

Metabolic Reprogramming and Prognostic Insights in Molecular Landscapes

Driven by Glycolysis in Ovarian Cancer

Mingwei Wang^{1#}, Qiaohui Ying^{2#}, Yuncan Xing³, Shuchang Dai¹, Jue Wang¹, Zhong Liu^{1*}

Affiliations

1. Institute of Blood Transfusion, Chinese Academy of Medical Sciences and Peking Union Medical College, Chengdu 610052, China
2. Institute of Oral Basic Research, School and Hospital of Stomatology, Cheeloo College of Medicine, Shandong University, Jinan 250012, China
3. National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100020, China.

Mingwei Wang and Qiaohui Ying contributed equally to this work

Supplementary materials

Supplementary tables

Supplementary table 1. Differential analysis results of 457 GRGs

Gene	conMean	treatMean	logFC	pValue	fdr
LINC01224	0.04895983	2.08313507	2.03417524	1.6167E-47	1.3145E-46
KLK10	3.22045862	5.44911263	2.228654	3.7454E-28	7.0748E-28
SLC2A1	3.14548337	6.1434471	2.99796373	1.2315E-43	4.6745E-43
MT-ND1	10.2476416	12.506313	2.25867141	1.6593E-41	5.3466E-41
PHLDA2	1.02816642	4.35483651	3.32667008	4.4221E-47	3.0351E-46
MIR100HG	5.60823179	2.48600976	-3.122222	6.5129E-45	2.8351E-44
LYZ	1.74082791	4.66694064	2.92611272	3.5862E-36	8.8087E-36
NR2F1	5.05839302	2.33147483	-2.7269182	2.4268E-44	9.894E-44
FGFR4	3.76138979	1.66198271	-2.0994071	3.2166E-39	9.0505E-39
SPI1	1.65453047	4.06476181	2.41023134	7.2182E-42	2.3799E-41
NRK	3.34519668	0.4403584	-2.9048383	1.0335E-46	6.3412E-46
SLPI	1.64482244	10.1797029	8.53488051	1.0231E-47	9.2008E-47
PDCD4	6.4029113	4.20771421	-2.1951971	3.8336E-46	2.0567E-45
GNG4	3.50099271	0.79334871	-2.707644	1.1219E-42	3.9269E-42
CDO1	2.69576547	0.67321815	-2.0225473	6.4045E-42	2.1203E-41
STAT1	3.23857713	5.55212876	2.31355163	2.9819E-47	2.1685E-46

ADAMTS9-AS2	2.6308394	0.12822825	-2.5026111	2.1634E-48	4.5929E-47
NEK2	0.16029567	3.1030763	2.94278063	2.2637E-48	4.5929E-47
CTHRC1	1.34249219	4.7135602	3.37106801	4.4574E-46	2.3527E-45
RBM4	5.54067657	2.11976341	-3.4209132	2.0546E-48	4.5929E-47
P3H3	4.70303919	2.40346085	-2.2995783	1.9323E-44	7.9884E-44
MUC1	2.40652204	7.00362134	4.5970993	1.5876E-46	9.3504E-46
SLC25A5	5.61024706	7.75171795	2.14147089	6.7159E-47	4.3535E-46
KLF4	4.43992274	2.27725768	-2.1626651	3.1939E-38	8.5962E-38
NUP210	0.75039279	3.82993938	3.07954659	2.8713E-48	4.6185E-47
FUS	7.41292061	5.11614669	-2.2967739	2.0806E-48	4.5929E-47
PDIA4	4.43796937	6.80146684	2.36349746	3.2799E-47	2.3537E-46
RACGAP1	1.09805028	3.7522947	2.65424441	2.658E-48	4.5929E-47
RPL14	8.85041791	6.72749365	-2.1229243	2.9431E-48	4.6229E-47
TYMP	2.11878583	4.27974515	2.16095932	1.416E-33	3.1465E-33
DPP3	2.2591004	4.37867184	2.11957145	3.6184E-48	4.8578E-47
FBP1	0.64595637	3.02149995	2.37554358	8.0394E-45	3.4695E-44
RHBDF1	5.18259125	2.69187089	-2.4907204	3.6186E-48	4.8578E-47
CIRBP	8.21770476	4.13695501	-4.0807497	2.054E-48	4.5929E-47
TEAD4	1.43504873	3.97993309	2.54488436	1.2027E-46	7.267E-46
SKP1	7.65319543	4.30643273	-3.3467627	2.0541E-48	4.5929E-47
EIF4A1	7.61319277	1.64723451	-5.9659583	2.0544E-48	4.5929E-47
ERBB3	0.92360877	4.15318592	3.22957716	4.0919E-44	1.6273E-43
LEFTY2	3.384337	0.58133164	-2.8030054	1.2495E-42	4.3553E-42
CYC1	5.04519754	7.26375571	2.21855817	4.3573E-48	5.3364E-47
TOP2A	0.47460324	4.04271758	3.56811434	2.6924E-48	4.5929E-47
MT-ND5	8.56541341	10.5829198	2.0175064	1.3816E-36	3.4474E-36
DSP	0.95792287	5.34216571	4.38424284	2.7297E-46	1.5136E-45
ATP1A2	2.57789158	0.45286846	-2.1250231	2.2102E-40	6.6296E-40
SLC25A27	5.54601243	1.54036356	-4.0056489	2.5574E-48	4.5929E-47
NCAPH	0.33435955	2.86641787	2.53205833	4.2215E-48	5.2569E-47
IRX3	0.63426758	2.74956214	2.11529455	1.1265E-24	1.9579E-24
GFPT2	3.95730609	1.48254368	-2.4747624	1.1435E-46	6.9563E-46
DEPDC1	0.14246537	2.17754566	2.03508028	3.4814E-48	4.7812E-47
FOXJ1	0.18861833	4.63851846	4.44990013	7.8774E-48	7.6545E-47
SUN2	5.91359459	3.49904136	-2.4145532	2.0355E-47	1.585E-46
EGLN2	5.01481397	1.9018098	-3.1130042	2.0813E-48	4.5929E-47
MATR3	3.99820487	0.40184654	-3.5963583	2.0546E-48	4.5929E-47
CENPA	0.22338808	3.11833188	2.8949438	4.2639E-48	5.2753E-47
LMCD1	5.03084107	2.29398759	-2.7368535	2.1148E-47	1.6344E-46
RPL13	12.0413425	8.25094028	-3.7904023	2.5456E-48	4.5929E-47
DHRS2	2.92090181	0.38409382	-2.536808	1.8621E-41	5.9812E-41
CYP11A1	3.91861578	1.01464664	-2.9039691	2.4842E-42	8.4701E-42
NME2	7.64445821	4.9014227	-2.7430355	2.0542E-48	4.5929E-47
DMTN	1.34520496	3.37853784	2.03333288	2.5446E-40	7.6129E-40
ADCY4	2.84519103	0.80961599	-2.035575	2.1188E-43	7.8842E-43
JUP	4.25589008	7.25191779	2.99602771	1.9542E-46	1.1244E-45
CDKN1A	6.21859151	4.02581622	-2.1927753	9.3307E-42	3.0542E-41
ADCY6	4.33873099	2.13126868	-2.2074623	6.0456E-48	6.4546E-47

MISP	0.25240514	3.9011643	3.64875916	1.461E-47	1.2132E-46
TPX2	0.35651533	5.0706413	4.71412597	2.1632E-48	4.5929E-47
ALDH1A1	5.95992656	2.907903	-3.0520236	3.5455E-45	1.6012E-44
UNG	2.85669245	5.00240657	2.14571412	6.0451E-48	6.4546E-47
TPM1	7.20534734	3.48457327	-3.7207741	2.0546E-48	4.5929E-47
CFH	6.2454667	2.5127898	-3.7326769	2.3471E-46	1.3239E-45
HSPB7	3.51351461	0.90420321	-2.6093114	1.7878E-45	8.4668E-45
RHOT2	5.93201669	3.86912414	-2.0628926	2.9459E-48	4.6229E-47
RPL22	8.19517854	5.86677615	-2.3284024	5.7044E-48	6.2233E-47
GATM	4.99688922	1.66272762	-3.3341616	5.6576E-46	2.9353E-45
EIF4EBP1	3.67196492	6.03481297	2.36284805	1.7562E-46	1.0211E-45
MT-TY	0	5.51172793	5.51172793	9.9684E-49	4.5929E-47
NDUFA11	6.59169738	3.32668667	-3.2650107	2.0547E-48	4.5929E-47
XIST	7.5333358	1.6500599	-5.8832759	2.0546E-48	4.5929E-47
RCC2	3.26552862	6.01972746	2.75419885	2.0545E-48	4.5929E-47
GPT2	1.18716524	3.34260307	2.15543783	2.3178E-46	1.3105E-45
TXNDC5	4.92049689	2.02539439	-2.8951025	2.5246E-48	4.5929E-47
FCGR3A	1.44024564	3.84983021	2.40958457	1.5416E-36	3.8414E-36
GAS5	8.47993719	6.17407413	-2.3058631	1.9137E-45	9.0334E-45
ALDH2	5.62069425	2.91164257	-2.7090517	7.233E-48	7.2289E-47
PIK3C3	3.74817418	1.49857017	-2.249604	2.2485E-48	4.5929E-47
OASL	0.2934579	2.48331356	2.18985566	4.2456E-44	1.6847E-43
CBX7	4.86243839	1.61649875	-3.2459396	2.1634E-48	4.5929E-47
PLK1	1.16540576	3.80642454	2.64101878	1.5773E-47	1.287E-46
FKBP5	5.34757758	2.37318383	-2.9743937	2.1578E-43	8.0228E-43
L1CAM	0.75534219	2.93595054	2.18060835	1.0172E-33	2.2706E-33
GLUL	8.28844501	5.62028092	-2.6681641	5.6686E-48	6.1934E-47
NEK9	5.09160555	2.50760813	-2.5839974	2.3071E-48	4.5929E-47
S100A4	3.81369653	6.61229114	2.79859461	3.5188E-34	7.9825E-34
PDLIM1	3.64203864	6.13418338	2.49214474	1.9426E-40	5.8533E-40
MIR25	0	2.77034449	2.77034449	1.7188E-48	4.5929E-47
FTL	9.13857998	11.6043305	2.46575052	2.2971E-48	4.5929E-47
PLD1	3.37472455	0.8296429	-2.5450817	1.3025E-47	1.1055E-46
DST	6.11290222	0.88592286	-5.2269794	2.0547E-48	4.5929E-47
MGME1	1.8253418	3.93018646	2.10484466	2.7982E-48	4.5929E-47
PPP1CA	4.03071605	6.61735425	2.5866382	2.2769E-48	4.5929E-47
GPX1	5.78879647	8.63954728	2.85075081	2.0502E-48	4.5929E-47
FOXQ1	0.08410905	4.23670665	4.15259761	1.3551E-47	1.1408E-46
ACTA2	7.56360358	5.18215266	-2.3814509	6.7485E-31	1.3757E-30
HSD11B1	4.2111998	1.27057794	-2.9406219	1.828E-44	7.5691E-44
ADH1B	5.35425634	0.65955136	-4.694705	6.3993E-46	3.278E-45
MYH11	5.81595881	0.84161809	-4.9743407	1.5774E-47	1.287E-46
FLCN	4.80941575	1.72900053	-3.0804152	2.0546E-48	4.5929E-47
CCL5	1.12240617	3.83251114	2.71010497	1.3504E-37	3.5188E-37
ATG16L2	4.59271643	1.51984409	-3.0728723	2.1913E-48	4.5929E-47
CDKN1C	6.34676174	4.06352193	-2.2832398	1.5361E-40	4.6595E-40
ANPEP	0.92355439	3.03038696	2.10683257	1.9768E-34	4.5247E-34
DHCR24	3.32011379	7.27617149	3.9560577	2.1952E-45	1.0268E-44

NDC1	1.44434089	3.74644763	2.30210674	2.0547E-48	4.5929E-47
EPB41L4A-AS1	6.37813318	2.92421934	-3.4539138	8.0127E-48	7.7419E-47
ZNF410	4.16819033	0.52463429	-3.643556	2.0548E-48	4.5929E-47
S100A2	0.96751246	3.71433027	2.74681781	1.2E-40	3.6668E-40
TK1	0.73331453	5.36682537	4.63351085	2.0812E-48	4.5929E-47
CLK1	6.91859399	3.58133819	-3.3372558	2.0547E-48	4.5929E-47
CASP9	4.57230835	2.19768332	-2.374625	3.8822E-46	2.0816E-45
NACA	9.27186683	5.92296409	-3.3489027	2.0531E-48	4.5929E-47
CBS	4.37163696	0.67297272	-3.6986642	3.3935E-48	4.7656E-47
BAK1	2.02581805	4.64150558	2.61568754	2.3071E-48	4.5929E-47
CDC20	0.50194061	5.4516229	4.94968229	2.2483E-48	4.5929E-47
AKT3	3.60524909	1.24924588	-2.3560032	4.5142E-44	1.7879E-43
TACC3	1.65856695	3.68338564	2.02481869	2.835E-46	1.5648E-45
LINC01503	1.2911085	3.72787069	2.43676219	1.2506E-42	4.3584E-42
IL4I1	0.36305592	4.73159236	4.36853644	4.6183E-48	5.5073E-47
INO80B-WBP1	3.15299535	0.0384804	-3.1145149	1.6541E-48	4.5929E-47
DDAH1	1.38355036	3.45397233	2.07042197	4.5706E-46	2.409E-45
PFKM	5.30538154	3.28102567	-2.0243559	4.6523E-47	3.1719E-46
SNRPB	5.4639712	8.0217756	2.5578044	2.0527E-48	4.5929E-47
BAMBI	4.58294143	1.59327695	-2.9896645	1.567E-41	5.0589E-41
CEBPA	0.66789306	2.7336249	2.06573184	1.6708E-43	6.2597E-43
NAP1L1	7.86950661	4.66758625	-3.2019204	2.0543E-48	4.5929E-47
HNRNPH1	7.77298233	4.68536381	-3.0876185	2.0539E-48	4.5929E-47
MKI67	0.28951745	3.28309122	2.99357377	2.9451E-48	4.6229E-47
CCND1	1.57093946	4.8533586	3.28241913	1.3585E-45	6.5745E-45
GSS	2.82528857	4.88721181	2.06192324	2.2197E-48	4.5929E-47
CALR	7.00573349	9.06638361	2.06065012	7.2162E-48	7.2289E-47
GAPDH	8.48099543	10.8543186	2.37332319	3.0533E-48	4.677E-47
KIT	2.83037165	0.54212516	-2.2882465	2.0051E-44	8.2801E-44
SPP1	1.83093836	7.44040276	5.6094644	2.0091E-47	1.5676E-46
MYCN	0.83852388	2.8446271	2.00610322	5.1879E-32	1.0918E-31
MACF1	5.87697061	2.52712276	-3.3498479	2.5247E-48	4.5929E-47
CHI3L1	1.65616058	6.21047101	4.55431043	1.9294E-41	6.1923E-41
PPARG	2.79892415	0.75089051	-2.0480336	2.1824E-45	1.0211E-44
MYBL2	0.26288315	5.0162575	4.75337435	2.1909E-48	4.5929E-47
EZR	4.19725838	6.42327683	2.22601845	3.5548E-46	1.9207E-45
PKP3	0.43487368	4.66461739	4.22974371	1.6382E-45	7.8085E-45
DYRK1B	2.58759861	4.91180858	2.32420997	2.1633E-48	4.5929E-47
NGF	3.08970389	1.00400165	-2.0857022	1.1093E-41	3.6113E-41
IFIT3	2.13240768	4.79262723	2.66021955	2.1764E-42	7.4424E-42
ATOH8	3.41703681	0.96013744	-2.4568994	1.2241E-44	5.1663E-44
FHL2	7.53814889	3.51982825	-4.0183206	1.2695E-47	1.0866E-46
MXRA7	5.98118816	3.70335822	-2.2778299	3.1415E-48	4.677E-47
SERPINA1	1.46269677	3.92624876	2.46355199	1.2907E-37	3.3671E-37
VIM	9.92752646	7.33726722	-2.5902592	6.4676E-45	2.8174E-44
KIF2C	0.58370348	3.54071206	2.95700859	3.4374E-48	4.7812E-47
GNG5	5.11615749	7.18225041	2.06609292	2.3062E-48	4.5929E-47
MIR503HG	5.16839671	1.19624935	-3.9721474	1.0735E-46	6.5691E-46

