

Table S1 Clinical features of gastric cancer in GSE84437

Clinical features	GSE84437, n (%)
Age (years)	
≤65	283 (65.4)
>65	150 (34.6)
Gender	
Male	296 (68.4)
Female	137 (31.6)
T stage	
1	11 (2.5)
2	38 (8.8)
3	92 (21.3)
4	292 (67.4)
N stage	
0	80 (18.5)
1	188 (43.4)
2	132 (30.5)
3	33 (7.6)

Table S2 DEGs list of CGC and NCGC

Gene	Up-regulated
<i>CRNN</i>	CGC
<i>KRT4</i>	CGC
<i>MUC21</i>	CGC
<i>TMPRSS11B</i>	CGC
<i>RHCG</i>	CGC
<i>KRT6C</i>	CGC
<i>SPRR2E</i>	CGC
<i>KRT13</i>	CGC
<i>IL36A</i>	CGC
<i>TMPRSS11A</i>	CGC
<i>KRT78</i>	CGC
<i>SERPINB11</i>	CGC
<i>IVL</i>	CGC
<i>KRT5</i>	CGC
<i>CRCT1</i>	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
<i>TMPRSS11E</i>	CGC
<i>SPRR3</i>	CGC
<i>SERPINB13</i>	CGC
<i>SPRR2A</i>	CGC
<i>KPRP</i>	CGC
<i>TMPRSS11D</i>	CGC
<i>CALML3</i>	CGC
<i>KLK5</i>	CGC
<i>SPRR2F</i>	CGC
<i>GBP6</i>	CGC
<i>KRTDAP</i>	CGC
<i>KRT6A</i>	CGC
<i>TMPRSS11BNL</i>	CGC
<i>CAPN14</i>	CGC
<i>KRT14</i>	CGC
<i>SPRR2D</i>	CGC
<i>A2ML1</i>	CGC
<i>MUC22</i>	CGC
<i>CLCA4</i>	CGC
<i>SPRR1A</i>	CGC
<i>MAL</i>	CGC
<i>TMPRSS11F</i>	CGC
<i>DYNAP</i>	CGC
<i>CAPNS2</i>	CGC
<i>MIR205HG</i>	CGC
<i>ADH7</i>	CGC
<i>CERS3</i>	CGC
<i>SERPINB12</i>	CGC
<i>CSTA</i>	CGC
<i>FAT2</i>	CGC
<i>AC011473.4</i>	CGC
<i>PSG4</i>	CGC
<i>SPRR1B</i>	CGC
<i>DSC3</i>	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
<i>FTLP10</i>	CGC
<i>TGM5</i>	CGC
<i>KRT16P6</i>	CGC
<i>KLK13</i>	CGC
<i>GJB6</i>	CGC
<i>SERPINB3</i>	CGC
<i>NCCRP1</i>	CGC
<i>ZNF750</i>	CGC
<i>SPINK5</i>	CGC
<i>LGALS7</i>	CGC
<i>TMEM40</i>	CGC
<i>BNC1</i>	CGC
<i>PKP1</i>	CGC
<i>RNF222</i>	CGC
<i>ANXA8</i>	CGC
<i>NKX6-1</i>	CGC
<i>KRT16</i>	CGC
<i>S100A7A</i>	CGC
<i>PADI1</i>	CGC
<i>IL36G</i>	CGC
<i>SCEL</i>	CGC
<i>SCGB3A1</i>	CGC
<i>KRT6B</i>	CGC
<i>GPR87</i>	CGC
<i>S100A2</i>	CGC
<i>SERPINB4</i>	CGC
<i>FOXE1</i>	CGC
<i>SCNN1G</i>	CGC
<i>LYPD3</i>	CGC
<i>SCNN1B</i>	CGC
<i>FAM83C</i>	CGC
<i>LY6D</i>	CGC
<i>IGFL1</i>	CGC
<i>CWH43</i>	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
<i>KRT15</i>	CGC
<i>AC009123.1</i>	CGC
<i>RNF225</i>	CGC
<i>ATP12A</i>	CGC
<i>LYPD2</i>	CGC
<i>TP63</i>	CGC
<i>DEFB4A</i>	CGC
<i>PNLIPRP3</i>	CGC
<i>ANXA8L1</i>	CGC
<i>SCGB1A1</i>	CGC
<i>LGALS7B</i>	CGC
<i>AC004147.4</i>	CGC
<i>KRT16P3</i>	CGC
<i>LIPF</i>	CGC
<i>FETUB</i>	CGC
<i>GRXCR2</i>	CGC
<i>AL079303.1</i>	CGC
<i>WNT7A</i>	CGC
<i>FAM83A</i>	CGC
<i>RAET1E</i>	CGC
<i>IRX4</i>	CGC
<i>VSIG8</i>	CGC
<i>LINC00707</i>	CGC
<i>TBX5-AS1</i>	CGC
<i>PSG9</i>	CGC
<i>IL20RB</i>	CGC
<i>KRT16P1</i>	CGC
<i>C5orf66-AS1</i>	CGC
<i>CYP24A1</i>	CGC
<i>LINC02560</i>	CGC
<i>AC006262.4</i>	CGC
<i>MUC15</i>	CGC
<i>KRT16P2</i>	CGC
<i>LINC01254</i>	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
AP003500.1	CGC
AQP3	CGC
DUOXA1	CGC
FAM83A-AS1	CGC
GRHL3	CGC
SOX15	CGC
SPAG17	CGC
BBOX1	CGC
CRISP3	CGC
LEXM	CGC
ANXA1	CGC
NTF4	CGC
MUC16	CGC
ADGRF1	CGC
PLAC4	CGC
PPL	CGC
DEFB1	CGC
UPK3B	CGC
AL162511.1	CGC
FSTL4	CGC
KLK7	CGC
KRT17P3	CGC
OTOP2	CGC
SFTPD	CGC
FAM167A	CGC
IL19	CGC
GSDMC	CGC
CLPSL1	CGC
DENND2C	CGC
DUOX1	CGC
RAET1G	CGC
KRT17P1	CGC
FGFBP1	CGC
ARHGAP40	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
KRT17P6	CGC
CYP4B1	CGC
SLC5A5	CGC
TBL1Y	CGC
DCAF12L1	CGC
RAET1L	CGC
TBX5	CGC
HPSE2	CGC
RDH12	CGC
RHOV	CGC
AC112236.1	CGC
NKX2-8	CGC
UNC5B-AS1	CGC
HAS3	CGC
AC011483.2	CGC
AL121950.1	CGC
AC024337.1	CGC
EPHX3	CGC
LINC00885	CGC
PRKG2-AS1	CGC
ALOX12B	CGC
EEF1A2	CGC
IFNWP19	CGC
KRT17	CGC
FZD10	CGC
MSLNL	CGC
KRTAP4-1	CGC
AC004808.2	CGC
AP000424.1	CGC
AL033397.1	CGC
STMND1	CGC
AC245041.1	CGC
KRT17P2	CGC
DSCAM-AS1	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
AC090541.1	CGC
KLK8	CGC
HPCA	CGC
LINC01564	CGC
LINC01269	CGC
AC025062.2	CGC
LINC00592	CGC
HSPA1A	CGC
LINC01460	CGC
AC080037.2	CGC
GJB2	CGC
ATP13A5	CGC
LINC02783	CGC
EREG	CGC
CDH26	CGC
MIR31HG	CGC
CNTN3	CGC
AC008406.3	CGC
UPK1A	CGC
KLK11	CGC
ARMC3	CGC
AP002800.1	CGC
AC133785.1	CGC
WNT7B	CGC
FAM153A	CGC
EYA2	CGC
HLA-V	CGC
DUSP13	CGC
AC023157.2	CGC
AL352984.1	CGC
ALDH1L1	CGC
CCDC190	CGC
GRHL1	CGC
PSCA	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
RASD1	CGC
AL163952.1	CGC
MANCR	CGC
CGB7	CGC
IRX3	CGC
DRC1	CGC
TACSTD2	CGC
ARHGEF4	CGC
COL6A5	CGC
SFTA2	CGC
OR7E91P	CGC
LINP1	CGC
VTCN1	CGC
LINC02057	CGC
SOX21-AS1	CGC
LINC02832	CGC
RNF39	CGC
BCAS1	CGC
ATP13A4	CGC
NUPR2	CGC
AL139039.1	CGC
AC004990.1	CGC
AC112518.1	CGC
ATP6V0A4	CGC
SOX21	CGC
LINC00887	CGC
LINC02188	CGC
ULBP2	CGC
AL445649.1	CGC
MUC5B	CGC
PCDHAC1	CGC
AC138305.1	CGC
TTC9	CGC
GNA15	CGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
<i>PLAAT1</i>	CGC
<i>AC008556.1</i>	CGC
<i>AL355312.3</i>	CGC
<i>KRT7-AS</i>	CGC
<i>SLPI</i>	CGC
<i>AREG</i>	CGC
<i>PCDHAC2</i>	CGC
<i>DKK1</i>	CGC
<i>PPP1R1C</i>	CGC
<i>RNF223</i>	CGC
<i>AC130456.2</i>	CGC
<i>CLIC6</i>	CGC
<i>AL118522.1</i>	CGC
<i>NMRAL2P</i>	CGC
<i>ECEL1P1</i>	CGC
<i>MYH16</i>	CGC
<i>ARL14</i>	CGC
<i>ELAVL4</i>	NCGC
<i>NEXN</i>	NCGC
<i>AC068473.3</i>	NCGC
<i>AC005291.2</i>	NCGC
<i>DMD</i>	NCGC
<i>PSPHP1</i>	NCGC
<i>ZNF177</i>	NCGC
<i>LINC00578</i>	NCGC
<i>SIX2</i>	NCGC
<i>CCND2</i>	NCGC
<i>LGR5</i>	NCGC
<i>CHRM2</i>	NCGC
<i>SYT6</i>	NCGC
<i>EPHA3</i>	NCGC
<i>GLP2R</i>	NCGC
<i>AC004080.3</i>	NCGC
<i>AC004080.2</i>	NCGC

