150685 0 8.042777 5.718114 11.047247 7.7599 8.647295 0
1.89533018524866 high
TCGA-BR-A4IV 2.38082191780822 1 10.314136 7.552614 10.693073 9.773144
9.150558 0 3.94901663035954 high
TCGA-BR-68032.6 0 8.786278 7.801593 11.278832 8.609033 8.687719 0
2.78332669170602 high
TCGA-IN-A7NR0.542465753424658 0 8.765568 6.360363 9.682448 6.512454 6.723668 0
1.48974752834068 high
TCGA-FP-7916 1.17260273972603 1 9.692505 8.399388 11.273671 7.065952 8.759608 0
2.95947030730327 high
TCGA-HU-8604 1.9013698630137 0 9.578628 5.02148 10.447725 6.975369
7.845661 0 1.89471791396289 high
TCGA-IN-A6RJ 1.03835616438356 0 9.805186 5.516911 7.869035 5.122237 5.90962 0
1.18444570071549 high
TCGA-CD-85291.02465753424658 0 8.650844 6.855174 8.640959 7.570617 8.721797 0
1.94109812910879 high
TCGA-BR-85900.778082191780822 1 9.480524 7.904503 11.207866 8.047574
9.704134 0 3.31557972638825 high
TCGA-F1-6875 6.01917808219178 1 7.976223 8.351879 5.959375 9.789535 7.056357 0
1.68511204173559 high
TCGA-HU-8249 2.41369863013699 0 8.936622 5.107113 6.901139 5.806322 6.463534 0
1.05537630005451 high
TCGA-CD-A486 0.526027397260274 1 7.647783 7.068826 12.100739 7.334287
8.051242 0 1.90908321520241 high
TCGA-CD-85341.00547945205479 0 8.309268 5.02148 11.108463 7.758417 7.100123 0
1.5930800464312 high
TCGA-HU-A4GQ 0.00821917808219178 1 9.38917 7.472495 9.437148 7.579588

7.235695 0 2.06706152448632 high
 TCGA-D7-A4Z01.230136986301370 8.374856 5.02148 8.48228 7.218669 7.294558 0
 1.3191139609126 high
 TCGA-D7-A6EZ1.69315068493151 1 9.116048 5.02148 6.372222 6.377643 7.662664 0
 1.25057133358258 high
 TCGA-D7-A4YU 1.36986301369863 0 9.777879 5.16027 8.167475 7.211892 8.169977 0
 1.80604620367469 high
 TCGA-CG-57251.25205479452055 1 7.964707 7.685705 8.606012 9.081036 6.913323 0
 1.74846069650365 high
 TCGA-VQ-A91Y 0.810958904109589 1 9.638719 9.819317 12.109728 8.957177
 9.120414 0 4.28695157581802 high
 TCGA-VQ-A8P8 2.58082191780822 0 9.142931 5.446252 9.477384 6.987492 7.607548 0
 1.67132321334679 high
 TCGA-VQ-A8PK 1.48767123287671 1 9.708409 8.177462 9.859519 8.543487 7.620609 0
 2.69595929809543 high
 TCGA-FP-8631 0.0465753424657534 0 8.98623 5.968999 10.454442 7.422028
 8.556849 0 2.08487752169315 high
 TCGA-HU-A4H2 1.07945205479452 0 7.998927 5.02148 7.813087 7.119358 6.821157 0
 1.11826008191864 high
 TCGA-HU-A4GJ 1.78082191780822 0 6.845985 5.02148 8.935674 6.711504 6.462578 0
 0.922637862149406 low
 TCGA-BR-84860.00273972602739726 0 8.846388 5.196264 8.585817 6.82828 7.509725 0
 1.43631333314907 high
 TCGA-HU-8238 0.126027397260274 0 7.470115 5.168246 8.456382 5.902367
 6.605583 0 0.944838453031695 low
 TCGA-IN-A6RL 1.11232876712329 1 8.420477 5.274504 11.228388 7.721323 6.50598 0
 1.55966226980251 high
 TCGA-BR-79570.756164383561644 1 10.127531 6.408203 11.044912 8.855424
 9.994488 0 3.60189928697876 high
 TCGA-D7-85781.76164383561644 0 9.729945 6.014097 8.689371 8.468513 9.802811 0
 2.65318376828481 high
 TCGA-BR-86870.684931506849315 1 8.012251 7.615582 8.722713 6.732707 8.055921 0
 1.60840099035369 high
 TCGA-BR-64531.32876712328767 0 7.32145 5.253662 11.460786 6.946443 6.926815 0
 1.28592957846753 high
 TCGA-VQ-A91U 0.142465753424658 1 8.948578 5.02148 10.036721 5.751222
 6.091542 0 1.23103540305867 high
 TCGA-CG-44420.00273972602739726 0 9.200659 5.495402 6.028053 8.165057 7.257573 0
 1.45286925895673 high
 TCGA-D7-A748 0.361643835616438 1 9.159438 6.679706 12.157728 7.434249
 9.364043 0 2.76730798238048 high
 TCGA-BR-42570.805479452054795 1 8.936876 5.727574 6.773156 7.834316 7.556439 0
 1.48990278134881 high
 TCGA-BR-83710.983561643835616 1 8.894922 6.835529 11.54719 9.23883 7.714544 0

2.54962079481848 high
TCGA-RD-A8N5 4.78630136986301 1 8.930749 5.170092 7.69956 7.757646 8.864406 0
1.72860942127395 high
TCGA-BR-82862.45205479452055 0 8.907154 5.469499 8.684739 7.302189 7.982311 0
1.63962166106838 high
TCGA-BR-80591.2027397260274 1 9.015982 7.340874 8.701457 7.881017 8.843449 0
2.24148070955992 high
TCGA-D7-65251.11232876712329 1 10.657678 9.721603 7.139114 10.058406
8.868584 0 3.92070684781453 high
TCGA-CG-57170.580821917808219 1 10.39464 5.02148 9.362819 5.973302 6.711156 0
1.6296456666642 high
TCGA-BR-84850.767123287671233 0 9.024788 5.268254 9.267336 6.93088 8.768872 0
1.79690398135396 high
TCGA-CD-A4MG 0.547945205479452 1 7.602825 5.02148 6.169515 6.380886
7.481885 0 0.944573167995023 low
TCGA-VQ-AA69 2.36712328767123 0 8.466041 5.295988 8.412471 5.564214 6.113636 0
1.03041894750119 high
TCGA-BR-64561.44109589041096 1 9.965637 9.185607 10.27938 8.215644 9.353825 0
3.65830264178913 high
TCGA-HU-A4GH 0.980821917808219 0 7.81077 5.146789 7.294773 6.47137
5.305755 0 0.847616765278626 low
TCGA-VQ-A8E2 3.61369863013699 0 9.542149 6.921056 10.889412 9.263537
9.068289 0 3.17047541984808 high
TCGA-KB-A93G 1.67945205479452 0 10.029705 5.20267 7.226335 8.556188
9.857944 0 2.4101840647572 high
TCGA-R5-A7ZF 0.70958904109589 1 7.956583 6.042508 5.668163 7.568482 5.953407 0
0.994245919162506 high
TCGA-VQ-AA6J 2.2958904109589 0 9.204247 5.514409 8.350743 8.615524 6.989386 0
1.71470027265954 high
TCGA-BR-77163.31506849315068 0 9.764377 5.820083 10.284281 7.054998 8.312599 0
2.1805053588428 high
TCGA-HU-A4GP 0.747945205479452 0 8.961629 5.134208 6.232974 5.980834
6.335204 0 1.01916730951801 high
TCGA-HU-8610 0.063013698630137 0 9.479897 5.02148 12.146927 6.433207
7.918293 0 1.99615576279404 high
TCGA-HF-71335.25479452054795 0 8.78788 5.206972 7.884343 8.127281 6.962229 0
1.44548644222721 high
TCGA-CD-A4MH 1.01643835616438 0 8.315341 5.88442 8.700336 6.350057 7.258724 0
1.30448080020121 high
TCGA-BR-64522.89041095890411 0 10.641387 6.133744 7.215215 6.432334 8.139452 0
1.95989685818669 high
TCGA-IN-A6RI 1.53150684931507 0 8.207334 5.02148 7.780768 6.074262 5.599627 0
0.919856664671714 low
TCGA-BR-77221.27671232876712 1 7.433566 8.064687 8.091336 6.861677 6.973406 0

1.31036815835703 high
TCGA-BR-64571.13972602739726 0 8.966041 7.362233 12.758653 8.78155 9.264637 0
3.29515982448441 high
TCGA-CG-43010.252054794520548 0 9.947735 8.568109 9.607249 7.372304 8.621149 0
2.84406877315842 high
TCGA-BR-86861.73972602739726 1 9.498157 5.02148 11.632769 7.472265 7.940595 0
2.13574030348943 high
TCGA-RD-A7BT 0.717808219178082 1 9.239981 5.099411 10.360613 5.6733
5.697861 0 1.26291341477667 high
TCGA-D7-65241.48767123287671 0 9.842446 5.18267 8.227272 8.308728 9.173274 0
2.26170400702661 high
TCGA-BR-85920.523287671232877 1 9.369639 9.513767 11.055125 9.163417
9.311268 0 3.88919390166419 high
TCGA-VQ-A91D 0.975342465753425 1 9.131733 6.954385 6.005463 5.97074
7.978496 0 1.42138339933449 high
TCGA-IN-A6RR0.561643835616438 1 8.175983 5.182811 8.620603 7.104107 5.890497 0
1.11035216536271 high
TCGA-BR-83731.23287671232877 0 10.64963 5.892837 11.47343 7.476591 9.196287 0
3.13180235286139 high
TCGA-CD-85331.28219178082192 0 8.365573 8.540783 10.585746 10.198022
8.838754 0 3.09703552991973 high
TCGA-IN-AB1V1.31232876712329 0 10.239954 5.02148 7.902539 7.06375 6.110785 0
1.49766493535782 high
TCGA-VQ-A8DV 1.1041095890411 1 8.540954 5.070792 7.035364 8.40858 5.659216 0
1.15936269230039 high
TCGA-RD-A8N2 9.6986301369863 0 9.450777 6.271158 10.899293 9.88691
8.273198 0 2.88663801737215 high
TCGA-CG-57183 1 7.36012 5.329144 9.976603 5.710406 6.691547 0
1.02871312921821 high
TCGA-VQ-A922 0.753424657534247 1 9.310803 5.489516 9.566597 8.9311
8.784007 0 2.35286530176014 high
TCGA-CD-57991.08493150684932 0 8.529919 5.337324 9.731525 6.432334 8.049516 0
1.51789370436485 high
TCGA-VQ-A94R 3.54520547945205 1 8.849298 5.644282 10.980898 7.029275
9.085896 0 2.09904963486418 high
TCGA-FP-8099 1.42191780821918 0 9.269659 9.018578 8.264839 8.361206 8.852367 0
2.71329526233431 high
TCGA-D7-A747 0.698630136986301 1 9.575449 5.846984 11.721782 9.005838
8.42175 0 2.81611899128168 high
TCGA-VQ-AA6K 1.03561643835616 1 9.441413 6.100172 8.712156 6.91573 8.32754 0
1.88760075620573 high
TCGA-R5-A8050.76986301369863 1 8.475183 6.69356 8.916956 6.534636 7.60347 0
1.5282234601494 high
TCGA-RD-A8N0 3.38630136986301 0 7.837193 5.02148 10.325346 7.386567

7.908171 0 1.47682962970714 high
 TCGA-CG-44443.92054794520548 0 7.679646 5.02148 8.192808 6.579658 7.991693 0
 1.17369399098303 high
 TCGA-BR-42790.797260273972603 1 10.290694 6.517572 13.22021 9.634568
 8.793669 0 4.05907239368513 high
 TCGA-BR-A4J5 2.36164383561644 0 9.280218 5.531162 9.496352 9.036322 9.480295 0
 2.54424041170016 high
 TCGA-HU-8602 1.86027397260274 0 9.546928 5.208495 4.768182 6.164708 7.41892 0
 1.1724011233623 high
 TCGA-BR-41870.386301369863014 1 9.330163 6.053101 12.178488 9.398162
 9.058215 0 3.14423244889216 high
 TCGA-F1-A448 1.77260273972603 0 8.297968 5.02148 6.903402 6.749842 8.284274 0
 1.25221242532966 high
 TCGA-HU-A4H0 0.175342465753425 0 9.949124 5.02148 6.786521 5.759115
 6.269385 0 1.19797010882597 high
 TCGA-CG-44384.50684931506849 0 9.060697 6.582394 10.220225 7.06481 7.627373 0
 1.91069249941369 high
 TCGA-RD-A8N4 5.94794520547945 0 8.233456 8.611087 10.549216 9.867866
 7.635671 0 2.59168822207128 high
 TCGA-D7-65270.854794520547945 1 7.444725 5.02148 8.432122 8.37671 7.031576 0
 1.22063895368354 high
 TCGA-CD-85251.04931506849315 0 7.530722 8.241875 12.69703 6.70968 7.358413 0
 1.87197055433179 high
 TCGA-HU-A4H6 1.76438356164384 0 8.071559 5.314725 7.475051 6.0218 6.462219 0
 0.985448157265351 high
 TCGA-BR-A4QL 1.34520547945205 1 6.071634 5.849648 7.871471 5.535573 6.748943 0
 0.749210812565728 low
 TCGA-CG-44411.16712328767123 1 9.10045 9.260755 7.850376 6.996351 8.653073 0
 2.26051914170558 high
 TCGA-BR-80583.1041095890411 0 9.091842 5.379084 9.563707 7.364142 9.799669 0
 2.17213453962969 high
 TCGA-HF-71326.44109589041096 0 8.741621 5.269586 10.610722 6.881561 8.504982 0
 1.81144978283873 high
 TCGA-CG-44620.00273972602739726 1 9.515449 5.118594 12.110375 9.187821
 10.008931 0 3.25586622526247 high
 TCGA-VQ-A91S 2.73972602739726 0 10.609671 5.154118 7.722963 6.059808
 6.732484 0 1.54929812755319 high
 TCGA-BR-A4J8 1.12602739726027 0 7.481474 9.148224 9.598072 7.472332 8.001134 0
 1.87455788083798 high
 TCGA-BR-83691.16986301369863 0 8.956808 6.270037 10.150003 7.65217 7.727359 0
 1.94634266926734 high
 TCGA-VQ-A8P2 3.17808219178082 0 8.880588 5.36048 5.604229 5.798014 5.796614 0
 0.912123279396916 low
 TCGA-HU-A4GF 2.15068493150685 0 6.93606 5.02148 6.80812 6.291253 5.891145 0

