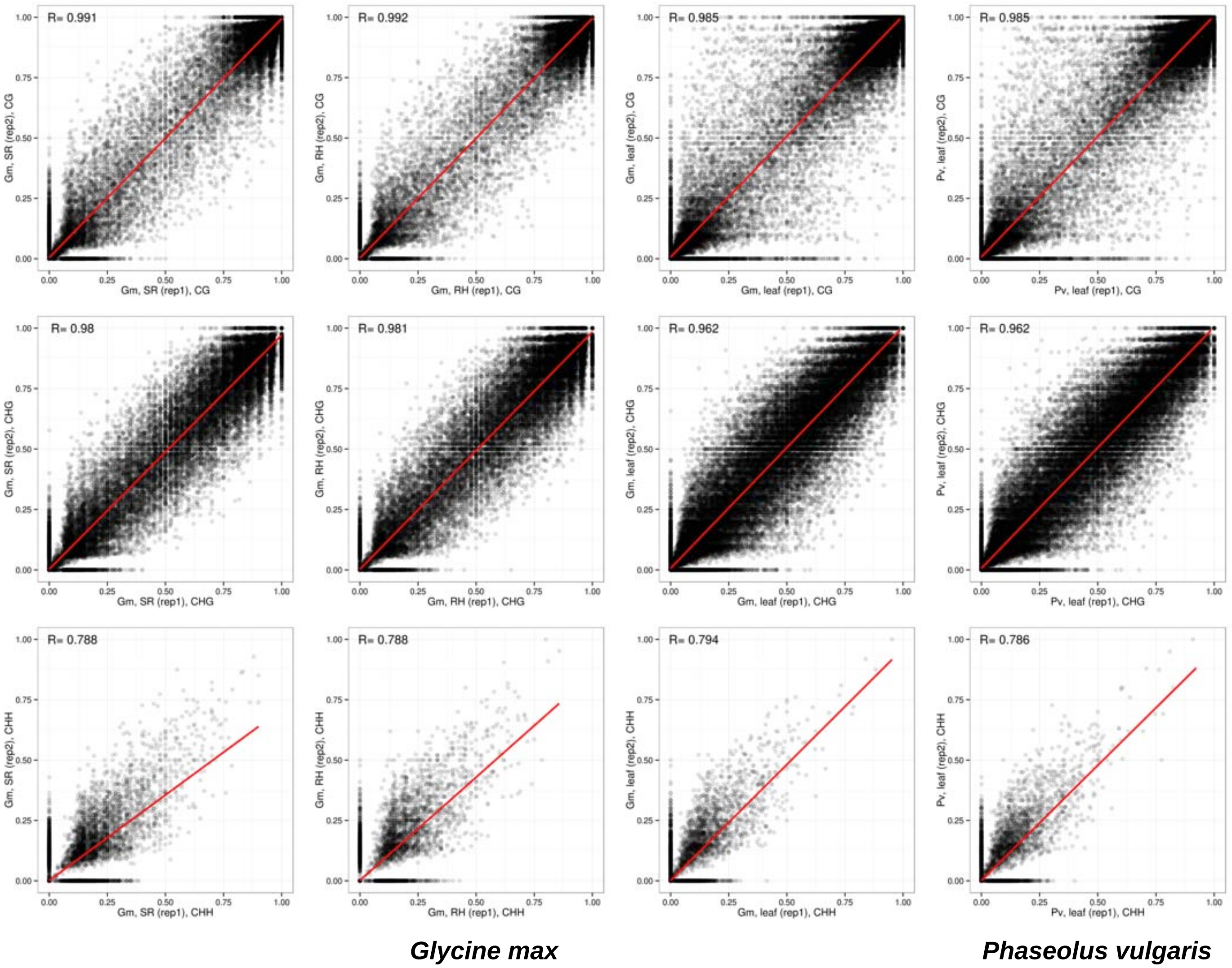
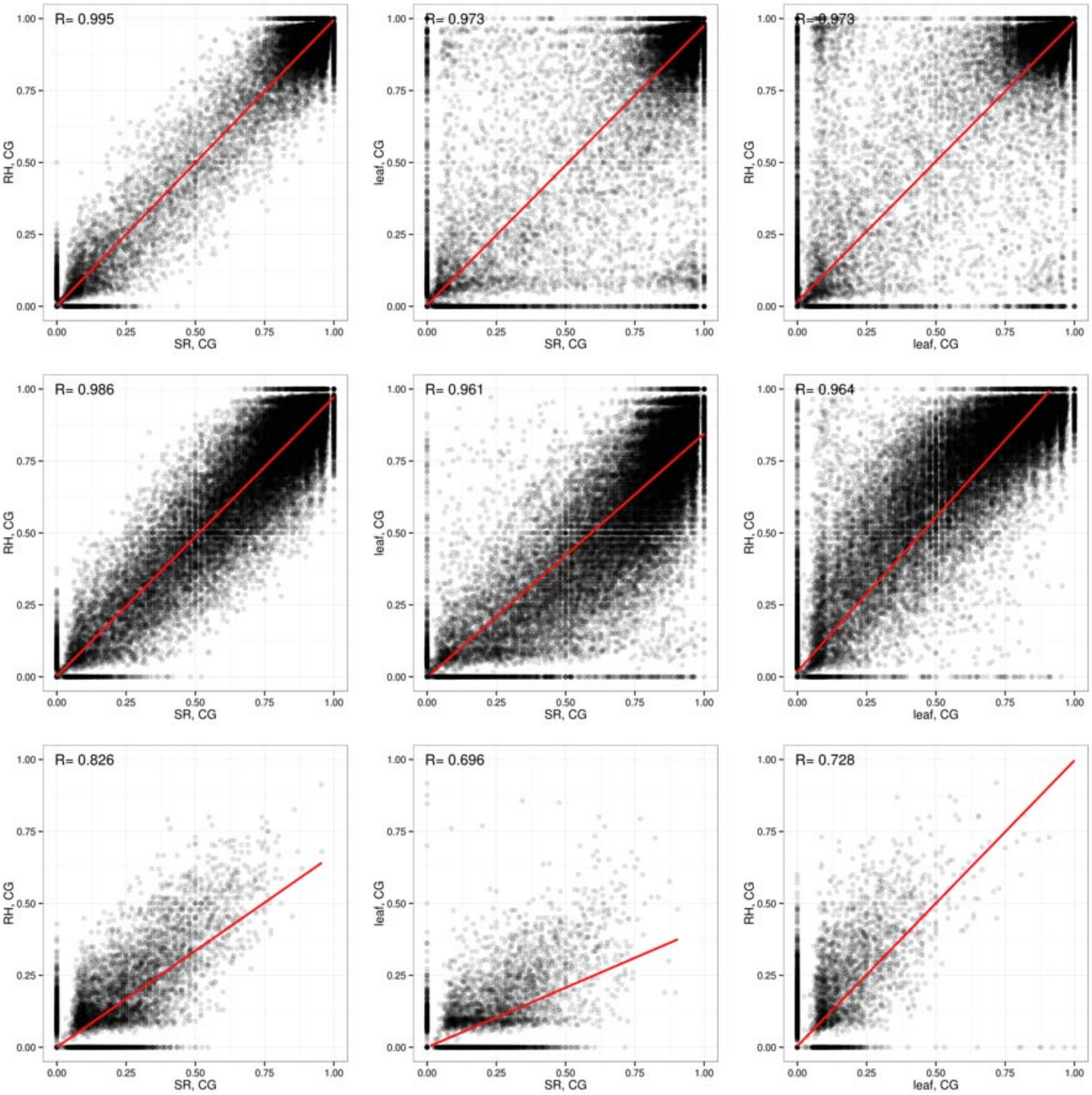
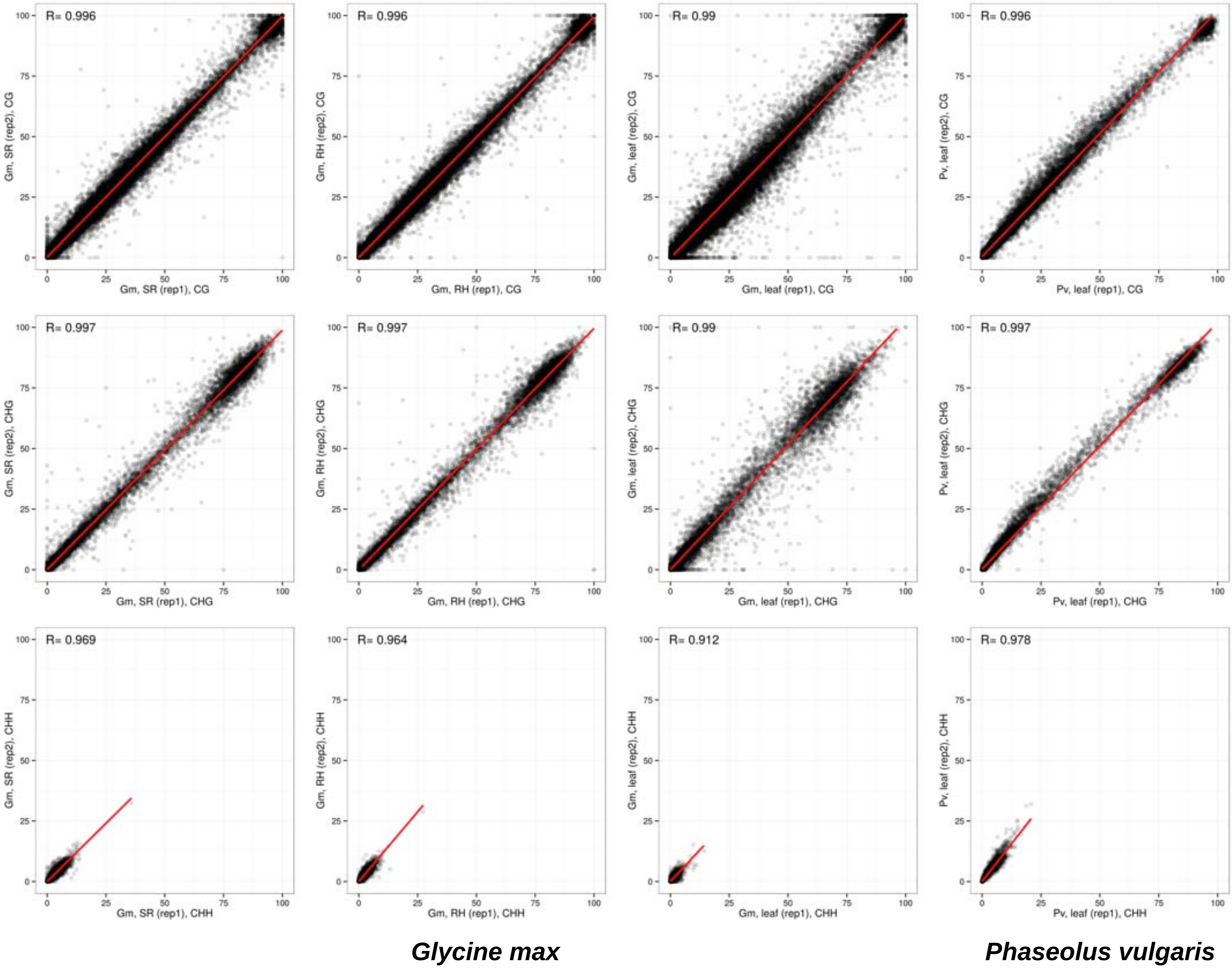


