

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.

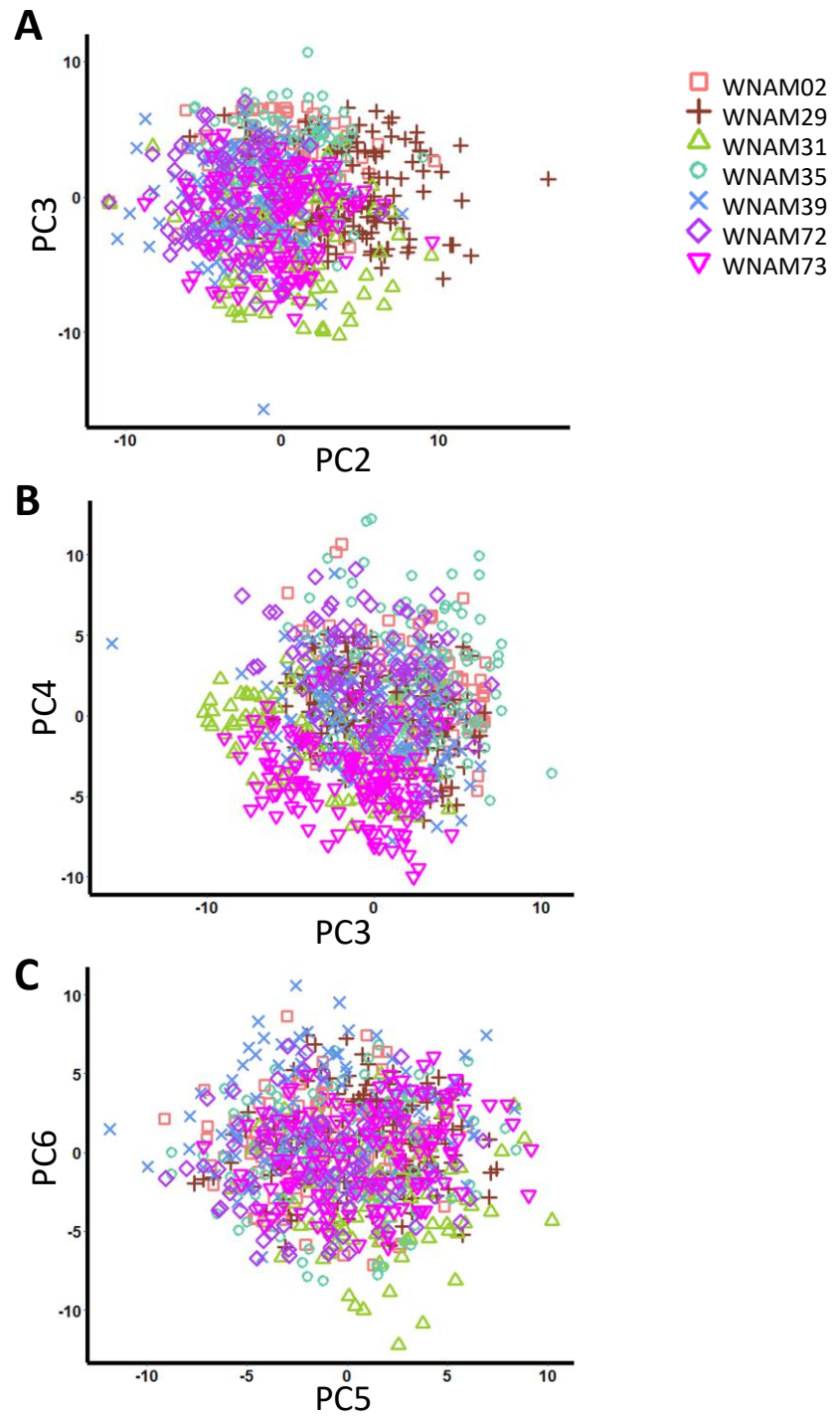


Figure S2. Probabilistic principal component analysis (PPCA) showing population structure in *aus* nested association mapping (*aus*-NAM) population. (A) PC2 vs PC3 (B) PC3 vs PC4 (C) PC5 vs PC6. Different shapes and colors represent different *aus*-NAM families.

