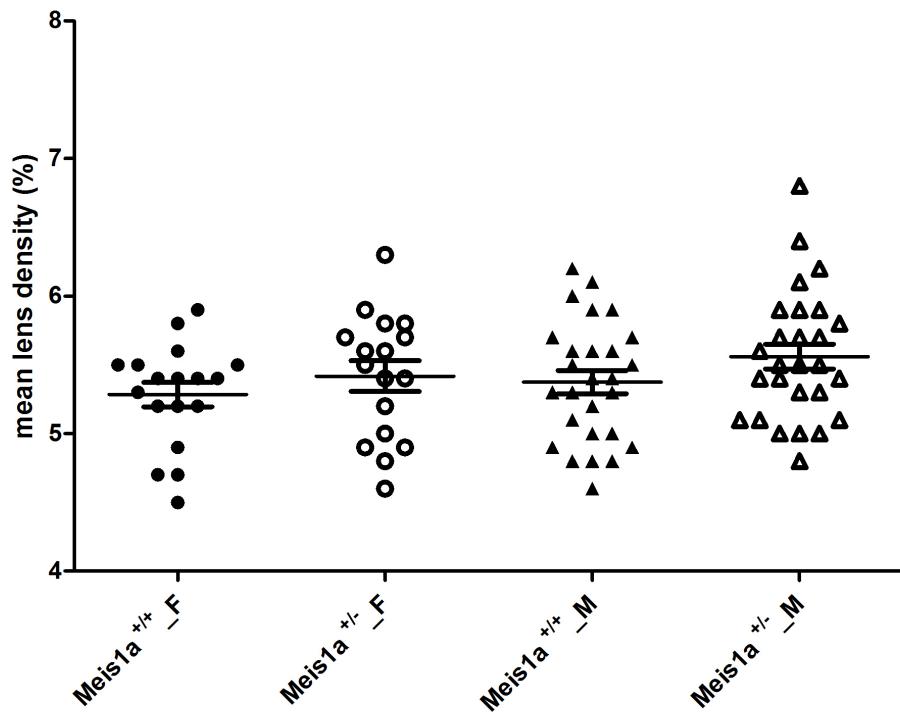
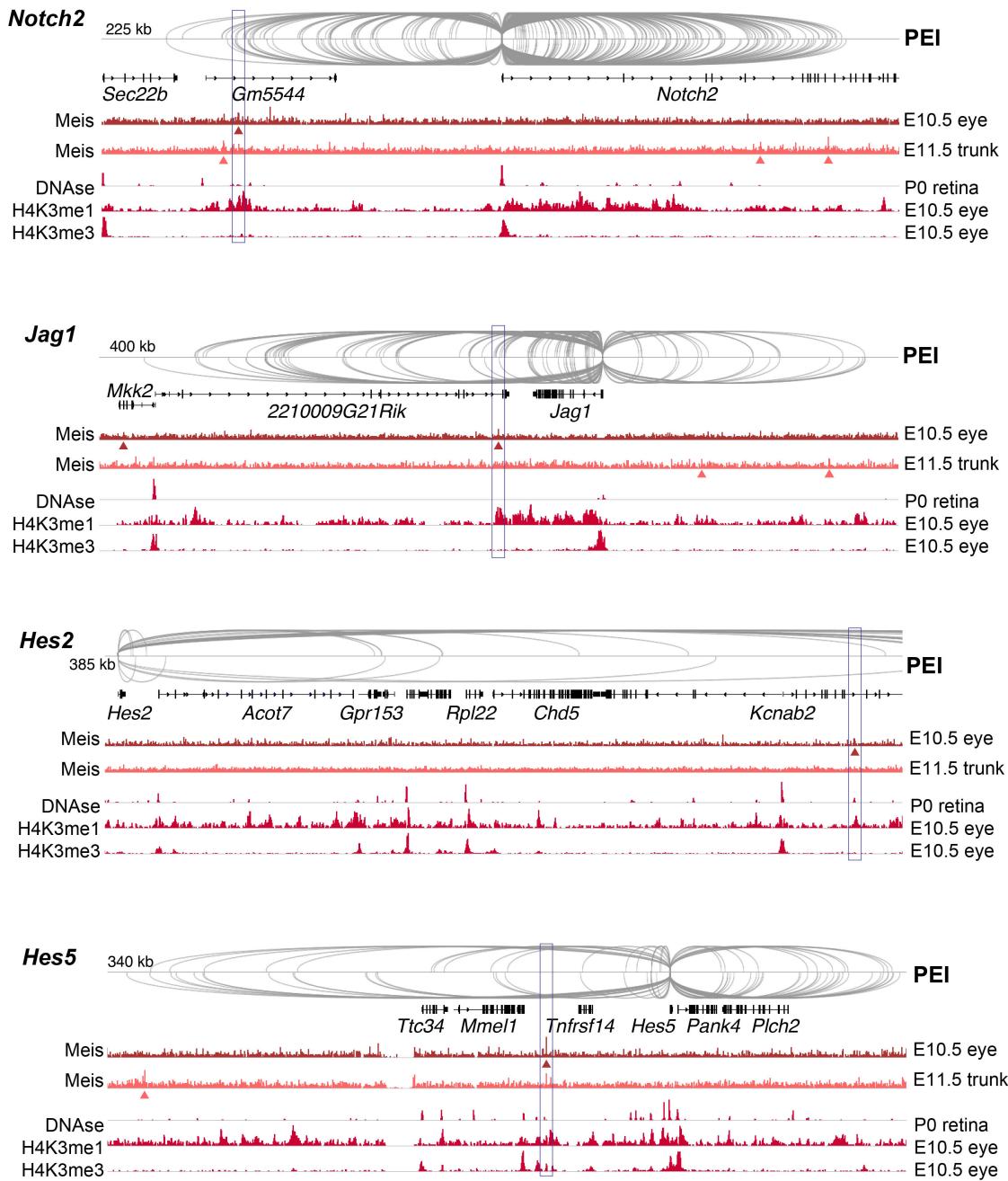


