Supplemental methods

Population Design

Step 1: During winter nursery 2007-2008, we performed a half diallel of the six parents.

Step 2: During summer 2008, we generated four-way hybrids by planting one row per F1 cross and making all possible crosses between them without reciprocals. We bulked the seed at harvest and included extra seeds of other crosses to account for any rare, failed crosses and to maintain population allele frequency at 1/6.

Step 3: During summer 2009, we randomly intermated plants. Approximately 28 rows were planted. Intermating was performed among the rows using individual plants only once, either as a pollen or seed parent. A minimum of 200 plants were used each intermating generation producing a minimum of 100 harvested ears. At harvest, we generated a seed bulk by including an equal number of kernels per ear.

Step 4: During summer 2010, we randomly intermated again by pollinating and harvesting as in step 3.

Step 5 **Subset A**: Fall 2010, we sent 500 kernels to AgReliant Genetics for DH induction.

Step 5 **Subset B:** During summer 2011, we randomly intermated one more generation as in step 3.

Step 6 **Subset B**: During summer 2012, we randomly intermated one more generation as in step 3.

Step 7 **Subset B**: March 2014, we sent 1500 more kernels to AgReliant Genetics for DH induction.

Exome Capture

Plate-based DNA library preparation with targeted exome enrichment for Illumina sequencing was performed on the PerkinElmer Sciclone NGS robotic liquid handling system using Kapa Biosystems library preparation kit and the Roche NimbleGen SeqCap EZ kit with the custom designed capture probes. 1ug of sample DNA was sheared to 600bp using a Covaris LE220 focused-ultrasonicator. The sheared DNA fragments were size selected by double-SPRI using AMPureXP beads, and then following Kapa's standard library protocol the DNA fragments were end-repaired, A-tailed, and ligated with Illumina compatible sequencing adaptors from IDT containing a unique molecular index barcode for each sample library. Following the SeqCap EZ protocol, the prepared library was then amplified by 7 cycles of LM-PCR, normalized and multiplexed with other libraries to create a pre-capture pool of sample libraries. xGen Universal Blocking Oligos from IDT were then added to the pre-capture pool followed by the addition of the custom capture probes. The samples were then incubated at 47C for 72 hours to allow for probe hybridization. After hybridization, SeqCap EZ Capture Beads were used to capture the targeted DNA, followed by 10 cycles of LM-PCR to amplify the captured DNA and generate the final enriched multiplexed sample libraries ready for Illumina sequencing. The enriched multiplexed libraries were quantified using KAPA Biosystem’s next-generation sequencing library qPCR kit and run on a Roche LightCycler 480 real-time PCR instrument. The quantified libraries were then prepared for sequencing on the Illumina HiSeq sequencing platform utilizing a TruSeq paired-end cluster kit, v4, and Illumina’s cBot instrument to generate a clustered flow cell for sequencing. Sequencing of the flow cell was performed on the Illumina HiSeq 2500 sequencer using HiSeq TruSeq SBS sequencing kits, v4, following a 2x150 indexed run recipe.