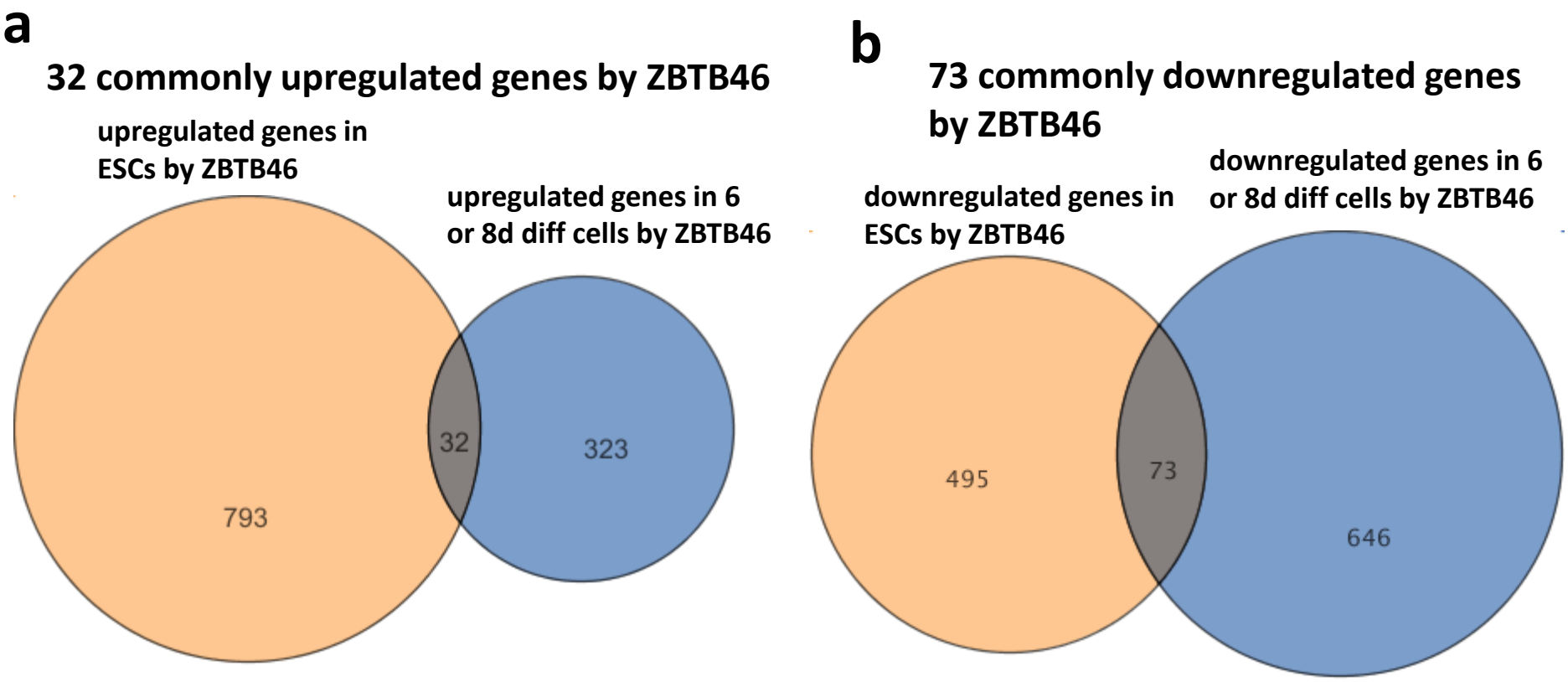

Figure S1. Venn diagrams visualizing overlap of regulated genes by ZBTB46 between the current ESC experiment and 6- or 8-day differentiated cells. (**a**) Upregulated genes. (**b**) Downregulated genes.

