a

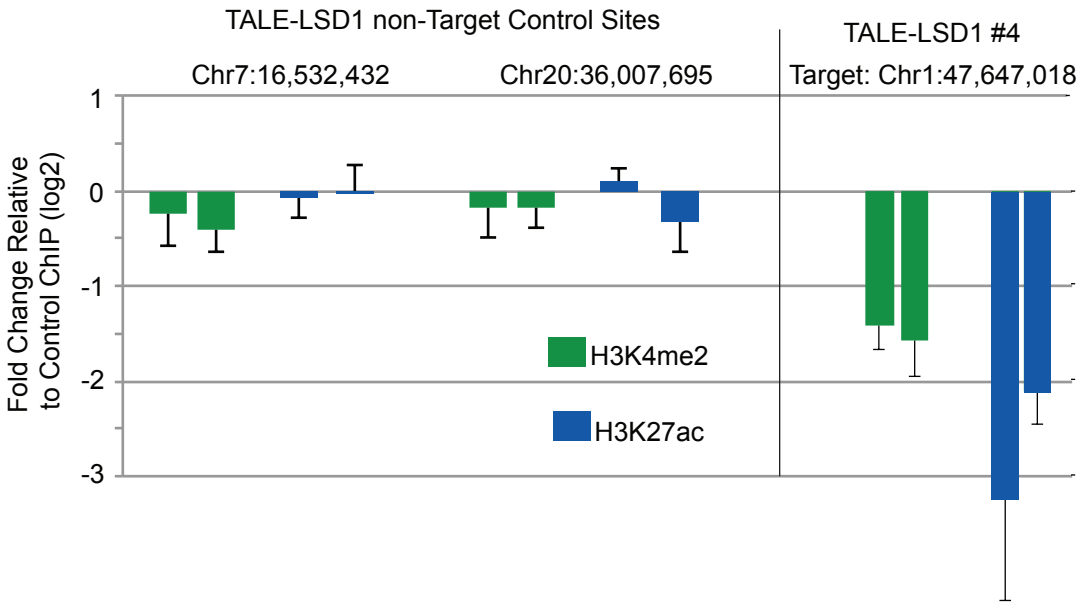
TALE-3X Flag ChIP-seq Peaks

chr location	Rep1 tags	Rep2 tags	pvalue
chr1:47,646,591-47,647,590	25	20	0.01
chr1:17,221,975-17,222,974	3	8	0.14
chr5:78,850,956-78,851,955	5	1	0.21
chr17:51,183,234-51,184,233	2	4	0.15

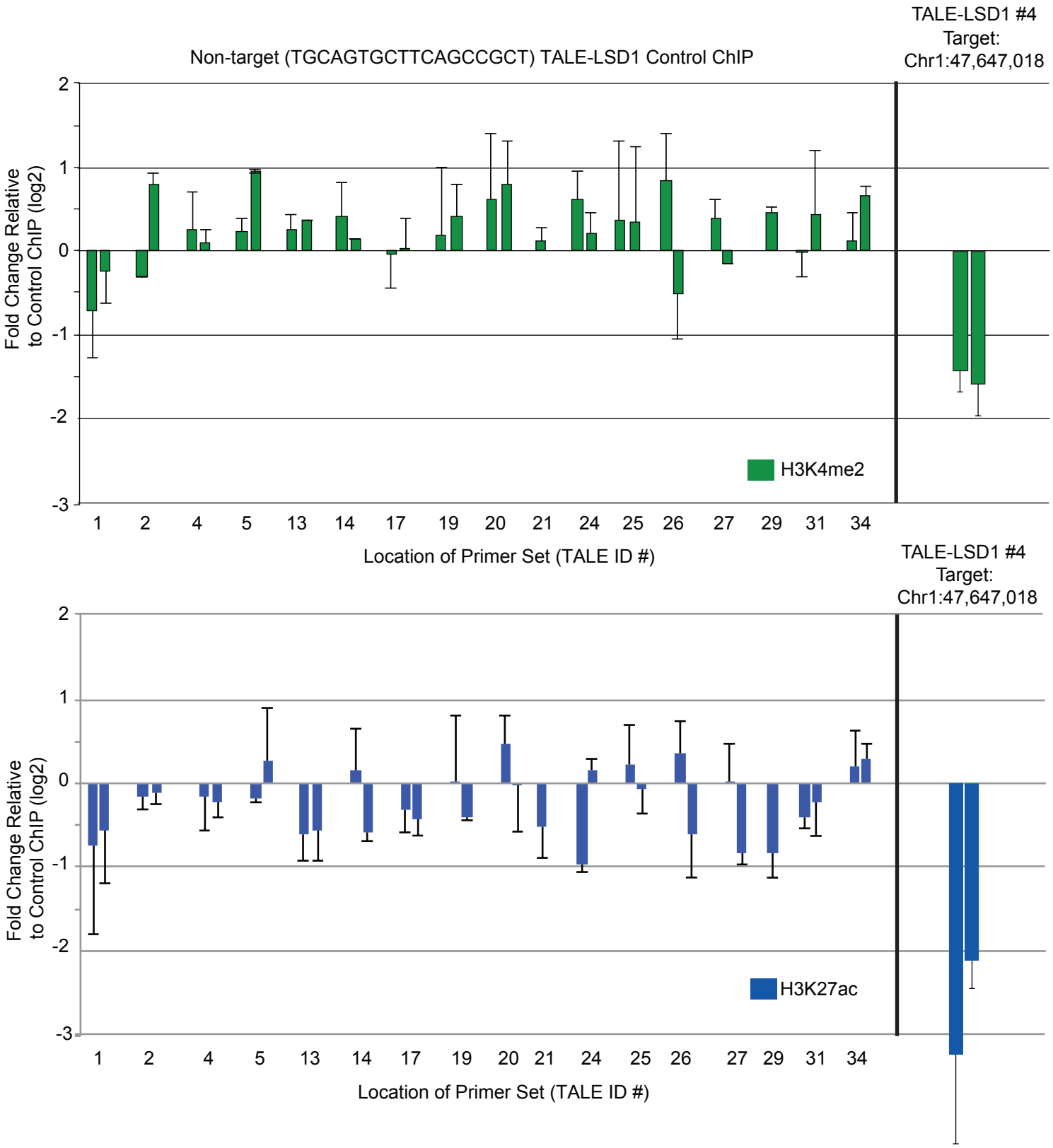
b