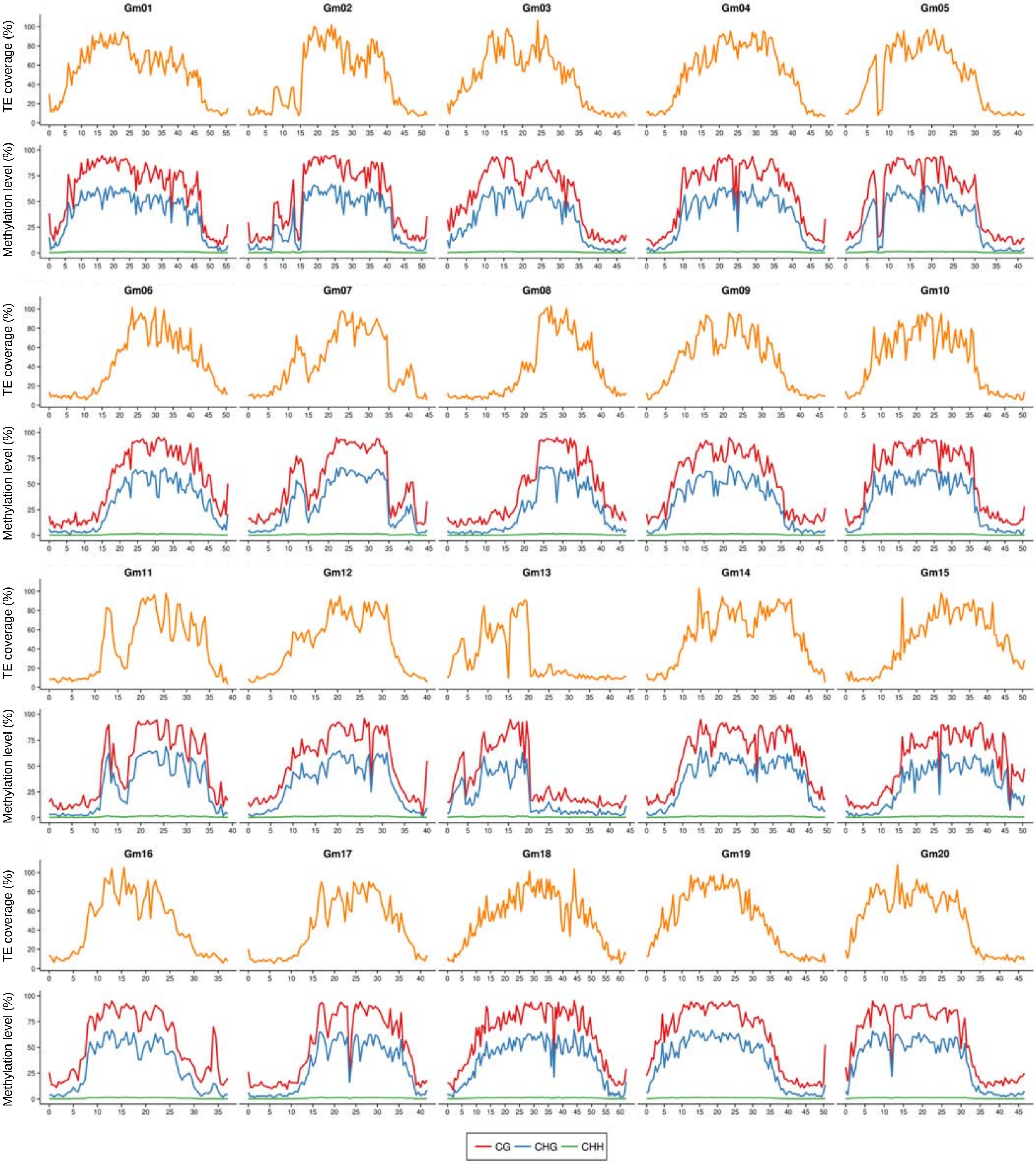
Supplemental Figure S1. Scatter plot of cytosine methylation between biological replicates. A total of 100,000 cytosine sites with more than 20 sequence reads were randomly selected. SR = stripped root, RH = root hair, R = Pearson correlation coefficient.