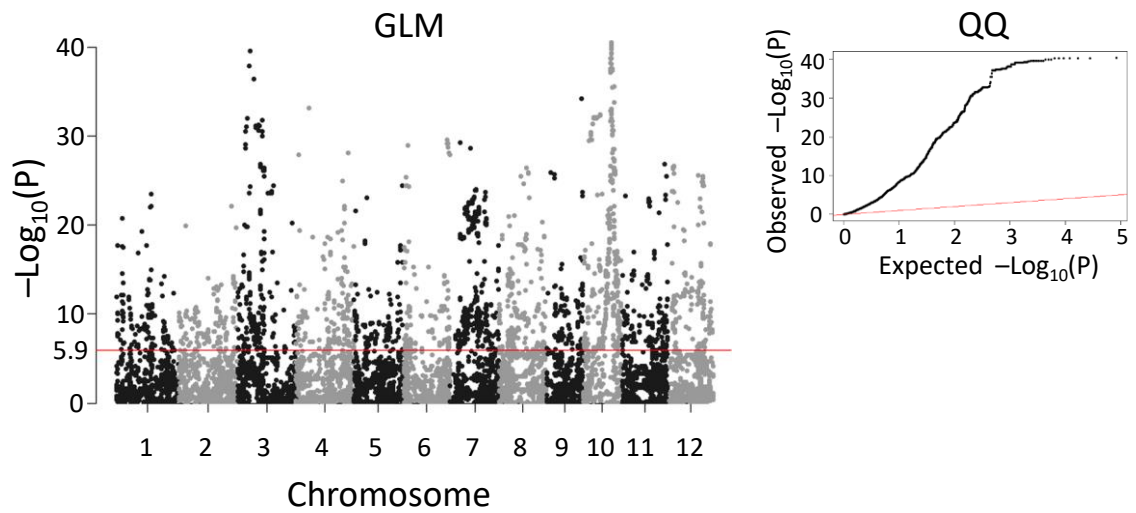


Figure S3. Manhattan plot of days to heading using general linear model (GLM). The red horizontal line marks the threshold for genome wide significance (5.9) on a $-\log_{10}$ scale. A quantile-quantile (QQ) plot is shown in the right panel, where the observed P-values (Y-axis) against the expected P-values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

Reference	1	MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCD
Hd1-Nipnbare	1	MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCD
Hd1_Ginbouzu	1	MNYNFGGNVFDQEVGVGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCD
Hd1_WRC39_Badar	1	MNYNFGGNVFDQEVGVRGEGGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASCD
consensus	1	*****.*****ZF-B box*****
Reference	61	RVHAANRVASRHERVRVCEACERAPAALACRADAAALCVACDVQVHSAN-----
Hd1-Nipnbare	61	RVHAANRVASRHERVRVCEACERAPAALACRADAAALCVACDVQVHSAN-----
Hd1_Ginbouzu	61	RVHAANRVASRHERVRVCEACERAPAALACRADAAALCVACDVQVYSANPLARRHQRPV
Hd1_WRC39_Badar	61	RVHAANRVASRHERVRVCEACERAPAALACRADAAALCVACDVQVHSANPLARRHQRPV
consensus	61	*****.*****ZF-B box*****
Reference	110	-PLPAITIPATSVLAEAVVATATVLGDKDEEVDSWLLLSKSDSNNNNNNNNDNDN--ND
Hd1-Nipnbare	110	-PLPAITIPATSVLAEAVVATATVLGDKDEEVDSWLLLSKSDSNNNNNNNNDNDN--ND
Hd1_Ginbouzu	121	APLPAITIPATSVLAEAVVATATVLGDKDEEVDSWLLLSKSDSNNNNNNNNDNDN--ND
Hd1_WRC39_Badar	121	APLPAITIPATSVLAEAVVATATVLGDKDEEVDSWLLLSKSDSNNNNNNNNDNDN--ND
consensus	121	.*****.*****
Reference	167	NNNSNSSNNGMYFGEVDEYFDLVGYNsYDNRIENNQDRQYGMHEQQEQQQQQEQMKEF
Hd1-Nipnbare	167	NNNSNSSNNGMYFGEVDEYFDLVGYNsYDNRIENNQDRQYGMHEQQEQQQQQEQMKEF
Hd1_Ginbouzu	179	NNNSNSSNNGMYFGEVDEYFDLVGYNsYDNRIENNQDRQYGMHEQQEQQQQQEQMKEF
Hd1_WRC39_Badar	181	NNNSNSSNNGMYFGEVDEYFDLVGYNsYDNRIENNQDRQYGMHEQQEQQQQQEQMKEF
consensus	181	*****.*****
Reference	227	AEKEGSECVVPSQITMLSEQQHSYGyGVVGADQAASMTAGVSAYTDSISNSISFSSMEAGI
Hd1-Nipnbare	227	AEKEGSECVVPSQITMLSEQQHSYGyGVVGADQAASMTAGVSAYTDSISNSISFSSMEAGI
Hd1_Ginbouzu	239	AEKEGSECVVPSQITMLSEQQHSYGyGVVGADQAASMTAGVSAYTDSISNSISFSSMEAGI
Hd1_WRC39_Badar	241	AEKEGSECVVPSQITMLSEQQHSYGyGVVGADQAASMTAGVSAYTDSISNRISFSSMEAGI
consensus	241	*****.*****
Reference	287	VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVLRYREKKKARKFEKTI
Hd1-Nipnbare	287	VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVLRYREKKKARKFEKTI
Hd1_Ginbouzu	299	VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVLRYREKKKARKFEKTI
Hd1_WRC39_Badar	301	VPDSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVLRYREKKKARKFEKTI
consensus	301	*****.*****CCT motif*****
Reference	347	RYETRKAyAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSyGTVVPWF
Hd1-Nipnbare	347	RYETRKAyAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSyGTVVPWF
Hd1_Ginbouzu	359	RYETRKAyAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSyGTVVPWF
Hd1_WRC39_Badar	361	RYETRKAyAEARPRIKGRFAKRSDVQIEVDQMFSTAALSDGSyGTVVPWF
consensus	361	*****

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.