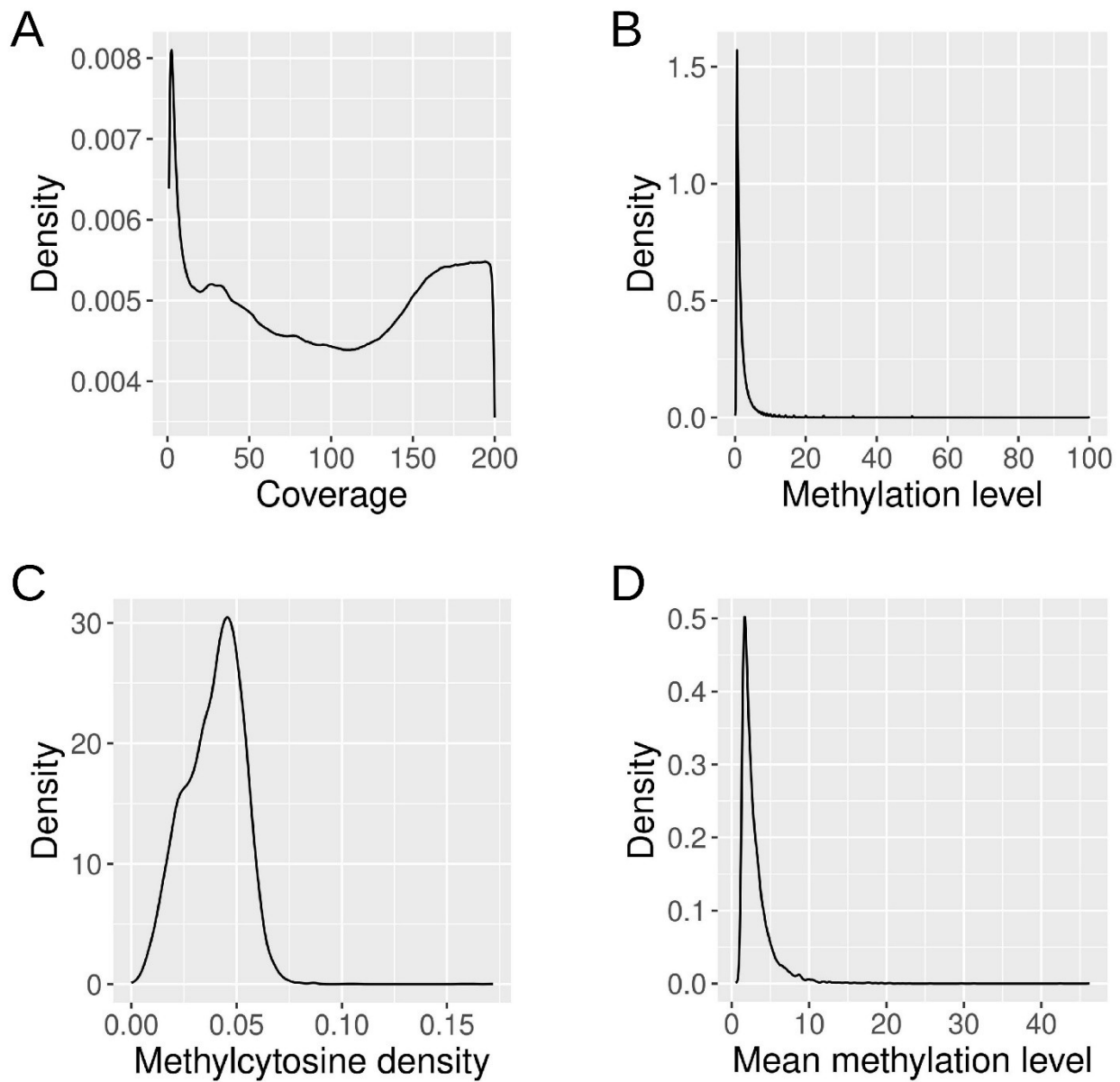
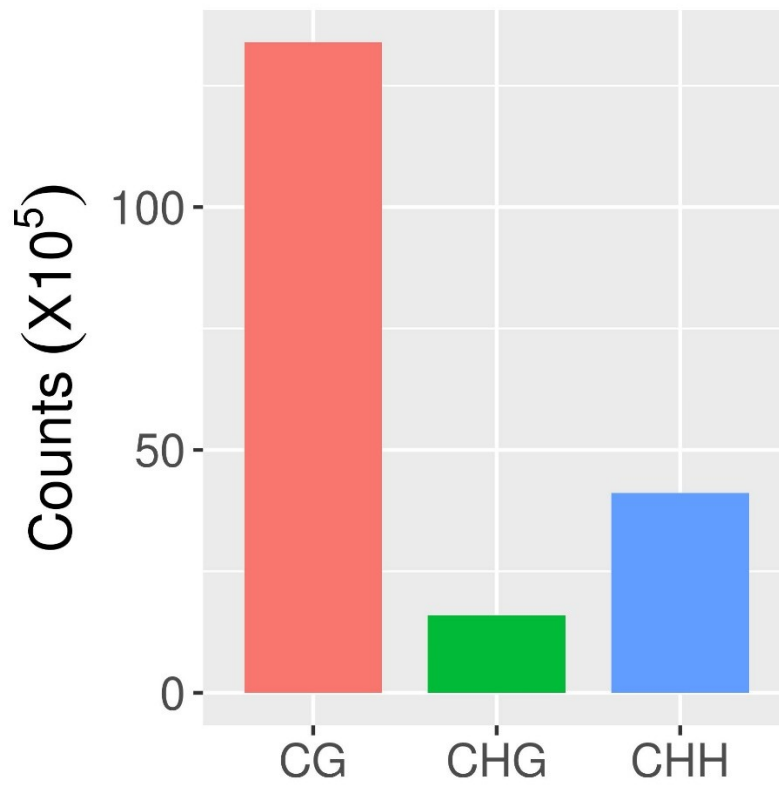
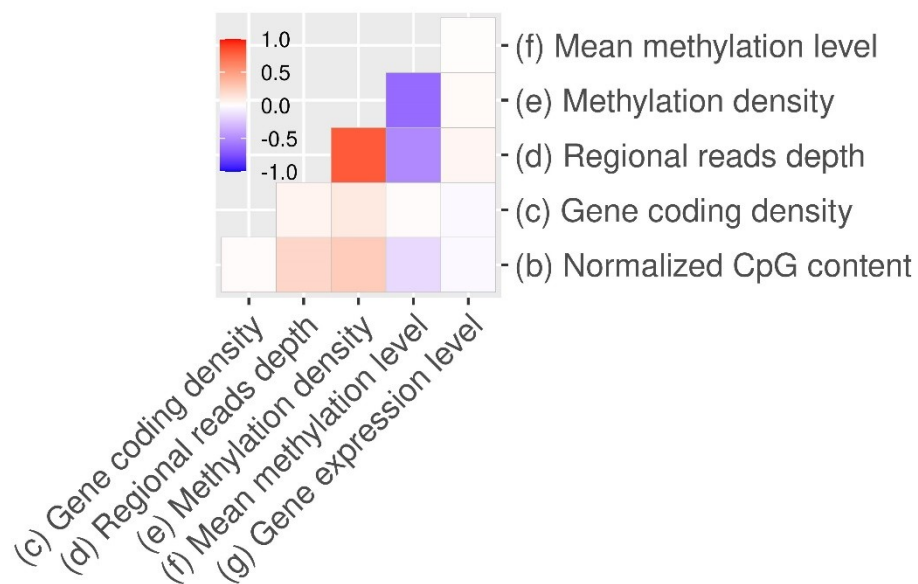