GATA6-AS1	3.54012909	1.08506213	-2.455067	5.6977E-44	2.2286E-43
MT-CO1	11.0498196	13.1791746	2.12935504	1.9455E-26	3.5278E-26
LAMB3	0.66420942	3.99311125	3.32890183	6.8279E-46	3.4775E-45
DIRAS3	4.29437935	1.41080756	-2.8835718	2.7306E-45	1.2579E-44
LINC01139	0.69258676	3.45087023	2.75828347	2.9076E-37	7.4593E-37
CA9	0.59886825	2.77732262	2.17845437	4.9035E-35	1.1478E-34
MAPK10	2.98462453	0.44322902	-2.5413955	4.0102E-48	5.1455E-47
GALT	5.00895046	2.52213467	-2.4868158	2.4605E-48	4.5929E-47
ACACB	3.35678493	1.13266607	-2.2241189	5.1835E-48	5.8723E-47
KLF2	5.80421626	3.41437014	-2.3898461	1.2508E-38	3.4305E-38
PCNA	3.78590473	6.51441927	2.72851454	2.6572E-48	4.5929E-47
PHKA2	4.47512732	2.44760875	-2.0275186	1.7467E-47	1.4031E-46
MAOA	4.14048341	1.34421601	-2.7962674	4.5455E-45	2.0218E-44
RPL10	11.997211	9.11988781	-2.8773232	2.3313E-48	4.5929E-47
TRIP13	0.77328349	3.47567159	2.70238811	2.0814E-48	4.5929E-47
MAP3K5	4.30764498	1.77896111	-2.5286839	1.8382E-47	1.4607E-46
LINC-PINT	3.98704255	1.56440184	-2.4226407	4.8329E-47	3.2711E-46
SMARCA2	5.66426712	3.0751765	-2.5890906	1.1463E-47	1.0022E-46
RHOD	2.57949069	4.59131995	2.01182926	4.4192E-43	1.6062E-42
RPL27A	9.57280769	7.50039159	-2.0724161	1.3245E-47	1.1221E-46
CSE1L	3.42038507	5.58966245	2.16927738	2.0545E-48	4.5929E-47
PMM1	4.80216526	2.02857605	-2.7735892	2.1356E-48	4.5929E-47
NR2F2	6.67240495	3.94698623	-2.7254187	7.3428E-47	4.7178E-46
MPST	5.27419807	3.10539502	-2.168803	8.8199E-48	8.2885E-47
TTN-AS1	3.34268816	0.2404626	-3.1022256	2.0547E-48	4.5929E-47
ISG15	2.59608291	7.08256388	4.48648097	4.9563E-47	3.3448E-46
PCBP2	7.82176787	5.71936358	-2.1024043	2.1345E-48	4.5929E-47
APOA1	2.88845405	5.34137703	2.45292298	1.2929E-23	2.1947E-23
KRT8	2.29116526	8.23020938	5.93904412	2.134E-48	4.5929E-47
CYBB	1.08034319	3.35519001	2.27484682	3.4199E-38	9.1952E-38
ARL6IP4	6.7741809	1.29733781	-5.4768431	2.0546E-48	4.5929E-47
BAIAP2L1	1.06568993	4.02802884	2.96233892	7.1409E-48	7.1794E-47
ARGLU1	6.77565948	4.34138249	-2.434277	3.1011E-48	4.677E-47
UCA1	0.15085452	3.06584583	2.91499131	4.6151E-43	1.674E-42
RPL23	9.99120842	6.83473187	-3.1564765	1.9537E-47	1.5348E-46
EPHA2	1.77600505	4.0261737	2.25016866	7.3719E-45	3.1926E-44
ASPH	4.34201649	2.3243142	-2.0177023	3.2652E-48	4.721E-47
MT-RNR2	9.03666585	12.9292693	3.89260349	1.7479E-48	4.5929E-47
OVOL2	0.0935639	3.36017628	3.26661238	6.1317E-48	6.5098E-47
ZNF185	1.79070463	3.94008399	2.14937935	1.52E-45	7.2976E-45
OAS3	1.45376291	4.09394295	2.64018004	1.461E-43	5.5094E-43
WSB1	6.37025769	3.14910114	-3.2211565	2.2776E-48	4.5929E-47
NMU	0.19007495	3.89930564	3.7092307	1.2641E-46	7.5991E-46
HBA1	3.99477722	1.42282673	-2.5719505	2.657E-31	5.4795E-31
PGAM5	1.98438842	4.00528219	2.02089377	2.9084E-48	4.6185E-47
ACTA2-AS1	2.93100766	0.62053497	-2.3104727	6.3633E-44	2.4738E-43
IFI27	4.73054798	6.80393695	2.07338897	1.0716E-24	1.8639E-24
ANXA6	6.24283544	3.94693965	-2.2958958	1.1317E-47	9.9372E-47

NR2F2-AS1	3.87714051	0.15956664	-3.7175739	2.0814E-48	4.5929E-47
AK1	5.77757926	2.07403102	-3.7035482	2.0547E-48	4.5929E-47
CYBA	4.16255796	6.50166201	2.33910405	4.2709E-45	1.9083E-44
UBE2C	0.58453754	6.20162667	5.61708912	2.2195E-48	4.5929E-47
CDCA5	0.54318104	3.42937342	2.88619238	4.1145E-48	5.2039E-47
PLA2G2A	6.31377404	1.23189944	-5.0818746	6.8308E-43	2.4359E-42
SNHG12	5.14983489	2.4922854	-2.6575495	2.658E-48	4.5929E-47
NDUFA1	5.14043892	7.36158991	2.22115099	4.7961E-48	5.6329E-47
CTSH	5.88458334	3.83802916	-2.0465542	7.1786E-46	3.644E-45
ANAPC4	3.94674645	1.9185161	-2.0282304	2.0546E-48	4.5929E-47
DNAJC7	4.97205902	2.47644771	-2.4956113	2.0547E-48	4.5929E-47
GSDME	3.21298458	0.82119214	-2.3917924	3.7128E-48	4.9272E-47
KLK6	0.45761938	6.47517031	6.01755093	6.2258E-47	4.0671E-46
KPNA2	1.7784004	5.72795152	3.94955112	2.3069E-48	4.5929E-47
PDGFRB	5.7750472	3.14270257	-2.6323446	1.3417E-45	6.5016E-45
KLF5	1.36958875	5.07247532	3.70288657	2.6956E-46	1.496E-45
IDO1	0.37828829	2.56826921	2.18998092	8.5849E-36	2.0714E-35
AMT	5.1724089	1.60033595	-3.572073	4.0102E-48	5.1455E-47
PRKCD	2.52717174	4.92714233	2.39997059	5.9682E-48	6.4098E-47
GNB3	3.08181674	0.48006486	-2.6017519	1.1463E-47	1.0022E-46
FOXM1	0.76360407	4.23424633	3.47064226	2.8345E-48	4.6115E-47
NDUFS6	3.71917298	5.80708155	2.08790857	7.2323E-48	7.2289E-47
TYMS	1.66170693	3.92542338	2.26371644	9.7079E-48	8.8658E-47
UCP2	1.60543795	7.29467391	5.68923595	2.0541E-48	4.5929E-47
HMMR	0.27477677	2.68560649	2.41082972	2.7983E-48	4.5929E-47
ECT2	0.79021116	3.9536167	3.16340554	2.2485E-48	4.5929E-47
MEST	3.0058383	5.1700455	2.1642072	2.0741E-42	7.1052E-42
DDX17	7.65401255	5.55032862	-2.1036839	3.4804E-48	4.7812E-47
EEF1A1	12.6775429	10.2229432	-2.4545997	5.4805E-47	3.6446E-46
RPL18	10.3476705	8.02934675	-2.3183237	3.135E-48	4.677E-47
PSMD9	4.07935685	1.77812766	-2.3012292	2.0547E-48	4.5929E-47
STAT5B	4.99989204	2.73828483	-2.2616072	2.3371E-48	4.5929E-47
SNHG5	7.8736397	5.16383486	-2.7098048	4.8016E-47	3.2582E-46
CDKN3	0.88684792	3.3543633	2.46751538	1.1174E-47	9.853E-47
ARF6	2.73193041	5.48711346	2.75518306	1.3023E-47	1.1055E-46
IRF6	0.91553442	3.79090198	2.87536755	4.0146E-45	1.8012E-44
LENG8	7.25202739	4.70101957	-2.5510078	3.9557E-46	2.1167E-45
PTTG1	1.03807726	4.66944376	3.6313665	6.5286E-48	6.75E-47
GLDC	0.17437923	2.80074605	2.62636682	3.5014E-45	1.5841E-44
FHL1	5.47400929	2.83063222	-2.6433771	5.9348E-45	2.5987E-44
RPL36A	9.44167842	5.54856146	-3.893117	2.0528E-48	4.5929E-47
XBP1	5.04246708	0	-5.0424671	6.914E-102	4.941E-99
ICMT	2.34392011	4.36400195	2.02008184	1.4062E-47	1.1768E-46
SRSF5	7.91613506	4.82194888	-3.0941862	2.0543E-48	4.5929E-47
PRKCI	2.90080725	5.39119767	2.49039043	7.2326E-48	7.2289E-47
U2AF1	5.02495191	0.24277662	-4.7821753	2.0547E-48	4.5929E-47
PODXL2	2.31481526	4.53146888	2.21665362	2.9746E-42	1.0072E-41
ITGB4	2.07669605	5.27633188	3.19963582	1.082E-42	3.7929E-42

SCARB1	5.58655173	2.94113458	-2.6454172	4.3509E-44	1.7251E-43
ADCY3	5.40132724	2.84657973	-2.5547475	3.3074E-48	4.7414E-47
MAOB	5.63847332	2.6057163	-3.032757	8.964E-44	3.4459E-43
SPTBN1	5.60780126	3.44155246	-2.1662488	3.1014E-48	4.677E-47
RAPGEF3	5.69577584	2.54060617	-3.1551697	7.5163E-48	7.4005E-47
CDK1	1.07928454	3.96438754	2.885103	5.1834E-48	5.8723E-47
EIF3L	7.9910379	5.24918994	-2.741848	2.9078E-48	4.6185E-47
MPRIP	5.24359749	2.65517818	-2.5884193	2.0546E-48	4.5929E-47
PMAIP1	0.39316704	2.40957334	2.0164063	8.6574E-47	5.4377E-46
CDCA8	0.47276038	3.9184703	3.44570992	2.1913E-48	4.5929E-47
CRTAC1	0.53467978	2.98263094	2.44795116	7.6208E-34	1.7092E-33
HSD17B4	5.3338487	3.27931254	-2.0545362	2.1355E-48	4.5929E-47
PCLAF	0.44347159	3.03879128	2.59531969	1.3362E-47	1.1299E-46
DARS2	1.46620682	3.78571334	2.31950652	2.0547E-48	4.5929E-47
NEAT1	8.71695483	3.7805642	-4.9363906	2.1079E-48	4.5929E-47
GSTM3	6.41209484	2.27022762	-4.1418672	9.5845E-48	8.7637E-47
CARMN	3.14167661	0.15275405	-2.9889226	2.0548E-48	4.5929E-47
IGLV3-19	0.92688422	3.51496312	2.5880789	2.2408E-17	3.3305E-17
CXCL1	0.72920778	2.84152379	2.11231601	4.9222E-29	9.5239E-29
CLDN1	1.6552398	4.83625616	3.18101636	7.4814E-42	2.4628E-41
LMNB1	1.33200473	4.13575409	2.80374936	2.3979E-48	4.5929E-47
RPL34	10.3073428	6.96363616	-3.3437066	2.1052E-48	4.5929E-47
F2RL1	0.37200847	3.13452877	2.7625203	4.7384E-48	5.5824E-47
FGFR1	6.30426147	3.82931911	-2.4749424	6.1761E-46	3.1726E-45
SERPINA3	4.35011786	0.17891348	-4.1712044	7.1077E-48	7.1729E-47
MUC16	0.34333053	4.04905875	3.70572822	9.0695E-46	4.5115E-45
PDK4	6.33555216	2.35954416	-3.976008	9.2236E-48	8.543E-47
SNCA	3.43828788	0.8807326	-2.5575553	1.9926E-46	1.1433E-45
CLDN6	0.0348824	4.64304473	4.60816233	4.2536E-48	5.2753E-47
NR2F1-AS1	3.62212606	0.68966644	-2.9324596	3.0619E-48	4.677E-47
ATXN3	3.0970086	1.08943435	-2.0075743	2.0547E-48	4.5929E-47
LSR	1.99236924	6.91544289	4.92307365	2.1348E-48	4.5929E-47
RNU1-4	2.2126282	0.14774859	-2.0648796	2.5537E-55	1.2823E-52
HDGF	5.59590309	7.69211319	2.0962101	2.2468E-48	4.5929E-47
TNF	0.12482543	2.14440613	2.0195807	5.7313E-46	2.9702E-45
CDH1	0.9897836	5.26012298	4.27033939	3.1747E-46	1.7323E-45
IGF2BP2	1.83612104	4.29034732	2.45422628	1.2335E-36	3.0837E-36
SKA3	0.19841598	2.60837567	2.40995969	2.2776E-48	4.5929E-47
TRMT10C	2.19413951	4.54565688	2.35151737	2.0546E-48	4.5929E-47
TRHDE-AS1	2.35612013	0.19831312	-2.157807	1.6714E-46	9.7961E-46
TUBB4B	4.98359295	7.69334917	2.70975622	8.6488E-48	8.181E-47
CEP55	0.23579513	3.52549992	3.28970479	2.458E-48	4.5929E-47
ETFB	4.65900613	2.5972835	-2.0617226	2.8345E-48	4.6115E-47
SDHC	5.35874831	3.31988632	-2.038862	2.0546E-48	4.5929E-47
SF3B1	7.10272015	4.87912593	-2.2235942	2.4287E-48	4.5929E-47
C12orf57	7.77395279	5.73901941	-2.0349334	2.9413E-45	1.3486E-44
UBE2T	0.72296523	4.85361225	4.13064703	2.1356E-48	4.5929E-47
TNS2	6.82456183	3.44536401	-3.3791978	2.3978E-48	4.5929E-47

KRT8P3	0.11289336	3.06676655	2.95387319	2.1702E-48	4.5929E-47
ANK2	3.00433724	0.6357765	-2.3685607	6.8062E-47	4.4045E-46
IDH2	3.04799084	6.0902499	3.04225905	1.1985E-47	1.0388E-46
SPC25	0.51910971	2.96092232	2.44181261	5.9685E-48	6.4098E-47
GPAT3	2.92304727	0.66056195	-2.2624853	7.6281E-47	4.8652E-46
ALDH18A1	2.86761471	5.03407124	2.16645653	2.0546E-48	4.5929E-47
PDZRN3	4.77222272	1.89552758	-2.8766951	1.0349E-47	9.2753E-47
ASS1	4.89485157	7.79606697	2.90121539	1.3338E-44	5.6112E-44
PFN1	6.75889246	9.18472084	2.42582838	2.1855E-48	4.5929E-47
GABBR1	5.57808994	1.76765424	-3.8104357	6.3635E-48	6.6495E-47
RPL26	10.4613769	6.77170469	-3.6896722	2.051E-48	4.5929E-47
GRHL2	0.18236618	3.08583638	2.9034702	8.1247E-47	5.1372E-46
MEG3	8.70149637	1.30549406	-7.3960023	2.0544E-48	4.5929E-47
MECOM	1.06922552	3.92064219	2.85141666	3.7859E-46	2.0329E-45
GGH	1.38247044	3.63459866	2.25212822	9.7651E-44	3.7376E-43
SFN	0.63686297	4.41616649	3.77930352	1.6259E-44	6.7685E-44
RUFY3	5.19886599	1.72697864	-3.4718873	2.0547E-48	4.5929E-47
AIFM1	2.68582476	4.75732755	2.0715028	1.8856E-47	1.4904E-46
SLX1A-SULT1A3	2.72713064	0.05469018	-2.6724405	2.0532E-48	4.5929E-47
LPAR3	0.70311564	4.33641639	3.63330075	1.8474E-46	1.0683E-45
GTF2I	5.5776072	3.12904497	-2.4485622	2.3673E-48	4.5929E-47
MT-TF	0	3.1861224	3.1861224	5.0824E-48	5.8145E-47
THEM6	1.68930177	4.99301999	3.30371822	2.0546E-48	4.5929E-47
CALCOCO1	6.10585849	3.50454033	-2.6013182	5.0522E-48	5.8145E-47
ACADVL	7.97901289	5.11168405	-2.8673288	5.8912E-48	6.3465E-47
RPL17	10.3840013	5.94515356	-4.4388477	2.0511E-48	4.5929E-47
UNC5B-AS1	0.35982827	3.68132077	3.32149249	1.3049E-46	7.8221E-46
VAPA	5.85104401	3.84337947	-2.0076645	2.2197E-48	4.5929E-47
THOC1	4.43459258	1.85773175	-2.5768608	2.4924E-48	4.5929E-47
RUNX3	0.40677381	2.76720078	2.36042697	1.2356E-42	4.3078E-42
PSMA3-AS1	4.89040862	2.20749214	-2.6829165	2.0547E-48	4.5929E-47
HAGLR	1.00107963	3.55907583	2.5579962	3.6412E-32	7.7077E-32
SNRNP70	7.57469734	5.03352483	-2.5411725	4.6173E-48	5.5073E-47
ZSCAN18	5.65993127	2.53862547	-3.1213058	2.0547E-48	4.5929E-47
RNU1-1	2.2126282	0.19001459	-2.0226136	4.4411E-50	1.8753E-47
DCN	9.23121152	4.14438175	-5.0868298	2.081E-48	4.5929E-47
NUMA1	6.68250596	4.42827737	-2.2542286	1.1244E-47	9.9062E-47
RAP2B	1.59881624	3.61047586	2.01165962	4.5938E-47	3.1378E-46
LINC00958	0.07566045	2.55648028	2.48081983	1.085E-46	6.6374E-46
USP15	4.38612327	1.46104254	-2.9250807	2.0547E-48	4.5929E-47
NR4A1	8.43842008	3.08813047	-5.3502896	1.0753E-47	9.5638E-47
NUDT4	5.3210359	2.33417857	-2.9868573	1.0482E-47	9.3765E-47
ATP6V0A1	4.54543907	2.36512543	-2.1803136	2.0546E-48	4.5929E-47
MRPS34	4.14967901	6.26069611	2.1110171	2.7617E-48	4.5929E-47
EFHD2	3.4287376	5.5290752	2.1003376	1.1317E-47	9.9372E-47
IGKV1-5	1.13688359	4.40180796	3.26492437	2.1284E-21	3.4416E-21
TRIM14	1.286994	3.29700855	2.01001456	1.4721E-46	8.7324E-46
MSTO1	4.78843805	2.16585977	-2.6225783	2.0547E-48	4.5929E-47