Table S2 (continued)

Table S2 (continued)

Clinical features	Up-regulated
<i>ASCL2</i>	NCGC
<i>OMD</i>	NCGC
<i>OTC</i>	NCGC
<i>TAC1</i>	NCGC
<i>XPNPEP2</i>	NCGC
<i>ODAM</i>	NCGC
<i>AC024651.1</i>	NCGC
<i>ASPN</i>	NCGC
<i>PRG4</i>	NCGC
<i>AC025594.1</i>	NCGC
<i>NRXN3</i>	NCGC
<i>FREM1</i>	NCGC
<i>PHYHIPL</i>	NCGC
<i>AL022324.3</i>	NCGC
<i>AC113133.1</i>	NCGC
<i>NCAM1</i>	NCGC
<i>DPEP1</i>	NCGC
<i>CILP</i>	NCGC
<i>CLVS2</i>	NCGC
<i>NRK</i>	NCGC
<i>VIP</i>	NCGC
<i>POPDC2</i>	NCGC
<i>PTPRO</i>	NCGC
<i>FGF10-AS1</i>	NCGC
<i>PSD</i>	NCGC
<i>TNN</i>	NCGC
<i>AC093702.1</i>	NCGC
<i>UTS2</i>	NCGC
<i>SMPX</i>	NCGC
<i>MIR486-1</i>	NCGC
<i>CTNNA2</i>	NCGC
<i>AP005018.2</i>	NCGC
<i>LINC02520</i>	NCGC
<i>CARTPT</i>	NCGC

Table S2 (continued)

Table S2 (continued)

Gene	Up-regulated
<i>GALNT9</i>	NCGC
<i>PLA2G2A</i>	NCGC
<i>KERA</i>	NCGC
<i>NKX2-5</i>	NCGC
<i>EPHA7</i>	NCGC
<i>FGF10</i>	NCGC
<i>SLC7A14</i>	NCGC
<i>MAB21L2</i>	NCGC
<i>HAND2</i>	NCGC
<i>ACTG2</i>	NCGC
<i>HAND2-AS1</i>	NCGC
<i>AC053503.5</i>	NCGC
<i>NKX6-3</i>	NCGC
<i>NKX3-2</i>	NCGC
<i>AC093787.1</i>	NCGC
<i>AQP12B</i>	NCGC
<i>SMYD1</i>	NCGC
<i>KCNA1</i>	NCGC

Abbreviations: DEGs, differentially expressed genes; CGC, cardia gastric cancer; NCGC, non-cardia gastric cancer.

