

Supplementary Figure S2. Transcription levels of *NPR1* in the barley transgenic lines wNPR1-OE and HvNPR1-Kd and the wild-type plants measured by qRT-PCR. Transcript levels are expressed relative to those of the endogenous control HvEF1a using the $2^{-\triangle CT}$ method. Each experiment, consisting of 4-11 biological replicates, was considered as a block. Calculations of the mean and standard error were performed using Microsoft Excel software. Data were transformed to restore normality, and two-sample t-test (** P < 0.01) was conducted using SAS software version 9.4.