Supplementary Information

The exon junction complex component *Magoh* controls brain size by regulating neural stem cell division

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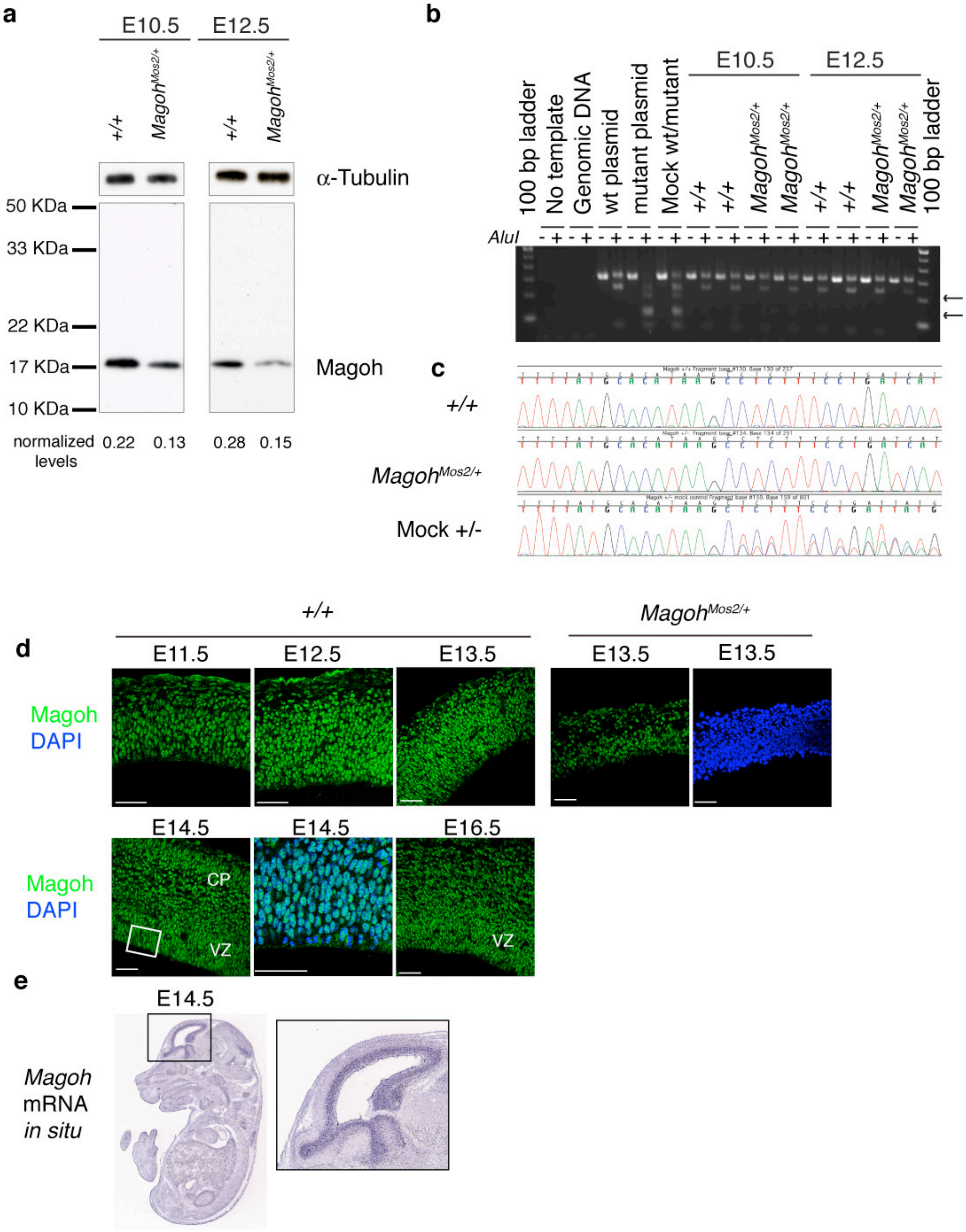
Supplementary Data 1 Serum chemistries, hematology, and organ weights of control and mutant animals