Table S3 The risk coefficient of signature genes

Gene	Coef
<i>KRT17</i>	0.106381
<i>PPP1R1C</i>	0.535501
<i>SLC5A5</i>	0.290156
<i>SYT6</i>	1.21479

Table S4 The estimated risk score for all samples in TCGA-STAD

ID	Risk score	Risk
TCGA-IN-AB1X	1.902343825	High
TCGA-FP-A9TM	1.209378381	High
TCGA-VQ-AA69	0.878972009	Low
TCGA-BR-7722	2.984975018	High
TCGA-BR-6852	0.735964123	Low
TCGA-IN-A6RI	0.950029291	High
TCGA-IN-A7NR	4.535595447	High
TCGA-IN-A6RL	5.464564434	High
TCGA-FP-8099	1.038968556	High
TCGA-VQ-AA68	1.246174262	High
TCGA-HF-7131	3.993521593	High
TCGA-VQ-AA6A	0.744991054	Low
TCGA-R5-A7O7	0.910109068	Low
TCGA-RD-A7BS	5.154254829	High
TCGA-R5-A805	2.283661559	High
TCGA-VQ-A91U	0.827331873	Low
TCGA-VQ-A8PK	1.553751307	High
TCGA-R5-A7ZE	1.623294265	High
TCGA-VQ-A8E7	1.295817057	High
TCGA-KB-A93G	0.779422397	Low
TCGA-IN-AB1V	1.660170081	High
TCGA-IN-8663	2.459843003	High
TCGA-RD-A8N9	0.909167396	Low
TCGA-BR-6710	2.86875831	High
TCGA-VQ-A91V	1.475980958	High
TCGA-IN-A6RS	1.065022297	High
TCGA-IN-A6RR	9.759355747	High
TCGA-FP-A4BF	1.195951424	High
TCGA-FP-7829	0.939984564	High
TCGA-FP-8631	0.975468354	High
TCGA-IN-A6RJ	0.885836362	Low
TCGA-IN-A7NT	1.721570317	High
TCGA-IP-7968	1.777911207	High
TCGA-IN-A6RO	2.397978939	High
TCGA-IN-7808	0.883572482	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-BR-7901	1.21710153	High
TCGA-HF-7133	2.21914491	High
TCGA-IN-7806	0.679985497	Low
TCGA-IN-A7NU	1.363515515	High
TCGA-IN-8462	3.178217301	High
TCGA-IN-A6RN	1.981876401	High
TCGA-D7-A74A	1.593244762	High
TCGA-VQ-AA64	1.838414095	High
TCGA-CG-5717	1.171017127	High
TCGA-BR-A4J8	0.560801724	Low
TCGA-CG-5732	0.841164984	Low
TCGA-CG-4477	1.387967885	High
TCGA-CG-5723	1.392202131	High
TCGA-CG-5725	0.775574104	Low
TCGA-VQ-AA6K	1.392994879	High
TCGA-BR-7196	0.755787284	Low
TCGA-CD-A4MG	0.635616803	Low
TCGA-D7-8570	0.485431724	Low
TCGA-BR-4201	1.464126291	High
TCGA-VQ-A94T	1.044108352	High
TCGA-D7-A6F0	1.018839175	High
TCGA-VQ-AA6G	1.133766166	High
TCGA-FP-8211	1.772507377	High
TCGA-D7-5577	1.540968793	High
TCGA-BR-6709	1.154380576	High
TCGA-BR-A44T	0.595721341	Low
TCGA-VQ-AA6F	0.734250332	Low
TCGA-BR-A4J6	1.828396188	High
TCGA-BR-4369	1.551293957	High
TCGA-D7-6519	2.180352412	High
TCGA-CG-4304	0.741345184	Low
TCGA-BR-6454	1.571760383	High
TCGA-CG-4466	0.84581477	Low
TCGA-CD-8532	1.279670719	High

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-VQ-A8PQ	1.241809214	High
TCGA-BR-8371	0.658376339	Low
TCGA-BR-8690	1.047290471	High
TCGA-D7-6525	2.690691697	High
TCGA-VQ-A8PM	1.832903468	High
TCGA-BR-7717	1.524092795	High
TCGA-BR-7959	0.933422818	High
TCGA-VQ-A91Q	1.156651746	High
TCGA-VQ-AA6J	0.596104231	Low
TCGA-CG-5720	0.772138391	Low
TCGA-CD-A486	1.360023508	High
TCGA-CD-A48A	1.497367241	High
TCGA-VQ-A92D	0.683258583	Low
TCGA-D7-6527	0.564817232	Low
TCGA-CG-4437	1.037539804	High
TCGA-VQ-A8PE	0.794383783	Low
TCGA-F1-6874	0.774961836	Low
TCGA-CG-4301	2.021284322	High
TCGA-BR-8060	0.660557521	Low
TCGA-BR-8687	0.951054937	High
TCGA-BR-7704	0.613066529	Low
TCGA-BR-6566	0.827660765	Low
TCGA-HU-8244	0.714669818	Low
TCGA-BR-8590	1.301088653	High
TCGA-HU-8610	0.965584107	High
TCGA-HU-8249	0.695826682	Low
TCGA-VQ-A8PJ	1.802820696	High
TCGA-BR-6565	0.63142986	Low
TCGA-VQ-A923	0.926769677	High
TCGA-D7-A4YU	0.719541324	Low
TCGA-BR-8679	0.62784203	Low
TCGA-CD-8535	0.881511727	Low
TCGA-BR-6458	0.736543217	Low
TCGA-HJ-7597	1.01087165	High

