**Supplementary Table 2. Methylation status in gastric cancer categorized by TCGA subtypes and their counterpart normal mucosa divided into GS subtype and others.**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | **TCGA subtype, no. (%)** | | | | ***P*-value\*** | **Counterpart Normal mucosa, no. (%)** | | ***P*-value\*** |
| **Locus** | | **Methylation status** | **MSI-high, n=13** | **EBV, n=7** | **CIN, n=52** | **GS, n=26** | **Non-GS subtype, n=72** | **GS subtype, n=26** |
| **Wnt** | ***SFRP2*-region 1** | Methylated | 12 (92%) | 6 (86%) | 46 (88%) | 14 (54%) | 0.0022 | 28 (34%) | 3 (12%) | 0.0102 |
| Unmethylated | 1 (8%) | 1 (14%) | 6 (12%) | 12 (46%) | 44 (66%) | 23 (88%) |
| ***SFRP2*-region 2** | Methylated | 12 (92%) | 5 (71%) | 42 (81%) | 11 (42%) | 0.0012 | 13 (18%) | 3 (12%) | 0.4409 |
| Unmethylated | 1 (8%) | 2 (29%) | 10 (19%) | 15 (58%) | 59 (82%) | 23 (88%) |
| ***APC* promoter 1A** | Methylated | 10 (77%) | 4 (57%) | 37 (71%) | 8 (31%) | 0.0036 | 27 (38%) | 6 (23%) | 0.1822 |
| Unmethylated | 3 (23%) | 3 (43%) | 15 (29%) | 18 (69%) | 45 (63%) | 20 (77%) |
| **Others** | ***CACNA1G*** | Methylated | 8 (62%) | 2 (29%) | 7 (13%) | 2 (8%) | 0.0003 | 0 (0) | 0 (0) |  |
| Unmethylated | 5 (38%) | 5 (71%) | 45 (87%) | 24 (92%) | 72 (100) | 26 (100) |
| ***CDKN2A*** | Methylated | 3 (23%) | 2 (29%) | 7 (13%) | 4 (15%) | 0.6751 | 1 (1%) | 0 (0) | 0.5458 |
| Unmethylated | 10 (77%) | 5 (71%) | 45 (87%) | 22 (85%) | 71 (99%) | 26 (0) |
| ***CHFR*** | Methylated | 11 (85%) | 4 (57%) | 13 (25%) | 5 (19%) | 0.0001 | 0 (0) | 0 (0) |  |
| Unmethylated | 2 (15%) | 3 (43%) | 39 (75%) | 21 (81%) | 72 (100) | 26 (100) |
| ***DCC*** | Methylated | 10 (77%) | 3 (43%) | 24 (46%) | 7 (27%) | 0.0316 | 6 (8%) | 2 (8%) | 0.9185 |
| Unmethylated | 3 (23%) | 4 (57%) | 28 (54%) | 19 (73%) | 66 (92%) | 24 (92%) |
| ***MGMT*-Eh region** | Methylated | 3 (23%) | 1 (14%) | 2 (4%) | 1 (4%) | 0.0788 | 0 (0) | 0 (0) |  |
| Unmethylated | 10 (77%) | 6 (86%) | 50 (96%) | 25 (96%) | 72 (100) | 26 (100) |
| ***MINT1*** | Methylated | 11 (85%) | 4 (57%) | 23 (44%) | 12 (46%) | 0.0663 | 2 (3%) | 1 (4%) | 0.7863 |
| Unmethylated | 2 (15%) | 3 (43%) | 29 (56%) | 14 (54%) | 70 (97%) | 25 (96%) |
| ***MINT2*** | Methylated | 8 (62%) | 3 (43%) | 17 (33%) | 10 (38%) | 0.296 | 2 (3%) | 0 (0) | 0.3905 |
| Unmethylated | 5 (38%) | 4 (57%) | 35 (67%) | 16 (62%) | 70 (97%) | 26 (100) |
| ***MINT31*** | Methylated | 6 (46%) | 2 (29%) | 3 (6%) | 1 (4%) | 0.0002 | 2 (3%) | 1 (4%) | 0.0944 |
| Unmethylated | 7 (54%) | 5 (71%) | 49 (94%) | 25 (96%) | 70 (97%) | 25 (96%) |
| ***MLH1*-A region** | Methylated | 11 (85%) | 2 (29%) | 10 (19%) | 4 (15%) | < .0001 | 0 (0) | 0 (0) |  |
| Unmethylated | 2 (15%) | 5 (71%) | 42 (81%) | 22 (85%) | 72 (100) | 26 (100) |
| ***MLH1*-D region** | Methylated | 11 (84.6%) | 0 (0) | 4 (8%) | 3 (11.5%) | < .0001 | 0 (0) | 0 (0) |  |
| Unmethylated | 2 (15.4%) | 7 (100) | 48 (92%) | 23 (88.5%) | 72 (100) | 26 (100) |
| ***RASFF2*-region 1** | Methylated | 7 (54%) | 2 (29%) | 5 (10%) | 2 (8%) | 0.0006 | 3 (4%) | 2 (8%) | 0.4837 |
| Unmethylated | 6 (46%) | 5 (71%) | 47 (90%) | 24 (92%) | 69 (96%) | 24 (92%) |
| ***RASFF2*-region 2** | Methylated | 11 (85%) | 4 (57%) | 29 (56%) | 7 (27%) | 0.0041 | 0 (0) | 0 (0) |  |
| Unmethylated | 2 (15%) | 3 (43%) | 23 (44%) | 19 (73%) | 72 (100) | 26 (100) |
| ***RUNX3*** | Methylated | 11 (85%) | 5 (71%) | 23 (44%) | 14 (54%) | 0.0512 | 7 (10%) | 2 (8%) | 0.7587 |
| Unmethylated | 2 (15%) | 2 (29%) | 29 (56%) | 12 (46%) | 65 (90%) | 24 (92%) |
| ***UNC5C*** | Methylated | 8 (62%) | 1 (14%) | 19 (37%) | 3 (12%) | 0.0082 | 4 (6%) | 1 (4%) | 0.7342 |
| Unmethylated | 5 (38%) | 6 (86%) | 33 (63%) | 23 (88%) | 68 (94%) | 25 (96%) |
| ***3OST2*** | Methylated | 12 (92%) | 5 (71%) | 42 (81%) | 17 (65%) | 0.2312 | 27 (38%) | 6 (23%) | 0.1822 |
| Unmethylated | 1 (8%) | 2 (29%) | 10 (19%) | 9 (35%) | 45 (63%) | 20 (77%) |

\**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).