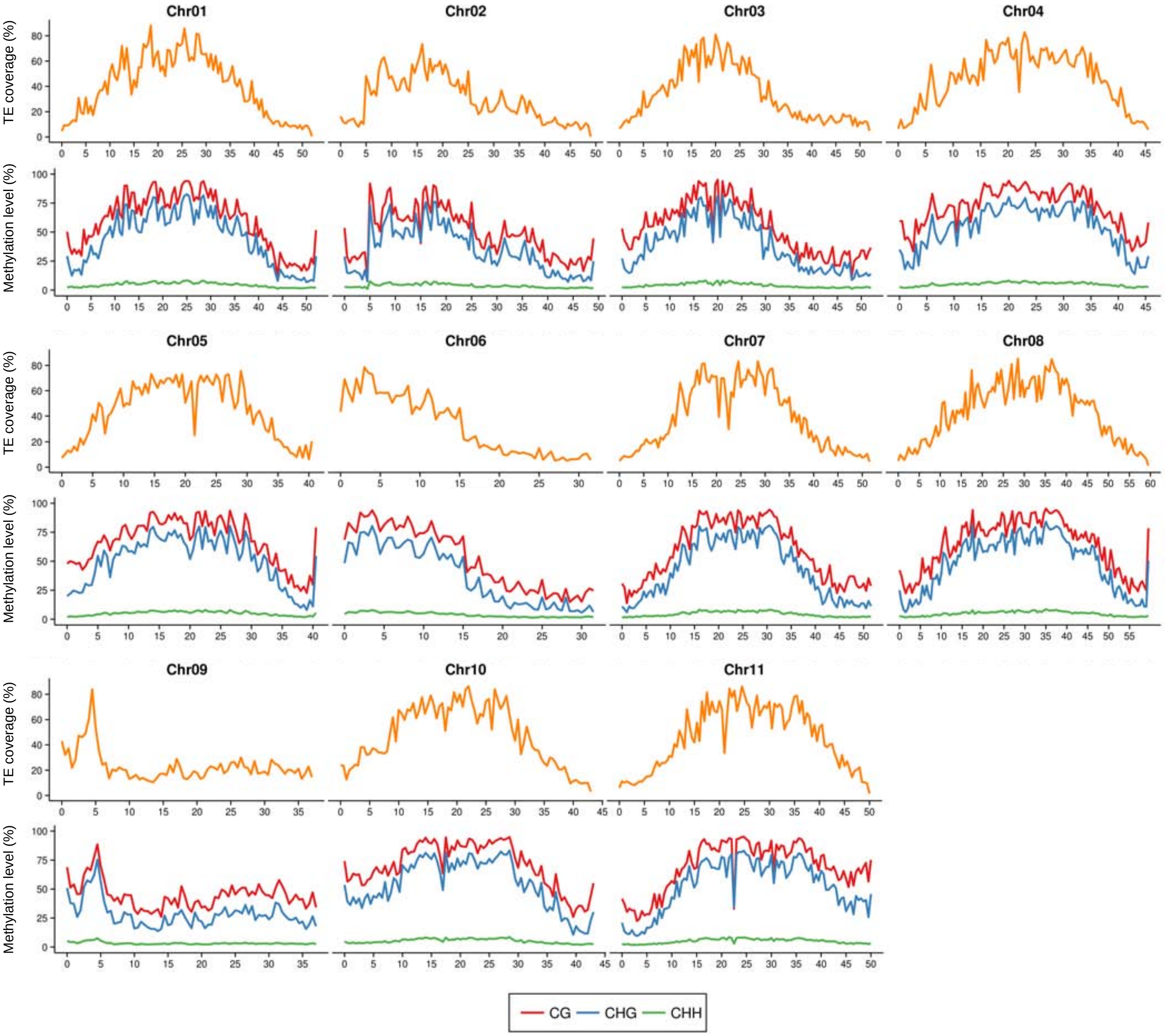
Supplemental Figure S2. Scatter plot of cytosine methylation between soybean tissues. A total of 100,000 cytosine sites with more than 20 sequence reads were randomly selected. SR = stripped root, RH = root hair, R = Pearson correlation coefficient.



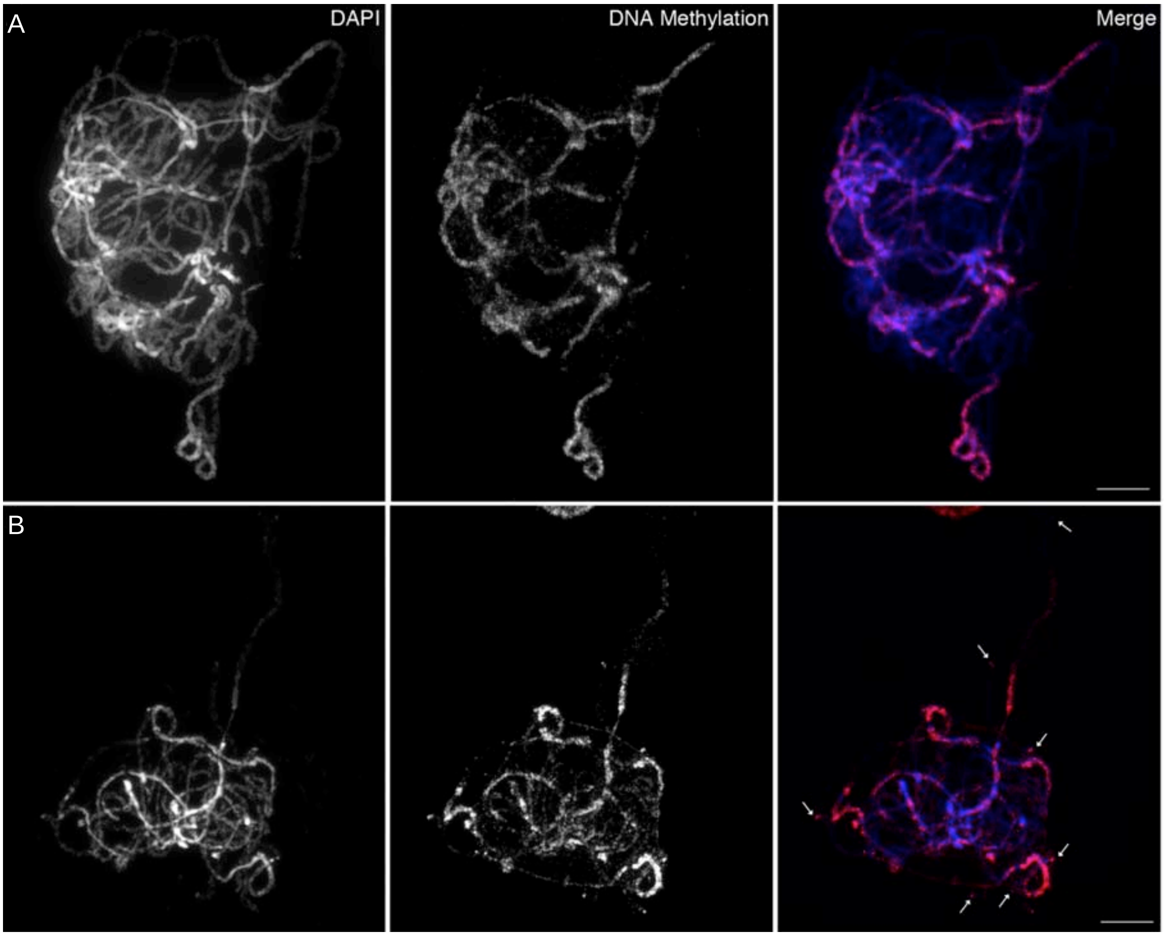
Supplemental Figure S3. Scatter plot of weighted methylation level of protein-coding genes between biological replicates. SR = stripped root, RH = root hair, R = Pearson correlation coefficient.



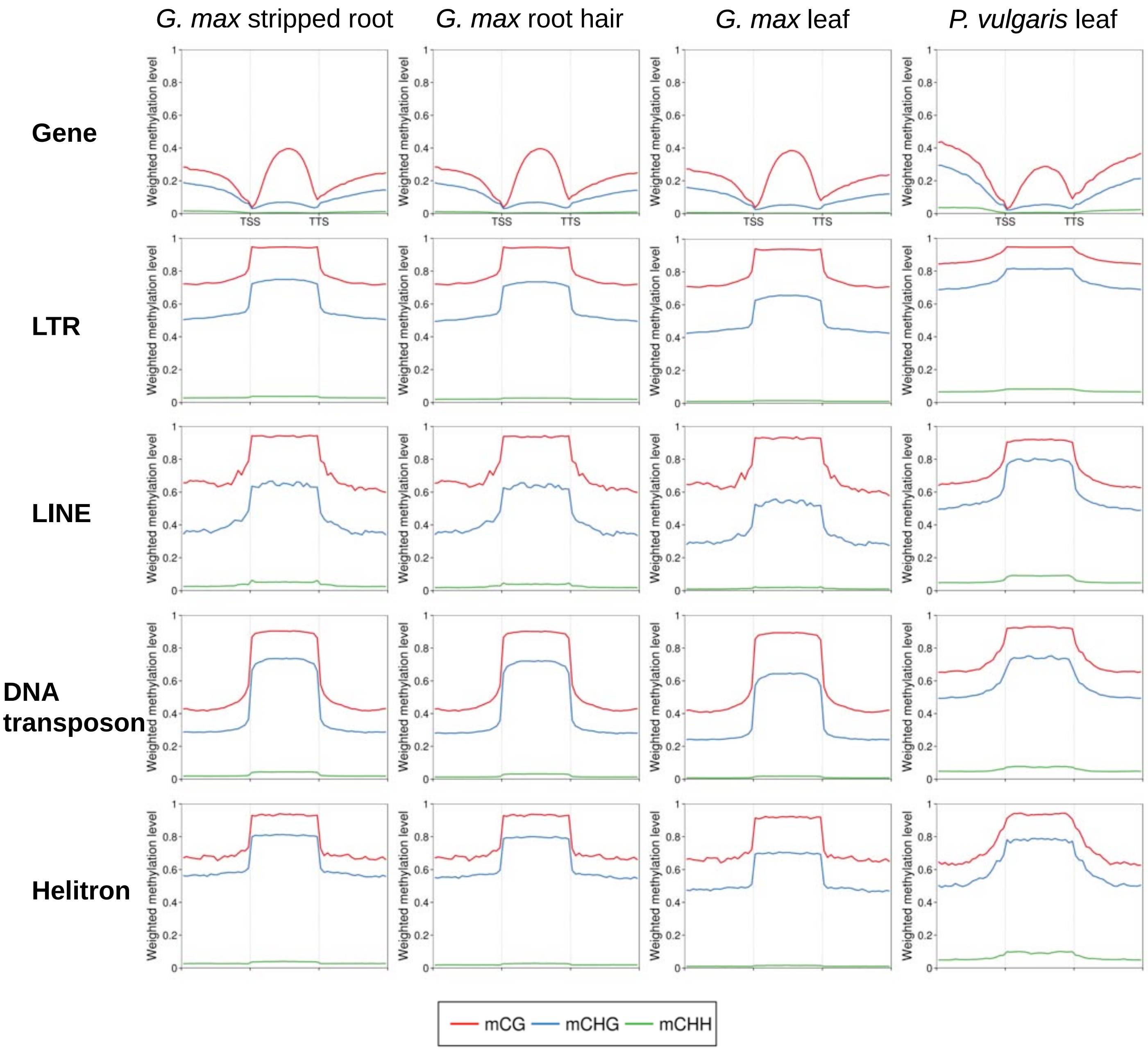
Supplemental Figure S4. Chromosome-wide distribution of methylation in *Glycine max* and correlation with annotated repeats in sliding 500kb windows.



