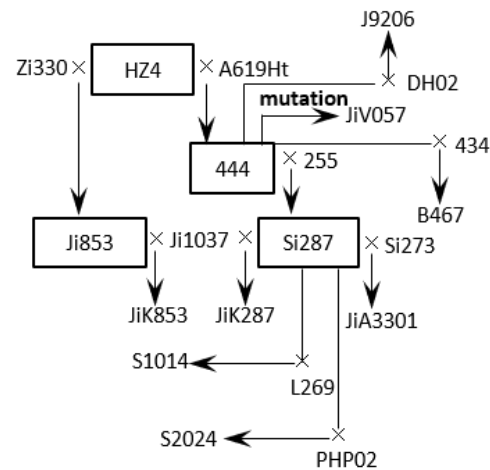
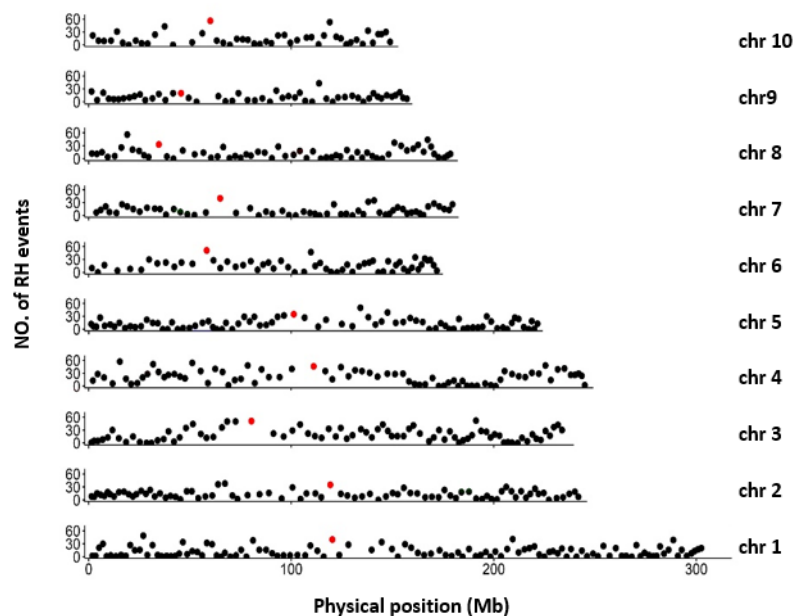


Underling Fundamental Parameters for Defining Maize Essentially-Derived-Varieties of Inbreds Using High Throughput Genome-wide SNP Markers

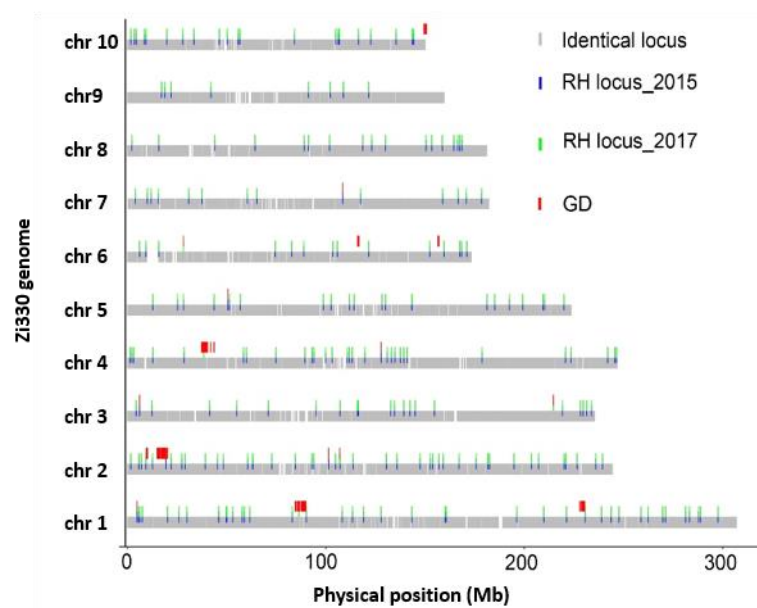


Supplementary Figure S1. Empirical pedigree networks of the analyzing maize inbreds.

