



Figure S6: Average gene expression levels in chromatin states: Gene expression values are derived from RNA-seq data in total barley seedling ([IBGSC 2012](#)) and expressed as \log_{10} RPKM of genes in each chromatin state (see Methods). Boxplots indicate median gene expression (central box line), interquartile range (IQR; Q3-Q1) and whiskers extend to 1.5 IQR in both directions. Points are outliers with gene expression greater than $Q3 + 1.5$ IQR. Chromatin states are colour-coded as in Figures 3-5.