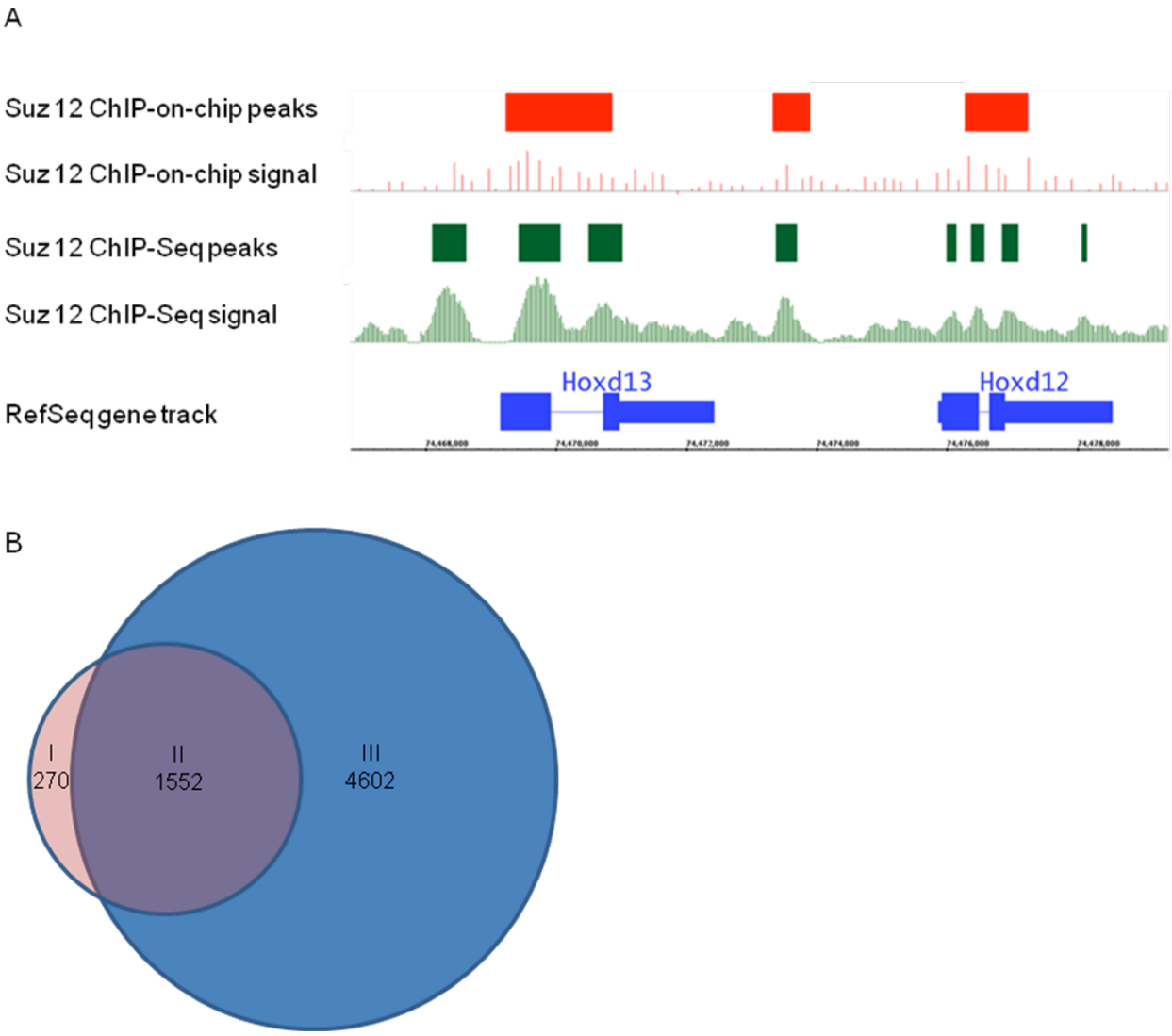
Usefulness of peak calling with ChIP-Seq experiments



Supplementary Fig S5: (A) Close up on the *Hoxd* cluster region shown in IGB (Integrated Genome Browser) for the enrichments of Suz12 ChIP-on-chip as previously described (red track), and ChIP-Seq (green track) experiments (Ku et al., 2008), respectively. For ChIP-Seq, peak detection was performed following conversion to GFF format (Perl script available for download at http://www.ciml.univ-mrs.fr/software/cocas/soft/wig2gff.pl). Main peaks (ChIP-on-chip in red blocks, ChIP-Seq in green blocks) show an overlap between both experiments. (B) Venn diagram representing overlap of ChIP-on-chip and ChIP-Seq Suz 12 peaks. I: ChIP-on-chip specific peaks, II: ChIP-on-chip and ChIP-Seq common peaks and III: ChIP-Seq specific peaks. Overlap with more than 1% between peaks was considered significant. ChIP-Seq encompasses 85% of the ChIP-on-chip peaks. Even though the amount of data generated by ChIP-Seq is extremely large due to its much higher resolution and genome-wide coverage, this shows that the peak detection algorithm is capable of handling ChIP-Seq data as efficiently as with ChIP-on-chip data.

References:

Ku,M. et al. (2008) Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains. *PLoS Genet,* 4, e1000242.