



Figure S7: Differential gene expression in the barley genome: DGE was calculated for HC genes using RNA-seq seedling leaf *versus* root tissue FPKM values (IBGSC 2012). Rolling averages are plotted in windows of 25 (red lines) or 250 genes (black lines). Chromatin State designations are overlaid at the top of the plots and are colour-coded as in Figure 3-5.