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Table S1 The expression profiles of 19 m6A-associated genes in pancreatic cancer patients collected from GSE21501 and TCGA-PAAD datasets

ID	METTL3	WTAP	ZC3H13	RBM15	RBM15B	YTHDC1	YTHDC2
YTHDF1	YTHDF2	YTHDF3	HNRNPC	FMR1	LRPPRC	HNRNPA2B1	
IGFBP2	IGFBP3	RBMX	FTO	ALKBH5			
TCGA_TCGA-HZ-8002			2.290268958		3.546464724		3.813320296
2.015384204		3.395529235		3.790118382		2.709145941	
3.697204733		3.942052978		3.645727001		4.231423659	
2.889595812		3.272908191		4.267434747		2.355971448	
4.534101788		3.667691761		2.639316615		3.780534579	
TCGA_TCGA-3A-A9IN			1.672207007		2.376945745		2.040614347
0.855660136		2.654321758		2.93168008		1.687660688	
3.713429515		2.741077015		2.142029079		2.951771975	
2.187665891		1.90146154		2.899001557		6.502280175	
3.061610111		2.745403404		1.675438651		4.318311026	
TCGA_TCGA-HZ-8519			1.834511	3.167514	3.388767	1.637131	2.829418
3.360749	2.631826	3.531582	3.397894	3.383435	3.799427	2.79228	2.931827
3.794299	2.232633	3.499427	3.306734	2.251995	3.588574		
TCGA_TCGA-FB-AAPY			1.66773545		2.51951181		2.047118822
1.514236152		2.393205633		2.712343598		1.502717186	
3.036332991		2.988297523		1.856649116		3.320301377	
1.55910186		2.010259033		3.180377569		2.47280716	
4.659408835		2.731758912		1.351849217		3.082441183	
TCGA_TCGA-IB-A7LX			2.436887511		2.730703321		3.223389172
1.862862275		2.948577998		3.498819122		1.882502153	
3.82668631		3.295169323		3.032890637		4.091444885	
3.527418631		2.99239683		4.361087963		1.946984523	
5.607232858		4.041393272		2.045858681		3.448608368	
TCGA_TCGA-XN-A8T5			1.890974562		3.598267658		2.905121397
2.080587757		3.097717442		3.177720206		2.405055656	
3.357493907		3.736740668		3.136327061		3.771919358	
2.531423429		2.574250216		3.763793432		4.097128309	
5.117798622		3.309922016		1.931290093		3.524791868	
TCGA_TCGA-3A-A9IX			1.635387871		2.915605235		3.011658329
1.525772062		2.990362134		3.201626951		2.031498902	
3.089622429		3.2773804		3.054561767		3.649380575	
2.467438821		2.521769197		3.460998971		3.17590362	
3.981902167		3.144724616		1.982788906		3.27538641	
TCGA_TCGA-3A-A9IB			1.57638746		2.926088373		2.41780948
1.515560342		2.809151869		2.93699129		1.821794241	
3.363155528		3.256811966		2.967768588		4.035688748	
2.30967441		2.715637579		3.725216776		3.670061619	
5.402911627		2.766219629		2.08725117		3.44464979	
TCGA_TCGA-IB-7646			1.307622	3.831617	2.914246	2.141686	2.793667

2.968276	1.705942	3.082192	3.69935	3.612472	4.580869	2.930992	2.686406
4.34724	2.054648	5.512493	3.243754	2.325965	3.536141		
TCGA_TCGA-2J-AAB4		1.798789873		3.428758329		2.454435589	
1.757691615	2.739221012		3.032673849		2.09120507		
3.292036279	3.451743315		2.397905219		4.079867457		
3.178130927	2.599423368		3.92508327		3.933165364		
5.518719079	2.867176655		1.904274944		3.39249677		
TCGA_TCGA-3A-A9IH		0.833962278		2.500037146		2.607808427	
1.741597697	3.121130651		3.04181485		2.19700407		
3.315049857	3.615688301		2.635941133		3.627469529		
2.47562956	2.515437169		3.896067961		3.67825531		
5.036631616	2.789710555		1.679209958		3.104632061		
TCGA_TCGA-IB-7890		1.443421	2.947529	3.666835	1.794047	3.278508	
3.290683	2.428844	4.110599	3.72947	3.964362	4.080938	2.72474	2.663509
3.904493	4.241372	6.448761	3.322679	2.79624	3.570642		
TCGA_TCGA-IB-AAUO		2.088853911		2.883604192		2.139634024	
1.666944252	2.437802469		2.773191829		1.749782849		
3.492153886	3.080688002		2.345525885		3.957276338		
2.445404109	2.185405595		3.9514546		1.093235329		
4.19657831	2.907112048		1.213859255		2.886425586		
TCGA_TCGA-HZ-A77O		1.327941347		2.356835083		2.494586401	
1.289381298	2.910707052		2.560248123		1.092595547		
3.308575829	2.922603284		2.400757775		3.566205564		
1.79011044	2.51955181		3.460145096		4.313935078		
3.047644802	2.844995807		1.666810424		2.877698244		
TCGA_TCGA-FB-AAPQ		0.939861701		3.759846363		2.427356399	
1.789339544	2.067191308		2.854245865		1.688031651		
3.432002398	2.614228162		3.113952198		3.852230741		
2.329679563	2.330335411		3.436194667		5.204975399		
5.26531131	2.624143585		1.415027577		3.215699925		
TCGA_TCGA-3A-A9IL		2.556283693		2.46086983		2.719925549	
1.172652137	3.248037803		3.135872578		2.178039342		
3.601758182	3.082430953		2.285945702		3.214722079		
2.3923882	2.139368402		3.116924765		4.421278203		
2.915213595	3.210807568		1.813144988		4.384698915		
TCGA_TCGA-HZ-8638		2.159797	3.103294	3.1931	1.680934	2.792896	
3.304622	2.686431	3.167882	3.49447	3.160366	3.827024	2.542605	2.743673
4.074958	1.364808	3.027755	3.282123	1.689025	3.632206		
TCGA_TCGA-FB-AAPS		1.834797827		3.564118744		2.541570549	
1.545153673	3.020656945		2.957453818		2.072347248		
3.232093774	3.194341232		2.502957064		3.655223577		
2.475681992	2.027382791		3.647207155		3.480958934		
5.362840631	2.896068244		2.125034723		3.484339064		
TCGA_TCGA-IB-A7M4		1.958799963		3.054557968		2.382229146	

1.573624795	3.11853696	3.028581549	1.483604363
4.01453844	3.320854028	2.600790627	4.337173297
2.379301494	3.471013936	3.702319749	2.026959295
5.322019957	3.078971598	1.523778866	2.870715766
TCGA_TCGA-IB-8126	0.725614898	2.188681999	2.264679939
0.987491526	1.831734459	2.487791913	1.555997887
2.242476786	2.40714087	2.236591455	2.76200206
1.777108662	1.788042811	2.451113185	3.85283319
2.701708342	2.329774529	1.295986143	2.552260887
TCGA_TCGA-HZ-8636	2.30319981	3.139591601	3.430040235
2.234936626	3.39580014	3.739719069	2.506260612
3.708116505	4.068102003	3.48874586	4.365622923
3.007783872	3.103340149	4.275671668	5.399338112
5.851289329	3.653881288	2.34545694	3.41023547
TCGA_TCGA-US-A77J	1.731531989	3.416379866	2.316148726
1.954332364	3.147634064	2.743147943	1.617863933
3.158346416	3.437591298	1.961185005	3.744882156
1.922715577	2.239907994	3.492136297	2.616414323
4.27498841	3.250151663	1.642676582	3.656313097
TCGA_TCGA-HZ-A8P0	1.406264	2.426778	2.423447
1.21974	2.495889		
2.665317	1.338011	2.486508	3.173123
2.354391	3.546725	1.816539	1.835983
3.35741	2.084648	4.259828	2.58515
1.10594	2.922502		
TCGA_TCGA-IB-AAUS	1.664416249	3.497505778	2.692425465
1.846670665	3.003766634	2.874670264	2.116314347
3.330071983	3.515452269	2.907453589	3.755113803
2.418622003	2.286147285	3.795057099	2.503829835
4.455241831	2.932315837	2.122833981	3.37242354
TCGA_TCGA-3E-AAAZ	2.054568	2.703037	3.051417
1.641767	3.090989		
3.007129	2.20161	3.597236	3.177401
3.042559	3.651604	2.375898	3.217786
3.771065	2.312504	4.069043	3.21221
1.781353	3.419207		
TCGA_TCGA-HZ-8001	1.46151333	3.000298882	2.512040333
1.616399738	2.910020276	2.629208237	1.473662136
3.171630538	3.692795145	2.335782349	4.092780707
2.315500883	2.521668312	3.361667413	3.725561808
4.875298918	3.26637401	1.840446403	3.553968523
TCGA_TCGA-S4-A8RO	1.794559	3.316501	2.913592
2.08163	3.211585		
3.045603	2.180495	3.974	3.241274
3.253427	4.193094	2.312068	3.3347
3.96855	6.191571	4.976315	3.429254
1.676666	2.928154		
TCGA_TCGA-IB-7889	1.246442	3.157805	2.751595
1.447838	3.071927		
2.95788	1.415108	3.165343	3.544963
2.615228	3.950426	2.257165	2.668401
3.672521	3.949247	4.31712	3.320999
1.563809	3.960635		
TCGA_TCGA-FB-AAPP	2.151774	2.792966	2.552611
1.321879	3.366727		
3.144852	1.976087	4.022422	3.640548
2.954891	3.502789	2.22331	2.863904
4.225676	-0.3462264	0.9184074	3.324682
1.36852	3.389765		

TCGA_TCGA-FB-A4P6	2.516549601	3.243983132	3.107696466
1.949091762	3.031230039	3.609778622	2.59637377
3.493101002	3.557959406	3.224007798	3.630083912
2.760571986	2.736485866	3.825800798	3.071630494
3.586860323	3.525433313	1.918732461	3.726836861
TCGA_TCGA-2L-AAQE	2.19016457	2.585490748	2.66097607
1.933664731	3.420402091	3.01549892	2.131765229
3.555384459	3.660714982	3.009854541	3.761972277
2.385608457	3.039340863	3.856191628	1.717796313
7.135695771	3.09647292	1.38488169	3.26123982
TCGA_TCGA-IB-A5SO	1.903718	2.916827	2.76473
1.922432	2.687378		
2.973538	1.991491	3.055266	3.336247
2.568337	3.786034	2.453759	2.363725
3.557227	2.173982	5.930626	2.896697
2.044037	3.278551		
TCGA_TCGA-FB-AAPU	1.093897	2.739347	2.329921
2.397846	2.616302		
2.987135	2.342295	3.289478	2.784427
2.521967	3.830142	2.886424	2.999209
3.666075	4.764339	4.357124	2.757349
1.398505	3.459746		
TCGA_TCGA-IB-7886	1.959273	3.353528	3.214722
2.145847	2.91866		
3.37526	2.5982	3.766156	3.603805
3.599561	4.313394	3.296518	3.712847
4.036949	0.4588233	5.358706	3.849924
2.601719	3.20784		
TCGA_TCGA-2J-AABR	1.991773	3.303215	2.908436
1.883013	3.227766		
3.138578	2.286528	3.270747	3.478246
2.924886	3.741835	2.587633	2.672685
3.807145	4.685205	3.841176	3.37252
2.036917	3.575967		
TCGA_TCGA-XD-AAUL	1.368182468	3.025361897	2.82272976
1.638967366	3.10016989	3.064306331	1.477417897
3.424359397	3.636404217	2.875511064	3.579863593
2.487024274	2.320130614	3.761765709	3.393452109
5.457524922	2.696765764	1.90955964	3.228110198
TCGA_TCGA-F2-A8YN	1.555297	2.2152	2.40964
1.571099	2.726517		
2.859888	1.780535	3.288376	3.443035
2.802648	3.85383	2.248154	2.776464
3.680476	2.60781	4.917647	2.658363
1.776994	2.646764		
TCGA_TCGA-HZ-A49I	2.075225626	3.247861704	2.641784959
1.725256611	2.743681599	3.108474057	2.029909621
3.757820992	3.464407129	2.65499894	3.855144963
2.530017015	1.966038437	3.591689116	4.448655992
5.676509746	3.060466208	1.93229354	4.051776678
TCGA_TCGA-2J-AABE	1.5483066	2.407665787	2.937670339
1.06305385	3.197577208	3.092406264	1.90574789
3.353006193	3.596153622	2.610005593	3.791876245
2.345818472	2.38907455	3.500713973	3.024099987
4.927172059	3.191111942	1.942254848	3.351849974
TCGA_TCGA-2J-AAB8	1.919072183	3.042187716	3.117012223
2.057805782	2.763262396	3.148776426	2.267905932
3.33261012	3.520336118	3.003975943	4.022014149
2.436515564	3.07256109	4.210831598	3.027950661

