**File S1**

**Supplemental methods:**

**Sequence capture probe maize genome conversion from AGPv2 to AGPv4**

**Target regions.** The sequences for each target region were extracted from the AGPv2 genome and were aligned to the AGPv4 genome using Blastn with the following parameters: evalue < 1e-20 and max\_target\_seqs < 3. Out of the 20,643 target regions, 18,436 can be mapped to the same chromosome in AGPv4 as in AGPv2 perfectly (identity = 100% over the entire region) and uniquely (only one position). Another 254 regions can also be perfectly and uniquely mapped but to different chromosomes, and 178 of them were mapped to contigs in AGPv4 (i.e., these regions were not assigned to the 10 maize chromosomes in AGPv4). There are 197 regions that can be perfectly mapped in AGPv4 but to multiple positions; here one mapping location was randomly selected. For the remaining regions that were not perfectly mapped we kept matches that have over than 95% identity over at least 90% of the query regions; of these, 1,382 regions mapped to same chromosome and 83 regions to different chromosomes. In total, 20,352 regions were mapped and 291 regions can’t be mapped (20643=18436+254+197+1382+83+291). The 20,352 regions correspond to 20,331 unique regions in AGPv4 as twenty-one regions were mapped to same positions on AGPv4 though they were located on different positions on AGPv2. These 20,331 non-redundant regions were used to summarize capture efficiency (“% on target”, <https://doi.org/10.13020/D69X0H>).

**Specific regions:** The specific regions are short in length - often 100bp - and are more likely to map to multiple positions. Therefore, we first mapped the AGPv2 specific regions to AGPv4 and then used the mapping position of the target region to cross-validate and calibrate the corresponding specific target loci. We first extracted the sequences of the 23,151 regions from the AGPv2 genome, aligned them to AGPv4 and selected the AGPv4 matches using the same criteria as for target regions. We then compared the alignment positions of the corresponding target and specific regions. For specific regions that were congruent with the mapping location of the target region (i.e., same chromosome and complete overlap), the positions were kept. For specific regions that mapped to different chromosomes or were mapped to same chromosomes but not overlapping, we used the mapping positions of the “target” region to derive a position of the “specific” region. The majority of the derived specific regions, mapped to multiple positions and the matches that overlapped the mapping position of the target region were kept. In total, 23,151 AGPv2 specific regions were used for alignment, and 22,974 could be mapped to AGPv4. Out of the 22,974 regions, 22,142 could be mapped to the same position as their corresponding “target” regions, and the corresponding mapping position was used. For the remaining 832 regions that mapped to different positions between the two alignments, their positions were derived from the mapping position of their corresponding “target” regions. The 22,974 regions correspond to 22,749 unique regions because (1) 201 regions were annotated as two classes and (2) twenty-four regions were mapped to same position on AGPv4 though they were at different positions on AGPv2 (22974-201-24=22749). The 22,749 non-redundant specific regions can be found in <https://doi.org/10.13020/D69X0H>.