

Table S1 Phenotype data of parents and F<sub>1</sub> plant under low-light treatment

Traits	lines	R1	R2	R3	R4	R5	R6	R7	R8	R9	Average
Plant height (PLH/cm)	WI	17.80	32.20	23.30	17.40	18.70	32.90	/	35.80	33.40	26.44
	F <sub>1</sub>	50.65	54.05	51.65	53.05	48.30	48.65	58.85	54.65	53.90	52.64
	M14	64.10	/	54.20	47.60	76.20	69.10	84.70	66.60	66.40	66.11
2nd internode length (nd2_NdL/cm)	WI	0.90	2.00	1.80	1.02	1.23	2.00	/	2.12	1.80	1.61
	F <sub>1</sub>	1.50	1.30	1.50	1.40	1.25	1.25	2.00	1.75	1.75	1.52
	M14	1.30	2.00	2.60	1.50	1.50	1.50	1.30	1.00	1.30	1.38

**Note:** R1、R2……, Repetition1、Repetition2……; WI, the low-light-tolerance line; F<sub>1</sub>, the hybrid of parents WI and M14; M14, the low-light-intolerance line.

Table S2. Quantity analysis of sequencing samples

Sample ID	Total reads	Q30 (%)	G C content (%)
WI	28 924 098	89.04	37.60
M14	28 536 117	89.53	38.27
F <sub>2</sub> population	2 119 013	94.04	41.50
Control	1 174 010	94.26	42.79
Total	296 908 762	93.96	41.44

Note: Q30, represent the identification reliability of a base reaches 99.9% in high-throughput sequencing. G C, base G C; WI, the low-light-tolerance line; F<sub>2</sub>, the second filial generation of parents WI and M14; M14, the low-light-intolerance line.

Table S3 Statistic of SNP Markers for the parental lines and offspring

Types	Number	Types	Number
Total SNP markers	1 076 599	ab × cc	137
Parent marker lack	206 481	cc × ab	36
4 × Depth not meet	56 612	ef × eg	57
No-poly marker	208 868	hk × hk	13 264
Remain marker	604 638	lm × ll	69 632
aa × bb	496 263	nn × np	25 249

Note: SNP, single nucleic acid polymorphism; aa × bb; ab × cc; cc × ab; ef × eg; hk × hk; lm × ll; nn × np, SNP genotyping.