**Table S15. Mutants and insertion lines used in this study.**

| related gene | mutants/genotypes | NASC ID | mutation/insertion | background | species | citations |
|---|---|---|---|---|---|---|
| *CHS* | *tt4-11* | N2105573 | T-DNA (SALK) | Col-0 | *A. thaliana* | Alonso et al., 2003; Appelhagen et al., 2014; Buer et al., 2007 |
| *TT7/F3'H* | *tt7-1* | N88 | EMS | L*er* | *A. thaliana* | Koornneef et al., 1982; Schoenbohm et al., 2000 |
| *TT3/DFR* | *tt3-1* | N84 | x-rays | L*er* | *A. thaliana* | Koornneef, 1981; Shirley et al., 1992 |
| *TTG1* | *ttg1-1* | - | EMS | L*er* | *A. thaliana* | Koornneeff et al., 1982 |
| *TT8* | *tt8-3* | N891 | T-DNA (Versailles) | Ws-2 | *A. thaliana* | Nesi et al., 2000 |
| *TT2* | *tt2-1* | N83 | x-rays | L*er* | *A. thaliana* | Koornneef, 1981; Nesi et al., 2001 |
| *HY5* | *hy5-215* | - | EMS | Col-0 | *A. thaliana* | Oyama et al., 1997 |
| *PAP1,PAP2, PAP3,PAP4* | *myb*RNAi | - | RNAi line | Col-0 | *A. thaliana* | Gonzalez et al., 2008 |
| *PAP1* | *pap1-D* | N3884 | T-DNA (activation tagging) | Col-0 | *A. thaliana* | Borevitz et al., 2000 |
| *COP1* | *cop1-6* | N69041 | EMS | Col-0 | *A. thaliana* | McNellis et al., 1994 |

Seeds were kindly propagated and provided by several persons or ordered from ABRC (see acknowledgement) Identifiers - when available - from the Nottingham Arabidopsis Stock Centre (NASC) are given as "NASC ID".

**Table S16. Primer**

| mutants/genotypes | primer name | enzyme for dCAPS primer | primer sequence | citation for primer |
|---|---|---|---|---|
| *tt4-11* | ANS571 | - | GATCACTCATGTCGTCTTCTG | Bowerman et al., 2012, plus SALK T-DNA primer |
| | ANS572 | - | TTAGAGAGGAACGCTGTGCAAGACG | Bowerman et al., 2012, plus SALK T-DNA primer |
| *tt7-1* | ANS701 | EcoRV | CACCAAACTCAGGAGCCAAACACATGGCATATAGATAT | this study |
| | ANS702 | EcoRV | CGGTCTAGTCTTGAAATAGTGAGAG | this study |
| *tt3-1* | ANS588 | - | ATGGTTAGTCAGAAAGAGACC | this study |
| | ANS589 | - | CTAGGCACACATCTGTTGTGC | this study |
| *ttg1-1* | ANS584 | PvuII | CTGATACGCCTTTGTTAAGAC | this study |
| | ANS585 | PvuII | CAATACCAATCCAATCAGGCTGCGAAGAAGACCACTGCAGCT | this study |
| *tt8-3* | BJ05 | - | CTTGAGTTTTGGTCATGC | this study, plus Versailles T-DNA-primer |
| | BJ06 | - | GGACAACGAACAACATCG | this study, plus Versailles T-DNA-primer |
| *tt2-1* | ANS586 | - | ATGGGAAAGAGAGCAACTACTAGTGTG | Nesi et al., 2001 |
| | ANS587 | - | TCAACAAGTGAAGTCTCGGAGC | Nesi et al., 2001 |
| *cop1-6* | ANS516 | KpnI, XhoI | GACAGATATTCTGTAAAGTTGCGGATG | this study |
| | ANS513 | KpnI, XhoI | CTTTTGGAGGAGGTAACATTCTTGTAAATCATGGTAC | this study |
| *hy5-215* | ANS546 | PsiI | GTTTGAAACTTTTCGTCTAAAGTCTCTTTTATGTTTTATA | this study |
| | ANS522 | PsiI | GTAAAAATGTAAATTCAATGAATAG | this study |

For designing dCAPS primers dCAPSfinder 2.0 was used (Neff et al., 2002)

**Methods S2**

**Experiments with external standards**

Precision and linearity were analysed using ten replicates of the standard mix (500 nM). The stability in dependence of FA and time was tested in triplicates with 500 nM per substance. In all cases D3-quercetin and D3-sakuranetin at final concentrations of 400 and 5 nM, respectively, were included. For spiking experiments, 10 µl of the individual external standards were added at the following concentrations: 75 µM (extracted samples), 12 µM (non-extracted samples) for seeds and 20 µM for seedlings. External standards were combined with 100 µM D3-quercetin (extracted seed samples), 200 nM D3-sakuranetin (non-extracted seed and all seedling samples).

**LC-MS (detailed)**

A KINETEX 2.6 µm C18 100 Å (4.6 mm x 50 mm) C18 column (Phenomenex, http://www.phenomenex.com) equipped with supplier's appropriate pre column was used for all samples. For all experiments, a QC was injected at least all 10 samples flanked by MeOH samples.

LC-ESI-MS-QTRAP(MRM): 10 µl of flavonoid standard or sample were separated by HPLC (1260 HPLC, Agilent, http://www.agilent.com/home) system applying a gradient (A: 0.1 % FA in water; B: 0.1 % FA in MeOH; flow rate 500 µl $min^{-1}$) with 5 % B for 0.5 min, a 2.5 min gradient to 100 % B, maintained for 3 min and returned to 5 % B for re-equilibration resulting in a total runtime of 10 min. Eluted substances were detected in positive ion mode with multiple reaction monitoring (MRM) using a QTRAP 5500 mass spectrometer equipped with a TurboV Source (ABSCIEX, http://sciex.com). The capillary voltage was set to 5.5 kV. The collision energy was optimized (30-61 eV) for each transition. For each flavonoid species, two MRM transitions were recorded (Table S2).

LC-ESI-MS-QTOF(AutoMSMS): 10 µl of sample (if not stated otherwise) was injected into a DIONEX 3000 RSL UPLC (Thermo Fisher, http://www.dionex.com) system and separated with the following gradient (A: 0.1 % FA in water; B: 0.1% FA in MeOH; flow rate 300 µl*$min^{-1}$) starting with 5 % B for 0.1 min followed by a 4 min gradient to

100 % B, maintained for 2 min and returned to 5 % B for re-equilibration. Mass-spectra were recorded on a maXis 4G (Bruker Daltonic, www.bruker.com) equipped with an ESI source. Samples were measured in positive ion mode in the range m/z 50-1000 at 3 spectra per second, capillary voltage was set to 4.5 kV, drying gas was set to 220°C at 12 L/min and rolling collisions energy was used. MS/MS data was recorded for selected flavonoids with a signal intensity above 20,000 counts.

LC-ESI-MS-QTOF (pseudoMS³):

For pseudoMS³ determinations the same LC conditions were used as for the AutoMSMS conditions. Mass-spectra were recorded on a maXis 4G (Bruker Daltonic, www.bruker.com) equipped with an ESI source. Samples were measured in positive ion mode in the range m/z 50-1000 at 3 spectra per second, capillary voltage was set to 4.5 kV and drying gas was set to 220°C at 12 L/min. In difference to the AutoMSMS runs, in-source collision induced dissociation (ISCID) was used. ISCID energy was set to 60V - 80V. MS/MS data was recorded for selected flavonoids with a signal intensity above 20,000 counts