**Supplementary table 1. Methylation status in gastric cancer and their counterpart normal mucosa estimated by each cut-off value.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Locus** | **Methylation status** | **Tumor, n=98 (%)** | **Normal mucosa, n=98 (%)** | ***P*-value\*** |
| **Wnt** | ***SFRP2*-region 1** | Methylated | 78 (80%) | 31 (32%) | < 0.0001 |
| Unmethylated | 20 (20%) | 67 (68%) |
| ***SFRP2*-region 2** | Methylated | 70 (71%) | 16 (16%) | < 0.0001 |
| Unmethylated | 28 (29%) | 82 (84%) |
| ***APC* promoter 1A** | Methylated | 59 (60%) | 33 (34%) | 0.0002 |
| Unmethylated | 39 (40%) | 65 (66%) |
| **Others** | ***CACNA1G*** | Methylated | 19 (19%) | 0 (0) | < 0.0001 |
| Unmethylated | 79 (81%) | 98 (100%) |
| ***CDKN2A*** | Methylated | 16 (16%) | 1 (1%) | 0.0001 |
| Unmethylated | 82 (84%) | 97 (99%) |
| ***CHFR*** | Methylated | 33 (34%) | 0 (0) | < 0.0001 |
| Unmethylated | 65 (66%) | 98 (100%) |
| ***DCC*** | Methylated | 44 (45%) | 8 (8%) | < 0.0001 |
| Unmethylated | 54 (55%) | 90 (92%) |
| ***MGMT*-Eh region** | Methylated | 7 (7%) | 0 (0) | 0.0071 |
| Unmethylated | 91 (93%) | 98 (100%) |
| ***MINT1*** | Methylated | 50 (51%) | 3 (3%) | < 0.0001 |
| Unmethylated | 48 (49%) | 95 (97%) |
| ***MINT2*** | Methylated | 38 (39%) | 2 (2%) | < 0.0001 |
| Unmethylated | 60 (61%) | 96 (98%) |
| ***MINT31*** | Methylated | 12 (12%) | 1 (1%) | 0.0016 |
| Unmethylated | 86 (88%) | 97 (99%) |
| ***MLH1*-A region** | Methylated | 27 (28%) | 0 (0) | < 0.0001 |
| Unmethylated | 71 (72%) | 98 (100%) |
| ***MLH1*-D region** | Methylated | 18 (18%) | 0 (0) | < 0.0001 |
| Unmethylated | 80 (82%) | 98 (100%) |
| ***RASFF2*-region 1** | Methylated | 16 (16%) | 5 (5%) | 0.0111 |
| Unmethylated | 82 (84%) | 93 (95%) |
| ***RASFF2*-region 2** | Methylated | 51 (52%) | 0 (0) | < 0.0001 |
| Unmethylated | 47 (48%) | 98 (100%) |
| ***RUNX3*** | Methylated | 53 (54%) | 9 (9%) | < 0.0001 |
| Unmethylated | 45 (46%) | 89 (91%) |
| ***UNC5C*** | Methylated | 31 (32%) | 5 (5%) | < 0.0001 |
| Unmethylated | 67 (68%) | 93 (95%) |
| ***3OST2*** | Methylated | 76 (78%) | 33 (34%) | < 0.0001 |
| Unmethylated | 22 (22%) | 65 (66%) |

\**P*-values were calculated by the chi-square test.

A and D regions in *MLH1* were defined by Deng and colleagues (24).

Eh and Mp regions in *MGMT* were defied by Nagasaka and colleagues (23).