

Table S1. Shapiro-Wilk test results. Normality test on the trait distributions among the generations using the Shapiro-Wilk test.

Trait	F ₂	F ₃	F ₆	F ₇
	W - p.value	W - p.value	W - p.value	W - p.value
HD	0.97 - 5.27 e-7	0.92 - 4.95 e-8	0.97 - 7.40 e-4	0.98 - 1.30 e-3
GH	0.79 - 8.38 e-15	0.93 - 5.06 e-7	0.98 - 5.68 e-2	0.97 - 2.98 e-5
PH	0.99 - 11.41 e-2	0.98 - 2.21 e-2	0.99 - 16.80 e-2	0.99 - 21.40 e-2
TTN	0.98 - 5.00 e-2	0.98 - 6.78 e-2	0.96 - 1.80 e-4	0.98 - 5.75 e-2
FTN	0.99 - 13.79 e-2	0.98 - 2.22 e-2	0.97 - 1.06 e-2	0.98 - 71.13 e-2

Table S2 Phenotypic correlations among the five investigated traits. r = Pearson correlation coefficients. HD = heading date; PH = plant height; GH = growth habit; TTN = total tiller number; FTN = fertile tiller number.

Pop.	Trait	r					p-value				
		HD	GH	PH	TTN	FTN	HD	GH	PH	TTN	FTN
F ₂	HD	1.00	0.15	-0.14	-0.05	-0.11	0	5.19E-02	0.0629363	5.20E-01	1.39E-01
	GH	0.15	1.00	-0.12	0.45	0.45	0.0519015	0.00E+00	0.1083925	4.32E-10	4.66E-10
	PH	-0.14	-0.12	1.00	-0.08	-0.04	0.0629363	1.08E-01	0	3.06E-01	5.84E-01
	TTN	-0.05	0.45	-0.08	1.00	0.98	0.5204431	4.32E-10	0.3063691	0.00E+00	7.03E-117
	FTN	-0.11	0.45	-0.04	0.98	1.00	0.1387115	4.66E-10	0.5836821	7.03E-117	0.00E+00
F ₃	HD	1.00	0.41	-0.28	0.16	0.17	0.00E+00	2.79E-08	0.0002209	4.05E-02	2.82E-02
	GH	0.41	1.00	-0.11	0.02	0.04	2.79E-08	0.00E+00	0.1477295	7.71E-01	6.26E-01
	PH	-0.28	-0.11	1.00	0.01	0.02	2.21E-04	1.48E-01	0	9.44E-01	7.44E-01
	TTN	0.16	0.02	0.01	1.00	0.90	4.05E-02	7.71E-01	0.9441459	0.00E+00	2.39E-62
	FTN	0.17	0.04	0.02	0.90	1.00	2.82E-02	6.26E-01	0.7438394	2.39E-62	0.00E+00
F ₆	HD	1.00	0.24	-0.27	0.23	0.20	0	0.0021329	0.0004956	3.72E-03	1.22E-02
	GH	0.24	1.00	0.04	0.19	0.21	0.0021329	0	0.6601272	1.40E-02	9.16E-03
	PH	-0.27	0.04	1.00	-0.08	-0.06	0.0004956	0.6601272	0	3.30E-01	4.18E-01
	TTN	0.23	0.19	-0.08	1.00	0.93	0.0037224	0.0139652	0.3297482	0.00E+00	2.44E-72
	FTN	0.20	0.21	-0.06	0.93	1.00	0.0121706	0.0091604	0.4176902	2.44E-72	0.00E+00
F ₇	HD	1.00	0.33	-0.06	0.08	0.04	0.00E+00	7.55E-06	0.4109153	2.68E-01	5.64E-01
	GH	0.33	1.00	0.06	0.15	0.11	7.55E-06	0.00E+00	0.4373474	5.13E-02	1.52E-01
	PH	-0.06	0.06	1.00	-0.09	-0.09	4.11E-01	4.37E-01	0	2.35E-01	2.57E-01
	TTN	0.08	0.15	-0.09	1.00	0.82	2.68E-01	5.13E-02	0.2351835	0.00E+00	1.33E-44
	FTN	0.04	0.11	-0.09	0.82	1.00	5.64E-01	1.52E-01	0.2571609	1.33E-44	0.00E+00

Table S3. Genetic map features. Main map characteristics concerning genetics maps constructed on F₂ and F₆ generations.

