**Supplementary table 3. Methylation status in gastric cancer categorized by histological classification.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 　 | 　 |  | **Histological subtype, no. (%)** | ***P*-value\*** |
| **Locus** | **Methylation status** | **pap, n=2** | **tub, n=46** | **muc, n=5** | **por, n=38** | **sig, n=5** | **special type, n=2** |
| **Wnt** | ***SFRP2*-region 1** | Methylated | 2 (100%) | 38 (83%) | 5 (100%) | 28 (74%) | 3 (60%) | 2 (100%) | 0.4714 |
| Unmethylated | 0 (0) | 8 (17%) | 0 (0) | 10 (26%) | 2 (40%) | 0 (0) |
| ***SFRP2*-region 2** | Methylated | 2 (100%) | 36 (78%) | 5 (100%) | 24 (63%) | 1 (20%) | 2 (100%) | 0.0296 |
| Unmethylated | 0 (0) | 10 (22%) | 0 (0) | 14 (37%) | 4 (80%) | 0 (0) |
| ***APC* promoter 1A** | Methylated | 2 (100%) | 29 (63%) | 4 (80%) | 21 (55%) | 1 (20%) | 2 (100%) | 0.1941 |
| Unmethylated | 0 (0) | 17 (37%) | 1 (20%) | 17 (45%) | 4 (80%) | 0 (0) |
| **Others** | ***CACNA1G*** | Methylated | 0 (0) | 11 (24%) | 1 (20%) | 7 (18%) | 0 (0) | 0 (0) | 0.7321 |
| Unmethylated | 2 (100%) | 35 (76%) | 4 (80%) | 31 (82%) | 5 (100%) | 2 (100%) |
| ***CDKN2A*** | Methylated | 0 (0) | 9 (20%) | 0 (0) | 7 (18%) | 0 (0) | 0 (0) | 0.6681 |
| Unmethylated | 2 (100%) | 37 (80%) | 5 (100%) | 31 (82%) | 5 (100%) | 2 (100%) |
| ***CHFR*** | Methylated | 0 (0) | 14 (30%) | 2 (40%) | 17 (45%) | 0 (0) | 0 (0) | 0.2238 |
| Unmethylated | 2 (100%) | 32 (70%) | 3 (60%) | 21 (55%) | 5 (100%) | 2 (100%) |
| ***DCC*** | Methylated | 0 (0) | 26 (67%) | 3 (60%) | 13 (34%) | 2 (40%) | 0 (0) | 0.0296 |
| Unmethylated | 2 (100%) | 20 (43%) | 2 (40%) | 25 (66%) | 3 (60%) | 2 (100%) |
| ***MGMT*-Eh region** | Methylated | 0 (0) | 2 (4%) | 2 (40%) | 3 (8%) | 0 (0) | 0 (0) | 0.094 |
| Unmethylated | 2 (100%) | 44 (96%) | 3 (60%) | 35 (92%) | 5 (100%) | 2 (100%) |
| ***MINT1*** | Methylated | 1 (50%) | 25 (54%) | 2 (40%) | 18 (47%) | 4 (80%) | 0 (0) | 0.4915 |
| Unmethylated | 1 (50%) | 21 (46%) | 3 (60%) | 20 (53%) | 1 (20%) | 2 (100%) |
| ***MINT2*** | Methylated | 1 (50%) | 19 (41%) | 3 (60%) | 14 (37%) | 1 (20%) | 0 (0) | 0.6618 |
| Unmethylated | 1 (50%) | 27 (59%) | 2 (40%) | 24 (63%) | 4 (80%) | 2 (100%) |
| ***MINT31*** | Methylated | 0 (0) | 7 (15%) | 2 (40%) | 3 (8%) | 0 (0) | 0 (0) | 0.3173 |
| Unmethylated | 2 (100%) | 39 (85%) | 3 (60%) | 35 (92%) | 5 (100%) | 2 (100%) |
| ***MLH1*-A region** | Methylated | 0 (0) | 12 (26%) | 3 (60%) | 11 (29%) | 0 (0) | 1 (50%) | 0.317 |
| Unmethylated | 2 (100%) | 34 (74%) | 2 (40%) | 27 (71%) | 5 (100%) | 1 (50%) |
| ***MLH1*-D region** | Methylated | 0 (0) | 10 (22%) | 2 (40%) | 7 (18%) | 0 (0) | 0 (0) | 0.794 |
| Unmethylated | 2 (100%) | 36 (78%) | 3 (60%) | 31 (82%) | 5 (100%) | 2 (100%) |
| ***RASFF2*-region 1** | Methylated | 1 (50%) | 6 (13%) | 1 (20%) | 8 (21%) | 0 (0) | 0 (0) | 0.5409 |
| Unmethylated | 1 (50%) | 40 (87%) | 4 (80%) | 30 (79%) | 5 (100%) | 2 (100%) |
| ***RASFF2*-region 2** | Methylated | 1 (50%) | 24 (52%) | 4 (80%) | 21 (55%) | 0 (0) | 1 (50%) | 0.2092 |
| Unmethylated | 1 (50%) | 22 (48%) | 1 (20%) | 17 (45%) | 5 (100%) | 1 (50%) |
| ***RUNX3*** | Methylated | 1 (50%) | 23 (50%) | 2 (40%) | 23 (61%) | 3 (60%) | 1 (50%) | 0.9198 |
| Unmethylated | 1 (50%) | 23 (50%) | 3 (60%) | 15 (39%) | 2 (40%) | 1 (50%) |
| ***UNC5C*** | Methylated | 0 (0) | 16 (35%) | 4 (80%) | 10 (26%) | 1 (20%) | 0 (0) | 0.1415 |
| Unmethylated | 2 (100%) | 30 (65%) | 1 (20%) | 28 (74%) | 4 (80%) | 2 (100%) |
| ***3OST2*** | Methylated | 1 (50%) | 37 (80%) | 4 (80%) | 30 (79%) | 3 (60%) | 1 (50%) | 0.7141 |
| Unmethylated | 1 (50%) | 9 (20%) | 1 (20%) | 8 (21%) | 2 (40%) | 1 (50%) |

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

Pap, papillary adenocarcinoma; tub, tubular adenocarcinoma; muc, mucinous adenocarcinoma; por, poorly differentiated adenocarcinoma; sig, signet-ring cell carcinoma.