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-B7-5818	0.567791436	Low
TCGA-BR-8588	1.084726884	High
TCGA-HU-A4G9	0.468961048	Low
TCGA-VQ-A91S	0.739105294	Low
TCGA-BR-8365	0.767079852	Low
TCGA-D7-5578	0.696252961	Low
TCGA-BR-6453	0.656724162	Low
TCGA-KB-A93H	0.713890371	Low
TCGA-CG-4476	1.802346571	High
TCGA-BR-8297	0.583121152	Low
TCGA-VQ-A91A	0.528505767	Low
TCGA-D7-6815	1.172085677	High
TCGA-CG-5719	1.164123854	High
TCGA-CD-8530	0.75376825	Low
TCGA-BR-7707	1.06877158	High
TCGA-VQ-A8P8	1.052121602	High
TCGA-VQ-A8DT	1.07307339	High
TCGA-CD-8526	2.405589976	High
TCGA-BR-7957	0.686253453	Low
TCGA-BR-6452	1.2554859	High
TCGA-BR-8592	0.910256493	Low
TCGA-D7-8573	0.606093142	Low
TCGA-FP-A8CX	2.090821456	High
TCGA-BR-8081	0.594064726	Low
TCGA-FP-7735	0.659426223	Low
TCGA-BR-8678	0.790111515	Low
TCGA-RD-A8N5	0.767567307	Low
TCGA-BR-8295	2.35847104	High
TCGA-CD-5813	0.633520399	Low
TCGA-CG-4444	0.611129464	Low
TCGA-BR-7851	0.553669731	Low
TCGA-CG-4443	1.077485286	High
TCGA-CG-5718	1.150746216	High
TCGA-BR-6455	0.837930822	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-BR-4363	1.31668419	High
TCGA-VQ-A8P5	1.303554546	High
TCGA-BR-8372	0.662844538	Low
TCGA-BR-8589	0.550469125	Low
TCGA-CG-5734	1.883807043	High
TCGA-BR-4294	0.50178646	Low
TCGA-D7-6822	1.096378019	High
TCGA-BR-6803	0.993723088	High
TCGA-BR-6457	0.623730955	Low
TCGA-BR-8367	0.846435244	Low
TCGA-D7-A6F2	0.546131746	Low
TCGA-D7-6521	0.842235718	Low
TCGA-BR-7723	0.600341798	Low
TCGA-VQ-A91D	0.786696984	Low
TCGA-KB-A6F7	1.181437799	High
TCGA-B7-A5TN	1.926407934	High
TCGA-VQ-A8E0	1.126701424	High
TCGA-VQ-A8PU	0.675814364	Low
TCGA-BR-4357	0.770219732	Low
TCGA-CG-4440	1.271774844	High
TCGA-BR-6802	1.461021071	High
TCGA-VQ-A8E2	1.876939806	High
TCGA-D7-6818	1.199673552	High
TCGA-BR-8059	0.632411764	Low
TCGA-D7-6526	0.606305241	Low
TCGA-BR-6801	0.617348257	Low
TCGA-CG-4460	1.271397163	High
TCGA-B7-A5TJ	0.695028588	Low
TCGA-D7-A6EZ	0.749579657	Low
TCGA-RD-A8MV	0.913506562	Low
TCGA-BR-8484	0.551016485	Low
TCGA-HU-A4H0	0.649542884	Low
TCGA-HF-7134	0.754071068	Low
TCGA-CG-4441	0.971776575	High

