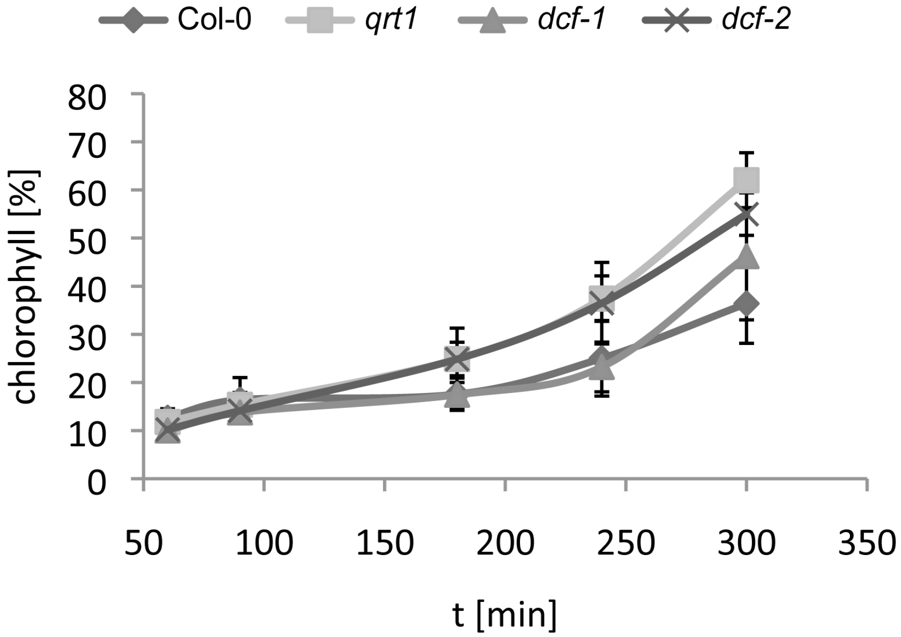
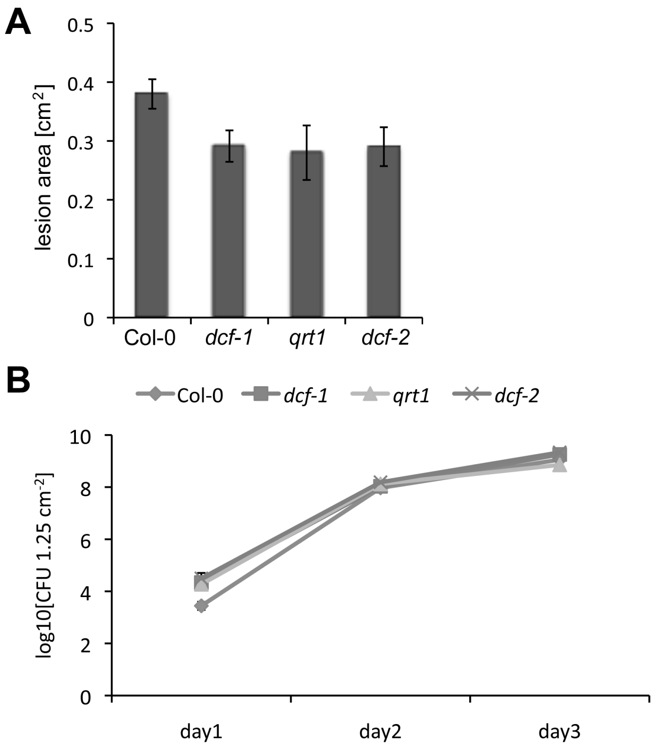


