

Figure S1. Boxplot illustrating sample counts across different treatment group ($N_{\text{Control}} = 6$, $N_{\text{BSp}} = 7$, $N_{\text{GTPs}} = 3$, $N_{\text{Combination}} = 3$) with no sample outliers.

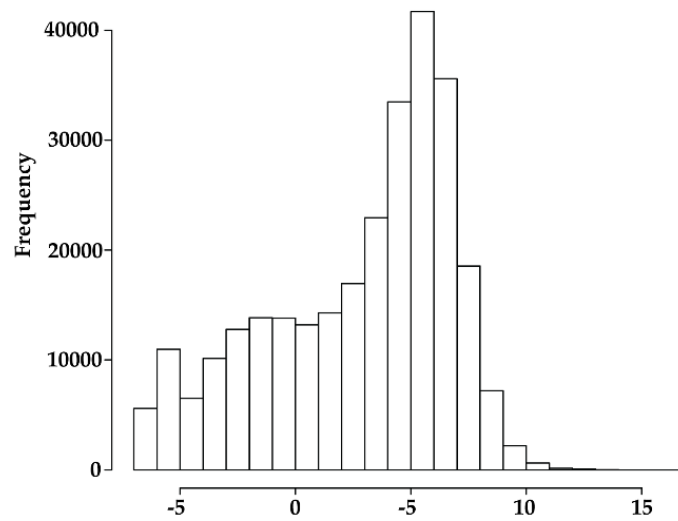


Figure S2. Histogram demonstrating normal distribution of total feature counts across different samples. Y-axis represents the total frequency across 19 samples and X-represents total feature by counts.

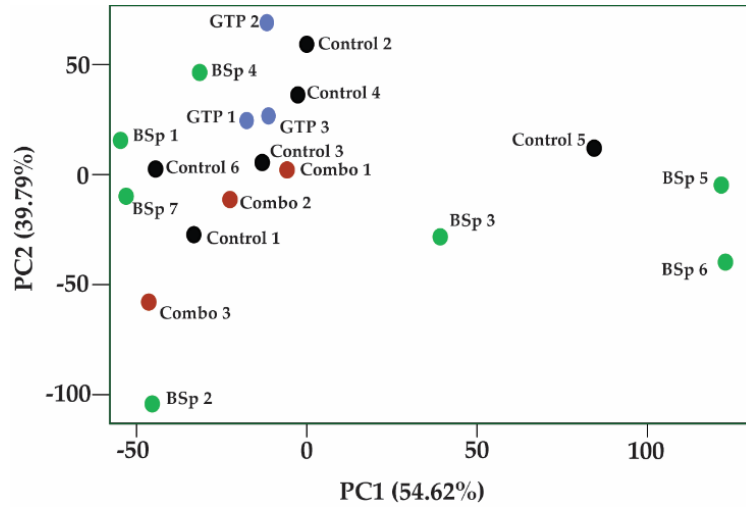


Figure S3. Normalized PCA across PC1 (54.62%) v/s PC2 (39.79%) using BSp, GTPs and Combination (BSp + GTPs) induced differentially expressed genes (DEGs).