0.737796631045052	low								
TCGA-BR-67091.01369863013699 1		7.601865	5.234309	6.003608	10.100184	10.2024	0		
1.79213293283227 high									
TCGA-BR-82840.671232876712329	1	8.771965	6.390321	8.666393	7.140579	9.208648	0		
1.93627835347037 high									
TCGA-CG-44650.750684931506849	1	8.795018	5.740723	7.324123	6.654919	7.67988	0		
1.37302195936307 high									
TCGA-BR-77042.93698630136986 0		8.468036	6.942489	7.313834	6.934262	7.007388	0		
1.36498963967091 high									
TCGA-CG-44751.91506849315068 0		9.847427	6.382836	10.600388	9.230039	9.243479	0		
3.18478026777121 high									
TCGA-B7-A5TJ 0.917808219178082	0	7.736224	6.912112	9.480089	5.975053	7.487604	0		
1.34014554466235 high									
TCGA-BR-86822.71506849315068 0		8.417674	6.12176	11.760839	8.131982	8.385131	0		
2.19301893610612 high									
TCGA-HU-A4G9 2.01643835616438 0		7.682278	5.096439	4.489568	5.23084	5.10034	0		
0.601127998340344 low									
TCGA-CG-57236.83835616438356 0		8.409176	5.127806	9.041516	7.744909	6.868488	0		
1.39096221192286 high									
TCGA-BR-42560.778082191780822	1	9.436951	6.03633	9.795206	8.583563	8.666554	0		
2.43469692174262 high									
TCGA-FP-A8CX0.0191780821917808	0	7.166653	5.02148	10.083656	6.294743				
5.908615 0 0.950137021200492 low									
TCGA-CG-57262.41369863013699 1		8.286478	5.02148	7.407974	6.826369	5.468996	0		
0.96116946260721 low									
TCGA-HU-8608 1.75616438356164 0		9.38122	5.02148	5.256384	6.322117	6.66436	0		
1.08569935322172 high									
TCGA-HU-A4H8 0.73972602739726 0		8.43092	5.02148	6.09014	5.448514	5.423782	0		
0.791989817381562 low									
TCGA-BR-67052.13424657534247 1		9.89401	6.622016	11.820667	8.750373	9.127847	0		
3.34573729012664 high									
TCGA-VQ-A928 0.476712328767123	1	9.366348	7.595194	11.35322	7.238647				
8.300781 0 2.55915779992475 high									
TCGA-IP-7968 0.210958904109589	0	8.428468	5.307465	6.85116	6.712848	9.120211	0		
1.42183405514172 high									
TCGA-FP-7829 1.62739726027397 0		8.984403	6.39324	7.216474	6.762628	8.055729	0		
1.55732979141411 high									
TCGA-CD-58131.03287671232877 1		8.691271	5.129992	12.949125	8.435648	8.507856	0		
2.38723717361117 high									
TCGA-VQ-A940 1.75342465753425 1		9.175455	5.112422	9.536494	6.506135	6.544773	0		
1.40203650428291 high									
TCGA-RD-A8NB 1.40547945205479 1		9.846122	6.995324	9.566791	7.856715	8.33727	0		
2.49845252410456 high									
TCGA-BR-85912.34520547945205 0		9.418232	7.01006	8.08154	6.353114	7.851053	0		

1.74976209216704 high
TCGA-VQ-AA6G 2.16986301369863 1 9.83345 5.097629 7.385526 5.684098 6.867386 0
1.30205592861757 high
TCGA-BR-42012.57534246575342 1 9.883141 6.613542 9.944038 8.890191 8.504265 0
2.79862597829813 high
TCGA-FP-A4BF0.46027397260274 1 9.419565 9.035707 10.510528 7.126587 8.860453 0
2.87869492184457 high
TCGA-BR-A44U 1.15616438356164 1 8.948212 9.569191 10.177991 6.202747
7.274634 0 2.1067712707368 high
TCGA-VQ-A8PO 0.772602739726027 1 8.37664 5.02148 5.671543 5.962767
7.077269 0 0.956617840755477 low
TCGA-CG-44760.00273972602739726 0 8.457179 5.099114 11.944418 8.229113
8.686095 0 2.14710823061648 high
TCGA-BR-79592.76712328767123 0 9.973605 6.842056 11.154427 8.229925 9.983411 0
3.45170515514636 high
GSM2235695 9.94520547945205 0 11.248906 5.199434 5.132278 7.575804 6.068453
10.644177 0.723107275760447 low
GSM2235698 1.89041095890411 1 7.102491 4.780256 6.859098 6.855386 6.333408
10.484157 0.386052411112011 low
GSM2235699 1.89041095890411 1 9.95658 9.518109 10.038753 8.017477 9.332265
11.082544 1.62194538037886 high
GSM2235703 3.53424657534247 1 9.471515 6.52327 9.71626 8.461168 7.871539
10.907682 1.04378464975854 high
GSM2235706 0.164383561643836 1 8.669892 6.681767 10.253926 7.321037
6.829879 10.806819 0.778216360061253 low
GSM2235708 8.95890410958904 0 8.899 5.322876 6.177257 5.854828 6.139654
11.001004 0.44544441233352 low
GSM2235710 1.06849315068493 1 10.573502 7.096673 7.073221 8.623213 7.99992
10.874353 1.13695059224959 high
GSM2235717 0.246575342465753 1 9.067941 5.267288 11.400046 8.732621
10.134326 10.768136 1.30338197657557 high
GSM2235723 9.6986301369863 0 7.936887 5.13876 8.204017 6.508023 7.349921
10.67506 0.529582538237186 low
GSM2235728 2.87671232876712 1 8.648365 4.997656 8.576039 8.206849 10.024447
10.349962 0.962053951896541 low
GSM2235729 0.410958904109589 1 9.190092 6.550684 11.159704 8.206025
7.868243 10.772231 1.08180003036568 high
GSM2235731 9.6986301369863 0 6.759594 4.867159 4.596736 4.443077 5.847143
9.470843 0.259466090892279 low
GSM2235733 11.8356164383562 0 10.039606 9.690769 6.378925 8.165857 9.615214
10.117393 1.47243888474737 high
GSM2235734 11.8356164383562 0 6.667518 5.058846 10.833186 7.464291 7.742279
10.708608 0.575982195733507 low
GSM2235737 3.6986301369863 1 7.813929 4.906036 8.466957 7.046846 6.714282

10.944552 0.49889395263024 low
 GSM2235739 1.15068493150685 1 9.089525 6.818877 5.472628 10.361394 7.056992
 10.79516 0.837952698448681 low
 GSM2235742 0.246575342465753 1 7.447369 5.604377 6.70108 6.535186 8.196396
 10.544675 0.509668281741065 low
 GSM2235746 9.12328767123288 0 8.093942 5.417502 8.542987 6.922846 5.094177
 10.60243 0.465450319098497 low
 GSM2235750 0.575342465753425 1 9.74498 9.461041 13.157778 7.745313
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 GSM2235751 8.3013698630137 0 9.081939 5.338439 5.958317 6.242568 5.889742
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 GSM2235752 12.2465753424658 0 8.514117 4.912161 7.068454 6.083925 4.87575
 10.709385 0.390630147660601 low
 GSM2235753 2.54794520547945 1 8.160055 5.071569 11.31501 7.670242 8.238837
 10.699145 0.817551784507581 low
 GSM2235755 7.15068493150685 1 9.946477 5.692236 11.135914 9.276085 9.010694
 10.783731 1.42435578428466 high
 GSM2235756 11.5068493150685 0 8.469678 5.212124 10.74559 8.0935 8.830965 11.2652
 0.891432082403612 low
 GSM2235757 3.28767123287671 1 9.812691 5.191569 8.107912 7.766121 7.919493
 10.532183 0.867093214321392 low
 GSM2235758 1.06849315068493 1 9.645242 4.903911 10.191601 9.34143 5.524927
 10.905905 0.82140035274992 low
 GSM2235759 0.986301369863014 1 10.165893 5.102859 8.084621 9.396852
 10.699169 11.213727 1.3582712419108 high
 GSM2235761 11.013698630137 0 8.890456 5.13876 10.698939 8.748494 9.632665
 10.178956 1.18566639023126 high
 GSM2235762 3.20547945205479 1 8.785077 6.00987 11.422372 7.170636 7.223698
 10.520514 0.85228785023264 low
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 10.530702 0.571593855929749 low
 GSM2235767 1.47945205479452 1 9.617208 9.19794 11.574997 9.223644 8.371408
 10.550592 1.73105275302844 high
 GSM2235772 4.93150684931507 1 8.961713 6.873559 9.178437 7.397022 8.008221
 10.616003 0.895651606988732 low
 GSM2235774 0.986301369863014 1 9.180633 8.532146 10.804675 7.916177
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 GSM2235776 1.64383561643836 1 9.400954 7.951957 11.294277 8.15802 8.663376
 10.486364 1.39717243535147 high
 GSM2235777 9.45205479452055 1 9.266807 7.870922 10.385841 7.768223 7.933968
 10.039665 1.17948036419715 high
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6.821267 11.113907 0.802501034412359 low
 GSM2235790 9.78082191780822 0 8.735153 5.45288 6.517742 6.117695 6.176615
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 GSM2235801 9.28767123287671 0 8.594731 4.948954 10.337544 7.666162 7.287581
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 10.817631 0.782747822860299 low
 GSM2235805 0.410958904109589 1 10.006078 9.911281 8.078415 7.880612
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 GSM2235820 1.97260273972603 1 9.6639 7.485909 11.447514 8.558158 8.822563
 10.720576 1.47357679228345 high
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10.605435 0.394379248473378 low
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GSM2235843 1.06849315068493 1 10.045948 6.17792 10.854812 7.405732
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GSM2235845 2.54794520547945 1 9.035455 5.587423 8.512973 6.25625 7.304454
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10.291138 1.10890066710835 high
GSM2235886 4.19178082191781 1 8.682104 6.162185 7.892384 7.717645 7.620721
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 GSM2235904 1.72602739726027 1 9.319806 9.531042 10.256077 8.060674 9.305998
 10.585872 1.53936863922847 high
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 7.594328 10.845654 1.14382500885418 high
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 11.370365 0.599480253534281 low
 GSM2235921 11.4246575342466 0 8.348555 5.998446 9.28454 5.635284 7.153887
 11.002869 0.574065352569062 low
 GSM2235924 11.0958904109589 0 8.682104 8.758246 8.995365 6.691468 8.528677
 9.995628 1.01703358870441 high
 GSM2235926 11.5068493150685 0 8.486339 6.343894 10.732705 7.06419 8.659729
 10.549135 0.918644436865582 low
 GSM2235928 10.8493150684932 0 9.673085 7.049653 7.314869 6.707167 7.609294
 10.539558 0.817519378241798 low
 GSM2235930 6.08219178082192 1 8.788011 6.281953 12.707584 7.215575 8.513867
 10.076506 1.12814404105554 high
 GSM2235931 10.8493150684932 0 8.282641 4.965662 5.781617 6.807464 6.486149
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 GSM2235933 3.36986301369863 0 9.711307 5.600095 10.284035 8.941619 9.809639
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 10.603982 0.616113965544624 low
 GSM2235935 1.56164383561644 1 8.376021 6.217957 9.790219 7.877715 8.098848
 10.48712 0.856342993228615 low
 GSM2235937 3.04109589041096 0 7.641328 4.937418 6.67411 6.45103 6.318102
 10.52196 0.404725333980446 low
 GSM2235938 7.56164383561644 0 8.527206 4.932375 7.048325 6.2681 5.785406
 11.03119 0.429057801407861 low
 GSM2235943 10.4383561643836 0 8.168438 5.173427 10.138271 8.616565 7.880886
 10.908553 0.790550298794381 low
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 10.442958 1.07794818937635 high
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 GSM2235947 10.6027397260274 0 7.325444 5.03937 6.989819 5.168502 6.856819
 10.09236 0.384097763610902 low
 GSM2235949 10.8493150684932 0 9.641487 5.727802 6.789231 6.586523 7.792957
 10.963459 0.692550285629099 low
 GSM2235950 10.5205479452055 0 9.101755 11.165237 12.561699 8.765656

7.505041 10.632667 1.72053392704386 high
 GSM2235953 0.821917808219178 1 9.694077 6.877766 11.973301 7.936095
 8.014772 10.763174 1.2606516149403 high
 GSM2235954 12.2465753424658 0 7.776076 5.618735 7.660173 6.352764 8.358027
 10.362098 0.581124592468936 low
 GSM2235955 12.2465753424658 0 9.684583 10.864642 12.523271 7.261388
 8.046597 10.605435 1.70530780135289 high
 GSM2235957 12.1643835616438 0 8.776802 5.916754 7.660173 6.192692 6.970102
 10.694469 0.58105661398108 low
 GSM2235958 12.4931506849315 0 8.711903 5.595642 9.936742 7.619321 8.930644
 9.984032 0.963055249085611 low
 GSM2235959 11.8356164383562 0 8.321099 5.156465 5.450708 5.108295 6.162065
 9.914061 0.386149658380753 low
 GSM2235964 1.80821917808219 1 8.653591 5.054138 9.99065 6.925032 8.042562
 10.516926 0.752477111639835 low
 GSM2235966 2.71232876712329 0 7.82933 5.05226 10.402557 7.881345 6.181785
 10.355253 0.610643987522647 low
 GSM2235967 0.821917808219178 1 5.701312 5.725136 7.557334 7.263795 6.293098
 10.664224 0.352954261331223 low
 GSM2235969 5.26027397260274 0 7.264014 5.445757 5.772647 3.965413 8.095411
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 GSM2235974 0.986301369863014 1 6.482377 5.525667 7.8269 6.548949 7.298847
 9.176853 0.466926493657982 low
 GSM2235976 4.52054794520548 0 7.157986 5.205525 5.092711 3.600076 7.171933
 9.271856 0.318030548322753 low
 GSM2235977 0.575342465753425 1 8.901802 6.503401 10.703172 6.9884
 9.762013 10.285855 1.13260213680455 high
 GSM2235979 3.45205479452055 0 8.171945 4.911429 9.255718 7.491431 7.294377
 10.794296 0.62449736961348 low
 GSM2235984 0.657534246575342 1 8.271285 5.587423 9.327254 8.490937 6.950647
 11.058202 0.697350861386064 low
 GSM2235986 2.87671232876712 0 7.452369 5.400734 9.349525 6.75109 6.483993
 10.96624 0.490784839379059 low
 GSM2235993 10.3561643835616 0 8.086897 5.186358 9.245455 7.313575 7.547638
 10.191484 0.664160184017984 low
 GSM2235994 10.1095890410959 0 8.744636 4.9723 7.55018 8.050076 7.314983
 10.195831 0.679810251321077 low
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 10.468513 0.485026392815599 low
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 8.582068 0.551749707605261 low
 GSM2235999 7.80821917808219 1 8.135035 4.964899 5.990537 5.807842 7.86111
 10.276158 0.476442756338119 low
 GSM2236000 10.027397260274 0 7.942528 6.183013 11.897677 6.648073 8.982903