6.134695413	3.100484853	2.425932828	3.596925888
TCGA_TCGA-US-A774	1.564583	2.774572	2.844591
1.624156	3.066211	2.918316	2.163894
3.38891	3.559104	2.784864	3.650188
2.259037	2.576418	3.331257	2.733764
3.826241	3.097734	1.906599	3.231833
TCGA_TCGA-IB-AAUV	1.907460765	3.413511784	2.995514567
1.842036555	3.219797167	3.026433128	2.30734722
3.306824726	3.553780523	3.222596067	3.781810754
2.762442103	2.493696573	3.674014415	2.486141514
4.626969075	3.220490417	2.418936564	3.703187537
TCGA_TCGA-2J-AABK	2.025659318	2.946597403	2.425659601
1.675881988	2.463049739	3.014887532	1.884581304
3.239485297	3.189613582	2.404655036	3.762583736
2.239043703	2.616409442	3.616756468	2.978071649
3.218783314	3.06541411	1.608600561	3.21885361
TCGA_TCGA-FB-A5VM	0.4988878	3.146633	1.966852
1.774751	2.866453	2.502243	0.495607
3.693196	3.142604	1.583746	3.910537
1.610215	2.828917	3.545797	3.147987
5.083055	2.891348	1.383959	3.229844
TCGA_TCGA-3A-A9I7	1.637283	2.723841	2.641974
1.593415	2.894547	2.887824	1.924193
3.287195	3.310103	2.953973	3.502228
2.461674	2.532127	3.610215	3.072319
4.586707	2.964262	1.636282	3.339185
TCGA_TCGA-IB-8127	1.867323	3.339908	2.924356
2.362351	2.888608	3.643353	2.52454
4.132633	3.81238	3.735246	4.398905
2.992532	3.10106	4.201757	3.830134
6.023808	3.469717	2.174514	3.270771
TCGA_TCGA-IB-AAUU	1.972887166	3.047774105	2.870630403
1.843866507	2.749335447	3.151055498	1.906255678
3.9563682	3.588322445	2.65757345	3.959481959
2.67438735	2.694162422	4.193578618	2.56547233
5.449160973	3.076496404	1.873742786	3.187635243
TCGA_TCGA-IB-7651	1.476945	3.112501	3.300678
1.855303	3.19208	2.788906	1.911227
3.438375	3.522526	3.220209	3.860475
2.681067	3.010092	3.219072	3.169512
5.839656	2.669966	2.153604	3.766608
TCGA_TCGA-S4-A8RP	2.160522249	2.72855103	3.021994806
1.821878635	3.232495107	3.431332517	2.327930446
3.58849284	3.402373392	3.262535432	3.84974433
2.679924559	2.790799363	4.050321272	3.188613627
5.460746274	3.399129628	1.936955874	3.405913383
TCGA_TCGA-HZ-A4BH	2.215030998	3.442294434	2.943172554
2.086939602	3.068157863	3.042506291	2.327327739
4.03045143	3.819538266	3.333885788	4.02548358
3.036149588	2.803241095	3.987249569	1.987485776
4.685193718	3.402220037	2.014021521	3.510294827
TCGA_TCGA-HV-AA8X	1.162959671	2.178334766	2.805187608
2.313329584	2.813354191	3.098797995	1.754857339
3.577757018	3.927172843	2.851304947	4.078782266

2.563303539	3.050673172	4.029551882	6.171044541
4.786580243	3.051943255	1.52408881	3.021657808
TCGA_TCGA-2J-AABV	-0.7170914	1.214862	0.4366912
0.3009125	1.331011	0.8840405	-0.2616904
1.678968	0.3299303	1.77815	0.2210368
4.164132	-0.3438123	1.283936	0.1465394
TCGA_TCGA-2J-AABO	1.883193052	2.868809526	2.758200282
1.668518062	2.943375704	3.089306771	1.746790744
3.747279445	3.500901464	2.814320283	3.834220758
2.187619011	2.514789794	3.737430325	3.806459748
5.942725067	3.102332364	1.685337237	3.413480845
TCGA_TCGA-US-A77E	1.506808	3.230606	2.46824
3.02509	2.113316	3.798984	3.626113
3.850183	2.408617	5.555031	2.744149
TCGA_TCGA-2J-AAB9	1.407609099	2.997285917	2.580911148
1.147508303	2.897659386	2.844607126	1.49125585
3.28157317	3.148582051	2.484641146	3.485190997
2.199843458	2.718634906	3.511633527	4.475281114
4.375505428	3.059708633	1.583695513	3.28633131
TCGA_TCGA-FB-AAQ1	1.610311366	2.526937504	2.265434716
1.693952174	2.634865673	2.618615136	1.481896045
2.973024121	3.169690716	2.421488641	3.866529947
2.176289494	2.12737309	3.915546466	2.186068188
3.846968913	2.979086179	1.516753852	3.227487493
TCGA_TCGA-LB-A9Q5	0.5400844	1.604319	1.972293
2.178899	2.152994	1.084982	2.319129
1.920995	2.453888	4.827509	4.442129
TCGA_TCGA-IB-A5SQ	1.250664	3.02813	2.604498
2.963464	2.016875	3.530592	3.495517
3.565549	3.74719	5.216222	3.070963
TCGA_TCGA-2J-AABA	1.488797766	2.556314381	3.000538305
1.896298186	3.225601457	3.184235109	2.514735847
3.620353609	3.355172543	3.178282871	3.557375485
2.257617694	2.799691657	3.548422559	3.409136792
5.949213111	3.229334718	1.967301521	3.546304917
TCGA_TCGA-F2-A44G	1.700581765	3.841076877	2.729298701
2.252836205	3.017170213	3.269059747	2.205881984
3.659231795	3.928807228	2.85472499	3.794313274
2.687268397	2.939620827	3.727437779	1.823673193
5.174987878	2.930743906	1.757175885	3.50805635
TCGA_TCGA-IB-AAUT	1.846111201	3.233802463	2.640791239
1.376604804	2.723384742	3.115299138	1.928438479
3.208185499	3.149608054	2.66699139	3.761861406
2.609493188	2.325583383	3.569306691	4.017143968

4.598403135	2.861828075	1.937656728	3.478842604
TCGA_TCGA-F2-6880	-0.07165801	0.9481838	1.426163
-0.1155749	1.453835	1.636609	0.5381573
0.9285238	1.654589	0.6821066	1.289713
-0.6313737	1.499762	0.8188352	1.970556
TCGA_TCGA-H6-A45N	2.060546368	2.909805446	3.040762929
1.456704104	3.141941159	3.099466463	2.184118745
3.485605486	3.45919869	2.94907734	3.682737191
2.563352507	2.763376429	3.615240736	2.872398026
4.985521345	3.276098203	2.039409092	3.676339772
TCGA_TCGA-LB-A7SX	1.835781	2.184862	2.547586
1.861925	2.491379	2.753824	1.730418
3.13353	3.399118	2.483584	3.46151
2.53024	2.752738	3.810596	2.417924
3.055064	2.975791	1.728298	2.789492
TCGA_TCGA-2L-AAQA	1.944470921	2.935264311	2.859885322
2.128211276	3.011842248	3.230382988	2.199215215
3.916843399	3.202988005	3.099588169	4.122511352
2.529593353	3.183185049	4.00345112	4.842174486
4.533437632	3.252267276	1.575945105	2.805839909
TCGA_TCGA-Z5-AAPL	3.021894586	3.869512722	3.144677306
2.61214514	2.787731632	3.683999265	3.10071398
3.439189976	3.677945012	2.842154471	4.321340929
2.911575552	2.817699136	4.55824905	0.99200572
3.288360476	3.991850379	1.818839193	3.592950771
TCGA_TCGA-HZ-7920	2.132721782	3.645980004	3.404175949
1.970197801	3.409353709	3.494150854	2.847369546
3.689529164	4.061643733	3.400639697	4.157290689
2.907746693	3.210460873	4.136894358	2.803438819
4.188606765	3.750163477	2.722912284	4.204224391
TCGA_TCGA-HZ-7918	1.218653537	2.910652213	2.918248931
1.57590599	2.978583456	3.160092798	1.681597965
3.6512226	3.399236905	3.177747007	3.766550872
2.766371245	2.80134383	3.375602134	5.592662593
4.949183628	3.09249275	2.171021455	3.453171569
TCGA_TCGA-US-A779	1.281644375	2.301122063	2.330849799
1.734079142	3.159974478	2.90400292	1.406396353
3.363421187	3.571046696	2.007328224	3.661667464
1.822548349	2.333919488	3.248583459	3.213411624
4.041404824	2.782623788	1.23770197	3.061968153
TCGA_TCGA-2J-AABT	2.02704761	3.104119324	3.149299717
1.673532905	3.100499597	3.005542545	1.977141596
3.188015972	3.281233451	2.896288443	3.579408604
2.406742465	2.73930114	3.623375016	3.02390127
4.67844595	3.04538795	2.062205377	3.743390112
TCGA_TCGA-XD-AAUH	1.927365	3.556847	2.881015
1.842618	3.179189		

3.149584	2.379431	3.574376	3.524836	3.008417	3.796978	2.467092	2.704204
3.716701	1.918925	4.171101	3.389863	2.130168	3.793428		
TCGA_TCGA-HZ-7924		2.013494	3.059537	3.401465	2.213472	3.172758	
3.431683	2.843659	3.447917	3.809776	3.530915	3.962338	2.469292	3.323942
4.048016	3.361485	2.63957	3.589585	1.88282	3.694284		
TCGA_TCGA-HZ-A4BK		1.651702265		3.070314145		2.670232758	
1.741917722	2.62973092		3.164863442		2.206958802		
3.92862779	3.466202587		2.805036102		3.670642846		
2.805738592	2.388795377		3.511587271		3.174171862		
4.425165047	3.154716066		1.859774667		3.319348823		
TCGA_TCGA-IB-AAUR		2.737323337		3.539628323		2.950132917	
2.37995784	3.279545755		3.359920981		2.629426163		
3.46579909	3.630085765		2.996188703		3.928643448		
2.576866	2.369883908	3.951833439		2.055864263		4.341178452	
3.566325511	1.898230152		3.71634818				
TCGA_TCGA-HZ-A9TJ		0.8974385		3.290469	2.850378	1.963564	
2.952407	2.864361	1.695494	3.63878	3.397423	2.52039	3.686349	2.418896
2.929568	3.900347	2.055105	3.785188	3.076516	1.981004	2.872677	
TCGA_TCGA-F2-A7TX		1.412386672		3.077067011		2.691397559	
2.024794454	2.922260434		3.102592757		1.951165809		
3.317147245	3.702435772		3.308226082		4.331296613		
2.807139198	3.068378761		4.199644246		3.362714243		
5.478680034	3.558854575		1.658308905		3.006327175		
TCGA_TCGA-HZ-7925		1.609247449		3.477398963		3.271393467	
1.704959667	3.03262634		3.131948256		2.475622425		
3.645156632	3.292185315		3.388394785		4.347443912		
2.902038296	3.135475418		3.742443572		3.759310606		
5.868770178	3.275552697		2.585138438		3.562801688		
TCGA_TCGA-3A-A9IC		1.213402	3.060314	2.261033	2.133776	3.002994	
2.855412	1.831574	3.54938	3.630881	2.675606	3.666066	2.493932	1.956442
3.880398	2.701555	5.096798	2.811601	1.749106	3.753989		
TCGA_TCGA-FB-A545		2.171632239		2.86684232		2.683771324	
2.096206645	3.265934955		3.451163053		2.077579084		
3.744514991	3.512941011		3.055726418		3.822361601		
2.320236091	2.687185933		3.801641758		1.949036743		
5.804303019	3.141829934		1.859425862		3.455277177		
TCGA_TCGA-XD-AAUI		1.691011806		3.352243643		2.629238221	
1.567121208	2.765697774		2.874767625		1.716499506		
4.058108684	3.427637599		2.561363986		3.786498731		
2.356202963	2.665734904		3.663014845		3.47762536		
4.953209256	2.915102525		1.568107096		3.314381367		
TCGA_TCGA-2J-AAB6		1.577449668		3.00961794		2.781034651	
1.439387076	3.093593921		2.715302164		1.542271743		
3.898782013	3.444851255		2.268364755		4.01821655		