Map Features	F ₂	F ₆
Linkage groups	39	38
Lenght (cM)	2,486.97	3,732.84
Marker density (Marker/cM)	1.37	1.00
Chr lenght average (cM)	118.43	177.75
Max chr lenght (cM)	231.56	360.26
Min chr lenght (cM)	5.01	3.93
Mean markers gap (cM)	1.15	1.50
N° SNPs Genome A	1,527	1,777
N° SNPs Genome B	1,569	1,691
N° SNPs Genome D	316	278
Genome A coverage (cM)	1,180.94	1,738.77
Genome B coverage (cM)	915.75	1,578.35
Genome D coverage (cM)	390.28	415.71
Genome A marker density*	1.29	1.02
Genome B marker density*	1.71	1.07
Genome D marker density*	0.81	0.67

*Marker/cM

Table S4 Genetic map data summary. Distribution of SNP markers across the twenty-one chromosome in the F₂ and F₆ genetic maps. Chromosome's length (cM), distance (cM), number of markers in common between F₂ and F₆, and coefficient of collinearity (Rho) were reported.

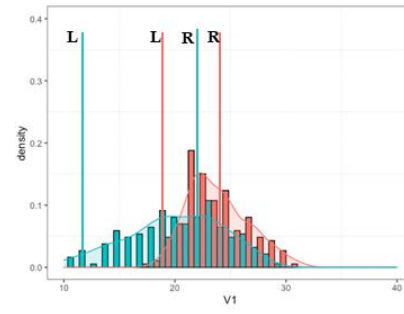
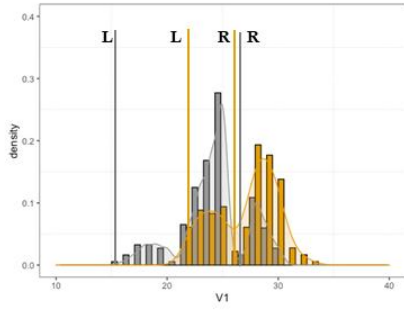
Cromosome	Chromosome lenght (cM)		Distance (cM) ^a		#Markers F ₂ /F ₆ ^b	Rho
	F ₂	F ₆	F ₂	F ₆		
1A	180.64	204.33	1.01	0.90	138	0.95
1B	231.56	289.12	0.6	0.81	190	0.81
1D	128.78	106.05	1.09	1.12	63	0.72
2A	145.86	186.23	0.6	0.55	224	0.91
2B	144.91	163.62	0.49	1.41	53	0.86
2D	100.55	82.24	2.23	3.16	10	-0.21
3A	178.51	232.65	0.74	1.62	103	0.92
3B	47.19	328.49	1.47	0.84	32	0.73
3D	5.01	9.35	0.26	2.34	0	/
4A	163.72	162	1.67	1.13	74	0.75
4B	133.62	155.29	0.81	1.51	58	0.86
4D	38.59	3.93	2.41	0.98	5	-0.89
5A	189.70	342.88	0.7	1.13	194	0.84
5B	203.32	360.26	0.55	0.93	234	0.91
5D	27.15	17.08	0.94	0.61	19	0.09
6A	128.13	302.43	0.46	1.04	182	0.82
6B	112.25	210.82	0.44	0.82	179	0.94
6D	35.16	69.67	0.49	0.71	67	0.83
7A	194.26	308.24	0.93	0.95	165	0.91
7B	42.90	70.75	0.75	0.96	51	0.84
7D	55.05	127.39	5.51	7.96	2	-1

^a Distance between adjacent markers

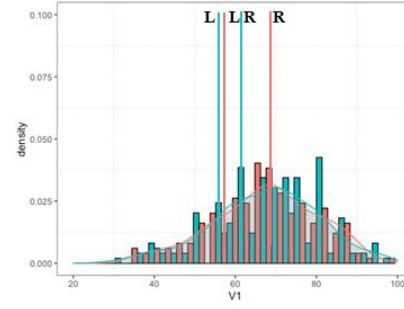
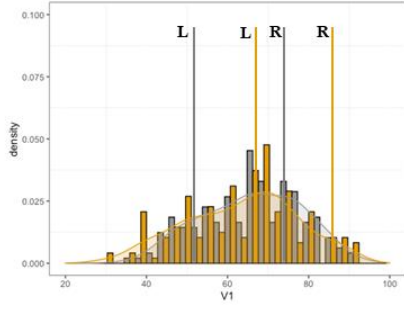
^b Number of markers in common between the two populations F₂ and F₇

^c Spearman's rho statistic is used to estimate a rank-based measure of association.

