Supplementary Figures

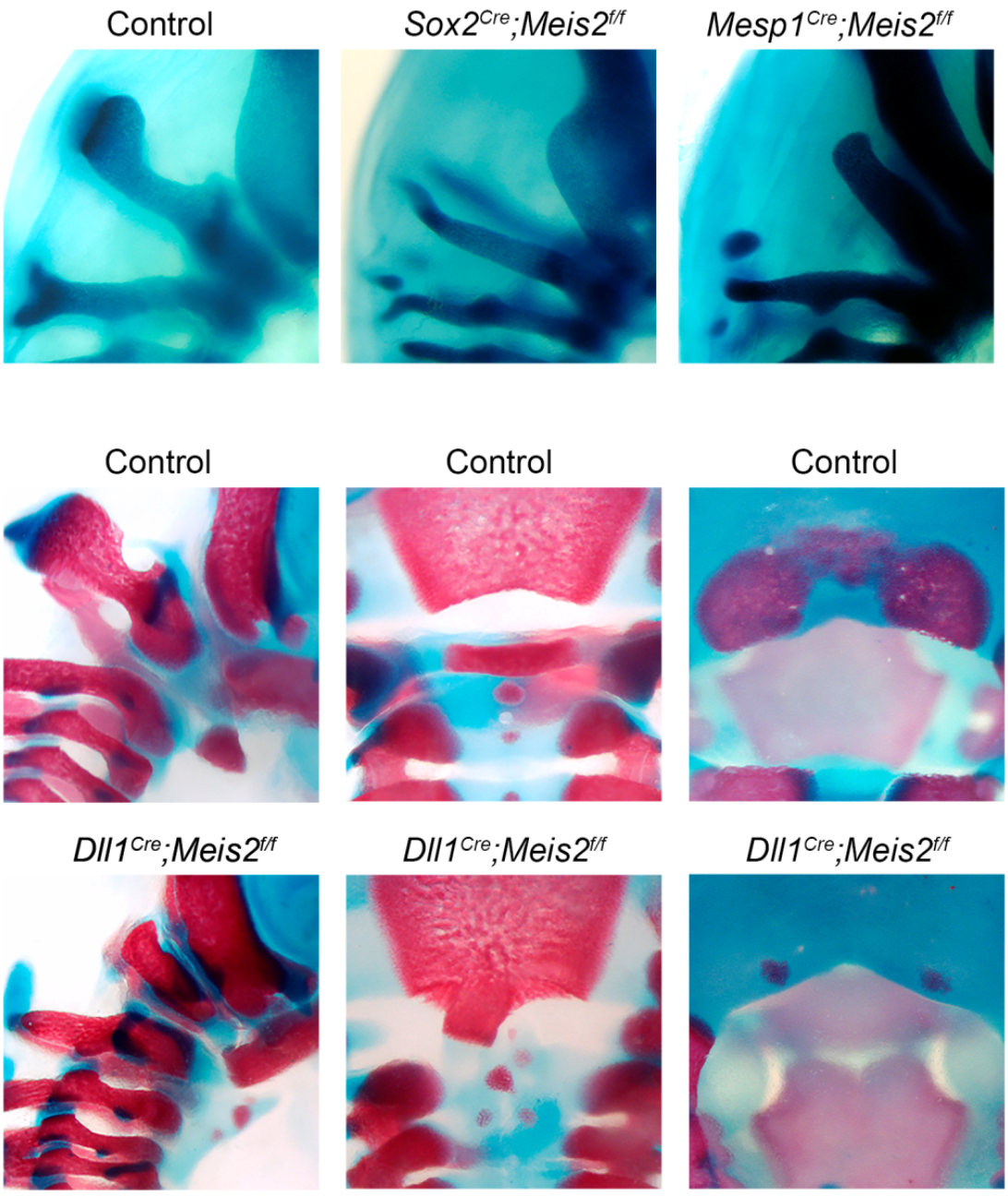

Figure S1. Magnified views (3.3X) of the specimens shown in Figure 2

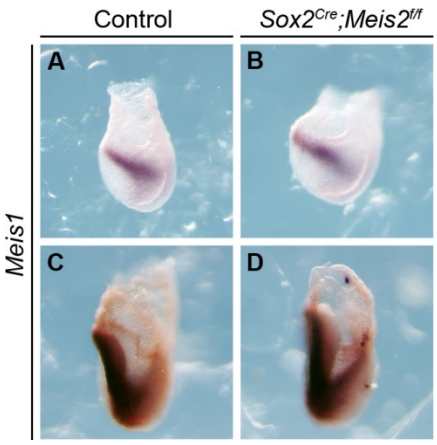

Figure S2. *Meis1* mRNA *in situ* hybridization in control and *Sox2*^{Cre};*Meis2*$^{f/f}$ embryos. (A and C) Control embryos at E7.5 and E8, respectively. (B and D) *Sox2*^{Cre};*Meis2*$^{f/f}$ embryos at E7.5 and E8, respectively.