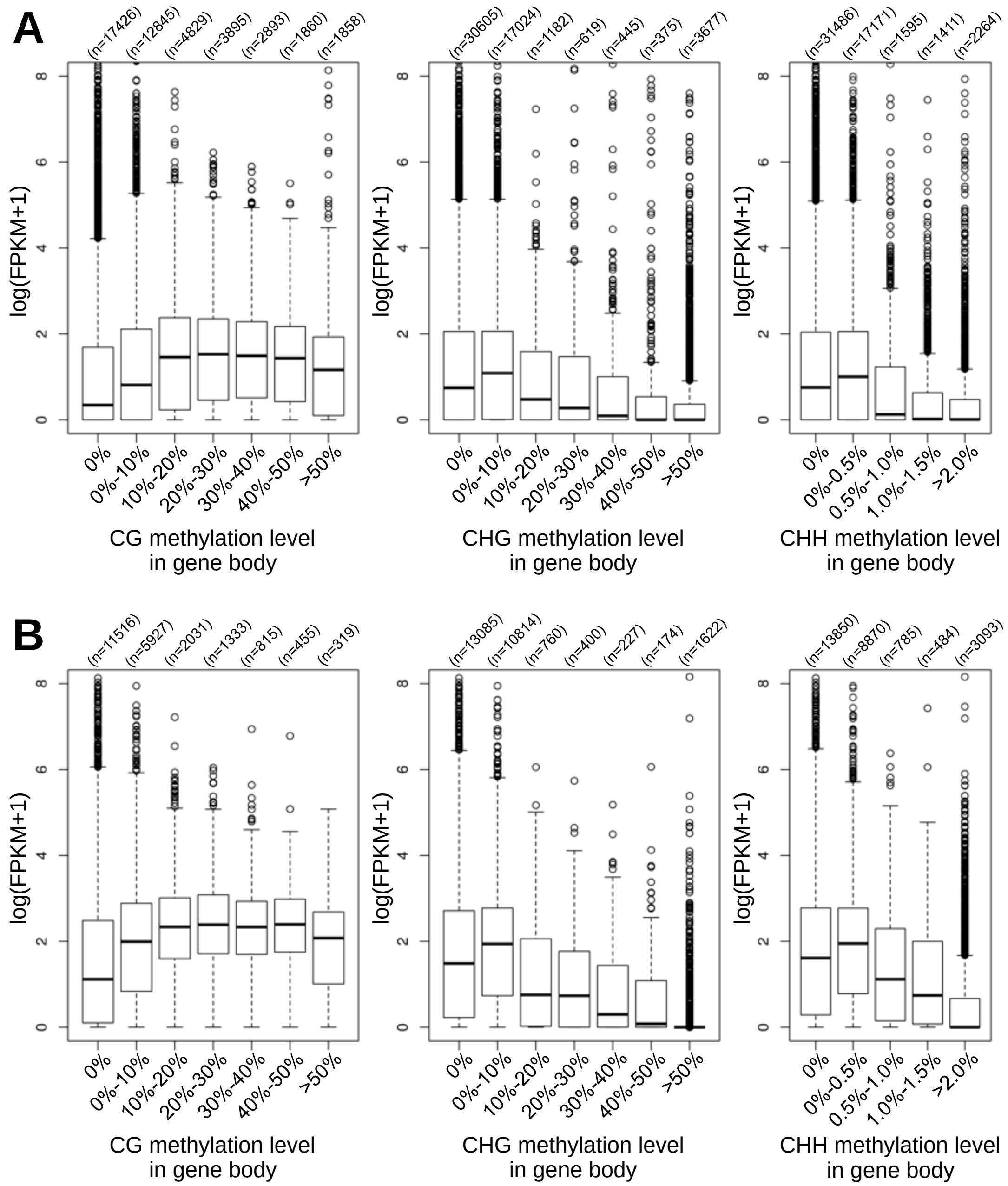
Supplemental Figure S5. Chromosome-wide distribution of methylation in *Phaseolus vulgaris* and correlation with annotated repeats in sliding 500kb windows.



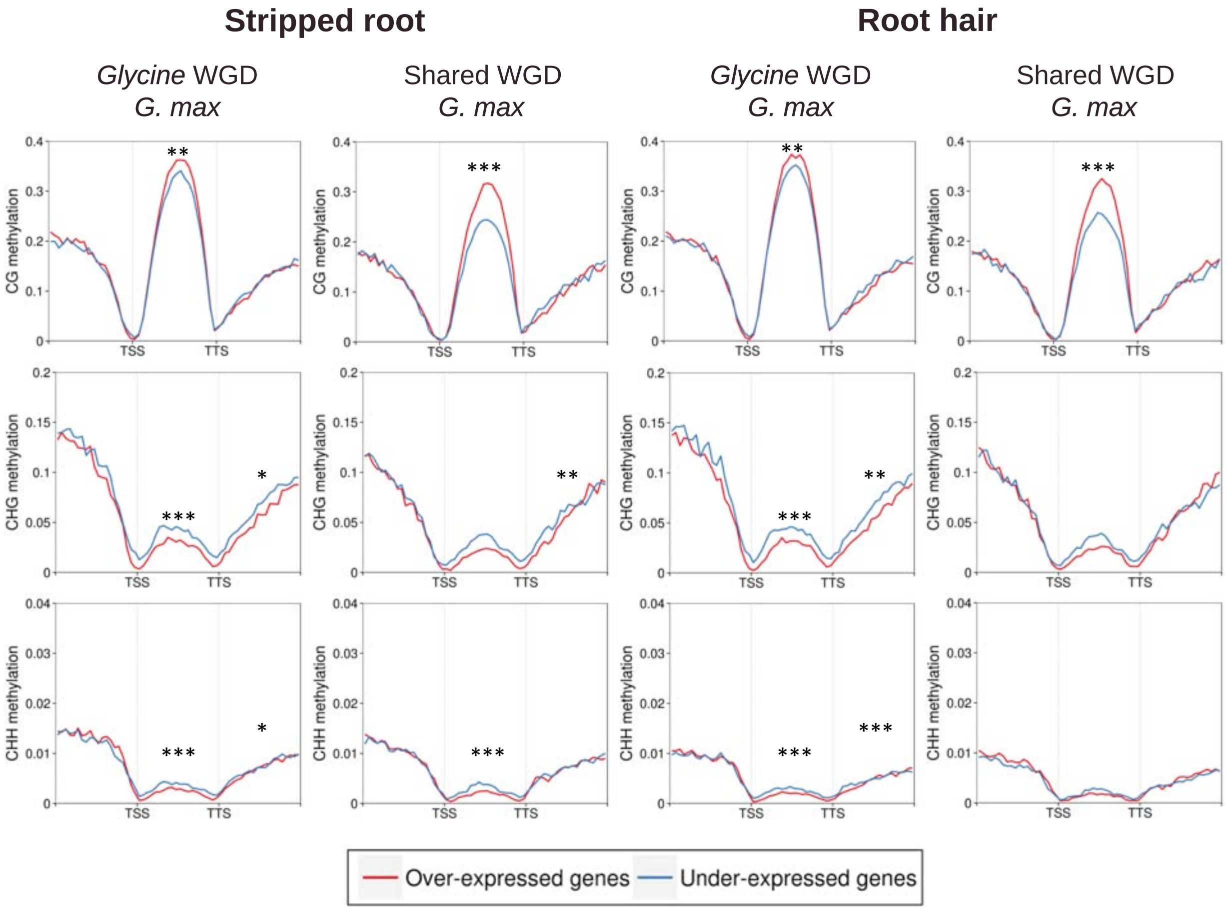
Supplemental Figure S6. Immunodetection of 5-methylcytosine on meiotic pachytene chromosomes of **(A)** soybean and **(B)** common bean. Arrows represent distinct heterochromatic knobs at chromosomal termini with strong 5-methylcytosine signals in common bean. Bars = 10 μm.