PDZK1IP1	0.50186822	5.00802511	4.50615689	9.3366E-46	4.6323E-45
HLF	3.64192718	0.344721	-3.2972062	3.3074E-48	4.7414E-47
RPN1	5.00770988	7.19773236	2.19002248	2.08E-48	4.5929E-47
CORO2A	0.29759013	2.892508	2.59491787	3.8093E-48	4.9881E-47
ADRB3	2.72873731	0.09645327	-2.632284	1.0815E-47	9.6139E-47
SNHG1	6.54020057	4.3568322	-2.1833684	5.3866E-48	6.0037E-47
KRT19	4.88404711	8.08460642	3.20055931	3.8315E-46	2.0562E-45
CDK3	2.78056525	0.40349099	-2.3770743	2.0548E-48	4.5929E-47
NCAM1	4.3588093	1.55069004	-2.8081193	3.692E-42	1.2415E-41
LTBP4	7.66301983	4.16976871	-3.4932511	5.7281E-46	2.9695E-45
TPM2	7.53728365	4.93909902	-2.5981846	1.7802E-47	1.4265E-46
NQO1	2.05226223	4.06757706	2.01531483	3.4577E-33	7.58E-33
PSMC1	5.00835105	2.64356091	-2.3647901	2.0546E-48	4.5929E-47
SNHG14	4.60449377	0.94557521	-3.6589186	2.0814E-48	4.5929E-47
NDUFS7	5.02209715	2.95256987	-2.0695273	2.3521E-48	4.5929E-47
ATM	3.69131214	1.32600454	-2.3653076	2.2198E-48	4.5929E-47
CRABP2	1.70266933	8.86950528	7.16683595	5.8104E-48	6.2912E-47
ACADL	3.07732086	0.11164132	-2.9656795	2.3167E-48	4.5929E-47
CDC45	0.34085937	2.41330586	2.07244649	1.1173E-47	9.853E-47
AIF1L	1.59111168	4.42911671	2.83800502	4.5698E-44	1.8084E-43
NDRG2	7.96760893	2.97660683	-4.9910021	2.0808E-48	4.5929E-47
KRT7	0.88603955	7.05092867	6.16488912	3.2643E-48	4.721E-47
BIRC5	0.39755978	3.94105951	3.54349973	2.3673E-48	4.5929E-47
DAPK1	4.62585372	2.34296084	-2.2828929	1.5916E-42	5.4972E-42
PGP	1.82147769	3.84128179	2.0198041	2.464E-47	1.8556E-46
SOCS2	2.91371821	0.60768677	-2.3060314	1.4908E-46	8.8294E-46
PSMA6	5.08435647	2.2104275	-2.873929	2.0547E-48	4.5929E-47
SPEG	3.95983919	1.36623575	-2.5936034	1.6913E-46	9.897E-46
MT1G	1.13142806	5.24860332	4.11717526	1.2647E-41	4.1036E-41
HMGB3	1.62932062	4.07056812	2.4412475	1.2064E-47	1.0444E-46
CYB5A	6.62165964	2.57225711	-4.0494025	2.0547E-48	4.5929E-47
KRT18	2.52582531	8.11755297	5.59172766	2.1069E-48	4.5929E-47
PSAT1	1.38736048	5.99150686	4.60414639	4.0972E-47	2.8503E-46
MTCH2	3.0517983	5.15347905	2.10168075	4.1672E-48	5.2213E-47
CDH2	1.29918288	3.39473003	2.09554715	2.1914E-28	4.1625E-28
SPARCL1	6.71004255	4.4877855	-2.222257	3.9198E-42	1.3161E-41
MT-TL1	0	2.6137329	2.6137329	5.0824E-48	5.8145E-47
MT-RNR1	7.62425483	11.3689074	3.74465257	1.9693E-48	4.5929E-47
ZNF224	3.36813841	0.94254272	-2.4255957	2.0814E-48	4.5929E-47
NDUFB11	4.55265837	6.84567024	2.29301187	6.0435E-48	6.4546E-47
SLC38A1	2.15369176	4.45223582	2.29854406	1.618E-47	1.3145E-46
MEX3A	1.46826087	3.73252272	2.26426185	1.172E-40	3.5821E-40
RBBP7	6.48769367	4.46832972	-2.019364	3.2597E-47	2.3412E-46
EWSR1	6.40556632	4.23701465	-2.1685517	2.0546E-48	4.5929E-47
HSPB1	7.66798561	9.74764556	2.07965994	4.3275E-39	1.2129E-38
GCKR	2.81923662	0.10574435	-2.7134923	2.0532E-48	4.5929E-47
SARNP	4.94676067	0.83098925	-4.1157714	2.0547E-48	4.5929E-47
TAGLN	8.50075732	5.02734928	-3.473408	6.008E-45	2.6277E-44

SAFB	5.47757594	3.44242087	-2.0351551	2.1083E-48	4.5929E-47
SLC29A2	0.87319292	4.24349373	3.3703008	3.7126E-48	4.9272E-47
C1QTNF1	4.79278074	2.67888179	-2.113899	4.3592E-40	1.2849E-39
CCL20	0.21295103	2.22921824	2.0162672	8.9342E-39	2.4679E-38
HMGA1	1.56264438	8.19925228	6.6366079	2.3055E-48	4.5929E-47
CDKN2A	0.5748078	5.18160419	4.60679639	2.6957E-46	1.496E-45
MPDZ	3.71979648	1.3519668	-2.3678297	3.4819E-48	4.7812E-47
PID1	3.37868975	0.86033193	-2.5183578	4.4222E-47	3.0351E-46
NUTM2B-AS1	3.04466248	0.97810509	-2.0665574	8.0131E-48	7.7419E-47
KRT17	0.55903594	4.49702827	3.93799233	3.096E-46	1.6928E-45
FCER1G	3.07697693	6.01129254	2.93431561	1.7479E-40	5.2775E-40
LUC7L	5.76783655	2.66263652	-3.1052	2.2775E-48	4.5929E-47
APOD	5.37770315	2.58746393	-2.7902392	1.1102E-43	4.231E-43
TYRO3	5.43412068	1.59436652	-3.8397542	1.4798E-47	1.2258E-46
PLCG1	5.84320894	2.89877597	-2.944433	2.0547E-48	4.5929E-47
LCN2	0.57675234	6.82884339	6.25209105	8.6012E-47	5.4078E-46
CAPG	2.9796242	5.70373615	2.72411196	1.6975E-44	7.0541E-44
DDX39B	7.53256098	3.9760222	-3.5565388	2.1628E-48	4.5929E-47
PPM1K	3.50381018	1.23363989	-2.2701703	5.6702E-48	6.1934E-47
IKBK	3.22780642	1.12570222	-2.1021042	2.0547E-48	4.5929E-47
UBR4	5.76469193	2.86343704	-2.9012549	2.0547E-48	4.5929E-47
PBX3	4.92522751	2.1923166	-2.7329109	1.4798E-47	1.2258E-46
TNFRSF21	1.76331915	4.61697992	2.85366077	8.8767E-48	8.3169E-47
MT-TC	0	4.3060432	4.3060432	9.9683E-49	4.5929E-47
RPL30	10.3722276	7.88435548	-2.4878721	3.2145E-48	4.7157E-47
MGST3	6.00290312	3.82376298	-2.1791401	3.0226E-48	4.6607E-47
NACC1	1.99161221	5.57869885	3.58708664	2.0544E-48	4.5929E-47
DIO3	2.73488785	0.38090284	-2.353985	2.5832E-45	1.1951E-44
PVT1	4.52131256	2.09188966	-2.4294229	2.6143E-45	1.2085E-44
PDZD11	3.39761022	5.46016655	2.06255633	2.798E-48	4.5929E-47
SLC7A2	4.90540347	2.01788712	-2.8875163	8.6636E-39	2.3949E-38
CXCR4	2.05372857	5.73495942	3.68123085	5.215E-47	3.4804E-46
E2F1	1.38732419	4.16863351	2.78130932	8.8767E-48	8.3169E-47
EEF1G	8.98750882	1.16954633	-7.8179625	2.0511E-48	4.5929E-47
MT-TP	0	11.9696556	11.9696556	9.5745E-49	4.5929E-47
SOX9	0.27878796	4.46582842	4.18704046	3.1416E-48	4.677E-47
E2F3	0.79945865	2.959646	2.16018734	2.7272E-48	4.5929E-47
CPEB1	2.24131458	0.21373493	-2.0275797	5.5981E-48	6.1398E-47
AGPAT2	3.08910397	5.44422089	2.35511693	3.3384E-46	1.8153E-45
NUAK2	0.82753818	4.89088748	4.0633493	7.4205E-48	7.357E-47
RBP1	8.47978767	5.01011134	-3.4696763	5.3797E-46	2.8002E-45
AURKB	0.45768683	3.5358721	3.07818527	4.1138E-48	5.2039E-47
MMP9	0.43608367	3.57748316	3.1413995	7.0613E-44	2.736E-43
LUC7L3	7.05511107	3.95424977	-3.1008613	2.2483E-48	4.5929E-47
TPT1	11.8571797	8.55224388	-3.3049358	2.9697E-48	4.6241E-47
SPART	5.04265436	2.96659112	-2.0760632	1.0088E-47	9.0982E-47
PPT2-EGFL8	3.52604207	0.35452682	-3.1715153	2.0547E-48	4.5929E-47
ACTR2	3.51895568	5.63335535	2.11439967	3.4368E-48	4.7812E-47

PLA2G6	5.04998418	2.11151149	-2.9384727	5.2504E-48	5.9156E-47
NR5A1	3.89425981	1.10323192	-2.7910279	5.1994E-38	1.3861E-37
BUB1B	0.40977555	2.65167655	2.241901	6.2025E-48	6.5512E-47
TREM2	0.84080855	3.62760145	2.7867929	3.4035E-44	1.3649E-43
BCL2L1	3.31568272	5.6447291	2.32904638	4.0616E-48	5.1797E-47
BDH2	5.28063273	2.74498201	-2.5356507	2.4924E-48	4.5929E-47
TAPBP	3.99546906	6.37042197	2.37495291	4.2207E-48	5.2569E-47
PYCR1	1.82969256	4.50608615	2.67639359	3.2908E-45	1.4974E-44
RPLP0P6	3.08569968	5.24739721	2.16169754	2.0305E-46	1.1644E-45

Supplementary table 2. The formula of GRG score*

Coefficients	Contents
0.292	LMCD1 expression
0.115	L1CAM expression
-0.145	MYCN expression
-0.310	GALT expression
-0.083	IDO1 expression
0.313	RPL18 expression
-0.242	XBP1 expression
-0.077	LPAR3 expression
0.118	RUNX3 expression
0.213	PLCG1 expression

***GRG score** = (0.292 × LMCD1 expression) + (0.115 × L1CAM expression) + (-0.145 × MYCN expression) + (-0.310 × GALT expression) + (-0.083 × IDO1 expression) + (0.313 × RPL18 expression) + (-0.242 × XBP1 expression) + (-0.077 × LPAR3 expression) + (0.118 × RUNX3 expression) + (0.213 × PLCG1 expression).

Supplementary table 3. Risk Group Stratification of Individuals Based on the Expression Profiles of the Ten GRGs

Id	futime	fustat	LMCD1	L1CAM	MYCN	GALT	IDO1	RPL18	XBP1	LPAR3	RUNX3	PLCG1	riskScore	risk
TCGA-13-1495	7.532	1	2.997	5.126	3.384	2.295	5.693	9.394	8.321	5.223	3.182	3.686	0.977	low
TCGA-24-1924	2.518	1	3.636	2.443	4.839	4.216	6.912	9.431	9.641	7.244	4.022	3.622	0.239	low
TCGA-13-1511	4.521	1	3.472	4.907	2.943	3.707	8.013	7.690	10.491	5.653	2.143	5.524	0.273	low
TCGA-59-A5PD	1.710	1	1.976	5.374	5.681	3.317	2.709	9.036	8.136	4.615	1.840	4.974	0.550	low
TCGA-29-1688	6.575	1	3.387	4.510	5.743	2.925	6.994	9.010	8.834	5.905	3.395	3.854	0.423	low
TCGA-13-1489	6.995	1	3.253	4.514	3.322	2.783	5.181	9.699	8.856	7.174	3.159	2.780	0.607	low
TCGA-25-1319	5.416	1	2.694	1.552	1.229	3.415	4.583	8.198	8.844	5.396	3.150	4.947	0.489	low
TCGA-23-1113	2.600	1	4.082	7.985	5.047	2.879	1.067	10.861	6.667	6.814	2.074	4.258	3.713	high
TCGA-24-1423	0.521	0	3.159	5.378	2.667	2.839	4.374	7.842	8.833	5.435	4.667	4.703	0.873	low
TCGA-13-1507	5.460	1	2.693	2.176	0.738	3.519	5.266	9.636	8.934	1.976	2.948	3.720	0.774	low
TCGA-24-1419	0.655	0	2.352	2.963	6.605	2.716	0.431	9.663	7.859	5.502	1.144	4.961	0.661	low
TCGA-61-2111	10.479	0	2.399	6.709	3.762	3.550	3.295	8.514	8.924	8.474	5.506	5.387	0.745	low
TCGA-25-1324	2.836	1	2.784	2.444	6.360	3.706	3.534	8.849	7.072	7.577	2.474	6.112	0.498	low
TCGA-61-1900	0.482	0	3.408	7.192	4.728	2.502	1.913	9.591	7.555	7.583	6.007	5.648	3.341	high
TCGA-24-1416	0.532	0	3.735	4.270	3.278	2.322	4.338	9.439	8.415	8.441	4.729	3.613	1.131	high
TCGA-24-1549	4.715	1	3.762	6.398	5.124	2.536	5.777	8.057	8.823	6.549	5.278	4.712	0.850	low
TCGA-61-2101	4.625	1	3.319	5.160	3.468	2.676	2.967	9.611	10.418	6.977	3.411	5.105	0.927	low
TCGA-29-1693	8.482	0	2.603	3.959	3.816	2.874	6.163	9.487	8.733	6.087	2.874	2.958	0.414	low
TCGA-24-2027	9.142	1	4.236	6.334	5.160	3.886	1.851	9.133	8.536	7.342	5.589	5.168	1.418	high
TCGA-13-0923	6.978	0	2.145	2.125	1.972	3.905	5.715	9.628	8.561	4.654	2.086	4.371	0.432	low