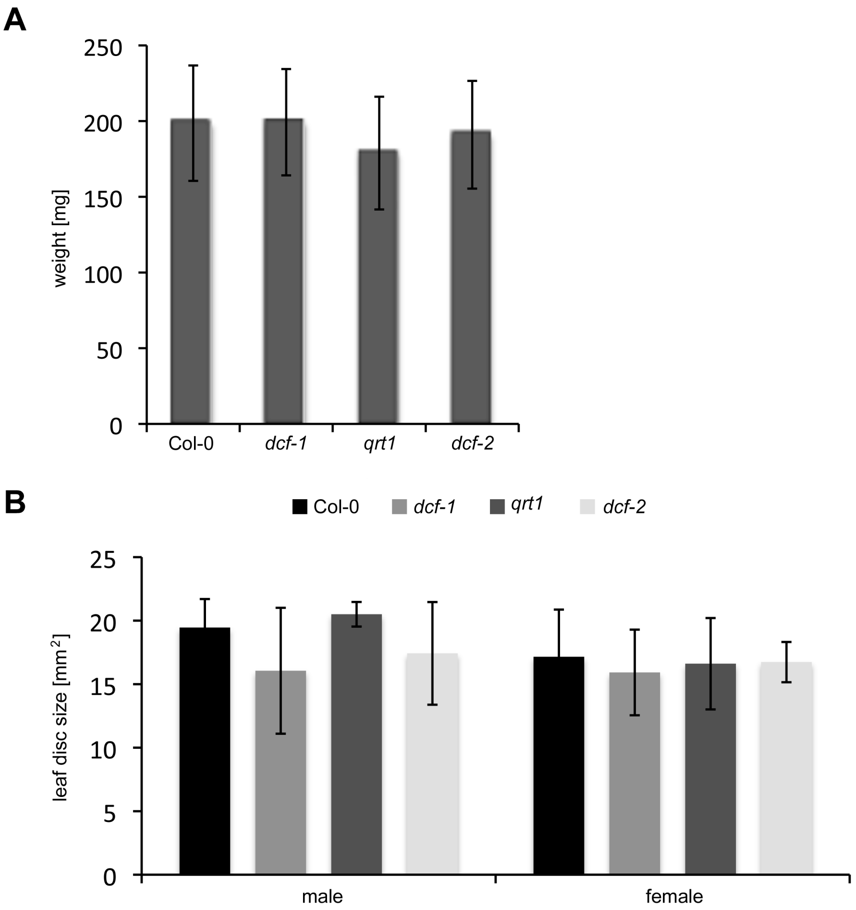
**Supplemental Figure 1.** Chlorophyll extraction from rosette leaves. Mature leaves derived from Col-0 and *qrt1* wild-type, and *dcf-1*, and *dcf-2* mutant plants were extracted with 80% ethanol. Data represent the mean ±SD of four replicates.



**Supplemental Figure 2.** Susceptibility of *dcf* mutants to fungal and bacterial pathogens.

A, Susceptibility to *Botrytis cinerea*. Mature leaves from 4-week-old plants were placed in Petri dishes containing 0.6% agar, with the petiole embedded in the medium. Inoculation was performed by placing 5 µl of a suspension of $5 \times 10^5$ conidiospores $ml^{-1}$ on each side of the middle vein. The plates were incubated at 22°C with a 12h photoperiod and lesion diameters were determined. Data represent the mean ±SD of three replicates.

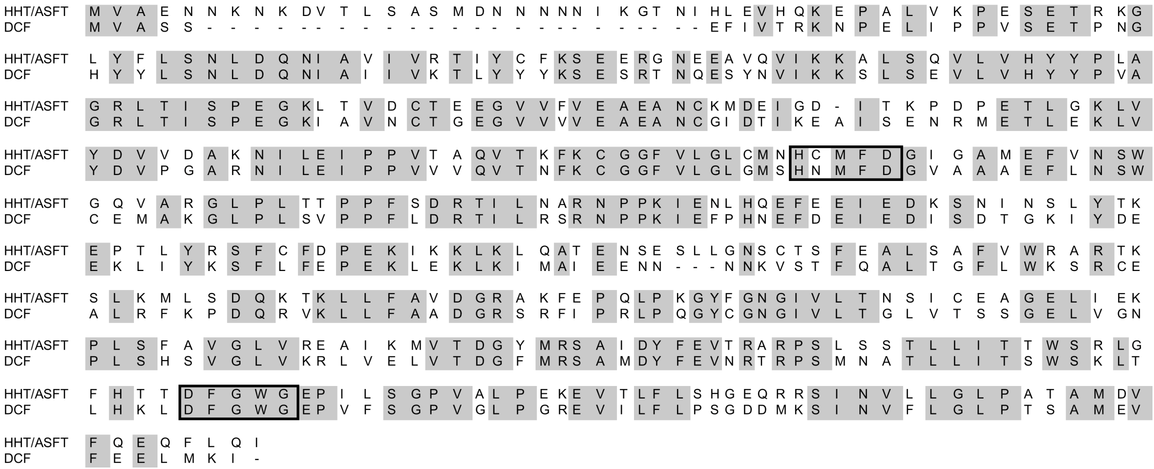
B, Susceptibility to *Pseudomonas syringae*. Fully expanded leaves were infiltrated with a diluted suspension of *Pseudomonas syringae* DC3000. At least four leaves were harvested from each genotype at each time point, surface sterilized, and the bacterial growth inside the leaves was enumerated after extraction of the bacteria by maceration of the leaves followed by direct counting of the colonies after growth in NYG medium for 2 days.