3.391225558	2.488863145	3.985791658	3.74283184
4.492026152	3.053884907	1.755696736	3.650956904
TCGA_TCGA-IB-AAUQ	1.711945165	3.069279024	2.573573491
1.242816921	2.856968502	2.760284106	1.944459693
3.178148465	3.312463608	2.151187211	3.750471166
2.281847014	2.392976734	3.656735514	4.055142882
6.642930236	2.879500358	1.780188515	3.291110517
TCGA_TCGA-HZ-A77Q	1.218198856	3.400549788	2.831707502
1.671372137	3.018610414	2.957004709	2.244095354
3.449679772	3.482022329	2.944995275	3.923742986
2.558390227	2.291771093	3.816155055	3.532690905
6.150186383	2.935505027	2.02033595	3.524409702
TCGA_TCGA-IB-7891	0.9008725	2.917553	3.033497 1.694488
2.927733 2.943574 2.018202 3.336241 3.573171 3.226865 3.822109 2.497067			
2.775745 3.50499 3.431751 5.040027 2.957535 2.08347 3.080688			
TCGA_TCGA-3A-A9IU	1.11138399	2.67114908	2.888899302
1.611461636	3.227962122	3.248913979	1.914968067
3.239661657	3.643714922	2.766555358	3.905254602
2.785726666	2.785336493	3.788278536	2.746639712
5.702209397	3.282866962	1.733072064	2.956999884
TCGA_TCGA-2L-AAQI	1.784127568	2.593506306	2.992431174
1.249721008	2.730995901	3.161292798	2.228630356
3.454935664	3.142112919	3.232732192	3.949469183
2.665684496	2.911434416	4.023475307	3.63856547
5.860945396	3.128488378	1.929175761	3.160378833
TCGA_TCGA-3A-A9J0	1.026776129	2.929166841	2.911194311
1.629940652	3.30291718	2.937945846	1.704524859
3.498787711	2.895649794	2.012387268	3.408865174
1.834643049	2.980378985	3.8604799	2.202277756
5.028134457	2.794003029	1.78049232	3.227618801
TCGA_TCGA-HV-A5A3	1.655783	2.372535 2.434715 1.706554 2.858505	
3.197995 1.895054 4.124904 3.633262 2.015909 3.590258 2.349964 2.40987			
3.431271 5.245227 6.572569 3.225261 1.422369 2.808132			
TCGA_TCGA-H8-A6C1	1.993905	3.026516 2.521026 1.772427 2.34582	
2.934608 2.071158 3.241909 3.446699 2.613548 3.528481 2.353339 2.680055			
3.68248 3.734463 4.115283 3.028071 1.256724 2.694106			
TCGA_TCGA-HZ-7926	1.758888321	3.221173586	3.278920653
2.214955337	3.338473972	3.418687347	2.846870321
3.69175542	3.768110894	3.521024119	4.121737213
2.76936533	3.132283094	4.089105274	3.372894971
3.390996449	3.588577947	2.034640033	3.552022912
TCGA_TCGA-IB-7645	1.914130004	3.64393516	3.809351759
2.308348844	3.102327899	3.30568936	2.503300198
3.701696374	3.901815144	3.615021456	4.034479592

2.82350847	2.84479326	4.079307476	3.272038409
4.627738218	3.453549093	2.402484264	3.52406959
TCGA_TCGA-IB-AAUN	1.415599349	2.7834748	2.886212603
1.557708674	3.250935653	3.181447482	2.208857622
3.334391927	3.249211974	3.189292437	3.609673075
2.547402326	2.747687919	3.957235369	3.140845834
4.695239403	3.222947206	1.694021352	2.9543898
TCGA_TCGA-3A-A9IS	2.48787517	2.555714127	3.032237128
1.599765095	3.261031484	3.970374256	2.418430434
4.198839458	3.07734317	3.465400236	3.898506019
2.602767918	2.925109179	3.960328607	6.966385374
5.621611291	2.911132813	2.211139895	4.219192365
TCGA_TCGA-IB-AAUM	1.412226	2.146998	2.093013
2.657524	1.468341	2.441785	2.271839
2.082181	2.844847	1.635395	1.960245
2.676124	3.861776	3.123479	2.503916
1.08683	2.601223		
TCGA_TCGA-IB-7885	1.527444986	2.830110814	2.633965033
1.597859654	3.025912657	2.894809115	1.904388276
3.437058917	3.761805	2.869187568	3.833335886
2.80809693	3.5471005	2.015538178	5.129471916
2.935151028	2.011450346	3.388490801	
TCGA_TCGA-HZ-A49G	2.108156249	3.148561238	2.736659629
1.48196745	2.712797303	3.298634796	2.186127996
3.301535287	3.362919069	2.894424812	3.670520498
2.63734858	2.509736284	3.560429173	3.418906222
4.66190321	3.108499096	1.972794413	3.430103897
TCGA_TCGA-XN-A8T3	2.051749	3.004983	2.895877
3.277713	2.057167	3.939836	3.817521
3.08995	3.938605	2.719709	2.59614
3.985648	5.309195	4.612701	3.421925
1.887869	3.419652		
TCGA_TCGA-2L-AAQM	2.816785769	2.380347785	2.936185127
0.851916739	2.711170186	3.317401506	1.879608348
3.946536279	2.550295532	1.984606254	3.569117701
2.416976454	1.862608928	3.361362628	6.618707433
6.18690197	3.006595761	1.642921151	5.105613166
TCGA_TCGA-FB-AAQ6	1.918897331	1.969123481	2.789382704
1.626654376	2.502371724	3.022114693	1.522785011
3.711612605	3.315688314	2.495596748	3.964487935
1.949398217	3.062552248	3.57615656	2.640173267
5.11686687	3.331399807	1.52305537	2.720134512
TCGA_TCGA-IB-7647	1.253260767	3.08157579	3.635651009
2.329947023	2.987987831	3.475552217	2.618892413
3.267782638	4.029737252	3.185385933	4.173726184
2.896196454	3.347886726	4.176566451	3.008442937
5.211791226	3.475791142	2.350600869	3.598873016
TCGA_TCGA-FB-A4P5	1.81645102	3.047650469	2.657493518

1.961263632	2.986905472	3.054585881	2.045211426
3.613400239	3.248945991	2.804731209	3.629513355
2.344035255	2.139222842	3.517673298	2.995381887
4.415466611	3.126973867	1.790242795	3.534201546
TCGA_TCGA-RB-AA9M	1.939559991	3.415492805	3.33081409
1.643336644	3.387007584	3.427985765	2.476495431
3.808527277	3.863053014	3.310133984	4.245654449
2.847598755	2.98155054	4.296957226	2.573521169
5.634370889	3.604713945	2.222502123	3.658110787
TCGA_TCGA-HZ-8005	1.733806247	3.403259308	3.120851205
1.949460158	3.455904982	3.103405445	1.723319501
4.269438633	3.894402228	3.322539844	4.406048755
2.79205753	3.388462198	4.040611916	1.684115007
5.149052676	3.202099262	2.507026148	3.467661877
TCGA_TCGA-3A-A9IO	2.00794	3.184203	2.49518
1.025373	2.003674	2.911966	2.034609
3.733475	3.104725	3.032391	3.6544
2.298286	2.483453	3.573014	5.852289
0.5719443		2.619457	1.987011
3.980697			
TCGA_TCGA-FB-A7DR	1.500308101	2.775407045	3.038875558
1.602710935	3.016215036	2.877203317	2.132368926
3.551605817	3.465664199	2.806091244	3.642695205
2.717924387	2.571063146	3.63291745	2.732629818
4.699892912	3.1300253	2.051226551	3.509977925
TCGA_TCGA-F2-6879	1.837664485	2.715425333	3.273995829
2.346957127	3.136340818	3.554905821	2.340694731
3.980806763	3.821887071	3.646236011	4.322463872
2.685743219	3.39348756	4.216776057	3.569363661
5.616925908	3.460414693	2.217861899	3.306270792
TCGA_TCGA-XD-AAUG	1.840240024	3.260497891	3.015881904
1.658709427	3.028547983	2.97978006	2.189214183
3.206031975	3.433771404	2.959708015	3.747444271
2.316137213	2.422308991	3.519664129	2.840482097
5.955330023	3.226707623	2.417691906	3.765656212
TCGA_TCGA-HZ-8315	1.842638027	3.052312506	3.262129871
1.362223846	2.777944906	3.539075656	2.50388222
3.343396075	3.623920612	3.068578677	3.988595518
2.75031592	2.61112949	4.040832042	2.01639221
6.118041485	3.408515489	2.097713387	3.016867557
TCGA_TCGA-HV-A5A5	1.602314416	2.936305514	2.658845728
1.279438016	2.742155547	2.901311248	2.082441511
3.432397013	3.221608771	2.543210816	3.502068888
2.385608457	2.455417746	3.346834293	3.112663772
4.253645532	2.848476127	1.800749515	3.471751753
TCGA_TCGA-3A-A9IR	2.206605	3.559854	2.477445
1.967005	3.365561	3.588055	2.40893
3.944244	3.867314	2.853198	4.153976
2.214351	2.875497		

4.074437	0.4090921	1.110349	3.496105	2.818664	4.425985
TCGA_TCGA-IB-7887		1.791549514		2.893833496	3.143817543
2.23841466	3.085632918		3.198443954		2.289011425
3.749138638	3.934048149		3.230903347		4.067659039
2.411247607	3.436722977		3.598160174		1.710560767
6.075575274	3.2304879		2.371097379		3.714448218
TCGA_TCGA-IB-A6UF		2.295493818		2.816872058	2.540183198
1.870395189	3.11507142		3.28667399		1.716278423
3.875884106	3.707462743		2.948561802		4.365369349
2.510630124	2.706759089		3.979717129		2.424108463
4.701003818	3.546998971		1.780897279		3.137096867
TCGA_TCGA-HZ-7923		2.026848	3.356906	3.245678	1.847647 2.916963
3.392449	2.552749	3.278312	3.575626	3.099451	3.743393 2.723654 2.648822
3.710056	2.143326	4.793043	3.529726	2.362576	3.57819
TCGA_TCGA-HZ-A49H		1.334234273		3.170635381	2.195244566
1.551811261	2.844353479		2.647857842		1.87267721
3.139376333	3.297328832		2.567661074		3.448285701
1.934602501	2.082409534		3.043207483		3.588367066
2.946030745	3.018630683		1.353953932		3.178956193
TCGA_TCGA-S4-A8RM		2.03087947		2.436750923	3.187564975
1.874701556	2.899053911		3.424988271		2.618706165
3.714123452	3.191019727		3.380340066		3.724310092
2.680531237	2.807738433		4.159347275		3.427452129
3.785176811	3.488510324		1.622497883		2.788181877
TCGA_TCGA-HV-AA8V		1.736197236		2.694321563	2.692874893
1.352139621	2.999528792		2.849162418		1.917011503
3.084973262	3.356115117		2.670467704		3.603671339
2.276714027	2.206507495		3.423585975		3.647162203
5.908448594	2.791577234		1.845298158		3.369570043
TCGA_TCGA-HZ-7289		0.6048349		2.434714	2.084638 1.669368
3.297086	2.78358	1.033044	3.693309	3.731707	3.194722 3.903023 1.234926
2.156642	3.075482	7.444888	2.531569	2.738183	0.9845567 3.36871
TCGA_TCGA-IB-A5SP		1.372325	2.044239	2.303221	1.561471 2.600489
2.553032	2.062006	3.208222	3.111021	2.554672	3.676336 2.15934 2.68694
3.434496	4.435605	3.831546	2.59806	1.647428	2.795922
TCGA_TCGA-OE-A75W		1.232653907		2.453631952	1.640781004
1.540891046	2.482362978		1.988086034		0.739129401
3.329843807	2.449989664		1.297540581		3.557308993
1.588201289	1.600947467		2.823192493		4.566389488
5.724395962	2.746848896		1.076519538		2.860833822
TCGA_TCGA-IB-7888		1.594133387		3.212861307	3.180248417
1.989152423	3.132426202		3.137287325		2.173475844
3.466414703	3.750847484		3.196607388		4.141416758
2.450730731	2.75237036		3.640429371		2.464460373

