

Figure S5. DNA methylation patterns of protein-coding genes and TEs in Sijihua and Beihua in the GF. A-C, Comparison of DNA methylation of TE-related genes and flanking 2 Kb regions in Sijihua and Beihua in CG(A), CHG(B), and CHH(C) contexts. D-F, Comparison of DNA methylation of TE-unrelated genes and flanking 2 Kb regions in Sijihua and Beihua in CG(D), CHG(E), and CHH(F) contexts. G-I, Comparison of DNA methylation in TE and flanking 2 Kb regions of Sijihua and Beihua in CG(G), CHG(H) and CHH(I) contexts