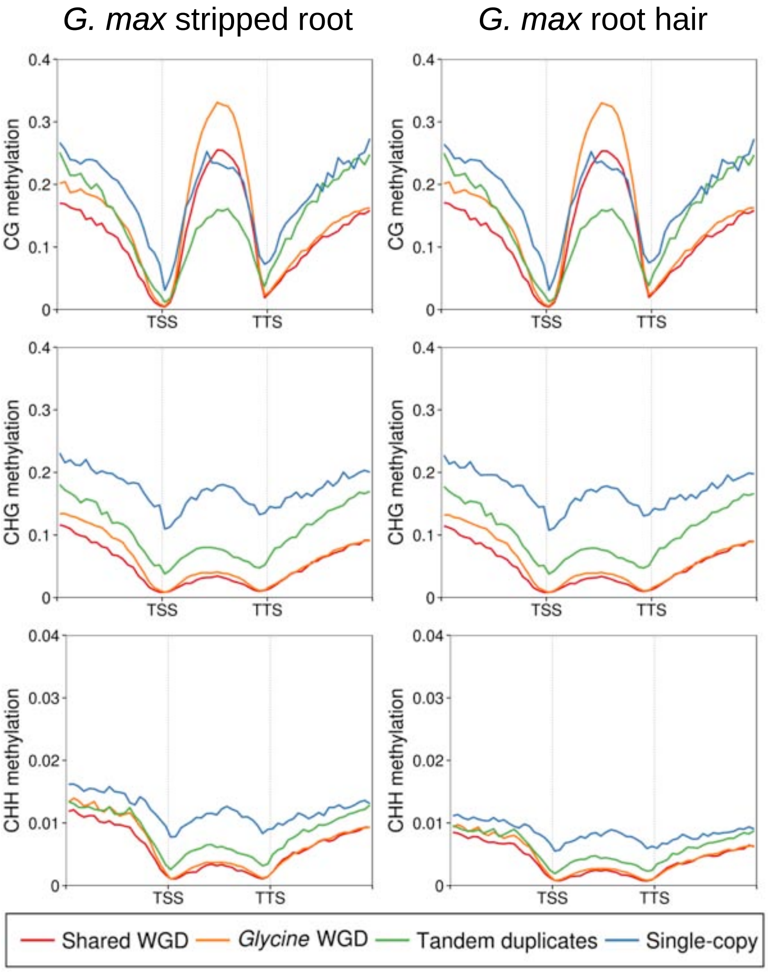
Supplemental Figure S7. Average distribution of DNA methylation over genes and TE categories in soybean and common bean. Flanking regions are 1kb. TSS = transcription start site. TTS = transcription termination site.



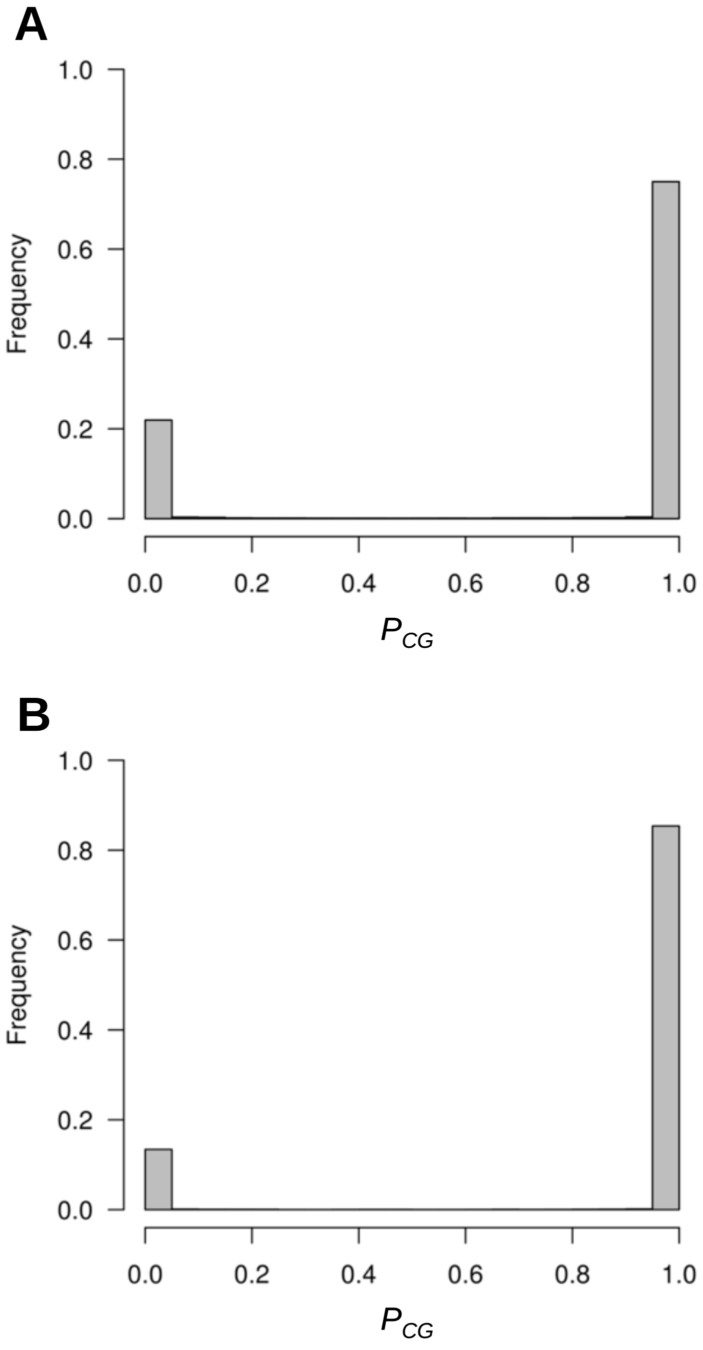
Supplemental Figure S8. Relationship between DNA methylation and gene expression in **(A)** soybean and **(B)** common bean. Within gene bodies, the expression levels are positively associated with CG methylation levels and negatively associated with CHG and CHH methylation levels. C methylated genes ($P_{CHG} < 0.05$ or $P_{CHH} < 0.05$) were removed for calculating CG methylation levels.



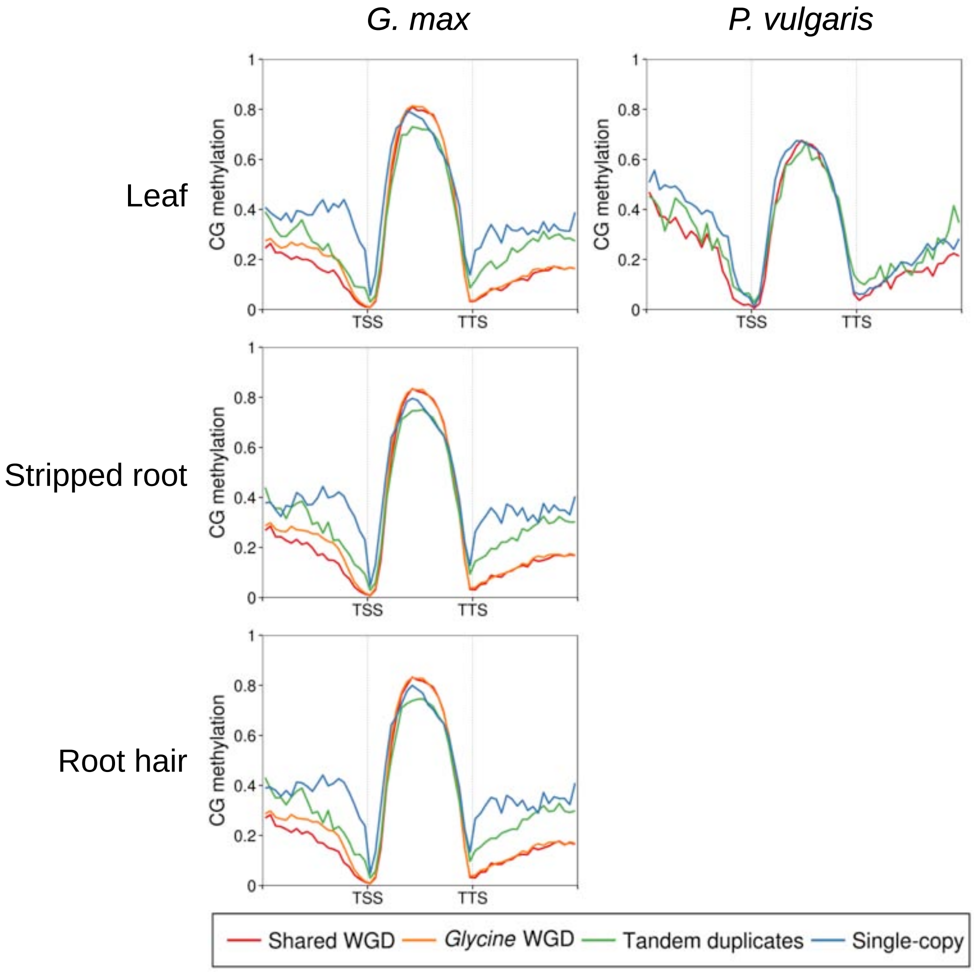
Supplemental Figure S9. Average distribution of DNA methylation of over- and under-expressed genes within paralogous gene pairs. Flanking regions are 1kb. TSS = transcription start site. TTS = transcription termination site. Methylation level of each cytosine context were compared using the Wilcoxon rank sum test. *** = $p<0.001$, ** = $p<0.01$, * = $p<0.05$



