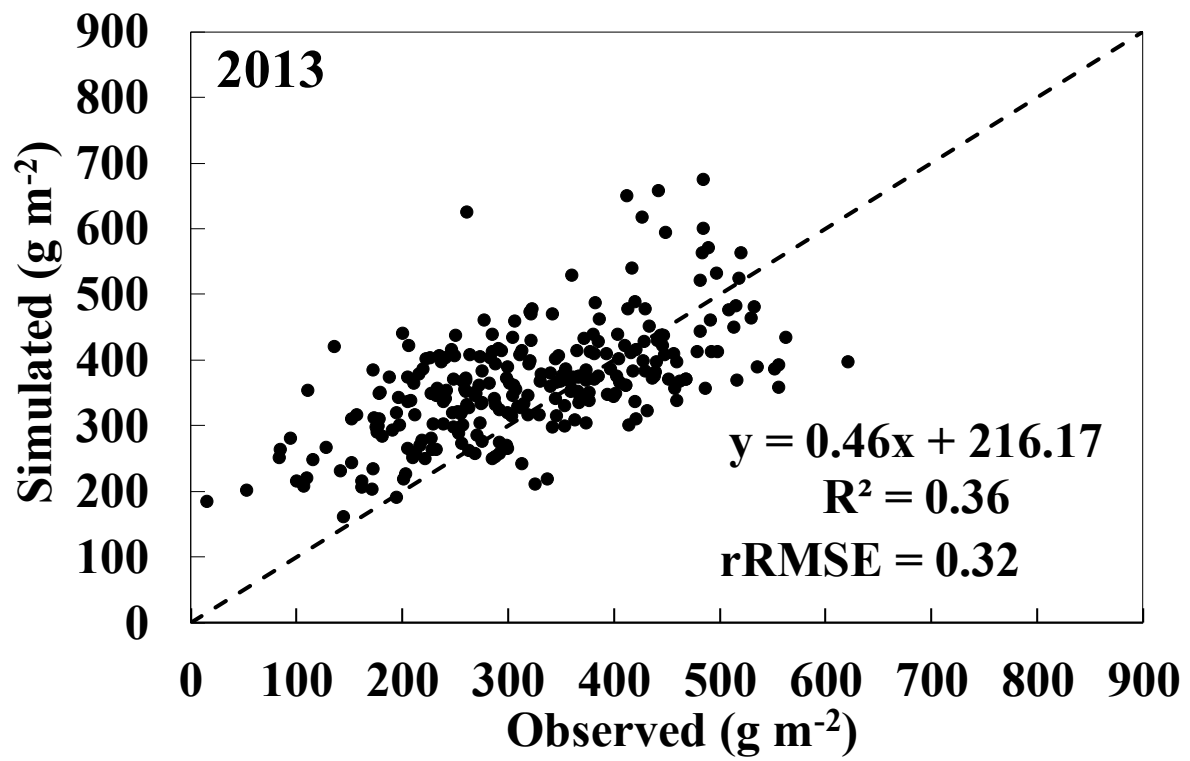
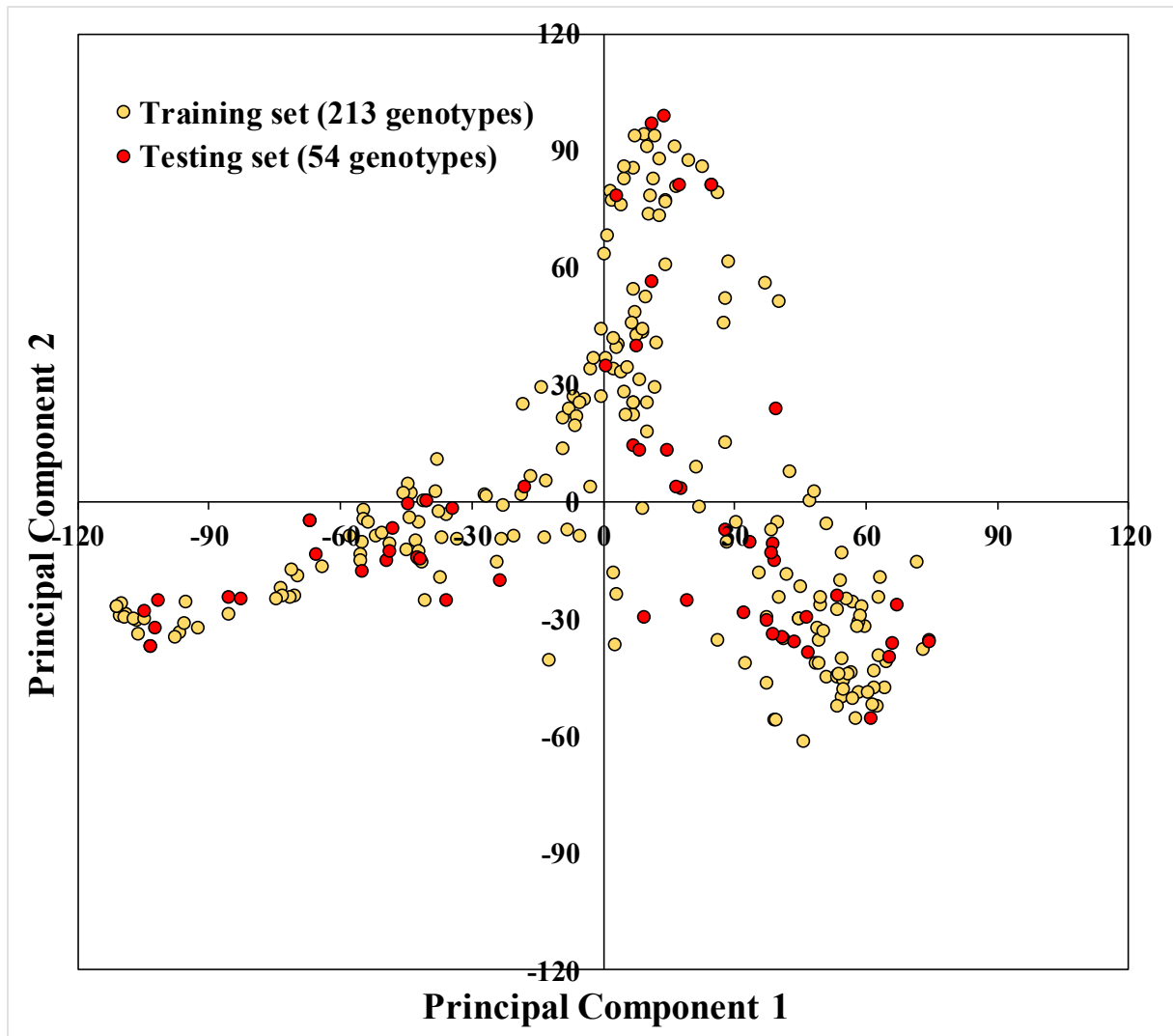


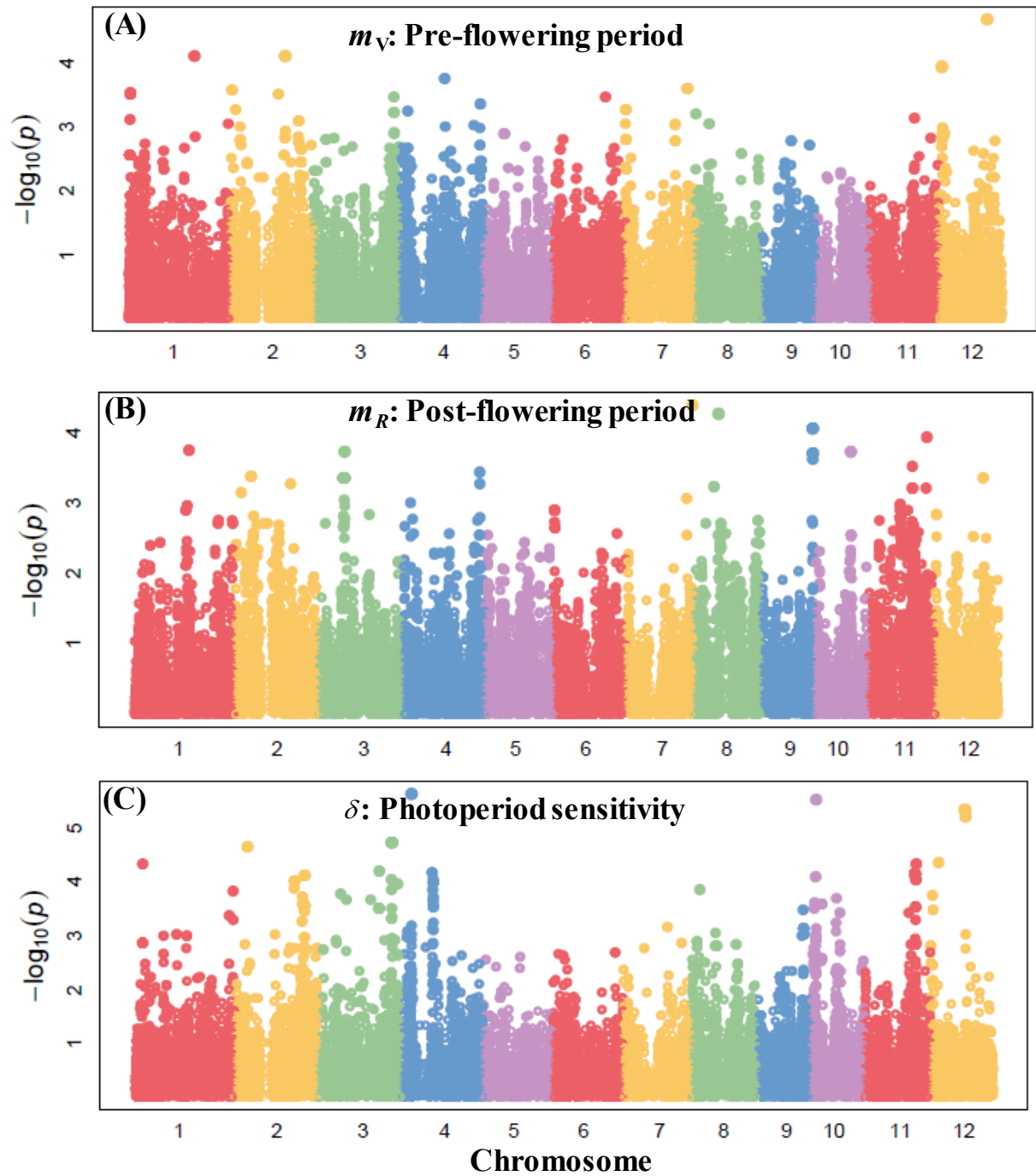
Supplementary Figure 1: Flow chart explaining the stepwise methodology adapted to combine the genome-wide association study (GWAS) with an eco-physiological crop model (GECROS). This flow chart was modified from [Gu et al. \(2014\)](#) Linking ecophysiological modelling with quantitative genetics to support marker-assisted crop design for improved yields of rice (*Oryza sativa*) under drought stress. *Annals of Botany* **114**, 499-511.



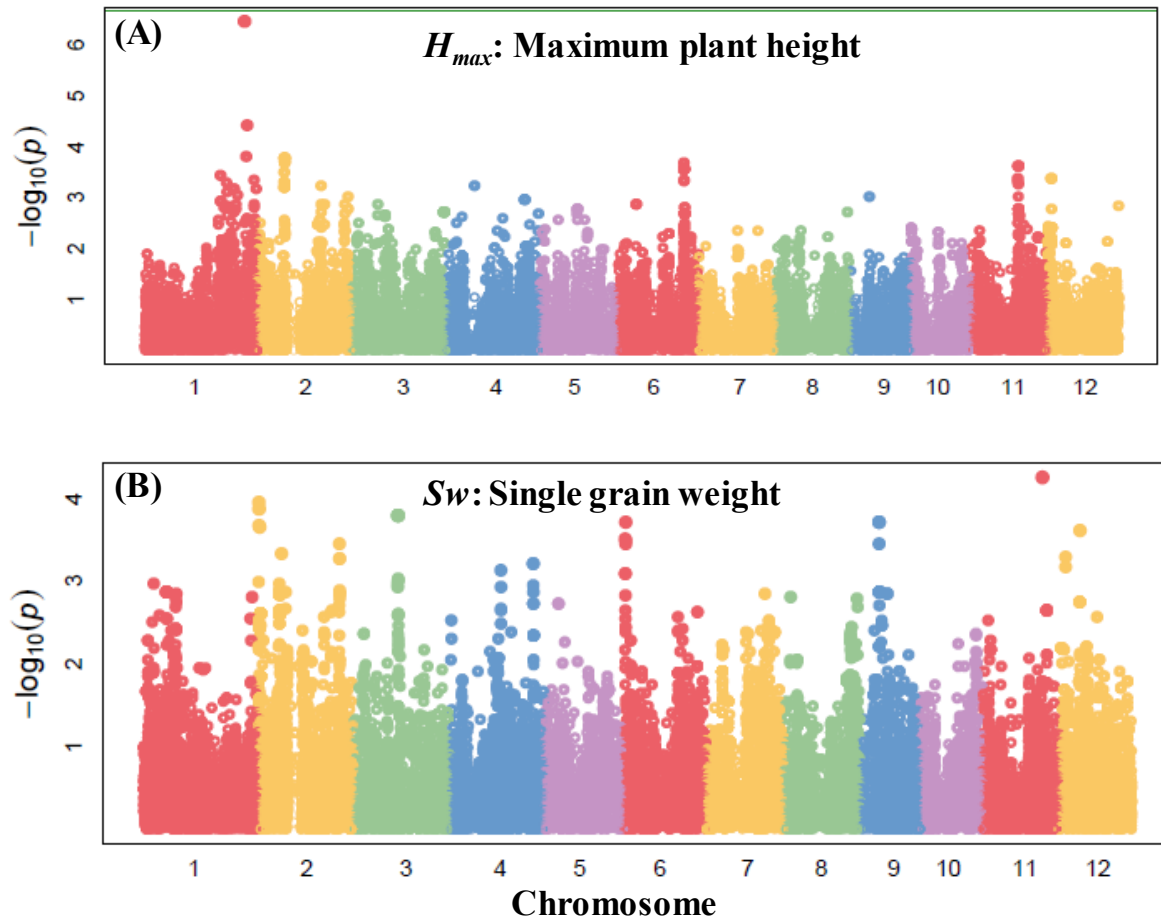
Supplementary Figure 2: Relationship between observed and simulated values of grain yield for the water-deficit stress treatment of the 2013 experiment, using the GECROS model without introducing the direct effect of panicle temperature on spikelet number.



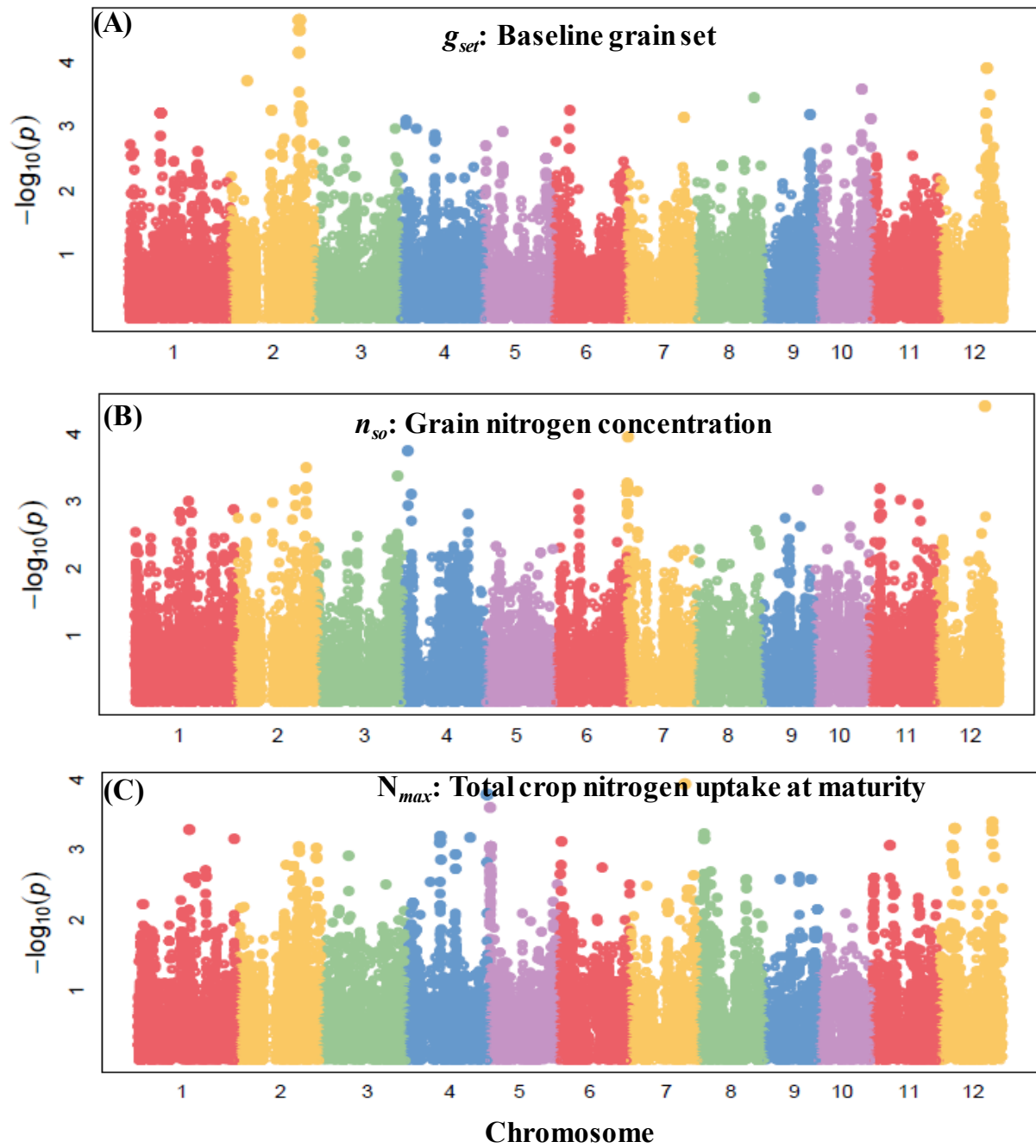
