

## **SUPPLEMENTARY FIGURE LEGENDS**

### **Figure S1. Quantification workflow**

A. Schematic flow of genome wide based quantification procedure followed by EpiMINE.

### **Figure S2. Differences in different modes of quantification, annotation of differentially regulated ROI and quantification of different ChIPs in Suz12 binding regions**

- A. Same as Figure 2C, where intensities are scaled independently for individual sample.
- B. Same as Figure 2C but with intensities scaled globally over all samples.
- C. Same as Figure 3A but without using strand information.
- D. Same as Figure 3B but without using strand information.
- E. Tissue specificity of genes whose promoters were differentially regulated in skeletal muscle identified in Figure 4A.
- F. Tissue specificity of genes whose promoters were differentially regulated in keratinocytes identified in Figure 4A.
- G. Heatmap with intensities presented for Ezh2, Ctbp2 and Suz12 in Suz12 binding regions.

## Genome Wide Based Quantification