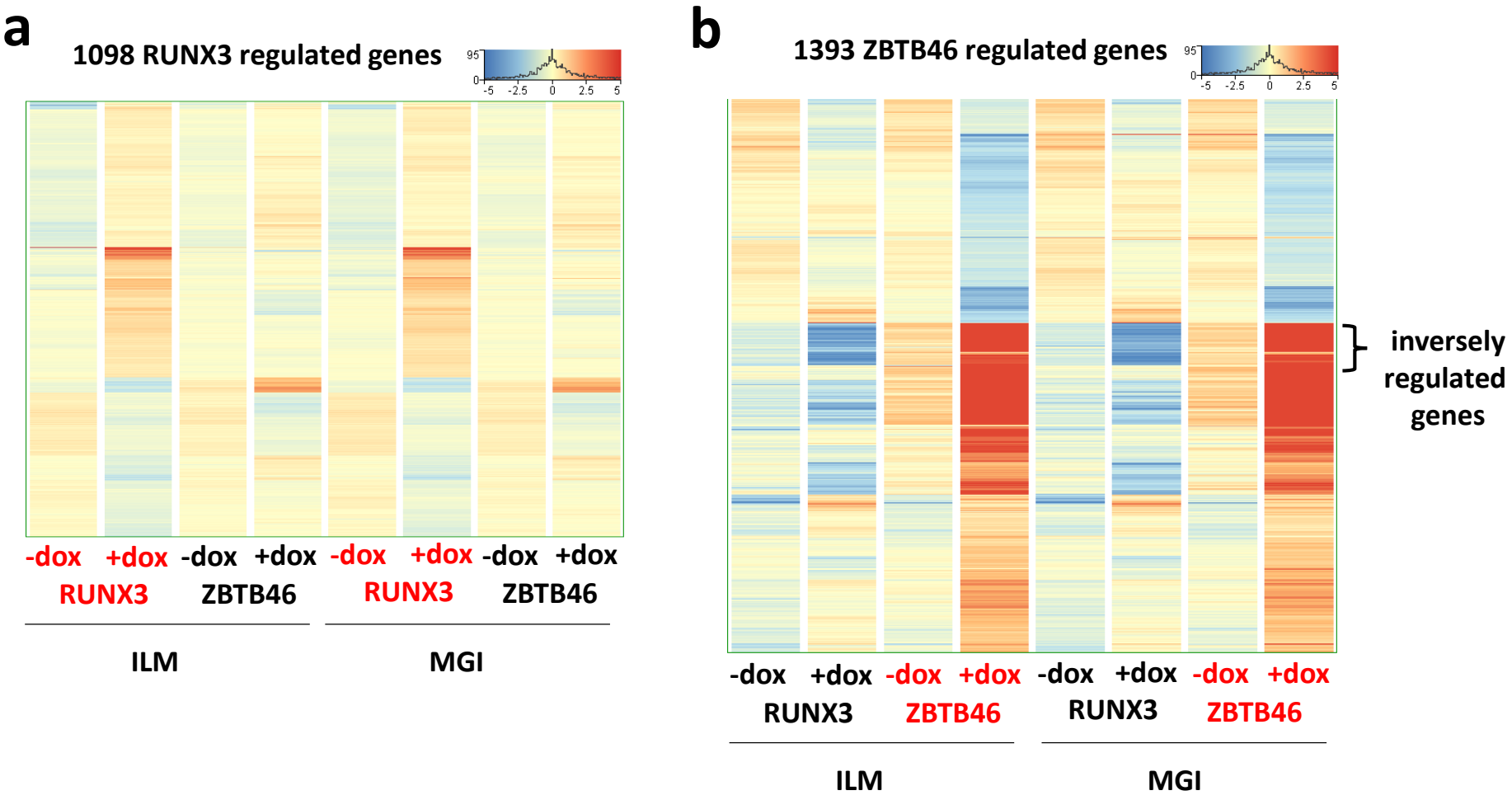

Figure S2. Heatmaps include both the RUNX3 and the ZBTB46 data obtained from the Illumina (ILM) or the MGI data sets. In these heatmaps the average expression of the four replicates are shown. Genes were hierarchically clustered. The indicated samples were treated with doxycycline (+dox) to induce *Runx3* or *Zbtb46*. (**a**) Heatmap showing normalized expression of 1098 transcripts regulated by RUNX3. (**b**) Heatmap showing normalized expression of 1393 transcripts regulated by ZBTB46. The indicated sector was oppositely modulated.

Figure S3. Principle component analysis for visualizing the MGI reagent and transgene dependent global gene expression changes. For this analysis 16 Standard- and 16 Hot-MPS samples were included and the four replicates were combined. The Hot-MPS samples were labelled with red, the Standard-MPS samples with green. The indicated samples were treated with doxycycline (+dox) to induce *Runx3* or *Zbtb46*.