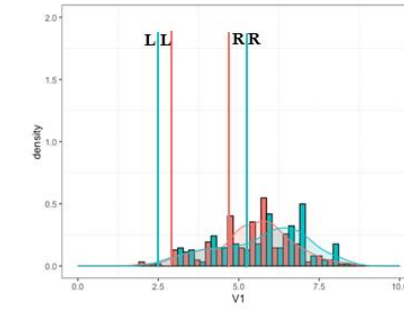
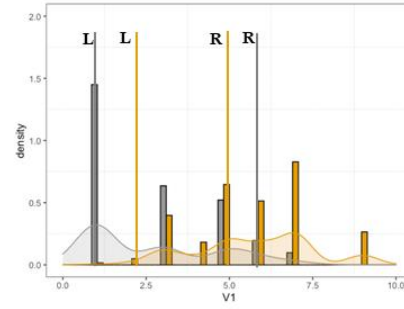
HD



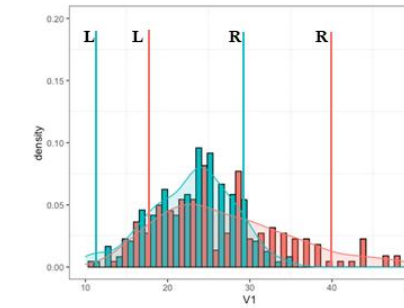
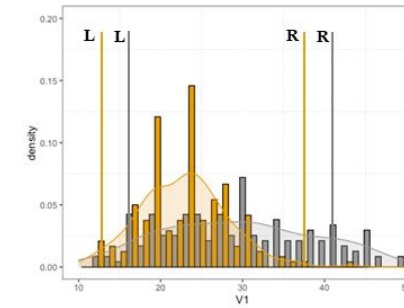
PH



GH



TTN



FTN

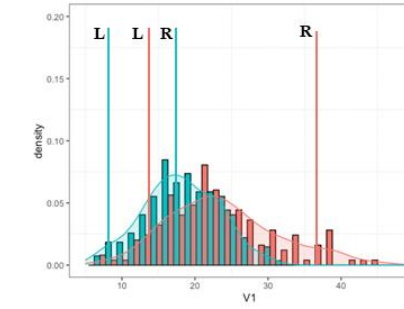
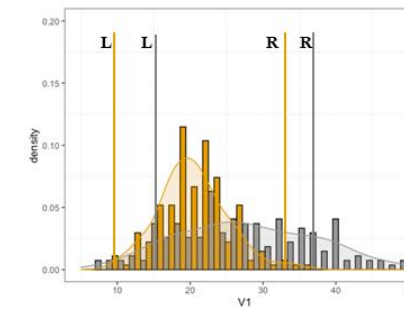


Figure S1 Phenotypic distribution for the five traits across the F₂ (grey bars), F₃ (orange bars), F₆ (red bars) and F₇ (green bars). The x-axis represents phenotypic values, whereas the y-axis corresponds to density. Phenotypic values of parental lines Lankaodali (L) and Rebelde (R) are also shown. HD = heading date; PH = plant height; GH = growth habit; TTN = total tiller number; FTN = fertile tiller number.

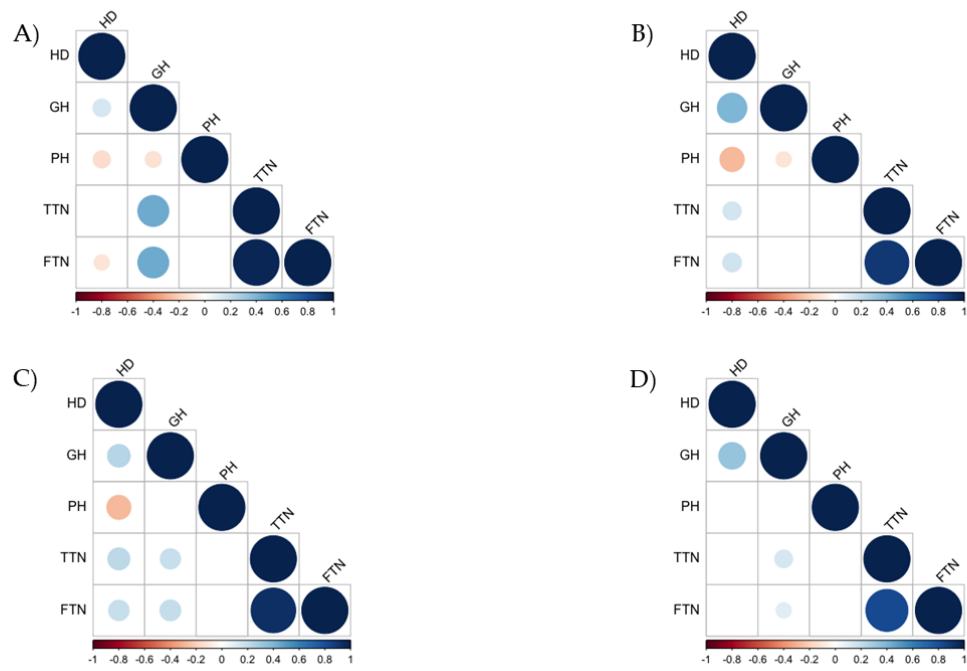


Figure S2 Pearson's correlation matrix for the five traits measured across the F₂ (A), F₃ (B), F₆ (C) and F₇ (D) populations. The square blank refers to the Pearson's correlation test yielded a non-significant p-value ($p > 0.05$). HD = heading date; PH = plant height; GH = growth habit; TTN = total tiller number; FTN = fertile tiller number.

