

Table S1 Significant differences in the distribution of somatic variations between metastatic and non-metastatic groups

Gene	Non-metastatic group	Metastatic group	P value
<i>ASTN1</i>	3	0	0.026
<i>HIST2H2AC</i>	3	0	0.026
<i>LRRC37A3</i>	3	0	0.026
<i>SAGE1</i>	3	0	0.026
<i>ZFHX4</i>	4	2	0.066
<i>ATAD3B</i>	0	7	0.074
<i>AHNAK</i>	3	1	0.084
<i>EYS</i>	3	1	0.084
<i>NALCN</i>	3	1	0.084
<i>STAB2</i>	3	1	0.084
<i>TAS2R30</i>	3	1	0.084
<i>VWF</i>	3	1	0.084
<i>ADRA1A</i>	2	0	0.094
<i>ALAS1</i>	2	0	0.094
<i>ANKRD36B</i>	2	0	0.094
<i>ANXA1</i>	2	0	0.094
<i>ARHGAP20</i>	2	0	0.094
<i>BAGE2</i>	2	0	0.094
<i>CTAGE1</i>	2	0	0.094
<i>DNHD1</i>	2	0	0.094

Table S2 Significant differences in the distribution of somatic variants between the TMB-H and TMB-L groups

Gene	TMB-H	TMB-L	P value
<i>AKAP9</i>	3	1	0.005
<i>PCLO</i>	3	1	0.005
<i>RELN</i>	3	2	0.011
<i>ASXL1</i>	2	0	0.014
<i>MMP2</i>	2	0	0.014
<i>PGR</i>	2	0	0.014
<i>TLR4</i>	2	0	0.014
<i>ATP2B3</i>	2	1	0.040
<i>KMT2D</i>	2	1	0.040
<i>NGFR</i>	2	1	0.040
<i>KAT6B</i>	2	2	0.076
<i>NOTCH2</i>	2	2	0.076
<i>KMT2C</i>	2	3	0.120
<i>MGA</i>	2	3	0.120
<i>ZFH3</i>	2	3	0.120

TMB-H, tumor mutation burden high (TMB score ≥ 300); TMB-L, tumor mutation burden low (TMB score < 300).

Table S3 Significant differences in the distribution of germline variants between metastatic and non-metastatic groups

Gene	Non-metastatic group	Metastatic group	P value
<i>ATP6V0A4</i>	2	0	0.094
<i>FANCM</i>	2	0	0.094
<i>PDGFRA</i>	2	0	0.094
<i>ALK</i>	0	4	0.287
<i>CFTR</i>	1	0	0.316
<i>DIS3L2</i>	1	0	0.316
<i>FH</i>	1	0	0.316
<i>HOXB13</i>	1	0	0.316
<i>MC1R</i>	1	0	0.316
<i>NF1</i>	1	0	0.316
<i>RAD50</i>	1	0	0.316
<i>RAD51D</i>	1	0	0.316
<i>RNASEL</i>	1	0	0.316
<i>SUFU</i>	1	0	0.316
<i>ATM</i>	3	3	0.357
<i>BRCA2</i>	3	3	0.357
<i>POLE</i>	1	6	0.395

Table S4 Overall survival and hazard ratios of cytoband amplification and deletion

Chromosomal	AMP/DEL	Patient count	HR	Median	P value
2q24.3	DEL	12	–	< Min	0.0455
9p24.1	DEL	11	–	< Min	0.0376
9p21.3	DEL	11	–	< Min	0.0403
19q13.33	AMP	7	–	< Min	0.0092
3p22.2	DEL	6	–	< Min	0.0001
9q31.1	DEL	6	–	< Min	0.0004
11q11	DEL	6	19	< Min	0.0035
12p13.33	DEL	5	9.588	< Min	0.0499
16p11.2	AMP	5	–	< Min	0.0066
22q12.3	DEL	4	–	< Min	0.0000
9p13.3	DEL	4	–	< Min	0.0002
11q12.1	DEL	4	19	< Min	0.0035
12q24.11	DEL	4	14	< Min	0.014
12q23.3	DEL	4	14	< Min	0.014
7q35	DEL	4	11.857	< Min	0.0258
3p22.3	DEL	4	11.857	< Min	0.0258
3p14.3	DEL	4	11.857	< Min	0.0258
19p13.12	DEL	4	11.857	< Min	0.0258
19q13.32	AMP	4	–	< Min	0.0000
9p	DEL	6	–	< Min	0.0002
3p	DEL	2	15.364	< Min	0.0096
17p	DEL	6	8	< Min	0.0939
11q	AMP	1	21.5	< Min	0.0018
16p	AMP	7	–	< Min	0.0143

AMP: amplification; DEL: deletion; HR: hazard ratio.

Table S5 Significant differences in the distribution of copy number variants between metastatic and non-metastatic groups

Gene	Non-metastatic group	Metastatic group	P value
<i>BCL11B</i>	3	0	0.026
<i>MNX1</i>	3	0	0.026
<i>MMP9</i>	0	9	0.036
<i>PTPN1</i>	0	9	0.036
<i>SSI8L1</i>	0	8	0.039
<i>HOXA3</i>	4	2	0.066
<i>SRSF2</i>	4	2	0.066
<i>ARFRP1</i>	0	7	0.074
<i>HIST1H2AL</i>	0	7	0.074
<i>IL10</i>	0	7	0.074
<i>ERF</i>	3	1	0.084
<i>FEV</i>	3	1	0.084
<i>SOX9</i>	3	1	0.084
<i>CIC</i>	2	0	0.094
<i>FGFR3</i>	2	0	0.094
<i>FOXA1</i>	2	0	0.094
<i>MGAM</i>	2	0	0.094
<i>MNI</i>	2	0	0.094
<i>SOX10</i>	2	0	0.094
<i>TPMT</i>	2	0	0.094

Table S6 Copy number variants frequently detected in gastric cancer between TCGA-STAD and this study

Gene	AMP/DEL	TCGA count with CNV	TCGA cohort total count	Our data count with CNV	Our data total count	P value
<i>ERBB2</i>	AMP	62	440	5	38	0.874
<i>CCNE1</i>	AMP	51	440	5	38	0.773
<i>IKZF3</i>	AMP	57	440	4	38	0.667
<i>CDKN2B</i>	DEL	51	440	4	38	0.844
<i>ZNF217</i>	AMP	48	440	4	38	0.942
<i>CSF3</i>	AMP	44	440	4	38	0.918
<i>GATA6</i>	AMP	42	440	4	38	0.844
<i>PTPNI</i>	AMP	39	440	4	38	0.731
<i>RARA</i>	AMP	38	440	4	38	0.693
<i>NFATC2</i>	AMP	35	440	4	38	0.578
<i>SALL4</i>	AMP	35	440	4	38	0.578
<i>TOP2A</i>	AMP	34	440	4	38	0.541
<i>SMARCE1</i>	AMP	32	440	4	38	0.466
<i>CEBPA</i>	AMP	12	440	4	38	0.019
<i>ZNF703</i>	AMP	5	440	4	38	0.000
<i>HIST1H3B</i>	AMP	1	440	4	38	0.000
<i>PTPRD</i>	DEL	82	440	3	38	0.097
<i>PGAP3</i>	AMP	61	440	3	38	0.300
<i>MYC</i>	AMP	58	440	3	38	0.349
<i>CDK12</i>	AMP	46	440	3	38	0.618
<i>CDK6</i>	AMP	35	440	3	38	0.990

AMP, amplification; DEL, deletion.