9.354837 0.97215319293948 high

GSM2236001 10.1917808219178 0 8.687584 5.712202 10.987652 7.317381 9.141098
10.517665 0.992125949274232 high

GSM2236003 10.3561643835616 0 8.209185 8.871431 12.819799 7.548928 8.485548
9.951412 1.31558001902757 high

GSM2236004 3.78082191780822 1 8.747352 6.75978 8.436417 5.651595 7.18432
10.551979 0.639475143328415 low

GSM2236005 0.73972602739726 1 8.273794 9.172423 7.672162 7.098693 8.707999
10.199677 0.940445400179416 low

GSM2236006 1.97260273972603 1 8.170783 4.969182 7.993526 5.991391 6.582133
10.170819 0.487769240789886 low

GSM2236010 3.12328767123288 1 8.052174 5.473224 9.849593 5.914619 6.765877
9.826186 0.583170324265146 low

GSM2236012 0.246575342465753 1 9.240525 6.440572 6.9429 8.692395 7.224867
10.892862 0.795347081943637 low

GSM2236015 9.04109589041096 0 9.011088 5.69656 10.491235 8.52157 7.571052
10.656522 0.94531307764269 low

GSM2236017 1.3972602739726 1 9.161605 6.983424 7.960915 7.892329 6.493126
10.79516 0.757285250453487 low

GSM2236018 9.53424657534247 0 9.033886 5.351346 6.606782 6.710289 6.485417
10.377702 0.551339139314936 low

GSM2236019 7.56164383561644 1 9.104871 6.335612 10.118582 6.565183 7.440913
11.007536 0.791390830988004 low

GSM2236020 8.95890410958904 0 7.785955 6.423652 5.776411 6.141391 6.20553
10.726969 0.415991812787829 low

GSM2236021 4.19178082191781 1 10.620012 6.860144 10.728548 8.790085
9.470867 10.940977 1.68782088214728 high

GSM2236024 8.46575342465753 0 8.419723 7.482133 8.132967 6.59831 7.722286
10.981335 0.704939590762811 low

GSM2236026 5.26027397260274 1 9.748908 5.049095 12.508754 9.019388 8.383652
10.89893 1.29739489977164 high

GSM2236027 10.1917808219178 0 9.979171 6.337625 11.703053 7.750177 7.863981
10.810974 1.19886938234662 high

GSM2236028 7.80821917808219 1 9.566708 5.218521 9.587278 6.390186 6.528024
10.957185 0.67600236398063 low

GSM2236029 11.3424657534247 0 7.54969 5.076619 6.964037 5.752513 5.381929
10.195831 0.356651782432919 low

GSM2236034 10.027397260274 0 10.328988 5.490517 8.784784 6.044365 8.057833
11.069797 0.841359811653846 low

GSM2236040 3.04109589041096 0 9.12664 4.890065 6.567753 5.768446 5.717884
10.61521 0.446861272811863 low

GSM2236041 3.36986301369863 0 8.684854 6.754968 11.312931 8.507067 7.857873
10.660386 1.05813352382801 high

GSM2236042 3.04109589041096 0 5.67685 5.417415 7.487614 6.009592 6.508238

10.565455 0.31366113349651 low
 GSM2236044 11.5890410958904 0 8.125822 5.809067 6.498578 7.141885 6.400429
 10.297491 0.507185498583947 low
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 10.113043 0.713003479249177 low
 GSM2236049 2.71232876712329 1 7.770552 5.044535 9.413535 7.180784 7.642608
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 GSM2236051 3.12328767123288 1 9.53421 5.074725 9.803229 8.109686 8.437569
 10.374267 1.0114136208861 high
 GSM2236055 10.9315068493151 0 6.754295 5.06895 8.786382 10.080125 5.194917
 10.527108 0.501821396619536 low
 GSM2236056 10.5205479452055 0 8.897557 5.192413 9.795885 6.477669 6.64429
 10.639569 0.639961532575615 low
 GSM2236057 3.04109589041096 1 9.746947 5.381847 11.051443 8.492713 8.354183
 10.917367 1.14872875153411 high
 GSM2236058 11.1780821917808 0 10.012338 7.64083 10.56198 7.408921 8.395365
 11.18145 1.23931563875221 high
 GSM2236059 11.2602739726027 0 9.092632 5.303621 6.985121 8.749476 9.37641
 10.427472 0.932118529012264 low
 GSM2236061 10.6027397260274 0 8.841725 5.212835 11.790027 8.012956 8.691854
 10.571483 1.04280225698092 high
 GSM2236065 9.78082191780822 0 10.092412 6.251747 9.118657 7.537054 6.610765
 10.510445 0.898245299889738 low
 GSM2236066 10.4383561643836 0 11.222376 5.534163 8.670022 7.69568 8.896598
 10.874353 1.25367361592144 high
 GSM2236067 1.3972602739726 1 10.945107 6.228132 9.277458 6.911208 6.575821
 11.22651 0.930445536442949 low
 GSM2236068 3.45205479452055 1 10.712564 6.197034 12.217033 9.083118
 8.341607 11.001004 1.62295184185587 high
 GSM2236070 10.1917808219178 0 11.173861 5.331482 4.951968 5.303636 6.352542
 11.314606 0.568430862751018 low
 GSM2236071 9.36986301369863 0 10.231819 5.555177 6.823779 5.866217 5.769556
 11.604554 0.542282563253145 low
 GSM2236073 1.80821917808219 1 8.346148 4.939453 8.068297 8.181059 6.889054
 10.894603 0.603789859889749 low
 GSM2236074 11.7534246575342 0 10.49618 5.418599 4.894606 8.454915 6.826499
 11.352853 0.715491405987053 low
 GSM2236082 10.7671232876712 0 8.379717 5.126125 8.194467 6.457402 6.229218
 10.315385 0.514966481290226 low
 GSM2236083 0.575342465753425 1 8.732437 5.089834 8.649629 6.797879 4.593822
 10.538015 0.47733365451627 low
 GSM2236084 10.5205479452055 0 8.552523 5.54947 8.44917 6.70929 7.492321
 10.927369 0.624581039298402 low
 GSM2236087 12.7397260273973 0 8.336123 5.661037 8.213577 7.167592 7.086715

10.681926 0.608766066534028 low
 GSM2236088 2.79452054794521 1 7.642399 5.073953 7.009552 8.66237 8.468093
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 GSM2236092 12.2465753424658 0 8.53264 5.653685 10.074911 8.637439 7.265506
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 11.510208 0.706363564943756 low
 GSM644520 1.8986301369863 1 10.046573 7.765043 11.49144 7.202762 9.082466
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 11.199287 0.956572293750366 low
 GSM644523 12.7643835616438 0 9.463116 3.619198 10.34944 7.802669 8.230946
 11.13477 0.830799088222237 low
 GSM644525 12.5013698630137 0 7.292158 3.545894 9.792065 8.062273 5.941848
 10.304491 0.474443023866153 low
 GSM644529 0.246575342465753 1 9.932977 6.373095 11.626217 8.472557
 8.770285 10.908413 1.38874965668191 high
 GSM644530 3.4027397260274 1 8.64549 5.111133 10.567172 7.447955 7.276329
 10.782223 0.742942423883632 low
 GSM644531 1.26575342465753 1 9.737167 6.255363 10.861602 8.161154 8.042531
 11.537157 1.08863328030258 high
 GSM644533 10.8328767123288 0 9.540157 4.967255 10.869637 8.466968 7.100383
 11.824999 0.867077824613499 low
 GSM644538 2.88493150684931 1 10.4461801 7.2226144 11.1488024 5.3355202
 10.092726 11.5571858 1.29072827609847 high
 GSM644539 4.76712328767123 0 9.546784 7.585553 11.550521 8.899603 7.074235
 12.067044 1.13790968201825 high
 GSM644540 0.756164383561644 1 10.02866 6.346184 10.811593 7.811609
 8.578023 11.516802 1.17765670957181 high
 GSM644541 8.9013698630137 0 7.409728 6.878091 10.555346 8.396873 7.338093
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 GSM644543 1.2986301369863 1 8.44627 6.486099 9.984166 8.35058 7.973534
 11.477145 0.859551583061798 low
 GSM644544 2.75342465753425 0 9.46573 6.4579 10.136584 7.603649 6.967542
 10.719386 0.906329097648167 low
 GSM644549 8.61369863013699 0 9.9993631 6.1942057 9.1800878 7.7032938
 6.3581045 11.4877593 0.814070652515345 low
 GSM644552 7.77534246575342 0 8.509116 5.980452 10.572396 7.530438 7.394609
 9.865928 0.848871609982158 low
 GSM644553 7.91506849315068 0 10.218403 5.1553668 8.8518881 7.9144419
 8.1016084 11.9785589 0.903040758567452 low
 GSM644554 7.63561643835616 0 9.573749 6.381353 10.52372 7.719765 8.950793
 11.293018 1.12832733940932 high
 GSM644556 0.986301369863014 1 10.094981 7.128341 10.782395 7.894484

7.966489 11.602406 1.18539397756763 high
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 9.717257 11.953954 1.51311646001914 high
 GSM644559 7.63561643835616 0 9.301471 6.835938 9.628695 6.835835 6.918112
 11.51618 0.769465465617946 low
 GSM644560 3.80547945205479 0 9.270893 7.380618 8.202208 6.168919 7.768062
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 GSM644561 7.36438356164384 0 9.671627 7.106139 10.405551 8.398609 8.92137
 11.838033 1.22910149078702 high
 GSM644562 1.06849315068493 1 9.075173 5.293518 10.536852 7.317585 8.284452
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 GSM644568 6.99452054794521 0 10.096214 7.536292 10.296229 7.685797
 9.419133 11.880472 1.33332076922507 high
 GSM644570 5.02191780821918 0 9.743028 5.056572 10.190132 8.093509 8.823446
 11.431574 1.03333024583584 high
 GSM644574 3.34520547945205 1 7.888838 7.828077 10.967192 7.965732 8.017468
 10.18188 0.990247870196649 high
 GSM644575 6.04931506849315 0 9.684544 7.413846 10.517139 6.767997 7.091995
 11.258814 0.937348247486365 low
 GSM644576 5.24383561643836 0 9.118714 6.634328 9.971003 8.09989 7.882653
 10.901077 0.978946262919061 high
 GSM644583 1.01917808219178 1 10.030569 6.782134 10.178207 8.281821
 9.255609 11.486489 1.31705473784884 high
 GSM644585 5.30958904109589 0 9.63426 7.684426 9.835312 7.707807 6.525827
 11.403947 0.922446985252074 low
 GSM644586 4.30684931506849 0 10.022761 6.656156 10.300778 7.957686
 7.697973 11.666461 1.06388083890178 high
 GSM644588 2.6958904109589 1 10.017751 7.730522 11.437548 8.258157
 8.700904 11.435195 1.45072013321845 high
 GSM644589 4.77534246575342 0 9.534722 6.571354 10.116169 7.905883 7.898012
 11.049968 1.0247708732181 high
 GSM644590 3.09041095890411 1 10.269013 6.96464 10.33191 8.056436 10.48104
 11.674893 1.54686373171137 high
 GSM644591 4.77534246575342 0 8.470899 5.554076 9.342322 6.086042 7.602751
 9.132953 0.710853308532106 low
 GSM644595 0.624657534246575 1 9.963379 3.8245457 7.902952 7.7495429
 7.2813211 11.5027961 0.684135194043973 low
 GSM644598 7.90684931506849 0 8.239505 3.788567 9.966358 8.000648 8.407427
 9.771438 0.769635447955734 low
 GSM644599 1.21643835616438 1 9.774393 8.082423 10.596683 4.823627 8.899554
 11.420171 1.01173671017905 high
 GSM644600 12.4767123287671 0 9.196592 7.123651 9.728736 7.196897 6.469587
 9.381934 0.8953482896178 low
 GSM644602 0.649315068493151 1 9.086534 7.860952 9.306333 7.568195 7.435715

