Figure S1 Correlation between the max read depth of one SNP site with the heterozygosity ratio (denoted by red curve) and MAF (denoted by green curve). Blue filled curves show the correlation between max read depths with SNP frequencies.
Figure S2 Population structure and pedigree network of GBS data. (a) t-SNE plot for F1 families (circle) and variety clones (triangle) (N ≥ 60). (b) The overview of pedigree for GBS data. F1 families (N ≥ 60) are denoted.
Figure S3 Linkage groups for the maternal lines of families (a) “247” and (b) “265”.

Unphased and phased (linkage for grandparents) groups are bounded by white and black frames individually. The degrees of Spearman’s correlation (rho) are color-coded.
Figure S4 Genome-wide views of the segregation distortion in three F1 families. Mendelian markers ((15% ≤ MAF ≤ 35%) and correlated (rho ≥ 0.3) segregation distortion (5% ≤ MAF < 15%) are represented by blue and red bars individually. F1 families (a) “144”. (b) “247”. (c) “265”.
Figure S5 Clustering patterns (derived from Locally-Linear Embedding method) of linkage group (LG) 1.2 (black), 2.1 (blue), 2.2 (red), 3.1 (yellow) in cross “265” (left axes) and linkage group LG 1.1 (black), 2.1 (blue+red), 3.1(yellow) in cross “144” (right axes). The initial azimuth (XY plane) angles are (a) 30, (b) 60, (c) 70 and (d) 90.
Figure S6  Association studies of sex determination in the F1 family “265” (N = 95, N_{male} = 13). Linkage group-based Manhattan-plot of MLM. Light and dark colors are used to distinguish two phases (linkage for grandparents) in coupling.
Figure S7 Linkage group (in family “247”)--based Fst heatmaps and the overall Fst distribution. Population differentiation (a) between modern cultivars (CV) and var. neomexicanus; (b) between CV and var. lupuloides; (c) between var. neomexicanus and var. lupuloides. (d) Spectrum of the overall Fst distribution.