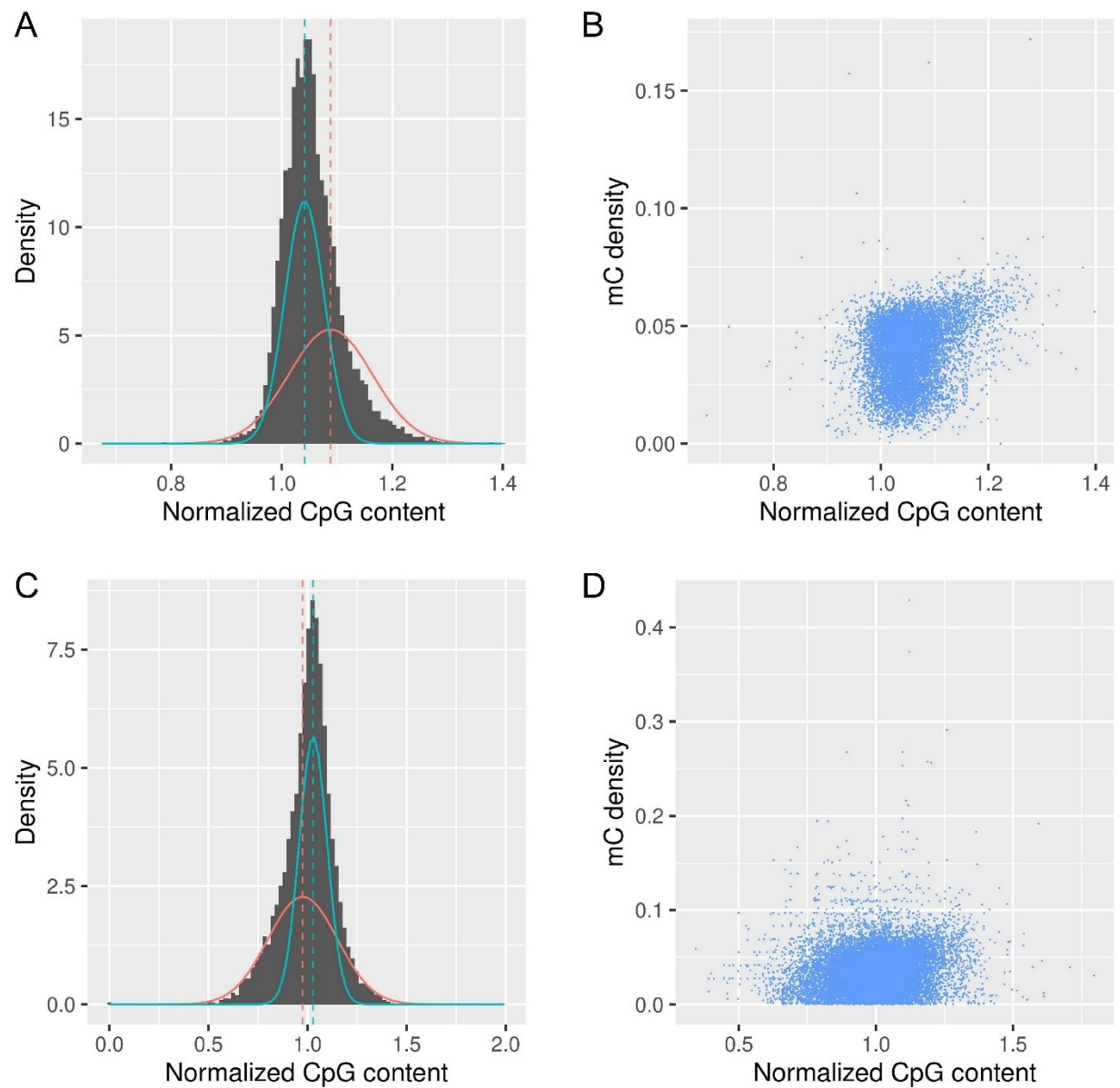
Supplementary Figure 1. Distribution of (A) sequencing depth, (B) single nucleotide methylation level, (C) 50-kb level methylcytosine densities, and (D) 50-kb mean methylation level.



