



Fig. S1. GO enriched categories in RNAseq experiment. Bubble network shows GO terms enriched among differentially expressed genes in *pep2-1*. Color represents p value, and size of the bubble represents the representation factor. Hypergeometric test Benjamini–Hochberg FDR correction. Cutoff 0.05. (A) Up regulated in *pep2-1* compared to the wild type (WT). (B) Up regulated in *pep2-1* compared to *pep1-1*. (C) Down regulated in *pep2-1* compared to the WT. (D) Down-regulated in *pep2-1* compared to *pep1-1*.







Fig. S3. The expression level of *miR156*, *AaSPL5* and *AaSPL15* does not differ between wild type and *pep2-1* plants growing in long days. Relative expression of miR156 (A), *AaSPL5* (B), *AaSPL9* (C) and *AaSPL15* (D) in wild type (WT) and the *pep2-1* mutant. Apices were harvested from WT and *pep2-1* seedlings growing for 3, 4 and 6 weeks in LDs. Asterisks stand for significant differences between WT and *pep2-1* at each time point determined by multiple pairwise comparisons using Benjamini-Hochberg-corrected p-values (α -value of 0.05). Values are the average of 2 biological replicates, error bars indicate s.d.m.



Fig. S4. *PEP2* regulates the age-dependent response of *A. alpina* to vernalization. Flowering time demonstrated as the number of days to flower emergence of 3-week-old wild type (WT), *pep1-1* mutant and *pep2-1* mutant, vernalized for 12 weeks. WT did not flower (NF). Error bars indicate s.d.m.



Fig. S4. *PEP2* regulates *AaFUL*, *AaTFL1*, *AaLFY* and *AaAP1* expression during vernalization in adult plants. Relative expression of *AaFUL* (A), *AaLFY* (B), *AaAP1* (C). 6-week-old wild type (WT) and *pep2-1* shoot apices were harvested before and during 12 weeks of vernalization. Asterisks stand for significant differences between the WT and *pep2-1* at each time point determined by multiple pairwise comparisons using Benjamini-Hochberg-corrected p-values (α -value of 0.05). Error bars indicate s.d.m.