Supplementary Figure 3: Principal component analysis (PCA) with first two principal components showing the population structure of training and testing set genotypes. PCA analysis was conducted using the 46K SNP data having minor allele frequency of ≥ 0.05 .



Supplementary Figure 4: Manhattan plot showing the results of GWAS through the single-locus compressed mixed linear model (CMLM) for model input parameters (Phenological; see Table 1): (A) m_v : pre-flowering period, (B) m_R : post-flowering period, and (C) δ : photoperiod sensitivity.



Supplementary Figure 5: Manhattan plot showing the results of GWAS through the single-locus compressed mixed linear model (CMLM) for model input parameters (Morphological; see Table 1): (A) H_{max} : maximum plant height, and (B) S_w : single grain weight.



Supplementary Figure 6: Manhattan plot showing the results of GWAS through the single-locus compressed mixed linear model (CMLM) for model input parameters (Physiological; see Table 1): (A) g_{ser} : baseline grain set, (B) n_{so} : grain nitrogen concentration, and (C) N_{max} : total crop nitrogen uptake at maturity.

Supplementary Table 1: Multiple linear regression (MLR) analysis of significant SNPs detected through the genome-wide association analysis against the model input parameters and grain yield. R^2 value represents the percentage of phenotypic variation explained by all SNP markers for a given parameter.

Parameters	Chromosome	Position	u	Additive effects (a_n)	P value	R^2 (%)
(A) Phenological						
m_v	1	28262688	64.19	2.5371	0.001111	74.2
	1	9243669		3.7197	5.24E-08	
	1	7344741		-1.5835	0.000138	
	2	4390533		3.6114	3.17E-12	
	2	23538671		-2.58	1.76E-11	
	3	10106310		-2.3681	0.000467	
	4	19591930		4.8726	5.21E-11	
	4	1258958		-2.6171	0.000878	
	6	26238067		-2.467	1.54E-05	
	7	99783		-4.3277	1.48E-13	
	9	18375567		-1.2878	0.000274	
	10	4760551		-1.3883	0.00039	
	12	1691770		-4.0529	4.73E-09	
	12	18314444		2.5202	9.73E-12	
12	3640868	-2.1222	6.73E-05			
12	7323204	-2.7144	1.81E-07			
m_R	4	33336957	32.95	0.6348	0.003947	51.6
	4	3661992		-2.5713	1.60E-09	