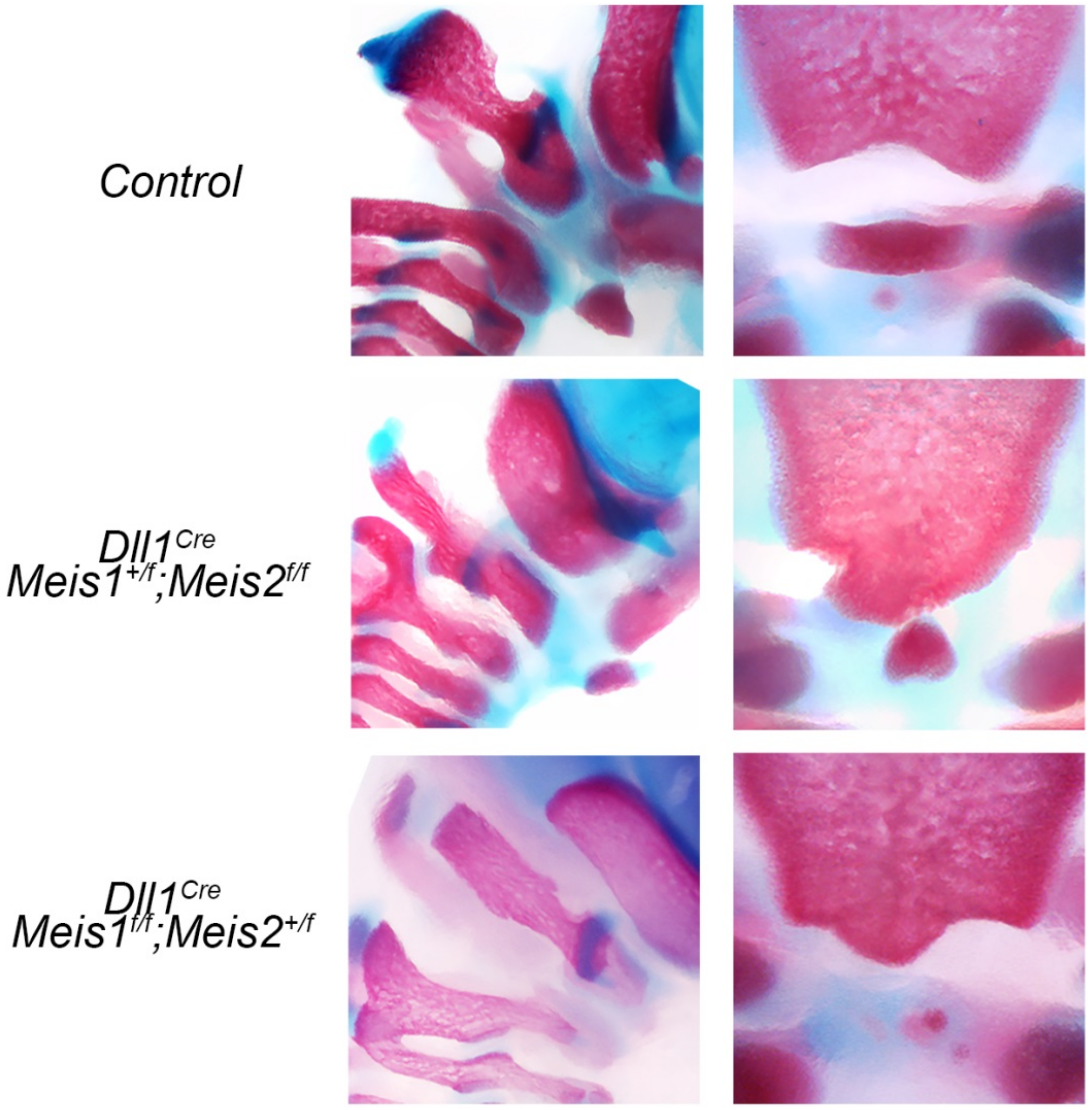

Figure S3. Magnified views (3.3X) of the specimens shown in Figure 3

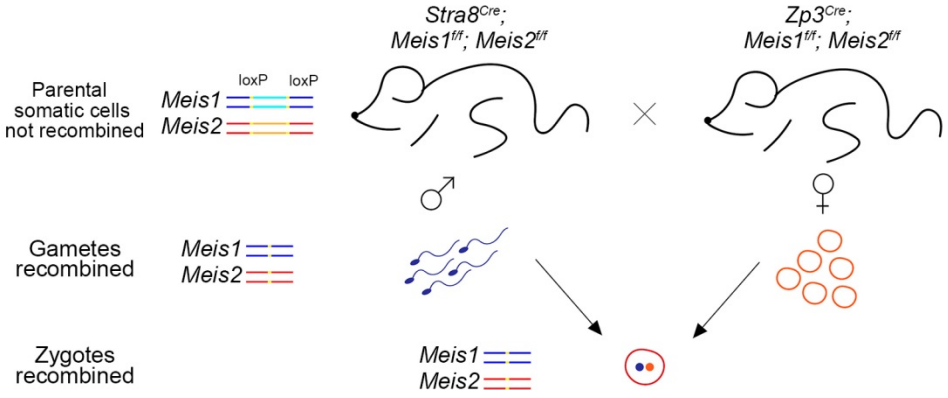

Figure S4. Schematic representation of crosses using biparental germ line Cre recombination to obtain complete zygotic elimination of *Meis1* and *Meis2*. *Meis1*$^{f/f}$;*Meis2*$^{f/f}$ males and females respectively carrying *Stra8*^{Cre} and *Zp3*^{Cre} alleles only recombine floxed alleles in the germ line. Parental mice are viable while their progeny is double-knockout from the zygotic stage.