Target Sequence	TALE-3X Flag ChIP tags per 1kb bin	Input tags per 1 kb bin
18/18 Target (n=1)	17.5	1
17/18 Targets (n=2)	0.5	0.5
16/18 Targets (n=52)	0.40	0.58

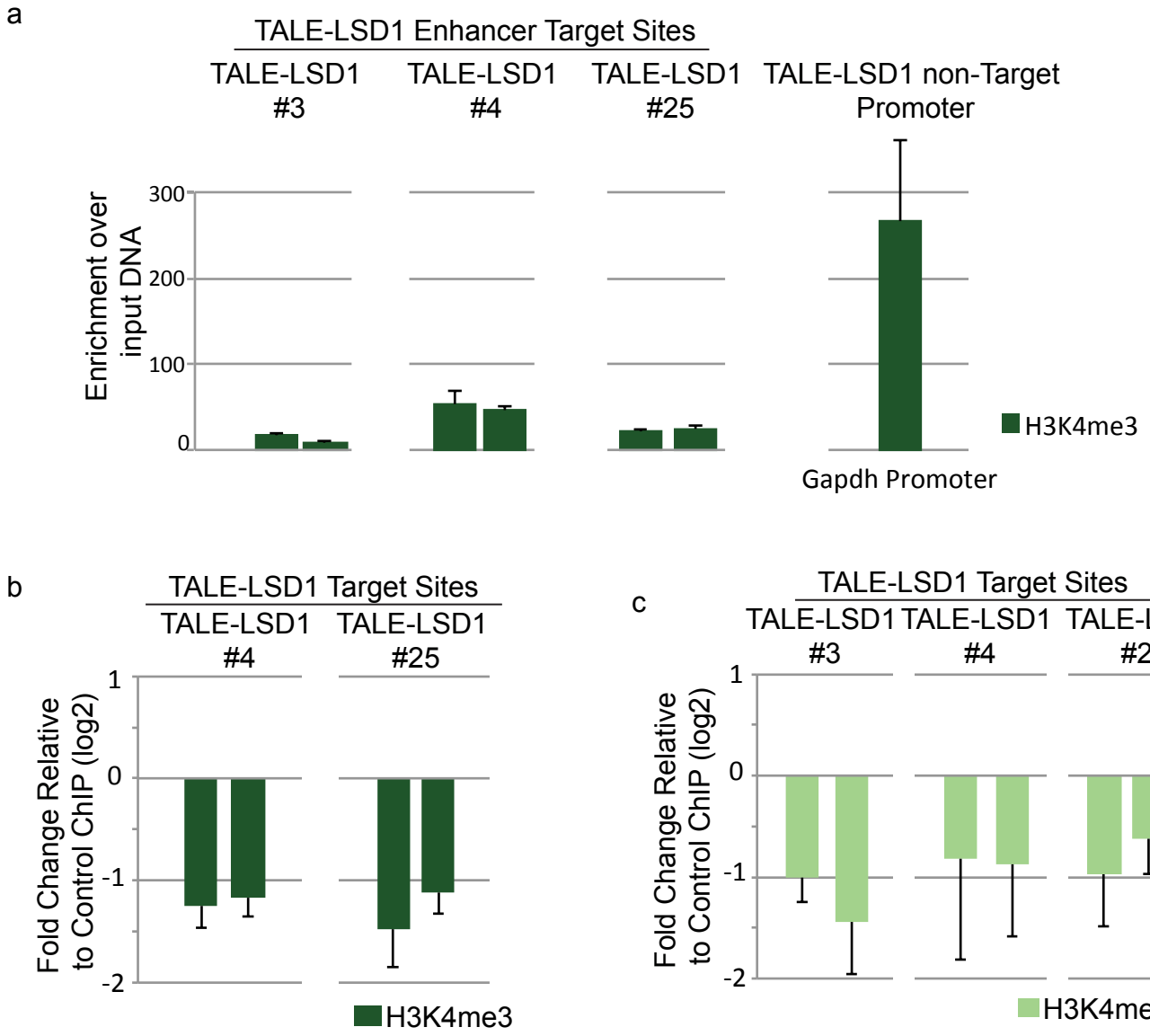
Supplementary Figure 1. Specificity of TALE binding determined by TALE-3X Flag ChIP-seq.
(a) Peak calls using MACS in two biologically independent replicates along with reads falling within a 1 kb window around the peak. Yellow shade indicates the target locus. P-values calculated by comparison of both biological replicates to the input control library.
(b) The sequence read count at 54 genomic loci with 1 or 2 mismatches compared to the perfect match target locus for the TALE-3X Flag.



