

**Table S1. Microarray data**

Expression level (ratio to control)	Abbreviation of gene name	Gene name	Accession number
<b>(A) Genes upregulated in <i>Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup></i> rostral forebrain at E9.5</b>			
0.111782	<i>Lhx8</i>	LIM homeobox protein 8	D49658.1
0.258314	<i>Hes5</i>	hairy and enhancer of split 5	BB561515
0.278592	<i>3830406C13Rik</i>	RIKEN cDNA 3830406C13 gene	BB763097
0.37488	<i>Crym</i>	crystallin	NM_016669.1
0.380651	<i>LOC382156</i>	similar to F-box- and WD40-repeat-containing protein	BM229128
0.400377	<i>Dchs1</i>	dachsous 1	AK014167.1
0.408742	<i>Igf1</i>	insulin-like growth factor 1	BG075165
0.4099378	<i>Prkab2</i>	protein kinase, AMP-activated, beta 2 non-catalytic subunit	AV223660
0.4137254	<i>Synpo</i>	synaptopodin	BB426294
0.43194	<i>Insm1</i>	insulinoma-associated 1	BB468410
<b>(B) Genes downregulated in <i>Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup></i> rostral forebrain at E9.5</b>			
10.58017	<i>Psmc6</i>	proteasome 26S subunit, non-ATPase, 6	BC006869.1
7.842105	<i>Cnm3</i>	Cyclin M3	BB236001
2.625724	<i>3110069A13Rik</i>	RIKEN cDNA 3110069A13 gene	AK014242.1
2.501182	<i>Strbp</i>	Spermatid perinuclear RNA binding protein	W488249
2.341556	<i>Ramp2</i>	Ramp2	BF537798
2.126619	<i>Wbscr1</i>	Williams-Beuren syndrome chromosome region 1 homolog	AU018978
2.104	<i>Lhx5</i>	LIM homeobox protein 5	NM_008499.1
2.08	<i>Plekha2</i>	pleckstrin homology domain-containing, family A member 2	BC010215.1
2.039887	<i>Tcf3</i>	transcription factor 3	BE994269
<b>(C) Genes upregulated in <i>Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup></i> rostral forebrain at E10.5</b>			
0.305256065	<i>3830406C13Rik</i>	RIKEN cDNA 3830406C13 gene	BB763097
0.307469181	<i>Cnm3</i>	Cyclin M3	BB236001
0.307507508	<i>Arnt</i>	aryl hydrocarbon receptor nuclear translocator	AV233793
0.31530782	<i>Smarb1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	AV310148
0.31838565	<i>Usp7</i>	Ubiquitin specific peptidase 7	AW548146
0.326007326	<i>Aldh1a3</i>	aldehyde dehydrogenase family 1, subfamily A3	NM_053080.1
0.327475103	<i>1810014B01Rik</i>	RIKEN cDNA 1810014B01 gene	AK017634.1
0.332063492	<i>Rpl27a</i>	ribosomal protein L27a	BG141806
0.335905711	<i>Hes5</i>	hairy and enhancer of split 5	BB561515
0.349477683	<i>Tmem69</i>	transmembrane protein 69	BB824992
<b>(D) Genes downregulated in <i>Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup></i> rostral forebrain at E10.5</b>			
8.68330362	<i>Psmc6</i>	proteasome 26S subunit, non-ATPase, 6	BC006869.1
3.470720721	<i>Arf5</i>	ADP-ribosylation factor 5	NM_007480.1
2.570723684	<i>Neurog2</i>	neurogenin 2	NM_009718.1
2.348777349	<i>Ptprz1</i>	protein tyrosine phosphatase, receptor type Z, polypeptide 1	BC002298.1
2.009538951	<i>2610017109Rik</i>	RIKEN cDNA 2610017109 gene	AW045679
<b>(E) Genes upregulated in <i>Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup></i> rostral forebrain at E12.5</b>			
0.24166203	<i>Dbx1</i>	developing brain homeobox 1	AI426026
0.25706371	<i>Irx5</i>	Iroquois related homeobox 5	NM_018826.1
0.28139535	<i>Tcf7l2</i>	transcription factor 7-like 2, T-cell specific, HMG-box	AF107298.1
0.28937117	<i>Irx2</i>	Iroquois related homeobox 2	AF295369.1
0.30982019	<i>Shox2</i>	short stature homeobox 2	AV332957
0.32046332	<i>Irx3</i>	Iroquois related homeobox 3	NM_008393.1
0.32054674	<i>Evi1</i>	ecotropic viral integration site 1	AI647591
0.35974026	<i>Ebf3</i>	early B-cell factor 3	AK014058.1
0.38888889	<i>Irx1</i>	Iroquois related homeobox 1	AF165984.1
0.39520028	<i>Fgf15</i>	fibroblast growth factor 15	NM_008003.1

List of genes, the expression of which was downregulated or upregulated in *Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup>* rostral forebrains at E9.5, E10.5 or E12.5 in comparison with wild-type rostral forebrains. The genes were selected according to the following criteria: (1) they display two-fold or more change in signal value between wild-type and *Fezf1<sup>-/-</sup>Fezf2<sup>-/-</sup>* rostral forebrains, (2) the signal intensities of the higher value should be greater than 100, and (3) the top-ten genes are shown in tables and raw data have been deposited in Gene Expression Omnibus (GEO) under the accession number GSE21156.