

В

Data set	FP	Random
Shared	91	29
p-value	6.86E-31	0.015

Fig. S1. Venn diagram showing the overlap of Foxa1/2-bound genes and those preferentially expressed in the midbrain floor plate at E10.5 (A) and statistical analysis of the shared genes in A and the same number of randomly selected genes (B).

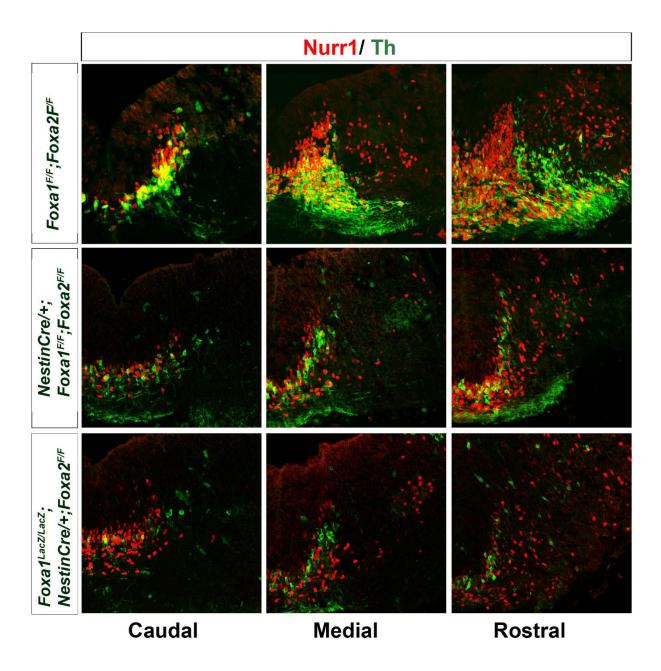


Fig. S2. A similar reduction was observed in the number of Nurr1+ and Nurr1+, Th+ mDA neurons in coronal sections through rostral, medial and caudal levels of the ventral midbrain of *NestinCre;Foxa1*^{F/F}; Foxa2^{F/F} and Foxa1^{lacZ/lacZ}; NestinCre;Foxa2^{F/F} compared with control Foxa1^{F/F}; Foxa2^{F/F} embryos at E12.5.

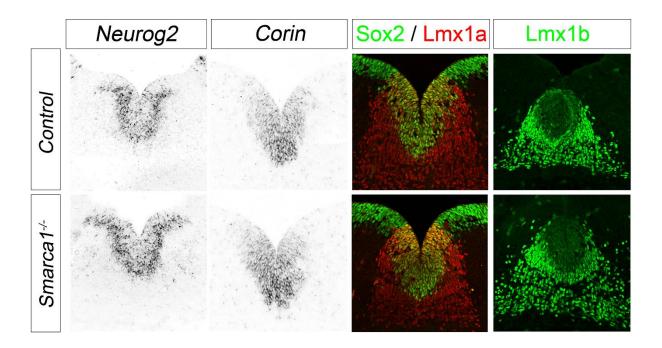


Fig. S3. Expression of mDA progenitor markers by *in situ* hybridisation and by immunohistochemistry was similar in coronal sections of the midbrain of control and *NestinCre;Foxa1/2* cko embryos at E12.5.

Table S1. Foxa1 ChIP-Seq peaks called by MACS. Data include: genomic coordinates, tag number, fold change, *P*-value, false discovery rate and closest TSS.

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Table S2. Foxa1 *in vivo* and Foxa2 *in vitro* co-bound genomic regions annotated to the closest TSS of genes expressed in mouse midbrain floor plate.

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Table S3. Overlap of differentially expressed genes identified by *in vivo* RNA-Seq analysis of wild-type versus *Nestin:Foxa1/2* cko ventral midbrains with genes associated to *in vivo* Foxa1 ChIP-Seq peaks. MGI identification codes and enriched Gene Ontology terms are also provided here.

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Table S4. Genomic coordinates discussed in the main manuscript including PCR primers used in ChIP-qPCR validation. Primers used in expression qPCR analysis are also mentioned here.
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Table S5. Foxa2 ChIP-Seq peaks called by MACS and their overlap with <i>in vitro</i> Foxa2-bound and <i>in vivo</i> Foxa1-bound genomic regions.
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Table S6. Overlap of Foxa2 in vivo ChIP-Seq peaks with Foxa1 in vivo ChIP-Seq peaks.
Click here to Download Table S6