Table S2 – High-confidence QTL effects in Ames-H and NAM-H, based on GWAS models and BSLMMs

Trait	Chr.	Position	Ames-H				NAM-H			
			AF	Effect	p (FDR)	WPIP	AF	Effect	p (FDR)	WPIP
DTS	1	5,819,499	0.76	0.14	0.37 (0.99)	< 0.01	**0.86**	**0.76**	**1.8×10^{-10} (8.0×10^{-7})**	**0.93**
	1	6,246,295	0.61	-0.31	0.022 (0.81)	< 0.01	**0.80**	**0.48**	**1.1×10^{-5} (0.011)**	**0.92**
	2	225,200,515	0.99	1.20	0.019 (0.80)	< 0.01	**0.91**	**0.74**	**4.1×10^{-7} (7.4×10^{-4})**	**0.73**
	2	225,463,382	0.61	0.18	0.19 (0.99)	< 0.01	**0.77**	**0.59**	**2.2×10^{-8} (6.2×10^{-5})**	**0.90**
	3	161,016,441	**0.58**	**-0.86**	**7.3×10^{-9} (2.6×10^{-3})**	**0.55**	0.88	-0.51	2.8×10^{-4} (0.13)	0.01
	4	202,429,351	**0.96**	**1.74**	**1.9×10^{-7} (0.014)**	**0.51**	0.89	0.03	0.86 (1.0)	< 0.01
	7	110,855,373	**0.99**	**3.69**	**6.3×10^{-10} (4.4×10^{-4})**	**0.94**	0.95	0.07	0.75 (1.0)	0.01
	8	126,761,299	**0.90**	**-1.04**	**3.8×10^{-7} (0.018)**	**0.59**	0.97	-0.70	0.023 (0.90)	0.01
	9	128,205,378	0.67	0.19	0.21 (0.99)	< 0.01	**0.74**	**0.55**	**2.3×10^{-6} (3.0×10^{-3})**	**0.89**
	9	146,679,383	**0.81**	**-0.73**	**3.5×10^{-6} (0.037)**	**0.72**	0.95	-0.54	0.010 (0.72)	< 0.01
	10	94,059,383	0.96	0.05	0.88 (1.0)	< 0.01	**0.95**	**2.23**	**1.3×10^{-25} (4.2×10^{-20})**	**0.99**
	10	94,453,179	0.97	0.80	0.041 (0.88)	< 0.01	**0.93**	**2.12**	**9.6×10^{-31} (2.4×10^{-24})**	**1.01**
GY	7	175,528,863	0.79	-0.05	0.54 (0.99)	0.04	**0.97**	**-1.09**	**2.0×10^{-8} (0.013)**	**0.70**

Values in bold describe high-confidence QTL (FDR ≤ 0.05 and WPIP ≥ 0.5). Chr.: Chromosome; Position: physical location; AF: frequency of the major allele (as per the Hapmap 3.2.1 panel) among female parents; Effect: estimated effect of minor allele from GWAS; p (FDR): p-value by Wald tests and false discovery rate estimated by the method of Benjamini and Hochberg (1995); WPIP: posterior inclusion probability for non-zero SNP effects in 500-kb sliding windows (250-kb steps), based on BSLMM (Guan and Stephens 2011).