SUPPLEMENTARY INFORMATION

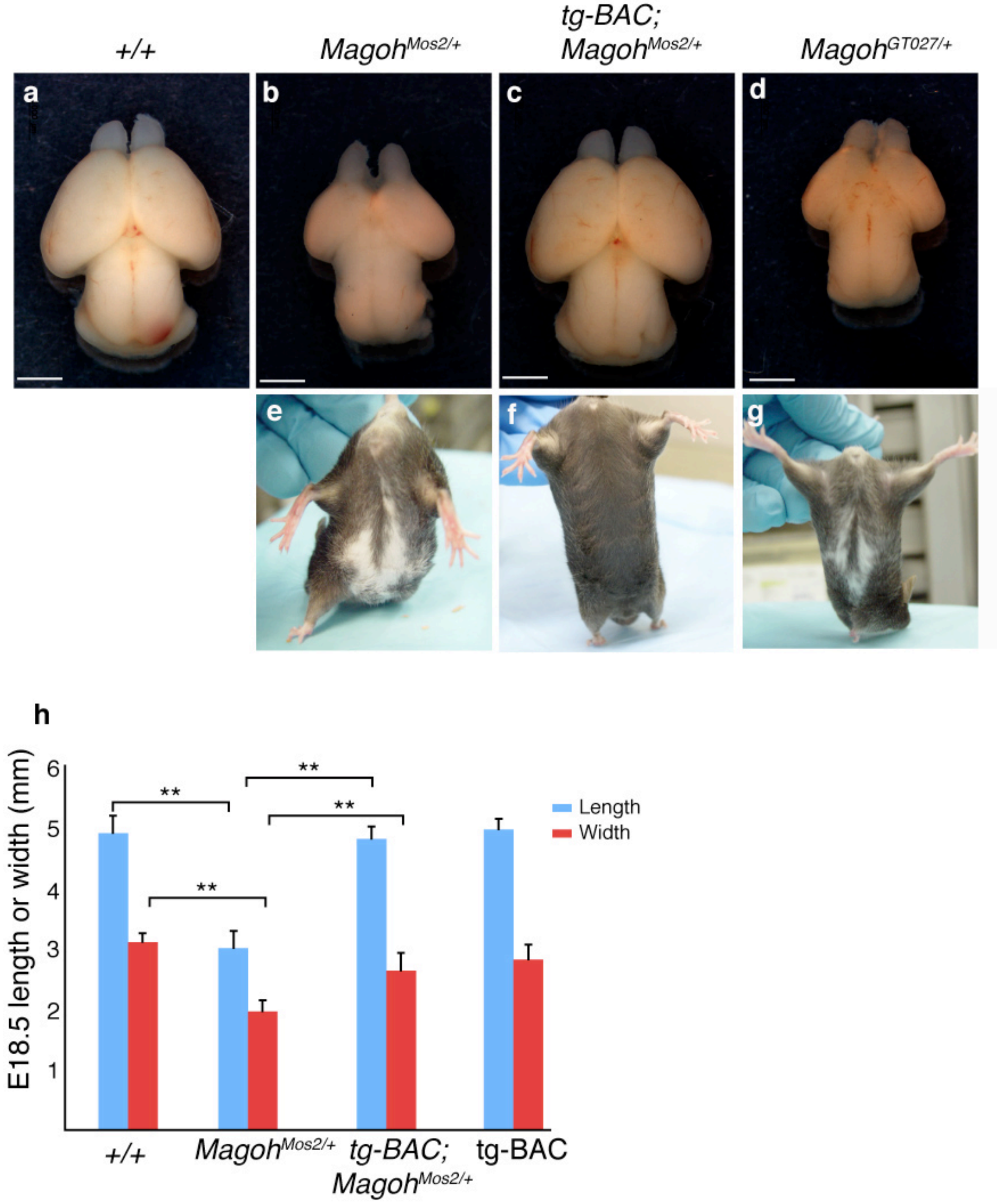
Supplementary Figure 1



Supplementary Figure 1 The *Mos2* allele results in haploinsufficiency. **a,** Representative Western blot analyses of E10.5 and E12.5 cortical lysates from indicated genotypes probed with anti-Magoh and anti-α-Tubulin, as a loading control. Below the blots are densitometry values normalized for loading. Note that in *Magoh*$^{Mos2/+}$, Magoh levels (17 kDa) are reduced (approximately two-fold) and there are no aberrantly sized proteins. Similar results were seen with antibodies recognizing either the whole protein or N-terminus. **b**, RNA from E10.5 and E12.5 cortices was used for first-strand cDNA synthesis and subsequent RT-PCR amplification using primers spanning exons 1 and 4. The gel image shows undigested and *AluI* digested PCR products from the indicated templates. The *wild-type* PCR product and cDNA plasmid positive control yields the expected 313 bp and upon digestion, the expected 2 fragments (240 bp and 73 bp). The *Magoh*$^{Mos2/+}$digested and undigested PCR product generates an identical pattern to wild-type. The mutant cDNA positive control yields the expected 3 fragments (126, 113, and 73 bp), due to an *AluI* site created by the *Mos2* mutation. A mock heterozygote sample, (1:1 mixture of wild-type