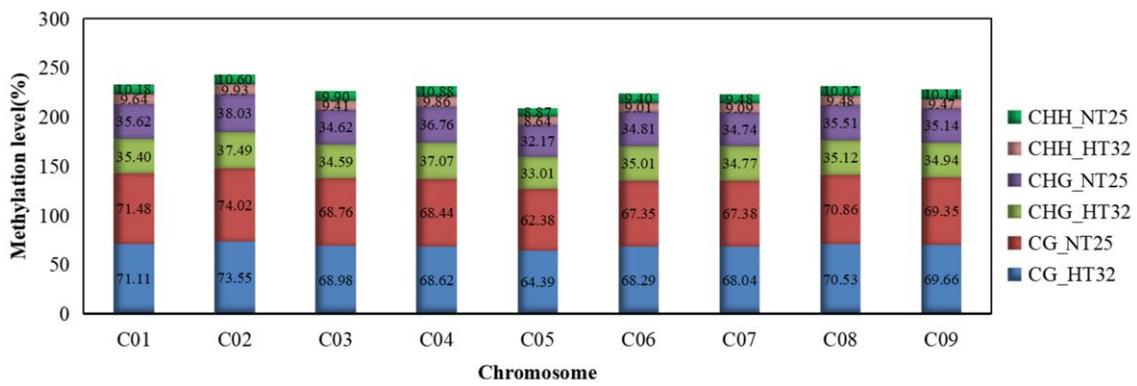
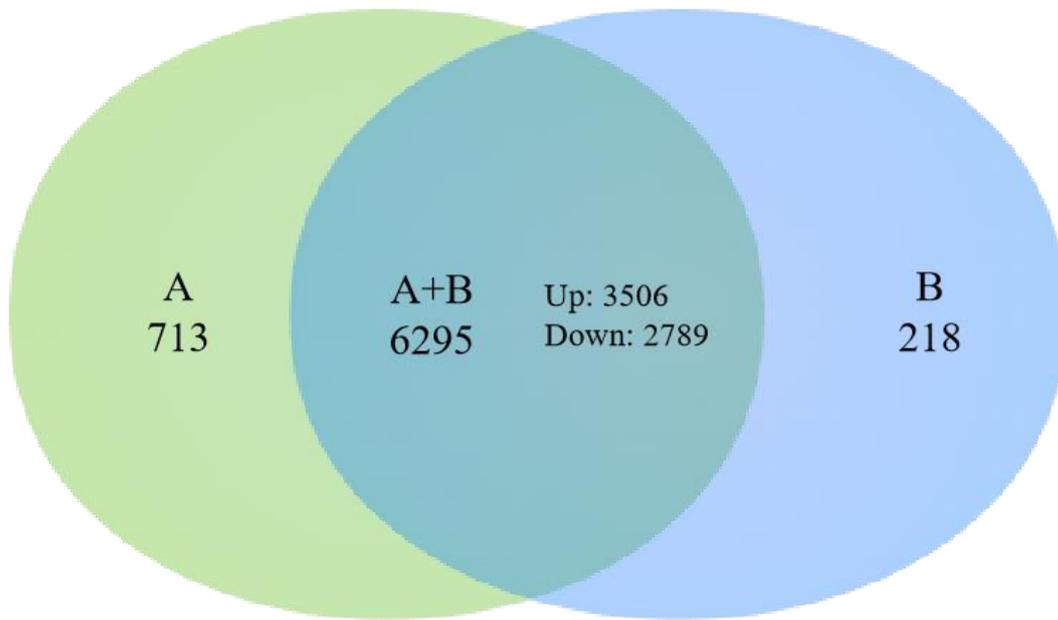