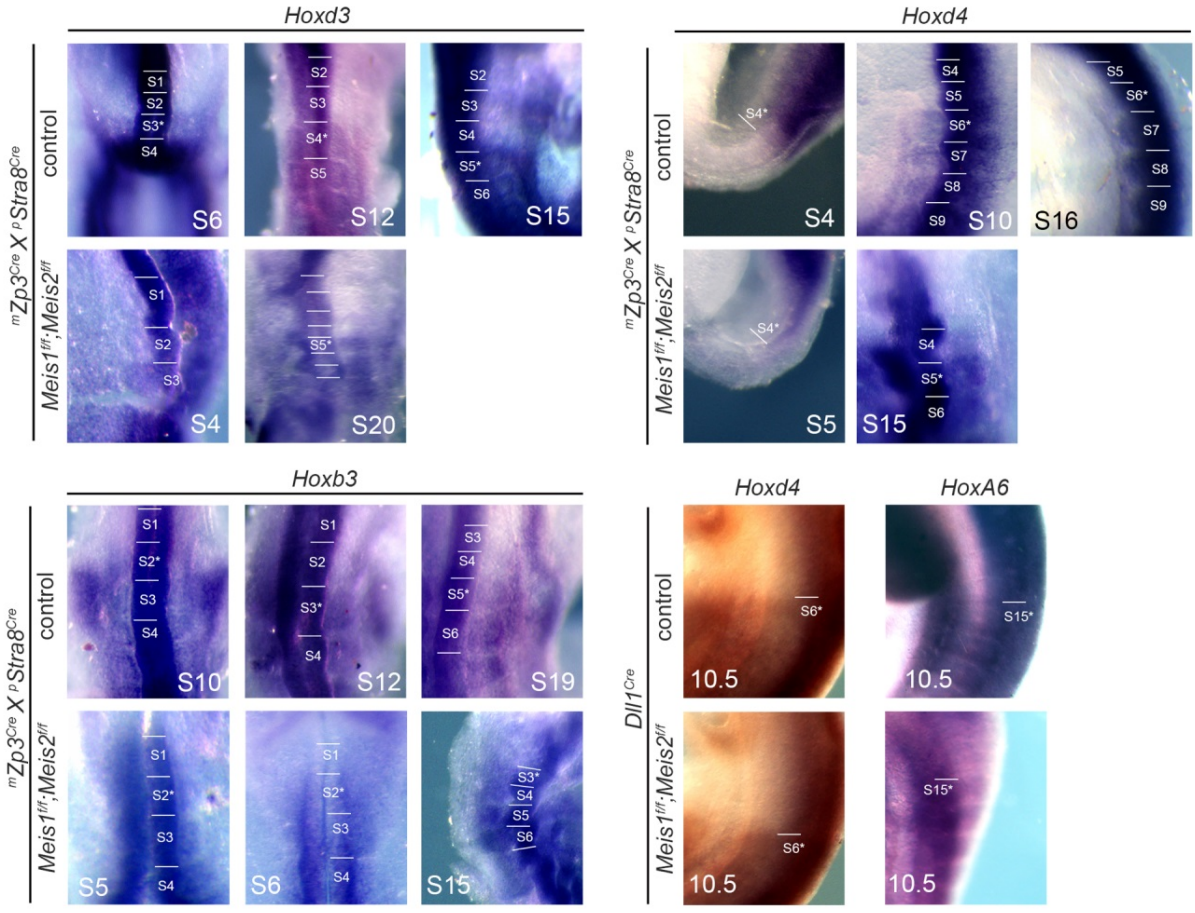

Figure S5. *Hox* gene mRNA expression patterns in *Meis* loss-of-function mutants mRNA *in situ* hybridization of the indicated *Hox* genes in control and *Meis2* conditional mutant embryos. The Cre recombination strategy is indicated to the left of the panels. The stage is indicated by the number of somites or day of development within each image. The visualized somites are indicated by S# and delimited by white lines. The first somite in which expression is clearly found is indicated with asterisks.