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-RD-A7BT	0.91729256	Low
TCGA-BR-8296	0.767372558	Low
TCGA-BR-6705	1.3543579	High
TCGA-BR-7716	1.155316234	High
TCGA-HU-8608	0.47974802	Low
TCGA-VQ-A8P3	1.376549543	High
TCGA-D7-8572	0.910755546	Low
TCGA-BR-8366	1.473592223	High
TCGA-D7-6528	0.791360533	Low
TCGA-BR-6707	0.837208567	Low
TCGA-BR-8368	0.589262084	Low
TCGA-BR-8361	0.575722501	Low
TCGA-VQ-A927	1.721103253	High
TCGA-VQ-A8PP	1.304272156	High
TCGA-RD-A7C1	1.774235043	High
TCGA-BR-6456	0.712770868	Low
TCGA-BR-A4CR	0.59736446	Low
TCGA-VQ-A8PF	0.706552914	Low
TCGA-BR-7715	0.645476863	Low
TCGA-D7-8575	1.129722084	High
TCGA-BR-8077	0.634467224	Low
TCGA-CD-8531	0.523960932	Low
TCGA-BR-8485	1.686449171	High
TCGA-HU-A4H5	0.98426575	High
TCGA-RD-A7BW	1.294925564	High
TCGA-BR-8486	0.634687994	Low
TCGA-D7-A4YX	0.744560986	Low
TCGA-BR-A4CS	1.255619538	High
TCGA-B7-A5TI	0.775568705	Low
TCGA-CG-5722	1.394462481	High
TCGA-D7-A748	1.184950112	High
TCGA-BR-8373	1.572931962	High
TCGA-HU-A4GH	0.875782513	Low
TCGA-VQ-A94P	0.61970771	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-BR-8364	1.292641489	High
TCGA-BR-8080	0.730301292	Low
TCGA-VQ-A8PD	1.274492701	High
TCGA-RD-A8N0	1.322833111	High
TCGA-BR-8289	0.642066869	Low
TCGA-HU-A4H3	1.280931134	High
TCGA-VQ-A8P2	0.716689513	Low
TCGA-BR-4253	0.709107052	Low
TCGA-BR-8381	0.912834968	Low
TCGA-FP-7998	0.667150458	Low
TCGA-R5-A7ZR	1.139499089	High
TCGA-BR-6564	0.71514372	Low
TCGA-VQ-A928	1.149130202	High
TCGA-BR-7958	0.779928834	Low
TCGA-BR-4187	0.611175367	Low
TCGA-BR-4256	1.687002362	High
TCGA-BR-4257	0.897984075	Low
TCGA-BR-4366	0.68796306	Low
TCGA-BR-4367	0.916583371	Low
TCGA-BR-4368	0.607847413	Low
TCGA-BR-4370	1.745282195	High
TCGA-BR-6563	0.887022977	Low
TCGA-BR-7197	0.595957194	Low
TCGA-BR-8058	1.172590723	High
TCGA-BR-8284	0.80663608	Low
TCGA-BR-8286	1.149751113	High
TCGA-BR-8291	0.562228551	Low
TCGA-BR-8369	0.83690545	Low
TCGA-BR-8380	0.890634194	Low
TCGA-BR-8382	0.902271135	Low
TCGA-BR-8384	0.686481609	Low
TCGA-BR-8483	0.945174553	High
TCGA-BR-8487	0.500047751	Low
TCGA-BR-8591	0.853776848	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-BR-8676	0.474743727	Low
TCGA-BR-8677	0.579827673	Low
TCGA-BR-8680	0.69232217	Low
TCGA-BR-8682	0.655178977	Low
TCGA-BR-8683	0.971059731	High
TCGA-BR-8686	0.695094822	Low
TCGA-BR-A44U	0.488876425	Low
TCGA-BR-A4IV	0.619604101	Low
TCGA-BR-A4J4	1.724389248	High
TCGA-BR-A4J5	1.071170658	High
TCGA-BR-A4J7	0.605267586	Low
TCGA-BR-A4J9	0.617262814	Low
TCGA-BR-A4PF	0.528159166	Low
TCGA-BR-A4QL	0.549535888	Low
TCGA-CD-5798	0.964564421	High
TCGA-CD-5799	0.629013816	Low
TCGA-CD-5800	1.399460498	High
TCGA-CD-5801	1.098666343	High
TCGA-CD-5803	0.840450342	Low
TCGA-CD-5804	1.032056253	High
TCGA-CD-8524	2.370349723	High
TCGA-CD-8525	1.671427158	High
TCGA-CD-8527	0.884405197	Low
TCGA-CD-8528	0.568152619	Low
TCGA-CD-8529	0.899660823	Low
TCGA-CD-8533	1.429180571	High
TCGA-CD-8534	0.505353399	Low
TCGA-CD-A487	1.110613531	High
TCGA-CD-A489	2.133870569	High
TCGA-CD-A48C	1.160179246	High
TCGA-CD-A4MH	0.677714947	Low
TCGA-CG-4305	1.084183862	High
TCGA-CG-4306	1.674393082	High
TCGA-CG-4438	0.790092714	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-CG-4442	0.988566884	High
TCGA-CG-4465	0.954312743	High
TCGA-CG-5716	2.176488948	High
TCGA-CG-5721	0.930556133	High
TCGA-CG-5724	1.539709953	High
TCGA-CG-5726	0.572120903	Low
TCGA-D7-6520	2.504150098	High
TCGA-D7-6522	0.69548813	Low
TCGA-D7-6524	1.090509476	High
TCGA-D7-8574	0.938289409	High
TCGA-D7-8576	1.572142277	High
TCGA-D7-8578	2.525394671	High
TCGA-D7-8579	0.990332859	High
TCGA-D7-A4Z0	0.886251838	Low
TCGA-D7-A6EV	0.859718369	Low
TCGA-D7-A6EX	1.462379139	High
TCGA-D7-A6EY	1.074495839	High
TCGA-D7-A747	0.96998933	High
TCGA-EQ-8122	0.70428746	Low
TCGA-F1-6177	0.689041434	Low
TCGA-F1-6875	0.764218021	Low
TCGA-F1-A448	0.704680173	Low
TCGA-F1-A72C	1.051055471	High
TCGA-FP-7916	1.100353274	High
TCGA-FP-8209	0.553618109	Low
TCGA-FP-8210	1.738949447	High
TCGA-HF-7132	1.961775144	High
TCGA-HF-A5NB	0.624840342	Low
TCGA-HU-8238	1.429198295	High
TCGA-HU-8602	0.619387795	Low
TCGA-HU-8604	0.464447476	Low
TCGA-HU-A4G2	0.621731201	Low
TCGA-HU-A4G3	1.219675687	High
TCGA-HU-A4G8	0.770194896	Low

Table S4 (continued)

Table S4 (continued)

ID	Risk score	Risk
TCGA-HU-A4GC	1.715917124	High
TCGA-HU-A4GD	1.320108553	High
TCGA-HU-A4GF	0.590389077	Low
TCGA-HU-A4GJ	1.065926376	High
TCGA-HU-A4GP	0.987115503	High
TCGA-HU-A4GQ	0.835477985	Low
TCGA-HU-A4GT	0.683944319	Low
TCGA-HU-A4GU	0.451666811	Low
TCGA-HU-A4GX	1.375457713	High
TCGA-HU-A4GY	0.633382294	Low
TCGA-HU-A4H2	0.615846199	Low
TCGA-HU-A4H4	0.604334796	Low
TCGA-HU-A4H6	1.505266892	High
TCGA-HU-A4H8	0.809037821	Low
TCGA-HU-A4HB	1.774710047	High
TCGA-HU-A4HD	0.813111337	Low
TCGA-MX-A5UG	1.187251753	High
TCGA-MX-A5UJ	0.967381953	High
TCGA-R5-A7ZF	1.502610806	High
TCGA-RD-A8MW	0.901521315	Low
TCGA-RD-A8N1	0.839982411	Low
TCGA-RD-A8N2	0.616257766	Low
TCGA-RD-A8N4	0.53980653	Low
TCGA-RD-A8N6	1.614565892	High
TCGA-RD-A8NB	0.817180074	Low
TCGA-SW-A7EA	0.919170578	Low
TCGA-SW-A7EB	8.580103893	High
TCGA-VQ-A8DU	1.419013505	High
TCGA-VQ-A8DV	1.294282799	High
TCGA-VQ-A8DZ	1.121357707	High
TCGA-VQ-A8E3	0.848345153	Low
TCGA-VQ-A8PB	0.86957499	Low
TCGA-VQ-A8PC	0.925461561	High
TCGA-VQ-A8PH	0.72138784	Low