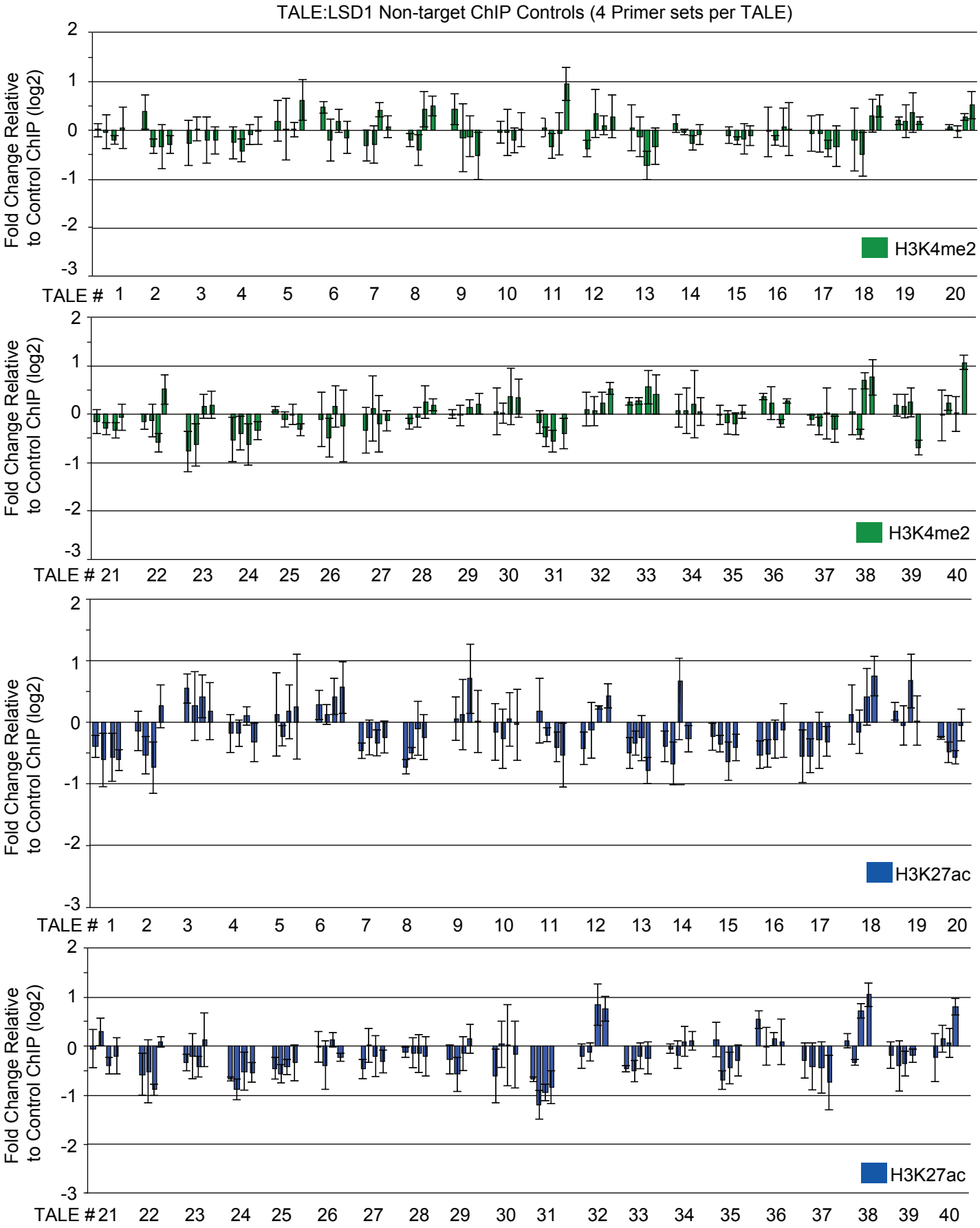
Supplementary Figure 2. ChIP-qPCR to test for off target effects of TALE-LSD1.
ChIP-qPCR for H3K4me2 (green) and H3K27ac (blue) at two non-target control enhancers. For comparision, the data from the target enhancer is shown.