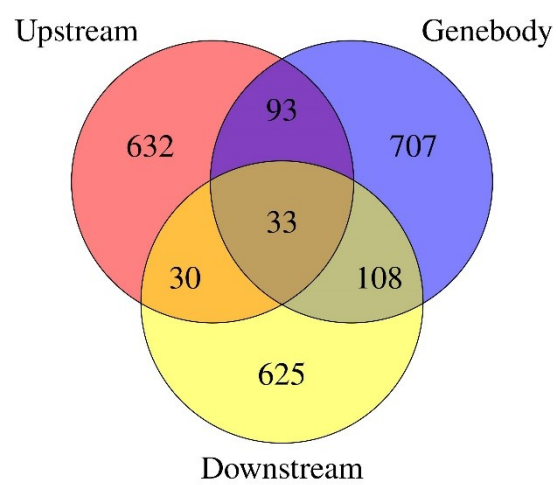
Supplementary Figure 2. Methylcytosine counts in CG, CHG, and CHH contexts.



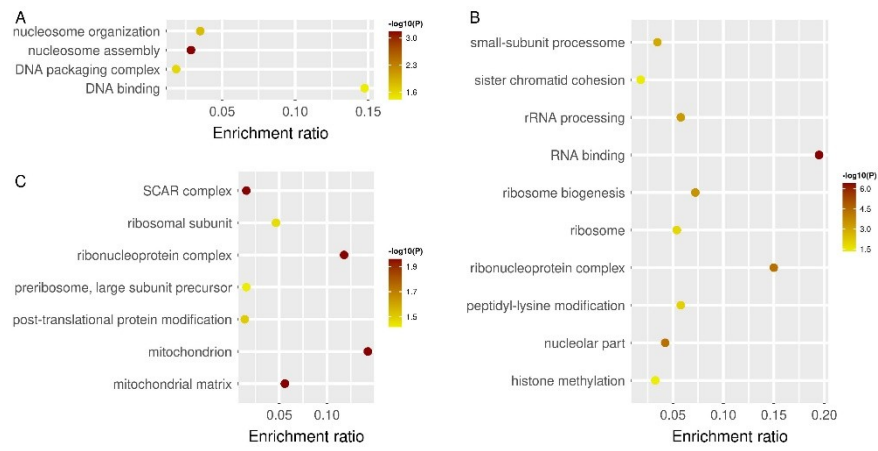
Supplementary Figure 3. Pairwise correlation between (b) normalized CpG contents, (c) gene coding density, (d) mean sequencing depth, (e) methylcytosine density, (f) mean methylation level, and (g) normalized *tags per kilobase per million mapped reads* (TPM) value at the 50-kb level.



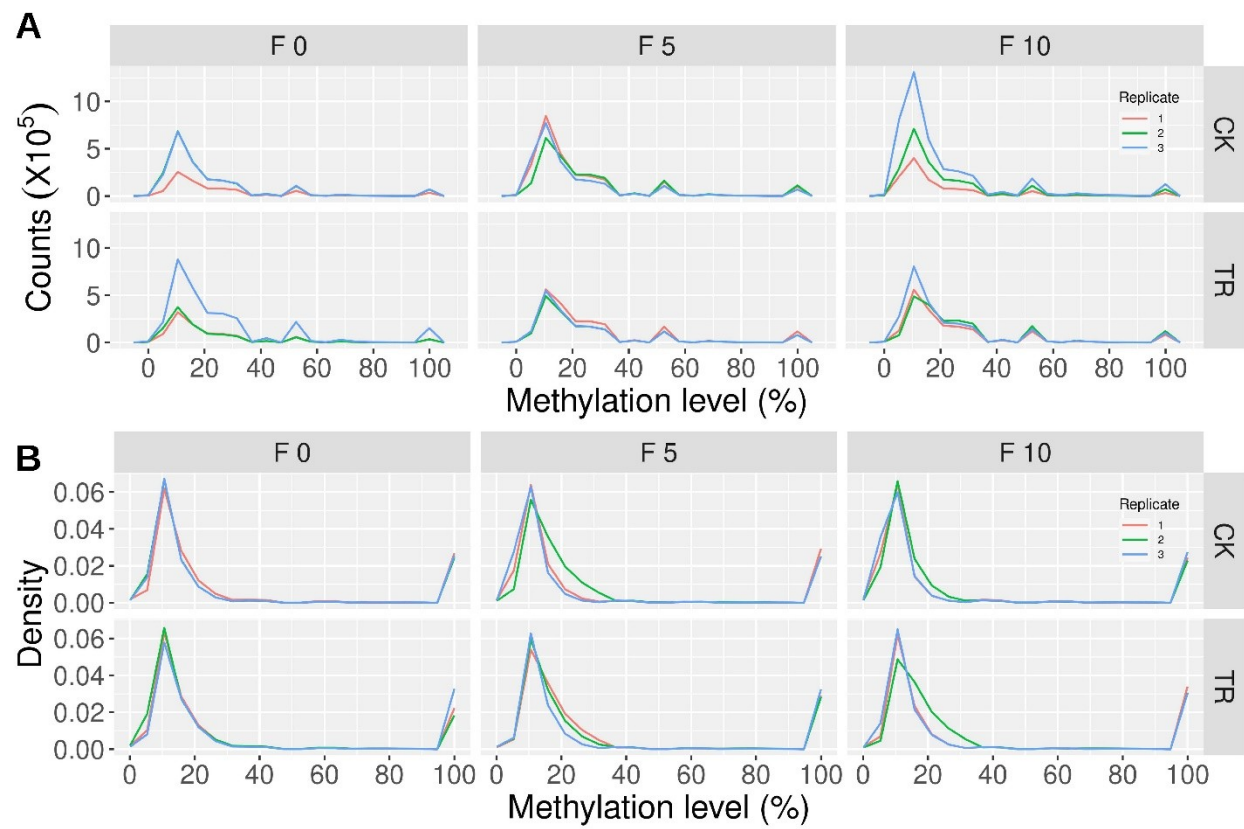
Supplementary Figure 4. (A) Distribution of genomic regional normalized CpG contents. (B) Correlation between genomic regional normalized CpG contents and mC densities. (C) Distribution of gene region normalized CpG contents. (D) Correlation between gene region normalized CpG contents and mC densities.