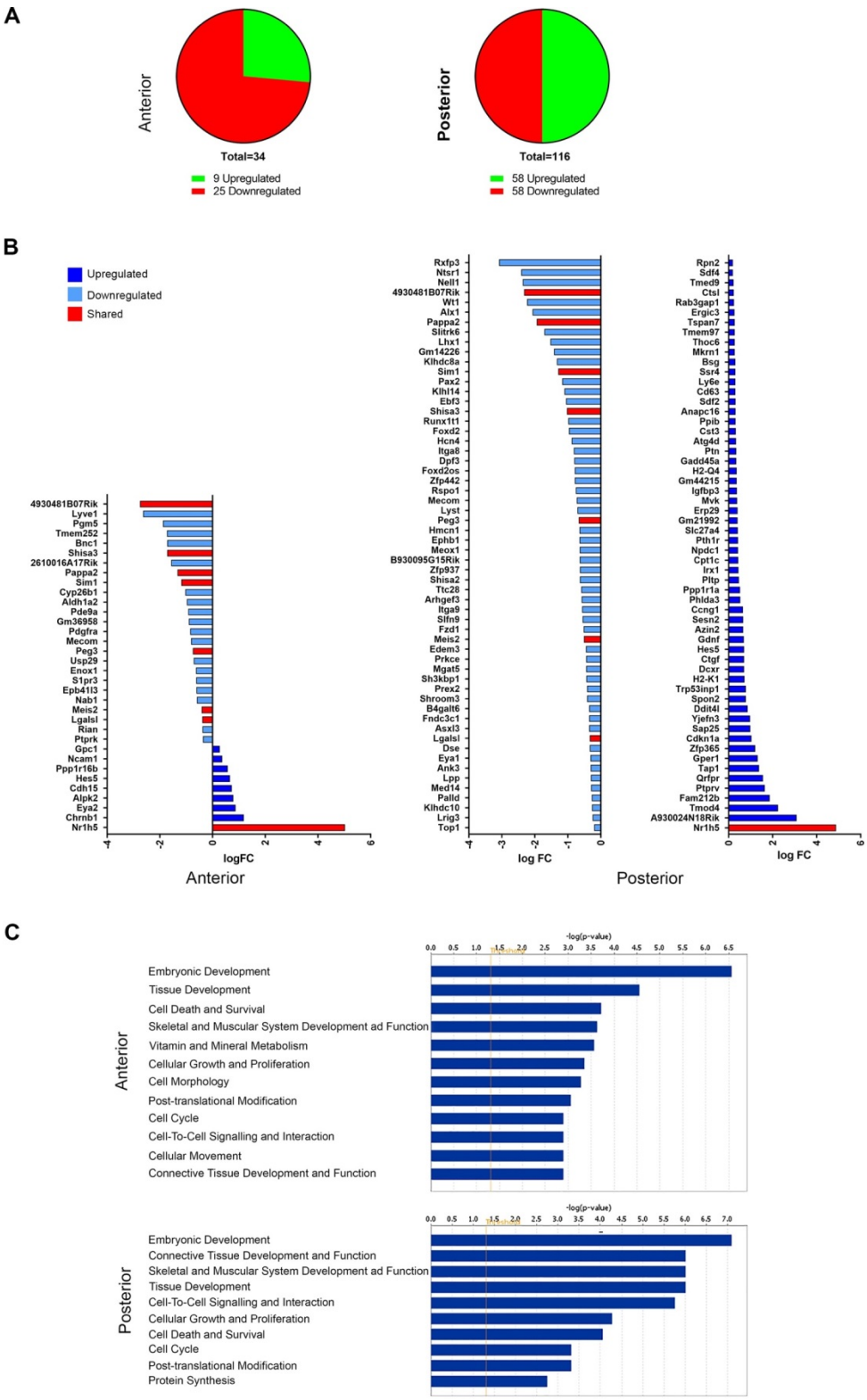

Figure S6. Comparative transcriptomic analysis of *Dll1^{Cre};Meis1$^{f/f}$;Meis2$^{f/f}$* and control embryos at E9.

(A) Representation of the number of genes differentially expressed in both anterior and posterior samples (adjusted p-value ≤ 0.05). (B) Fold change representation (adjusted p-value ≤ 0.05) from anterior and posterior samples (upregulated and downregulated genes are colored in dark and light blue, respectively). Genes colored in red are differentially expressed in both, anterior and posterior. (C) Functions affected in *Dll1^{Cre};Meis1$^{f/f}$;Meis2$^{f/f}$* embryos from the Ingenuity Pathway analysis in anterior and posterior regions.

