



Supplementary Figure S4. Quantile-quantile plots comparing the observed trait-marker association scores with those expected in case of no significant association, for a GWAS based on 9,828 SNPs and 134 white lupin recombinant inbred lines performed for grain yield under moisture-favorable (Yield_NS) and drought conditions (Yield_S), onset of flowering (Flowering), and adjusted grain yield as yield deviation from the expected value according to the linear regression of yield as a function of onset of flowering.