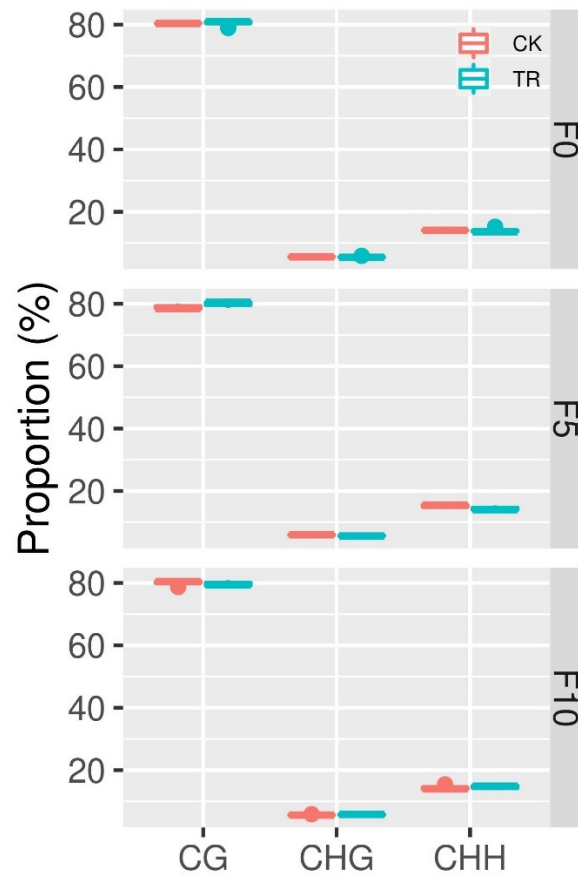
Supplementary Figure 5. Intersection relationship of top 5% high methylcytosine density genes in the upstream, genebody, and downstream.



Supplementary Figure 6. GO enrichment analysis of the top 5% high methylated genes in the (A) upstream, (B) genebody, and (C) downstream.

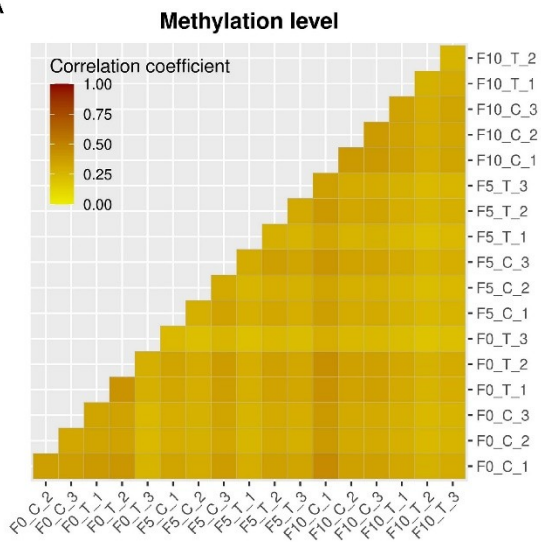


Supplementary Figure 7. Histogram of methylation levels in (A) counts and (B) density. The three colors represent three biological replicates.

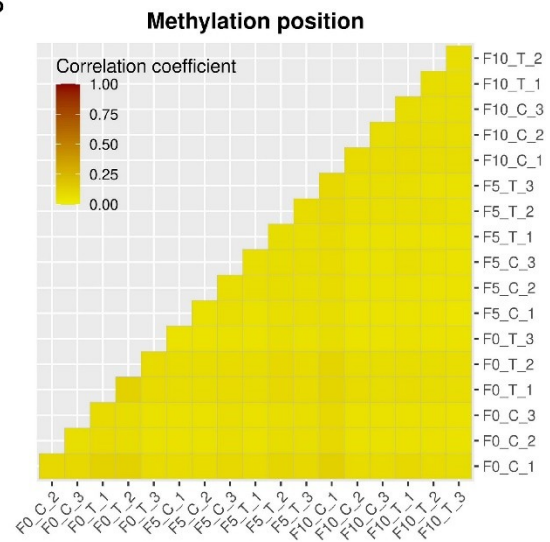


Supplementary Figure 8. Methylated context proportions in F0, F5, F10, and their Vip3Aa-treated groups.

