FN Line	Illumina paired-end read length (bp)	Raw sequencing data			Aligned sequencing data		
		Number of reads	Total number of bases sequenced	Genome fold coverage*	Number of Reads	Total number of bases sequenced	Genome fold coverage*
F_2-1	90	34,283,104	3,085,479,360	25.8	22,902,760	2,061,248,400	17.2
F_2-2	90	34,490,180	3,104,116,200	25.9	23,405,658	2,106,509,220	17.6
F_2-3	90	35,115,388	3,160,384,920	26.4	23,468,808	2,112,192,720	17.7
E71 (M_3)	75	62,395,014	4,679,626,050	39.1	42,804,110	3,210,308,250	26.8
E99 (M_3)	75	64,339,922	4,825,494,150	40.3	44,727,908	3,354,593,100	28.0
E125 (M_3)	51	99,141,632	5,056,223,232	42.3	70,754,626	3,608,485,926	30.2
E128 (M_3)	75	38,859,106	2,914,432,950	24.4	27,575,704	2,068,177,800	17.3
E138 (M_3)	75	61,425,202	4,606,890,150	38.5	42,935,852	3,220,188,900	26.9
E216 (M_3)	51	113,915,698	5,809,700,598	48.6	77,689,046	3,962,141,346	33.1
E99 (M_4)	101	82,128,064	8,294,934,464	69.3	51,187,102	5,169,897,302	43.2
E125 (M_4)	101	80,463,600	8,126,823,600	67.9	50,895,650	5,140,460,650	43.0
Progenitor	36, 75 and 76	83,936,186, 63,810,862 and 30,731742	10,143,129,738	84.8	59,184,147, 45,247,612 and 18,127,179	6,901,865,796	57.7

Supplemental Table 7. Genome sequencing summary table for plants used in this study. DNA from three independent non-irradiated progenitor F_2 lines (F_2-1 to -3), six FN-induced elongated hypocotyl mutants E71, E99, E125, E128, E138 and E216 (M_3 generation) and two M_4 generation E99 and E125 plants were sequenced along with the DNA from the progenitor line using Illumina sequencing technology. Several lanes of 36, 51, 75, 76, 90 and/or 101 bp paired-end runs were generated for each line. Between 34 and 176 million reads were obtained for each plant lineage equating to 24 – 85 fold sequence coverage (raw sequencing data) for each genome and 17 – 58 fold sequence coverage (aligned data) for each genome.. *The parental reference genome size of 119,649,590 bp was used to determine genome fold coverage.