	4	20195438		3.362	2.53E-11	
	4	20014494		-1.7035	7.79E-06	
	5	16151637		0.8617	3.29E-05	
	9	22561421		-13.2386	4.75E-16	
	9	22561709		11.0251	1.79E-12	
	9	16415255		0.6762	0.002308	
11	19245430	1.1817	0.000162			
δ	1	27113695	0.13	-0.022173	0.001154	65.1
	2	5508005		0.024534	0.000143	
	2	30150945		0.039265	3.27E-08	
	4	4499266		0.03125	4.75E-08	
	5	5619386		0.017076	0.000126	
	10	2718469		-0.028512	5.49E-07	
	11	22826451		0.019679	0.000269	
	11	6520591		0.026071	2.78E-05	
12	15123621	0.043865	< 2e-16			
(B) Morphological						
H_{max}	1	39255482	1.29	-0.06984	0.000147	77.0
	1	38286772		-0.1849	< 2e-16	
	1	21100541		0.10041	1.64E-06	
	1	852462		0.04606	0.000382	
	1	37707297		0.06128	1.44E-05	
	1	6077035		-0.03864	0.000458	
	2	24267632		-0.047	0.000128	
	2	774705		0.05459	1.56E-05	
	4	16556278		0.03247	0.001486	
	7	58252		-0.11813	1.34E-13	
	8	7880762		-0.10699	7.32E-12	
8	19677137	0.08531	0.000217			
10	2506985	-0.06651	0.002954			

	2	554478		0.0008908	3.21E-08	
	2	30699332		0.0008471	3.22E-06	