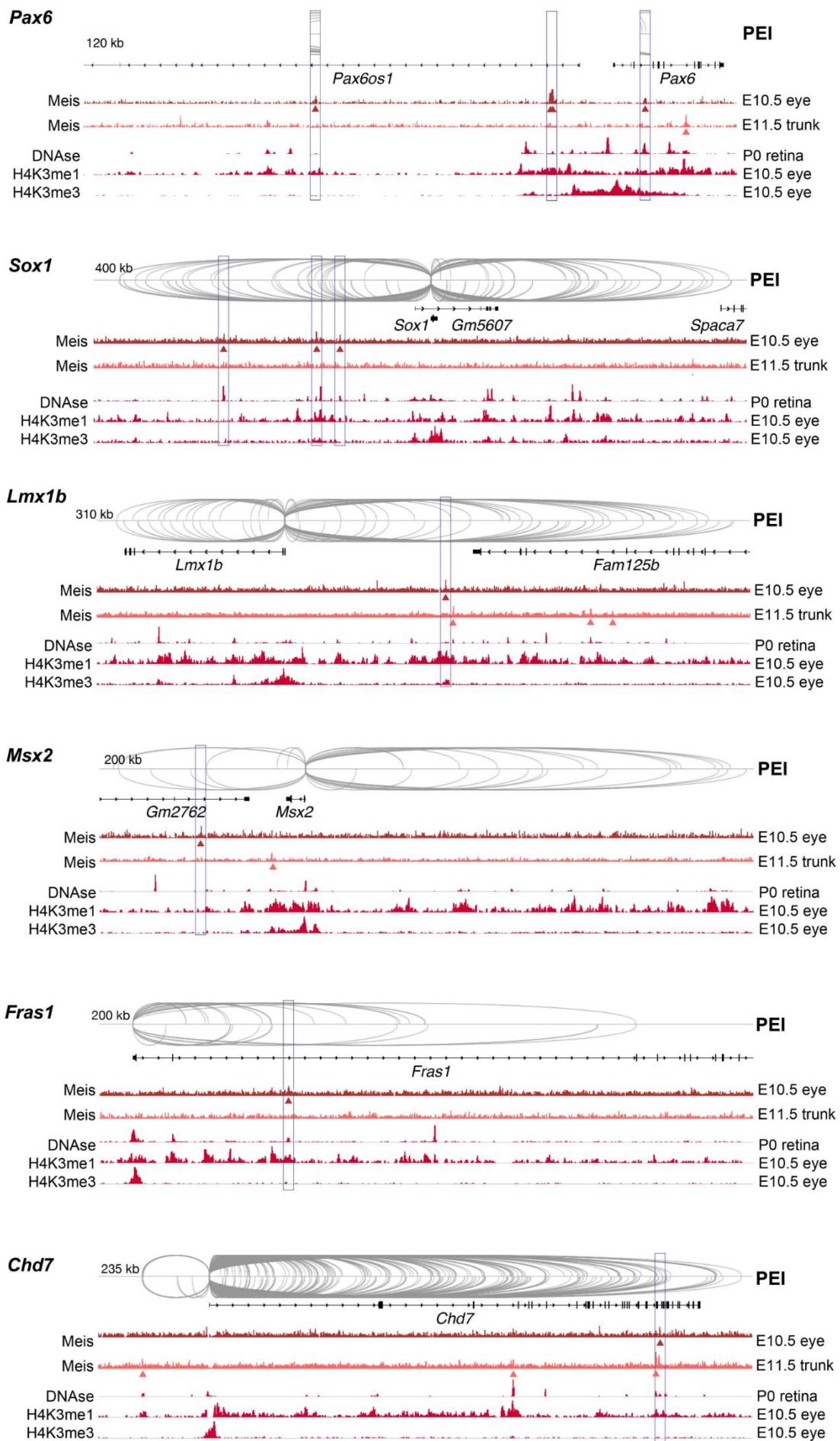
Supplementary Figure 1. *Meis1* is cell autonomously required for retinal neurogenesis. A-I) Frontal cryostat sections through the optic cup of wt, *Meis1^{+/-}* and *Meis1^{-/-}* embryos at the stages indicated in the panels stained with DAPI to determine general optic cup morphology or immunostained with antibodies against BrdU, Otx2 and Pax2. Note the decrease in eye size and BrdU incorporation in the mutants. Neuronal differentiation, marked by Otx2 expression is also strongly decreased in both heterozygous and homozygous *Meis1* mutants. Similarly, the expression of Pax2, restricted to the optic disc in wt, is extended to both the dorsal and ventral retina in *Meis1^{-/-}* embryos. This defect, although present, is less evident in *Meis1^{+/-}* optic cup. Dotted lines in the different panels delineate the extent of marker labeling Abbreviations: lv, lens vesicle; od, optic disc.