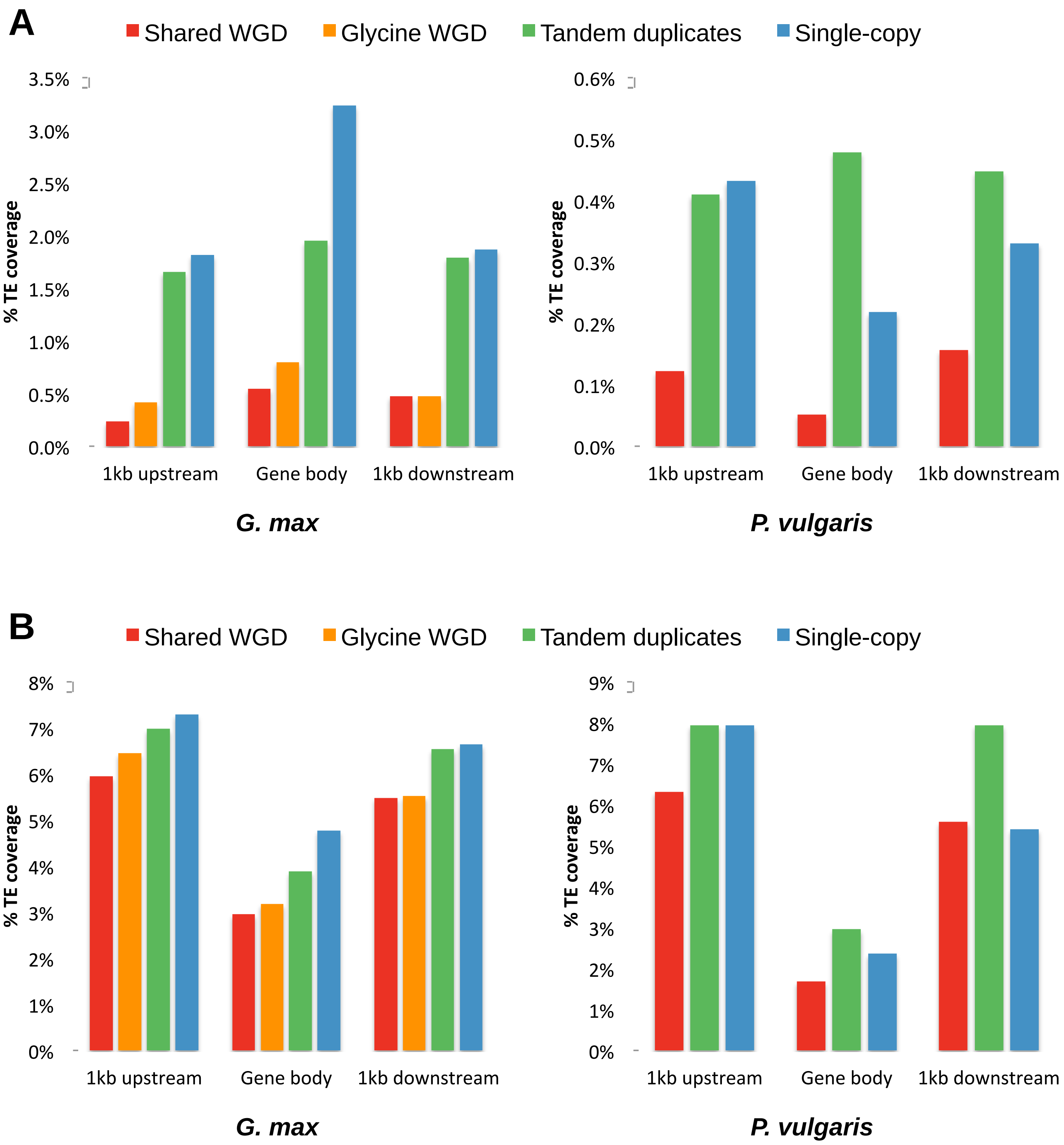
Supplemental Figure S10. Average distribution of DNA methylation from soybean root over different gene categories. Flanking regions are 1kb. TSS = transcription start site. TTS = transcription termination site.



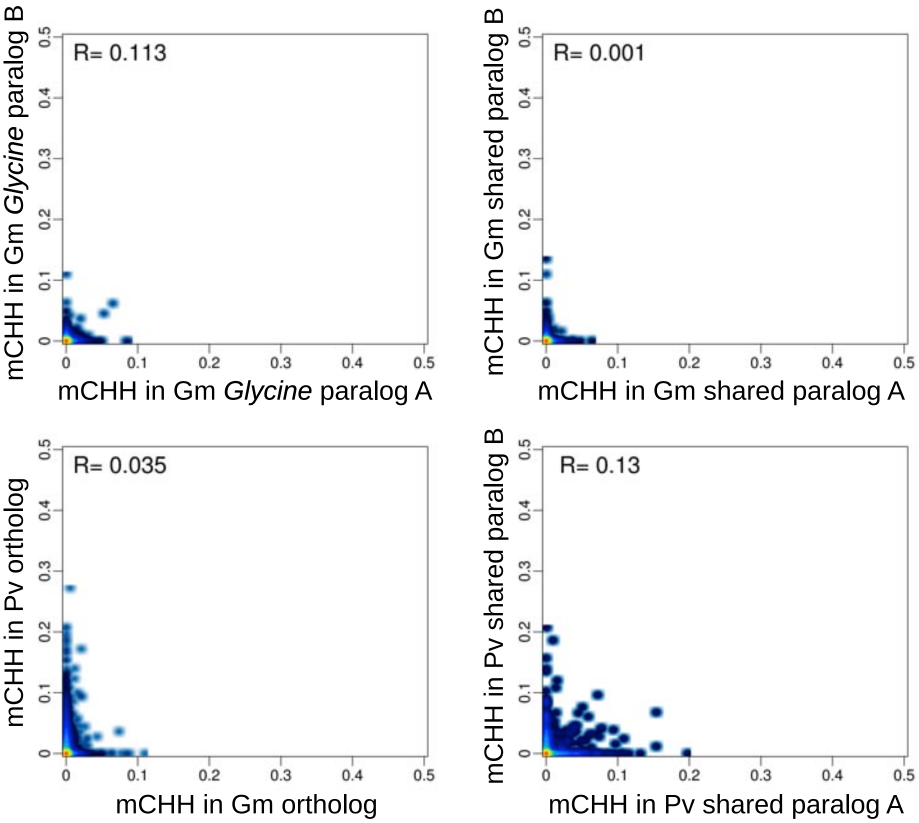
Supplemental Figure S11. Frequency distribution of P_{CG} after removing C methylated genes ($P_{CHG} < 0.05$ or $P_{CHH} < 0.05$) in **(A)** soybean and **(B)** common bean.