	2	17222218		-0.0015312	2.41E-06	
S_w	2	11071729	0.022	0.0005774	0.000404	47.3
	3	16725807		0.0009015	1.12E-07	
	3	12717890		-0.0007547	7.25E-06	
	7	23227646		-0.0008358	3.21E-07	
	12	7731908		0.0011273	1.92E-10	
(C) Physiological						
	2	29373768		-0.05334	2.54E-07	
	6	6585943		0.031565	2.00E-07	
g_{set}	10	14926494	0.732	0.02464	1.97E-05	42.2
	10	18906753		0.023826	9.76E-05	
	12	20014218		-0.032433	3.48E-06	
	12	21173768		0.016498	0.00755	
	1	42643627		4.52E-04	9.10E-05	
	1	6765299		2.66E-04	0.001454	
	1	22900197		-2.82E-04	0.000543	
	2	34358656		6.35E-04	7.67E-10	
	3	25074645		-5.29E-04	5.34E-06	
	3	16529108		5.79E-04	1.92E-12	
	4	1982000		-3.23E-04	0.000173	
n_{SO}	4	31449324	1.13E-02	-3.09E-04	0.000703	70.0
	5	14030811		-3.43E-04	1.59E-05	
	7	467419		-7.43E-04	1.95E-15	
	7	4568023		-4.87E-04	5.93E-10	
	7	9524268		-6.50E-04	1.34E-05	
	9	7207743		-4.18E-04	0.000483	
	11	25041651		-7.32E-04	4.89E-07	
	12	20907521		8.55E-04	< 2e-16	
	12	17569836		-5.84E-04	1.54E-07	