4.737229158	3.432203326	2.423374723	3.309911814
TCGA_TCGA-LB-A8F3	0.8924691	2.861112	1.942446 1.36976
2.81822 2.129124 0.9125258		3.340507 2.971407	1.782732 3.473037
2.191962 2.350907 3.489678 4.463816 4.241161 3.03538		1.207536 3.294408	
TCGA_TCGA-3A-A9IJ	1.398875465	2.724848848	1.784233412
0.922351344	2.392950552	2.388504976	0.886918776
2.749921537	2.694407927	1.552402168	3.5828335
1.475158269	2.138224279	2.905674019	3.470024944
0.465143972	2.801283323	2.278574304	3.616246076
TCGA_TCGA-IB-AAUW	1.983263247	3.243150667	3.148752645
1.834293363	3.115481928	3.332179679	2.440859732
3.422462653	3.791051198	3.200922746	3.913999483
2.664165753	2.84958806	3.895531859	2.985093233
3.800083948	3.304401141	2.082313374	3.507918272
TCGA_TCGA-2J-AABU	1.860996	2.764615 2.699996	1.922472 2.782393
3.221475 1.894002 3.461857 3.745954 2.804201 3.961849 2.27243		3.098487	
4.050756 2.657875 5.531084 3.142765 1.881028 3.386261			
TCGA_TCGA-IB-7644	1.669967	2.971723 3.610471	2.628996 3.424192
3.719311 2.160477 3.827656 4.197943 3.459354 4.338361 2.581316 3.26949			
3.945056 2.553492 5.140176 3.465103 2.341366 3.117981			
TCGA_TCGA-Q3-AA2A	1.700012554	2.664294887	2.305702505
1.501052018	2.422533148	2.849762238	2.079221959
3.376597229	3.390410473	2.294896019	3.543086302
2.148047118	2.001132824	3.635175188	2.639225961
4.669245918	2.660040319	1.078606042	3.044119261
TCGA_TCGA-IB-A5ST	1.393989	3.274699 2.827717	2.25101 3.017878
3.121157 1.670224 3.537388 3.700771 2.813018 3.667085 2.31928 2.397111			
3.526307 4.158289 4.77848 3.104808 1.8861 3.705436			
TCGA_TCGA-2J-AAB1	1.373548	2.508213 2.736727	1.347937 2.744501
3.178038 2.089756 3.038126 2.919046 2.37294 3.602375 2.180492 2.377822			
3.427504 2.77724 4.33266 2.967432 1.700491 3.500351			
TCGA_TCGA-HZ-7922	1.709849884	3.051215202	3.640935164
2.162066701	3.324987369	3.28236835	1.962321885
3.84301132	3.84067585	3.697014487	4.016234384
2.950707656	2.876278526	3.732163119	2.177442283
6.112792417	3.390675492	2.414421408	3.359192945
TCGA_TCGA-Q3-A5QY	1.591325144	3.357089482	2.52455121
2.107438009	2.836877669	3.073505589	1.993538146
3.298465279	3.138883277	2.262136147	3.743129228
2.130433647	2.011153825	3.59873471	3.270357678
4.409401975	3.332318183	1.411284211	3.255043434
TCGA_TCGA-HV-A5A6	1.757618907	3.268451924	3.045498483
1.913648517	3.338858347	3.118353842	1.46290344
3.53982836	3.763287028	3.32038783	3.818797372

2.653477381	2.647853431	4.370807811	3.954797407
4.521579202	2.960609069	1.466738226	2.877948162
TCGA_TCGA-IB-7654	1.02669054	3.018949339	3.147375913
1.457673423	2.77933857	3.196623383	2.167608367
3.55107045	3.398497561	3.294826372	3.726333313
2.494759243	2.993078848	3.536108991	3.051432241
5.433205184	2.929313358	2.025562456	2.995289915
TCGA_TCGA-HZ-8003	1.011779	2.227156	2.533983
1.287869	2.198952		
2.441712	1.602197	2.529825	2.693611
2.476065	2.903288	1.924582	2.026896
2.747136	4.097006	3.92356	2.409641
1.50542	2.612203		
TCGA_TCGA-IB-7649	1.013902774	2.85506303	2.908091257
1.476130737	2.754320935	2.89271447	1.579408531
2.996866469	3.352001923	2.996866839	3.745784835
2.378227109	2.616903797	3.286278855	3.014429047
5.679251759	2.966559683	1.999126463	3.200056177
TCGA_TCGA-HV-A7OL	0.8908838	2.061105	1.376071
1.875644			
2.517523	2.202014	0.967341	3.189631
3.200432	1.652928	3.778292	1.605854
2.050737	3.392938	4.32834	3.628021
2.535784	0.8952399	2.702964	
TCGA_TCGA-IB-7652	1.539765	3.158607	3.613242
1.902976	2.911754		
3.23062	2.050537	3.346469	3.273111
3.334133	4.141226	3.14835	2.838578
3.854294	4.938944	4.962853	3.300409
2.30396	3.217339		
TCGA_TCGA-US-A77G	1.601482774	2.383683462	2.826331144
2.35811221	3.207880387	3.342347702	2.087658476
3.603334283	3.713716932	2.85225361	3.49706753
2.56468792	2.680464157	3.873604993	4.35854423
3.107212895	3.282158637	1.356856954	2.82109435
TCGA_TCGA-3E-AAAY	1.830036	3.143097	2.635179
1.586271	2.609833		
3.090392	2.233432	3.451723	3.557865
2.786434	3.668	2.572574	2.261126
3.954773	3.663446	5.100674	3.24453
1.606744	3.263146		
TCGA_TCGA-2J-AABH	1.645358584	2.110094493	2.800061813
1.028532884	2.747243917	2.723202836	1.573242702
3.757336019	2.715412067	2.093703593	3.630711735
1.781813248	2.384553201	3.290200172	2.99285456
3.855105366	2.702540134	1.516483679	2.822427072
TCGA_TCGA-3A-A9IZ	1.766804412	3.148765066	2.275427597
2.622786041	2.921941152	3.292969184	1.826838677
3.124665752	3.49770124	3.380025782	4.375005957
2.554993893	3.353131811	3.898587275	5.550399395
4.720601928	3.076431921	1.436705244	3.630579092
TCGA_TCGA-YH-A8SY	1.252326547	2.89950995	2.587144388
1.400983222	2.903143304	2.687997149	1.784099624
3.632482857	3.496621276	2.760391255	3.582913582
2.391060719	1.899377154	3.772303458	4.717201242
5.02629311	2.575248724	1.957198324	3.215760818

TCGA_TCGA-F2-7273	1.270774523	3.374426888	3.322931241
1.865084476	3.053451334	3.244550677	2.277332668
3.478081432	3.547704745	3.459571532	3.92537863
2.770639571	3.002418	3.595790023	3.889453033
3.055779567	2.476010312	3.786362984	4.744686417
TCGA_TCGA-IB-A5SS	1.146674	2.572041	2.859597
3.070214	1.762052	3.629818	3.356888
3.572294	4.421808	6.530351	3.099497
TCGA_TCGA-FB-AAPZ	1.494379019	3.094228981	2.764225131
1.78633051	2.706610208	3.157797015	2.014381869
3.754626503	3.5997571	2.706730166	4.010218872
2.63194903	2.928445229	3.977806485	3.282810384
5.564905351	3.179323077	1.920093606	3.682710158
TCGA_TCGA-IB-7897	2.270508226	3.666941323	3.893965656
2.429569919	3.247161274	3.822823363	3.081733857
3.708754308	4.060582386	3.728978659	4.100303799
3.306338456	3.194958344	4.242832956	1.943315192
4.115562103	3.951970908	2.892248137	3.753271807
TCGA_TCGA-L1-A7W4	2.394692057	2.958259501	2.341713396
1.778571915	3.148998551	3.167939267	1.951563935
3.463439983	3.727659009	2.799793503	3.935742399
3.148891071	3.801964814	3.944313669	0.734139036
4.875275187	3.137676957	1.912619561	3.773211331
TCGA_TCGA-F2-A44H	0.6994305	2.205898	2.431369
2.331074	2.397096	1.621054	2.72911
2.312262	2.823728	4.110522	4.59506
TCGA_TCGA-HV-A7OP	-1.104233	1.927493	1.251465
2.2666	1.386458	-0.2514204	2.951559
2.404991	0.9861832	2.304922	2.033915
2.523933	0.2359443	2.587738	0.1543361
TCGA_TCGA-2J-AABP	2.3829425	3.319439367	2.214772575
1.504120709	3.543752626	2.565575881	1.612860725
3.94051161	3.835555322	2.45896551	3.89550401
2.338804028	2.1036403	4.295427527	5.353603736
5.434570701	3.222840315	1.84609964	4.244153712
TCGA_TCGA-IB-7893	1.853126	3.269174	3.569671
3.074319	2.188335	3.706753	3.703433
4.137603	2.139465	5.308567	3.266236
TCGA_TCGA-IB-A6UG	1.765766	2.808817	2.292315
2.867021	1.483567	3.061645	2.873061
3.503526	3.116723	3.314749	3.316366
TCGA_TCGA-FB-AAQ0	1.433351	2.904101	2.38785
3.022871	1.890689	3.672459	3.438507
3.795325	2.580912	5.168442	2.984127