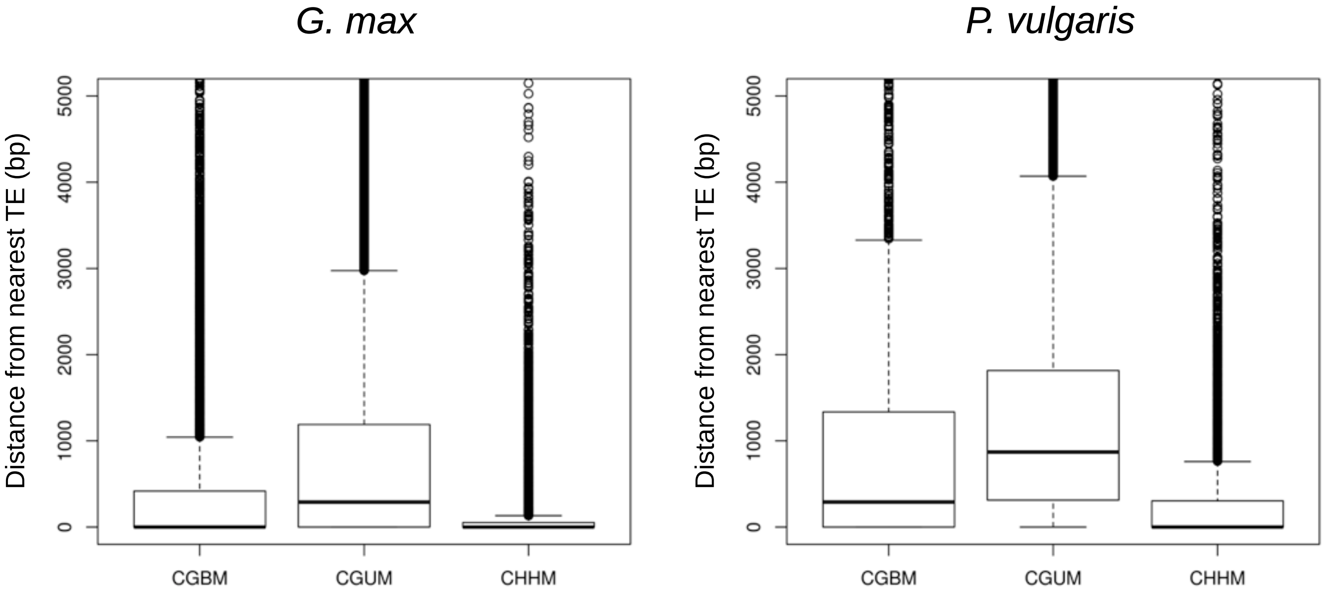
Supplemental Figure S12. Average distribution of DNA methylation in over CG body-methylated genes. Flanking regions are 1kb. TSS = transcription start site. TTS = transcription termination site.



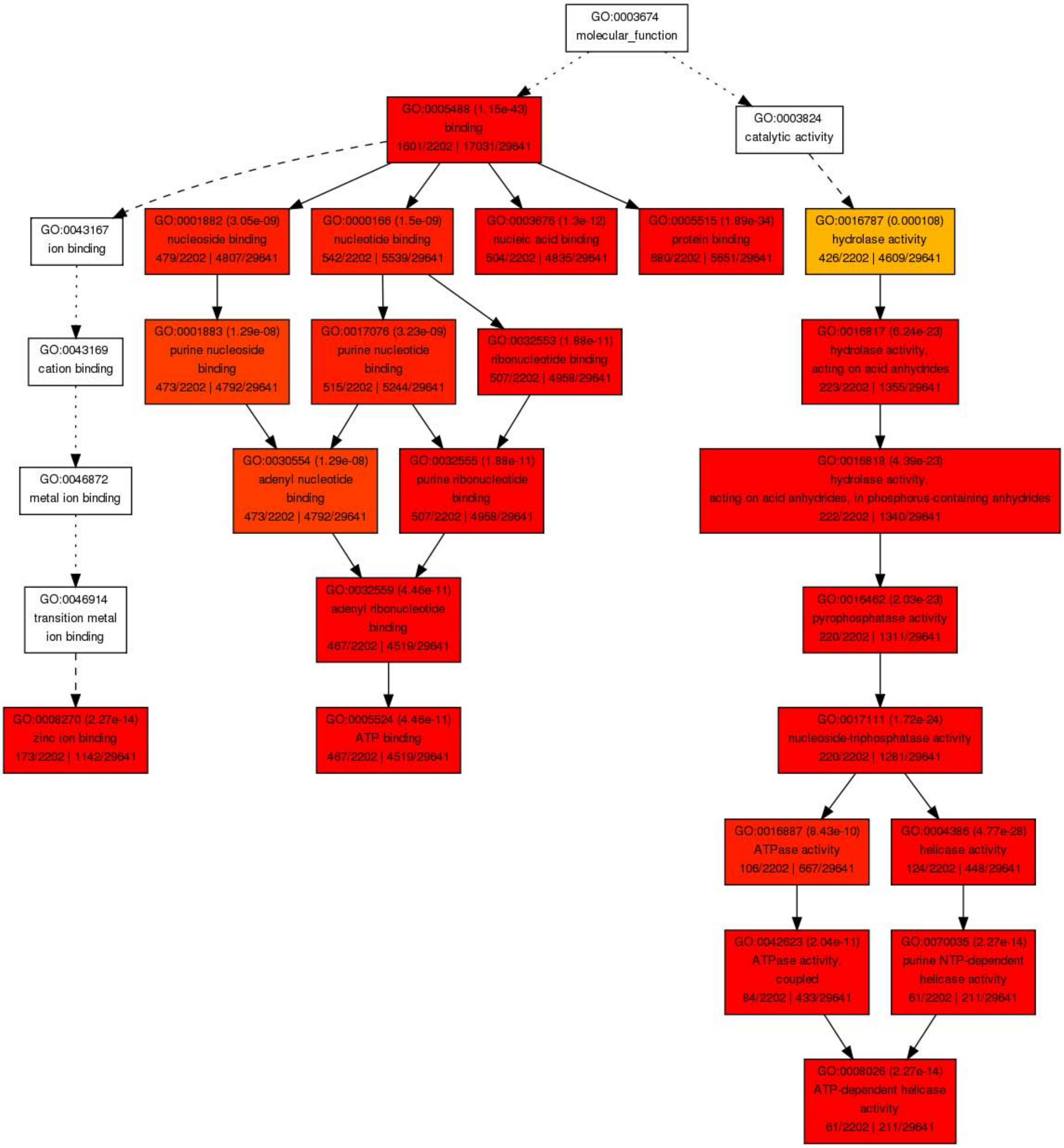
Supplemental Figure S13. Percent total TE in genic regions in gene categories in soybean and common bean. **(A)** Long TE (>4kb). **(B)** Short TE (<500bp).



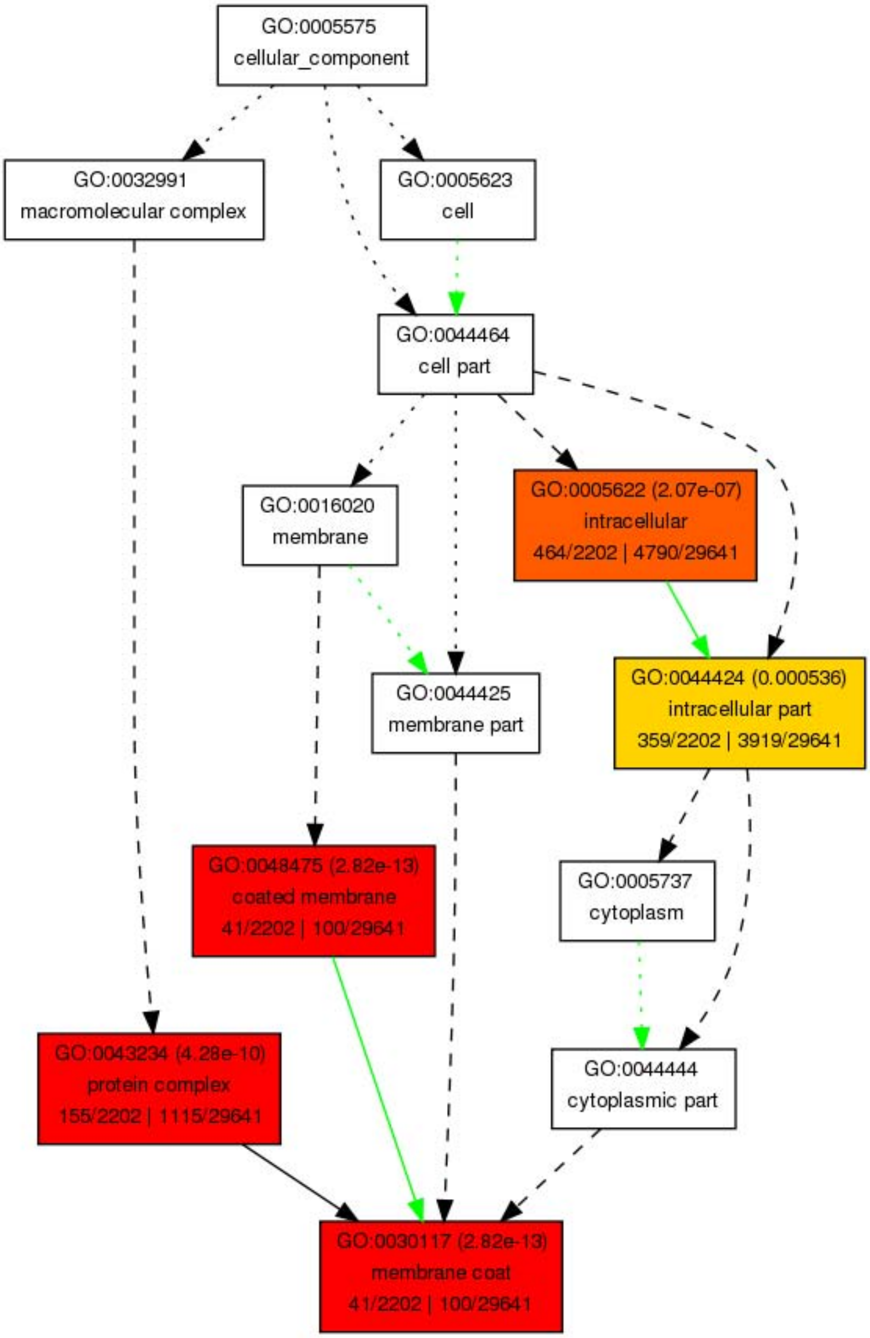
Supplemental Figure S14. Pairwise comparisons of CHH methylation levels between paralogous and orthologous gene pairs. R = Pearson correlation coefficient.



