**Supplemental Data**

**Figure S1. Technical validation of 450K BeadChip array data.** Correlation between array-derived β-values (*x*-axis) and methylation percentage as determined by pyrosequencing (*y*-axis) for 5 CpGs (cg07778029, cg14456683, cg01227537, cg05661282 and cg26465391) across 24 samples is shown. Spearman-rank correlation coefficient r=0.912; *P*<0.00001.

**Table S1. Sample characteristics.**

**Table S2. List of 256 differentially methylated genes.**

**Table S3. Methylation in discovery and investigation high-grade tumor cohorts.**

**Table S4. Frequency and mean levels of methylation in 25 genes for high- and low-intermediate-grade tumors.**

**Table S5. Gene Ontology and KEGG pathway annotation lists.**

**Table S6. Primer sequences.**