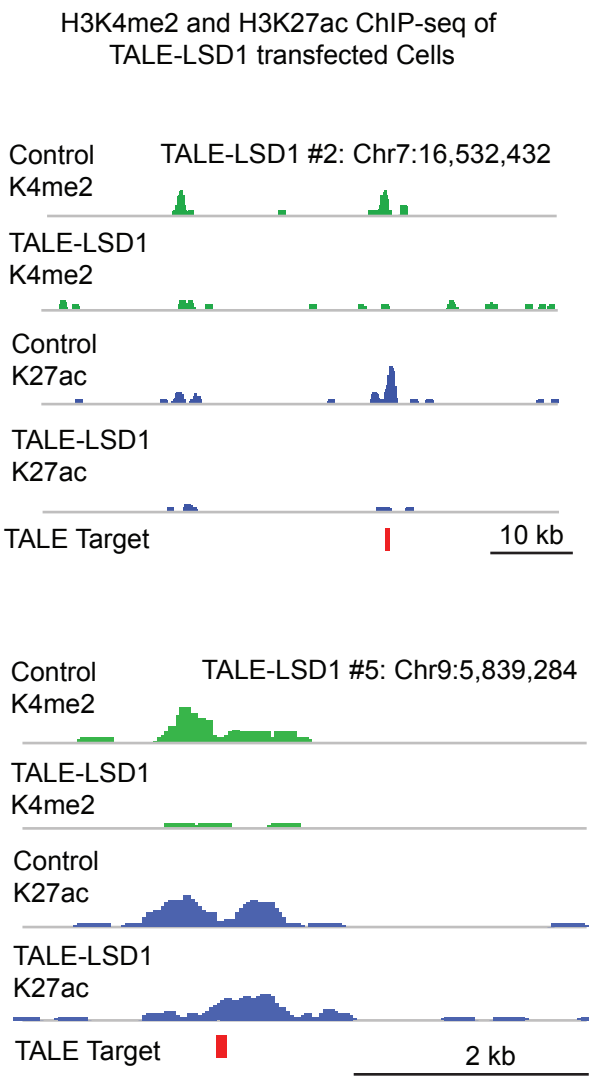
Supplementary Figure 3. ChIP-qPCR values for the non-target control TALE-LSD1.
A TALE-LSD1 construct targeting a sequence not present in the human genome was transfected into K562 cells as a control for non-specific effects. Data is shown as ratio of enrichment to mCherry plasmid control for a subset of enhancers shown in figure 2. For comparision, an 'on target' TALE-LSD1 construct at it's targeted enhancer is shown (TALE-LSD1 #4).



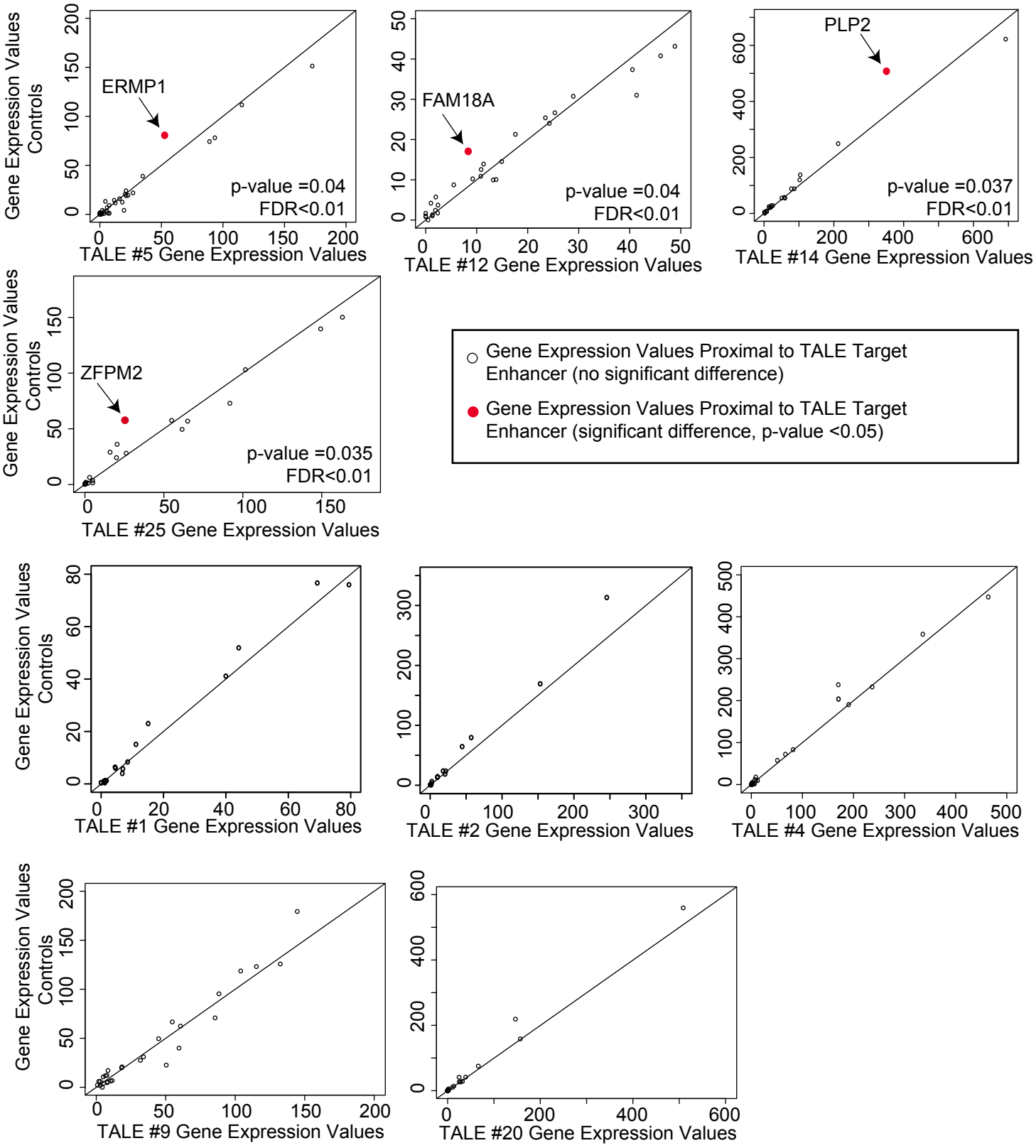
Supplementary Figure 4. ChIP-qPCR to test for effects of TALE-LSD1.
(a) ChIP-qPCR enrichment of H3K4me3 for three target enhancers, selected based on prior evidence of H4K4me3 (#4, #25) and one typical enhancer (#3) lacking K4me3. For comparision, data from a H3K4me3 enriched promoter is shown.