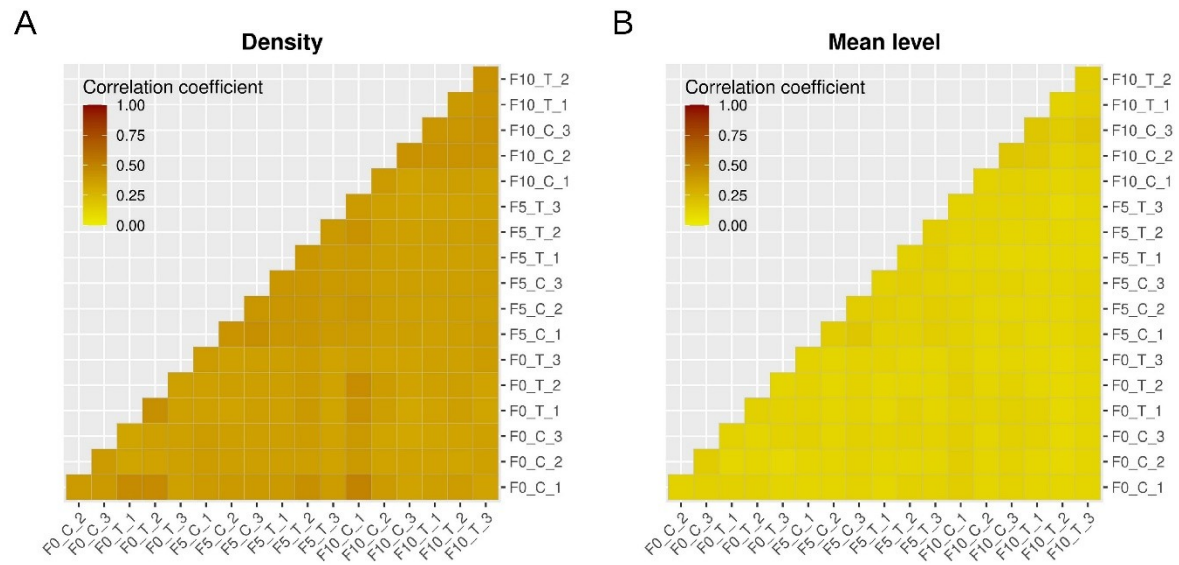
A



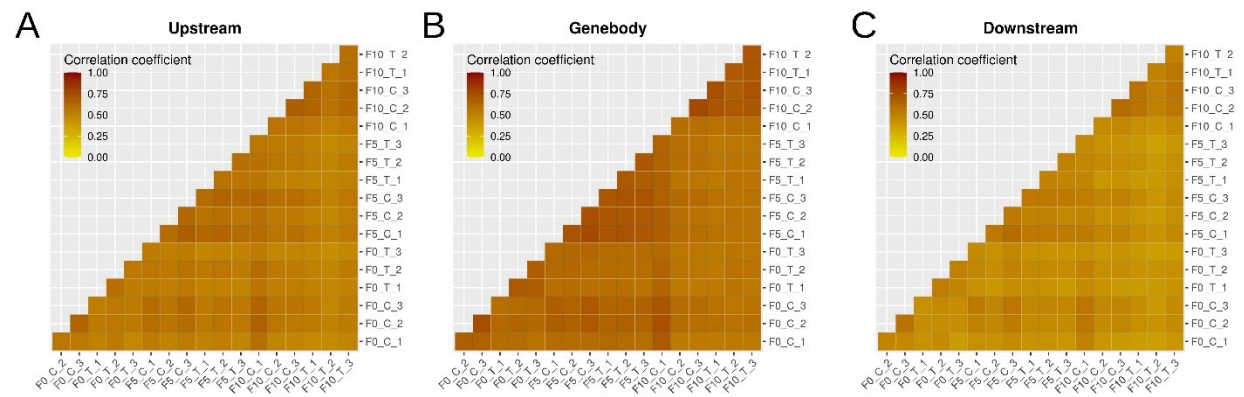
B



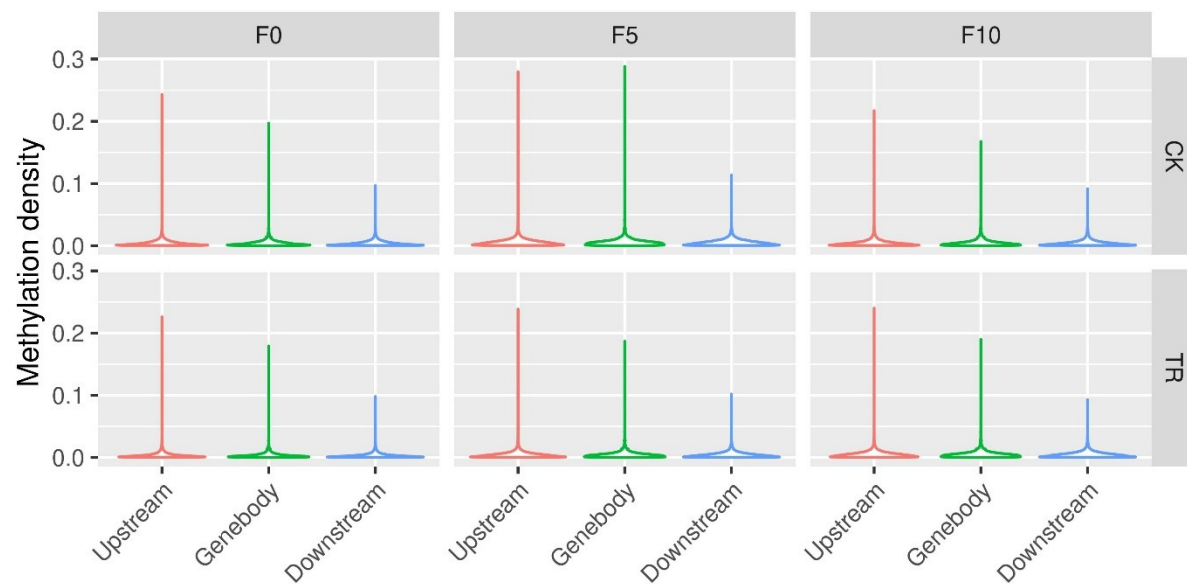
Supplementary Figure 9. Pairwise correlation of (A) methylation levels and (B) methylated sites between samples.



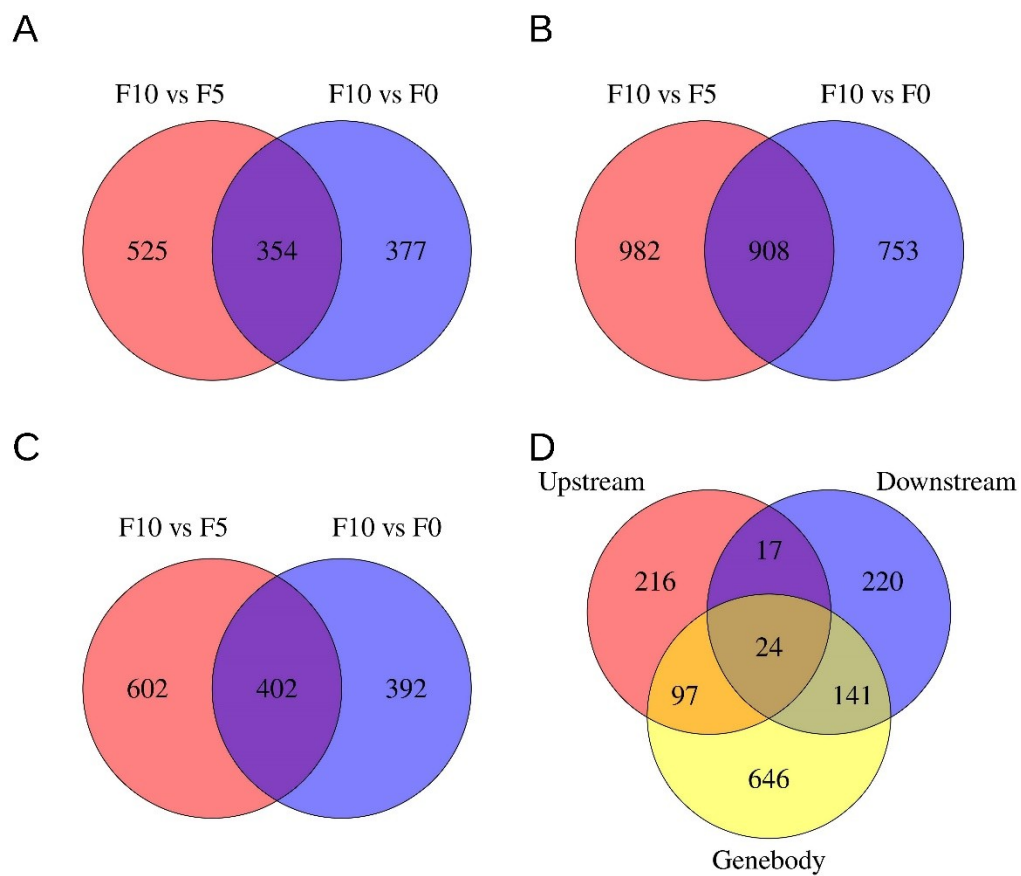
Supplementary Figure 10. Pairwise correlation of (A) methylcytosine densities and (B) mean methylation levels between samples at the 500-bp level.



