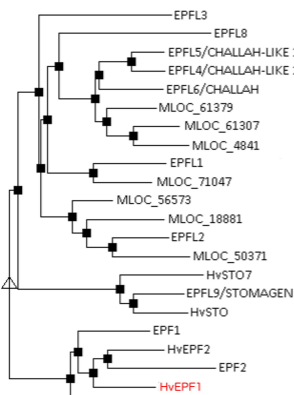
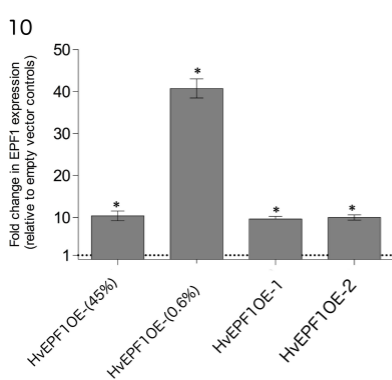
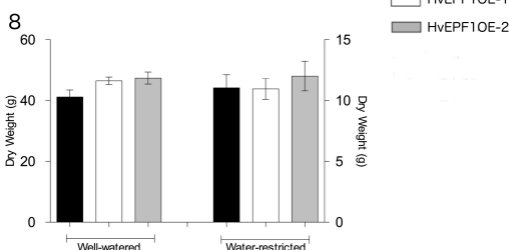
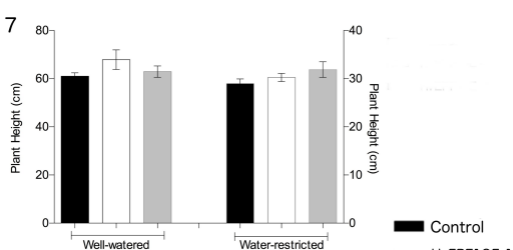
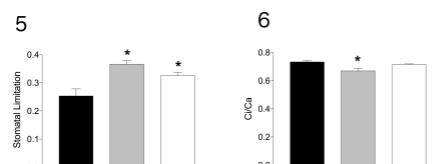
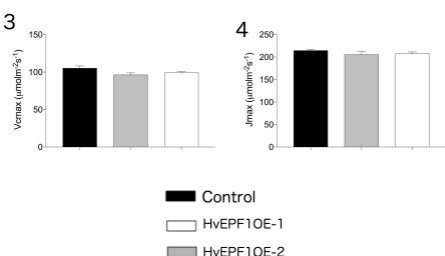


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Supplemental Figure 1. Phylogenetic tree of predicted Arabidopsis and barley epidermal patterning factor peptide sequences constructed using Maltalin. Barley annotations taken from Ensembl Plants apart from HvSto7, which is a putative unannotated EPFL9/Stomagen on Chromosome 7. HvEPF1 highlighted in red.

Supplemental Figure 2. Growth of barley plants is inhibited by the water-restricted conditions used in this study (25% soil water content) in comparison to growth in well-watered conditions (60% soil water). From left to right: Control plant well-watered, control water-restricted, HvEPF1OE-1 well-watered, HvEPF1OE-1 water-restricted, HvEPF1OE-2 well-watered and HvEPF1OE-2 water-restricted.

Supplemental Figure 3 and 4. Maximum velocity of Rubisco for carboxylation ( $V_{cmax}$ ) and the potential rate of electron transport under saturating light ( $J_{max}$ ) were obtained using the Farquhar C3 photosynthesis model and the landflux Aci curve fitting tool ([www.landflux.org](http://www.landflux.org)) as previously described (Franks et al., 2015). No significant differences were observed indicating that photosynthetic potential in the HvEPF1OE plants is unaltered.

Supplemental Figure 5. Stomatal limitation was estimated using the Farquhar graphical method. At 500ppm CO<sub>2</sub> both HvEPF1OE lines showed significantly increased stomatal limitation.

Supplemental Figure 6. Ratio of internal to atmospheric CO<sub>2</sub> concentration ( $C_i/C_a$ ) in leaves of well-watered plants. A significant reduction in  $C_i/C_a$  was observed in HvEPF1OE-1.

Supplemental Figure 7. Plant heights of controls and HvEPF1OE-1 or HvEPF1OE-2 were not significantly different within either well-watered or water-restricted conditions. Error bars represent SE.

Supplemental Figure 8. Above ground biomass of control and HvEPF1OE-1 or HvEPF1OE-2 plant lines were not significantly different under either well-watered or water-restricted conditions. N=5 plants. Error bars represent SE.

Supplemental Figure 9. Schematic of the gene expression construct inserted into the barley genome to overexpress the HvEPF1 gene.

Supplemental Figure 10. qPCR results confirming significant overexpression of HvEPF1 the barley lines detailed in the manuscript. N=5 plants, asterisk indicates significance to at least  $P < 0.05$  (Dunnnett's tests after one-way ANOVA). Error bars represent SE.