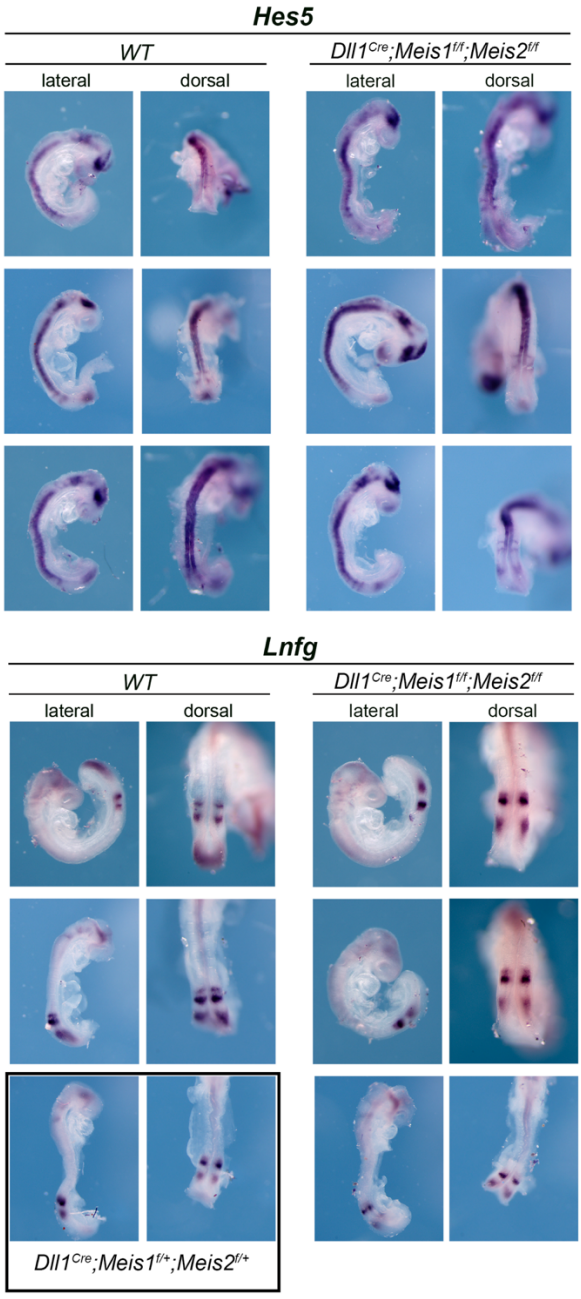

Figure S7. Expression of segmentation clock genes. (A-C) *In situ* hybridization of *Hes5* and (D-F) *Lnfg* in Control and *Dll1*^{Cre}*;Meis1*$^{f/f}$*;Meis2*$^{f/f}$ at E8.5. Dorsal view of the posterior bud of the embryos is shown in the bottom right of each image.

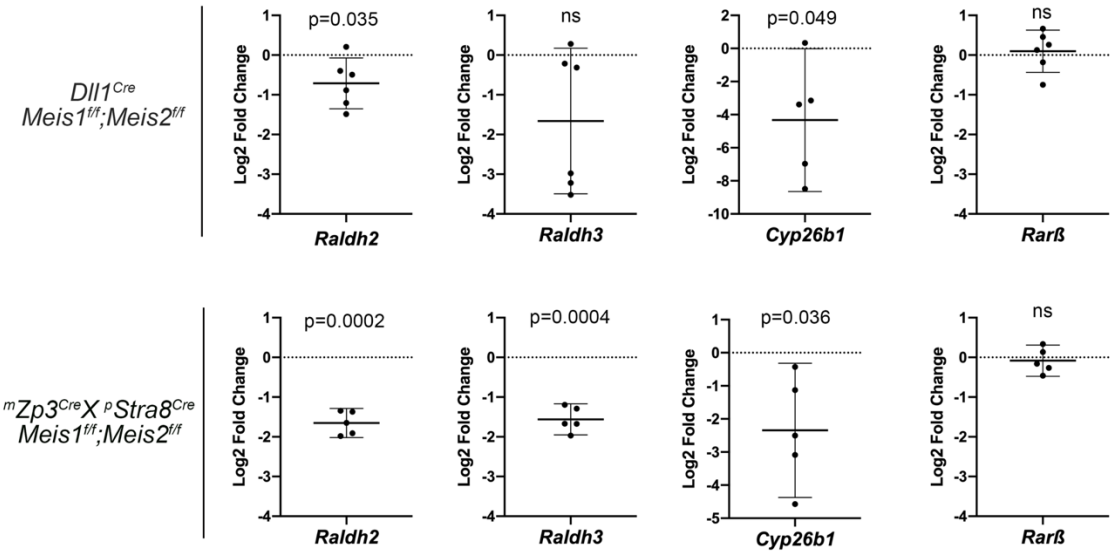

Figure S8. Expression analysis of retinoic acid pathway genes in *Meis* mutants. Graphs show log2 of mRNA fold change measured in individual embryos for *Raldh2*, *Raldh3, Cyp26b1* and *Rarß*, deduced from quantitative reverse-transcription PCR comparing control embryos with *Dll1*^{Cre};*Meis1*$^{f/f}$;*Meis2*$^{f/f}$ or *Meis1*$^{f/f}$;*Meis2*$^{f/f}$ embryos derived from ^{m}*ZP3*^{Cre} x ^{p}*Stra8*^{Cre} crosses. Embryos and controls were matched for somite stage, which were 20-24 somites for the experiments with the *Dll1*^{Cre} driver and 14-18 for the experiments with the maternal/paternal recombination strategy. Each dot in the graph represents the difference of individual mutant embryos to their somite-matched controls. Graphs show the 95% confidence interval of the mean and the significance measured using a 1-sample t-test for deviation of the mean from 0.

