Supplementary Table 1. Association between genomic DNA methylation level and the risk of colorectal cancer according to subsites of large bowel

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| Subsites of cancer (cases/controls) | 1st quintile (3.628-4.107) | 2nd quintile (4.108-4.196) | 3rd quintile (4.198-4.272) | 4th quintile (4.273-4.353) | 5th quintile(4.354-4.788)  | *P* for trend |
|  Colon (249/620) | 1.00 | 1.15 (0.72-1.85) | 1.02 (0.63-1.66) | 0.96 (0.59-1.56) | 1.17 (0.73-1.89) | 0.74 |
|  Rectum (70/620) | 1.00 | 1.52 (0.59-3.95) | 1.94 (0.78-4.82) | 1.37 (0.52-3.58) | 2.09 (0.84-5.20) | 0.16 |
|  Proximal (175/620) | 1.00 | 1.00 (0.58-1.72) |  1.01 (0.58-1.76) | 0.91 (0.52-1.59) | 1.26 (0.73-2.16) | 0.51 |
|  Distal (94/620) | 1.00 | 1.38 (0.70-2.73) | 1.00 (0.48-2.07) | 0.86 (0.40-1.82) | 0.84 (0.44-1.77) | 0.37 |

Multivariate models are adjusted for age at blood draw, date of blood draw, race, height (continuous), fasting status, pack-years of smoking (continuous), body mass index (continuous), physical activity (in quartiles), family history of colorectal cancer (yes or no), history of colonoscopy or sigmoidoscopy (yes or no), alcohol intake (continuous), intake of red and processed meat (in quartiles), vitamin D intake (continuous), calcium intake (continuous), and aspirin use (non-users vs. ever users).