and mutant plasmid clones before PCR amplification), generates bands expected if the *Mos2* transcript is expressed in *Magoh*$^{Mos2/+}$. The *Magoh*$^{Mos2/+}$ samples show no evidence of the *Mos2* transcript (arrows). **c**, Sequence chromatograms of RT-PCR products from +/+ cortices (top), *Magoh*$^{Mos2/+}$ cortices (middle) and mock heterozygote showing double peaks beginning at 198delG mutation (bottom). Consistent with the RT-PCR data, these show no evidence of the mutant *Mos2* transcript. **d,** Confocal micrographs of coronal sections, from the indicated genotypes and ages, stained with rabbit anti-Magoh (green) and DAPI (blue). Note that MAGOH is nuclear, is expressed throughout the cortex, and is reduced in *Magoh*$^{Mos2/+}$ brains. At

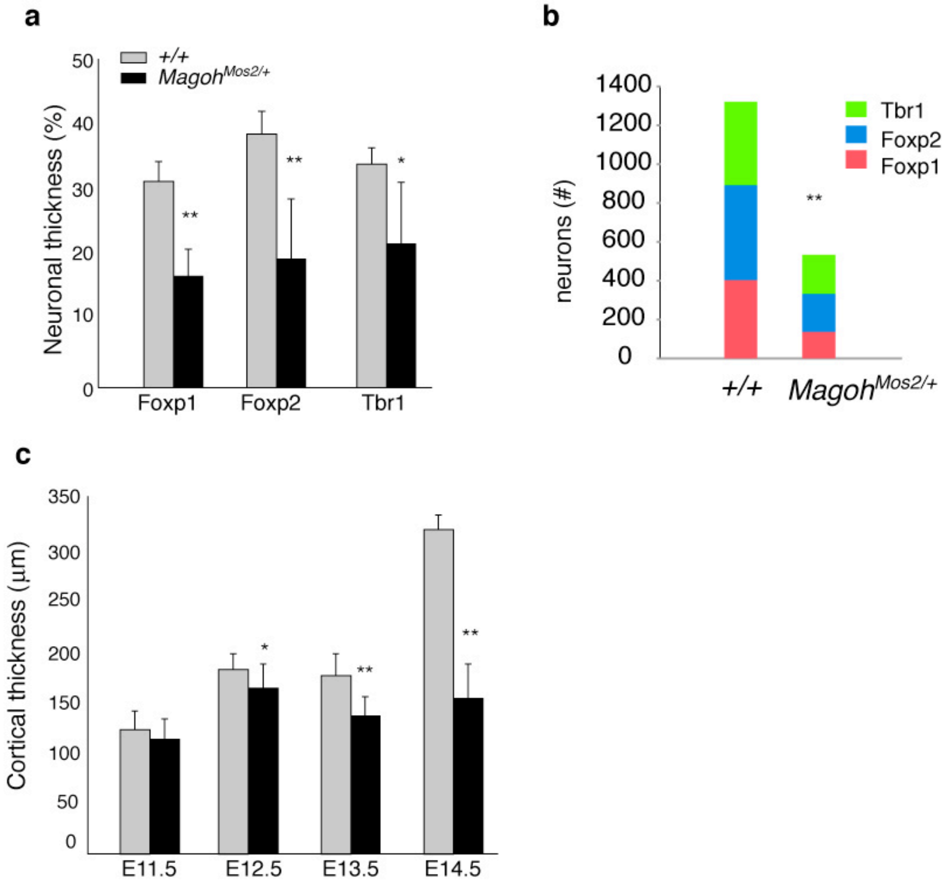
E14.5 and E16.5, MAGOH expression is enriched in the VZ/SVZ and CP. In E14.5 images, the boxed square indicates the higher magnification image shown to the right. **e**, *Magoh* mRNA *in situ* hybridization of E14.5 sagittal section, with square indicating higher magnification image of the developing cerebral cortex. The enriched expression of *Magoh* in the VZ/SVZ is especially evident with this technique. *In situ* images were taken from Genepaint.org but also repeated to confirm the expression pattern. Scale bars=50 μm.