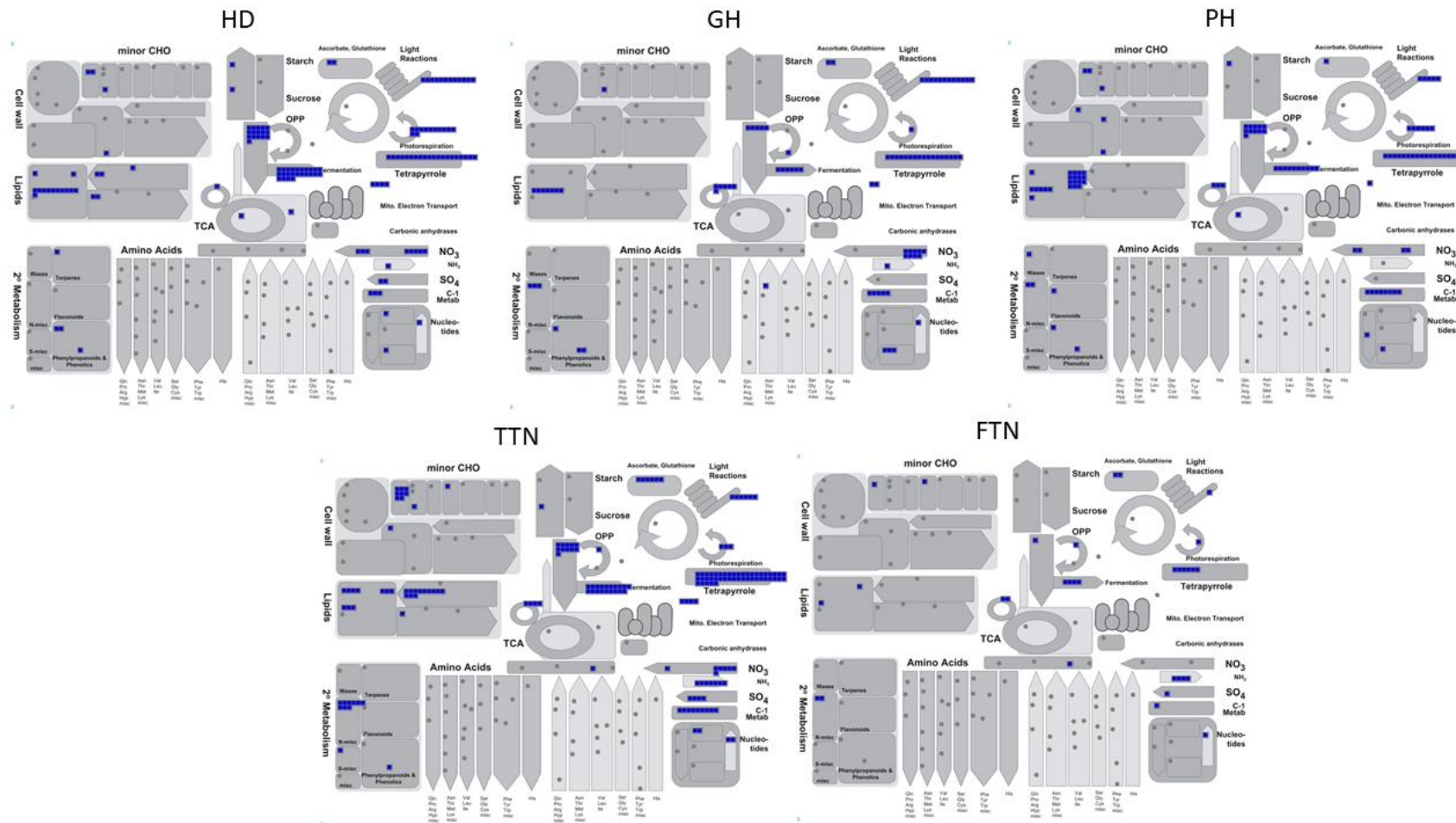


Figure S3 MapMan analysis. The blue squares indicated the major pathways of metabolic processes in which candidate genes were involved. HD = heading date; PH = plant height; GH = growth habit; TTN = total tiller number; FTN = fertile tiller number.