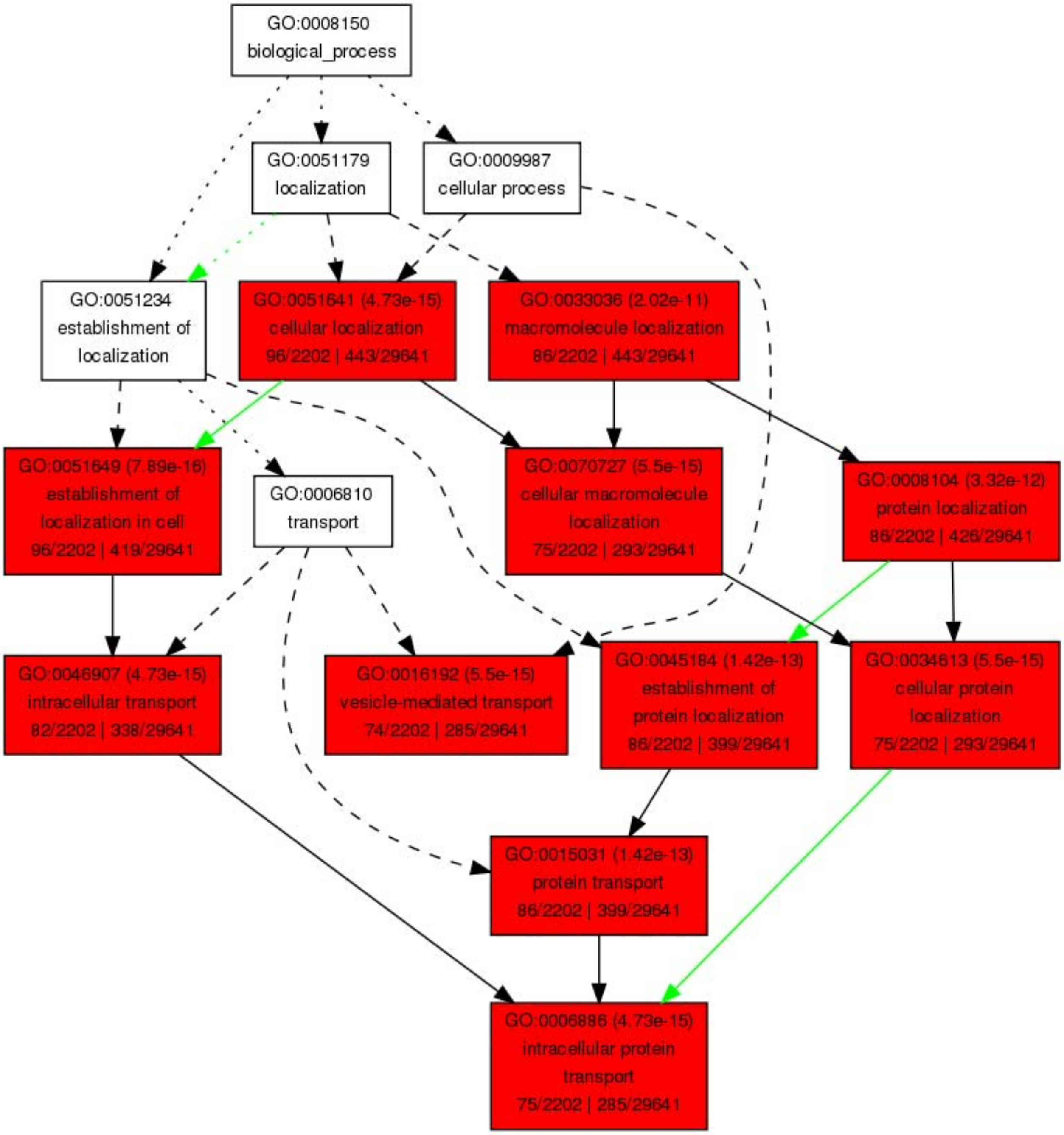
Supplemental Figure S15. Distance from nearest TE (transposable element) for CG body-methylated (CGBM), unmethylated (CGUM), and C methylated genes (CHHM).



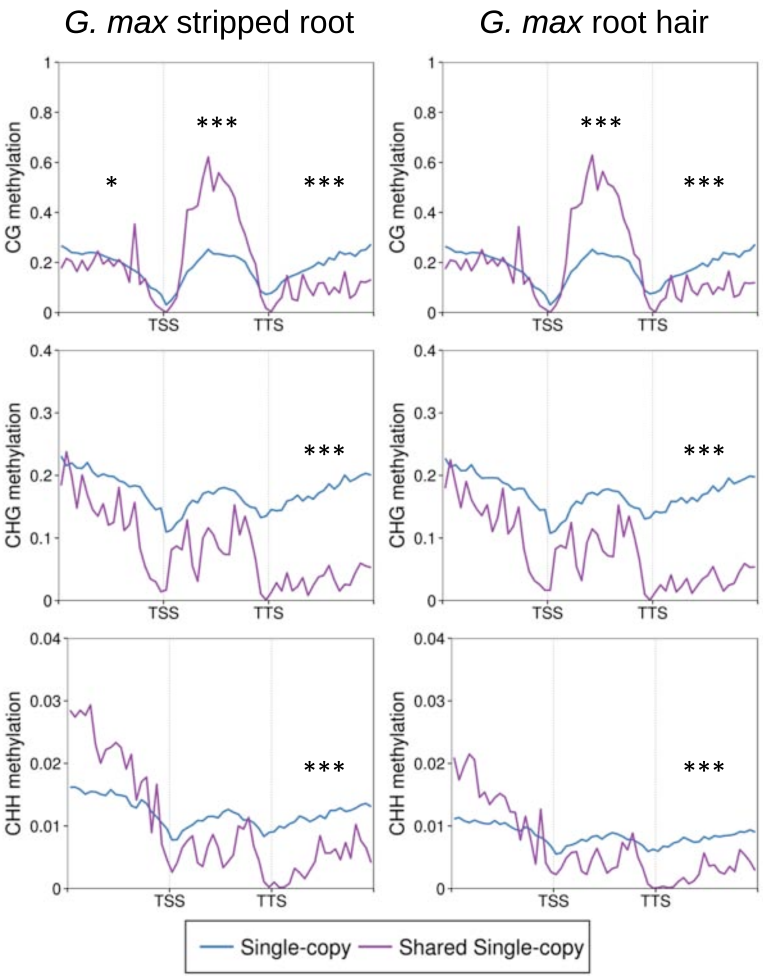
Supplemental Figure S16. GO categories (molecular function) enriched for conserved CG body-methylated genes.



Supplemental Figure S17. GO categories (cellular component) enriched for conserved CG body-methylated genes.



Supplemental Figure S18. GO categories (biological process) enriched for conserved CG body-methylated genes.



Supplemental Figure S19. Average distribution of DNA methylation from soybean root in shared single-copy and species-specific single-copy genes. Flanking regions are 1kb long. TSS = transcription start site. TTS = transcription termination site. Methylation level of each cytosine context was compared using the Wilcoxon rank sum test. *** = $p<0.001$, * = $p<0.05$.