10.644106	0.950145423449914	low			
GSM644605	7.093150684931510	8.936614	7.657786	10.021324	5.131698 5.855001
7.858752	0.788351087647605	low			
GSM644606	3.443835616438360	9.091425	7.382793	10.181552	8.01239 6.94492
11.675575	0.888919895761137	low			
GSM644607	12.27123287671230	7.841577	6.071319	10.633815	4.833797 6.281956
10.307208	0.515900727529639	low			
GSM644608	2.186301369863011	9.352064	5.758723	10.485064	8.439701 7.734785
10.697776	1.01136523197219	high			
GSM644609	9.632876712328770	8.9349358	7.3345412	10.8696373	5.1398781
7.3215023	11.6977375	0.720364388140463	low		
GSM644610	0.509589041095891	8.425355	7.475763	10.411458	7.87299 8.302622
11.286654	0.957362180941675	low			
GSM644613	8.728767123287670	9.9932778	7.6584727	10.7658596	7.7328841
7.3380931	11.8357407	1.09960463003311	high		
GSM644614	9.945205479452050	9.793242	6.964203	10.776316	8.314382 7.444874
11.357083	1.113534447564	high			
GSM644615	1.627397260273970	9.897524	7.574308	9.82518	6.373397 6.052751
11.325094	0.806700833345871	low			
GSM644618	10.01095890410960	9.147864	7.507516	10.655938	4.772541 8.560108
10.799506	0.878973225883033	low			
GSM644619	6.016438356164380	9.8257742	7.2154923	7.2587445	5.6528125
7.2995344	11.4207853	0.696954826179843	low		
GSM644620	9.534246575342470	9.426956	6.956389	10.736543	7.678364 8.404869
11.184107	1.10667261206435	high			
GSM644622	7.717808219178080	9.722065	6.550144	10.657356	7.932146 8.508884
11.371242	1.1428328079206	high			
GSM644623	1.627397260273971	10.015452	7.838865	10.430885	7.937458
8.096465	11.286654	1.26000529603587	high		
GSM644624	5.087671232876710	9.513455	6.847982	10.661545	7.769648 8.082426
11.164239	1.08036931616832	high			
GSM644625	4.956164383561640	9.65081	3.539019	8.766979	6.397608 6.130706
11.400985	0.528365690024447	low			
GSM644626	9.065753424657530	9.783518	7.598866	9.792065	7.837149 7.804097
11.370637	1.08963329299906	high			
GSM644628	8.441095890410960	9.717266	7.291957	10.050312	7.669638 7.75519
11.270169	1.05558250634041	high			
GSM644631	1.117808219178081	9.736138	7.458389	11.62936	7.538962 8.545698
10.712799	1.33138447645873	high			
GSM644632	0.493150684931507	1	9.64307	3.593146	10.950212 6.518421
8.113878	11.269604	0.771544067485296	low		
GSM644633	4.060273972602741	7.227157	7.188769	10.716037	7.673584 8.556731
10.346288	0.846968440458007	low			
GSM644636	1.027397260273971	9.7688333	7.4211954	9.3867312	4.8101719

7.1507688 10.625203 0.77743319317349 low
 GSM644638 3.99452054794521 1 9.385696 6.88436 10.49658 7.164214 8.602138
 11.202544 1.04690997502797 high
 GSM644639 5.07123287671233 0 10.076416 6.879765 10.665836 5.992787
 6.144596 11.756889 0.78496480281949 low
 GSM644640 7.56164383561644 0 8.889882 7.897108 10.027066 7.349013 6.229796
 10.466336 0.843179960726729 low
 GSM644642 2.29315068493151 1 9.731346 7.405831 10.755436 7.804596 8.120817
 10.715648 1.22515249584599 high
 GSM644643 1.68493150684932 1 7.846201 3.516737 5.516999 8.109924 6.391795
 9.782727 0.429823438685751 low
 GSM644645 0.567123287671233 1 9.382382 6.825409 10.044532 4.730412
 7.860174 11.311786 0.740576330477831 low
 GSM644646 1.68493150684932 1 10.130773 5.902754 9.777786 7.391864 9.092424
 11.282161 1.11812639285492 high
 GSM644653 6.48493150684931 0 9.449115 7.52995 9.941343 5.859108 6.857993
 10.489216 0.831380165803334 low
 GSM644654 6.39452054794521 0 7.461696 6.13042 11.146814 4.842964 7.557288
 10.841288 0.556020545284111 low
 GSM644655 0.789041095890411 1 8.878963 5.595396 10.639354 6.857914
 6.699436 10.54406 0.729868514286954 low
 GSM644656 1.72602739726027 1 9.376679 3.597649 10.482542 7.704017 7.542862
 10.553863 0.79170065355033 low
 GSM644658 1.66027397260274 1 8.562402 4.035391 10.429636 6.950987 7.371163
 11.184107 0.625390486705871 low
 GSM644659 5.02191780821918 0 9.618495 6.627068 8.802627 7.670009 6.627805
 10.051406 0.879264743620345 low
 GSM644660 0.953424657534247 1 9.555166 6.989506 8.941113 5.330423 7.887653
 9.3765 0.875897534947455 low
 GSM644661 5.52328767123288 0 9.644714 7.090307 10.223625 7.236431 8.31756
 10.808098 1.0958201936898 high
 GSM644669 3.99452054794521 0 7.25727 5.53007 9.43389 5.160434 8.012424
 10.594059 0.504953913663509 low
 GSM644672 3.97808219178082 0 10.287469 7.318976 10.058194 7.718979
 7.556418 11.468611 1.12652448345104 high
 GSM644673 1.32328767123288 1 9.887712 8.66442 10.614466 8.65107 9.498448
 11.506516 1.62862216358957 high
 GSM644675 4.70958904109589 0 7.416614 4.559055 4.175471 7.472929 7.233706
 9.810528 0.410718506901585 low
 GSM644678 7.59452054794521 0 8.145331 6.553157 4.157507 4.737434 7.744939
 8.293882 0.49617061497074 low
 GSM644680 1.77534246575342 1 7.14285 8.229495 10.547535 7.24694 9.302976
 10.402523 0.930755183755768 low
 GSM644681 12.0904109589041 0 9.407633 7.84561 9.170257 8.171789 8.425823

10.276601 1.19722823637801 high
 GSM644682 11.7698630136986 0 9.896795 7.641097 9.758609 7.949657 9.362705
 10.18282 1.44680427260645 high
 GSM644683 0.641095890410959 1 10.099828 7.084299 8.90114 5.250208
 9.104945 10.156752 1.02912572271879 high
 GSM644684 8.15342465753425 0 8.892593 7.145096 9.385313 7.375119 8.751436
 11.106749 0.95665523861706 low
 GSM644685 10.6849315068493 0 8.106447 6.8928 4.973058 4.674236 7.828061
 10.238176 0.465361679852089 low
 GSM644686 3.26301369863014 1 9.623872 8.345806 10.010712 4.699656 8.127005
 7.395765 1.18118371118064 high
 GSM644687 2.24383561643836 1 7.276644 5.891912 4.626622 8.403783 6.610454
 7.005782 0.573233087111799 low
 GSM644688 10.5041095890411 0 7.069757 6.435349 4.401897 4.909268 6.442585
 10.410823 0.317248662927056 low
 GSM644689 9.55068493150685 0 7.312932 6.800236 7.819857 7.447955 7.222951
 9.029713 0.644189435780744 low
 GSM644691 9.18082191780822 0 8.813414 6.457166 9.494594 8.207446 6.336087
 8.067574 0.934664273388548 low
 GSM644692 7.23287671232877 0 9.767753 5.676866 8.389797 7.976038 9.559018
 9.629437 1.18233919064434 high
 GSM644696 9.38630136986301 0 9.51043 7.008883 8.993844 7.785042 8.151372
 9.812396 1.09174866676643 high
 GSM644698 9.01643835616438 0 9.6120755 7.0146498 4.8824994 7.7085212
 9.0890496 9.941154 0.925035046593259 low
 GSM644701 8.01369863013699 0 9.205963 6.375328 9.687508 4.737717 6.52927 8.06292
 0.744323346721748 low
 GSM644702 1.8 1 9.788032 7.713085 5.603005 8.450555 8.094742 9.870739
 1.01974102851951 high
 GSM644707 1.01095890410959 1 8.898128 6.841731 9.364931 7.424407 8.013249 9.2973
 0.987532742820777 high
 GSM644708 5.4986301369863 0 7.315678 7.698355 4.487766 5.354892 5.594872
 7.080402 0.444257430698681 low
 GSM644711 2.11232876712329 1 9.610357 6.983373 10.150104 5.012639 7.806642
 7.796657 1.031510123433 high
 GSM644714 1.2986301369863 0 9.79856 4.78822 4.983581 5.608633 5.865571
 10.72461 0.443518132594757 low
 GSM644715 6.16438356164384 0 7.716197 6.717846 8.074448 8.27926 6.261645
 9.600652 0.649436684878088 low
 GSM644716 5.11232876712329 1 9.82059 8.149389 8.485901 7.251793 6.496156
 9.662418 0.979978768002269 high
 GSM644719 5.76164383561644 0 8.424353 6.741771 10.157351 6.175643 8.89435
 10.175835 0.877643294137321 low
 GSM644725 0.904109589041096 1 9.451798 7.68805 8.42282 7.560643 8.62182

10.606729 1.06945488945576 high
 GSM644729 4.81643835616438 0 9.861754 5.967028 9.612411 5.044517 8.610789
 9.965044 0.895295927721721 low
 GSM644732 4.05205479452055 0 10.149021 7.457187 8.252253 6.927761 8.07116
 11.031994 1.00406095217375 high
 GSM644733 3.73972602739726 0 8.959379 7.192211 7.494747 7.353885 7.721005
 8.696096 0.913268952828604 low
 GSM644735 7.40547945205479 0 9.200384 6.8966 5.845893 5.305431 7.07758
 9.174026 0.622550056304939 low
 GSM644737 3.4027397260274 0 7.805647 6.505829 7.092027 7.289123 7.679338
 9.320991 0.659582338180411 low
 GSM644738 10.158904109589 0 9.336814 7.186818 10.140737 4.653268 8.373488
 10.294903 0.859552386811263 low
 GSM644740 0.682191780821918 1 10.020414 7.9325581 8.5963573
 8.0193106 7.9367804 10.6879293 1.16625893419042 high
 GSM644741 0.312328767123288 1 9.0434641 7.9192518 10.1460037
 8.1862925 9.1715406 9.9787488 1.33976922075948 high
 GSM644742 2.55616438356164 1 8.092631 6.398715 9.787927 8.257623 6.153603
 10.627557 0.689599081786973 low
 GSM644744 4.23287671232877 1 7.563865 6.074398 9.074228 8.360646 8.671573
 9.343384 0.854269557644926 low
 GSM644745 2.62191780821918 0 7.3872578 3.7688742 8.6643109 8.0492799
 7.0324025 7.79818 0.613643491071547 low
 GSM644747 2.05479452054795 1 7.4425004 7.6670818 3.98521 8.6650056
 9.6756874 7.7444048 0.877492053636134 low
 GSM644750 3.02465753424658 1 7.996575 3.686312 4.523403 4.728305 7.963866
 7.194326 0.437861170718147 low
 GSM644751 9.62465753424657 0 8.57668 3.864361 9.176118 8.348351 7.462053
 10.812893 0.672458080178247 low
 GSM644752 1.35616438356164 1 9.419349 3.811016 10.442041 9.006809 8.201311
 10.368683 0.991728480845136 high
 GSM644753 2.41643835616438 1 7.087771 4.003811 4.143514 9.061178 7.558129
 10.711859 0.417279920799643 low
 GSM644754 1.28219178082192 1 7.3095692 5.421416 9.7239428 8.9284892
 6.1706054 7.2079361 0.762962352258045 low
 GSM644756 6.11506849315068 0 8.37993408 5.98552798 9.92114131 4.76294868
 8.47705365 7.1608017 0.844007772688651 low
 GSM644757 6.13150684931507 1 7.587332 3.917638 10.088166 7.921008 8.578907
 10.359126 0.682376822590499 low
 GSM644758 10.0438356164384 0 7.870761 7.98895 3.893763 8.539341 8.304378
 10.62616 0.664753768506479 low
 GSM644759 1.21643835616438 0 7.881353 5.925098 9.287726 8.839272 7.512646 8.00823
 0.916506782991847 low
 GSM644761 6.61643835616438 0 9.671627 6.850814 8.699424 8.118268 8.85179

9.700503 1.21727389908743 high
 GSM644762 9.25479452054794 0 7.321586 6.995196 9.93858 8.064062 6.758227
 9.736481 0.719212594313768 low
 GSM644763 9.28767123287671 0 8.0548056 7.0403968 4.2591393 8.6342642
 7.9770313 10.8966403 0.621646445290886 low
 GSM644764 1.66849315068493 1 7.815466 6.73381 7.317808 8.327749 8.059871
 8.483059 0.83131828077782 low
 GSM644767 8.36712328767123 0 7.802974 6.28061 8.744867 7.417821 7.870561
 10.594059 0.679295113021561 low
 GSM644770 1.75068493150685 1 9.04044 6.824565 6.12496 7.824971 7.258812
 10.24687 0.730485308199991 low
 GSM644771 8.0958904109589 0 8.562039 3.743144 9.742879 8.096179 5.81991 7.41193
 0.722173861674756 low
 GSM644772 6.42739726027397 1 9.098629 5.124856 7.07982 7.224963 8.28702
 10.364134 0.718898067844694 low
 GSM644777 2.13698630136986 1 7.485288 3.74886 9.51991 8.592978 5.995304
 7.249914 0.64407356705507 low
 GSM644779 6.18082191780822 0 8.858931 7.014225 9.639935 8.382439 8.166994
 8.555486 1.18636241022136 high
 GSM644780 7.25753424657534 0 7.9651392 3.65542 10.0193608 8.2119422
 6.9373807 7.0322807 0.775519928622226 low
 GSM644781 5.4986301369863 0 8.100017 6.323236 8.451774 5.269835 6.569733
 10.207965 0.515243552561338 low
 GSM644782 1.51232876712329 1 9.683855 8.072168 9.642248 8.51153 8.977756
 10.337081 1.4334897841757 high
 GSM644783 1.12602739726027 0 9.560798 8.315249 10.950212 8.09989 9.051194
 10.474921 1.4980788875725 high
 GSM644784 4.33972602739726 1 9.365756 4.816365 9.058393 7.780382 8.088552
 9.122841 0.939531784075411 low
 GSM644785 6.92054794520548 0 9.161724 6.692356 9.140391 8.146873 9.227304
 10.030364 1.1597203064966 high
 GSM644787 3.01643835616438 0 7.319455 3.628557 9.317561 8.182433 7.534428
 8.982842 0.61407457587907 low
 GSM644789 1.66849315068493 1 8.644155 6.338429 6.39078 8.000193 7.021557
 9.750748 0.68818613207834 low
 GSM644790 6.57534246575342 0 7.192838 6.458638 10.400631 8.356654 7.760292
 9.148039 0.830319505075158 low
 GSM644798 0.665753424657534 1 9.585365 7.317925 10.296229 8.652502 9.23982
 10.822098 1.39495153702923 high
 GSM644800 4.86575342465753 0 7.230747 3.650303 4.964365 7.931315 5.705392
 7.351605 0.412716702603188 low
 GSM644805 2.4 0 8.171674 5.511249 8.223212 8.207969 6.84869 7.854971
 0.771215243436481 low
 GSM644806 1.22465753424658 1 7.378139 3.548851 4.088039 7.580022 6.547455

