SUPPLEMENTAL MATERIAL

Shakya et al., http://www.jem.org/cgi/content/full/jem.20150363/DC1

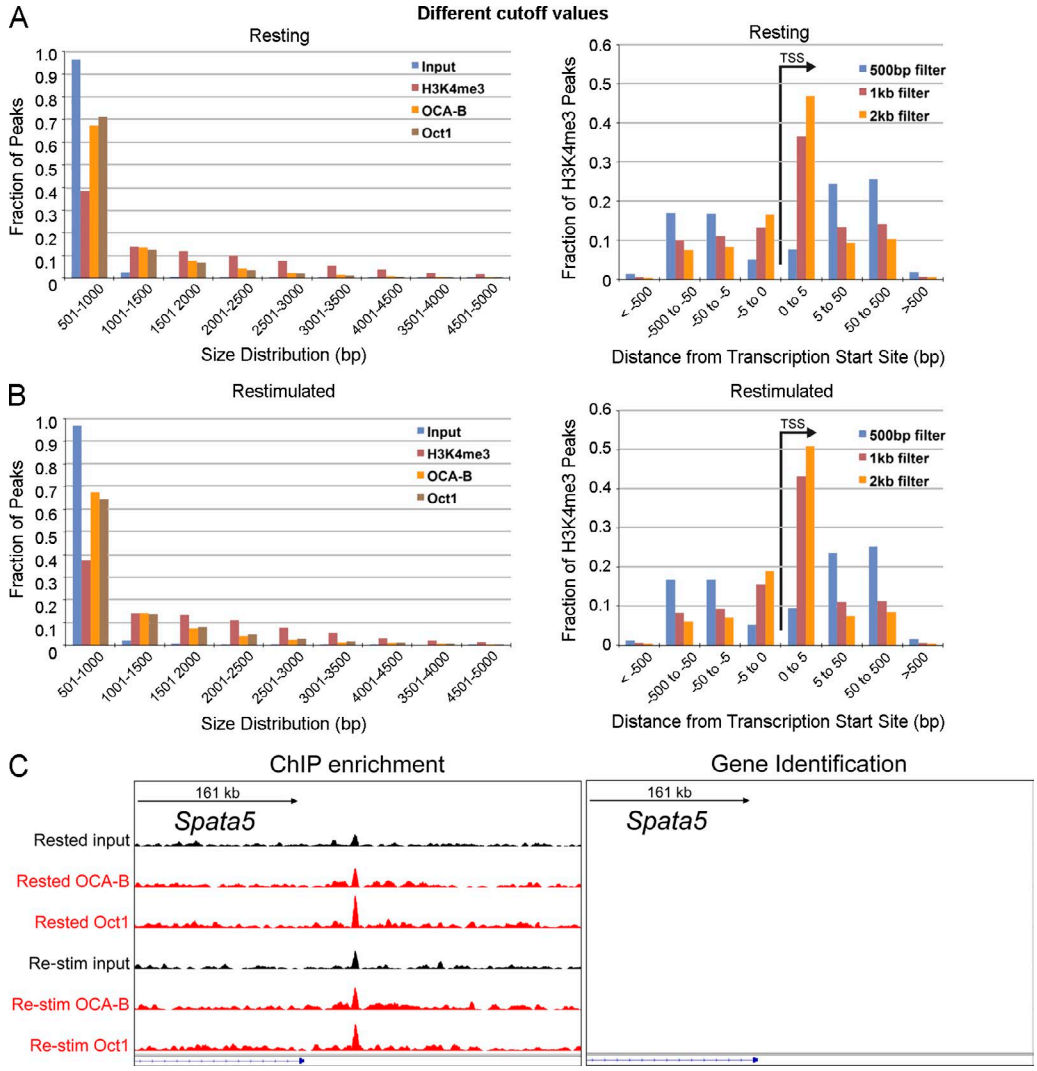

Figure S1. **ChIPseq analysis workflow.** (A) Analysis of ChIPseq enrichment using different values for peak calling comparing input with IP data. Because the longer cross-linker DSG increased the width of spurious background peaks in the ChIPseq data, peak size cutoffs higher than the commonly applied 500-bp limit were required to remove background peaks. 96% of peak calls from the input-DNA ChIPseq data were <1 kb. (B) Analysis of ChIPseq enrichment using different cutoff values in resting and restimulated cells using an H3K4 trimethyl (H3K4me3) antibody and DSG cross-linking. H3K4me3 should enrich for transcription start sites (TSSs). The best enrichment around TSSs was observed with peaks filtered at 2 kb. The OCA-B and Oct1 ChIPseq data were therefore filtered at 2 kb to remove spurious peaks presumably from the DSG cross-linking. (C) IGV images of a spurious peak (present in input) near the *Spata5* gene. Peak calling is shown on the right.

Table S1. **Numbers of offspring with the indicated genotype from *Oct1*$^{-/+}$ and *Oct1*$^{fl/+}$ intercrosses**

Genotype	Number of offspring observed (expected)
Oct1$^{-/+}$	
+/+	21 (7)
−/+	7 (14)
−/−	0 (7)
Total	28
P-value	4.4×10^{-8}
Oct1$^{fl/+}$	
+/+	15 (11)
fl/+	20 (23)
fl/fl	10 (11)
Total	45
P-value	0.38

P-values are based on χ^2 test.

Table S2, included as a separate Excel file, shows normalized RNAseq gene expression changes.
Table S3, included as a separate Excel file, shows Oct1/OCA-B target gene identification using ChIPseq.
Table S4, included as a separate Excel file, shows Gene Ontology enrichments for ChIPseq data.