TCGA-09-2051	5.258	0	2.998	6.327	5.091	3.877	6.637	8.377	8.269	5.617	6.058	4.634	0.610	low
TCGA-04-1517	1.666	1	4.565	5.749	2.928	3.703	4.570	10.025	8.292	6.537	7.168	5.120	3.028	high
TCGA-29-1701	1.411	1	3.454	2.535	3.575	2.665	2.585	10.537	9.429	5.775	2.224	3.347	0.809	low
TCGA-59-2354	2.866	1	4.159	6.074	2.713	3.541	5.075	9.178	8.242	6.680	5.294	4.421	1.541	high
TCGA-24-2019	0.405	0	4.534	4.374	5.883	3.611	5.227	8.191	8.534	7.890	6.122	5.530	0.752	low
TCGA-24-1467	8.833	1	3.711	3.249	3.613	2.731	2.349	8.717	8.588	7.649	1.751	4.530	0.688	low
TCGA-24-1847	0.940	0	5.031	5.747	4.000	3.571	6.204	8.864	9.846	8.238	4.173	4.395	0.681	low
TCGA-61-1741	2.805	1	3.356	4.553	5.041	4.617	3.520	8.742	7.893	7.807	2.765	5.477	0.482	low
TCGA-04-1365	2.595	0	2.433	3.910	2.820	3.353	4.913	8.345	8.068	5.437	4.194	4.638	0.625	low
TCGA-30-1891	2.504	1	3.072	5.346	5.475	3.020	2.540	9.818	7.714	2.954	2.091	3.584	1.064	high
TCGA-13-1506	2.847	1	3.388	4.161	5.356	3.168	5.947	9.292	9.440	7.709	5.728	4.209	0.507	low
TCGA-29-1778	1.244	0	5.418	1.092	3.791	3.024	5.743	8.910	8.380	5.635	3.030	4.323	0.861	low
TCGA-23-1114	5.723	1	3.816	3.415	4.013	3.695	1.001	8.611	7.953	7.498	4.937	5.714	1.212	high
TCGA-23-1111	0.268	0	3.371	3.723	1.412	4.144	5.402	10.269	8.580	7.098	6.387	5.477	1.628	high
TCGA-61-2092	4.310	0	3.039	1.617	0.293	3.351	6.209	10.185	8.702	3.220	1.418	3.598	0.774	low
TCGA-13-1477	4.553	1	1.878	0.643	3.302	3.184	1.702	9.926	6.542	3.774	3.312	3.754	0.942	low
TCGA-61-2012	2.553	0	2.861	4.164	2.255	3.044	5.676	8.587	8.673	4.490	6.080	4.472	0.987	high
TCGA-29-1770	2.030	0	5.471	5.386	4.831	2.911	2.292	9.827	7.863	5.696	1.576	4.073	2.040	high
TCGA-13-0899	5.512	1	3.132	4.180	2.780	3.520	2.538	9.313	8.224	4.557	3.931	4.381	1.177	high
TCGA-13-0920	4.066	1	2.591	2.201	2.671	3.250	3.525	9.729	9.253	5.911	3.564	3.303	0.496	low
TCGA-10-0934	0.559	1	3.291	4.905	0.414	2.835	1.852	9.990	9.151	0.044	5.167	2.402	2.618	high
TCGA-24-1849	0.482	0	3.999	5.449	3.423	3.311	4.564	8.876	8.087	4.602	4.012	5.235	1.569	high
TCGA-36-1568	2.397	0	2.725	5.465	2.509	3.361	3.258	9.785	8.586	1.605	8.895	4.385	2.989	high
TCGA-23-2077	9.658	0	3.415	4.339	3.996	3.787	2.857	8.891	8.559	4.884	2.833	4.561	0.704	low
TCGA-09-2056	1.038	0	3.135	3.697	5.428	2.518	3.863	9.944	8.322	4.456	4.497	2.572	0.809	low
TCGA-24-0970	0.970	1	3.380	6.327	6.224	2.161	3.023	9.527	6.432	7.974	3.914	4.822	2.003	high
TCGA-09-1667	5.156	0	4.460	4.264	1.778	3.115	7.048	8.612	9.263	7.881	3.994	4.210	0.741	low
TCGA-29-1769	1.915	0	3.103	4.847	4.034	3.590	3.835	10.112	7.594	5.856	3.490	3.370	0.956	low
TCGA-25-1318	2.915	1	4.275	5.463	3.238	2.224	2.905	9.124	8.185	4.448	6.921	4.928	3.962	high
TCGA-09-1665	3.468	1	2.866	2.231	2.336	3.700	4.792	8.503	8.721	5.903	3.089	3.185	0.317	low
TCGA-13-0900	11.170	0	3.530	2.741	4.489	3.198	5.882	9.364	7.595	5.673	2.196	4.036	0.602	low
TCGA-5X-AA5U	0.989	0	3.993	3.266	5.129	5.128	1.580	8.274	7.745	4.863	2.151	6.844	0.693	low
TCGA-29-1697	2.600	1	2.873	5.603	4.953	4.087	5.760	8.677	7.090	7.771	4.770	5.181	0.665	low
TCGA-13-2060	6.490	0	2.317	0.730	1.087	2.477	6.033	8.723	7.348	5.690	2.167	3.396	0.511	low
TCGA-25-1628	1.718	1	4.684	5.641	5.735	3.706	6.950	8.630	7.413	6.928	4.728	6.052	1.201	high
TCGA-09-2053	3.312	0	2.830	5.362	4.732	3.480	4.396	9.391	8.007	6.011	3.108	4.488	0.724	low
TCGA-61-1724	1.745	1	4.954	6.503	0.982	3.667	3.672	8.683	9.441	5.075	7.547	4.631	2.803	high
TCGA-13-1410	6.751	0	4.004	5.437	3.566	3.771	5.335	9.647	9.109	5.361	4.738	5.194	1.265	high
TCGA-25-1328	5.504	1	3.877	2.888	4.796	3.171	2.674	10.055	7.567	1.791	5.031	5.296	2.627	high
TCGA-09-0366	4.814	1	2.752	2.264	2.041	3.791	3.809	8.755	7.469	3.143	5.380	4.072	0.972	low
TCGA-61-2110	3.710	1	3.409	7.453	4.571	3.335	2.034	10.503	6.137	5.094	1.539	4.387	2.761	high
TCGA-09-0364	2.430	1	2.290	3.058	8.219	3.379	0.474	10.125	7.524	7.245	0.652	6.001	0.544	low
TCGA-13-0913	9.110	0	3.392	1.705	2.322	3.758	5.176	9.918	8.597	7.607	2.144	3.665	0.462	low
TCGA-04-1338	3.885	0	2.828	2.413	4.513	2.835	3.078	9.139	7.639	6.841	3.462	3.341	0.561	low
TCGA-30-1855	0.205	1	3.704	4.803	4.154	3.161	3.770	8.299	7.807	4.398	4.585	4.253	1.059	high
TCGA-04-1361	2.710	0	4.144	4.585	3.983	3.589	5.227	9.438	7.350	6.640	2.710	4.076	0.968	low
TCGA-09-0367	1.499	1	3.029	2.571	2.843	3.176	6.275	10.565	8.152	4.309	5.983	2.685	1.044	high
TCGA-25-1632	4.929	1	3.224	2.467	2.966	4.005	1.620	9.258	9.239	6.514	7.072	4.864	0.953	low
TCGA-24-2289	5.614	1	4.056	3.272	1.518	3.111	2.403	8.242	8.369	5.660	4.286	5.221	1.514	high
TCGA-24-1471	0.099	0	4.097	2.147	2.435	3.918	2.796	10.255	6.162	7.808	2.460	3.280	1.284	high
TCGA-25-2399	1.666	1	4.697	4.453	3.031	3.850	5.065	8.374	7.647	5.907	4.883	5.100	1.364	high

TCGA-13-0886	12.781	0	3.637	3.777	1.872	2.985	6.252	8.583	7.646	8.375	3.432	4.252	0.806	low
TCGA-24-1463	6.077	1	2.504	6.433	3.910	3.192	4.765	8.012	8.435	5.484	6.769	5.416	1.019	high
TCGA-13-1505	5.474	0	3.447	0.921	6.247	3.624	1.939	8.953	7.940	5.270	2.332	5.475	0.518	low
TCGA-61-2109	1.723	1	4.243	5.511	3.189	4.002	2.756	9.760	7.413	8.285	5.137	4.293	1.797	high
TCGA-29-1783	0.603	0	4.292	6.733	2.998	2.304	3.328	8.946	7.682	7.164	2.904	5.062	2.494	high
TCGA-24-1470	0.288	0	3.027	1.852	3.198	3.762	6.432	7.955	7.951	4.283	6.593	4.508	0.554	low
TCGA-20-1685	1.392	0	3.196	2.306	2.847	3.055	2.713	9.266	8.909	8.522	3.808	4.565	0.687	low
TCGA-13-0760	0.962	1	2.573	2.292	0.298	3.146	2.381	8.730	7.238	3.958	4.797	2.640	1.109	high
TCGA-31-1956	3.677	0	4.286	2.206	4.225	3.012	5.240	8.652	8.534	6.013	3.827	4.113	0.627	low
TCGA-29-1785	3.025	1	2.808	3.425	4.575	3.758	5.485	9.836	8.053	6.150	3.612	3.595	0.487	low
TCGA-29-1694	3.252	1	3.935	4.360	5.303	2.131	4.651	9.018	7.492	4.288	3.301	4.337	1.391	high
TCGA-29-2414	7.181	1	3.626	3.387	2.485	3.861	4.154	9.748	8.374	7.117	4.992	5.506	1.331	high
TCGA-24-1430	2.364	1	4.147	2.199	3.405	3.141	1.133	9.176	7.931	6.299	1.083	6.026	1.327	high
TCGA-61-1910	3.088	0	2.995	3.453	5.795	3.664	4.501	9.827	7.486	3.981	4.223	5.486	1.051	high
TCGA-20-1686	0.244	0	2.451	1.128	3.070	1.575	2.273	9.023	7.714	6.335	1.976	3.529	0.725	low
TCGA-13-0730	1.485	1	2.931	5.386	6.356	4.479	4.061	8.944	7.094	2.437	4.011	6.532	1.097	high
TCGA-24-1923	1.890	1	4.389	3.470	5.126	3.664	1.962	10.383	6.362	6.064	2.929	4.619	2.042	high
TCGA-29-1705	1.521	1	3.926	6.043	4.275	2.075	1.416	9.660	7.407	3.236	2.877	5.004	3.855	high
TCGA-30-1857	0.022	1	3.360	6.044	0.996	2.609	4.169	9.144	7.592	3.124	6.161	3.650	3.211	high
TCGA-25-2392	0.085	1	3.050	3.439	3.587	2.926	2.232	8.102	8.374	5.555	4.339	4.370	0.741	low
TCGA-30-1892	4.066	1	3.513	3.324	3.881	2.950	2.697	10.505	6.925	4.313	4.834	3.344	2.162	high
TCGA-61-1914	4.718	0	2.760	3.195	3.032	2.856	6.298	9.796	9.814	6.356	3.712	3.857	0.491	low
TCGA-24-1562	3.792	1	3.959	7.128	5.231	3.607	4.233	10.161	7.470	6.686	5.753	4.281	2.011	high
TCGA-25-1329	1.252	1	2.937	4.651	1.675	3.780	6.028	10.175	9.252	4.519	7.550	5.551	1.916	high
TCGA-61-1740	0.203	1	2.840	2.988	4.964	3.872	5.957	9.232	8.196	2.102	5.749	4.266	0.666	low
TCGA-29-A5NZ	2.981	1	3.801	3.047	3.621	3.522	2.519	8.690	8.299	4.509	4.940	6.855	1.723	high
TCGA-24-1417	0.652	0	4.525	4.460	5.102	4.728	7.038	9.351	8.432	9.883	4.381	4.854	0.460	low
TCGA-23-1021	3.962	1	3.349	4.751	2.815	2.615	2.469	9.634	7.027	4.038	4.656	2.988	2.207	high
TCGA-24-1552	3.449	1	4.167	3.245	2.254	2.736	1.354	8.893	7.344	8.424	2.164	3.915	1.284	high
TCGA-36-1580	2.019	1	4.008	4.622	2.488	2.765	3.352	9.207	8.011	1.800	3.593	4.845	2.631	high
TCGA-20-0991	2.184	0	1.481	3.000	1.642	2.858	7.313	9.344	8.640	4.513	3.515	3.329	0.431	low
TCGA-04-1648	2.386	1	2.438	2.053	1.907	3.455	6.432	7.630	9.096	4.217	4.909	4.624	0.366	low
TCGA-24-1550	3.422	1	2.474	1.849	5.326	2.751	3.343	8.953	8.397	3.701	5.863	5.384	0.869	low
TCGA-29-2425	5.416	0	4.325	1.523	3.418	2.787	2.910	9.718	8.141	6.231	1.843	5.475	1.368	high
TCGA-24-1553	4.841	1	4.832	4.750	5.212	3.594	5.742	10.168	8.227	7.120	5.051	4.429	1.344	high
TCGA-61-1736	4.066	1	6.355	4.247	2.585	3.127	6.198	9.384	6.975	9.397	2.740	4.335	2.136	high
TCGA-24-1469	0.759	0	4.191	4.783	4.913	4.007	3.353	8.411	9.506	5.069	3.180	4.843	0.545	low
TCGA-57-1994	2.085	0	3.708	5.342	3.535	3.589	3.659	8.316	7.713	7.537	4.666	5.235	1.097	high
TCGA-13-0906	9.915	0	2.740	3.961	5.669	2.596	5.290	9.331	7.933	5.145	2.214	4.467	0.612	low
TCGA-04-1530	9.923	1	4.253	4.646	2.529	3.577	4.022	8.253	8.235	4.639	2.604	4.808	1.033	high
TCGA-61-2104	6.405	0	3.334	6.252	2.690	3.242	6.288	8.522	8.161	7.269	3.591	5.101	0.924	low
TCGA-61-1728	2.323	0	4.446	5.688	4.055	3.393	4.772	9.405	8.194	7.478	2.669	4.504	1.081	high
TCGA-23-1119	10.830	0	2.496	5.019	4.711	3.480	4.004	8.922	9.094	7.235	3.886	2.571	0.288	low
TCGA-09-0369	2.964	1	3.068	1.697	6.993	4.297	2.286	9.605	7.405	7.387	1.188	5.961	0.412	low
TCGA-13-1485	1.723	1	3.876	3.856	2.418	2.380	2.984	8.985	7.303	3.480	2.802	4.826	2.401	high
TCGA-25-1317	0.167	1	3.558	3.513	5.019	2.988	3.475	10.227	8.360	6.655	1.563	5.556	1.036	high
TCGA-25-1625	2.301	1	3.238	5.960	2.815	2.069	7.296	9.576	9.128	3.962	6.415	3.862	1.716	high
TCGA-13-1482	5.142	1	4.206	3.876	3.826	3.603	5.255	9.283	8.942	6.389	2.022	4.383	0.600	low
TCGA-13-1487	1.866	1	3.261	5.863	3.213	3.214	2.861	9.686	7.246	6.101	2.858	4.637	1.753	high
TCGA-23-1026	2.236	0	4.206	4.885	3.990	3.181	5.964	9.021	7.998	3.846	4.779	3.695	1.192	high
TCGA-09-1673	0.252	0	2.948	1.733	4.633	3.762	3.744	8.727	7.269	3.582	2.650	5.265	0.635	low