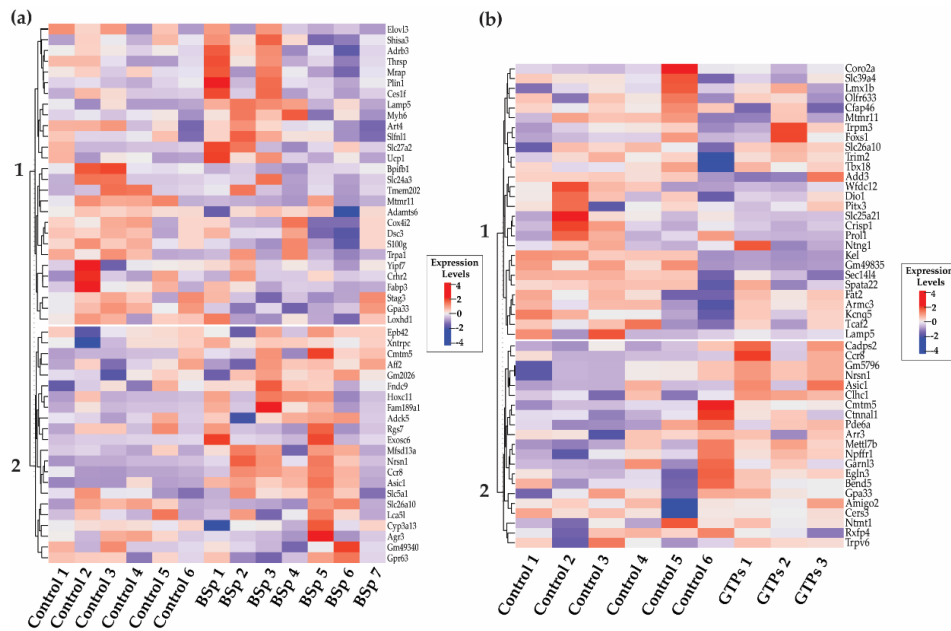


Figure S4. Heatmap representing the top 50 DEGs in (a) BSp treatment group and (b) GTPs treatment group based on p value. Each row corresponds to differentially expressed transcripts and each column represents biological replicates in control ($N_{\text{Control}} = 6$), BSp ($N_{\text{BSp}} = 7$) and GTPs ($N_{\text{GTPs}} = 3$) treatment group.

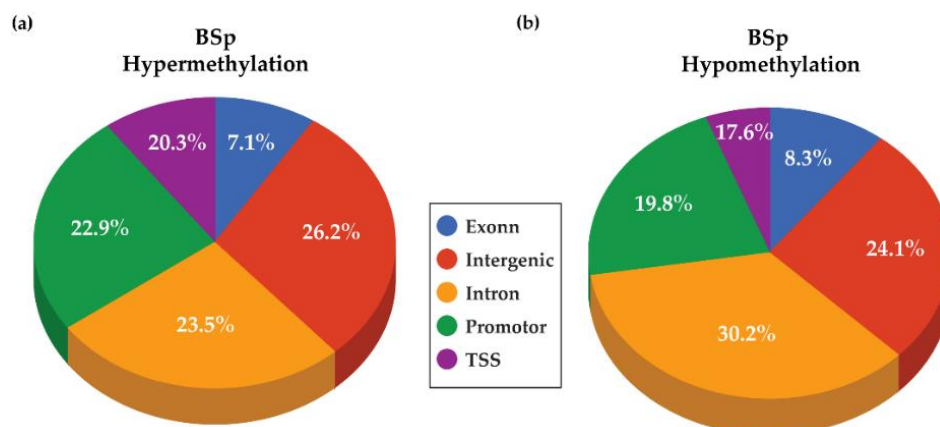


Figure S5. Pie charts representing genomic distribution of differentially methylated genes (DMGs) by BSp treatment in (a) hypermethylated regions and (b) hypomethylated regions.

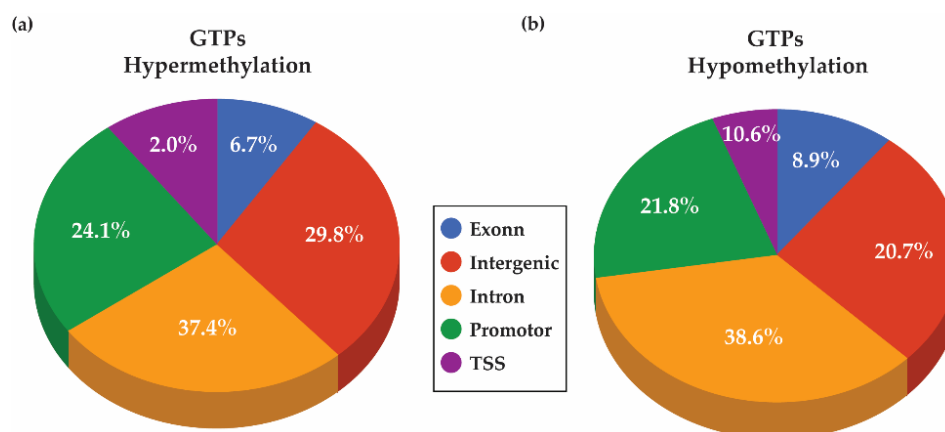


Figure S6. Pie charts representing genomic distribution of DMGs by GTPs treatment in (a) hypermethylated regions and (b) hypomethylated regions.