7.490469	0.415741845870902	low					
GSM644808	4.02739726027397 0	8.61054	5.671971	7.803987	7.784662	7.506053	
	10.092177	0.717105215047124	low				
GSM644809	4.23287671232877 0	9.858582	6.518549	5.092106	5.270392	6.395812	
	7.481453	0.671131301793759	low				
GSM644810	1.03561643835616 0	7.12001	3.658915	8.614085	7.708521	6.345099	7.98861
	0.515233660750702	low					
GSM644812	3.01643835616438 0	8.37508	3.677213	9.130628	7.395306	7.204531	
	8.366823	0.6797632028448	low				
GSM644814	10.027397260274 0	8.7239418	4.6105257	4.9051916	8.8489033		
	7.1549662	6.9243463	0.743195064911231	low			
GSM644815	1.9972602739726 1	7.9939914	3.8352632	8.9650809	5.4638199		
	7.6996805	10.1416371	0.496690674112062	low			
GSM644817	0.978082191780822	1	10.174245	7.365575	9.790455	8.88492	
	10.025186	10.998052	1.63791259254199	high			
GSM644818	10.4630136986301 0	8.00773	4.011712	9.150711	8.590899	6.762437	
	7.232246	0.76039386498541	low				
GSM644821	6.14794520547945 0	6.9089692	3.8170376	5.9432348	8.6687659		
	8.1208174	7.9065269	0.563392049363537	low			
GSM644822	1.07671232876712 1	7.898257	3.866976	10.705968	6.050752	6.910602	
	8.864289	0.583814916365781	low				
GSM644823	0.501369863013699	1	7.1006389	6.5291179	8.402036	5.0804143	
	5.587709	7.8860841	0.463481400156274	low			
GSM644827	7.46301369863014 1	9.7764738	3.5053106	9.379612	8.7864678		
	7.5756615	6.8074834	1.13574171059544	high			
GSM644829	6.46027397260274 0	7.734005	4.460652	4.532541	7.553543	6.83695	
	7.438507	0.503640588675525	low				
GSM644831	8.54794520547945 0	8.97274	6.331374	4.679214	8.429567	7.377914	
	8.192263	0.785840504643384	low				
GSM644832	7.74246575342466 0	8.838636	7.394048	9.227089	8.030361	7.184281	
	10.370511	0.906133839204068	low				
GSM644835	4.89041095890411 1	8.9474146	4.4292605	9.9174525	8.5979112		
	8.0399587	7.6412027	1.07405013561605	high			
GSM644836	0.978082191780822	1	7.467181	5.552972	4.040923	8.984342	7.311172
	9.213615	0.537342833226058	low				
GSM644838	1.33972602739726 1	8.528139	3.59518	9.501175	8.327238	8.362217	
	7.950162	0.902122554563743	low				
GSM644839	6.76438356164384 0	7.056435	6.292222	9.003755	8.875814	6.961723	
	8.070087	0.761629826398269	low				
GSM644841	7.30684931506849 0	7.237148	3.630004	4.069584	8.502032	6.941606	
	8.629354	0.427058503910349	low				
GSM644843	7.01917808219178 0	8.97239	3.573912	7.954849	7.256618	7.451788	
	8.333206	0.700231749396413	low				
GSM644844	1.56986301369863 1	7.080587	5.87343	8.052859	8.005037	7.245409	

8.664662 0.633863402959465	low
GSM644845 7.22465753424658 0	7.165363 6.36039 9.094609 8.436697 8.32467
7.117444 0.934107797336897	low
GSM644847 0.747945205479452	0 9.059646 3.875616 4.165892 8.363415 7.23883
9.340625 0.572138031643118	low
GSM644848 5.57260273972603 0	7.1226723 7.2993854 6.9223826 9.1052382
3.7596352 7.2712111 0.558673177607042	low
GSM644849 2.42465753424658 1	7.204228 3.886129 8.651817 8.440303 8.506242
9.752653 0.633165245036303	low
GSM644850 6.80547945205479 0	7.619188 3.893058 8.558919 8.761686 8.148004
7.439115 0.789847880985767	low
GSM644856 5.54794520547945 0	7.744405 6.888149 4.129653 7.48185 6.220027
6.933869 0.574171592341908	low
GSM644857 0.813698630136986	1 7.430413 3.578857 10.34944 8.997565 6.788916
7.381625 0.744154727690055	low
GSM644858 2.06301369863014 1	7.523975 3.756833 9.294045 8.905841 7.516037 7.39836
0.766277513550564	low
GSM644860 5.71232876712329 0	7.29835 4.101798 7.56715 7.566093 6.670412
6.985913 0.564113419179481	low
GSM644862 5.05479452054795 0	7.250465 4.852622 9.546223 8.559359 7.310361
8.029827 0.735096719423136	low
GSM644863 5.02191780821918 0	10.117479 4.982467 6.728183 8.375695 7.288806
9.135686 0.896362789804188	low
GSM644869 3.22191780821918 0	8.788883 4.187432 7.965182 7.535393 6.506051
7.675197 0.693764328752858	low
GSM644870 0.912328767123288	0 10.4615945 3.6477408 4.0077513
8.2656979 6.1895008 9.7906725 0.599953508488841	low
GSM644872 4.1013698630137 0	7.458458 5.572447 5.493259 8.612053 5.889127 7.33496
0.56118368179771	low
GSM644876 6.05753424657534 0	7.578889 4.535668 4.008379 4.94857 4.85126
7.538392 0.301264248605424	low
GSM644877 7.7013698630137 0	7.411376 7.018228 9.518381 6.928124 6.812551
9.833251 0.640150666567424	low
GSM644880 1.2986301369863 1	9.652485 6.602156 9.647894 5.274945 6.901613
7.507706 0.925862938995688	low
GSM644882 0.641095890410959	1 9.434054 4.740245 9.467491 4.746475 7.930694
8.151285 0.773806556142702	low
GSM644883 3.54246575342466 1	9.509287 7.241276 8.550487 8.085248 7.781607
10.526494 1.01346141644228	high
GSM644884 9.78904109589041 0	9.51378 7.092642 9.025593 7.616693 7.71675
10.758455 0.966927115762454	low
GSM644889 0.394520547945205	1 7.578363 7.266901 8.022881 7.692866 5.403561
9.473249 0.576288049036246	low
GSM644892 9.43561643835617 0	7.783232 7.183331 10.159405 4.760135 9.185111

9.34798	0.786789061399419	low					
GSM644893	10.0109589041096 0	7.685798 5.327131 9.809718 4.640009 6.70107					
7.745907	0.555849855441079	low					
GSM644894	8.30958904109589 0	9.886282 6.750137 4.396063 7.741941 6.186267 7.15113					
0.825018018950446	low						
GSM644896	0.345205479452055	1 9.225147 7.176069 6.657981 6.952453 8.175787					
9.496399	0.861769180440757	low					
GSM644900	2.25205479452055 1	9.7757865 4.7231337 9.3306044 6.4899894					
6.203239	7.5809742 0.823256600486203	low					
GSM644901	0.526027397260274	1 7.224347 7.196574 9.267777 7.547164 6.936521					
10.707572	0.62380457769066	low					
GSM644902	4.53698630136986 0	9.58 4.842561 8.648941 6.716074 8.71957 11.002677					
0.804177682918114	low						
GSM644903	8.47397260273973 0	9.93186303 3.58093877 8.84305495 7.64071741					
9.17408704	10.15346635 0.94938410111365	low					
GSM644906	5.21917808219178 1	9.930783 4.200895 10.032854 7.836742 9.131841					
10.284309	1.08139946322482	high					
GSM644907	3.93698630136986 1	9.839654 6.977266 9.229834 8.04749 8.263403					
9.677006	1.22217364438173	high					
GSM644910	0.452054794520548	1 9.792886 7.320051 8.628358 7.663787 7.057425					
10.588547	0.951344351156718	low					
GSM644911	3.39452054794521 1	8.22256 6.28099 10.110197 8.04575 7.803247					
10.61454	0.83526720246312	low					
GSM644912	7.48767123287671 0	9.597766 6.870143 9.37754 4.68506 8.114775					
9.603828	0.853831244406181	low					
GSM644913	6.99452054794521 0	8.503189 7.326443 9.635859 8.154065 7.444874 9.03468					
1.0036626690866	high						
GSM644917	7.21643835616438 0	7.635905 5.85011 9.834493 7.354579 7.579129					
9.888349	0.695315577483891	low					
GSM644919	1.04383561643836 1	8.5777 7.594238 9.398893 7.67577 7.299534					
9.566492	0.926389056512006	low					
GSM644922	5.1041095890411 0	8.005543 5.668171 9.639142 7.822958 8.079039					
9.845536	0.794610918357215	low					
GSM644924	6.94520547945205 0	9.654184 7.401417 9.20437 8.366723 6.532572					
10.558867	0.981841660018109	high					
GSM644927	6.55890410958904 0	9.226164 7.244311 9.298842 7.972171 8.218571					
10.297196	1.07135601543939	high					
GSM644928	1.52876712328767 1	9.569153 6.777684 10.170877 4.805496 7.607009					
9.766776	0.840528355010882	low					
GSM644930	6.33698630136986 0	9.450436 7.627981 9.317561 8.088924 7.307906					
10.731664	1.01891666086708	high					
GSM644933	6.10684931506849 0	7.944598 6.345825 4.392512 6.678462 6.4236					
10.641293	0.419745675318245	low					
GSM644936	2.95068493150685 0	9.732023 5.275916 7.412612 6.986507 6.773212					

10.487408 0.679752398644761 low
GSM644937 1.47123287671233 1 9.430998 6.331374 8.730787 5.914257 7.389659 9.03468
0.823967602067182 low
GSM644939 2.57260273972603 1 9.503449 7.022732 9.986976 6.671119 8.310501
9.684029 1.07913592465658 high
GSM644940 4.93150684931507 0 7.197806 6.442073 10.434583 7.806183 6.792197
9.468645 0.696213779559811 low
GSM644943 1.77534246575342 1 9.419694 6.485343 9.242628 6.924537 7.849832
10.255982 0.908455244191993 low
GSM644946 4.1013698630137 1 10.265335 7.109003 10.315823 7.883897
9.062249 10.717986 1.41471629781149 high
GSM644947 4.10958904109589 0 9.033939 6.906742 9.696357 4.781892 7.517711
7.082646 0.905086437417486 low
GSM644949 0.698630136986301 1 9.656554 4.96145 4.659486 5.522512 6.583047
7.23321 0.593404860357686 low
GSM644950 3.60821917808219 0 8.937974 6.564492 9.698026 7.153194 6.697001
7.350262 0.968747999750507 low

risk.train

id	futime	fustat	PLS3 GRP	APOD	SGCE	COL8A1	VAMP7	riskScore	risk
TCGA-BR-65642	1.17534246575342	1	8.904285	8.328912	11.615144	9.010114	9.065679	0	3.26765979865963 high
TCGA-CD-85301	0.03287671232877	0	9.683478	5.236078	11.666171	8.688737	9.457866	0	2.95446045735552 high
TCGA-MX-A5UJ	1.64383561643836	0	9.391702	6.587037	8.823479	7.108749	7.773073	0	1.87961063585998 high
TCGA-BR-43670	0.00273972602739726	0	9.877328	8.741068	7.003012	7.669356	8.759202	0	2.50993198641509 high
TCGA-VQ-A8PX	5.38082191780822	0	8.266041	5.02148	6.081387	5.734897	5.213482	0	0.773311433599876 low
TCGA-HU-A4G8	1.89041095890411	0	8.956279	5.213748	5.834617	5.945369	6.779076	0	1.0438642070845 high
TCGA-VQ-A923	0.00273972602739726	1	9.474692	5.23635	8.94596	6.560918	7.212463	0	1.54530659258245 high
TCGA-BR-67100	0.747945205479452	0	7.330225	7.369912	9.299819	6.671698	5.376009	0	1.09184377906462 high
TCGA-D7-85731	0.62465753424658	0	8.99178	5.099411	5.662742	5.744946	6.130312	0	0.942140922787776 low
TCGA-VQ-A91E	1.81917808219178	0	10.036905	5.02148	6.243045	5.923561	5.324831	0	1.07611876198861 high
TCGA-HU-A4GC	0.271232876712329	0	7.915723	8.434371	9.47364	7.72265	7.428088	0	1.81589847994744 high
TCGA-CG-57190	0.0849315068493151	0	8.972264	9.389396	11.978876	7.982944	8.969545	0	3.31300926251493 high
TCGA-CD-85320	0.96986301369863	1	8.438149	7.026429	10.150567	7.28876	7.832139	0	1.85611932737249 high
TCGA-BR-42800	0.550684931506849	1	7.853324	5.02148	5.211636	5.745096	6.035834	0	0.746737528499992 low
TCGA-VQ-A8PE	1.84931506849315	1	9.095207	5.71201	10.203159	7.978284	7.374417	0	1.89665900314233 high
TCGA-D7-68151	0.33150684931507	0	8.717911	5.919927	11.104101	7.317208	8.210181	0	1.97809357269697 high
TCGA-F1-6874	1.20547945205479	0	9.242152	5.331961	5.240246	7.18009	7.648779	0	1.3068448839899 high
TCGA-HU-8244	2.03287671232877	0	7.193186	5.02148	5.396169	5.263755	4.905967	0	0.574610731729641 low
TCGA-BR-43660	0.00273972602739726	0	8.973808	6.74561	10.634165	8.401263	8.489156	0	2.43168952764809 high
TCGA-D7-65191	0.71232876712329	0	9.270992	7.456509	8.717636	8.916167	7.813046	0	2.3250214036804 high
TCGA-F1-A72C0	0.947945205479452	0	8.708915	7.5921	8.131513	6.282271	7.639786	0	1.58902934835316 high
TCGA-BR-8365	1.46027397260274	1	9.373379	10.303969	11.229842	9.181907			