TCGA-24-2024	4.847	1	5.251	2.500	4.775	3.406	3.584	9.161	8.868	6.969	1.735	4.466	0.682	low
TCGA-13-0804	2.940	1	3.375	3.514	1.581	3.774	4.200	9.555	7.671	2.671	2.785	3.318	1.113	high
TCGA-24-2038	3.710	1	3.762	2.365	4.261	3.066	1.338	10.399	7.063	1.591	1.464	3.629	1.752	high
TCGA-13-0800	7.290	0	3.656	2.765	6.982	3.360	1.541	8.880	8.349	7.007	1.928	5.367	0.495	low
TCGA-24-1436	0.712	1	3.167	3.895	1.540	3.260	7.492	8.941	8.018	5.761	3.852	4.657	0.886	low
TCGA-13-0901	1.614	0	3.263	1.213	3.436	2.017	1.587	10.409	5.492	4.590	1.436	2.850	1.993	high
TCGA-13-0916	4.890	0	2.537	2.478	4.989	2.607	5.543	8.570	7.182	5.782	2.523	4.524	0.495	low
TCGA-30-1866	3.052	1	5.776	1.367	3.294	2.862	4.475	9.336	7.856	8.508	4.885	2.755	1.146	high
TCGA-24-2288	0.068	1	4.203	4.873	1.371	4.203	5.159	9.278	8.547	3.493	4.492	4.496	1.512	high
TCGA-13-0766	4.726	1	3.751	4.505	3.787	3.588	4.675	9.705	7.580	5.886	2.514	3.005	0.780	low
TCGA-13-0891	8.570	1	3.974	1.280	0.743	3.787	4.177	9.751	6.852	7.062	2.865	2.632	0.930	low
TCGA-36-1569	2.425	0	4.493	5.359	4.498	2.746	4.194	9.379	8.255	3.338	4.615	5.479	2.641	high
TCGA-30-1853	3.022	1	3.786	1.250	1.840	2.612	0.597	10.374	6.407	0.962	1.444	4.305	3.792	high
TCGA-OY-A56P	3.307	0	4.311	3.452	3.328	3.261	3.398	9.410	7.199	6.089	3.935	7.000	2.921	high
TCGA-10-0938	1.742	1	5.375	3.044	2.784	3.378	2.019	9.997	9.901	7.431	2.534	5.180	1.440	high
TCGA-24-2020	12.668	1	2.886	2.056	5.526	4.138	0.810	10.167	10.019	3.485	1.017	5.434	0.448	low
TCGA-24-1431	1.597	1	3.611	5.646	0.553	2.330	2.835	10.798	7.318	7.700	2.750	4.280	4.127	high
TCGA-25-2397	1.000	1	2.288	4.893	1.690	3.642	2.848	9.446	7.244	2.885	3.556	4.537	1.631	high
TCGA-24-1413	0.526	0	3.426	4.745	4.079	3.266	6.371	8.957	8.639	6.930	2.010	4.760	0.520	low
TCGA-24-2026	2.901	1	4.117	2.477	0.403	3.594	4.282	8.508	8.115	7.676	2.578	3.997	0.758	low
TCGA-24-1556	5.885	1	3.557	4.293	3.723	4.200	6.183	8.483	8.438	7.254	2.934	4.875	0.414	low
TCGA-61-1737	3.737	0	3.962	5.459	3.814	3.483	5.672	9.579	8.918	7.201	6.107	4.682	1.205	high
TCGA-29-1781	0.699	0	3.349	3.713	5.675	3.716	5.537	9.229	9.256	5.393	3.041	2.877	0.267	low
TCGA-61-1918	1.312	1	4.194	5.196	3.463	2.807	4.013	9.042	8.045	7.896	3.064	4.536	1.247	high
TCGA-57-1583	0.948	1	3.670	2.956	1.479	2.577	3.559	9.212	6.761	5.517	1.246	4.446	1.682	high
TCGA-23-1032	0.230	1	4.121	3.908	2.478	3.418	3.253	9.285	7.389	6.206	3.874	4.372	1.638	high
TCGA-24-1422	0.063	1	3.885	4.113	1.439	3.432	3.751	8.852	8.291	4.808	4.104	4.699	1.497	high
TCGA-13-0893	3.614	1	4.225	1.984	3.540	3.364	6.330	8.897	7.841	6.993	3.814	3.939	0.619	low
TCGA-13-0725	1.033	1	3.483	4.012	2.412	4.012	4.189	9.541	6.995	6.758	2.416	3.620	0.876	low
TCGA-13-1408	4.603	1	3.112	6.291	2.814	3.446	4.150	9.260	7.907	4.223	4.835	4.985	1.833	high
TCGA-04-1651	3.019	1	2.908	6.002	4.208	3.455	6.702	9.621	8.541	6.601	2.125	3.944	0.512	low
TCGA-25-2404	2.419	1	3.751	5.536	3.091	3.653	5.011	9.092	7.426	4.662	6.178	4.611	1.894	high
TCGA-13-0799	6.945	0	3.463	3.167	3.481	3.919	4.527	9.177	6.635	5.487	1.877	4.940	0.905	low
TCGA-13-0726	2.600	1	3.187	6.236	3.803	3.924	3.040	8.444	7.533	4.767	4.132	2.505	0.673	low
TCGA-13-0727	1.266	1	4.242	7.037	4.750	4.513	1.120	10.243	6.627	5.759	2.743	6.143	3.193	high
TCGA-61-1919	3.181	1	3.821	2.096	4.429	2.872	2.794	9.550	8.702	7.262	3.325	4.091	0.727	low
TCGA-04-1356	4.107	1	2.910	2.838	4.761	3.138	2.777	8.635	8.523	7.323	1.975	4.125	0.358	low
TCGA-61-1907	2.608	0	2.051	2.137	5.123	4.528	4.373	9.235	7.302	6.458	2.741	3.050	0.210	low
TCGA-04-1364	2.805	1	4.809	2.777	6.028	3.334	0.598	9.767	8.749	9.474	0.622	5.775	0.804	low
TCGA-24-2298	4.438	1	4.195	3.482	1.429	3.314	5.319	9.061	7.920	3.642	2.607	3.913	1.259	high
TCGA-29-1762	7.216	1	2.901	6.405	5.627	4.228	0.662	9.454	9.417	5.569	2.984	5.097	0.666	low
TCGA-24-2297	4.655	1	3.148	3.581	3.861	4.917	4.806	8.814	8.224	8.091	5.589	4.889	0.448	low
TCGA-13-0884	8.932	1	4.552	4.100	3.556	3.139	5.162	9.402	6.470	7.697	2.849	3.209	1.208	high
TCGA-10-0931	2.740	1	4.068	2.697	2.771	3.334	5.103	9.740	6.408	6.539	1.479	3.155	0.981	low
TCGA-31-1950	1.564	0	1.837	3.879	1.179	3.082	6.548	7.569	8.394	6.315	3.492	5.081	0.432	low
TCGA-04-1655	3.781	1	3.203	5.101	5.643	2.995	0.413	9.545	5.893	4.420	2.587	4.505	2.074	high
TCGA-25-1312	0.085	1	3.364	4.387	3.048	2.870	2.103	9.305	7.789	7.105	5.040	5.260	1.970	high
TCGA-24-2262	0.030	1	3.987	1.801	3.070	3.538	5.182	8.806	8.527	5.279	3.191	5.194	0.719	low
TCGA-20-1684	1.592	0	4.354	4.060	4.301	2.482	2.853	9.079	7.757	8.725	1.057	4.044	0.894	low
TCGA-10-0926	2.159	1	3.818	3.986	5.131	3.059	2.069	10.342	7.304	2.157	1.987	4.070	1.851	high
TCGA-61-1911	3.542	0	2.371	3.426	1.166	3.268	5.045	9.298	9.995	6.201	5.543	3.061	0.500	low

TCGA-59-2355	0.178	1	3.489	4.632	4.941	3.077	5.018	9.567	8.070	6.798	4.142	4.005	0.841	low
TCGA-10-0927	6.822	1	2.932	1.818	3.550	2.845	1.217	10.216	5.972	4.105	1.064	4.068	1.644	high
TCGA-25-1631	0.025	1	3.696	5.998	3.080	3.731	5.403	9.579	9.575	6.734	6.452	5.085	1.254	high
TCGA-24-1474	1.852	1	4.023	4.392	2.653	2.633	2.423	8.610	6.829	7.581	2.843	5.989	2.337	high
TCGA-61-2002	1.499	0	3.725	3.021	1.962	3.358	7.712	9.229	8.159	4.798	3.773	3.833	0.800	low
TCGA-04-1514	4.712	1	3.656	5.723	6.789	3.904	2.648	9.037	6.720	7.280	3.095	6.301	1.178	high
TCGA-13-0887	5.556	1	3.005	5.042	1.754	3.524	5.754	9.453	8.147	6.677	2.960	3.465	0.737	low
TCGA-24-1548	1.351	1	2.695	4.305	3.587	3.060	4.488	8.915	8.677	7.075	4.395	5.386	0.782	low
TCGA-24-1418	0.666	0	4.315	5.746	4.059	2.431	3.048	9.353	7.781	3.097	3.738	5.293	3.326	high
TCGA-WR-A838	0.833	1	4.095	2.392	3.965	3.725	3.150	9.836	7.407	7.440	2.622	5.333	1.150	high
TCGA-29-1711	2.885	0	3.223	2.996	5.452	3.170	6.894	7.938	8.351	5.595	5.098	4.386	0.372	low
TCGA-30-1861	2.899	1	3.547	6.639	3.143	3.824	2.681	9.155	8.205	9.202	4.007	5.163	1.199	high
TCGA-24-1464	1.038	1	2.600	4.350	1.232	3.139	3.249	9.736	7.104	7.579	1.757	3.741	1.091	high
TCGA-VG-A8LO	0.066	1	4.073	5.640	1.589	2.752	5.802	9.586	6.978	6.518	7.661	5.170	4.900	high
TCGA-13-0890	12.121	0	3.961	6.551	4.341	4.023	3.606	9.086	8.278	5.794	3.679	4.482	1.020	high
TCGA-30-1860	3.742	1	4.028	1.316	3.844	2.801	5.876	9.600	8.078	5.963	3.650	3.621	0.747	low
TCGA-09-2045	2.929	1	2.928	4.401	5.588	3.623	5.037	8.995	7.940	6.057	7.511	3.762	0.689	low
TCGA-25-1627	1.079	1	2.901	4.786	2.672	2.248	1.566	9.119	9.986	7.007	2.695	5.066	0.979	low
TCGA-57-1993	2.090	0	3.498	5.106	1.977	4.072	1.666	9.273	7.380	6.222	5.825	5.348	2.427	high
TCGA-10-0936	3.077	1	3.322	4.282	1.607	5.412	6.209	8.970	7.588	6.282	5.575	4.930	0.766	low
TCGA-61-2102	0.540	1	4.237	3.013	5.837	3.534	3.176	8.556	8.026	0.071	2.770	6.804	1.474	high
TCGA-25-1326	3.422	1	3.868	5.339	4.897	3.143	3.984	8.815	9.466	6.911	5.346	4.834	0.842	low
TCGA-24-1426	0.447	0	3.619	5.107	4.890	2.870	2.293	8.924	6.189	5.741	2.731	4.922	1.789	high
TCGA-25-2391	4.088	1	3.437	3.850	5.767	3.195	5.193	8.818	8.713	7.212	3.525	4.697	0.451	low
TCGA-29-1776	0.986	0	4.905	3.414	4.090	3.651	4.291	10.111	8.516	7.551	3.207	4.233	1.049	high
TCGA-09-2054	1.745	1	3.933	3.580	5.388	3.884	1.104	9.001	8.076	5.171	2.931	6.586	1.221	high
TCGA-13-0801	3.833	1	3.511	2.408	4.684	3.527	5.152	10.424	7.971	5.291	4.759	3.261	0.808	low
TCGA-24-0975	1.816	1	2.954	5.402	3.139	2.700	3.401	9.338	7.047	0.742	3.104	4.312	2.355	high
TCGA-29-1761	1.447	1	2.070	2.541	2.068	2.828	4.365	10.626	7.243	5.572	2.536	3.258	0.995	high
TCGA-24-2254	4.756	1	4.738	2.507	4.401	3.837	2.987	8.650	7.567	7.077	5.786	5.576	1.351	high
TCGA-61-1725	2.619	0	3.289	3.771	4.626	3.357	5.046	9.591	6.880	4.612	4.713	3.909	1.147	high
TCGA-3P-A9WA	1.151	0	3.015	1.649	3.836	3.902	3.368	8.214	8.193	8.581	4.332	5.738	0.444	low
TCGA-24-1557	3.323	1	4.666	6.078	4.615	3.468	3.989	8.370	7.828	8.845	6.829	4.476	1.340	high
TCGA-25-1321	2.830	1	3.295	2.818	3.025	2.682	1.270	8.704	8.506	8.912	2.774	4.967	0.800	low
TCGA-24-1544	2.247	1	3.414	6.193	4.260	4.207	2.521	9.938	7.620	4.426	4.348	5.010	1.797	high
TCGA-29-1763	5.567	0	5.290	4.803	4.519	5.002	5.859	8.436	8.034	8.358	3.477	5.430	0.623	low
TCGA-24-1603	7.512	1	3.593	5.818	4.130	3.209	4.074	8.251	8.116	7.086	4.063	4.696	0.853	low
TCGA-04-1536	2.425	1	3.242	3.626	1.661	2.296	3.638	9.101	6.584	5.513	1.427	3.390	1.392	high
TCGA-24-2281	3.718	0	2.663	3.127	3.062	3.212	4.045	9.304	8.943	5.565	3.551	4.569	0.654	low
GSM642933	20.222	0	3.828	4.453	2.372	3.335	5.215	7.991	7.657	7.706	6.044	4.985	1.163	high
GSM642935	6.044	1	3.527	3.291	4.009	3.733	5.863	8.499	8.672	8.211	2.946	5.581	0.428	low
GSM642937	4.225	1	3.367	6.275	4.448	2.352	4.083	8.737	8.226	6.726	5.922	4.384	1.424	high
GSM642938	2.353	1	3.966	5.676	6.944	2.813	3.898	8.874	7.258	6.656	2.468	5.730	1.142	high
GSM642939	2.126	1	3.559	5.064	4.098	3.278	4.004	9.189	7.888	8.254	7.415	3.561	1.157	high
GSM642940	4.759	1	2.616	3.166	1.573	3.097	5.380	9.035	8.588	6.737	3.416	4.149	0.614	low
GSM642945	4.099	0	3.555	2.992	2.502	2.526	5.711	8.820	8.289	3.732	4.719	4.737	1.346	high
GSM642946	1.479	1	4.042	5.276	5.846	3.153	4.188	9.124	7.996	6.735	3.530	6.372	1.341	high
GSM642948	5.025	1	3.654	4.644	4.494	3.244	5.657	9.124	9.183	6.648	5.918	4.398	0.766	low
GSM642950	1.847	1	3.576	3.716	1.847	4.189	5.154	8.636	8.018	6.830	3.058	4.589	0.640	low
GSM642956	11.142	0	3.197	3.460	4.923	4.777	1.734	8.228	9.196	7.271	3.746	5.297	0.319	low
GSM642958	1.849	1	3.601	5.835	5.251	2.863	3.197	9.071	6.602	6.055	4.354	4.654	1.806	high

