



Supplementary Fig. S2 Comparison of expression profiles of representative genes as measured by RNA-seq and qRT-PCR. Columns represent expression determined by qRT-PCR (left y-axis). (a-d) Relative expression was calculated using the *ACTIN* (a), *HISTONE* (b), *SAND*(c), *WL40* (d). Values represent the means \pm SE of 3 biological replicates. Lines represent expression by RNA-seq in relative to FPKM values at first sample time point (right y-axis). Circles represent 6-BA treatment group, triangle represent control group. Correlations between qRT-PCR and RNA-seq expressions were calculated and their associated *P*-values are indicated.