

Figure legends

Supplementary Fig. S1. TMA analysis of the protein expression level of STAT2 in GC tissues by using the IHC analysis ($\times 200$).

Supplementary Fig. S1. TCGA analysis of the association of STAT2 expression with its genetic and epigenetic alterations in GC samples.

Supplementary Tables

Table S1 The association of STAT2 expression with clinicopathologic features in GC patients

| features | Cases n=89 | STAT2 Expression | | P |
|------------------------------|---------------|------------------|----|-------|
| | | - | + | |
| | n=22 | n=67 | | |
| Age | | | | |
| ≥ 60 | 29 | 9 | 20 | |
| <60 | 60 | 13 | 47 | 0.34 |
| Gender | | | | |
| Female | 20 | 8 | 12 | |
| Male | 69 | 14 | 55 | 0.074 |
| Tumor size (cm) | | | | |
| <3.5 | 17 | 7 | 10 | |
| ≥ 3.5 | 72 | 15 | 57 | 0.082 |
| Pathological stage | | | | |
| I/II | 32 | 14 | 18 | |
| III/IV | 57 | 8 | 49 | 0.002 |
| T classification | | | | |
| T1/T2 | 11 | 5 | 6 | |
| T3/T4 | 78 | 17 | 61 | 0.09 |
| N classification | | | | |
| N0/N1 | 39 | 13 | 26 | |
| N2/N3 | 50 | 9 | 41 | 0.098 |
| Lymph node metastasis | | | | |
| Negative | 23 | 2 | 21 | |
| Positive | 66 | 20 | 46 | 0.040 |

Table S2 TCGA analysis of the association of STAT2 expression with clinicopathologic characteristics in GC patients

| Variables | Cases (n) | STAT2 | | <i>P</i> value |
|---------------------------|--------------|-------|-----|----------------|
| | | High | Low | |
| Total | 301 | 10 | 291 | |
| <i>Age (years)</i> | | | | |
| ≥60 | 206 | 10 | 196 | |
| <60 | 95 | 0 | 95 | 0.034 |
| <i>Gender</i> | | | | |
| Male | 189 | 8 | 181 | |
| Female | 112 | 2 | 110 | 0.332 |
| <i>Pathological stage</i> | | | | |
| I / II | 145 | 2 | 143 | |
| III/IV | 156 | 8 | 148 | 0.106 |
| <i>T stage</i> | | | | |
| T1/T2 | 80 | 2 | 78 | |
| T3/T4 | 221 | 8 | 213 | 1.000 |
| <i>N stage</i> | | | | |
| Negative | 104 | 1 | 103 | |
| Positive | 197 | 9 | 188 | 0.173 |
| <i>M stage</i> | | | | |
| Negative | 272 | 8 | 264 | |
| Positive | 29 | 2 | 27 | 0.249 |

Table S3 The association of miR-605-5p expression with clinicopathologic characteristics in GC patients

| Variables | Cases (n) | miR-605-5p | | <i>P</i> value |
|---------------------------|--------------|------------|-----|----------------|
| | | High | Low | |
| Total | 160 | 149 | 11 | |
| <i>Age (years)</i> | | | | |
| ≥60 | 105 | 97 | 8 | |
| <60 | 55 | 52 | 3 | 0.750 |
| <i>Gender</i> | | | | |
| Male | 103 | 97 | 6 | |
| Female | 57 | 52 | 5 | 0.523 |
| <i>Pathological stage</i> | | | | |
| I / II | 76 | 72 | 4 | |
| III/IV | 84 | 77 | 7 | 0.540 |
| <i>T stage</i> | | | | |
| T1/T2 | 36 | 32 | 4 | |
| T3/T4 | 124 | 117 | 7 | 0.269 |
| <i>N stage</i> | | | | |
| Negative | 59 | 57 | 2 | |
| Positive | 101 | 92 | 9 | 0.331 |
| <i>M stage</i> | | | | |
| Negative | 143 | 133 | 10 | |
| Positive | 17 | 16 | 1 | 1.000 |

Table S4 Cox regression analysis of miR-605-5p expression as a survival predictor in GC patients

| Variables | Univariate Cox regression analysis | | Multivariate Cox regression analysis | |
|------------------------------|------------------------------------|---------|--------------------------------------|---------|
| | RR (95% CI) | P value | RR (95% CI) | P value |
| <i>Age (years)</i> | | | | |
| ≥ 60 vs. < 60 | 1.601 (0.909 to 2.819) | 0.103 | NA | NA |
| <i>Gender</i> | | | | |
| Male vs. Female | 1.507 (0.859 to 2.643) | 0.153 | NA | NA |
| <i>Pathological stage</i> | | | | |
| III/IV vs. I / II | 2.072 (1.209 to 3.551) | 0.008 | 1.754 (0.981 to 3.136) | 0.058 |
| <i>T stage</i> | | | | |
| T3+T4 vs. T1+T2 | 2.147 (1.050 to 4.390) | 0.036 | 2.038 (0.922 to 4.502) | 0.078 |
| <i>N staging</i> | | | | |
| Positive vs. Negative | 1.712 (0.975 to 3.004) | 0.061 | NA | NA |
| <i>M stage</i> | | | | |
| Positive vs. Negative | 3.220 (1.623 to 6.387) | 0.001 | 3.255 (1.629 to 6.507) | 0.001 |
| <i>miR-605-5p expression</i> | | | | |
| High VS. Low | 0.350 (0.148 to 0.825) | 0.016 | 0.315 (0.131 to 0.760) | 0.010 |

NA: not analyzed