TCGA_TCGA-YB-A89D	1.663811	2.941261	2.918037	1.226889	2.681667
3.12487	1.94418	3.415465	3.165884	2.846736	3.933933
3.939608	4.657508	5.872658	2.899364	2.250924	3.535779
TCGA_TCGA-HZ-A77P	1.949138	2.734743	3.164731	1.523853	3.164763
3.122145	2.060611	3.443482	3.628444	2.819434	3.725956
3.638945	3.387352	3.825756	3.163808	2.027147	3.661706
TCGA_TCGA-HZ-8637	2.434936	3.298732	3.137762	1.908363	2.619141
3.158351	2.386527	3.247272	3.396635	3.371667	4.015559
3.948943	1.473578	2.560265	3.541653	1.591536	3.217051
TCGA_TCGA-2L-AAQL	0.482407295	2.815316868	2.083455307		
1.231161664	2.751802368	2.664353583	0.938162254		
3.562758536	3.149318823	2.060295138	3.675162235		
1.858422875	2.059403348	3.534417169	3.79579647		
4.750561311	2.700237019	1.13224638	3.060259248		
TCGA_TCGA-M8-A5N4	2.000643	2.733016	2.469249	1.868794	2.662484
2.804701	1.72159	3.543686	3.392431	2.869177	3.587274
3.5233	2.180627	4.687975	2.739889	1.659312	2.977219
TCGA_TCGA-US-A776	2.213154	2.739505	2.517043	1.773574	3.185446
3.157807	1.358787	3.527746	3.796881	2.644525	3.642701
3.794286	4.590458	0.5703447	3.465075	1.112904	3.41307
TCGA_TCGA-PZ-A5RE	1.088261	2.640059	2.300611	1.748106	2.922203
2.798141	1.490285	3.130367	3.298419	2.026156	3.993596
3.807702	1.4663	6.294148	2.735521	1.636093	3.12498
TCGA_TCGA-2L-AAQJ	0.649398879	2.964546693	2.479775161		
1.362423204	2.436509575	2.78381084	1.507702261		
3.40078563	3.183314364	2.481702467	3.679036028		
2.146799077	2.482049387	3.475562249	3.838363424		
3.717445897	2.678467253	1.26415172	2.757931851		
TCGA_TCGA-HV-A5A4	1.643855427	2.929600348	2.990845653		
1.757194272	3.046779766	3.255694376	2.384014707		
3.565862716	3.248585723	2.762416377	3.871380241		
2.59544788	2.74199234	3.573106889	5.060013913		
5.98432457	3.348377074	1.643428949	3.261144772		
TCGA_TCGA-FB-AAQ2	2.067899	2.311716	3.073862	1.866857	3.092075
2.721884	2.226954	3.460483	3.002344	2.914072	4.080358
3.743978	2.50473	4.955871	3.226352	2.099958	3.033851
TCGA_TCGA-F2-7276	1.932198478	3.735686246	3.46739959		
1.922579649	3.332817407	3.40916864	2.580905827		
3.506179866	3.921832687	3.489970125	4.019464203		
2.876708219	2.90286413	3.913561949	3.368275614		
4.810614552	3.323404378	2.356034805	3.699320686		
TCGA_TCGA-H6-8124	2.470273	2.982821	3.438399	2.21647	3.606165
3.509032	2.4293	3.558516	4.162859	3.252647	4.356996
4.133112	3.57119	6.366317	3.665544	2.304429	3.740587

TCGA_TCGA-2J-AABF	2.114999	3.353371	3.361167	1.941783	3.153706
3.252499	2.158953	3.570889	3.523196	3.104569	3.941865
4.0926	3.789879	4.619258	3.445473	2.054575	3.424931
TCGA_TCGA-FB-AAQ3	0.5277254		2.50524	1.734384	1.449769
1.795186	2.444956	0.9810173	2.65176	3.08982	2.336698
2.002292	1.934003	3.037762	3.218746	5.008714	2.680088
2.167968					0.6994908
TCGA_TCGA-3A-A9I5	1.397699198		2.906599585		2.17119995
1.34551781	2.419494296		2.369580492		1.385920959
3.378903615	2.885248589		2.98339319		3.915652129
2.169840895	2.44424248		3.609920256		2.77113452
3.22602277	2.891840746		1.271284256		3.294540937
TCGA_TCGA-HZ-8317	1.153859203		2.66379641		2.731051438
0.93662475	2.481731177		2.667609543		1.969293779
2.77117782	2.946478373		2.596458166		3.323089081
1.99170711	2.346442412		3.427110929		3.65083241
2.8120191	2.704184467		1.643692172		2.864964758
TCGA_TCGA-RB-A7B8	1.26157	2.507503	2.465823	1.156232	2.732368
2.568483	1.664049	2.841628	2.802719	2.243546	3.464782
3.574821	2.776595	5.604237	2.600032	1.561244	2.932798
TCGA_TCGA-HZ-A8P1	1.561270162		2.803853114		2.909850171
1.463011379	2.158877096		3.051882567		2.521827761
3.597327549	2.990099513		2.969890229		3.937489747
2.268570961	2.987283917		3.912192817		4.424839411
3.764587285	3.2714438		1.263720458		3.016394242
TCGA_TCGA-FB-A78T	2.303496613		3.050117073		2.552334945
2.117938728	2.930499363		3.159210788		2.04638705
3.555931001	3.479254297		2.319685723		3.725556201
2.146731319	2.36216052		3.728847823		3.431640751
3.415983713	3.375498701		1.39086294		2.848508138
TCGA_TCGA-IB-AAUP	2.40019781		3.300694372		3.137525422
2.152175083	2.933064137		3.329625135		2.487311581
3.32960592	3.460190284		2.929082746		4.019713283
2.752696029	2.590990379		4.108263755		3.757728813
4.874676886	3.524883722		2.085169554		3.377322947
TCGA_TCGA-HZ-7919	1.660964167		2.943117276		3.322866241
2.402712017	3.399329571		3.528794455		2.715289587
3.756805111	4.022675093		3.416150774		4.382543742
2.914334635	3.075584934		4.355109739		2.48120113
6.444511614	3.456223987		2.417661284		3.204335355
TCGA_TCGA-RL-AAAS	1.28430655		3.123118203		2.465844254
1.239689253	2.980046889		3.060242758		1.620867158
3.185945126	3.365820277		2.266744257		3.925796309
2.083050373	2.302281379		3.763384922		3.286375439

3.920050885	3.197810795	1.927538857	3.480272049
TCGA_TCGA-3A-A9I9	1.109257	2.142017	1.902488 0.9022004
2.341363 2.469088 1.287081	3.265387	2.54423	2.112263 2.933307 2.034652
1.585007 2.921218 4.299496	3.988232	2.351122	1.021243 2.703288
TCGA_TCGA-2J-AABI	2.158938222	2.900016193	2.791515538
1.566603765	3.103962875	3.180413382	1.750722298
3.511364238	3.089196547	2.38153267	3.963131744
2.04912742	3.279588437	3.827327968	4.258063399
5.222097138	3.550499491	2.140829209	3.343274102
TCGA_TCGA-3A-A9IV	2.155974	2.244049	3.169552 0.9115851
2.676781 3.195639 1.928357	3.981935	2.531166	2.510477 3.525148 2.697926
2.842649 3.371836 4.575832	5.605119	2.994656	2.509317 5.046367
TCGA_TCGA-YY-A8LH	2.040891	2.441516	2.44916 1.798138 2.722788
3.08843 1.884567 3.740519	3.427958	2.606493	4.078538 2.662393 2.889706
4.243819 4.075388 3.958928	3.214629	1.404627	2.963257
GSE21501_GSM535948	2.802315888	3.218114457	1.799396553
2.048526454	2.651209243	2.916128009	1.137821841
3.167215406	2.924886447	2.718628166	4.160535119
1.474719355	2.277634446	4.251463602	2.519682913
3.433261296	3.641238608	1.941050867	3.425760908
GSE21501_GSM535949	1.993847581	3.033154736	3.875759078
1.927217166	2.565585104	2.93964299	2.53946237
2.869691079	3.465784933	2.801663375	3.780566104
2.966303718	2.339905061	4.037900012	1.705164045
3.353864378	4.020991805	1.649024167	3.096826132
GSE21501_GSM535950	2.284773	2.886473	3.7458 2.05142 3.079562
2.681414 3.30645 3.515135	3.332664	2.721529	3.98283 3.199229 2.374955
3.662273 2.335439 3.121956	3.496201	1.36683	3.364824
GSE21501_GSM535951	3.004579	2.7498	3.343703 2.334879 2.729847
2.895783 2.143931 3.591604	3.33483	2.732312	4.004482 1.924488 2.719469
4.102456 1.785461 3.180401	3.812314	1.753063	3.036039
GSE21501_GSM536032	1.253340227	3.151698884	3.980585212
2.63229687	2.964473214	2.766730654	2.084477725
2.848601074	3.709222939	2.334537726	4.429409487
2.997855537	2.663604962	3.879567897	3.107580685
2.64799963	4.133405236	1.593147479	4.258886183
GSE21501_GSM536033	2.246911302	2.732690019	2.883368361
1.176682314	3.025142807	2.396678161	1.304642725
2.804944364	3.025141954	2.968924066	3.539900191
1.629622623	2.563085554	3.949296224	4.690900391
3.457346186	3.534546279	1.28024301	3.392532007
GSE21501_GSM536034	3.172534703	3.474332919	3.243568348
2.039277156	2.406371384	3.652031457	2.038912261
3.491194791	3.105859638	3.184688928	4.469996071

2.322707422	2.910771956	4.617233871	2.077734717
4.204184364	3.493411287	1.191573101	3.906935414
GSE21501_GSM536035	0.8105597	3.107983	2.966468 1.845835
2.466176 2.509749 1.123227 3.327808 3.149782 3.01788	3.947613 2.721828		
2.050938 3.185892 2.760491 4.778427 3.205766 1.938874 3.430723			
GSE21501_GSM536036	1.979549 2.39475 2.899987 1.909468 2.668662		
3.332927 2.000587 3.507198 3.516918 2.34807 4.337528 2.118515 2.02237			
4.094307 2.885568 2.941482 2.672725 1.727865 3.614337			
GSE21501_GSM536037	2.026135 2.331765 2.818404 1.418356 2.634499		
3.315859 1.669964 3.460882 2.899146 2.244633 4.156032 2.505776 2.043784			
3.763013 3.50092 3.231781 2.250883 1.918966 4.020339			
GSE21501_GSM536038	2.401097145	2.790316875	2.027836612
1.758049666	2.836822754	2.825347201	1.503559297
3.509597934	2.741281119	3.730000464	4.105839228
3.52554937	2.402572022	3.551263013	3.01587485
4.353318149	3.097187826	1.035644172	4.140121696
GSE21501_GSM536039	2.047628568	1.888283124	2.706328369
1.203043154	2.741371123	2.989154484	1.791717124
3.012157486	2.946154521	2.255630953	3.695089308
1.902459283	2.367503362	3.749256554	4.257454124
5.317468157	2.901571937	1.678173275	3.234498161
GSE21501_GSM536040	2.417426 2.605128 3.215188 1.546942 2.428393		
3.110392 1.661809 2.765772 2.929357 2.448692 3.393537 1.663321 3.329434			
3.840946 4.385052 3.263691 3.667674 1.557707 2.830741			
GSE21501_GSM536041	2.65422238	2.659045319	2.445185754
1.498490128	2.58537282	3.573380805	1.73681017
3.366697102	3.377963396	2.25024236	3.314796951
1.589760282	2.741333831	3.471288117	4.982002548
3.897797766	2.957635321	1.612109291	3.088139984
GSE21501_GSM536042	0.7586755	2.733567	3.084156 2.379553
2.914408 2.765321 1.382043 2.96771 3.389329 3.082707 3.568969 2.90871			
2.712789 3.652539 4.144616 4.066161 3.13791 1.470936 2.984548			
GSE21501_GSM536043	2.88744 3.077595 2.433956 1.894882 2.377788		
2.734979 1.842514 3.28084 3.401236 2.231027 4.010529 1.966005 2.111123			
3.601063 0.9049795	7.250268 3.179872 2.14079 3.707516		
GSE21501_GSM536044	1.737442 2.316119 2.508913 2.211208 2.588915		
2.446195 2.465509 3.734479 3.504641 2.310835 3.590985 3.184984 2.008504			
3.644371 1.984256 6.064983 3.025615 2.258289 3.1484			
GSE21501_GSM536045	4.644395 3.142594 2.343579 1.989804 1.802343		
2.820778 3.436815 3.667574 3.740807 3.536403 4.229 1.929475 4.361294			
5.063918 2.889873 10.32852 4.580298 1.399854 3.737004			
GSE21501_GSM536046	1.699366298	3.360955517	2.967218089
1.825937977	3.348540126	3.690613717	1.939066419
3.171433434	3.439753219	2.527195142	3.584890722