GSM642959	2.978	1	3.616	5.524	4.773	3.185	3.271	8.793	8.163	6.166	1.961	2.082	0.458	low
GSM642960	1.901	1	3.703	4.056	2.728	2.523	5.029	9.072	7.152	5.496	2.084	4.502	1.411	high
GSM642961	8.195	0	3.194	6.774	6.763	3.574	4.417	8.930	8.813	4.644	3.646	4.682	0.602	low
GSM642963	6.510	0	2.536	2.503	2.569	3.547	7.823	9.206	9.087	4.674	7.957	3.613	0.571	low
GSM642964	6.258	1	3.502	5.040	2.827	2.914	6.582	8.909	7.506	6.026	2.594	3.217	0.774	low
GSM642965	3.901	1	3.900	7.316	4.036	2.842	3.136	10.058	6.533	7.919	2.708	5.161	3.101	high
GSM642967	5.326	1	3.877	3.880	2.730	3.914	6.884	9.501	8.117	5.509	2.234	4.211	0.701	low
GSM642972	6.795	1	3.115	4.982	2.500	3.543	2.905	9.230	7.244	5.783	3.500	3.813	1.219	high
GSM642973	4.556	1	4.217	5.424	2.483	3.066	2.941	9.512	7.508	6.251	5.244	4.327	2.776	high
GSM642975	0.255	1	3.332	2.515	2.816	2.883	1.360	9.536	7.834	2.829	2.021	4.115	1.396	high
GSM642976	2.479	1	3.365	4.705	2.542	2.352	3.567	10.015	8.175	6.229	4.111	5.122	2.420	high
GSM642977	6.671	0	3.073	2.342	2.472	2.378	5.531	9.006	8.562	6.723	5.271	2.095	0.554	low
GSM642978	4.693	0	3.323	5.101	2.515	3.446	4.469	9.973	8.103	5.292	5.837	3.340	1.503	high
GSM642982	1.145	1	3.360	2.618	1.832	3.203	2.174	8.615	7.747	6.274	5.415	3.395	1.046	high
GSM642983	2.014	1	2.555	6.403	4.623	3.265	4.339	10.253	7.367	7.173	5.936	5.520	1.999	high
GSM642985	8.578	0	2.596	2.764	5.795	3.619	2.146	8.538	9.106	6.933	2.176	5.469	0.300	low
GSM642986	8.014	0	2.578	2.292	2.688	3.875	3.975	9.238	8.654	3.413	1.966	4.238	0.480	low
GSM642987	8.337	0	3.143	2.850	4.223	3.369	4.021	8.159	9.417	8.187	5.001	3.478	0.281	low
GSM642988	7.627	1	3.493	3.836	4.439	4.043	2.836	9.439	9.546	8.102	4.234	3.659	0.419	low
GSM642990	6.203	0	3.033	2.860	2.501	4.848	2.227	10.017	9.000	5.063	1.980	5.436	0.687	low
GSM642992	2.833	1	3.439	2.767	4.543	3.419	1.267	9.334	8.411	2.758	3.931	4.114	1.014	high
GSM642993	1.729	1	3.655	2.199	3.379	2.984	1.239	9.510	7.891	2.877	2.381	4.879	1.598	high
GSM642998	2.156	1	4.895	2.804	3.114	5.108	1.378	10.330	8.924	4.610	1.969	5.318	1.206	high
GSM643001	1.263	1	3.890	5.087	2.397	2.885	7.384	9.172	7.904	3.106	5.779	4.015	1.866	high
GSM643002	2.299	1	2.949	7.258	4.889	3.366	2.316	10.147	7.499	7.795	5.504	4.571	1.893	high
GSM643003	4.756	0	3.517	2.401	5.756	3.391	1.022	9.622	8.332	2.815	1.956	4.489	0.819	low
GSM643005	5.241	0	3.850	2.038	4.527	2.948	4.962	9.305	8.991	3.123	4.117	5.294	0.988	high
GSM643010	0.532	1	5.449	2.357	2.429	3.049	5.413	9.217	7.458	3.721	4.542	5.631	3.144	high
GSM643018	7.723	0	2.352	2.632	2.753	3.902	2.037	9.784	9.037	2.894	1.935	5.058	0.720	low
GSM643019	2.805	1	4.656	5.275	3.068	3.541	2.140	9.886	6.948	8.797	3.197	4.363	2.201	high
GSM643020	6.455	0	2.407	5.751	5.402	3.757	0.752	8.865	7.659	7.340	2.104	5.616	0.710	low
GSM643022	5.860	0	3.139	2.659	3.575	2.873	7.955	8.048	7.624	7.519	2.917	4.233	0.367	low
GSM643023	0.677	1	3.250	6.493	5.426	2.650	5.725	8.506	8.681	4.486	6.518	4.969	1.173	high
GSM643024	3.047	1	3.719	3.915	2.496	3.018	5.013	8.876	8.848	7.915	4.821	4.855	0.955	low
GSM643025	1.460	1	3.715	4.335	5.775	3.755	2.316	8.236	6.448	4.509	5.756	7.088	2.123	high
GSM643027	2.567	1	3.928	5.628	2.237	2.845	6.876	9.396	7.712	4.163	3.924	4.401	1.960	high
GSM643028	2.707	1	4.341	6.335	4.440	3.908	2.201	9.405	7.688	8.269	3.450	4.688	1.367	high
GSM643029	1.318	1	3.625	4.417	2.861	3.652	5.696	8.698	7.550	7.630	4.535	4.127	0.795	low
GSM643033	5.608	0	3.107	2.945	3.336	3.393	4.032	9.600	8.255	5.998	6.346	3.882	0.998	high
GSM643034	6.611	0	2.200	2.339	2.633	3.484	4.752	9.472	9.458	2.878	2.707	4.864	0.531	low
TCGA-04-1347	5.258	0	2.682	4.555	3.332	3.713	1.362	10.395	6.268	6.088	3.371	5.287	2.348	high
TCGA-24-2267	3.962	1	4.204	2.085	2.584	3.267	8.212	9.012	8.285	6.632	4.637	4.587	0.762	low
TCGA-29-1691	4.027	1	3.283	2.371	5.932	4.669	3.307	8.679	7.737	7.219	3.428	5.136	0.346	low
TCGA-23-1122	3.258	1	3.904	6.440	2.764	3.930	4.155	9.140	8.193	5.545	3.725	4.642	1.347	high
TCGA-20-0987	1.921	1	1.348	4.764	0.534	2.714	5.664	9.381	8.429	5.128	5.239	3.385	0.900	low
TCGA-24-1844	0.310	0	3.938	2.915	3.211	4.161	3.266	8.820	8.105	9.791	6.485	4.947	0.839	low
TCGA-59-2363	0.452	0	4.179	4.762	4.360	3.217	4.377	9.734	8.253	7.221	6.211	5.937	2.156	high
TCGA-04-1343	0.989	1	3.412	6.266	1.036	3.769	4.304	10.337	7.894	4.696	3.976	4.892	2.764	high
TCGA-09-1674	0.712	0	3.114	6.757	7.288	2.840	0.695	7.989	7.639	7.918	4.947	5.809	1.061	high
TCGA-13-1488	5.901	1	3.418	3.483	1.789	4.182	7.311	9.238	7.973	6.454	3.825	3.359	0.532	low
TCGA-25-1634	2.989	1	3.422	5.835	6.278	2.090	0.753	9.715	7.791	6.096	2.280	4.887	1.730	high

TCGA-24-1565	0.855	1	2.325	1.743	1.896	3.290	2.426	8.839	6.668	7.110	2.685	2.822	0.553	low
TCGA-23-1110	4.542	0	3.075	4.682	4.730	4.085	1.252	9.396	7.397	7.414	0.428	6.418	0.887	low
TCGA-23-1023	3.378	0	3.477	6.491	4.208	3.307	7.884	9.236	9.306	4.983	5.080	5.051	0.909	low
TCGA-09-1669	2.542	0	4.414	4.155	4.729	3.548	3.832	9.755	8.360	6.187	3.189	4.374	1.027	high
TCGA-25-1322	0.249	1	3.879	7.084	4.541	2.928	4.810	8.700	8.488	8.768	4.216	4.395	0.916	low
TCGA-61-2098	5.460	0	4.269	5.438	7.490	3.268	0.704	8.990	8.384	7.496	4.831	5.391	1.154	high
TCGA-20-1687	0.222	0	3.738	4.254	3.259	2.545	5.040	9.444	8.156	6.274	5.725	3.431	1.360	high
TCGA-04-1331	3.660	1	2.710	4.992	3.827	3.583	3.948	8.735	7.955	6.356	4.722	5.693	0.965	low
TCGA-25-1877	2.000	1	3.310	2.237	6.280	3.759	4.548	9.916	7.809	4.632	2.472	4.953	0.593	low
TCGA-24-1843	0.290	0	2.741	2.353	2.064	2.578	2.304	8.791	8.293	5.919	4.529	3.873	0.933	low
TCGA-04-1332	3.416	1	4.258	4.465	4.616	3.825	3.454	9.430	8.732	7.297	2.421	5.557	0.872	low
TCGA-25-1314	2.751	1	3.904	4.897	2.027	3.635	2.941	10.240	7.310	1.741	1.967	5.041	3.150	high
TCGA-25-2393	3.170	1	2.857	4.124	4.579	3.191	5.798	10.225	7.561	3.011	4.640	5.275	1.627	high
TCGA-24-2033	1.540	1	4.984	0.970	4.133	3.087	0.639	10.386	7.730	4.565	1.312	4.689	1.897	high
TCGA-25-1320	3.164	1	3.875	3.768	4.608	3.713	3.136	8.548	7.560	6.899	4.950	5.660	1.097	high
TCGA-13-1498	5.512	1	4.096	4.254	2.297	2.507	5.557	8.829	7.894	4.195	6.691	3.349	1.912	high
TCGA-13-0762	9.315	0	3.380	6.068	2.999	3.031	1.077	9.073	7.111	6.787	1.471	4.661	1.624	high
TCGA-24-0979	3.463	1	5.827	4.822	2.878	3.247	4.808	9.390	8.360	7.492	2.243	3.904	1.446	high
TCGA-09-1668	4.614	0	4.858	3.410	3.866	3.797	6.228	7.673	7.989	6.776	3.774	4.493	0.553	low
TCGA-25-1871	2.082	1	3.436	6.117	6.230	3.687	1.311	8.055	6.696	6.333	0.764	6.600	0.965	low
TCGA-23-1029	0.734	0	5.289	3.174	4.822	3.874	5.540	9.408	8.746	8.896	4.431	5.115	0.824	low
TCGA-24-1428	1.449	0	3.351	3.038	2.160	4.311	6.873	9.255	7.572	6.088	4.240	3.926	0.632	low
TCGA-09-1659	0.833	1	2.014	2.543	2.023	3.501	4.847	10.176	8.602	4.378	3.438	3.954	0.680	low
TCGA-13-1509	6.679	0	4.069	2.768	3.656	3.689	1.659	9.876	7.036	6.237	3.950	3.520	1.378	high
TCGA-23-1123	2.789	1	3.507	2.026	4.544	4.370	5.911	8.361	8.171	7.281	3.701	6.079	0.393	low
TCGA-24-1545	4.784	1	3.571	4.554	3.799	2.507	5.333	8.421	9.136	7.213	3.314	4.697	0.643	low
TCGA-13-1496	0.353	1	1.931	4.923	0.437	2.529	6.350	8.504	7.287	4.060	3.803	2.873	0.908	low
TCGA-23-2084	4.153	1	4.537	6.663	2.541	3.091	6.172	9.119	8.274	6.106	3.142	4.284	1.520	high
TCGA-61-2000	1.208	0	1.875	4.241	5.404	2.747	3.003	9.038	9.227	5.152	4.581	4.320	0.503	low
TCGA-04-1348	4.063	1	4.100	4.200	3.298	3.455	5.110	8.346	7.891	6.748	4.474	3.865	0.773	low
TCGA-61-2008	2.553	0	4.593	4.755	3.966	3.841	4.136	9.881	8.434	8.486	7.270	5.342	1.963	high
TCGA-23-1120	0.356	0	2.924	0.920	5.020	3.952	6.109	8.867	9.205	7.633	4.601	4.693	0.224	low
TCGA-29-1695	3.367	1	4.752	3.692	2.596	3.412	3.755	9.187	8.467	5.560	3.415	4.845	1.492	high
TCGA-13-0883	5.745	1	4.600	4.341	6.171	3.315	3.131	9.548	6.865	4.558	2.889	5.624	1.970	high
TCGA-25-2400	3.501	1	4.136	4.921	3.295	2.059	3.466	9.002	7.953	6.541	4.913	4.551	2.248	high
TCGA-31-1951	1.874	0	3.740	6.290	4.168	3.960	5.920	8.764	8.104	4.713	3.453	5.211	0.934	low
TCGA-OY-A56Q	1.578	0	3.322	2.082	5.357	4.105	0.662	8.145	7.773	6.702	0.683	5.827	0.399	low
TCGA-24-1104	5.296	1	2.600	3.599	2.884	3.075	6.476	8.995	6.559	4.279	5.281	4.200	1.201	high
TCGA-29-1768	2.608	1	4.040	0.661	3.505	2.720	5.750	9.863	8.576	7.333	2.347	2.930	0.485	low
TCGA-30-1718	4.326	1	4.006	4.961	4.528	2.625	5.673	9.658	9.190	6.018	3.424	4.600	1.021	high
TCGA-13-1409	4.773	1	3.126	6.201	3.173	2.768	1.629	10.528	6.028	3.515	2.946	4.868	5.077	high
TCGA-25-1635	4.337	1	3.965	3.544	3.678	3.100	3.198	8.459	7.637	5.839	6.417	4.768	1.538	high
TCGA-25-2398	3.751	1	4.900	5.862	4.106	3.435	3.443	8.786	9.222	4.889	5.253	6.006	2.018	high
TCGA-61-2003	0.334	0	4.123	7.819	4.282	2.919	2.962	8.565	7.734	1.657	4.314	5.681	3.439	high
TCGA-61-1743	3.641	1	3.100	3.505	2.445	3.955	5.209	9.060	8.297	4.834	1.326	5.820	0.704	low
TCGA-36-1575	0.712	0	2.953	3.984	2.985	4.515	0.836	9.276	6.455	5.899	1.239	6.459	1.391	high
TCGA-13-0797	5.811	0	2.788	4.636	2.615	3.315	7.066	8.183	6.815	5.062	4.595	2.903	0.631	low
TCGA-23-1107	0.025	1	3.017	3.304	2.626	4.404	4.947	10.761	8.129	6.263	3.247	3.247	0.670	low
TCGA-24-2035	2.348	1	3.671	2.614	2.437	2.723	4.576	9.117	7.154	5.416	2.866	4.246	1.277	high
TCGA-24-1567	1.436	1	3.582	1.321	4.941	2.844	1.951	9.596	9.498	5.899	5.445	5.299	0.963	low
TCGA-61-2088	0.397	0	1.869	1.217	2.627	4.951	1.430	7.897	6.971	5.698	3.353	5.347	0.381	low

TCGA-31-1944	3.797	0	3.490	5.732	5.123	3.368	3.385	8.667	8.065	6.405	3.255	5.000	0.844	low
TCGA-13-1405	2.378	1	3.593	5.838	4.905	3.215	5.996	8.860	8.371	3.112	6.012	5.071	1.371	high
TCGA-23-1809	0.044	0	3.870	7.710	4.755	3.728	1.686	9.298	7.425	6.502	4.417	6.562	2.905	high
TCGA-09-1670	1.499	0	4.019	5.770	4.266	3.073	4.070	10.147	7.751	7.264	3.062	4.275	1.557	high
TCGA-25-1870	1.247	1	3.096	4.066	2.273	3.130	1.163	9.337	7.955	6.713	2.202	4.963	1.315	high
TCGA-13-0795	1.696	1	2.077	4.634	0.374	3.208	2.569	9.840	8.021	4.483	3.568	3.150	1.302	high
TCGA-61-2016	0.099	1	3.466	6.606	4.114	3.892	6.658	8.958	7.940	7.086	6.753	4.346	0.978	low
TCGA-04-1519	0.066	0	4.343	3.906	4.919	2.645	1.340	9.369	7.393	5.049	0.868	4.682	1.536	high
TCGA-13-1499	9.589	0	3.795	3.901	3.911	3.545	4.259	8.836	7.724	6.051	3.780	4.567	0.895	low
TCGA-23-2078	7.290	0	4.026	5.181	5.130	3.713	4.711	9.308	8.724	7.107	5.654	5.375	1.057	high
TCGA-24-2280	5.871	0	4.271	4.356	3.965	4.332	1.110	8.989	8.112	5.646	2.330	6.298	1.313	high
TCGA-13-1411	1.455	1	3.319	3.461	2.714	2.764	3.356	8.676	8.004	5.048	4.644	4.484	1.262	high
TCGA-13-0885	9.282	0	2.426	2.967	1.165	4.245	6.395	10.037	7.409	7.104	3.630	3.158	0.570	low
TCGA-23-1109	4.279	1	5.296	1.294	3.799	4.277	2.681	9.790	6.706	8.072	4.099	4.687	1.491	high
TCGA-24-2261	0.066	1	3.008	3.363	3.891	3.604	3.696	9.125	7.439	7.871	4.984	4.987	0.886	low
TCGA-20-1682	2.293	0	4.054	2.355	3.183	3.199	4.906	9.216	8.834	6.578	3.340	4.356	0.710	low
TCGA-04-1350	5.332	1	4.365	0.705	4.797	3.024	0.841	10.379	6.956	6.107	1.363	4.366	1.405	high
TCGA-29-1696	2.827	1	2.621	4.756	3.900	3.208	5.275	9.917	8.813	5.243	4.821	2.729	0.627	low
TCGA-61-1738	2.984	1	1.879	5.511	0.545	2.808	8.792	9.481	8.321	0.590	4.033	4.108	1.302	high
TCGA-09-1666	4.800	0	3.874	2.631	3.734	3.477	6.652	9.968	7.240	7.306	2.770	4.606	0.885	low
TCGA-13-0924	7.162	0	3.021	5.032	3.102	3.163	4.910	10.273	7.808	6.597	4.930	3.864	1.415	high
TCGA-25-1313	2.247	1	5.023	2.879	3.591	2.792	5.740	8.901	8.816	7.314	2.803	4.024	0.751	low
TCGA-31-1953	0.559	0	3.714	5.221	2.340	2.760	5.223	8.832	8.041	5.455	4.863	4.547	1.647	high
TCGA-25-1623	1.548	1	3.914	6.966	2.708	3.184	4.824	8.601	8.116	4.239	4.851	5.080	2.059	high
TCGA-24-1555	7.375	1	3.437	3.539	4.494	3.344	3.820	10.047	7.269	7.129	2.949	3.810	0.908	low
TCGA-24-2290	3.019	1	3.899	4.524	2.157	3.539	5.105	9.551	9.152	6.694	4.359	4.664	1.098	high
TCGA-23-2081	6.416	1	2.652	3.731	4.011	2.998	4.783	8.275	7.854	6.592	5.278	4.058	0.587	low
TCGA-24-1850	0.460	0	3.613	3.552	5.647	3.625	4.820	9.476	8.311	5.070	5.549	5.604	1.037	high
TCGA-61-2097	5.052	0	4.797	4.567	5.011	3.087	3.964	8.902	9.223	6.400	5.060	5.004	1.151	high
TCGA-23-1030	2.427	0	3.763	3.976	3.216	2.491	2.707	8.635	7.235	4.560	2.464	4.081	1.427	high
TCGA-31-1946	2.515	0	4.267	4.072	3.994	3.564	4.823	8.396	8.776	6.035	6.626	4.280	0.874	low
TCGA-25-2396	0.252	1	5.180	0.442	4.931	3.440	3.621	9.130	8.147	7.533	3.263	4.472	0.689	low
TCGA-23-1027	2.674	1	3.648	4.583	3.814	3.231	4.007	10.097	7.390	3.484	3.315	4.446	1.913	high
TCGA-24-1845	0.318	0	2.941	0.853	0.429	2.998	7.146	9.405	8.921	7.926	3.589	3.463	0.453	low
TCGA-25-2409	2.249	1	4.748	3.897	5.565	3.567	6.236	8.487	6.890	5.661	3.117	4.495	0.807	low
TCGA-59-2350	1.860	1	2.932	5.488	5.042	3.435	4.775	9.723	7.619	6.829	2.884	5.131	0.909	low
TCGA-31-1959	0.184	0	4.006	6.504	5.240	3.290	4.655	9.004	8.565	6.045	4.827	4.796	1.133	high
TCGA-10-0928	1.542	1	3.296	4.018	4.737	3.665	2.011	9.157	6.847	6.444	1.937	3.430	0.676	low
TCGA-13-1403	6.425	1	2.921	3.982	2.981	3.798	4.879	8.276	8.302	4.948	3.703	4.961	0.602	low
TCGA-57-1584	1.762	0	4.931	2.176	4.028	3.680	4.655	8.718	8.991	8.415	6.558	4.491	0.753	low
TCGA-36-1577	2.145	0	3.153	6.297	4.902	3.181	0.768	9.294	7.768	3.424	5.886	5.240	2.620	high
TCGA-29-1702	1.995	1	3.782	6.016	6.172	4.206	1.073	9.001	8.694	6.224	1.885	5.378	0.679	low
TCGA-29-1710	2.605	1	2.904	7.316	1.121	2.964	3.840	8.252	8.807	4.927	4.666	4.136	1.342	high
TCGA-25-1626	1.419	1	4.750	6.766	5.538	3.119	4.170	8.562	8.203	6.533	4.688	5.451	1.581	high
TCGA-29-1774	1.444	0	3.425	1.734	6.573	3.820	1.911	9.963	7.448	2.918	3.873	4.935	1.006	high
TCGA-24-0966	0.636	0	3.676	1.173	0.874	3.959	4.579	9.592	7.583	7.130	5.246	2.824	0.829	low
TCGA-24-1434	1.556	1	4.113	5.370	3.453	3.122	3.012	8.903	7.750	3.473	3.642	4.882	2.045	high
TCGA-24-1424	0.501	0	4.601	6.332	5.887	3.260	2.890	8.413	7.863	6.523	4.250	5.861	1.567	high
TCGA-61-1733	2.649	0	3.734	5.461	5.764	3.303	2.038	8.793	6.372	3.223	1.276	5.478	1.604	high
TCGA-61-1721	0.926	0	4.099	1.724	3.184	3.484	1.530	10.719	7.099	0.761	2.115	5.223	3.216	high
TCGA-04-1337	0.167	1	3.713	5.764	1.493	3.415	5.371	9.244	7.426	3.454	3.094	5.529	2.461	high

