

## Descriptions of Additional Supplementary Files

### **Supplementary Data 1**

**Description:** List of the differentially expressed genes in the RNAseq experiment. List of the differentially expressed genes identified in the RNA-seq in root tips of wild-type (WT), *sgn3-3*, *esb1-1*, *myb36-2*, *esb1-1 sgn3-3*, *sgn3-3 myb36-2* plants. Treatment with 100 nM CIF2 was applied as indicated (+CIF2) for WT and *sgn3-3* plants. Cluster numbers refer to the clusters defined in Fig. 3a.

### **Supplementary Data 2**

**Description:** Metabolite profiling in response to the activation of the Schengen-pathway.

### **Supplementary Data 3**

**Description:** Absence of endodermal apoplastic barrier triggers major ionic changes. Elemental content in shoot of *sgn3-3*, *myb36-2* and *sgn3-3 myb36-2* mutants compared to WT using different growth conditions in agar plates (long day, n=10), in hydroponics (short day, n=6), natural soil (short day, n≥13) and compost at 80 and 60 % relative humidity (RH) (long day, n=9). Element concentration were determined by ICP-MS. Data are presented as mean ± standard deviation (SD). t tests were performed to determine the significant differences to WT for agar plates, hydroponics and natural soil. For compost, t tests were performed to determine the significant differences between 80 and 60 % RH for each genotype. The corresponding p-values are presented.

### **Supplementary Data 4**

**Description:** List of primers used for qPCR analysis