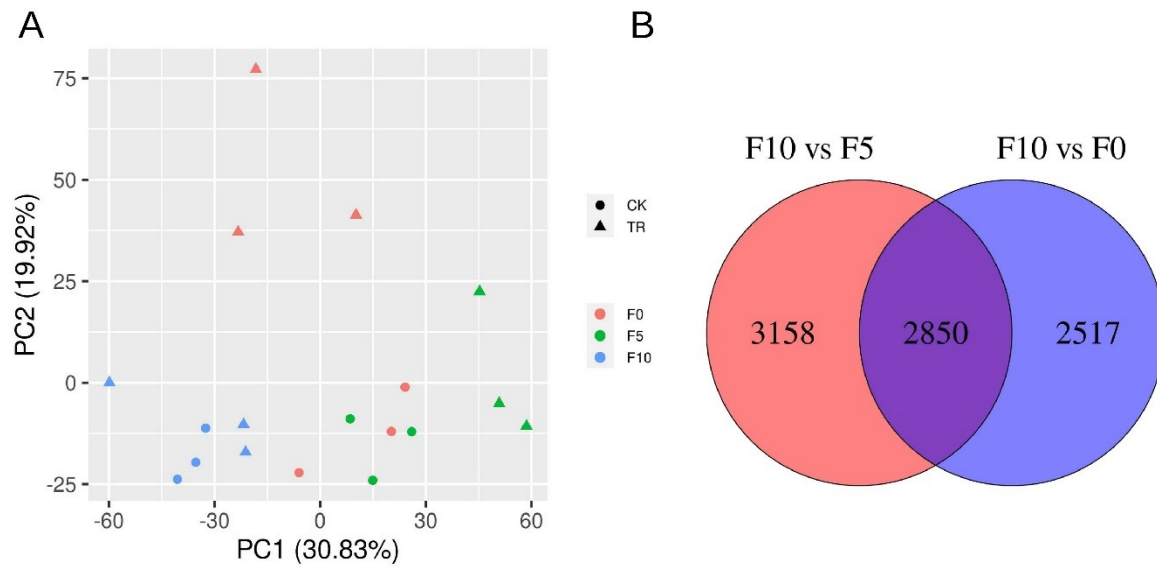
Supplementary Figure 11. Pairwise correlation of the (A) upstream, (B) genebody, and (C) downstream methylcytosine densities between samples.



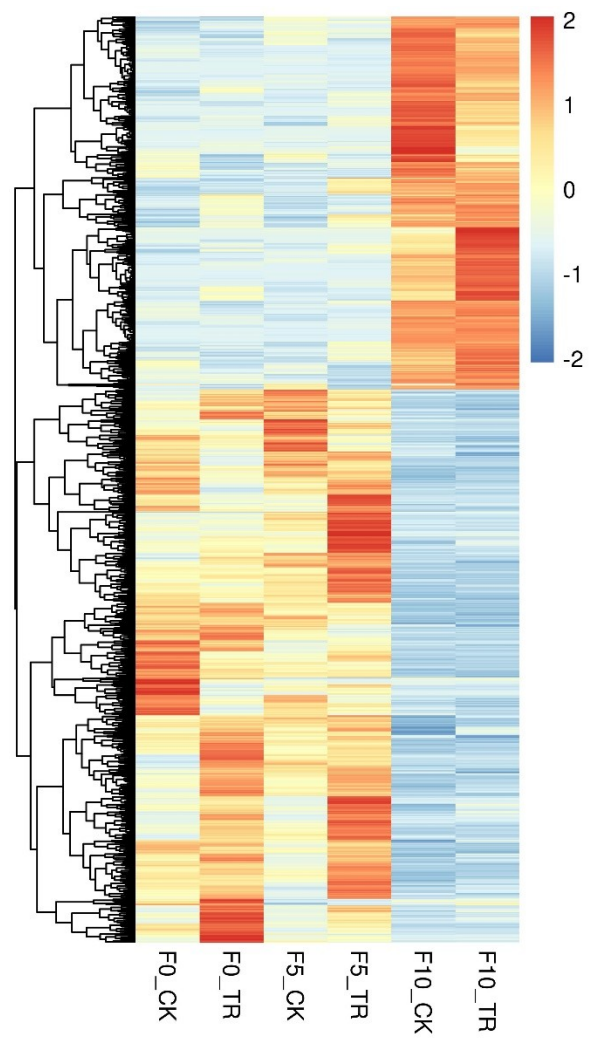
Supplementary Figure 12. Distribution of methylcytosine densities for each gene stream in F0, F5, F10, and their Vip3Aa-treated groups.