	1	22221764		-0.43691	3.05E-06	
	1	18893159		0.37043	7.18E-05	
	1	41741982		-0.40857	0.000239	
	4	34815309		-0.77981	1.62E-10	
	5	658940		-0.2115	0.000765	
	6	1360962		0.34729	3.56E-05	
N_{max}	7	23760855	5.84	-0.75225	3.80E-08	66.8
	8	2341829		0.28059	0.000122	
	8	20492803		-0.32529	8.02E-08	
	11	10143495		0.27417	7.34E-06	
	11	965990		-0.3564	0.001213	
	12	6720935		-0.45876	5.80E-09	
	12	19666909		-0.46896	1.32E-06	
	1	37302008		-10.331	0.27545	
	1	537855		1.933	0.78126	
	2	26263170		15.201	0.16315	
	2	26654759		19.416	0.05706	
	4	10502119		31.805	0.02564	
Grain yield	5	658940	406.63	-43.576	3.53E-09	44.3
	6	10086748		-20.301	0.01844	
	8	2756338		1.809	0.83464	
	8	2341829		24.607	0.02028	
	11	7789963		-48.323	0.0011	
	11	10101900		-20.479	0.00836	
	12	22741407		-46.749	8.56E-07	

Supplementary Table 2: The SNPs-based GECROS model accounting for the phenotypic variance of grain yield in a rice association mapping panel (n=267) by different sets of simulations by stepwise fixing one marker at a time.

