**Figure headings/legends: (will add separately as part of online submission)**

**Figure 1.**

TITLE: Frequency distribution of methylation ratios for CpG dinucleotides in oyster gill tissue.

LEGEND: A total of  2,625,745 CpG dinucleotides with ≥ 5x coverage are represented.

**Figure 2.**

TITLE: Comparison of the total CpG versus methylated CpG in oyster gill tissue by genomic feature.

LEGEND: Proportion of all CpG (blue) and methylated CpG (red) in gill tissue across genomic features of C. gigas. Percent of CpG dinucleotides in Exons, Introns, Transposable Elements (TE), promoters (Pro) and unannotated intergenic regions (Other) are reported.

**Figure 3.**

TITLE: DNA methylation among genes with increasing transcript abundances.

LEGEND: Expressed genes were grouped into deciles by transcription abundance. Genes not expressed in gill (i.e. RPKM=0) are also shown (leftmost column).. Error bars represent 95% confidence intervals.

**Figure 4**

TITLE: PCA ordination of oyster genes by gene attributes.

LEGEND: Variables loadings shown by purple arrows. Variables significantly contributing to PC1 and PC2 include: methylation ratio (Methylation), the coefficient of variance of expression between tissues (%CV), the number of exons (Exons), the length of the mRNA in base pairs (mRNA) and the number of CpG dinucleotides in the gene (CpG).  Variables that did not significantly contributes to PC1 and PC2 include the mean transcript abundance (Expression). Inset depicts ordination of the genes analyzed on PC1 and PC2 (n= 27,181).

**Table 1.**

Title: Summary of PCA for gene attributes.