Table S4 (continued)**Table S4** (continued)

ID	Risk score	Risk
TCGA-VQ-A8PO	0.842543473	Low
TCGA-VQ-A91E	1.25377843	High
TCGA-VQ-A91K	1.175747268	High
TCGA-VQ-A91N	0.979597971	High
TCGA-VQ-A91X	0.622736473	Low
TCGA-VQ-A91Y	0.971315868	High
TCGA-VQ-A91Z	0.981187114	High
TCGA-VQ-A922	7.339485318	High
TCGA-VQ-A924	0.60002817	Low
TCGA-VQ-A925	1.341233534	High
TCGA-VQ-A94O	1.072206937	High
TCGA-VQ-A94R	0.672081045	Low
TCGA-VQ-A94U	0.821204074	Low
TCGA-VQ-AA6D	0.821878573	Low
TCGA-ZA-A8F6	0.516257684	Low
TCGA-ZQ-A9CR	0.783703731	Low

TCGA-STAD, The Cancer Genome Atlas of Stomach Adenocarcinoma.

Table S5 The estimated risk score for all samples in GES84437

ID	Risk Score	Risk
GSM2235556	0.910214298	Low
GSM2235557	1.480597696	High
GSM2235558	0.875772968	Low
GSM2235559	1.908629448	High
GSM2235560	1.159905892	High
GSM2235561	0.8402981	Low
GSM2235562	1.528635084	High
GSM2235563	1.342492179	High
GSM2235564	0.959524917	High
GSM2235565	1.037586552	High
GSM2235566	1.024689911	High
GSM2235567	0.716778405	Low
GSM2235568	1.218538145	High
GSM2235569	0.626212571	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235570	0.922992015	High
GSM2235571	0.779169193	Low
GSM2235572	1.275150603	High
GSM2235573	1.523473901	High
GSM2235574	1.382891636	High
GSM2235575	0.782013312	Low
GSM2235576	2.11217861	High
GSM2235577	1.053628699	High
GSM2235578	0.604841868	Low
GSM2235579	1.631789317	High
GSM2235580	1.235631879	High
GSM2235582	0.796651761	Low
GSM2235584	0.788129944	Low
GSM2235585	0.929075785	High
GSM2235586	0.874302923	Low
GSM2235587	2.361493524	High
GSM2235588	0.710461096	Low
GSM2235589	2.073709844	High
GSM2235593	0.654367032	Low
GSM2235595	0.719283343	Low
GSM2235596	0.684336404	Low
GSM2235597	0.830239415	Low
GSM2235598	1.232937117	High
GSM2235599	1.097460974	High
GSM2235600	0.878149881	Low
GSM2235601	1.15200955	High
GSM2235602	0.776907212	Low
GSM2235603	1.139181165	High
GSM2235604	0.556133023	Low
GSM2235605	0.829484034	Low
GSM2235606	0.907496859	Low
GSM2235607	0.561937052	Low
GSM2235608	1.115047179	High
GSM2235609	1.565887113	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235610	0.85291947	Low
GSM2235611	1.25885041	High
GSM2235612	0.853204255	Low
GSM2235613	1.150884142	High
GSM2235614	0.888937112	Low
GSM2235615	0.666432969	Low
GSM2235616	1.759605314	High
GSM2235617	0.736386745	Low
GSM2235618	0.853690057	Low
GSM2235619	0.586032015	Low
GSM2235620	0.758824163	Low
GSM2235621	0.541763979	Low
GSM2235622	1.199206636	High
GSM2235623	1.863214438	High
GSM2235624	1.308648364	High
GSM2235625	0.948621163	High
GSM2235626	0.848102874	Low
GSM2235627	0.766385293	Low
GSM2235628	1.200352504	High
GSM2235629	1.057743829	High
GSM2235630	0.651128083	Low
GSM2235631	1.061492327	High
GSM2235632	0.486315875	Low
GSM2235633	0.902949834	Low
GSM2235634	0.745658962	Low
GSM2235635	1.637412947	High
GSM2235636	0.732318671	Low
GSM2235637	0.747819434	Low
GSM2235695	0.868441164	Low
GSM2235696	0.730379377	Low
GSM2235697	0.81242176	Low
GSM2235698	0.875724376	Low
GSM2235699	0.621876488	Low
GSM2235700	0.997001337	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235701	0.615720546	Low
GSM2235702	0.888265272	Low
GSM2235703	0.687287223	Low
GSM2235704	0.741684439	Low
GSM2235705	0.633758772	Low
GSM2235706	1.054616776	High
GSM2235707	0.743660877	Low
GSM2235708	0.918912812	Low
GSM2235709	0.619104008	Low
GSM2235710	0.971152652	High
GSM2235711	0.511191768	Low
GSM2235712	1.053044266	High
GSM2235713	0.864618054	Low
GSM2235714	1.14716796	High
GSM2235715	0.773309931	Low
GSM2235716	0.534611654	Low
GSM2235717	0.581766944	Low
GSM2235718	0.756628148	Low
GSM2235719	0.673112984	Low
GSM2235720	0.92676764	High
GSM2235721	1.009484752	High
GSM2235722	0.710377359	Low
GSM2235723	0.935001332	High
GSM2235724	0.968586896	High
GSM2235725	0.702069784	Low
GSM2235726	0.638587037	Low
GSM2235727	0.548219739	Low
GSM2235728	0.509450286	Low
GSM2235729	0.912988716	Low
GSM2235730	0.692302934	Low
GSM2235731	0.654530468	Low
GSM2235732	0.785562368	Low
GSM2235733	1.530479344	High
GSM2235734	0.65248439	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235735	1.3480503	High
GSM2235736	0.888039934	Low
GSM2235737	0.871386425	Low
GSM2235738	0.602333244	Low
GSM2235739	1.421273637	High
GSM2235740	0.844681578	Low
GSM2235741	1.241959733	High
GSM2235742	0.987837468	High
GSM2235743	1.404694064	High
GSM2235744	1.316516917	High
GSM2235745	0.538715482	Low
GSM2235746	1.464166313	High
GSM2235747	1.709688442	High
GSM2235748	0.714601425	Low
GSM2235749	2.352418579	High
GSM2235750	1.105558498	High
GSM2235751	0.79000029	Low
GSM2235752	1.882289645	High
GSM2235753	1.336909898	High
GSM2235754	0.736347894	Low
GSM2235755	0.682241795	Low
GSM2235756	0.42894017	Low
GSM2235757	1.261460607	High
GSM2235758	1.812194922	High
GSM2235759	1.631328382	High
GSM2235760	1.119915034	High
GSM2235761	0.835346853	Low
GSM2235762	0.565458982	Low
GSM2235763	2.655882228	High
GSM2235764	1.102749942	High
GSM2235765	1.921004593	High
GSM2235766	0.581044794	Low
GSM2235767	1.105700385	High
GSM2235768	1.101012147	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235769	1.153298959	High
GSM2235770	1.388672698	High
GSM2235771	1.608634642	High
GSM2235772	1.003659824	High
GSM2235773	1.240106217	High
GSM2235774	1.196498958	High
GSM2235775	1.351632211	High
GSM2235776	1.205607496	High
GSM2235777	1.213380422	High
GSM2235778	1.01746287	High
GSM2235779	0.631780256	Low
GSM2235780	1.036940407	High
GSM2235781	0.990882282	High
GSM2235782	1.499684903	High
GSM2235783	1.303752736	High
GSM2235784	0.46528454	Low
GSM2235785	0.620983766	Low
GSM2235786	0.831202386	Low
GSM2235787	1.055606154	High
GSM2235788	0.889871477	Low
GSM2235789	0.93436003	High
GSM2235790	1.37615878	High
GSM2235791	0.778413337	Low
GSM2235792	1.510675916	High
GSM2235793	0.834388275	Low
GSM2235794	0.814966067	Low
GSM2235795	0.668698327	Low
GSM2235796	0.931362468	High
GSM2235797	0.861186486	Low
GSM2235798	0.638704742	Low
GSM2235799	0.763007961	Low
GSM2235800	1.081363248	High
GSM2235801	1.069341516	High