	9.170602 0	4.13393481097026 high					
TCGA-VQ-A91A	3.28767123287671 0	10.426987	5.15927	6.488632	7.334143		
	9.417952 0	2.08296384057443 high					
TCGA-CG-44601.83287671232877 1	8.906564	5.02148	8.573613	7.396678	7.191217 0		
	1.45561574959268 high						
TCGA-VQ-A94P	0.221917808219178	1	9.845141	5.816993	11.891801	10.217483	
	8.601487 0	3.38415756017279 high					
TCGA-BR-83800.0575342465753425	0	9.200179	10.76424	11.164893	9.242793		
	9.402876 0	4.27819170019885 high					
TCGA-D7-65201.56986301369863 0	9.358727	9.383502	12.540388	9.198774	8.716568 0		
	3.98290086508547 high						
TCGA-R5-A7O7	3.80547945205479 0	8.029111	5.336687	7.725605	5.981908	6.916943 0	
	1.04245723185465 high						
TCGA-CD-58040.00273972602739726	0	8.443626	8.023576	11.765983	7.14711		
	8.024349 0	2.24977165376473 high					
TCGA-IN-8663 0.282191780821918	1	11.753348	10.071246	6.447572	5.91804		
	7.637258 0	2.76066314786149 high					
TCGA-BR-83810.613698630136986	0	8.847984	6.326712	9.134556	6.489407	8.629552 0	
	1.77980518925997 high						
TCGA-BR-77232.39452054794521 1	7.151852	5.124596	10.462447	6.899593	8.219537 0		
	1.32728432488543 high						
TCGA-R5-A7ZE 1.51780821917808 1	9.957235	5.02148	9.515935	6.68359	5.902598 0		
	1.49934375028111 high						
TCGA-BR-86830.821917808219178	1	10.209555	7.150314	9.902431	8.484634	9.45099	
	0	3.27663964626197 high					
TCGA-MX-A663	0.821917808219178	1	9.596502	6.4171	12.029065	8.680287	
	8.701387 0	3.01603587103724 high					
TCGA-D7-A6EX	0.942465753424658	0	7.375571	8.461335	9.565036	9.925229	7.69323
	0	2.11104749640315 high					
TCGA-BR-83722.60547945205479 0	10.131165	5.178724	7.864026	6.493972	6.769863 0		
	1.51340264896869 high						
TCGA-CD-A489	0.942465753424658	1	9.539792	9.547477	11.970762	9.420581	
	9.082003 0	4.2517710649082 high					
TCGA-BR-85892.26027397260274 0	9.518264	5.02148	6.835603	6.230697	5.669377 0		
	1.09641493040782 high						
TCGA-VQ-A91V	3.55342465753425 0	9.869486	5.608908	8.063534	5.687788	5.787978 0	
	1.26961711508884 high						
TCGA-CD-A48C	0.967123287671233	1	8.475668	9.419329	10.236194	6.306682	
	8.664967 0	2.26706492973206 high					
TCGA-CD-58011.0986301369863	1	8.308528	5.63008	7.531523	5.454507	7.258545 0	
	1.09000443720065 high						
TCGA-VQ-A8E7	3.11780821917808 0	9.119904	6.353332	7.845408	6.029822	7.429454 0	
	1.44514879470603 high						
TCGA-VQ-A8DU	0.454794520547945	1	9.058469	5.268254	9.470615	7.739889	

7.678114 0 1.7542863938692 high
 TCGA-BR-64540.00273972602739726 0 9.078596 6.352401 9.820905 12.310582
 7.583983 0 2.95745958328147 high
 TCGA-VQ-A94T 0.936986301369863 1 10.422474 5.02148 5.290792 6.112764
 7.29075 0 1.35441009270439 high
 TCGA-HJ-7597 2.20547945205479 1 9.279929 5.639562 6.506531 6.092195 6.688507 0
 1.19381808894479 high
 TCGA-KB-A93H 3.13698630136986 0 8.480966 5.373489 5.689266 6.421834 5.339518 0
 0.867007276136837 low
 TCGA-BR-41911.52876712328767 1 10.120459 5.364745 10.291125 7.870957
 7.397013 0 2.17963124259808 high
 TCGA-VQ-A8PC 3.85479452054795 1 9.341776 5.167393 8.731997 7.102263 7.296899 0
 1.57292902124787 high
 TCGA-BR-85881.06575342465753 0 8.505065 6.514277 9.708434 7.207618 8.712138 0
 1.91041853128411 high
 TCGA-VQ-AA6A 3.24383561643836 0 9.949657 5.02148 10.084398 6.696288
 6.672748 0 1.68985758538185 high
 TCGA-BR-43710.00273972602739726 0 9.098764 5.276228 6.332892 6.26384 6.019773 0
 1.05270728114093 high
 TCGA-CD-85351.06849315068493 0 9.502914 7.692034 7.429944 8.809506 7.291874 0
 2.11891224801651 high
 TCGA-VQ-A8DZ 1.08493150684932 1 8.15847 5.150099 9.863213 9.194148 7.212029 0
 1.67245987531438 high
 TCGA-BR-79010.287671232876712 1 9.349539 8.969458 11.099694 8.673675
 8.907856 0 3.40880248562332 high
 TCGA-D7-68181.03013698630137 1 8.619484 7.445188 10.4865 7.714191 8.371208 0
 2.22609861959538 high
 TCGA-SW-A7EB 0.482191780821918 0 6.911706 5.02148 10.455561 7.020799
 5.891894 0 0.996209959116124 high
 TCGA-BR-79582.46301369863014 0 8.959307 6.543389 7.556924 6.653539 8.117011 0
 1.59903127195304 high
 TCGA-BR-A4J6 0.0547945205479452 0 8.877748 8.265075 10.642987 7.067827
 8.182471 0 2.31142064508206 high
 TCGA-FP-8209 4.96164383561644 1 9.229959 7.115578 11.324839 9.753358 9.401753 0
 3.41176863793078 high
 TCGA-VQ-A924 4.61917808219178 1 9.498684 5.480587 9.090271 6.243586 6.924262 0
 1.50332911074152 high
 TCGA-BR-80800.8 1 9.170692 5.02148 10.858574 8.308037 9.386222 0
 2.42778786045503 high
 TCGA-CD-85270.597260273972603 1 7.688697 6.609597 9.953079 10.875627
 7.658838 0 2.14076595922309 high
 TCGA-BR-43690.00273972602739726 0 9.40565 5.253797 9.735955 8.653716 7.935668 0
 2.11045152513084 high
 TCGA-B7-A5TK0.789041095890411 0 10.963503 6.319051 10.347576 8.092656

8.098767 0 2.98144858072618 high
 TCGA-BR-65633.26027397260274 0 8.217034 5.940937 11.22149 8.058093 8.796922 0
 2.09686940700813 high
 TCGA-IN-AB1X 1.12602739726027 0 9.82765 5.295334 7.525261 6.114785 6.682627 0
 1.36000319289432 high
 TCGA-BR-43700.00273972602739726 0 10.172835 5.83387 8.138636 9.198529
 8.704656 0 2.57948387392407 high
 TCGA-HU-A4GX 1.68767123287671 0 7.677433 5.847535 7.279218 5.917349 6.563452 0
 0.952487425297818 low
 TCGA-IN-7806 3.03013698630137 0 7.582554 6.20151 9.591164 6.233807 7.459867 0
 1.27053048659265 high
 TCGA-VQ-A8P5 0.643835616438356 1 9.955936 7.234841 7.634376 7.545445
 8.308333 0 2.21504797782221 high
 TCGA-MX-A666 1.16986301369863 0 8.080172 5.09852 9.098461 7.428595 6.558804 0
 1.23987648948813 high
 TCGA-B7-A5TN 0.786301369863014 0 9.911672 10.232124 7.494793 7.907712
 9.460491 0 3.23170689307444 high
 TCGA-BR-42530.33972602739726 1 11.574243 5.109475 5.936251 6.326932 7.155158 0
 1.72706484560978 high
 TCGA-ZQ-A9CR 0.0657534246575342 1 9.159995 7.528785 6.595453 7.597929
 8.054663 0 1.81837889778371 high
 TCGA-VQ-A91Q 1.73424657534247 1 9.186508 8.497951 7.53153 10.273946
 8.743154 0 2.88630774170788 high
 TCGA-BR-80770.0575342465753425 0 7.749579 5.227622 9.562167 6.156673 6.938127 0
 1.13293926659956 high
 TCGA-RD-A8MV 10.1917808219178 0 7.535988 5.02148 8.770297 6.176153 7.018021 0
 1.03290516653372 high
 TCGA-D7-A6EY0.953424657534247 1 9.080116 8.71099 10.297014 7.120869
 8.209521 0 2.43908582380338 high
 TCGA-RD-A8N1 9.64109589041096 0 8.168354 5.02148 11.283993 6.742474 8.12867
 0 1.60154719030888 high
 TCGA-FP-8210 0.419178082191781 1 9.264421 6.66926 11.741843 8.698156
 9.337669 0 3.0670602732137 high
 TCGA-CD-A487 1.02465753424658 0 9.249843 6.689813 8.377778 7.171872 8.168895 0
 1.88754353705438 high
 TCGA-CD-57981.11780821917808 0 8.975604 7.469571 10.011724 8.83718 9.069062 0
 2.74032129100178 high
 TCGA-VQ-A8PF 0.208219178082192 1 9.435788 5.02148 9.380248 6.512875
 7.425108 0 1.58170605356384 high
 TCGA-R5-A7ZI 6.21095890410959 0 7.048105 5.307855 5.579642 6.335847 5.416783 0
 0.677213365657601 low
 TCGA-HU-A4H4 1.98630136986301 0 8.77964 5.02148 5.596446 5.919559 6.157477 0
 0.917689548287604 low
 TCGA-BR-83641.84931506849315 0 10.100235 8.081936 12.741424 9.270122

9.959549 0 4.73023160699499 high
 TCGA-IN-8462 1.56712328767123 0 9.087404 6.092097 10.678182 7.122141 7.583441 0
 1.90295779326476 high
 TCGA-HU-A4GU 0.547945205479452 0 8.393905 5.268254 4.413771 5.515878
 6.611055 0 0.82285670583443 low
 TCGA-CD-85311.04931506849315 0 6.10121 5.291925 7.711626 7.972646 7.219804 0
 0.938465696396891 low
 TCGA-VQ-A8E0 1.53972602739726 1 8.98694 5.02148 10.182111 7.750811 5.6246
 0 1.42966382416554 high
 TCGA-BR-83660.0794520547945206 0 9.643126 6.26336 11.051929 7.031844
 8.540531 0 2.37965358907218 high
 TCGA-VQ-AA6D 1.42739726027397 0 9.52103 5.65149 11.674876 8.707419
 6.495236 0 2.16730284102273 high
 TCGA-D7-A6EV 0.936986301369863 0 8.927065 5.245841 5.43208 5.7139
 7.177648 0 1.03668749630872 high
 TCGA-F1-6177 0.00273972602739726 0 7.907219 5.02148 5.093563 5.648258 6.471998 0
 0.776528369671768 low
 TCGA-BR-A4J7 2.70958904109589 0 9.168086 6.379309 11.317713 8.922326 9.005022 0
 2.82726877267345 high
 TCGA-BR-77152.8027397260274 0 8.997099 5.274239 9.862366 7.174434 8.237075 0
 1.79669063656713 high
 TCGA-D7-85751.51780821917808 1 9.121032 5.583965 10.859073 6.37574 6.762885 0
 1.58989885371384 high
 TCGA-BR-43630.00273972602739726 0 9.889343 8.047358 9.377888 8.464185 8.967198 0
 3.05638741721261 high
 TCGA-IN-A7NU 0.975342465753425 0 8.454931 9.527406 8.653267 6.58414
 7.504191 0 1.86183478601102 high
 TCGA-CG-44400.334246575342466 1 9.812301 6.649258 8.08539 8.668019 6.866882 0
 2.02012379329585 high
 TCGA-HU-A4G3 0.465753424657534 0 7.847315 5.02148 7.801651 5.984858
 6.005059 0 0.899489221430774 low
 TCGA-HU-A4HD 2.78356164383562 0 7.743653 5.35784 8.664734 6.982583 7.535191 0
 1.24104832536247 high
 TCGA-FP-A9TM 0.517808219178082 0 8.494902 5.104303 7.650282 5.973975
 5.537502 0 0.947258101878183 low
 TCGA-D7-65281.26849315068493 0 9.624686 7.055189 4.887897 5.847535 6.822265 0
 1.26149207109923 high
 TCGA-CG-44370.671232876712329 0 8.403079 6.438776 8.739331 6.349944 7.728876 0
 1.4579979073948 high
 TCGA-VQ-A8DT 4.06575342465753 0 8.364525 5.179852 6.917019 6.835545 6.124171 0
 1.02536438283892 high
 TCGA-CG-44360.665753424657534 0 9.375384 5.02148 9.749386 5.704317 6.148659 0
 1.29827938270549 high
 TCGA-VQ-A8PD 1.35890410958904 1 9.42535 5.87686 7.009889 7.280647 8.066649 0

