Supplementary Fig. 1 Increased leaf size of leaf epidermal cells in the fha2 mutants.

a Morphology of the 7th leaf from the wild-type and the fha2 mutant plants at 4 weeks after germination.

b The abaxial epidermal cell size of the first true leaf was measured by light microscopy at 4 weeks after germination (n=150).
Supplementary Fig. 2 Development of wild-type and the fha2-1 flowers during anther stages 12 to 14 according to Sanders et al. (1999). Anthers dehisced at the stage 13.
Supplementary Figure 3

(a) WT      fha2-1      fha2-2      fha2-3

(b) WT      fha2-1      fha2-2      fha2-3

(c)
<table>
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<th>Aborted pollen (%)</th>
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<td>23.6</td>
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<td>fha2-3</td>
<td>25.8</td>
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Supplementary Fig. 3 Alexander staining of pollen and in vitro pollen germination assays.

a Alexander staining of mature pollen grains from the wild-type and the fha2 mutants to test pollen viability. The fha2-1 mutant was homozygous for the qrt1 mutation (Preuss et al. 1994). Scale bars = 20 μm.

b In vitro germination assays of mature pollen grains from the wild-type and the fha2 mutants. Scale bars = 200 μm.

c Pollen abortion rates. The number of aborted pollen in the wild-type and the fha2 mutants was counted after Alexander staining of mature pollen grains (n=500).
Supplementary Fig. 4 DAPI staining of mature pollen.

a Mature pollen grains from the qrt1 control and the fha2-1 mutant were stained with DAPI. Please note that some pollen grains of the qrt1 control were not in tetrads.

b Numbers of pollen nuclei were counted and the frequency of 1, 2, or 3 nuclei in the qrt1 control (n=320) and the fha2-1 pollen (n=500) was presented in percentages. Scale bars = 20 μm.
Supplementary Fig. 5 Expression profiles of AtFHA2 (At3g07220) based on the Genevestigator program (https://www.genevestigator.com/). These expression profiles were derived from multiple transcriptome analyses. Relative transcript levels of AtFHA2 in flower buds (a), flower organs (b), and pollen (c) in different developmental stages are plotted in comparison with the level in rosette leaves.
Supplemental Fig. 6 Relative AtFHA2 transcript levels in stamens.

Real-time quantitative RT-PCR analysis was performed with RNA isolated from stamen filaments and anthers in flower stages 12 and 14. Each value represents the mean ± SD of three replicates per experiment.
Supplementary Fig. 7 Semiquantitative RT-PCR analyses of the transcript levels of jasmonate-related genes in the control stamen (Col-3 and Col-0) and the fha2 stamen.