

Figure S1. Violin plots showing the frequency distributions for days to heading (DTH) in *aus* nested association mapping population. Yellow and blue dots represent the population founders, *aus* and T65 respectively. Black dots show the recombinant inbred lines average in each family. Groups with no significant difference by Tukey HSD with a 95% confidence level are represented by the same letters shown above the plots.

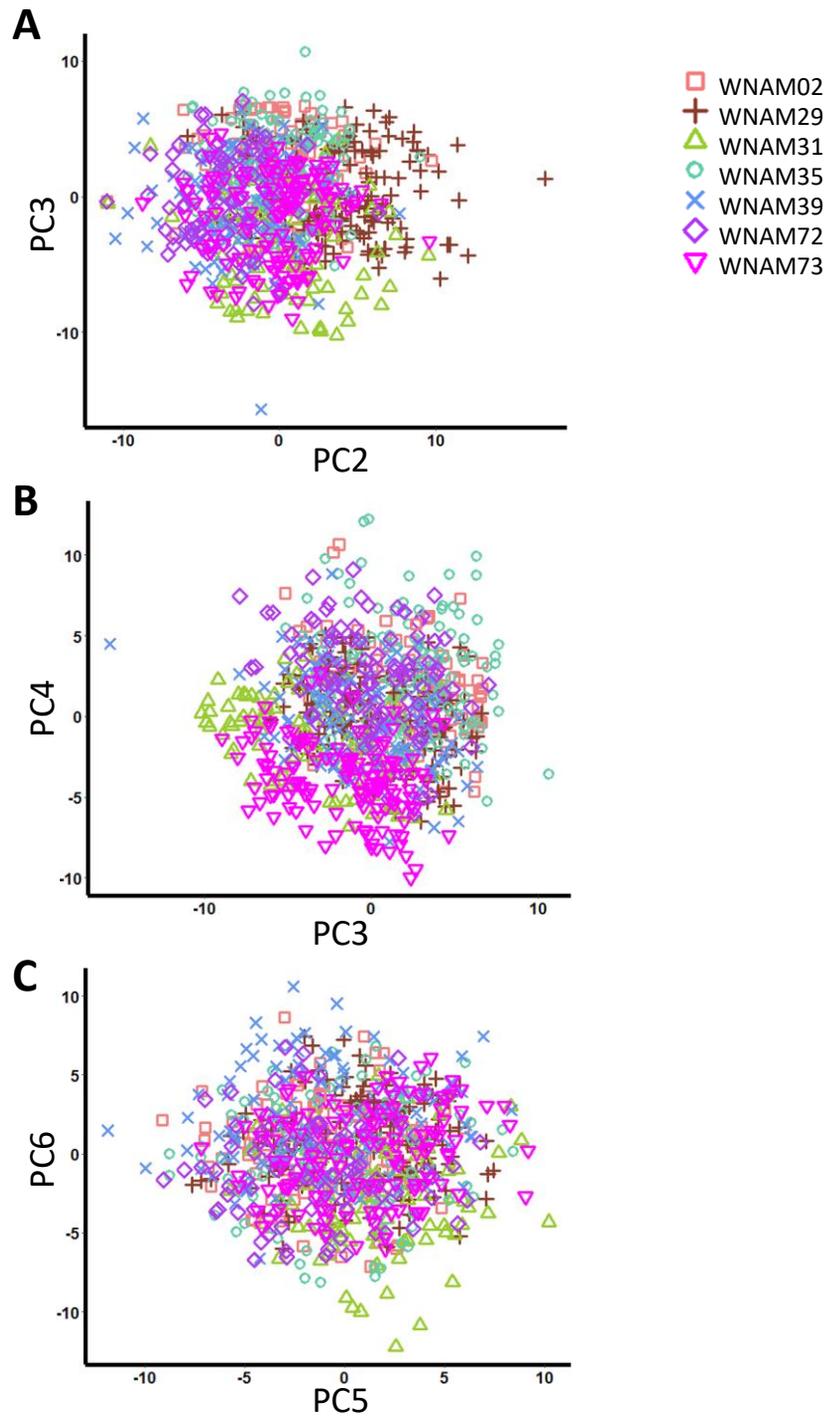


Figure S2. Probabilistic principal component analysis (PPCA) showing population structure in *aus* nested association mapping (*aus*-NAM) population. (A) PC2 vs PC3 (B) PC3 vs PC4 (C) PC5 vs PC6. Different shapes and colors represent different *aus*-NAM families.

