



**Supplementary Figure 12.** RNA-seq analysis reveals to large extent that SUMO represses transcription by CDK9 sumoylation and that MYC amplifies gene expression by antagonizing CDK9 sumoylation. (a) On the basis of RNA-seq data, the genes repressed by PIAS1/SUMO-1 were divided into genes that were not repressed and repressed by PIAS1/SUMO-1 in KO-CDK9K/R cells. The two groups of genes were further divided according to whether they were derepressed by MYC, thus resulting in four different types of genes. (b). The representative genes from each group were analyzed by qRT-PCR and the results were in general consistent with the RNA-seq data.