

Figure S2. DNA methylation landscape of Beihua and Sijihua. A-C, DNA methylation differences between Sijihua and Beihua at CG (A), CHG (B), and CHH (C) contexts in WB stage. The dotted lines indicate no difference in methylation between Sijihua and Beihua. D, Circos plot showing gene density, TE density, SNP density, and DNA methylation levels for all three contexts of golden flower. E-G, DNA methylation differences between Sijihua and Beihua at CG (E), CHG (F), and CHH (G) contexts in GF stages.