Supplemental Data:
Supplemental Tables:

Table S1. Marker selection steps during genotyping of the IL.

Selection step	No. markers excluded	No. remaining markers
overall	56,110	56,110
Genome Studio output (GenTrain ≤ 0.9, Call Frequency ≠ 1)	-39,966	16,144
not included in the CoreSet [a]	-9,775	6,369
no confirmed genome position	-106	6,263
monomorphic between the parents	-4,402	1,861

[a] selection of 32,650 SNP which were found to show highly reproducible results across a diverse set of inbred lines.

Table S2. Single environment estimates of genotypic (σ^2_g) and residual error (σ^2) variance components as well as estimates of repeatability of seven traits evaluated in the field and in the greenhouse.

Trait [a]	Experimental condition	σ^2_g	σ^2	rep. [c]
$\Delta^{13}C$	field	0.04	0.05	0.44
	greenhouse	0.06	0.16	0.27
Fflow	field	2.58	3.70	0.41
	greenhouse	0.94	5.68	0.14
Mflow	field	1.58	3.11	0.34
	greenhouse	0.43	3.07	0.12
PH	field	112.76	90.51	0.55
	greenhouse	191.12	369.38	0.34
SenL	field	- [b]	-	-
	greenhouse	0.89	4.04	0.18
SPAD	field	5.07	8.66	0.37
	greenhouse	2.17	13.63	0.14
$F_VF_M^{-1}$	field	- [b]	-	-
	greenhouse	- [b]	-	-

[a] $\Delta^{13}C$; stable carbon isotope discrimination [‰], Fflow; time to female flowering [days], Mflow; time to male flowering [days], PH; plant height [cm], SenL; percentage of senescent leaves [%], SPAD; chlorophyll content of the ear leaf, $F_VF_M^{-1}$; maximum photosynthetic capacity
[b] not significant at $P < 0.05$
[c] repeatability

Table S3. Donor genome target regions associated with time to female flowering (Fflow), time to male flowering (Mflow), plant height (PH), chlorophyll content of the ear leaf (SPAD) detected by stepwise regression on means averaged across greenhouse and field environments and for seed germination vigor (GV) evaluated in a growth chamber experiment.

Trait [a]	Target region ID	Chr [b].	Target region position [c] [Mbp]		Length of target region [Mbp]	ADD [d]	R_i^2 [e] [%]
			start	end			
Fflow	5	1	36.05	39.28	3.23	0.59	0.06
	9	1	75.20	81.36	6.16	-1.18	0.13
	24	1	254.97	257.03	2.06	0.56	0.04
	26	1	257.96	260.23	2.27	0.71	0.01
	48	2	187.29	204.90	17.61	0.54	0.03
	51	2	214.32	216.39	2.07	0.47	0.02
	76	5	10.68	19.76	9.08	-0.53	0.04
	88	5	206.83	208.78	1.95	0.78	0.10
	96	6	120.84	130.41	9.57	0.70	0.04
	122	8	6.73	8.43	1.70	-0.64	0.05
	133	8	151.27	156.26	4.99	-0.61	0.06
	146	9	16.72	132.74	116.02	0.49	0.02
	160	10	74.91	125.89	50.98	0.77	0.06
Mflow	5	1	36.05	39.28	3.23	0.43	0.06
	10	1	81.36	156.35	74.99	-0.68	0.11
	29	1	294.50	297.61	3.11	-0.36	0.03
	54	2	227.75	232.32	4.57	0.38	0.03
	128	8	74.35	78.88	4.53	-0.66	0.02
	129	8	78.88	119.48	40.60	0.99	0.05
	133	8	151.27	156.26	4.99	-0.81	0.12
PH	6	1	39.28	41.79	2.51	7.44	0.05
	9	1	75.20	81.36	6.16	-12.45	0.10
	59	3	147.33	175.14	27.81	12.11	0.10
	77	5	19.76	58.79	39.03	-13.70	0.13
	147	9	132.74	138.99	6.25	-14.98	0.05

Table S3 continued

Trait[a]	Target region ID	Chr.[b]	Target region position[c] [Mbp]		Length of target region [Mbp]	ADD[d]	R_i^{2e} [%]
			start	end			
SPAD	1	1	4.53	10.19	5.66	-0.43	0.01
	19	1	228.16	230.52	2.36	-0.45	0.01
	24	1	254.97	257.03	2.06	0.99	0.04
	29	1	294.50	297.61	3.11	-0.53	0.01
	32	2	6.56	9.18	2.62	0.37	0.01
	35	2	12.66	19.06	6.40	0.56	0.02
	49	2	204.90	211.90	7.00	-1.32	0.03
	54	2	227.75	232.32	4.57	1.06	0.02
	59	3	147.33	175.14	27.81	1.10	0.05
	70	3	225.22	225.82	0.60	-0.79	0.02
	71	4	15.97	31.62	15.65	-1.06	0.02
	76	5	10.68	19.76	9.08	0.84	0.03
	88	5	206.83	208.78	1.95	-0.77	0.05
	94	6	0.00	3.17	3.17	1.46	0.04
	118	7	139.73	147.07	7.34	0.99	0.05
	123	8	8.43	13.78	5.35	-0.81	0.02
	124	8	13.78	17.60	3.82	1.26	0.04
	128	8	74.35	78.88	4.53	-1.49	0.08
	130	8	119.48	124.17	4.69	0.84	0.02
	133	8	151.27	156.26	4.99	-1.29	0.08
	140	8	168.94	174.25	5.31	-0.95	0.03
	141	9	0.00	6.63	6.63	-0.94	0.01
	142	9	6.63	9.21	2.58	1.36	0.02
	143	9	9.21	11.31	2.10	-1.58	0.05
	147	9	132.74	138.99	6.25	-0.75	0.01
	151	9	152.80	153.85	1.05	0.89	0.04
	161	10	125.89	133.15	7.26	-1.41	0.07
	162	10	133.15	135.71	2.56	0.75	0.02

Table S3 continued

Trait[a]	Target region ID	Chr.	Target region position[c] [Mbp]		Length of target region [Mbp]	ADD[d]	R_i^{2e} [%]
			start	end			
GV	3	1	17.09	27.72	10.63	-0.09	0.02
	68	3	216.97	219.65	2.68	0.04	0.02
	82	5	167.69	168.95	1.26	0.09	0.04
	89	5	208.78	212.15	3.37	-0.10	0.13
	122	8	6.73	8.43	1.70	0.17	0.11
	123	8	8.43	13.78	5.35	-0.11	0.07
	140	8	168.94	174.25	5.31	-0.10	0.06
	150	9	151.12	152.80	1.68	-0.06	0.02
	156	10	6.42	9.18	2.76	-0.05	0.04

[a] Fflow; time to female flowering [days], Mflow; time to male flowering [days], PH; plant height [cm], SPAD; chlorophyll content of the ear leaf, GV, seed germination vigor [%],[b] chromosome, [c] estimated borders of the target regions. The start of a target region was calculated as the position of the first SNP marker on the target region minus half the distance to the next marker flanking the target region. The end of a target region was calculated as the position of the last SNP marker on the target region plus half the distance to the next marker flanking the target region, [d] additive effect of the target region carrying the donor alleles relative to the recurrent parent, [e] percentage of phenotypic variance explained.