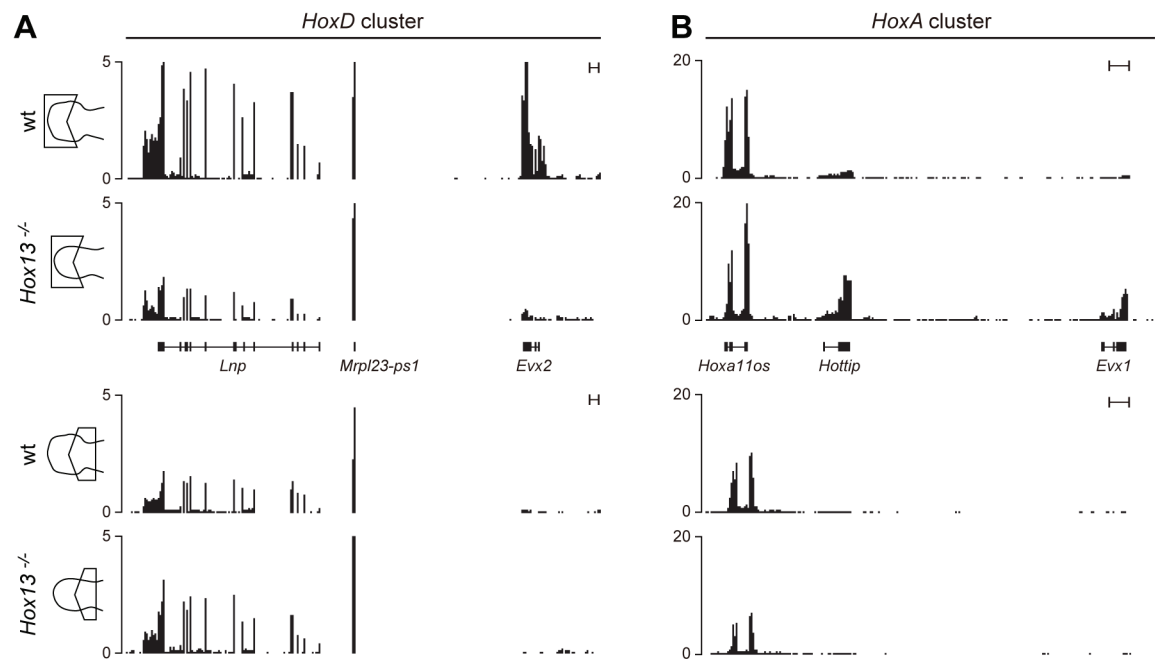


**Supplemental Figure 2 (Figure S2, related to Figure 1)**



**Figure S2. Expression of non-*Hox* genes at both the *HoxD* and *HoxA* loci in double *Hoxa13*<sup>-/-</sup>;*Hoxd13*<sup>-/-</sup> forelimb buds. (A-B)** Transcription profiles of the *Hox* antisense strands in the distal and proximal domains of either wild type (wt) or *Hoxa13*<sup>-/-</sup>;*Hoxd13*<sup>-/-</sup> (*Hox13*<sup>-/-</sup>) double mutants forelimbs at both the *HoxD* (left) and *HoxA* (right) loci. The Y axis represents the strand-specific RNA-seq read counts, divided by the total number of million mapped reads. Transcriptomes from *Hox13*<sup>-/-</sup> mutant were aligned to a manually engineered version of the genome including the sequences introduced in the targeted approaches (see Material and Methods). For visualization, the profiles of the wild type *Hoxa* and *Hoxd* genes lying downstream of the *Neomycin* (*Neo*) and the *LacZ* (*Lac*) integration sites were shifted to align with the mutant genome annotations. Scale bar, 4 kb. Both the *Lnp* and *Evx2* genes were down-regulated in *Hox13*<sup>-/-</sup> mutant limbs. At the *HoxA* locus, while the *Hotip* lncRNA (Wang et al., 2011) and the *Evx1* gene were also down regulated in mutant limb buds, the *Hoxa11* antisense transcript (Hsieh-Li et al., 1995) remained unaffected.