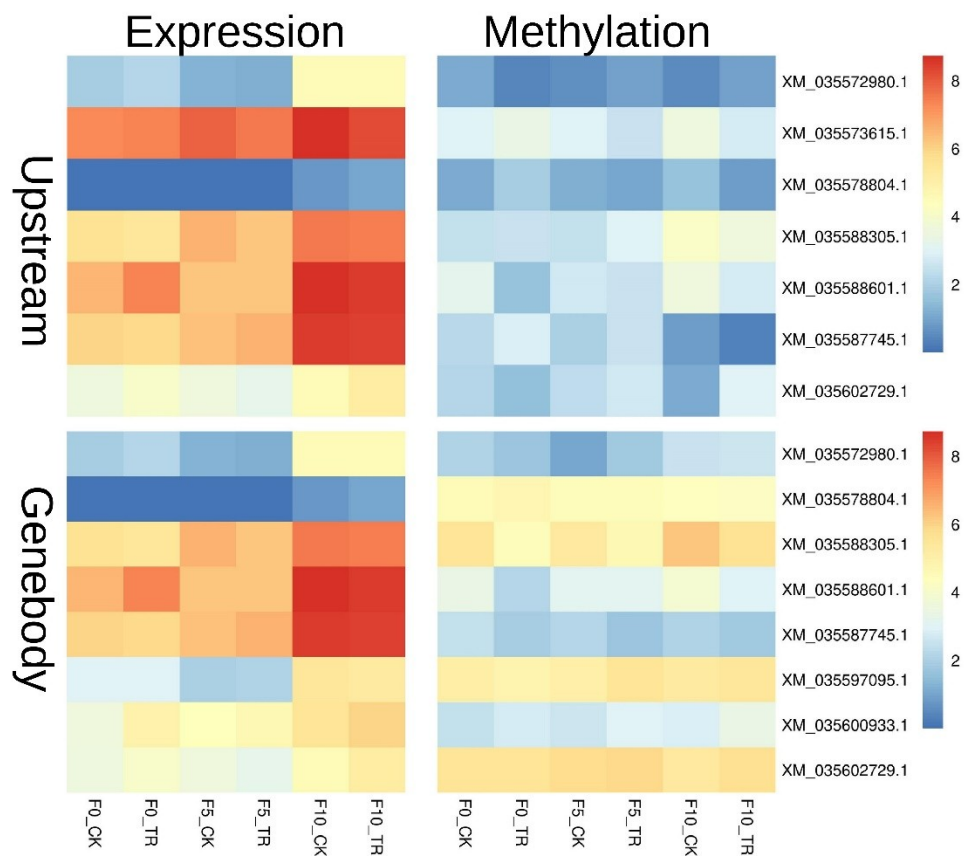
Supplementary Figure 13. Differentially methylated gene (DMG) counts identified based on the comparison of (A) upstream, (B) genebody, and (C) downstream methylcytosine density. (D) Numbers of DMGs identified from upstream, genebody, and downstream and their relationship.



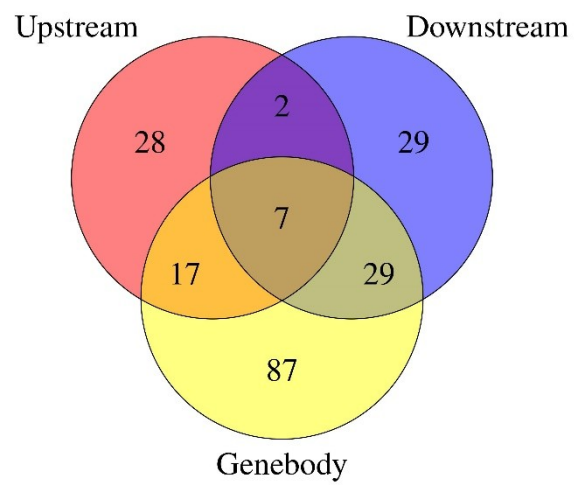
Supplementary Figure 14. Sample relationship by transcriptome and the numbers of differentially expressed genes identified. (A) PCA of whole genomic gene expression values. (B) Numbers of differentially expressed genes identified based on the comparison between tenth generation (F10) to fifth generation (F5) samples, and between F10 to wild-type (F0) samples.



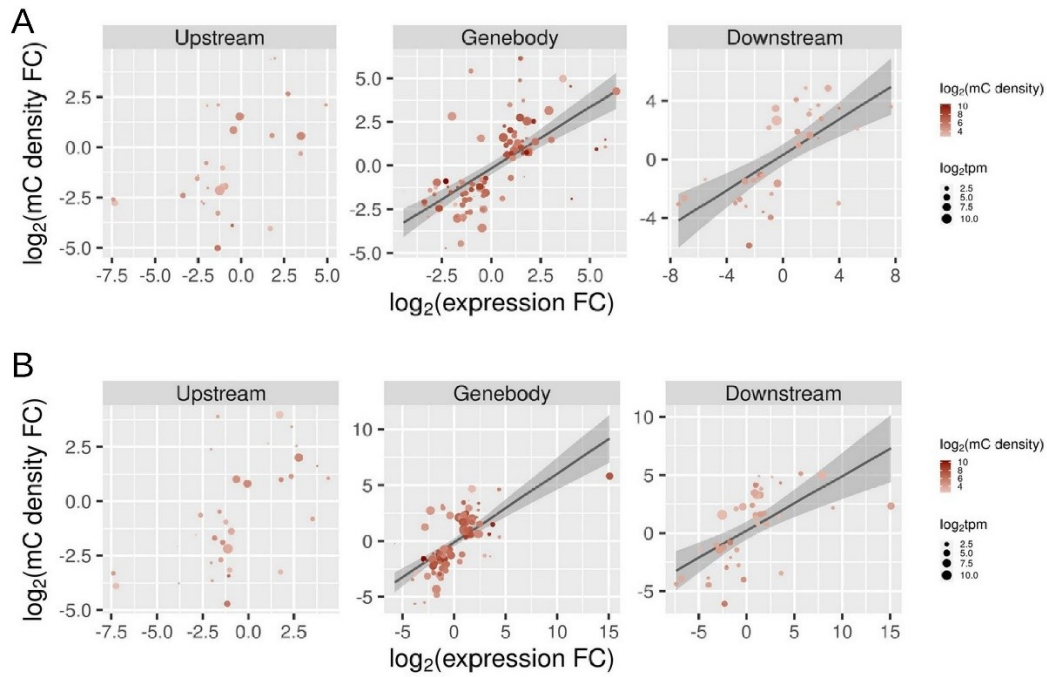
Supplementary Figure 15. Expression pattern of differentially expressed genes.