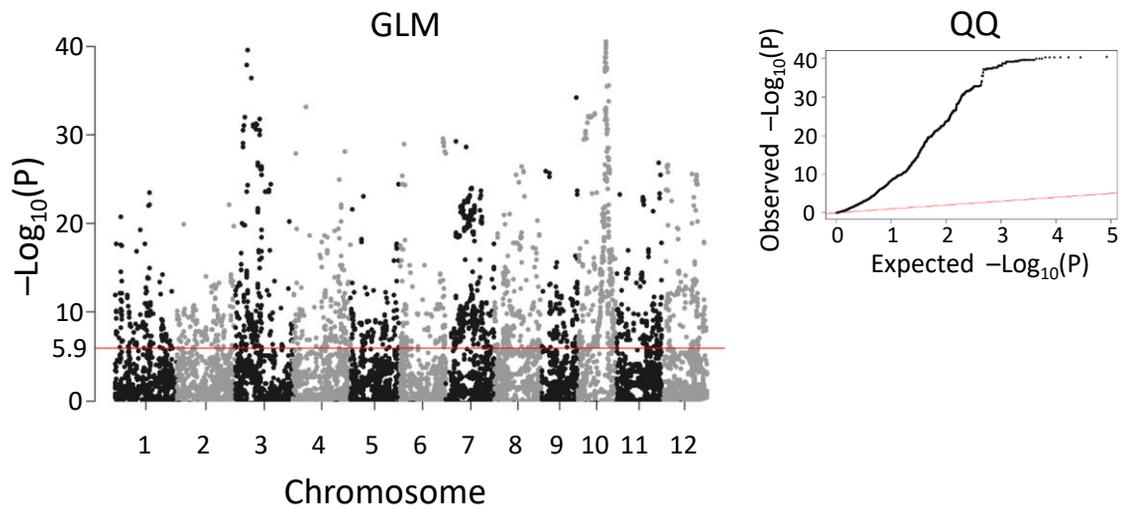


Figure S3. Manhattan plot of days to heading using general linear model (GLM). The red horizontal line marks the threshold for genome wide significance (5.9) on a $-\log_{10}$ scale. A quantile-quantile (QQ) plot is shown in the right panel, where the observed P-values (Y-axis) against the expected P-values (X-axis) under the null hypothesis of no association are plotted on a $-\log_{10}$ scale. Each black dot indicate a SNP.

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Reference      1  MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCDA
Hdl-Nipnbare  1  MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCDA
Hdl_Ginbouzu  1  MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCDA
Hdl_WRC39_Badar  1  MNYNFGGNVFDQEVGVREGGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCDA
consensus      1  *****.*****ZF-B box

Reference      61  RVHAANRVASRHERVRCACERAPAALACRADAALCVACDVQVHSAN-----
Hdl-Nipnbare  61  RVHAANRVASRHERVRCACERAPAALACRADAALCVACDVQVHSAN-----
Hdl_Ginbouzu  61  RVHAANRVASRHERVRCACERAPAALACRADAALCVACDVQVYSANPLARRHQRPV
Hdl_WRC39_Badar  61  RVHAANRVASRHERVRCACERAPAALACRADAALCVACDVQVHSANPLARRHQRPV
consensus      61  *****.*****ZF-B box

Reference      110 -PLPAITIPATSVLAEAVVATATVVLGDKDEEVDSWLLLSKDSNNNNNNNNNDNDN--ND
Hdl-Nipnbare  110 -PLPAITIPATSVLAEAVVATATVVLGDKDEEVDSWLLLSKDSNNNNNNNNNDNDN--ND
Hdl_Ginbouzu  121 APLPAITIPATSVLAEAVVATATVVLGDKDEEVDSWLLLSKDSNNNNNNNNNDNDN--ND
Hdl_WRC39_Badar  121 APLPAITIPATSVLAEAVVATATVVLGDKDEEVDSWLLLSKDSNNNNNNNNNDNDNND
consensus      121 .*****.*****

Reference      167  NNNSNSNNGMYFGEVDEYFDLVGYSYDNRIENNQDROYGMHEQQEQQQQQEQEMQKEF
Hdl-Nipnbare  167  NNNSNSNNGMYFGEVDEYFDLVGYSYDNRIENNQDROYGMHEQQEQQQQQEQEMQKEF
Hdl_Ginbouzu  179  NNNSNSNNGMYFGEVDEYFDLVGYSYDNRIENNQDROYGMHEQQEQQQQQEQEMQKEF
Hdl_WRC39_Badar  181  NNNSNSNNGMYFGEVDEYFDLVGYSYDNRIENNQDROYGMHEQQEQQQQQEQEMQKEF
consensus      181  *****.*****

Reference      227  AEKEGSECVVPSQITMLSEQQHSYGVVGVGADQAASMTAGVSAITDSISNSISFSSMEAGI
Hdl-Nipnbare  227  AEKEGSECVVPSQITMLSEQQHSYGVVGVGADQAASMTAGVSAITDSISNSISFSSMEAGI
Hdl_Ginbouzu  239  AEKEGSECVVPSQITMLSEQQHSYGVVGVGADQAASMTAGVSAITDSISNSISFSSMEAGI
Hdl_WRC39_Badar  241  AEKEGSECVVPSQITMLSEQQHSYGVVGVGADQAASMTAGVSAITDSISNRIISFSSMEAGI
consensus      241  *****.*****

Reference      287  VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVRLRYREKKKARKFEKTI
Hdl-Nipnbare  287  VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVRLRYREKKKARKFEKTI
Hdl_Ginbouzu  299  VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVRLRYREKKKARKFEKTI
Hdl_WRC39_Badar  301  VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVRLRYREKKKARKFEKTI
consensus      301  *****.*****CCT motif

Reference      347  RYETRKAAYAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSYGTVPWF
Hdl-Nipnbare  347  RYETRKAAYAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSYGTVPWF
Hdl_Ginbouzu  359  RYETRKAAYAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSYGTVPWF
Hdl_WRC39_Badar  361  RYETRKAAYAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSYGTVPWF
consensus      361  *****

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Figure S4. Alignment of amino-acid sequences of *Hd1* in functional alleles of Nipponbare and Ginbouzu, and Badari Dhan (WRC39). The amino acid sequences were deduced from genomic sequences. Regions of the 2 ZF-B box and CCT motif are indicated. The sequence of Badari Dhan contained 6 non-synonymous mutations, but it was considered that the allele retains function.