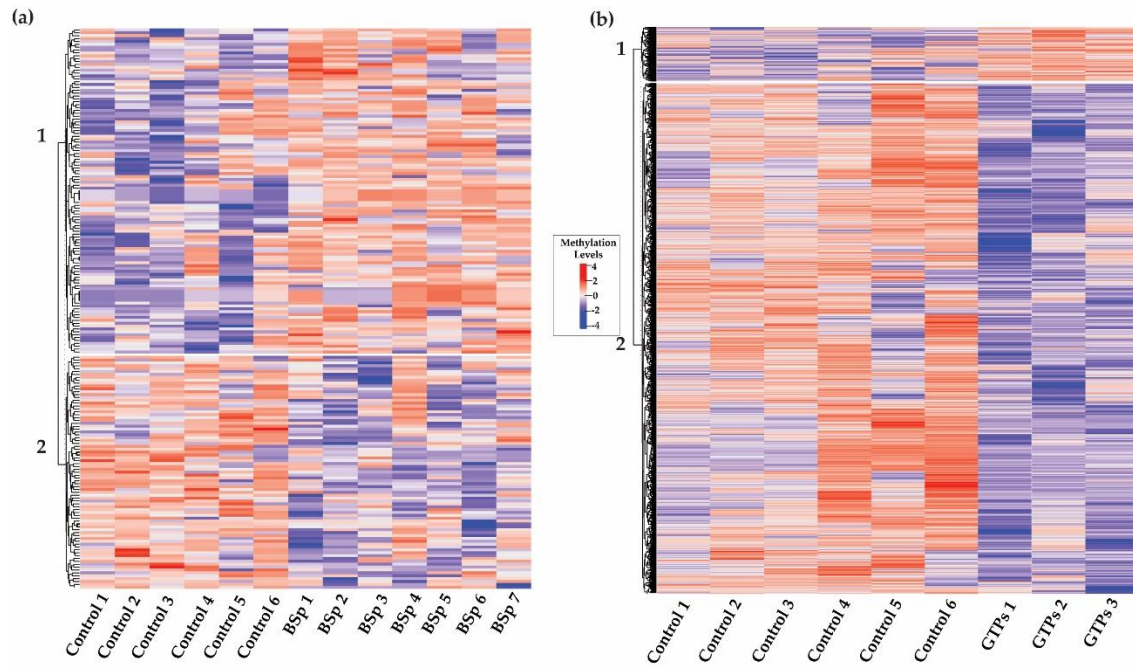


Figure S7. Heatmap representing DMGs in (a) BSp treatment group and (b) GTPs treatment group based on q value. Each row corresponds to differentially expressed transcripts and each column represents biological replicates in control ($N_{\text{Control}} = 6$), BSp ($N_{\text{BSp}} = 7$) and GTPs ($N_{\text{GTPs}} = 3$) treatment group across two heatmap clusters (1 and 2).

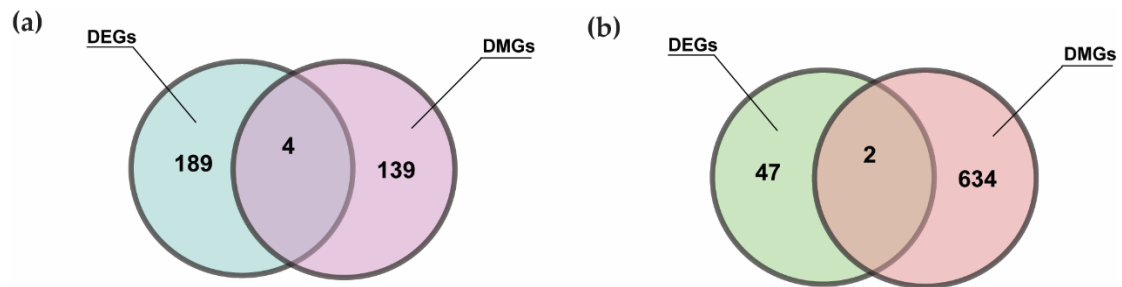


Figure S8. Venn diagram representing unique DEGs and DMGs in (a) BSp treatment group and (b) GTPs treatment group.