Supplementary Figure 2. Adult *Meis*⁺⁻ mice present no anterior segment abnormalities. The graph show the mean lens density, determined with a Pentacam, in male and female adult *Meis*⁺⁻ animals as compared to wt littermates. No differences were detected (mean \pm S.E.M., scatter plot).



Supplementary Figure 3. Meis binding and histone modification profiles for Notch pathway genes. Representative of the *Notch2*, *Jag1*, *Hes2*, and *Hes5* genes showing their described Promoter Enhancer Interactions (PEI) according to Shen et al. ([Shen et al., 2012](#)); the Meis1 ChIP seq read profile from E10.5 eye and E11.5 trunk ([Penkov et al., 2013](#)); the P0 DNAse-seq profile (from the ENCODE project; GEO:GSM1014188; ([Consortium, 2012](#)), and the H3K4me1 and H3K4me3 ChIP seq profiles. Detected Meis1 BS are shown by arrowheads below the read profiles. Boxes highlight the E10.5 eye Meis BS regions and their coincidence with Histone modification marks and described enhancer promoter interactions.



Supplementary Figure 4. Meis binding and histone modification profiles at microphthalmia-related genes. Representaon of the *Pax6*, *Sox1*, *Lmx1b*, *Msx2*, *Fras1* and *Chd7* genes showing their described Promoter-Enhancer Interacons (PEI) according to ([Shen et al., 2012](#)); the Meis1 ChIP-seq read profile from E10.5 eye and E11.5 trunk ([Penkov et al., 2013](#)); the P0 DNase-seq profile (from the ENCODE project; GEO:GSM1014188), and the H3K4me1 and H3K4me3 ChIP-seq profiles. Detected Meis1-BSs are shown by arrowheads below the read profiles. Boxes highlight the E10.5 eye Meis-BS regions and their coincidence with Histone modification marks and described enhancer-promoter interactions.

Table S1. Genes upregulated in *Meis1* knockout

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Table S2. Genes downregulated in *Meis1* knockout

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