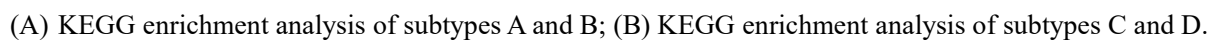
TCGA-13-0714	0.518	1	2.633	2.425	1.735	2.938	3.421	9.329	6.544	3.907	2.943	3.383	1.228	high
TCGA-13-0908	5.049	1	3.104	4.793	5.567	3.254	2.803	8.068	7.136	5.852	3.884	4.952	0.797	low
TCGA-10-0933	1.222	1	3.032	5.222	5.629	3.107	1.185	8.758	6.269	5.611	3.199	4.797	1.353	high
TCGA-04-1542	7.016	1	4.040	4.021	3.709	2.610	0.738	9.537	7.345	7.156	1.088	3.492	1.301	high
TCGA-13-0897	5.978	1	3.407	4.171	4.261	3.422	5.761	9.567	7.756	5.418	5.900	3.225	0.908	low
TCGA-36-1578	2.321	0	3.289	1.383	0.489	3.669	7.882	9.611	8.367	7.054	3.158	4.225	0.589	low
TCGA-29-1703	4.973	1	3.917	5.383	0.966	3.647	3.925	10.093	7.983	5.401	5.576	4.665	3.095	high
TCGA-25-1633	5.181	1	4.255	4.462	5.682	3.295	3.339	9.093	7.257	2.441	3.721	5.631	1.967	high
TCGA-13-1481	7.255	1	3.331	4.328	5.152	2.846	2.445	8.470	7.980	7.529	4.080	4.144	0.701	low
TCGA-10-0937	1.666	1	3.394	2.448	3.552	2.779	3.943	9.433	6.726	4.175	4.163	2.386	1.076	high
TCGA-24-1928	0.921	1	3.661	5.057	4.691	3.593	3.429	8.803	8.769	6.009	7.627	6.036	1.539	high
TCGA-24-0982	1.860	1	3.554	4.781	3.390	3.058	2.744	8.937	7.606	7.403	1.841	4.895	1.071	high
TCGA-30-1714	3.173	1	2.345	2.440	3.822	2.790	2.040	8.761	8.415	6.302	3.071	2.953	0.403	low
TCGA-24-1551	4.326	1	2.949	1.466	4.087	2.809	6.657	8.566	8.272	8.082	4.367	4.277	0.368	low
TCGA-13-0724	0.227	1	3.517	5.138	1.949	3.711	3.455	9.796	7.286	6.491	4.880	3.510	1.691	high
TCGA-24-2271	2.636	1	4.251	3.918	5.926	3.149	3.568	8.651	7.817	7.570	3.466	4.228	0.674	low
TCGA-29-1707	3.499	0	2.707	1.917	4.937	3.007	9.725	8.200	6.892	5.934	2.288	4.266	0.267	low
TCGA-25-1630	3.184	1	2.476	4.704	2.226	3.103	4.289	10.078	8.470	6.486	5.205	4.301	1.297	high
TCGA-13-0720	3.712	1	3.236	2.552	3.626	3.551	7.922	8.966	7.895	4.834	6.665	3.935	0.674	low
TCGA-59-2351	9.677	0	4.151	2.536	2.719	2.339	2.882	8.986	9.087	8.490	3.012	4.330	0.889	low
TCGA-09-2044	0.510	0	3.568	4.294	3.667	3.777	2.894	9.691	7.491	7.400	3.361	4.206	1.038	high
TCGA-29-1699	3.030	1	3.237	4.247	0.747	3.713	8.923	7.945	8.602	7.009	6.493	4.956	0.686	low
TCGA-23-1024	1.282	0	2.003	4.200	4.711	3.179	3.611	9.647	7.616	5.943	1.526	3.874	0.510	low
TCGA-57-1582	2.003	1	3.630	4.682	4.171	2.423	1.422	9.499	8.145	9.381	1.946	4.902	1.196	high
TCGA-23-1116	1.622	1	3.557	4.945	1.737	2.954	4.725	9.329	8.138	2.862	5.187	3.707	1.974	high
TCGA-29-2427	5.205	0	3.692	1.704	3.129	3.278	6.824	8.488	9.318	6.841	4.221	3.952	0.351	low
TCGA-59-2352	0.784	1	3.832	4.164	4.327	2.840	5.066	9.196	8.698	5.602	5.110	5.444	1.318	high
TCGA-25-1316	3.504	1	2.530	5.264	6.646	3.202	3.541	10.150	7.656	2.478	5.432	5.015	1.553	high
TCGA-20-1683	2.115	0	2.771	0.610	0.867	3.656	1.870	9.060	8.495	5.211	1.935	3.776	0.536	low
TCGA-36-1571	1.904	1	4.034	3.375	5.580	2.900	1.802	8.820	9.547	8.435	1.249	4.883	0.449	low
TCGA-61-2113	1.852	1	3.467	4.823	2.660	2.866	5.646	8.546	8.712	4.434	6.635	6.105	1.887	high
TCGA-59-2348	15.016	0	4.350	5.333	4.494	2.876	3.827	8.842	8.337	6.993	2.179	3.828	0.826	low
TCGA-29-1777	1.025	0	3.122	4.354	4.114	3.281	5.135	10.533	8.228	4.505	2.829	2.632	0.761	low
TCGA-25-1323	1.082	1	4.015	6.990	4.823	3.054	2.441	9.632	8.757	7.268	5.937	5.428	2.276	high
TCGA-25-1315	4.337	1	3.367	3.210	4.332	3.038	1.792	9.344	7.555	6.731	4.718	5.141	1.442	high
TCGA-13-1501	3.600	1	3.818	3.610	2.998	3.061	2.466	9.709	6.779	7.699	5.517	3.503	1.907	high
TCGA-36-1576	2.507	0	4.604	5.082	4.270	3.473	3.805	8.475	9.091	7.630	3.784	5.283	0.866	low
TCGA-57-1586	1.860	0	3.343	4.505	2.868	2.773	4.018	9.211	7.963	7.977	5.227	4.432	1.336	high
TCGA-13-1492	10.463	1	2.775	6.975	6.141	3.688	3.088	9.466	7.427	4.873	3.710	6.117	1.429	high
TCGA-29-1766	3.285	1	4.317	3.027	1.963	2.958	4.342	9.725	8.037	6.764	2.845	3.865	1.328	high
TCGA-13-0765	3.805	1	2.973	5.404	4.710	3.064	4.189	9.532	6.763	1.432	5.305	2.202	1.409	high
TCGA-09-1662	7.444	1	4.225	5.003	5.535	2.995	3.219	9.550	7.220	5.753	4.762	4.420	1.851	high
TCGA-04-1341	0.090	0	3.559	4.694	3.159	3.744	2.741	9.939	7.531	5.001	4.778	4.002	1.740	high
TCGA-29-1698	5.693	0	4.093	4.481	3.727	3.844	2.827	8.940	8.249	6.080	6.224	5.892	1.767	high
TCGA-61-1995	0.167	0	3.658	5.214	5.475	3.371	3.326	8.753	7.003	5.942	3.702	5.913	1.404	high
TCGA-24-1425	0.496	0	4.712	3.864	4.691	3.539	6.014	8.597	7.779	5.798	3.225	5.569	0.975	low
TCGA-13-1404	6.764	0	2.783	2.436	4.772	3.257	2.150	9.398	7.037	6.567	4.108	4.198	0.841	low
TCGA-24-1546	5.356	1	4.183	5.770	3.724	2.710	4.919	9.257	9.114	5.948	4.548	5.326	1.654	high
TCGA-24-1604	7.364	1	4.437	3.195	3.004	3.215	4.662	9.140	8.646	5.481	4.176	5.239	1.350	high
TCGA-61-2009	3.321	0	4.100	5.600	5.421	2.932	3.396	9.572	9.672	6.564	4.750	3.867	0.905	low
TCGA-13-1407	6.942	0	3.099	2.782	6.182	3.398	0.716	9.370	6.884	5.631	0.622	5.038	0.739	low

TCGA-57-1585	0.145	1	4.460	5.195	3.831	3.242	2.616	9.393	9.099	5.094	5.239	4.922	1.889	high
TCGA-61-2094	5.978	0	3.936	5.966	3.051	4.283	8.332	8.057	9.568	3.379	4.988	4.558	0.539	low
TCGA-36-1570	1.795	0	3.987	1.891	2.654	3.365	3.731	9.790	8.130	9.643	4.230	3.838	0.831	low
TCGA-24-1563	3.975	1	3.915	3.572	3.231	2.899	5.659	9.410	9.003	7.019	3.258	3.942	0.718	low
TCGA-24-1435	3.627	1	3.842	3.105	4.609	3.348	5.954	8.293	7.763	8.017	4.757	4.511	0.550	low
TCGA-29-1784	0.447	0	3.097	1.244	1.307	3.714	5.138	9.510	8.973	8.551	4.765	3.524	0.468	low
TCGA-23-1118	7.167	0	4.036	4.120	4.121	2.626	6.368	9.221	8.540	6.468	4.907	2.923	0.769	low
TCGA-24-1616	3.186	1	3.427	7.412	5.369	2.568	4.433	9.479	8.118	4.394	4.181	3.776	1.455	high
TCGA-24-1103	4.510	1	2.797	1.996	3.572	2.903	7.236	9.421	9.493	8.366	0.875	4.225	0.232	low
TCGA-25-2042	1.085	1	5.117	5.309	3.793	2.474	1.794	9.035	7.764	5.639	6.930	5.083	4.739	high
TCGA-13-1510	3.723	1	3.091	2.364	1.353	2.790	3.520	9.190	7.611	4.695	3.048	3.854	1.192	high
TCGA-13-0888	7.701	1	2.727	5.504	4.615	2.746	0.850	9.533	7.467	4.950	0.437	4.879	1.255	high
TCGA-24-1564	2.156	1	2.839	3.781	3.930	3.004	3.452	8.179	8.789	6.034	4.394	4.859	0.607	low
TCGA-13-A5FT	5.871	0	3.020	8.000	3.058	2.913	6.043	10.092	8.427	7.495	4.678	4.352	1.611	high
TCGA-36-1581	2.058	0	3.207	2.882	1.711	3.059	5.526	7.626	9.451	4.909	3.876	5.610	0.600	low
TCGA-23-1022	4.140	1	3.548	3.732	4.278	2.691	2.219	10.236	7.505	5.577	3.284	4.234	1.778	high
TCGA-24-1842	0.693	0	3.277	5.412	1.889	2.939	4.707	9.800	9.945	6.796	3.634	4.118	0.949	low
TCGA-30-1862	0.510	1	4.051	4.332	2.982	3.738	3.220	9.989	8.358	3.416	5.108	5.400	2.505	high
TCGA-13-1512	1.211	0	2.874	4.317	4.430	2.835	5.070	9.571	7.520	6.591	2.787	3.644	0.718	low
TCGA-13-0905	10.263	0	2.525	4.043	2.707	2.837	6.735	9.147	8.951	6.220	1.706	3.452	0.378	low
TCGA-36-1574	1.879	0	4.967	3.097	2.298	2.826	6.187	8.507	8.784	7.255	5.182	4.307	1.096	high
TCGA-13-0911	3.712	1	4.289	4.710	2.184	4.215	3.410	9.307	7.243	5.300	4.594	3.582	1.562	high
TCGA-24-2293	1.386	1	4.911	6.633	2.826	3.244	5.195	8.527	8.135	6.628	4.558	5.167	1.974	high
TCGA-24-2023	3.737	1	4.991	5.183	3.849	2.686	6.937	8.572	8.559	6.063	6.120	4.287	1.446	high
TCGA-09-1661	3.203	1	3.285	3.343	4.135	1.482	0.925	8.840	6.907	4.457	5.029	3.899	2.425	high
TCGA-13-1497	10.605	0	4.218	0.828	5.884	2.787	5.135	8.056	7.994	7.154	3.529	3.944	0.360	low
TCGA-24-2036	5.334	1	4.427	3.158	4.107	3.101	2.736	7.858	7.880	6.505	6.943	5.552	1.534	high
TCGA-25-2401	0.247	1	4.438	2.983	2.723	2.322	6.536	9.454	8.527	2.776	4.347	4.730	1.984	high
TCGA-61-1998	0.460	0	3.787	4.323	3.997	3.254	2.749	9.668	7.330	7.447	2.633	4.711	1.325	high
TCGA-29-2428	3.759	0	3.354	5.855	5.127	3.403	5.187	9.781	8.312	6.756	5.818	4.452	1.095	high
TCGA-29-1690	3.967	1	3.352	4.321	2.935	2.762	4.403	9.953	8.329	3.573	2.450	3.505	1.209	high
TCGA-13-0919	7.044	0	2.977	6.007	4.998	4.199	4.448	8.901	7.701	5.076	3.405	3.774	0.551	low
TCGA-61-2095	5.137	1	3.208	4.417	3.171	3.322	3.644	9.775	8.131	2.312	5.919	5.991	2.838	high
TCGA-13-0768	4.888	1	3.804	2.680	1.200	3.190	8.920	8.129	7.514	1.802	4.622	4.654	1.152	high
TCGA-24-1560	3.674	1	3.130	3.702	3.276	2.743	3.335	9.221	6.995	6.773	1.953	4.646	1.140	high
TCGA-24-1558	1.627	1	3.721	3.107	4.388	2.670	0.994	8.145	8.558	5.531	2.777	5.663	0.986	high
TCGA-13-1483	2.452	1	3.377	5.270	2.424	2.434	5.427	8.926	7.315	4.254	5.007	4.478	2.177	high
TCGA-04-1362	3.693	1	4.723	5.721	3.652	3.270	6.005	8.725	7.922	8.987	7.478	3.873	1.386	high
TCGA-09-2048	0.378	1	2.895	2.667	5.954	3.786	0.865	9.303	6.494	7.843	1.188	4.128	0.498	low
TCGA-24-1427	0.403	0	4.016	4.465	5.145	2.546	2.151	8.889	7.568	5.611	4.138	5.197	1.802	high
TCGA-24-1846	0.364	0	3.993	2.613	3.915	3.808	4.245	9.025	7.019	8.647	3.730	4.433	0.750	low
TCGA-23-1028	4.118	0	3.417	4.776	4.769	2.730	6.655	9.695	8.096	4.691	4.187	2.445	0.732	low
TCGA-24-1105	3.951	1	2.266	4.656	3.031	2.869	3.682	8.773	7.373	5.828	3.057	4.956	0.994	high
TCGA-24-1930	6.759	1	3.516	5.001	2.279	3.446	4.137	8.767	8.301	7.497	4.435	4.162	0.931	low
GSM642934	9.718	0	2.369	2.377	3.920	3.062	7.599	9.154	8.224	6.404	4.071	4.935	0.464	low
GSM642936	2.474	1	3.569	3.302	3.710	3.342	6.807	9.187	7.664	7.035	3.819	4.454	0.714	low
GSM642941	9.090	0	2.640	3.424	3.902	3.024	0.969	9.717	7.944	4.873	6.120	4.238	1.570	high
GSM642942	2.959	1	4.133	6.256	5.354	3.262	0.840	9.272	6.571	7.146	4.972	5.265	2.833	high
GSM642943	2.715	1	3.501	2.501	4.617	4.039	5.051	7.452	7.038	6.794	3.707	4.196	0.336	low
GSM642944	4.622	1	4.121	4.134	3.767	3.916	3.750	8.868	8.287	6.548	4.078	4.806	0.887	low
GSM642947	4.625	0	3.405	6.077	4.212	3.619	5.431	9.232	7.448	8.563	2.139	5.138	0.808	low