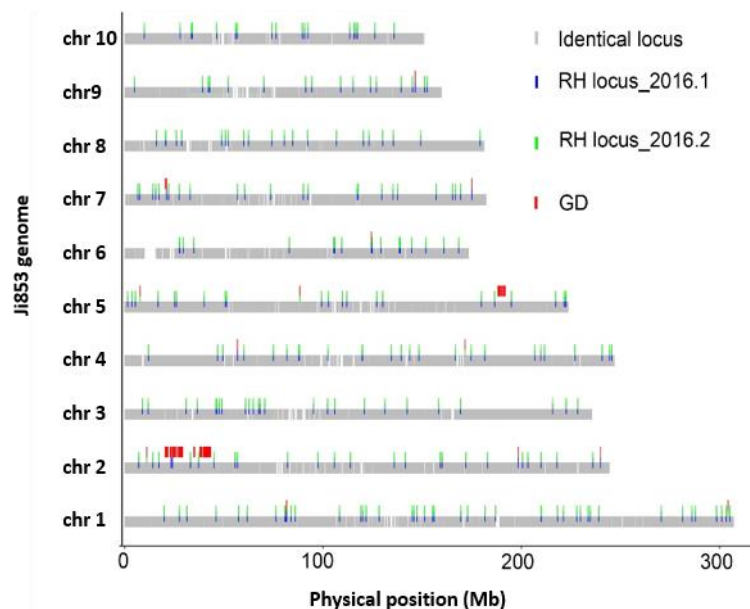


Supplementary Figure S2. Sliding window analysis of the RH abundance distribution along each 10 chromosomes of 28 accessions.

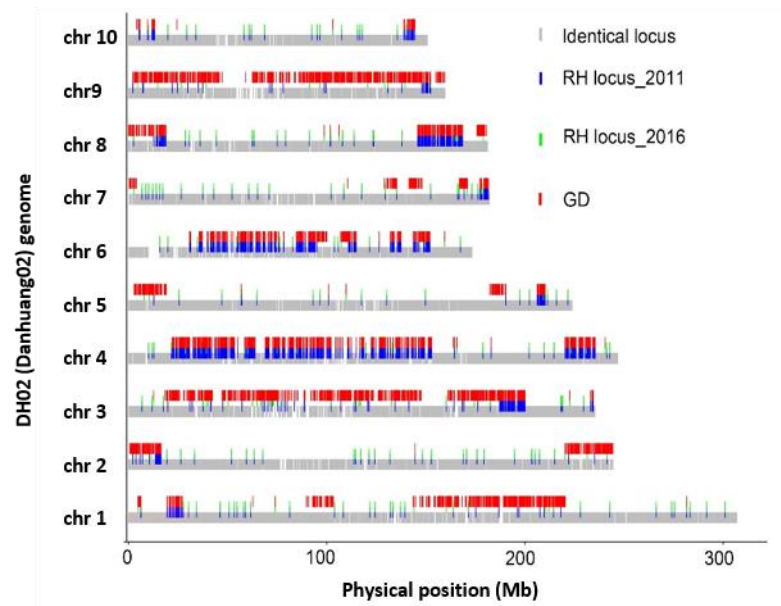
Sliding window size: 50 SNPs; Y variables, Numbers of RH events found in each window among 28 accessions. X axis, physical position in Mb scale. Dots in red, the window across centromere regions.



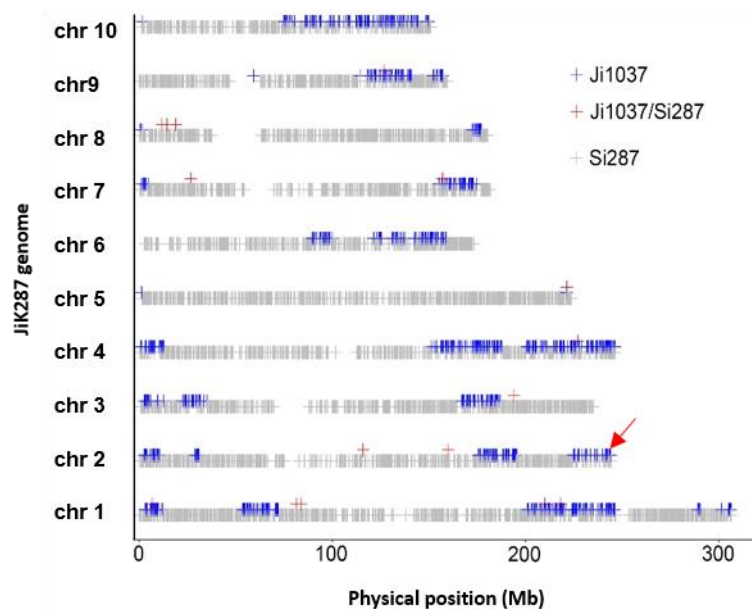
Supplementary Figure S3. Comparison of residual heterozygotes (RH) and genetic drifts (GD) between 2 accessions of Zi330, one of the classic maize founder lines of wide applied germplasm.



