Figure S1: Effects of inbred correction on genotype calling in predominantly homozygous inbred lines shown for two variants.

For marker AX-90525761 (top), the cluster positions change after inbred correction, whereas for marker AX-90525759 (bottom) cluster positions are stable. Left: without inbred correction, right: with inbred correction; X-axis: contrast of the two color channels for allele A and B, respectively, Y-axis: signal intensity; blue circles: homozygous for allele A, yellow triangles: heterozygous genotypes, red circles: homozygous for allele B, grey rectangles: no calls.
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**Figure S2:** Representative cluster plots for the six categories according to SNPolisher.

From left to right: PHR - “PolyHighResolution” with three clearly separated and called clusters; OTV - “Off-Target Variant” indicated by a potential cluster split and/or low signal intensity calls; NMH - “NoMinorHom” with one homozygous cluster without genotype calls; MHR - “MonoHighResolution” with calls belonging to one genotype cluster only; CR - “CallRateBelowThreshold” associated with overlapping and mis-assigned clusters; Other - several criteria not fulfilled.
Figure S3: Variant density shown for the screening arrays (light grey) and for the 616 k variants of the Affymetrix® Axiom® Maize Array (black) across the 10 maize chromosomes. Centromere positions are indicated by a black horizontal bar.
Figure S3 continued
**Figure S4**: Cross-validation errors from ADMIXTURE for different values of K for 155 maize lines based on 251,152 variants including OTVs (markers in LD with $r^2 > 0.8$ were excluded).
Figure S5: Subgroups identified in 155 maize lines of the validation panel as revealed by ADMIXTURE for K = 7 based on 251,152 variants including OTVs (markers in LD with $r^2 > 0.8$ were excluded).

Yellow: Iodents, red: BSSS Dents, brown: LSC, orange: non BSSS Dents, green: (sub)tropical lines or lines with ancestors of (sub)tropical origin, blue: Northern Flints, purple: non Northern Flints.
Figure S6: Cross-validation errors from ADMIXTURE for different values of K for 155 maize lines based on 27,099 flanking OTVs (markers in LD with $r^2 > 0.8$ were excluded).
Figure S7: Subgroups identified in the 155 public lines of the validation panel as revealed by admixture for $K = 3$ based on 27,099 flanking OTVs (markers in LD with $r^2 > 0.8$ were excluded).

Yellow: (sub)tropical lines or lines with ancestors of (sub)tropical origin, red: Dent, blue: Flint.