Parameters	Chr	Position	Control		Water-deficit	
			R ² (%)	Rank	R ² (%)	Rank
(A) Phenological						
<i>mv</i>	1	28262688	30.5	29	20.5	5
	1	9243669	29.4	12	16.0	2
	1	7344741	31.5	49	29.4	86
	2	4390533	29.1	10	18.0	3
	2	23538671	29.6	14	24.0	14
	3	10106310	33.1	87	29.4	85
	4	19591930	28.6	8	14.9	1
	4	1258958	31.8	65	29.1	84
	6	26238067	31.5	47	28.7	80
	7	99783	29.9	19	30.0	88
	9	18375567	31.6	60	26.6	62
	10	4760551	30.9	34	26.9	66
	12	1691770	31.9	69	31.0	89
	12	18314444	31.7	64	23.6	9
	12	3640868	32.1	75	29.0	83
12	7323204	32.7	82	29.5	87	
<i>mr</i>	4	33336957	32.0	70	25.8	40
	4	3661992	29.9	20	25.9	44
	4	20195438	32.6	81	25.9	45
	4	20014494	30.7	31	25.6	37
	5	16151637	32.0	71	26.2	57
	9	22561421	29.8	18	26.0	49
	9	22561709	33.5	90	25.0	33
	9	16415255	31.6	50	25.4	35
11	19245430	31.7	61	25.8	41	
<i>δ</i>	1	27113695	31.6	53	26.1	50
	2	5508005	30.6	30	24.5	24
	2	30150945	30.7	32	23.9	12
	4	4499266	30.2	24	24.2	19
	5	5619386	30.5	27	24.9	30
	10	2718469	31.9	66	26.8	63
	11	22826451	30.3	25	24.9	31
	11	6520591	30.1	21	24.5	25
12	15123621	30.1	22	24.1	18	
(B) Morphological						
<i>H_{max}</i>	1	39255482	32.3	78	28.9	82
	1	38286772	32.0	73	31.7	90
	1	21100541	32.3	79	28.4	79
	1	852462	31.5	46	27.4	72
	1	37707297	30.5	28	27.3	71
	1	6077035	31.2	39	25.7	39
	2	24267632	31.4	42	24.8	28
	2	774705	31.6	57	28.2	76
	4	16556278	31.1	35	26.3	59
	7	58252	28.8	9	20.5	4
	8	7880762	31.4	41	25.8	42
	8	19677137	32.0	74	28.2	77
10	2506985	30.4	26	23.6	8	

	2	554478	31.5	43	26.2	58
	2	30699332	31.7	62	26.0	47
	2	17222218	31.4	40	26.1	55
S_w	2	11071729	31.5	45	26.1	54
	3	16725807	31.6	54	26.1	51
	3	12717890	31.6	55	26.1	53
	7	23227646	32.0	72	26.1	56
	12	7731908	31.5	44	26.1	52
(C) Physiological						
	2	29373768	31.5	48	24.6	26
	6	6585943	31.6	58	26.5	60
g_{set}	10	14926494	31.6	51	24.4	21
	10	18906753	29.6	17	24.0	15
	12	20014218	31.6	59	24.0	17
	12	21173768	31.6	52	25.3	34
	1	42643627	31.2	37	26.0	48
	1	6765299	31.7	63	27.0	68
	1	22900197	31.2	38	25.0	32
	2	34358656	29.6	15	24.0	16
	3	25074645	32.9	85	26.9	65
	3	16529108	27.7	5	22.4	7
	4	1982000	33.1	86	27.8	74
	4	31449324	31.9	68	27.1	70
n_{SO}	5	14030811	32.6	80	27.0	69
	7	467419	31.9	67	23.7	10
	7	4568023	33.4	89	27.7	73
	7	9524268	33.2	88	26.8	64
	9	7207743	32.9	84	27.9	75
	11	25041651	31.6	56	26.0	46
	12	20907521	32.9	83	24.7	27
	12	17569836	31.2	36	26.9	67
	1	22221764	27.5	4	24.4	22
	1	18893159	29.2	11	24.5	23
	1	41741982	30.2	23	25.8	43
	4	34815309	32.2	77	25.7	38
	5	658940	29.4	13	25.5	36
	6	1360962	25.9	1	21.5	6
N_{max}	7	23760855	26.0	2	24.8	29
	8	2341829	28.1	7	24.0	13
	8	20492803	32.2	76	28.7	81
	11	10143495	30.8	33	28.3	78
	11	965990	29.6	16	26.5	61
	12	6720935	27.2	3	24.3	20
	12	19666909	27.9	6	23.8	11
Baseline simulation			31.6		26.1	