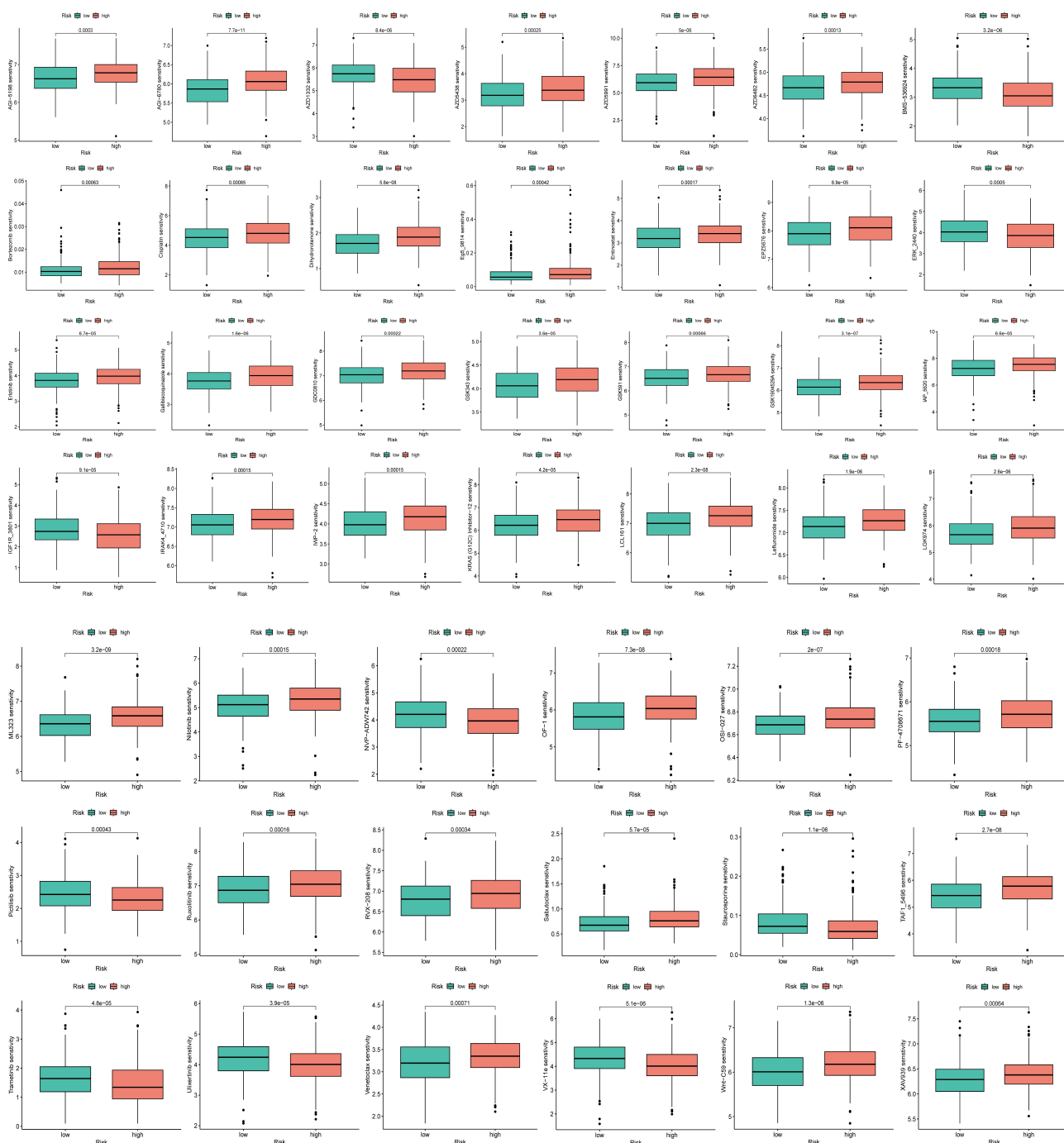
GSM642949	0.745	0	4.207	2.628	3.539	2.320	2.912	9.751	8.691	3.380	4.207	4.714	2.110	high
GSM642951	1.688	1	4.170	4.788	3.345	2.804	6.935	10.217	8.150	4.862	5.102	3.389	1.673	high
GSM642952	1.096	1	3.331	4.652	3.278	3.843	1.068	10.047	8.939	3.014	1.877	3.400	0.950	low
GSM642953	2.422	1	6.149	4.102	3.645	3.300	4.253	8.876	6.260	5.106	3.963	4.402	3.126	high
GSM642954	12.216	0	2.882	2.485	3.753	4.513	1.324	9.622	8.212	3.162	2.065	4.411	0.631	low
GSM642955	1.814	1	3.844	2.054	3.316	3.806	3.374	8.127	7.747	7.981	3.900	4.357	0.528	low
GSM642957	0.690	1	4.357	4.976	4.603	3.077	4.189	9.424	7.768	7.508	2.021	4.498	1.068	high
GSM642962	2.173	1	2.403	2.372	2.665	3.264	6.143	10.215	8.650	4.732	2.216	4.388	0.608	low
GSM642966	1.430	1	3.942	4.302	3.096	3.858	5.377	9.025	5.393	5.868	4.916	4.531	1.955	high
GSM642968	10.060	0	2.752	7.237	3.902	3.168	3.426	9.011	7.648	4.549	4.417	3.599	1.238	high
GSM642969	2.181	1	3.839	6.256	2.830	3.281	3.982	9.102	7.875	6.434	4.178	5.130	1.855	high
GSM642970	2.460	1	2.630	2.076	3.945	3.281	1.346	9.435	8.025	2.858	1.985	4.294	0.777	low
GSM642971	9.992	0	2.550	3.133	3.475	4.020	2.215	10.017	7.725	3.159	2.339	3.675	0.782	low
GSM642974	0.838	1	3.295	5.560	3.886	3.331	2.016	8.943	10.409	8.154	2.048	4.730	0.468	low
GSM642979	1.553	1	3.769	5.495	2.613	3.341	5.561	9.406	8.789	2.851	4.960	4.739	1.734	high
GSM642980	3.803	1	4.110	4.147	4.483	2.694	3.160	9.029	7.398	8.217	1.997	3.975	0.920	low
GSM642981	3.877	1	4.334	2.041	3.726	2.557	2.334	9.923	8.282	8.076	2.156	3.447	0.944	low
GSM642984	10.290	0	5.043	3.402	3.828	2.830	5.847	9.348	8.575	6.626	2.272	4.752	1.071	high
GSM642989	3.378	1	4.472	2.575	4.562	3.044	1.734	10.024	7.645	7.283	5.224	5.095	2.187	high
GSM642991	5.022	0	4.860	3.203	4.295	2.757	2.845	9.358	9.001	7.280	2.490	4.127	0.940	low
GSM642994	9.293	1	2.748	2.581	4.039	2.586	4.310	8.648	7.598	5.812	2.011	3.632	0.490	low
GSM642995	1.397	1	2.656	4.647	3.076	2.887	6.915	9.815	8.016	3.831	4.105	5.795	1.573	high
GSM642996	1.586	1	3.841	4.331	2.644	2.971	3.542	9.353	9.121	4.897	4.145	4.992	1.519	high
GSM642997	0.784	1	5.417	2.090	2.175	2.512	3.110	9.692	5.644	6.931	1.989	5.890	4.923	high
GSM642999	7.356	1	3.644	4.170	3.597	3.276	6.639	8.985	8.227	7.840	2.942	2.877	0.421	low
GSM643000	3.490	1	4.156	2.897	4.073	2.912	4.553	9.025	8.015	8.027	3.798	4.087	0.789	low
GSM643004	0.923	1	4.572	5.350	2.089	3.329	1.574	11.401	7.447	5.902	7.696	7.373	16.057	high
GSM643006	1.567	1	4.305	2.586	2.474	2.349	5.544	9.069	7.665	5.863	2.597	4.365	1.319	high
GSM643007	0.775	1	1.621	8.899	3.430	3.335	2.226	9.061	8.302	3.187	2.744	5.234	1.356	high
GSM643008	6.112	1	3.293	2.577	4.128	3.587	5.935	8.587	7.213	8.119	4.095	4.659	0.522	low
GSM643009	1.879	1	3.558	3.536	4.794	3.081	2.928	9.332	7.267	7.272	4.578	4.088	1.070	high
GSM643011	0.008	1	4.217	5.808	4.078	2.899	5.655	8.737	8.299	4.928	4.464	5.124	1.503	high
GSM643012	9.611	0	4.395	4.751	2.869	4.019	5.326	8.905	8.093	8.120	4.364	4.699	0.948	low
GSM643013	9.279	0	4.095	2.680	5.213	3.122	2.832	9.607	6.231	4.127	2.941	5.640	2.175	high
GSM643014	2.493	1	2.832	6.550	4.228	5.279	6.667	8.752	7.277	8.491	6.923	3.494	0.434	low
GSM643015	3.811	1	3.987	2.772	2.234	2.969	5.547	9.463	9.346	6.935	2.859	4.246	0.731	low
GSM643016	3.000	1	4.659	6.149	6.498	3.188	1.909	8.662	8.050	8.763	2.090	4.019	0.720	low
GSM643017	7.759	0	3.197	3.741	2.657	3.236	4.277	8.826	8.079	5.498	3.958	4.336	0.902	low
GSM643021	0.507	1	2.878	2.291	3.413	3.487	0.783	9.846	7.478	3.027	1.826	3.766	1.021	high
GSM643026	3.110	1	3.826	2.636	4.268	3.613	6.909	8.794	8.602	8.136	2.413	3.740	0.282	low
GSM643030	2.310	1	3.279	5.189	4.335	3.728	2.980	8.730	7.864	6.702	6.175	4.235	0.970	low
GSM643031	3.984	1	3.760	3.780	2.316	2.370	3.896	10.056	8.483	6.447	6.792	2.832	1.900	high
GSM643032	0.052	1	3.807	7.337	5.623	3.012	5.841	8.473	7.405	3.343	3.406	5.983	1.656	high
GSM643035	2.658	1	4.537	4.605	3.908	2.993	4.288	9.103	7.904	6.159	4.012	4.294	1.428	high
GSM643036	2.170	1	3.404	2.360	2.491	3.167	7.047	9.588	8.279	7.166	3.805	4.667	0.761	low
GSM643037	5.827	0	3.432	2.574	4.502	3.466	6.046	8.834	7.947	5.631	2.171	4.508	0.448	low
GSM643038	3.814	1	3.142	2.532	3.287	2.845	4.913	8.252	7.025	3.783	5.572	4.553	1.178	high
GSM643039	0.405	1	2.508	3.378	2.205	3.257	2.050	8.993	8.284	2.747	3.568	6.140	1.569	high

<https://docs.google.com/spreadsheets/d/1J8bR2AyEwb0bZcMGpo2V8lwZBgv63aVP/edit?usp=sharing&oid=100551137938415125175&rtpof=true&sd=true>

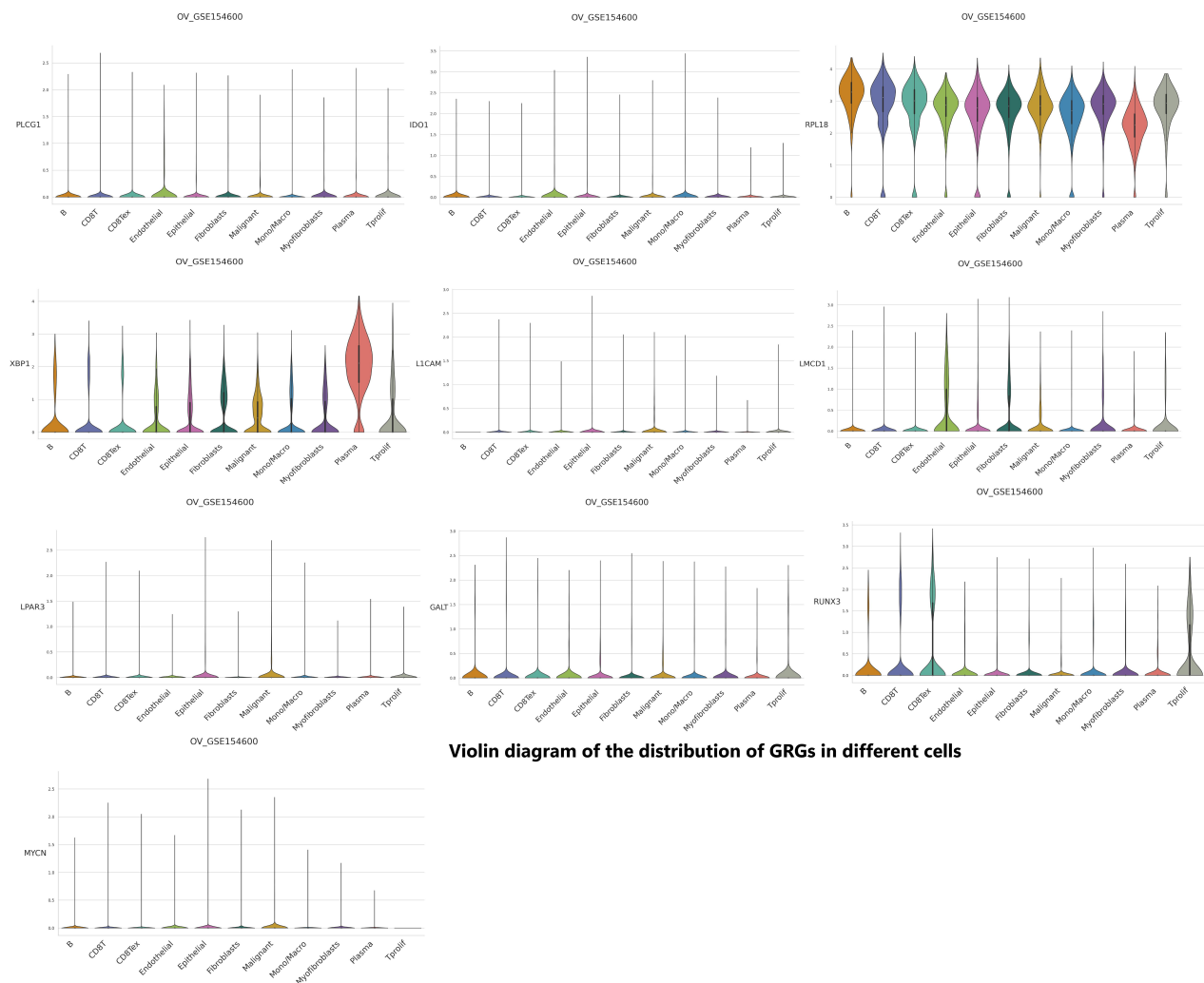
Supplementary figure1. Enrichment analysis of different molecular subtypes



Supplementary figure2. Drug sensitivity analysis



Supplementary figure3. Analysis of CRG expression levels in different subgroups



Violin diagram of the distribution of GRGs in different cells