1.6651672960116 high
 TCGA-CG-44432.4986301369863 0 7.880975 5.492635 6.336674 6.42304 7.194337 0
 1.00976767216589 high
 TCGA-VQ-AA68 3.63835616438356 0 9.746311 5.092716 7.233173 5.704012 6.632393 0
 1.24102697005296 high
 TCGA-D7-85761.22191780821918 1 6.629324 5.245571 6.912968 6.510455 8.356427 0
 0.956135372900999 low
 TCGA-BR-86772.22739726027397 0 9.724272 7.294644 10.269797 8.080361 9.001263 0
 2.87758132482317 high
 TCGA-VQ-A925 0.378082191780822 1 10.033907 5.181825 7.680788 7.204253
 6.220816 0 1.48157885115446 high
 TCGA-BR-83840.30958904109589 0 9.43143 8.628779 10.973141 9.608638 9.028497 0
 3.68267789505872 high
 TCGA-BR-77171.51232876712329 1 7.60161 9.075989 9.097402 6.610639 7.506622 0
 1.6118954978748 high
 TCGA-BR-42670.515068493150685 1 9.284738 5.455971 5.968307 6.082991 7.254141 0
 1.20728375950201 high
 TCGA-BR-43680.00273972602739726 0 8.452734 6.149885 8.510867 7.849274 8.152214 0
 1.70059624480057 high
 TCGA-CG-57200.0821917808219178 1 7.753653 5.02148 10.958089 6.69822 7.57959
 0 1.37529682584635 high
 TCGA-CD-58001.0958904109589 0 7.774043 5.204892 10.774988 7.2255 6.562673 0
 1.30197169523379 high
 TCGA-VQ-A8PJ0.224657534246575 1 9.697103 5.144339 13.228979 7.845345
 6.378192 0 2.16277360774638 high
 TCGA-D7-55772.14246575342466 1 9.229498 6.551784 6.569005 6.260654 6.570153 0
 1.28125916071349 high
 TCGA-RD-A8MW 3.15890410958904 1 7.022779 5.833128 8.66533 7.063994 8.048663 0
 1.21887735420334 high
 TCGA-D7-A6F01.85753424657534 0 7.877665 5.497359 12.36727 9.774413 6.823827 0
 1.95445673168402 high
 TCGA-D7-A4YX 3.03561643835616 0 9.623552 5.02148 5.602721 5.89735 7.041925 0
 1.15717232904825 high
 TCGA-IN-A7NT0.884931506849315 0 12.026265 5.02148 6.290515 7.528303
 7.917069 0 2.29121342329701 high
 TCGA-CD-85241.06301369863014 0 9.957868 10.737774 11.159387 9.401148
 8.729158 0 4.56130024558733 high
 TCGA-HU-A4GD 1.8958904109589 0 7.545983 5.669214 8.808108 6.39902 5.702142 0
 0.96735732908177 low
 TCGA-IN-A6RS 1.04931506849315 0 8.553469 5.02148 6.885191 5.533924 6.676486 0
 0.981206313235338 high
 TCGA-BR-42940.00273972602739726 0 7.168575 5.02148 6.771346 8.241454 6.100731 0
 0.935810534988265 low
 TCGA-BR-65662.73150684931507 0 7.37162 6.607452 7.045697 6.07709 7.807502 0

1.09899097549172 high
TCGA-VQ-A91X 0.791780821917808 1 8.372433 5.02148 6.757641 5.338974
5.008482 0 0.77559953648398 low
TCGA-BR-65650.764383561643836 1 8.522991 5.339872 10.937801 6.924276
7.754313 0 1.66253825139984 high
TCGA-HU-A4GY 0.0219178082191781 0 8.557956 5.14015 11.270534 7.798504
8.531315 0 1.98148933172068 high
TCGA-KB-A6F75.3013698630137 0 5.3 5.02148 10.646617 6.774222 5.437591 0
0.720821518467661 low
TCGA-BR-77072.98630136986301 0 8.826979 5.137544 6.064724 6.08504 7.248767 0
1.09851412795906 high
TCGA-D7-68221.02739726027397 0 9.432993 5.02148 7.501368 8.851407 7.19212 0
1.69230028353048 high
TCGA-VQ-A8P3 3.1013698630137 0 8.295597 5.142318 7.563685 6.353228 7.750969 0
1.20105143020788 high
TCGA-VQ-A927 0.547945205479452 1 8.670228 5.155551 7.409562 6.725185 6.93189
0 1.19953206365754 high
TCGA-D7-65211.54520547945205 0 9.282209 5.885049 8.448441 6.826551 9.038293 0
1.90253908242683 high
TCGA-BR-84842.0986301369863 1 9.452497 5.092716 9.105697 6.861409 8.636582 0
1.84275940691766 high
TCGA-BR-71961.82465753424658 0 9.826583 5.542493 11.422838 8.421828 9.251344 0
2.91088699529495 high
TCGA-VQ-A91Z 4.63013698630137 0 9.750724 5.246652 5.745736 7.83998 5.901283 0
1.28423214116121 high
TCGA-CG-43051.32876712328767 0 8.979385 10.032241 11.080162 6.998287 8.29843
0 2.79747912050728 high
TCGA-D7-85741.43287671232877 0 8.418101 5.102822 9.414645 7.764519 9.338723 0
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TCGA-BR-83672.19452054794521 1 9.399484 5.119181 13.819725 8.170954 8.932264 0
2.89599136056818 high
TCGA-BR-82961.2986301369863 1 8.311184 6.535659 7.928902 6.877297 7.786936 0
1.45024686567391 high
TCGA-CG-57241.0027397260274 1 8.913126 8.608362 7.501337 6.701982 7.197068 0
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TCGA-CG-44772.58082191780822 0 9.86493 5.461043 8.440238 7.653477 7.567411 0
1.86419337697903 high
TCGA-CG-44661.58082191780822 0 5.58003 5.103267 9.804521 5.843678 6.192804 0
0.715932321398065 low
TCGA-VQ-A8PQ 1.3041095890411 1 9.780659 6.993428 10.443707 8.298477
8.368691 0 2.7341026960409 high
TCGA-RD-A8N6 0.745205479452055 1 9.09986 7.276019 12.364474 8.082304
7.937982 0 2.65143019132405 high
TCGA-BR-84830.449315068493151 0 8.829958 10.237316 11.614767 7.860001

7.630317 0 2.89409610907411 high
 TCGA-D7-A6F21.3041095890411 0 8.826241 5.327862 8.750426 5.956531 7.357124 0
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 TCGA-BR-A4CS0.123287671232877 1 8.274909 6.277522 12.675357 5.684406 7.52921
 0 1.67601035572038 high
 TCGA-BR-82970.616438356164384 0 9.50258 7.153224 10.444621 9.321748
 8.556592 0 2.96599669145238 high
 TCGA-BR-64581.61095890410959 1 9.751254 6.871335 9.250348 12.420276 9.215496 0
 3.99097875797217 high
 TCGA-CG-57210.501369863013699 0 9.350342 5.02148 7.953945 6.196311 7.222753 0
 1.35108188358765 high
 TCGA-FP-8211 1.13150684931507 0 8.221557 7.133345 6.803993 5.993418 6.441354 0
 1.11099637641542 high
 TCGA-VQ-A92D 5.56712328767123 0 10.493763 7.909589 6.988501 6.024696
 7.165377 0 1.88166242355095 high
 TCGA-ZA-A8F6 1.43835616438356 0 8.887055 5.097034 11.901779 8.301345 7.869344 0
 2.11832629567815 high
 TCGA-D7-A74A 1.66301369863014 0 9.9425 6.472524 6.286587 5.437339 5.860978 0
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 TCGA-FP-7998 1.85753424657534 0 9.67107 5.231447 8.893415 7.157377 8.805448 0
 1.99307843541294 high
 TCGA-BR-86782.06575342465753 0 8.400626 8.010387 5.922839 8.719506 8.594115 0
 1.87546024269619 high
 TCGA-BR-43610.00273972602739726 0 10.242607 6.982937 9.84477 7.533506
 9.372472 0 2.94262511566728 high
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 8.765115 0 2.63041007098654 high
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 2.05464140094725 high
 TCGA-BR-82890.221917808219178 1 9.439912 5.346729 10.422669 7.917438 8.88646
 0 2.31382737169861 high
 TCGA-BR-A4J9 0.0383561643835616 0 9.067245 6.601679 11.177347 9.08336 7.87935
 0 2.52211403121546 high
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 0.694815099942411 low
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 8.069436 11.694247 1.21417473978025 high
 GSM644648 0.821917808219178 1 9.19147 7.276249 9.836188 7.161388 7.807507
 11.304969 0.913001060430952 low
 GSM644649 1.372602739726031 9.80486 7.336722 8.784958 5.930274 7.078449
 10.804305 0.81115720909604 low
 GSM644650 6.106849315068490 9.371459 7.276748 4.233329 6.653811 7.055763
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 GSM644651 4.964383561643840 10.02276055 7.19320287 4.09427024 5.56569803
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 GSM644652 4.947945205479450 7.359657 5.839086 9.625623 5.208298 7.56466
 9.952745 0.534251212456507 low
 GSM644657 1.824657534246581 8.897463 6.760536 10.280372 8.199494 8.740314
 11.437101 1.03564188123703 high
 GSM644662 4.964383561643840 9.838935 6.319859 10.116169 7.337472 8.610789
 11.315769 1.06135658172666 high
 GSM644663 5.038356164383560 9.412335 5.631328 9.253419 4.877383 6.212831

10.325156 0.586668471682732 low
 GSM644664 4.71780821917808 0 9.176972 3.615569 8.579881 7.561381 7.037401
 7.148107 0.810932355819125 low
 GSM644665 2.36712328767123 1 8.784239 3.624681 8.618043 5.004427 8.351804
 9.425688 0.588774273281979 low
 GSM644666 1.06027397260274 1 10.018121 7.125939 9.67951 7.897318 7.842912
 10.820127 1.13789660684244 high
 GSM644667 1.54520547945205 1 10.18951 8.414783 10.134482 8.132732 9.178347
 11.233553 1.52804761703289 high
 GSM644668 4.87397260273973 0 9.638309 7.004937 9.685145 7.904663 8.180156
 10.958981 1.08818882045797 high
 GSM644670 0.542465753424658 1 7.639799 6.160473 10.304244 6.831891
 6.593059 10.297658 0.611804674408512 low
 GSM644671 0.6 1 8.898803 3.644175 10.768856 8.240305 7.354119 10.718914
 0.761415095500073 low
 GSM644674 3.13150684931507 1 10.069757 6.975071 10.147061 4.837836
 9.680291 7.681906 1.34861494991218 high
 GSM644676 9.22191780821918 0 9.562456 4.315117 9.376843 8.304363 7.434823
 10.420836 0.84791999526717 low
 GSM644677 3.02465753424658 0 9.119745 6.885637 9.535897 7.305378 8.663035
 7.970095 1.2132543692566 high
 GSM644679 9.75616438356164 0 7.980704 5.161832 9.728736 8.678585 8.071967
 10.719386 0.776123925526584 low
 GSM644690 10.7424657534247 0 7.852407 7.014225 7.437601 4.825226 6.354035
 10.665505 0.443863483022295 low
 GSM644693 9.58356164383562 0 9.305219 7.743383 6.064934 5.379758 9.196848
 9.936878 0.821830393460665 low
 GSM644694 10.3315068493151 0 10.111723 7.662703 9.969184 5.063456 8.057208
 8.5784 1.13913673799737 high
 GSM644695 6.4027397260274 0 9.568164 7.330838 8.109491 7.614083 6.096317
 7.234184 1.01539131845191 high
 GSM644697 9.58356164383562 0 7.925208 6.423406 9.716727 5.318188 9.438774
 9.439948 0.791841523767091 low
 GSM644699 1.32328767123288 1 8.853896 7.827265 5.333629 7.526904 7.270531
 7.446766 0.869040179315525 low
 GSM644700 5.40821917808219 0 9.585365 6.883125 7.459588 5.147809 6.612106
 10.635773 0.620500957057423 low
 GSM644703 4.07671232876712 1 8.634492 8.021672 7.708469 6.937921 8.165263
 10.302205 0.842528575197841 low
 GSM644704 9.44383561643836 0 10.194685 7.602292 8.994439 4.744721 6.099479
 10.790828 0.723241201397163 low
 GSM644705 0.50958904109589 1 9.436741 7.01242 4.130499 5.380348 6.968391
 11.489643 0.491699039919948 low
 GSM644706 6.94520547945205 0 8.678672 4.081164 9.483458 5.24914 7.239671 7.70208

0.652503501758428 low

GSM644709 6.15616438356164 0 9.437391 7.465592 10.073186 5.153004 8.748052
9.755018 1.00813981939616 high

GSM644710 5.86027397260274 0 7.4872749 7.3700953 4.1689399 5.0174406
7.8247828 8.9119542 0.470537772546306 low

GSM644712 1.30684931506849 1 9.388655 7.166286 9.117605 7.950942 6.957512
10.009118 0.961798052962925 low

GSM644713 1.59452054794521 0 8.378966 4.7489 8.407126 5.130746 7.408046
9.102897 0.55573405516968 low

GSM644717 2.0958904109589 1 10.174245 7.637563 9.057747 7.841137 9.477367
9.934487 1.47603218880635 high

GSM644718 5.81917808219178 0 8.374093 5.149306 5.145847 5.308802 7.424815 8.74192
0.484675900378557 low

GSM644720 5.00547945205479 0 9.328016 3.618764 8.61635 4.909615 6.570539
6.975557 0.62885535346747 low

GSM644721 5.0958904109589 0 7.776563 6.163814 4.086465 4.82334 5.121461 7.46496
0.363956678221413 low

GSM644722 3.61643835616438 0 9.972057 7.267428 9.289094 5.319018 8.340476
10.034075 0.980700037158518 high

GSM644723 5.62191780821918 0 9.530338 7.189292 8.176747 6.415945 6.983727
9.553969 0.834823840004927 low

GSM644724 5.35068493150685 0 9.872941 7.120353 9.078067 7.318622 7.105289
8.785558 1.08388545012099 high

GSM644726 0.468493150684932 1 10.60753 7.506295 8.272802 5.406461 8.62687
10.810486 1.02046026779507 high

GSM644727 1.01917808219178 1 7.374043 7.274224 7.687741 8.017606 6.216809
7.524065 0.706400741741282 low

GSM644728 5.02191780821918 0 9.566161 7.55479 9.934838 7.605068 10.017184
9.599298 1.49266519184731 high

GSM644730 1.04383561643836 1 9.780052 5.39911 10.117299 7.124155 8.314095
8.409899 1.14561752562536 high

GSM644731 4.42191780821918 0 9.534386 6.739392 7.537243 7.900194 6.97612 9.04429
0.919105787351022 low