**Supplemental Figure 3.** Susceptibility of *dcf* mutants to herbivors.

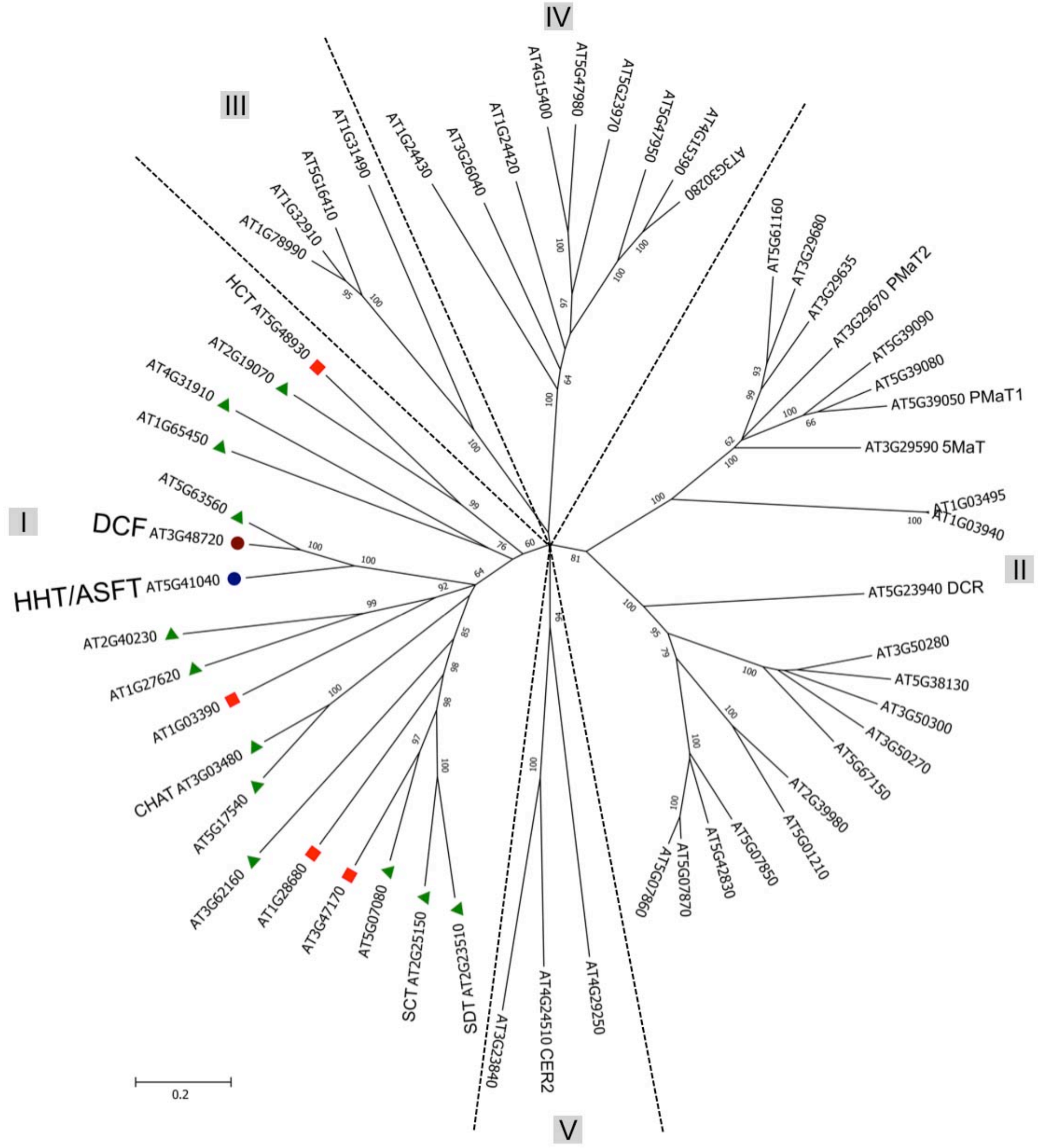
A, Feeding of white cabbage butterfly (*Pieris rapae*) larvae on Arabidopsis plants. Caterpillars were placed on a single plant two days after hatching on radish plants and weighted after seven days of feeding. Data represent the mean ±SD of ten replicates.

B, Feeding of flea beetles (*Phyllotreta nemorum*) on Arabidopsis leaf discs. Leaf discs (20 $mm^2$) obtained from *dcf* mutants and from wild-type plants were presented to adult male and female flea beetles in a choice test. Remaining leaf areas were measured after 24 hours of feeding. Data represent the mean ±SD of two replicates.



**Supplemental Figure 4.** Pairwise alignment of HHT / ASFT and DCF full-length amino acid sequences.

The BAHD family characteristic -HXXXD- and -DFGWG- motifs are framed. Identical amino acids are shaded in grey.



**Supplemental Figure 5.** Bootstrapped neighbor-joining tree of the Arabidopsis BAHD gene family of acyl-CoA dependent acyl-transferases.

The neighbor-joining tree was generated from an alignment of 56 BAHD family full-length amino acid sequences comprising the characteristic -HXXXD- motif. Assignment into major subclades (I-V) was done according to Yu et al. (2009). Green triangles within the DCF clade (I) indicate genes for those homozygous knockout mutants comprising T-DNA insertions in exon or intron seuences were identified and analyzed for wall-bound hydroxycinnamate contents. Red squares indicate genes where no insertion mutants could be identified or confirmed.