2.894875267	2.755851655	3.475088723	2.625026286
2.697587407	3.086338151	2.922707564	4.646538953
GSE21501_GSM536443	1.483222	2.017123	2.741551
1.6679	2.898114		
3.176049	1.535014	2.851195	3.294796
1.715393	3.307769	2.128539	1.663733
3.278949	3.648873	6.008016	2.905652
1.644682	3.487548		
GSE21501_GSM536444	1.597323	2.795205	2.216279
1.82303	2.738096		
3.487528	2.05015	3.592656	3.197079
3.181267	3.667068	2.161294	2.165601
3.784045	2.564081	4.280654	3.086041
1.184865	3.820204		
GSE21501_GSM536445	1.583098	2.690726	2.671665
1.284996	2.88971		
2.369935	2.722982	3.179705	3.811599
2.464943	3.78747	2.150685	1.931886
3.473409	2.223011	5.852034	3.242949
2.215924	3.719396		
GSE21501_GSM536446	2.461301	2.753528	2.450149
1.640538	3.714873		
3.41696	1.310426	3.823843	4.000277
2.542166	4.839065	2.375799	3.130057
4.574282	6.717552	5.620686	3.150304
1.29884	3.052339		
GSE21501_GSM536447	0.9903191	2.73741	2.225748
1.598083			
3.707158	3.063335	0.6027558	3.280317
3.410592	2.948403	4.008238	
1.994455	3.257061	4.674359	5.388353
1.265385	3.680417	1.157275	3.280675
GSE21501_GSM536448	1.180178042	2.676131772	2.313697945
1.977368904	2.60480752	3.085954814	1.795373092
3.445477523	4.004088649	2.110319678	3.641798723
2.246586296	1.16818159	3.302672873	3.019683605
5.344649046	2.850493855	1.524475191	3.435489385
GSE21501_GSM536449	1.397233	3.201225	2.257329
1.297777	2.884026		
3.431798	1.805524	3.288272	3.726339
2.404527	3.318576	2.274006	2.330392
3.497452	2.894858	5.858134	2.980359
2.391048	3.699138		
GSE21501_GSM536450	1.290120982	3.247304406	2.801140526
1.207438285	2.883067023	3.041301264	1.302122152
2.956078697	3.317333888	3.113011156	3.321146767
2.301693038	2.839751475	3.730305371	6.18042875
3.202762037	3.241052658	2.308942056	3.042198812
GSE21501_GSM536451	1.195681	2.734158	2.643809
1.164731	2.61253		
2.863569	1.625217	3.366905	3.210802
2.697684	3.228254	2.08797	2.46338
3.577908	4.935248	3.708581	3.297398
2.36502	2.903089		
GSE21501_GSM536452	0.634729426	2.613641716	3.038748483
1.92308062	2.860854975	2.823121502	2.347537092
3.820519638	3.659383239	2.0345779	3.891192277
2.575159718	2.451138637	3.492591075	1.755925314
5.156990683	3.084429228	2.934059959	3.11694476
GSE21501_GSM536453	1.386381866	2.495475245	2.451466436
1.816021228	2.796266168	3.061595454	1.584138645
3.030520516	3.29971585	1.860259867	3.420684193
1.930221063	1.348983934	3.10347617	3.127100793
6.459969391	3.117545269	2.332481844	3.143550294
GSE21501_GSM536454	1.459313196	3.100514866	2.595049184

1.815564431	2.919646146	2.929920898	2.712005377
3.81404474	3.783174038	2.313363546	3.829637191
3.046892786	2.401809161	3.791456474	5.831823439
4.837380003	3.043999207	1.784020983	3.902873301
GSE21501_GSM536455	2.556111405	2.397529183	3.847634418
2.088307091	2.983127029	3.725156326	2.121578564
3.361697827	3.798641364	2.268936339	4.518382363
2.486816709	3.00935144	4.130335598	4.349741234
3.879888779	3.384724488	1.872248683	3.046615229
GSE21501_GSM536456	1.956009	3.110018	2.498729
1.928335	2.953707		
3.229691	2.42511	3.607748	3.659513
2.867572	4.097529	2.458734	2.437777
3.828446	2.907158	2.799448	2.873131
1.429113	3.734265		
GSE21501_GSM536457	1.675823	2.116058	3.18035
1.947184	2.893555		
2.998461	1.87411	3.347459	3.199025
2.630277	3.885005	2.581255	2.482191
3.807528	2.078917	5.444982	2.995627
2.141443	3.614068		
GSE21501_GSM536458	1.420164079	3.04687549	2.471200514
1.480672057	2.713753959	3.035500034	2.189689587
3.678255447	2.98025587	3.279956833	3.794780942
2.477286702	2.484333784	3.918001022	4.171544024
5.311887788	3.115533912	1.668704061	3.674410017
GSE21501_GSM536459	1.621726	2.823913	2.834477
1.516597	3.167851		
3.330029	2.487222	2.750217	2.976619
2.703791	3.713508	2.865009	2.820287
3.885444	4.263849	3.787456	3.256804
1.816489	4.710919		
GSE21501_GSM536460	1.784228947	2.971357436	2.259682747
1.641959312	3.148499022	2.962402927	1.839247215
4.449486431	3.64128725	3.133222531	4.041400249
2.527977244	2.444655698	3.873858568	3.454751933
6.497597817	3.00356284	1.55734658	3.445264714
GSE21501_GSM536461	1.886711	3.082779	2.835399
1.627814	3.369044		
3.007473	2.435595	3.211918	3.447698
2.820648	4.195982	2.533935	2.396532
3.889801	2.708758	5.132709	3.26948
1.768953	3.665242		
GSE21501_GSM536462	1.789701164	3.198346349	2.491002775
1.282872907	3.277060982	3.493942144	1.290259659
3.427444792	3.309195104	3.091101887	3.564235782
1.969469856	2.808559946	4.058167782	4.720911105
3.481000127	3.506981759	1.467796174	3.229572806
GSE21501_GSM536463	1.580062874	3.159443907	2.674989041
1.42909105	2.939566004	2.813443113	2.377332494
3.223037848	3.304200661	3.464336478	3.856685746
2.726257836	2.152912507	3.837618937	2.448576586
3.995301385	3.242948895	1.815631235	3.948349781
GSE21501_GSM536464	1.457862	3.181925	2.798874
1.446559	3.227121		
2.471611	2.159429	3.065587	3.474453
2.960899	3.964856	2.502698	2.751341
3.879568	3.103644	4.287226	2.980359
2.027385	3.840367		

GSE21501_GSM536465	2.653841	3.047219	2.297162	1.958674	2.920413
3.715884	2.560884	3.424594	3.606726	2.100277	4.072119
2.343875	2.715493	3.991399	3.941823	3.801223	3.123527
1.138932	3.437778	GSE21501_GSM536466	1.555005	2.069574	3.471147
3.261277	2.53248	2.795064	2.117509	3.655823	3.34567
2.555451	4.150099	2.628629	2.216517	3.7043	3.28555
4.605401	3.057383	1.476269	3.344812	GSE21501_GSM536467	1.596950173
3.272501747	2.833174354	1.21792785	3.371715448	3.384282727	1.574760475
3.491013211	3.541782716	3.213068314	3.714597166	2.039158038	2.574427187
4.182263656	2.329001776	4.789023459	2.999735631	1.464389684	3.464442624
GSE21501_GSM536468	1.654716102	3.04226533	2.722637385	2.19273004	2.907415078
3.484335437	2.14705826	3.812423221	3.781245764	2.635285204	3.675149799
3.882920293	3.034288295	2.142693088	2.774276664	3.294544089	2.960779762
1.4279561	3.473061078	GSE21501_GSM536469	1.765049	2.987622	2.51138
1.512926	2.859102	2.676798	2.042048	3.103138	3.186718
3.518239	4.115068	2.561662	2.248262	4.227268	2.538471
5.933126	3.207414	1.731362	3.565833	GSE21501_GSM536470	1.488019
2.566511	2.758536	1.924603	2.775695	2.868934	2.078206
3.499489	3.292819	2.214128	4.148747	2.550799	2.853519
3.282903	2.541298	4.698515	2.838763	1.947697	3.456591
GSE21501_GSM536471	1.327888	2.868878	2.168517	1.817816	2.868241
2.261025	2.495787	2.753656	3.536673	2.983931	4.30358
2.417094	2.425817	4.214278	2.234577	4.816448	3.750945
1.262891	3.796659	GSE21501_GSM536472	1.274687	3.007273	2.80039
1.544403	3.033169	2.510245	2.545487	3.410874	3.657697
2.689389	4.043644	2.848178	2.391437	4.046476	4.152886
6.131469	3.302062	1.680751	3.83104	GSE21501_GSM536473	1.49024
2.910579	3.235883	1.543581	3.0297	2.887103	2.429397
3.615521	3.449093	2.659011	3.895395	2.62231	2.612951
3.714198	3.55787	3.847462	3.222055	1.751052	3.288679
GSE21501_GSM536474	2.167829	3.385658	2.467461	1.548726	2.990044
2.898262	1.350949	3.578741	3.42524	3.077307	3.963869
2.685617	2.429988	4.233944	2.79279	4.969709	3.053425
1.373452	3.101047	GSE21501_GSM536475	1.447259	2.094232	2.840178
1.415075	3.618768	2.957341	2.643893	3.379529	3.721481
2.904029	3.853165	2.473724	2.521708	3.995155	3.292092
6.739441	3.260112	2.062848	3.456903	GSE21501_GSM536476	2.11407137
2.920295548	2.486320969	1.681703066	2.998163115	3.536364496	2.287445693
3.59069756	3.536780951	2.409335062	3.809181425	2.610492472	2.551349999
3.651868168	4.267287543	3.128480009	3.13604088	1.475040092	3.072238915
GSE21501_GSM536477	2.007703669	2.952985519	2.292781283	2.069580692	2.143394651
2.925197365	1.773487585				

3.423156294	2.983701276	2.806381304	3.829444632
2.632791121	2.553566873	3.889801118	5.699102258
4.445639435	3.253659035	1.392701865	3.016478316
GSE21501_GSM536478	1.912433	2.295133	2.913257 2.362109 2.702558
3.133972 2.442495	3.478836 3.76669	2.192468 4.097718	3.056434 2.718638
3.817876 5.386467	3.053921 3.298921	1.506148 3.026986	
GSE21501_GSM536479	2.636446776	2.665607074	2.973610301
2.557820407	3.767432601	2.308529554	0.191042342
3.133593988	2.491135552	1.004079796	4.657185954
0.626153834	3.007234384	5.462177567	3.983524256
5.154364534	3.921264432	2.604834392	4.48451986
GSE21501_GSM536480	1.580062874	1.987880803	2.59701168
2.047012052	2.775910555	3.229739383	2.43445389
3.373931901	3.791717946	1.973687197	4.123419614
2.099235405	2.818030811	3.890257878	2.975969903
4.887915919	3.386885311	1.834069591	3.410664605
GSE21501_GSM536481	1.704983293	3.077686443	2.564370565
1.410337982	2.960935878	3.240845715	2.154672846
3.448553338	2.955265424	2.589950186	4.158327883
2.683306025	2.441146382	3.750089633	4.057367736
5.774809825	2.881943778	2.027137207	3.815477985
GSE21501_GSM536482	1.385167388	2.935547918	2.437684914
1.717453642	3.191324622	2.829167224	2.536545514
3.655892936	3.63805677	3.518658315	3.99802657
2.12378859	2.172717938	4.07003081	2.858320822
3.863201501	3.038944752	1.628093355	3.326989231
GSE21501_GSM536483	2.082466258	2.496589328	3.414813261
2.02040082	2.698875931	3.06372357	1.684613787
3.716821579	3.589717555	2.789927748	4.220589501
2.016915398	2.573967192	4.260783422	3.141322536
3.919473414	2.771181589	1.485550022	3.391912337
GSE21501_GSM536484	1.963184017	2.571629816	2.771479141
1.877095883	3.066484917	3.831900858	2.311786379
3.58049306	3.753251702	2.504837011	3.906812061
2.247175365	2.86743933	3.707640715	3.118784775
5.367965324	2.931166425	1.42815608	3.001556649
GSE21501_GSM536485	1.795362	2.240236 3.008471	2.179502 3.210057
3.495347 2.754681	3.521106 3.963085	2.105112 4.104658	2.770151 2.526374
3.950865 3.27064	4.38729 3.222478	1.565065 3.508513	
GSE21501_GSM536486	1.8227701	3.116146921	2.79133173
1.429886781	3.089209262	3.352165005	2.155972696
3.249760457	3.419560258	2.686455648	3.807530931
2.50624066	2.661339348	3.886673387	3.201489106
5.400531786	3.22577232	1.958135118	3.837233809

