## SUPPLEMENTARY TABLES

### Supplementary Table 1. Oligonucleotides sequences.

| Experiment                  | Name            | Position or orientation | Sequence (5’-3’)                                      |
|-----------------------------|-----------------|-------------------------|------------------------------------------------------|
| **Luciferase construction** | R:              | 95~ 77                  | TCCGCTCGAG GATTCCCCCGTCAGTCAC(XhoI)                  |
| SUZ12                       | L: SUZ12p1-WT   | -91~ -84                | F: 5’ - GGGGTACCATTCCCGCAATTCTAGTT (Kpn I) -3’       |
|                             | L: SUZ12p2-WT   | -1395~ -1388            | F: 5’ - GGGGTACC AGGCTTCAAGGAGCTCTGAGAA (Kpn I) -3’ |
|                             | R:              | 271~ 251                | TCCGCTCGAG CAAAATCGCAGGCTAGTAA (XhoI)                |
| CCDC43                      | L: CCDC43p1-WT  | -737~ -714              | F: 5’ - GGGGTACC GAAGCTTCTCAGGAGAATT (Kpn I) -3’     |
| Leggere construction        | L: SUZ12p1-MT   | -91~ -84                | F: ACTGACCGGAATTCTAGTTA                              |
|                             | L: SUZ12p2-MT   | -1395~ -1388            | F: AGGCTTCAGAAGTTACC and AGGCTTCAGAAGTTACC          |
| Site-directed               | L: SUZ12p3-MT   | -91~ -84 and -1395~ -1388 |
| mutagenesis                 | L: CCDC43p1-MT  | -737~ -714              | F: TGTTTTGTTTTGAGAGCGLAGCTC                        |
|                             | L: CCDC43p2-MT  | -1395~ -1389            | F: GAAGCTTCAGAAGTTACC and GAAGCTTCAGAAGTTACC        |
| **Chip**                    | R:              | -179~ -155              | CTAAGGATCTAGACTCGCTAAACC                             |
| SUZ12                       | Chip 1          | R: 92~ 77               | GATTCCTCGAGCTACGCA                                  |
|                             | R:              | 1477~ 1457              | GTGCCCAAGAGCTAACAG                                   |
|                             | R:              | 1296~ 1272              | CAGGCACTGTGCTCAGCTACATAGA                            |
|                             | R:              | -564 ~ -544             | CCTGGGTTGGTTGTGTTG                                  |
|                             | R:              | 1404~ -1384             | GGAAGACCCCGGTCCTACT                                  |
|                             | R:              | 1228~ -1204             | CATCATCCTGGAGAAACAGA                                 |
| CCDC43                      | Chip 1          | L: 92~ 77               | CTAAGGATCTAGACTCGCTAAACC                             |
| Chip 2                       | L:              | 1477~ 1457              | GTGCCCAAGAGCTAACAG                                   |
|                             | R:              | 1296~ 1272              | CAGGCACTGTGCTCAGCTACATAGA                            |
|                             | L:              | -564 ~ -544             | CCTGGGTTGGTTGTGTTG                                  |
|                             | L:              | 1404~ -1384             | GGAAGACCCCGGTCCTACT                                  |
|                             | L:              | 1228~ -1204             | CATCATCCTGGAGAAACAGA                                 |

*Bold and italic: HMGA1 binding sites; underline: mutated nucleotide residues.*
Supplementary Table 2. Correlation between HMGA1 protein expression and the clinicopathological parameters of gastric carcinoma.

| Features                              | Total number (n=51) | HMGA1 expression | P   |
|---------------------------------------|---------------------|------------------|-----|
|                                       |                     | Low              | High|     |
| Age (years)                           |                     |                  |     |
| <60                                   | 30                  | 10(33.3%)        | 20(66.7%) | 0.249|
| >60                                   | 21                  | 11(52.4%)        | 10(47.6%) |     |
| Gender                                |                     |                  |     |
| Male                                  | 34                  | 15(44.1%)        | 19(55.9%) | 0.764|
| Female                                | 17                  | 6(35.3%)         | 11(64.7%) |     |
| Differentiation                       |                     |                  |     |
| Well                                  | 11                  | 8(72.7%)         | 3(27.3%) | 0.028|
| Moderate                              | 16                  | 7(43.8%)         | 9(56.2%) |     |
| Poor                                  | 24                  | 6(25.0%)         | 18(75.0%) |     |
| Lymph node metastasis                |                     |                  |     |
| Yes                                   | 36                  | 10(27.8%)        | 26(72.2%) | 0.004|
| No                                    | 15                  | 11(73.3%)        | 4(26.7%)  |     |
| Tumor size(cm³)                       |                     |                  |     |
| <5                                    | 27                  | 16(59.3%)        | 11(40.7%) | 0.009|
| ≥5                                    | 24                  | 5(20.8%)         | 19(79.2%) |     |
| AJCC stage                            |                     |                  |     |
| T1,T2                                 | 11                  | 8(72.7.6%)       | 3(27.3%) | 0.035|
| T3,T4                                 | 40                  | 13(32.5%)        | 27(67.5%) |     |
| AJCC TNM stage                        |                     |                  |     |
| I I                                   | 16                  | 12(75.0%)        | 4(25.0%) | 0.002|
| III IV                                | 35                  | 9(25.7%)         | 26(74.3%) |     |