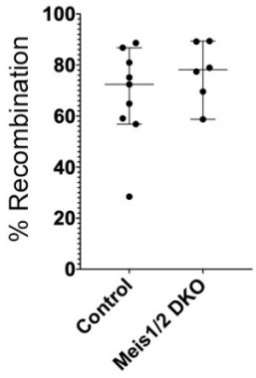

Figure S9. Frequency of recombination induced by *Dll1*^{Cre} in the paraxial mesoderm. The graph shows the frequency of recombined cells measured in the 3 newly formed somites of E8.5-E10.5 *Dll1*^{Cre};*Rosa26R*^{Tomato} embryos wild type for *Meis1* and *Meis2* (controls) or carrying the *Meis1*^{f} and *Meis2*^{f} alleles in homozygosity (*Meis1/2* DKO). Graphs show individual measurements, the median and its 95% confidence interval.

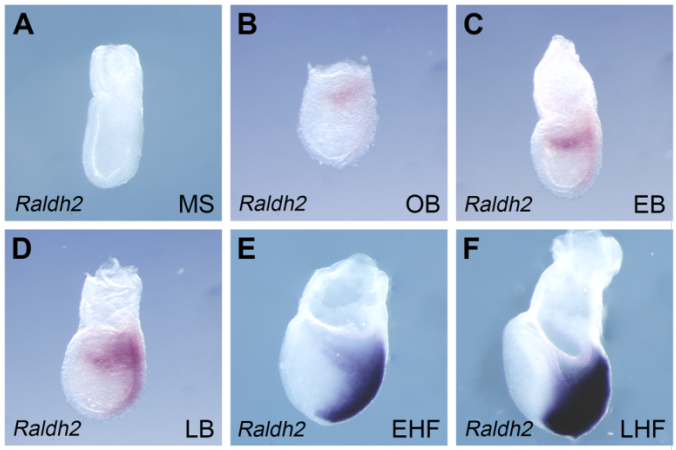

Figure S10. *Raldh2* expression pattern in early embryo.
(A-F) Whole-mount mRNA *in situ* hybridization of *Raldh2* from E7 to E7.75. MS, mid-streak; OB, no allantoid bud; EB, early allantoid bud; LB, late allantoid bud; EHF, early headfold; LHF, late headfold. All images are oriented with the anterior to the left.