GSE21501_GSM536487	2.10688	3.54728	3.400656	2.312538	3.308412
3.643274	2.887958	3.652443	3.705803	2.589855	4.147173
3.900229	3.821513	4.020084	3.530726	1.831329	3.981968
GSE21501_GSM536488	1.292113	3.198639	3.0368	1.172179	3.048462
2.922595	1.971079	2.852235	3.324783	3.023021	3.347614
3.586566	3.043322	3.579249	3.208534	2.455539	3.708741
GSE21501_GSM536489	1.419099641		3.323377158		2.451950542
1.447270536	3.230442935	3.19479909		1.698506493	
2.903971037	3.053713157	4.018579066		3.345821124	
2.307772476	3.075179244	3.415959382		5.385158095	
2.863802466	2.531223197	1.487163748		2.793875357	
GSE21501_GSM536490	1.803223301		3.498900419		2.583525753
1.236387287	3.136200314	3.590701425		1.422129979	
3.581979615	3.132345091	2.940186933		3.389623557	
1.892548948	2.549318704	3.359537218		2.327839461	
3.877368855	2.425899763	2.444499258		3.036428328	
GSE21501_GSM536491	1.137214	2.312696	3.106081	2.465194	2.655212
2.725388	1.654595	3.451969	3.935319	2.437726	4.128606
3.73558	5.334287	4.001493	3.22883	2.273967	2.85329
GSE21501_GSM536492	1.566288732		3.58248978		2.919371151
1.49012016	3.022626152	3.764009587		2.085428275	
3.549407258	3.470024491	2.928153094		3.036977693	
2.437965252	2.935181502	3.050046268		2.59139109	
2.470097176	2.38268295	1.586921239		3.22013095	
GSE21501_GSM536882	1.599335	3.086479	2.945233	1.401993	2.989855
3.703916	1.634779	3.185177	3.110459	2.75621	3.507417
3.66179	3.136795	5.993167	2.349318	1.732521	3.320884
GSE21501_GSM536883	1.529252974		3.156929116		1.933186339
1.599659984	2.691374844	3.233350437		1.927292168	
4.49710268	3.80428557	2.541374155		3.514673113	
2.588343494	2.529750054	3.421634472		2.416131839	
4.231449041	2.771576371	2.22513854		3.080286516	
GSE21501_GSM536884	1.430768	2.971083	2.731277	1.460908	2.993002
3.372109	1.421733	4.181013	3.902228	2.668674	3.61735
3.61466	2.879741	4.07528	2.800683	1.664526	2.62163
GSE21501_GSM536885	1.417730337		2.786508349		3.000539313
2.053498536	2.917201204	3.178901151		2.02893987	
4.071253489	3.390656434	2.715794329		3.399201108	
2.009091375	2.735425053	3.1834909		2.364603328	
4.234923955	2.241498948	1.779088224		3.384184996	
GSE21501_GSM536886	1.476254841		2.576642433		2.73676427
1.164892596	3.422332033	2.777635268		2.200070203	
3.724952731	3.437024105	2.327249279		3.931682684	
2.048706432	2.310066057	3.430212148		2.526980529	

5.744188041	2.858937872	2.043721424	2.61788719
GSE21501_GSM536887	1.050491	3.430178	3.200717 2.048117 2.681489
2.475875	2.044942 3.628474	4.347791	2.963509 3.721931 3.663202 3.5839
3.695807	0.07156561	4.435707	3.281719 1.828401 2.722048
GSE21501_GSM536888	0.9230822	3.743016	1.951748 1.651818
2.867441	2.65142 1.969729	3.717135	3.378691 2.342706 3.516548 2.113269
3.003171	2.451072 2.076633	3.639106	3.107342 2.067162 2.805442
GSE21501_GSM536889	1.726327099	1.761434738	3.526756725
2.844382393	2.931173933	1.821306221	1.382748344
2.073339055	3.044596577	3.301079826	3.934923495
1.673946915	2.232223945	3.952784674	3.285641969
3.811784661	2.748364037	2.581368607	3.831797301
GSE21501_GSM536890	1.261572589	3.321848356	2.308890323
1.303203309	2.97482355	2.665534334	1.647963464
4.320029423	3.356267704	2.956965101	3.354179937
1.995155925	3.094583868	3.37832059	4.831712023
5.481144508	3.022536176	2.221324843	2.778786628
GSE21501_GSM536891	1.867704917	1.934236596	2.770306146
2.103592729	2.603678731	2.321641294	2.222481401
3.801037429	3.906454088	2.251044635	4.247694169
2.059185625	2.929172493	2.956021177	0.754445305
2.903749765	3.725640555	1.332328875	2.840299419
GSE21501_GSM536892	0.9796702	3.609198	1.894213 1.496188
2.848954	3.11746 2.219136	3.397786	2.963192 3.037951 3.615759 2.698291
3.337368	3.753771 3.248967	6.034049	2.705783 2.66147 3.149138
GSE21501_GSM536893	0.975928196	3.749555476	1.6219555
1.14225243	3.074558444	2.485683444	1.249704134
3.841043978	2.997324904	2.568292201	2.945251083
1.866618915	2.943683043	2.532710112	4.810645047
4.836293762	3.338707199	2.589479202	2.853105633
GSE21501_GSM536894	2.285006567	3.414174872	2.601476433
1.627186583	1.957610338	3.312865849	2.308608944
3.596794966	3.633374879	2.717010301	3.346623608
2.590107579	2.688461288	2.908572516	3.200254905
4.32029537	2.700422215	0.840973827	2.672996173
GSE21501_GSM536895	1.231272	4.022873	2.306554 1.21085 3.745548
3.376729	1.661455 3.990009	3.795673	3.198025 3.755947 2.27954 2.61642
3.590187	3.664327 3.907789	2.846702	2.116644 3.785091
GSE21501_GSM536896	0.9769983	1.909699	2.934499 1.684071
3.094996	2.834288 1.549366	3.11516	4.063342 2.044618 3.273346 2.045346
2.563086	3.332938 6.645992	4.338021	3.291659 1.679293 3.171243
GSE21501_GSM536897	1.4770987	3.386356349	2.918296418
1.496491356	2.699393682	2.918659568	2.438214952
3.184098432	3.792465839	2.513074662	3.163697715

2.832426356	3.172502787	2.926434555	5.104164658
3.129179828	3.049248145	1.867085241	3.083864103
GSE21501_GSM536898	0.7635781	2.881492	2.172409 1.550579
2.361901 2.897136 2.405462	3.079606 4.112009 2.575231	3.812264 2.900326	
2.714611 2.67031 3.137339	5.410072 3.234443 1.497743	2.669219	
GSE21501_GSM536899	1.192663 4.211784 2.210711	1.309101 3.567938	
3.1054 2.409842 3.977374	3.532291 3.019818 3.423271	2.290734 2.829045	
3.411441 3.398987 4.393053	2.897589 1.925112 3.036428		
GSE21501_GSM536900	1.124239 2.959795 2.120868	1.443302 3.261176	
3.02532 1.759868 3.749004	3.190245 2.348806 3.169497	1.583101 2.811403	
2.71913 3.468832 5.438161	2.957635 2.358276 3.047463		
GSE21501_GSM536901	1.437825 2.313839 3.143167	2.22281 3.130518	
2.95848 1.61659 3.476815	4.752578 2.772995 4.307335	2.132713 2.906077	
4.449195 0.7349004	1.884078 3.878686 1.527615	3.118769	
GSE21501_GSM536902	1.539268 3.53815 2.731499	1.357012 2.256523	
3.319962 2.095322 3.126023	3.469818 3.306515 3.498676	2.457527 2.64116	
2.815835 1.269875 3.450029	2.65464 1.811965 2.469306		
GSE21501_GSM536903	0.6637817	3.305437 2.208729 1.550525	
2.702189 2.809427 1.516175	4.255446 3.167945 2.9845	4.056396 2.927931	
2.892895 3.951291 2.827366	3.659418 3.17117 2.405547	3.082011	
GSE21501_GSM536904	1.2888931	3.013174695	2.323221981
1.101121546	2.982480985	3.223840808	1.631543318
2.928622738	3.230000269	2.141475401	3.581527631
2.751450527	2.204420558	3.311926953	2.925936885
4.763710655	2.997839472	2.461726661	3.929557628
GSE21501_GSM536905	1.686200924	2.146258623	2.712657623
1.383731492	2.893771418	2.282821548	1.994431393
4.022086994	3.117085869	3.23952464	4.080714071
2.998936554	2.409303909	3.74338045	1.458992539
3.369640779	3.062985822	0.76884475	2.67803738
GSE21501_GSM536906	1.528153786	2.971309602	2.394120015
1.887008941	2.448888357	2.920663663	1.964803419
3.840829097	3.195165939	2.364876139	3.59113393
2.743756059	2.252175704	3.55107408	2.357908381
5.54992572	2.759778797	1.879169511	3.2061931
GSE21501_GSM536907	0.6621798	2.704506	2.702396 3.2454
1.891311 3.047993 2.832285	3.072305 3.733669 2.435389	4.463134 2.930816	
2.599873 3.276604 3.77047	4.931009 3.454564 1.959532	3.250283	
GSE21501_GSM536908	1.799124 2.289582 3.131478	1.968854 2.314986	
3.021767 2.163841 3.952144	2.688182 2.03017 3.728743	2.852457 1.915608	
3.169635 2.132927 6.285538	2.063898 1.584591 2.801372		
GSE21501_GSM536909	1.182151 2.025622 3.651413	1.640431 2.422003	
2.742409 2.644741 3.189583	4.21109 2.006727 3.515137	3.131595 2.73104	
3.260659 2.276394 6.274816	3.028537 1.839659 2.662317		

GSE21501_GSM536910	1.022034	3.480275	3.038405	1.329205	2.994663
3.271319	1.828361	3.219887	3.924256	3.159641	3.711166
3.12733	1.949499	4.489861	2.644736	2.157669	3.19856
GSE21501_GSM536911	0.8920244		3.100515	2.835643	1.474955
3.693846	3.43479	1.958259	3.95137	2.88426	4.089655
2.488462	3.76946	2.086056	4.932719	3.214694	1.544112
GSE21501_GSM536917	0.814897577		3.031247863		2.376856518
1.730221586	2.634938781		3.587859686		2.048394823
3.771336409	4.012492091		3.629481016		3.587820106
3.010967142	2.985696385		3.409664404		3.783067435
4.937411316	2.798663382		1.637669872		2.916745974
GSE21501_GSM536918	0.7793141		3.181971	2.685727	1.685614
3.110781	2.788386	2.129258	3.248108	3.442898	2.200475
2.348614	3.05972	2.582751	3.323296	3.254594	3.087315
GSE21501_GSM536919	1.826987	2.814217	2.56126	1.142844	3.538304
3.824636	1.249409	3.845723	2.562161	4.588925	3.758011
3.267628	4.854804	4.655652	3.230206	1.049484	2.342509
GSE21501_GSM536920	1.149191222		2.898593507		2.921318101
1.134845166	2.455519556		2.882226637		1.459068502
3.111827661	3.695348449		3.815299402		3.829540911
2.500291372	2.381292813		3.617901165		1.994381857
7.386213226	2.858614815		2.018657568		3.670540118
GSE21501_GSM536921	1.109062684		4.065563399		3.152544864
1.368704754	2.599467711		3.557395629		1.388338512
3.474008911	2.584260614		3.740289704		3.577667503
2.129435643	3.329162326		3.121866453		3.102069049
6.076079482	3.100334758		1.424341984		3.527088351
GSE21501_GSM536922	1.675655	2.99816	2.804018	1.283265	3.185274
3.161852	1.257076	3.060497	2.77689	2.197418	2.87036
3.595951	6.221161	2.802185	3.502971	1.756005	3.939019
GSE21501_GSM536923	1.182151006		3.168324506		2.171462654
1.79654112	2.789866455		2.809233487		2.183630215
3.098704939	3.617162127		2.421576351		3.043531374
2.079517675	3.092828922		2.643102058		2.549929705
3.743144551	2.750573629		2.44650602		2.858760931
GSE21501_GSM536924	0.9857888		2.710732	2.664364	1.753463
2.828026	2.737347	1.776074	3.373552	3.472637	2.770071
2.077419	3.487097	3.507234	4.337307	2.916752	2.229776
GSE21501_GSM536925	1.111641	2.248029	2.564723	2.116299	2.903321
3.015749	2.063667	4.00844	3.78244	2.353091	4.028258
3.913911	1.804501	4.691405	2.594968	1.76955	2.5808
GSE21501_GSM536926	1.606951	3.329345	2.227506	1.343595	2.946714
2.799308	1.629826	3.112873	3.100071	2.952602	2.904866
3.2709	4.567873	3.433781	2.997435	1.495676	2.866756