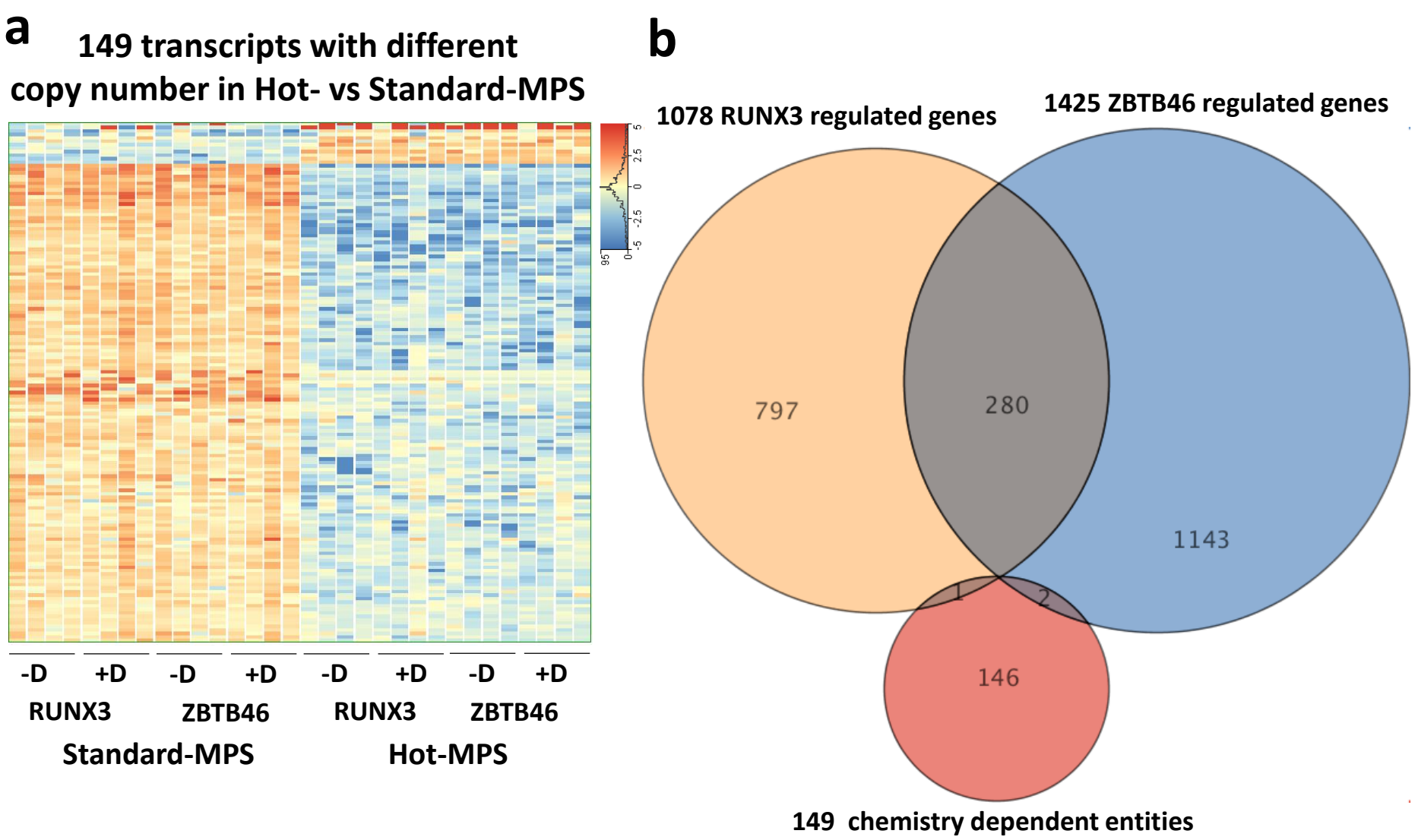

Figure S4. (**a**) Heatmap showing expression pattern of 149 transcripts which exhibited significantly different copy number comparing the Hot- to the Standard-MPS sequencing results. Genes were hierarchically clustered. Samples were derived from the RUNX3- or the ZBTB46-inducible cells. The indicated samples were treated with doxycycline (+D) to induce *Runx3* or *Zbtb46*. (**b**) Venn diagram visualizing overlap of differently expressed genes by RUNX3, ZBTB46 and the chemistry dependent gene entities.