



S3 Fig. Pyrosequencing methylation analysis in the methylation-variable transitional-CpG sites. (A, B, C) Upper panels show the sequences of transitional-CpG sites near *ARRDC4*, *CDKN2A*, and *CDH1* and lower panels display the bisulfite-modified sequences. Red-colored letters indicate CpG sites analyzed by radioisotope MSP, and CG¹ and CG² by pyrosequencing. Underlined letters indicate the sequences amplified by pyrosequencing common polymerase chain reaction (PCR). (B) Left panel shows pyrograms for the relative density of methylation (%). Note that methylation densities analyzed from same specimen are different depending on annealing temperature of common PCR. (C) Left panel shows scattergram for the relationship between methylation levels of semiquantitative radioisotope methylation-specific PCR and relative methylation densities of pyrosequencing. Correlation coefficients were determined by Spearman's correlation analysis.