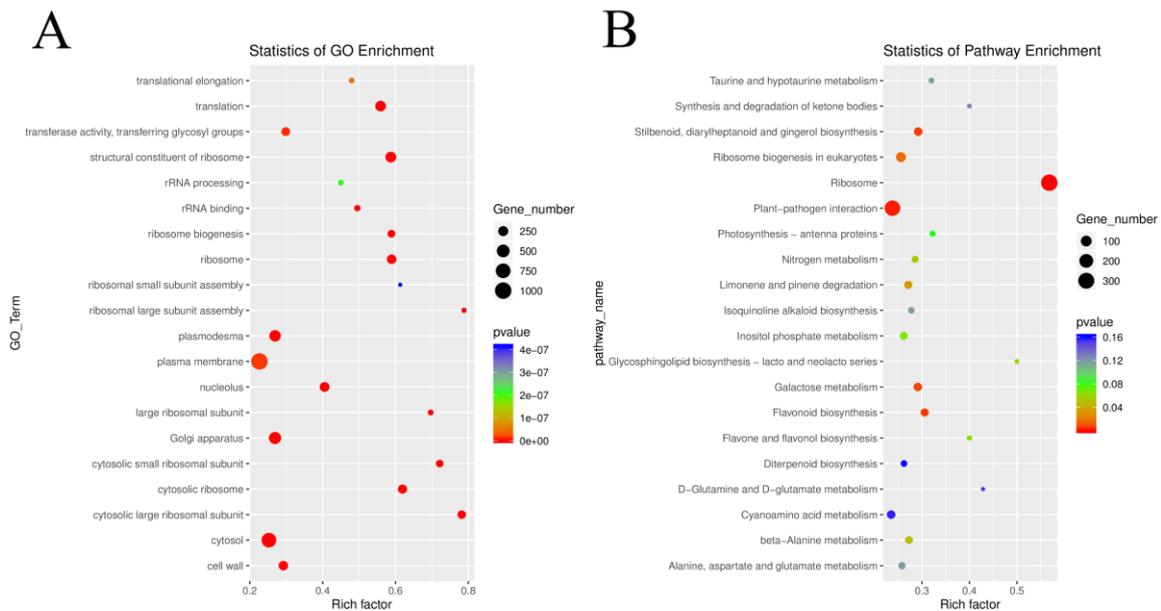
**Figure S1.** Levels of CG, CHG and CHH methylation in the whole cabbage genome.



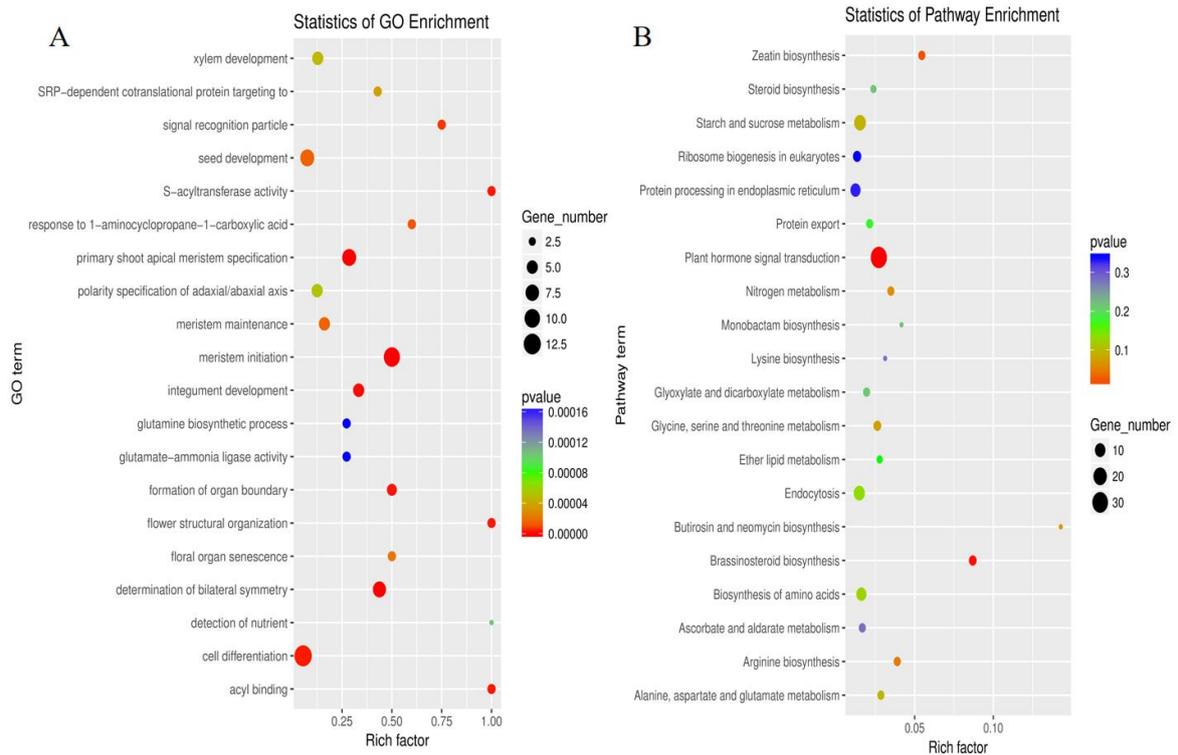
**Figure S2.** DNA methylation levels in nine chromosomes.



**Figure S3.** Ven diagram of DEGs in HT32 and NT25. A indicates the unique DEGs in HT32. B indicates the unique DEGs in NT25. A+B indicates the common DEGs in both samples.



**Figure S4.** GO and KEGG enrichment of DEGs in microspores after HS. (A) GO enrichment of DEGs in microspores after HS. (B) KEGG enrichment of DEGs in microspores after HS.



**Figure S5.** GO and KEGG enrichment of genes targeted by DERs. (A) GO enrichment of genes targeted by DERs. (B) KEGG enrichment of genes targeted by DERs.