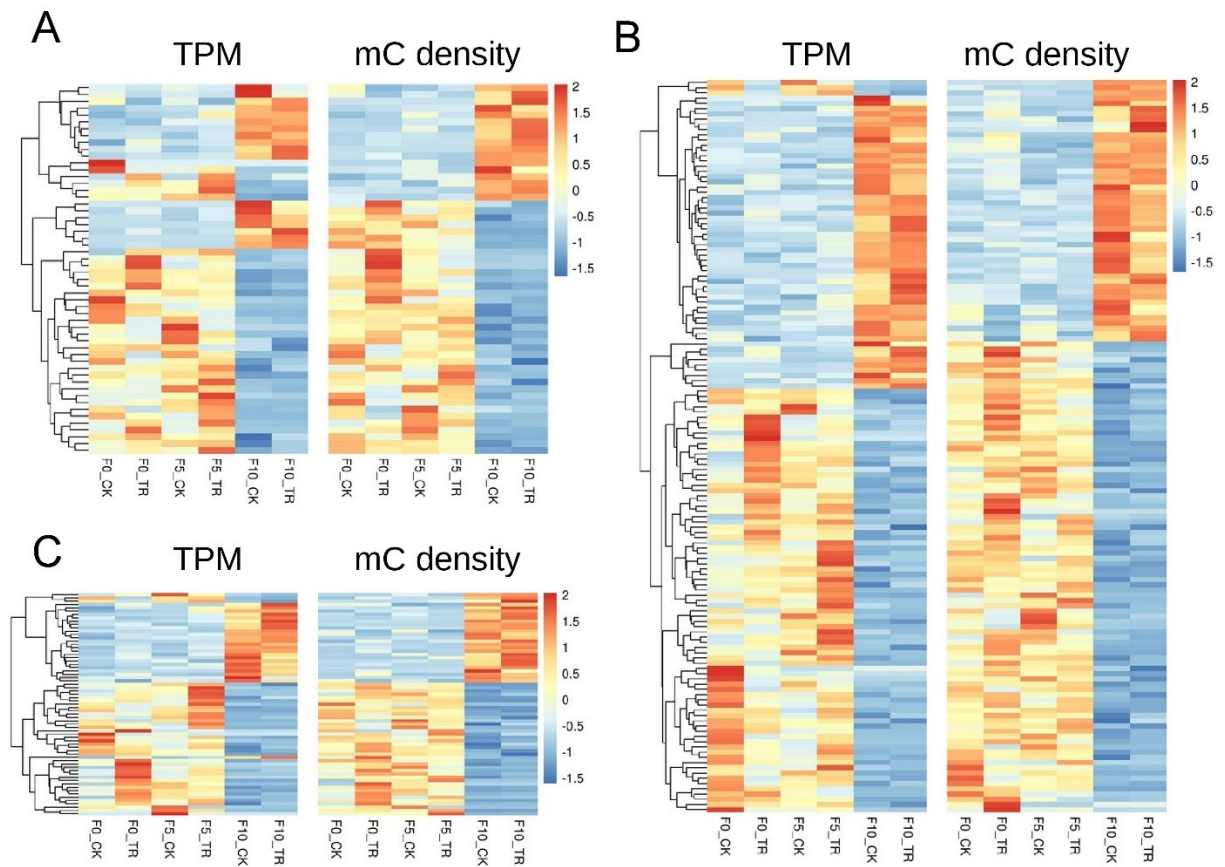
Supplementary Figure 16. Expression level and methylcytosine density patterns of upstream and downstream of significantly enriched P450 genes.



Supplementary Figure 17. Relationship among upstream, genebody, and downstream differentially methylated and expressed genes.



Supplementary Figure 18. Point plots of differentially expressed and methylated genes in the upstream, gene body, and downstream. Comparison of $\log_2$ fold changes of mC densities and expression levels between F10 and F0 (A) and between F5 and F0 (B) control groups. The lines were produced by loess analysis, and the dark grey area represents the 95% confidence interval. The size and color for each point represents the maximum values of $\log_2$ transformations of mC densities and TPM in F10 and F0, or in F10 and F5 for each gene.



Supplementary Figure 19. Patterns of the genes that were both differentially expressed and methylated in the (A) upstream, (B) gene body, and (C) downstream.

Supplementary Table 1.

Generation	Vip3Aa concentrations (ng/cm ²)
F0	0, 5, 10, 20, 40, 80, 160
F5	0, 4, 8, 16, 64, 128, 256
F10	0, 15, 45, 135, 405, 1215
F11-	0, 5, 15, 45, 135, 405, 1215
F12-	0, 5, 15, 45, 135, 405, 1215
F13-	0, 5, 15, 45, 135, 405, 1215

Vip3Aa concentrations for bioassays.

Supplementary Table 2.

Primer name	Primer sequence	Comment
dsGFP_F	TAATACGACTCACTATAGGGGCATCGACTTCAAGGAGGAC	For dsRNA
dsGFP_R	TAATACGACTCACTATAGGGCTACTTGTACAGCTCGTCCA	For dsRNA
dsSfPDE_F	TAATACGACTCACTATAGGGGCGGAACCAAGAACACTCAG	For dsRNA
dsSfPDE_R	TAATACGACTCACTATAGGGTTAGTAAGCCCAATAGCAGCAC	For dsRNA
SfPDE_F	GTCTTCTACGCCAAGTCCAG	For qRT-PCR
SfPDE_R	ATCATCATTCTCTTCACCAGCA	For qRT-PCR
GAPDH_F	CGGTGTCTTCACAACCACAG	For qRT-PCR
GAPDH_R	TTGACACCAACGACGAACAT	For qRT-PCR

List of primers used.