Table S4
Novel Coding Mutations in *BADH2*

Allele #	IRGC #	Code #	Accession Name	Origin	Subpopulation	[2AP]	Marker	Mutation	Exon
*badh2.2**	28473	ANF4/8203	Hsiang-Keng-Nuo	China	*tropical japonica*	0.66	BadHapG1	7 bp deletion	2nd
badh2.3	69874	ANF10	Rasomotrafotsy	Madagascar	*tropical japonica*	0.74	BadHapG1	2 bp deletion	1st
badh2.4	27348	ANF3	Pare Baine Pulut	Indonesia	*tropical japonica*	0.59	BadHapG7	_ ➔T (1 bp insertion)	10th
badh2.5	52787	ANF9	Vishunparag	India	*aus*	0.41	BadHapG7	G➔T (substitution)	10th
badh2.6	13453	ANF1	Padi Wangi	Malaysia	*indica*	0.7	BadHapG7	T➔_ (1 bp deletion)	10th
badh2.7	34975	ANF6	Katak Tara	India	*aus*	0.37	BadHapG9	_➔G (1 bp insertion)	14th
	36394	ANF7	Suwanda Al	Sri Lanka	*aus*	0.3	BadHapG9		14th
	44204	ANF8	UPRB28	India	*aus*	0.42	BadHapG9		14th
	82408	ANF11	Basmati Bahar (Longer Grain)	India	*aus*	0.38	BadHapG9		14th
	83308	ANF12	Basmati	Nepal	*aus*	0.32	BadHapG9		14th
	83309	ANF13	Basmati	Nepal	*aus*	0.77	BadHapG9		14th
badh2.8	33858	ANF5	Yangon Saba	Myanmar	Group V	0.31	BadHapG9	__➔TAT (3 bp insertion)	13th
	32960	F22	Balugyun	Myanmar	Group V	0.42	BadHapG9		13th
	97793	SR5	Paw San Hmwe	Myanmar	Group V	0.43	BadHapG9		13th
	N/A	8149	Paw San Hmwe (META-PHOR)	Myanmar	Group V	0.49	BadHapG9		13th
	33064	8172	Emata Longyu	Myanmar	Group V	0.14	BadHapG9		13th
badh2.9	18438	ANF2	Pandan Wangi	Indonesia	*tropical japonica*	0.29	BadHapG9	G➔T (substitution)	14th
	18438	PW1	Pandan Wangi	Indonesia	*tropical japonica*	0.19	BadHapG9		14th
	N/A	SR8	Pandan Wangi	Indonesia	*tropical japonica*	0.14	BadHapG9		14th
	N/A	SR9	Pandan Wangi	Indonesia	*tropical japonica*	0.18	BadHapG9		14th
	79569	8517	Mentik Wangi	Indonesia	*tropical japonica*	N/A	BadHapG9		14th
	N/A	8151	Pandan Wangi8 (META-PHOR)	Indonesia	*tropical japonica*	0.08	BadHapG9		14th

badh2.10	78746	8192	Tainung 72	Taiwan	*tropical japonica*	0.35	BadHapG9	C➔T (substitution)	13th
	5394	8215	Shiratama	Japan	*tropical japonica*	N/A	BadHapG9		13th
WT	90687	ANF14	Khau Tan Luong	Vietnam	*tropical japonica*	0.79			
	LG6732	K2/C7/8156	Kay Noi Leuang	Laos	*tropical japonica*	0.76			

*The *badh2.2* allele was first identified by Shi et al., 2008 (Ref. 15)