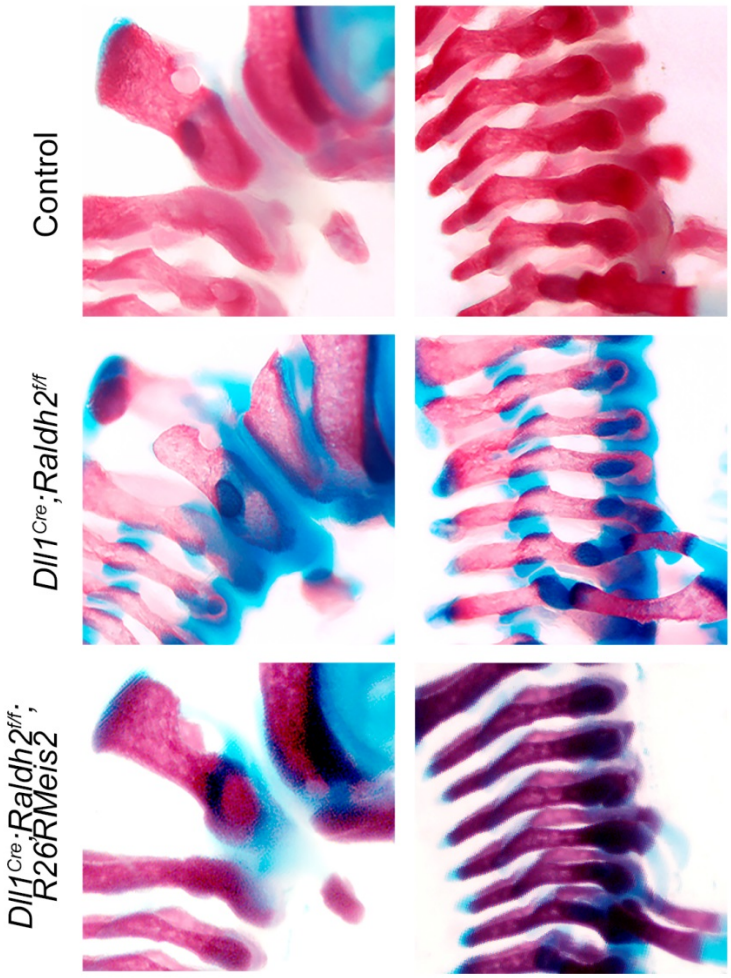

Figure S11. Magnified views (3.3X) of the specimens shown in Figure 7

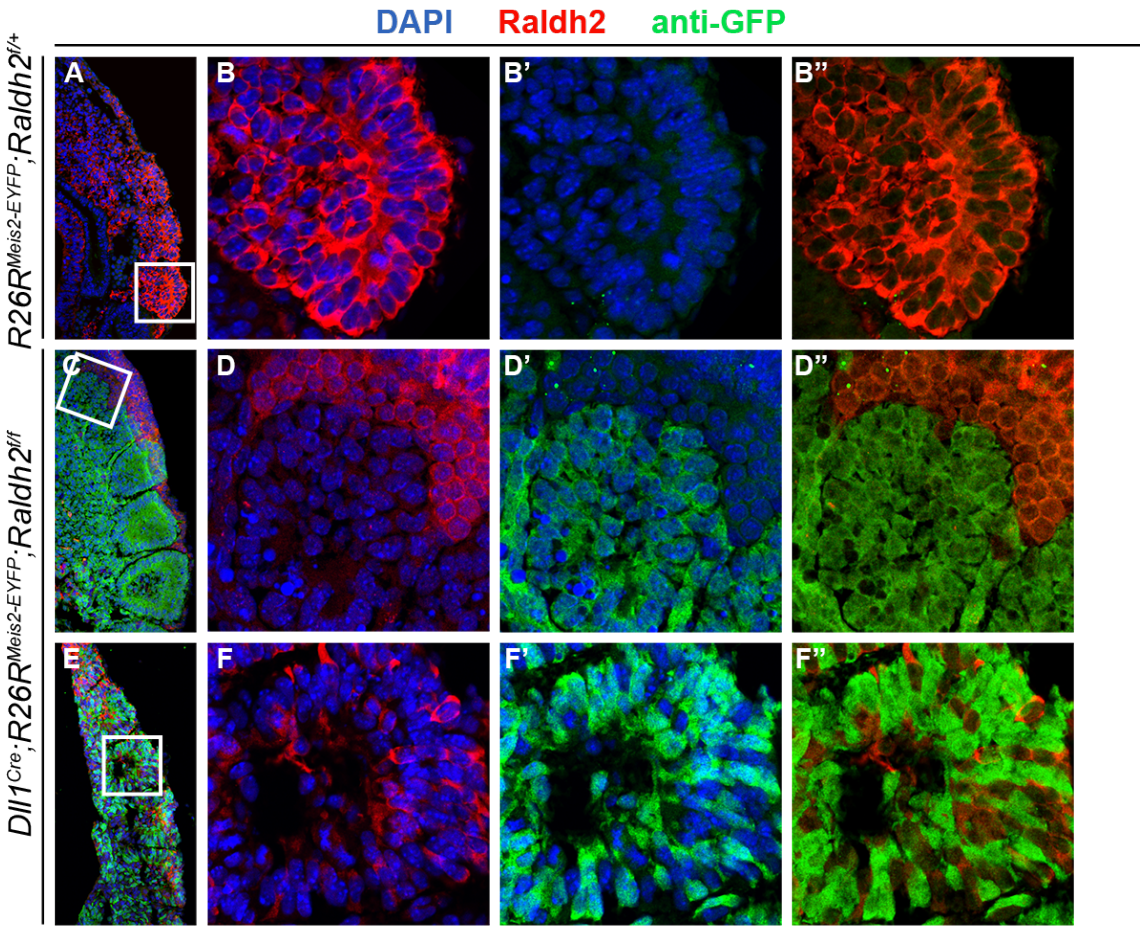

Figure S12. Overlap between *Raldh2* deletion and *Meis2*$^{IRES-EYFP}$ in *Dll1*^{Cre}*;R26RM2;Raldh2*$^{f/f}$ embryos. Immunostaining for RALDH2 and EYFP in *R26RM2;Raldh2*$^{f/+}$ without Cre (A-B'') and *Dll1*^{Cre}*;R26M2;Raldh2*$^{f/f}$ (C-F'') in the somite region of E9.5 embryos. B, D and F show the magnification of the area squared in A, C and E, respectively.

Table S1

Click here to Download Table S1

Table S2

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