Supplementary Figure S4. Comparison of residual heterozygotes (RH) and genetic drifts (GD) between 2 accessions of Ji853, one of the classic maize founder lines of wide applied germplasm.

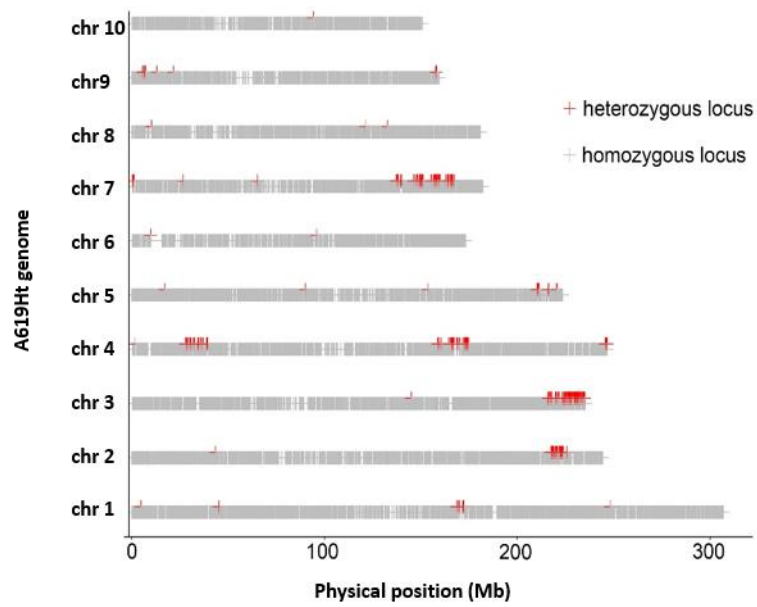


Supplementary Figure S5. Comparison of residue heterozygotes (RH) and genetic drifts (GD) between 2 accessions of DH02, one of the classic maize founder lines of wide applied germplasm.

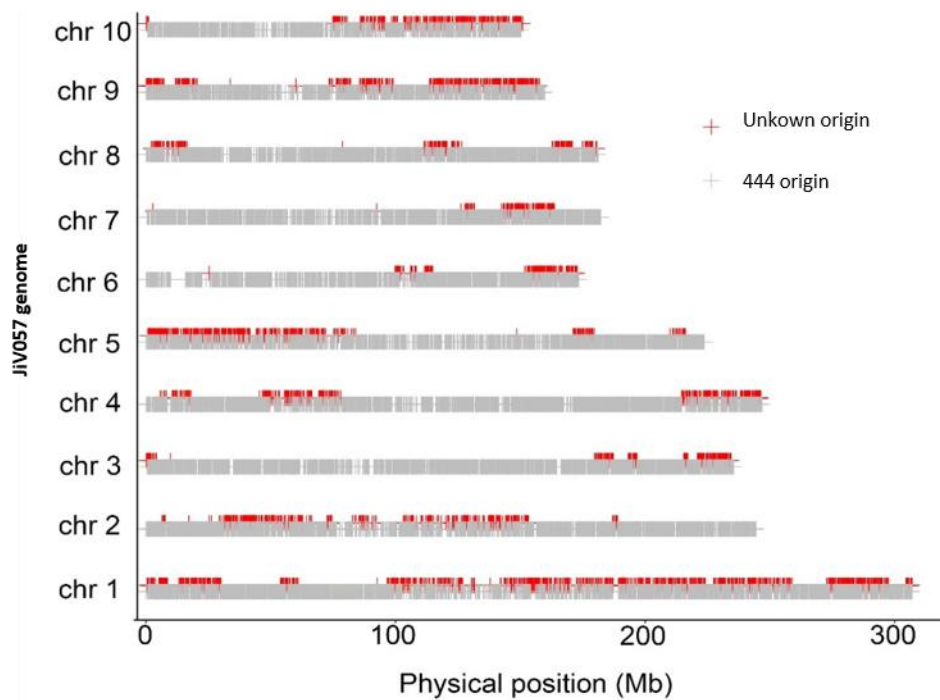


Supplementary Figure S6. Characterization of both donor (Ji1037) and recurrent (Si287) parental genome contributions to JiK287, which was essentially derived varieties of Si287 through backcross breeding.

The red arrow indicated the introgression contain head smut resistance genome region from Ji1037.



Supplementary Figure S7. EDV analysis of A619Ht genome from A619 (homologous loci) and unknown origins (heterozygous loci).



Supplementary Figure S8. Identification of JiV057 genome, which was essentially derived from 444 with around 14.98% genome introgression from unknown origins but not 444 with a single or multiple loci mutations.