



Figure S6 Steady state expression of *FLC* in early and late flowering allohexaploids. RNA was isolated from two late flowering (5-1-1-4; 12-19-9-1) and six early flowering allohexaploid individuals, DNase-treated, and reverse transcribed. Intron-spanning primers for *FLC* were used in RT-PCR (809 bp for genomic DNA, 266 bp for cDNA). Loading control experiments to ascertain that similar amounts of cDNA were loaded were performed with actin and tubulin (data not shown). PCR products were digested with *Clal* which uses a polymorphic site that distinguishes between *FLC* alleles derived either from *A. thaliana* or from *A. arenosa/suecica*. *Clal* digest showed that both types of alleles were expressed (data not shown). The data suggest that *FLC* expression in these non-vernalized plants is not the primary cause for the difference in flowering time.