GSM2235802	0.724688419	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235803	0.706816187	Low
GSM2235804	1.149790712	High
GSM2235805	1.260096695	High
GSM2235806	1.143298675	High
GSM2235807	1.338324202	High
GSM2235808	1.464420694	High
GSM2235809	0.991896564	High
GSM2235810	0.88818667	Low
GSM2235811	0.897726537	Low
GSM2235812	1.165652227	High
GSM2235813	1.166264706	High
GSM2235814	1.780648872	High
GSM2235815	1.045672662	High
GSM2235816	0.999665375	High
GSM2235817	0.559872619	Low
GSM2235818	1.326492156	High
GSM2235819	1.01396877	High
GSM2235820	0.887110263	Low
GSM2235821	0.599908905	Low
GSM2235822	0.709791698	Low
GSM2235823	0.58512608	Low
GSM2235824	0.748248285	Low
GSM2235825	0.49447361	Low
GSM2235826	1.283122393	High
GSM2235827	0.988915382	High
GSM2235828	0.635437439	Low
GSM2235829	1.166037701	High
GSM2235830	0.977285901	High
GSM2235831	0.96523409	High
GSM2235837	1.433912607	High
GSM2235838	3.37071556	High
GSM2235839	1.202297316	High
GSM2235840	0.773949745	Low
GSM2235841	1.346879878	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235842	1.007831786	High
GSM2235843	1.660599211	High
GSM2235844	2.135776701	High
GSM2235845	1.907174728	High
GSM2235846	0.997728041	High
GSM2235847	0.909566809	Low
GSM2235848	1.050775683	High
GSM2235849	1.228760949	High
GSM2235850	0.644032728	Low
GSM2235851	0.960558086	High
GSM2235852	0.804265598	Low
GSM2235853	0.75313405	Low
GSM2235854	0.740850306	Low
GSM2235855	0.543773323	Low
GSM2235862	0.920357524	High
GSM2235863	1.323631207	High
GSM2235864	0.847978642	Low
GSM2235865	0.921895643	High
GSM2235866	1.863255612	High
GSM2235867	1.479792415	High
GSM2235878	1.027009771	High
GSM2235879	1.056469286	High
GSM2235880	0.812677826	Low
GSM2235881	0.856824782	Low
GSM2235882	1.173123552	High
GSM2235883	0.927321304	High
GSM2235884	0.843635138	Low
GSM2235885	1.848787193	High
GSM2235886	1.18399363	High
GSM2235887	0.886384973	Low
GSM2235888	0.926193329	High
GSM2235889	0.830424659	Low
GSM2235899	3.354803867	High
GSM2235900	0.884827534	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235901	1.167817668	High
GSM2235902	0.672248396	Low
GSM2235903	0.87082946	Low
GSM2235904	0.928228098	High
GSM2235905	0.780286628	Low
GSM2235906	1.433551435	High
GSM2235907	1.876745096	High
GSM2235908	0.789418761	Low
GSM2235909	0.699361253	Low
GSM2235910	0.730287636	Low
GSM2235921	0.84027114	Low
GSM2235922	0.463380902	Low
GSM2235923	1.274661122	High
GSM2235924	1.563845987	High
GSM2235925	1.139097788	High
GSM2235926	0.819302691	Low
GSM2235927	1.014427865	High
GSM2235928	2.341338037	High
GSM2235929	0.509740685	Low
GSM2235930	0.767804447	Low
GSM2235931	0.794598265	Low
GSM2235932	1.561448382	High
GSM2235933	1.36943005	High
GSM2235934	0.704456299	Low
GSM2235935	1.114069264	High
GSM2235936	0.815183188	Low
GSM2235937	0.560687404	Low
GSM2235938	0.714059083	Low
GSM2235939	1.133534978	High
GSM2235940	0.934497644	High
GSM2235941	0.805136639	Low
GSM2235942	0.984593743	High
GSM2235943	1.051726691	High
GSM2235944	0.702512091	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235945	0.898993824	Low
GSM2235946	1.519375751	High
GSM2235947	0.815385708	Low
GSM2235948	0.612716716	Low
GSM2235949	0.718652441	Low
GSM2235950	0.681304637	Low
GSM2235951	0.776592949	Low
GSM2235952	2.054888041	High
GSM2235953	0.903877817	Low
GSM2235954	0.860135481	Low
GSM2235955	0.857224698	Low
GSM2235956	1.513055386	High
GSM2235957	0.800943136	Low
GSM2235958	0.688287428	Low
GSM2235959	0.748528352	Low
GSM2235960	1.100482056	High
GSM2235961	0.767497943	Low
GSM2235962	0.791745821	Low
GSM2235963	0.733939306	Low
GSM2235964	0.673878948	Low
GSM2235965	1.457924718	High
GSM2235966	0.8120066	Low
GSM2235967	0.94181134	High
GSM2235968	0.474542874	Low
GSM2235969	0.864702498	Low
GSM2235970	1.450007792	High
GSM2235971	0.515285331	Low
GSM2235972	0.981129207	High
GSM2235973	0.46768181	Low
GSM2235974	1.138111348	High
GSM2235975	0.658383784	Low
GSM2235976	0.847818551	Low
GSM2235977	1.390846733	High
GSM2235978	0.550240818	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2235979	0.717379118	Low
GSM2235980	1.03062588	High
GSM2235981	0.706469107	Low
GSM2235982	0.987121871	High
GSM2235983	0.83440334	Low
GSM2235984	2.208034021	High
GSM2235985	1.390212713	High
GSM2235986	0.849729553	Low
GSM2235987	1.029275456	High
GSM2235988	1.035594409	High
GSM2235991	2.510573526	High
GSM2235992	1.373004888	High
GSM2235993	0.685736545	Low
GSM2235994	1.783777052	High
GSM2235995	1.448048625	High
GSM2235996	8.928647432	High
GSM2235997	1.072218468	High
GSM2235998	1.201510739	High
GSM2235999	1.055464736	High
GSM2236000	1.400526313	High
GSM2236001	0.759019998	Low
GSM2236002	1.179201038	High
GSM2236003	0.769322118	Low
GSM2236004	0.552968695	Low
GSM2236005	0.816498327	Low
GSM2236006	2.144814392	High
GSM2236007	1.562406926	High
GSM2236008	2.132758846	High
GSM2236009	0.793534486	Low
GSM2236010	0.497007155	Low
GSM2236011	1.766396871	High
GSM2236012	1.568527274	High
GSM2236013	0.890231701	Low
GSM2236014	1.011178328	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2236015	1.128673274	High
GSM2236016	1.912605999	High
GSM2236017	1.192271093	High
GSM2236018	1.806877925	High
GSM2236019	0.854465795	Low
GSM2236020	1.406765827	High
GSM2236021	1.256227136	High
GSM2236022	0.784639987	Low
GSM2236023	1.505219928	High
GSM2236024	1.269398219	High
GSM2236025	0.857581258	Low
GSM2236026	3.501048358	High
GSM2236027	10.80259878	High
GSM2236028	1.511753537	High
GSM2236029	0.939662514	High
GSM2236030	1.021148682	High
GSM2236031	1.86610606	High
GSM2236032	0.74278003	Low
GSM2236033	1.165675269	High
GSM2236034	1.10207386	High
GSM2236036	1.42720136	High
GSM2236037	1.047784287	High
GSM2236038	1.837641465	High
GSM2236039	1.104519498	High
GSM2236040	1.111438753	High
GSM2236041	1.154257693	High
GSM2236042	0.595244014	Low
GSM2236043	1.198687448	High
GSM2236044	0.983964996	High
GSM2236045	2.314437105	High
GSM2236046	1.112879837	High
GSM2236047	0.970562166	High
GSM2236048	0.950717481	High
GSM2236049	1.319392716	High