(b) ChIP-qPCR for H3K4me3 (dark green) at the two TALE-LSD1 targeted enhancers that showed some H3K4me3 enrichment. The data represent the decrease in enrichment at the target enhancer.
(c) ChIP-qPCR enrichment of H3K4me1 for target enhancers of three TALE-LSD1 fusions.
The data represent the decrease in enrichment at the target enhancer.



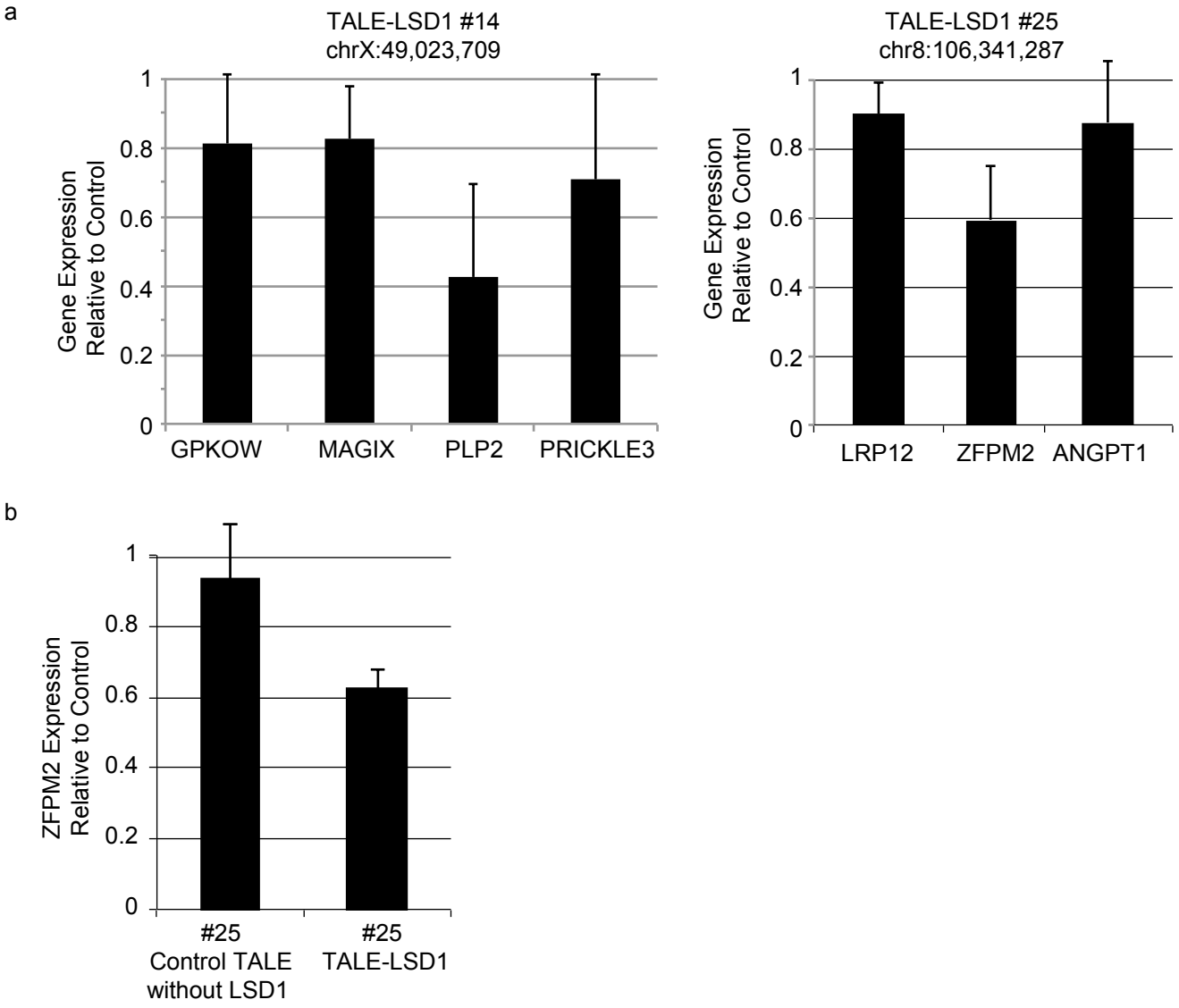
Supplementary Figure 5. ChIP-qPCR for H3K4me2 and H3K27ac at non-target sites. Data is shown for all 40 TALE-LSD1 constructs used in Figure 2. Four primers sets were used to measure ChIP enrichment at two non-target enhancer loci for each TALE construct. No non-target enhancer showed a significant decrease (>2 fold decrease in 2/4 primer sets) in ChIP enrichment.



Supplementary Figure 6. ChIP-seq maps for H3K4me2 and H3K27ac for control cells and cells transfected independently with 2 TALE-LSD1 fusions.



Supplementary Figure 7. Mean normalized 3' Digital Gene Expression Values for the 10-25 genes nearest the TALE target enhancer. Genes with values below 10 were considered unexpressed in K562 cells. Red data points represent genes with a significant decrease in the TALE-LSD1 transfected cells. Significant decrease was considered if both biological replicates represented the two outlying values across all 22 RNA-seq datasets (see Methods).



Supplementary Figure 8. Quantatitative PCR confirmation of 3' DGE. (a) RT-qPCR expression analysis for genes near two TALE-LSD1 target sites.
(b) RT-qPCR data showing gene expression for *Zfpm2* in cells transfected with a TALE #25 control plasmid that lacks the LSD1 protein, with data from the TALE-LSD1 for comparision. Error bars represent +SEM, n=2 biological replicates.