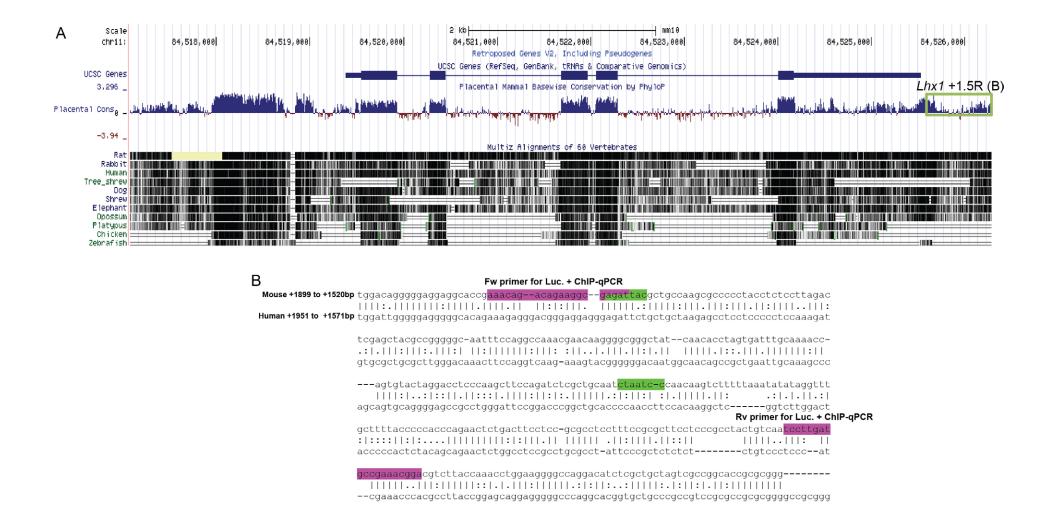
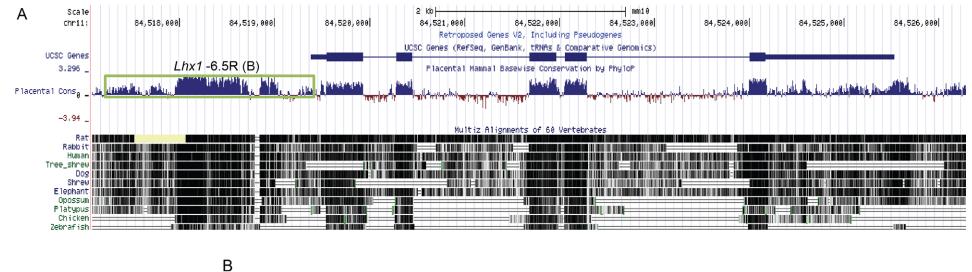


Supplementary Fig. S1. Mouse +30R region of *Lhx1***.** (**A**) Genomic information of the *Lhx1* locus in mouse obtained from the University of California, Santa Cruz (UCSC) genomic browser. *Lhx1* is in antisens orientation. Thick blue boxes indicate coding sequences and thin blue boxes indicate untranslated regions. Placental mammal basewise conservation (Placental Cons) histogram shows the result of multiple sequence alignment for 60 vertebrate species. The conservation score was measured by phyloP. The blue bar indicates positive score in which the regions are conserved, whereas regions with negative score in red indicate are not conserved. Gray scale density plot display pairwise alignments for each species (Rat, Rabbit, Human, Tree_shrew, Dog, Shrew, Elephant, Opossum, Platypus, Chicken and Zebrafish). Gray scales with darker values indicate higher level of overall conservation scored by phastCons. The green box delineates the conserved genomic location covering the *Lhx1* +30R region. (**B**) Basewise sequence alignment of the mouse (+30128 to +29810 bp upstream of START codon) and the human (+30668 to +30327 bp upstream of START codon) +30R regions. Sequences of the primers used for ChIP-qPCR and luciferase (Luc.) assay are highlighted in purple. Fw, forward primer; Rv, reverse primer. Sequences highlighted in green refer to OTX2 binding motifs or motifs close to an OTX2 binding motif.



Supplementary Fig. S2. Mouse +1.5R region of *Lhx1.* (**A**) Genomic information of the *Lhx1* locus in mouse obtained from the University of California, Santa Cruz (UCSC) genomic browser. *Lhx1* is in antisens orientation. Thick blue boxes indicate coding sequences and thin blue boxes indicate untranslated regions. Placental mammal basewise conservation (Placental Cons) histogram shows the result of multiple sequence alignment for 60 vertebrate species. The conservation score was measured by phyloP. The blue bar indicates positive score in which the regions are conserved, whereas regions with negative score in red indicate are not conserved. Gray scale density plot display pairwise alignments for each species (Rat, Rabbit, Human, Tree_shrew, Dog, Shrew, Elephant, Opossum, Platypus, Chicken and Zebrafish). Gray scales with darker values indicate higher level of overall conservation scored by phastCons. The green box delineates the conserved genomic location covering the *Lhx1* +1.5R region. (**B**) Basewise sequence alignment of the mouse (+1899 to +1520 bp upstream of START codon) and the human (+1951 to +1571 bp upstream of START codon) +1.5R regions. Sequences of the primers used for ChIP-qPCR and luciferase (Luc.) assay are highlighted in purple. Fw, forward primer; Rv, reverse primer. Sequences highlighted in green refer to OTX2 binding motifs or motifs close to an OTX2 binding motif.



Supplementary Fig. S3. Mouse -6.5R region of *Lhx1***.** (**A**) Genomic information of the *Lhx1* locus in mouse obtained from the University of California, Santa Cruz (UCSC) genomic browser. *Lhx1* is in antisens orientation. Thick blue boxes indicate coding sequences and thin blue boxes indicate untranslated regions. Placental mammal basewise conservation (Placental Cons) histogram shows the result of multiple sequence alignment for 60 vertebrate species. The conservation score was measured by phyloP. The blue bar indicates positive score in which the regions are conserved, whereas regions with negative score in red indicate are not conserved. Gray scale density plot display pairwise alignments for each species (Rat, Rabbit, Human, Tree_shrew, Dog, Shrew, Elephant, Opossum, Platypus, Chicken and Zebrafish). Gray scales with darker values indicate higher level of overall conservation scored by phastCons. The green box delineates the conserved genomic location covering the *Lhx1* -6.5R region. (**B**) Basewise sequence alignment of the mouse (-6564 to -6875 bp downstream of START codon) and the human (-6782 to -7099 bp downstream of START codon) -6.5R regions. Sequences of the primers used for ChIP-qPCR and luciferase (Luc.) assay are highlighted in purple. Fw, forward primer; Rv, reverse primer. Sequences highlighted in green refer to OTX2 binding motifs or motifs close to an OTX2 binding motif.