

Supplementary Table S1: *A. thaliana* *f3h/fls1/ans* mutant *de novo* ONT genome assembly statistics.

Parameter	Value
Number of contigs	162
Maximal contig length	16,321,703 bp
Assembly size	160,571,748 bp (160.6 Mbp)
GC content	39.11 %
N50	8,170,251 bp
N90	246,021 bp
BUSCOs	95.5% complete BUSCOs [Single: 88.3%. Duplicated: 7.2%]; Fragmented: 1.7%. Missing: 2.8%

Abbreviations: ONT, Oxford Nanopore Technologies; BUSCOs, Benchmarking Universal Single-Copy Orthologs

Supplementary Table S2: Oligonucleotide primers used in this work.

Gene	Name	Sequence (5'-3')	Description
<i>F3H</i>	MM70	GAGGTGACTAGAGACGATGAATCC	genotyping primer for the <i>F3H</i> wildtype and <i>tt6-2</i> mutant allele
	I250	AATGACGATTGGGATTTTTGTAAC	genotyping primer for the <i>F3H</i> wildtype allele
	8409	ATATTGACCATCATACTCATTGC	GABI-KAT T-DNA LB primer
<i>FLS</i>	UH9	CACTGAGATCTGTATGAGCCGGTACACC	genotyping primer for the <i>FLS</i> wildtype and <i>fls1-2</i> mutant allele
	RSt647	TTACACATATCAACACGTACTIONTTA	genotyping primer for the <i>FLS</i> wildtype allele
	RSt645	CCGGATCGTATCGGTTTTTCG	RIKEN Ds-transposon primer
<i>ANS</i>	B078	TTCCCCTGTTTTAAGTTTTATT	genotyping primer for the <i>ANS</i> wildtype and <i>tds4-4</i> mutant allele
	B079	AGAAAGACACAAACACATTATAAAA	genotyping primer for the <i>ANS</i> wildtype allele
	RS630	GCGTGGACCGCTTGCTGCAACTCTCTCAGG	SALK T-DNA LB primer