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2236050	0.725435295	Low
GSM2236051	0.920866015	High
GSM2236052	0.822242455	Low
GSM2236053	1.032055797	High
GSM2236054	1.203716521	High
GSM2236055	0.763794091	Low
GSM2236056	0.833300803	Low
GSM2236057	1.067465981	High
GSM2236058	0.803186106	Low
GSM2236059	0.752289504	Low
GSM2236060	1.104540511	High
GSM2236061	0.590518577	Low
GSM2236062	1.323315957	High
GSM2236063	0.822147249	Low
GSM2236064	0.938683277	High
GSM2236065	1.184074559	High
GSM2236066	4.004189466	High
GSM2236067	2.671240637	High
GSM2236068	1.104451009	High
GSM2236069	1.935930023	High
GSM2236070	0.955448616	High
GSM2236071	0.911304268	Low
GSM2236072	1.274737342	High
GSM2236073	0.788974431	Low
GSM2236074	0.545639066	Low
GSM2236075	0.804997687	Low
GSM2236076	1.59676895	High
GSM2236077	1.082435354	High
GSM2236078	1.221390585	High
GSM2236079	0.97099485	High
GSM2236080	0.688692817	Low
GSM2236082	0.612726546	Low
GSM2236083	0.63122848	Low
GSM2236084	0.74182598	Low

Table S5 (continued)

Table S5 (continued)

ID	Risk Score	Risk
GSM2236085	0.663575337	Low
GSM2236086	1.591772913	High
GSM2236087	1.216954285	High
GSM2236088	1.068162629	High
GSM2236089	0.7262057	Low
GSM2236090	1.238290004	High
GSM2236091	1.128900214	High
GSM2236092	1.068980131	High
GSM2236093	0.759615596	Low
GSM2236094	1.323740033	High
GSM2236095	1.074296658	High