GSM644734 0.410958904109589 1 9.748144 7.298287 10.610308 7.56749
7.039059 9.694875 1.13169164390686 high

GSM644736 8.76164383561644 0 9.90762 7.955403 8.21991 7.820237 6.917325
11.072731 0.957850070270697 low

GSM644739 9.46027397260274 0 9.908359 7.438982 9.490159 7.689884 7.963866
10.352235 1.16343288423013 high

GSM644743 4.66027397260274 0 9.7083749 3.6400409 9.5736168 4.7371751
6.2993264 7.4020734 0.661393388483832 low

GSM644746 0.789041095890411 1 7.72432125 3.67238967 4.69144757
8.54065906 8.09820788 7.09534217 0.613673269650784 low

GSM644748 3.7972602739726 1 7.8084604 3.5218735 9.2076302 8.2864173

7.5236601 10.3686828 0.597593504152031 low
 GSM644749 11.9835616438356 0 8.425682 3.966337 9.897835 4.850446 7.387166
 8.841598 0.574702995679109 low
 GSM644755 2.13698630136986 0 8.66202925 4.15534506 6.06167565 8.67707949
 5.63657263 7.87309646 0.597277072113999 low
 GSM644760 9.16438356164384 0 9.000664 6.543493 9.605337 8.521148 8.27228
 7.021155 1.33615335511716 high
 GSM644765 5.13698630136986 0 8.13603296 3.89101671 4.35636895 5.85339965
 6.44258544 8.34192443 0.39039457411318 low
 GSM644766 3.81369863013699 0 8.953887 3.6546561 8.5447598 7.6381683
 7.6691754 10.0415492 0.683990547836225 low
 GSM644768 1.91506849315068 1 7.67803 3.610405 10.555346 8.282861 7.968202
 7.150123 0.851028161880759 low
 GSM644769 4.73424657534247 0 7.812734 3.707453 4.173296 5.472007 3.466414
 9.836603 0.226938832471526 low
 GSM644773 7.96438356164384 0 7.125164 5.462352 9.570568 8.592289 8.591694
 9.742127 0.769706722478505 low
 GSM644774 5.68767123287671 0 7.64598 6.259397 8.545334 8.341787 6.510128
 10.572508 0.61465964078312 low
 GSM644775 4.92328767123288 0 7.475756 6.602526 9.437581 8.329913 7.977907
 7.162688 0.974189647508419 high
 GSM644776 2.49041095890411 1 7.239237 6.91095 8.878297 8.089841 7.927272
 9.682561 0.750652376848485 low
 GSM644778 7.17534246575342 0 8.695663 3.73662119 7.29133529 8.3706901
 7.00061019 6.97086777 0.756245878514063 low
 GSM644786 6.04109589041096 1 9.319119 7.004504 9.531367 7.911559 8.581419
 8.260838 1.29835808383622 high
 GSM644788 5.97534246575342 0 7.420894 6.079658 7.586074 8.43793 7.036546
 10.002413 0.610472228223168 low
 GSM644791 6.57534246575342 0 7.920502 5.588428 9.538003 7.409229 7.917798
 9.164972 0.768831890193486 low
 GSM644792 5.62191780821918 0 9.311398 6.380984 3.74371 8.290586 6.23642
 10.066745 0.598466506637566 low
 GSM644793 1.16712328767123 1 7.244168 6.577766 9.313306 8.013262 7.752609
 7.993852 0.828880471833245 low
 GSM644794 6.04109589041096 0 9.482366 6.978603 9.35222 8.337957 7.863627
 10.956459 1.04211358598968 high
 GSM644795 0.772602739726027 1 9.371774 7.262306 10.280372 8.260128
 8.485634 9.376974 1.32289333616221 high
 GSM644796 5.95890410958904 0 8.935622 4.925094 9.157262 8.20343 7.619859
 9.488011 0.855739748262319 low
 GSM644797 5.16164383561644 0 7.913962 3.683777 4.466684 4.769571 5.583683
 7.923189 0.317281349337485 low
 GSM644799 5.45753424657534 0 7.639799 5.558555 9.019369 7.936238 7.623378

9.031949 0.727219068036545 low
 GSM644801 0.526027397260274 1 7.43981 4.4123191 8.8873574 8.7511286
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 GSM644802 0.156164383561644 1 8.610195 4.251199 10.4953 8.269851 8.885202
 9.538785 0.96356557131808 low
 GSM644803 5.0958904109589 0 9.998623 6.835534 10.189105 7.744944 9.338342
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 4.1520064 7.4206139 0.276341961640765 low
 GSM644807 0.378082191780822 1 8.22191 3.889884 4.317888 8.95177 8.172218
 7.95055 0.65062155082434 low
 GSM644811 3.6 0 7.8121 3.845023 4.116364 4.69291 6.01938 7.730721
 0.325946955818962 low
 GSM644813 1.627397260273971 9.305937 7.091236 10.335361 8.35554 9.752914
 7.724007 1.68812360073945 high
 GSM644816 10.7342465753425 0 7.245483 6.57627 9.660412 7.751429 7.843789
 7.441888 0.869900276079887 low
 GSM644819 0.805479452054795 1 8.392868 3.941535 9.726312 8.534784 5.991263
 8.91683 0.67788772938413 low
 GSM644820 10.2657534246575 0 9.968677 4.962924 5.138755 8.91899 9.741541
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 GSM644824 2.05479452054795 1 7.664236 6.631277 8.404884 8.127572 8.784041
 7.014108 1.0188488665174 high
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 GSM644826 4.27397260273973 0 7.072719 3.687895 4.234948 9.465632 6.212045
 8.772153 0.422089989189455 low
 GSM644828 1.43835616438356 1 8.2183388 3.9062871 4.1645861 5.7517048
 5.9788926 7.2140938 0.400152065858468 low
 GSM644830 1.33150684931507 1 7.760682 6.971188 9.766735 8.063603 7.999293
 8.283805 0.968321290745743 low
 GSM644833 8.0958904109589 0 9.388995 5.573533 4.604049 8.721633 5.583683
 10.407578 0.56910402404549 low
 GSM644834 1.17534246575342 1 7.225881 7.437292 10.003064 8.187271 7.875756
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 GSM644837 5.087671232876710 8.163982 6.376847 9.946021 8.431386 7.573097
 9.510488 0.902979615478892 low
 GSM644840 2.31780821917808 0 7.407369 3.744016 10.090206 8.730371 5.434918
 8.733936 0.564961016835639 low
 GSM644842 7.01917808219178 0 7.1622697 3.7366212 4.1836531 8.4136883
 6.2164223 7.7168323 0.420089600085213 low
 GSM644846 4.73424657534247 1 7.01504549 3.59794085 10.45722034 8.01717633
 7.15418424 8.40683395 0.6185872936664 low
 GSM644851 1.47945205479452 1 7.337393 3.56423 9.598407 8.50966 8.230946

7.760445	0.757203016343658	low		
GSM644852	2.95890410958904 0	7.358305 5.552601 8.930845 8.291101 7.228724		
8.119138	0.730054132261454	low		
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7.097074	0.656867039191618	low		
GSM644854	1.89041095890411 1	9.174541 6.425703 9.780294 8.627101 7.958661 8.30613		
1.22563266747269	high			
GSM644855	4.9972602739726 0	7.543337 5.357274 6.408064 8.409573 6.698596		
8.133016	0.600048508008161	low		
GSM644859	5.08767123287671 0	9.126701 6.737821 9.484937 8.243836 7.86627		
8.785558	1.12884524295345	high		
GSM644861	5.54794520547945 1	7.887262 6.174099 8.806772 8.812554 7.794435		
7.503311	0.967115467320634	low		
GSM644864	4.91506849315068 0	8.312807 3.8112122 4.3805068 5.4668409		
8.0982079	9.8983603 0.412032339276669	low		
GSM644865	5.17808219178082 0	7.299367 3.637361 9.002497 8.595768 8.107811		
6.948902	0.768055191261231	low		
GSM644866	0.879452054794521	1 7.108061 6.815203 9.82518 7.836742 8.091999		
7.50644	0.902593441109351	low		
GSM644867	5.02191780821918 0	7.255537 5.609663 9.399613 8.408987 7.913593		
8.733495	0.773716378280193	low		
GSM644868	0.986301369863014	1 8.108381 5.225565 7.629924 7.817109 6.431831		
9.14666	0.603175371296538	low		
GSM644871	4.21643835616438 0	8.529452 4.459655 9.20243 8.765752 6.978712		
9.883228	0.739309031530346	low		
GSM644873	3.26301369863014 0	7.167489 5.026004 9.716727 8.852506 6.852926		
7.415406	0.760112558849283	low		
GSM644874	1.91506849315068 1	8.608823 7.218004 10.179335 7.417493 8.224782		
9.972143	0.995922932733674	high		
GSM644875	12.6986301369863 0	9.61411063 6.4831178 7.94360686 7.2385302		
8.45199761	8.85546103 1.04730913347911	high		
GSM644878	2.12876712328767 1	9.022702 5.268993 4.998905 7.341274 7.835924		
10.486946	0.598695361205496	low		
GSM644879	1.59452054794521 0	9.4350439 3.7005811 4.4337798 7.6962366		
6.2331247	10.0434298 0.489925856691873	low		
GSM644881	11.8191780821918 0	7.566358 7.314784 8.245537 5.006279 7.061651		
10.231836	0.517452485971929	low		
GSM644885	2.07123287671233 1	7.135568 6.951971 9.180735 6.072074 7.416549		
7.695358	0.685455333438317	low		
GSM644886	7.87397260273973 0	6.979151 6.876401 7.80573 7.11333 6.205613		
9.218281	0.525621932893674	low		
GSM644887	2.4986301369863 1	9.814297 6.772833 7.867222 7.871777 8.482212		
9.169062	1.14549755412924	high		
GSM644888	0.517808219178082 1	9.500089 7.011067 9.835312 7.947081 8.917163		

9.674162 1.28163759884889 high
 GSM644890 1.45479452054795 1 7.69333148 7.2119804 10.06926653 7.43843716
 8.88435858 10.68288396 0.868844573934712 low
 GSM644891 7.15890410958904 1 9.424968 4.5176765 4.1847856 4.7610619
 5.8353199 7.9704953 0.436234042477099 low
 GSM644895 9.53424657534247 1 9.487328 6.90208 9.694676 8.386416 7.408046
 11.492704 0.975292024793045 high
 GSM644897 4.25753424657534 0 9.146845 6.686959 9.090133 5.152264 7.136667 8.38618
 0.787288959467006 low
 GSM644898 2.76164383561644 0 8.501851 6.478201 8.939329 5.24378 6.378543
 10.519294 0.549524804070291 low
 GSM644899 1.07671232876712 1 7.614151 5.507533 9.750436 4.921491 7.527876
 9.943578 0.531046461261058 low
 GSM644904 1.33972602739726 1 8.820221 7.972102 8.614085 6.911921 7.451788
 10.180053 0.855444971348388 low
 GSM644905 2.35068493150685 1 9.93372 7.673591 9.429701 7.775376 8.444967
 10.727421 1.22453353747985 high
 GSM644908 5.8027397260274 1 7.581863 5.951441 8.65238 4.723245 8.810518
 9.538785 0.591184733721976 low
 GSM644909 0.542465753424658 1 9.8286193 7.1580918 9.9138198
 6.2787376 8.8877571 11.1642392 1.05576443926401 high
 GSM644914 6.15616438356164 0 9.831485 7.623234 10.44077 8.147347 7.929835
 10.147372 1.30784091331374 high
 GSM644915 6.77260273972603 0 9.51378 7.878953 9.649463 7.696608 9.049518
 8.010672 1.51962686384697 high
 GSM644916 6.86301369863014 0 9.418043 7.228203 8.730787 7.715974 6.79964
 10.891319 0.854876081148943 low
 GSM644918 1.43835616438356 1 9.989104 7.22103 10.032854 7.88224 9.182507
 10.89857 1.33878587897893 high
 GSM644920 4.58630136986301 0 9.6298347 7.2423106 8.641492 5.9574909
 7.9144597 10.5969372 0.862885032106304 low
 GSM644921 0.558904109589041 1 9.79928 7.732784 7.513088 7.520848 7.891045
 10.675312 0.981611471517793 high
 GSM644923 7.03561643835616 0 9.741653 7.030456 9.307704 7.106715 7.40299
 8.947202 1.06995175279313 high
 GSM644925 2.04657534246575 1 10.205415 7.462587 10.481312 7.826168
 9.693237 10.563137 1.56751304369124 high
 GSM644926 6.77260273972603 0 8.519591 7.272643 9.585335 5.794621 7.164185
 9.721479 0.742177754874031 low
 GSM644929 1.18356164383562 1 9.376353 4.514252 9.112399 8.003705 8.025919 8.33497
 0.989878761137947 high
 GSM644931 2.48219178082192 1 9.376353 8.263857 9.482744 8.446324 8.290385
 10.172968 1.27949114896324 high
 GSM644932 6.07397260273973 0 9.5624563 8.0324226 7.0454086 4.7614704

8.153145 10.9658712 0.732770719028682 low
GSM644934 6.0986301369863 0 8.731518 6.762061 8.00181 8.372931 7.095393
10.045287 0.818535244450672 low
GSM644935 1.45479452054795 1 10.020025 7.275741 9.246003 7.565003 9.209603
10.086149 1.32647954404932 high
GSM644938 5.06301369863014 0 9.267808 5.534124 6.927335 6.789055 6.252735
9.887892 0.604085439670382 low
GSM644941 5.02191780821918 0 9.300439 7.854176 9.391005 7.831686 7.669999
10.671082 1.03706612120828 high
GSM644942 3.62465753424658 1 9.619179 5.751437 8.568012 7.294702 8.444967
9.209965 1.00859408088282 high
GSM644944 5.17808219178082 0 7.907396 6.044595 9.126121 4.699005 5.880175
7.364415 0.552244170330096 low
GSM644945 0.435616438356164 1 8.122477 4.23286 9.507885 7.095731 5.250052
7.785169 0.574371625709419 low
GSM644948 4.47123287671233 0 7.71965 6.605557 4.514685 8.326703 5.611025
7.873096 0.542343623683316 low