GSE21501_GSM536927	1.536508656	2.996425011	2.614246591
1.921701975	3.175980539	3.512004446	1.780802175
3.596040735	3.50212624	1.978396127	3.464715049
2.439525184	3.253776321	2.961690474	2.986436075
6.017252447	2.736973975	2.108269735	2.717651141
GSE21501_GSM536928	1.748663601	2.902109853	2.638948594
1.532459388	2.920528189	3.765313013	1.535185447
3.539639721	3.275186111	2.659573966	3.423270868
2.124875631	2.704441786	3.387917624	2.908322322
5.419407718	2.332905435	1.762360632	3.405771297
GSE21501_GSM536929	1.355803	2.689466	2.357779
1.910498	2.737588	2.509527	1.756921
3.23505	4.138145	2.482869	2.959608
2.172052	2.663511	2.621075	3.888834
4.460529	2.737458	1.958893	2.937346
GSE21501_GSM536930	1.249873	3.556769	2.791332
1.684127	3.432204	3.086265	1.671788
4.48319	3.008397	2.798844	3.136103
2.772585	3.68694	3.332327	1.084531
4.342167	2.327923	1.450896	3.137764
GSE21501_GSM536931	0.989179223	2.952315921	3.167742607
1.830636839	3.111896741	2.936324593	2.864215016
3.352909779	3.474278335	2.575373407	3.981169576
2.511351476	2.743511942	3.454338638	3.870706277
6.011145138	3.116343598	2.45869051	3.427038914
GSE21501_GSM536932	1.435086608	3.171883067	3.187496839
1.751426808	2.573585226	2.41550519	2.751582045
3.338281484	3.073333186	2.713715588	4.21850872
2.423313376	3.407433966	3.852853441	4.307935172
3.603680059	3.143326488	0.739201875	3.444742561
GSE21501_GSM536933	1.580816273	2.359803039	2.921040778
1.823674236	3.574807907	2.577310956	1.613369132
3.936969262	3.060927226	3.86851386	4.439641608
2.500439186	1.841731165	4.067747738	2.508511646
5.344512871	3.391767528	2.622573569	3.645244722
GSE21501_GSM536934	2.068121	3.12563	2.855732
0.8559762	3.046632	3.186622	1.489847
3.316781	2.823345	3.212027	3.851486
2.211435	2.365548	3.7001	3.287516
4.177249	3.032856	2.226263	3.496036
GSE21501_GSM536935	2.003117	3.040309	3.170727
1.407581	2.070558	2.437331	1.794447
3.633037	2.602293	3.347046	3.800727
2.633626	3.235159	3.734175	5.198945
4.741726	3.256533	1.698772	3.779642
GSE21501_GSM536936	1.303488955	1.974245607	3.119905128
1.729935306	2.753228726	2.869697932	2.165597081
3.295382022	3.373723755	1.999908916	3.6150017
2.091365528	2.359132654	3.38019119	4.808967167
6.500947395	2.835768812	2.101351945	3.522118771
GSE21501_GSM536937	1.633683	2.807276	2.086548
1.278725	2.808457	2.589278	1.716529
3.179705	3.08876	3.341184	3.952994
2.271422	2.265407		

4.197378	2.637944	5.727147	3.056211	2.356258	3.001838		
GSE21501_GSM536938		2.029881	2.863672	2.253837	1.137197	2.597335	
2.791343	1.821377	3.440523	2.862644	3.973547	4.07867	2.441588	2.486311
4.080043	4.454189	6.215511	3.023056	1.839162	2.861391		
GSE21501_GSM536939		1.921508343		3.398340656		2.634863367	
1.240225952	2.826504675		2.564104031		1.491524761		
3.60588537	3.157679503		2.753644738		3.689702066		
2.411807183	2.504864803		3.96784818		1.693481147		
3.674524408	3.188602967		1.011782143		3.598414662		
GSE21501_GSM536940		1.991384179		2.898039634		3.957884942	
2.040460726	2.791028541		3.606752382		3.091508673		
2.964200086	3.220374595		2.669809324		3.899043225		
3.206367194	2.69834682		3.795955754		3.223647839		
4.520113462	3.329492868		2.066867729		3.659978034		
GSE21501_GSM536941		2.023472	3.026691	3.743816	1.658928	2.821144	
3.013564	2.468718	3.135706	3.346474	2.901995	3.586036	2.85164	2.448979
3.885061	4.229737	4.512385	2.976703	1.792683	2.89475		
GSE21501_GSM536942		1.78761	2.980323	2.857831	1.830014	3.13683	
2.723982	1.533375	3.073497	3.186203	2.668909	3.440455	2.233308	1.914465
3.281897	3.377683	5.439305	2.611469	1.80341	3.606363		
GSE21501_GSM536943		2.175456	2.659242	2.439732	1.004429	2.961901	
2.910703	1.303392	3.131284	2.608737	3.626687	3.746666	2.281571	2.645448
4.222307	3.440455	5.786158	3.05555	1.453313	3.038225		
GSE21501_GSM536944		2.008055	3.203202	2.218796	1.242079	2.69618	
2.814041	1.94854	4.040445	3.18273	3.768391	3.964856	2.57281	2.745035
4.251669	4.229345	5.04512	3.020465	1.629291	2.91552		
GSE21501_GSM536945		1.776443	3.365109	2.358457	0.971171	3.04281	
3.301331	1.767425	3.769976	2.494581	3.821176	3.992659	2.101004	2.887972
4.127995	4.025522	6.50153	3.068535	1.744383	3.069111		
GSE21501_GSM536946		1.372576	3.152832	3.352888	1.614089	2.890066	
2.456939	1.231245	2.862208	3.415841	3.535226	3.5784	2.058769	2.628291
3.927127	5.126873	3.285876	2.72544	1.702306	3.674341		
GSE21501_GSM536947		1.483958111		2.770683656		3.086961648	
1.331396784	3.013825171		2.872675577		1.778268224		
3.164527641	2.632722159		3.02204907		4.012963829		
2.421158584	2.402281021		3.317336961		3.571942962		
5.825294591	2.770367838		2.269974443		3.253287469		
GSE21501_GSM536948		1.977688	2.937212	2.934064	1.112923	2.569689	
3.07036	1.099405	2.851195	2.663686	2.338816	3.514386	2.076004	2.775221
3.977434	5.997928	3.143033	3.119786	1.998875	3.26369		
GSE21501_GSM536949		1.505969653		2.590470862		2.808147852	
2.000475115	3.03596822		3.06345401		1.571728896		
3.513620141	2.684769508		2.963509405		4.075621555		
2.275915319	2.419049048		3.446246695		2.941550185		

5.664341195

2.736488717

1.648191529

3.597395537

Table S2 39 differentially expressed genes between m6Acluster A and m6Acluster B were remarkable relevance to the prognosis

id	HR	HR.95L	HR.95H	pvalue
IGFBP2	0.863428573684647			0.767749740835227
0.97103113449973	0.0142643092888903			
ANXA1	1.24878513929778	1.09139217094104	1.42887622401244	
0.00122793314946246				
COL8A1	1.16720919219629	1.04081915970768	1.30894717457943	
0.00818932380896084				
VCAN	1.17062717307255	1.04415047888274	1.31242383741674	
0.00692215400980968				
TGM2	1.27163957680644	1.11576519834878	1.44928988257884	
0.000316040321741817				
COL12A1	1.12752436154479	1.01394620554579	1.25382508354342	
0.0267168603681125				
COL5A2	1.17757414231052	1.04777760521048	1.3234496077627	
0.00608375326857736				
GREM1	1.1398386502359	1.04645593143059	1.24155457439611	
0.00268938731643593				
COL3A1	1.14343136099867	1.02438543120323	1.27631186220558	
0.0168723395795536				
MFAP5	1.12639919135158	1.025125558512	1.23767779248345	
0.0132782649043387				
COL1A2	1.12714181625645	1.01692236075449	1.24930744271501	
0.0226326961448307				
SULF1	1.11899299422324	1.01662609452879	1.23166750082396	
0.0216286068136121				
MUC16	1.16243325970851	1.05202809313457	1.28442490470995	
0.00311566193236833				
UCA1	1.21635893064114	1.11795063074406	1.32342968236955	
5.3576695305364e-06				
GABRP	1.09626001598457	1.02113352978482	1.17691368228771	
0.0111694857917737				
SCEL	1.18389640703047	1.08471337752364	1.29214844365568	
0.000155884430462082				
FNDC1	1.10747776243467	1.00569396923032	1.21956284099622	
0.0379500111901132				
INHBA	1.1522658591013	1.02651332946691	1.29342364286683	
0.016226614648026				
GJB2	1.24269700782366	1.11460851475243	1.38550516420277	
9.04315123561753e-05				
THBS2	1.11293572691079	1.0128884681411	1.22286507467859	
0.0259855985054849				
KRT7	1.31761556660312	1.18220964230632	1.46853038515905	

6.18470147637641e-07
PSCA 1.12391991974616 1.05547386871431 1.19680460449574
0.000268339757424185
FN1 1.1586473913301 1.04739806217301 1.2817130620338
0.00424825163144701
KLK10 1.25071458243962 1.12639010255014 1.38876128544238
2.81401613543722e-05
DKK1 1.19562876620166 1.10028444016648 1.29923508356858
2.50980621862807e-05
COL10A1 1.12960905448025 1.03750623012733 1.22988814805204
0.00497793101338779
COL11A1 1.13304092753621 1.05046777578157 1.22210483088541
0.00121538341716074
POSTN 1.10622078627686 1.01369416833413 1.2071929248661
0.0235031291387653
COL17A1 1.21802213784362 1.11846756882067 1.32643803864734
5.80330458175875e-06
EPYC 1.10608061606138 1.02121428957295 1.19799961841341
0.0133101556346393
MSLN 1.14424610732634 1.06156797705 1.23336346087786
0.000429361609518174
CST6 1.13897927725561 1.05042556502939 1.2349983065972
0.00162559986530347
BEX1 0.898201897172069 0.835962198947319
0.965075513102651 0.00338735729665407
LY6D 1.16187203613772 1.08675650883178 1.24217947386389
1.08366034393406e-05
CXCL5 1.1199031768702 1.04689644385236 1.19800113270882
0.000993219264096411
KRT6A 1.10907363872026 1.04115885973352 1.18141849786404
0.00132273499099849
KLK7 1.12785684397166 1.05364164929439 1.20729952289339
0.000531107212642063
CEACAM6 1.15170153758496 1.06177545837255 1.24924382195519
0.000661444763027247
S100P 1.11769627500685 1.04711174187589 1.1930388259482
0.000828448327271783