**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).