Fig 3: Marginal plot of fold changes of expression and number of E-box

(A) Genes differentially expressed in the *ams* anther compared with wild-type anther were selected (more than two fold changes with P<0.05). The logarithm 2 ratio of fold-changes and the number of AMS binding sites (E-box) within 1kb putative promoter sequence upstream of the start codon were plotted. (B) Randomly selected genes were plotted as control.