Supplementary Figure 2



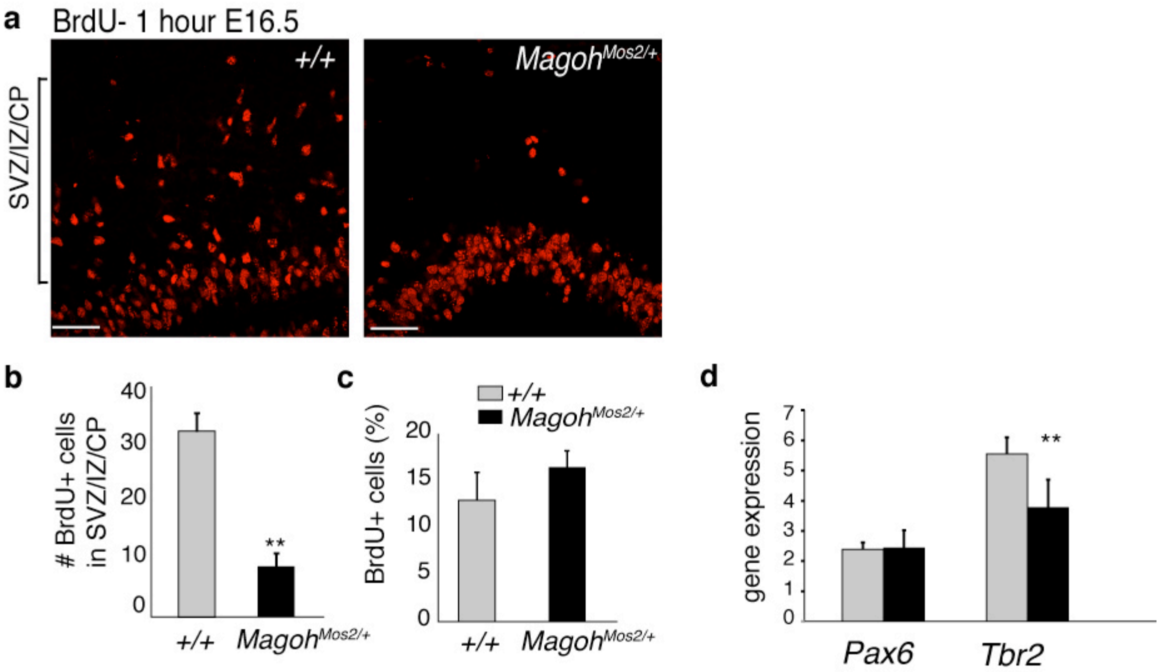
Supplementary Figure 2 Microcephaly and hypopigmentation in *Magoh* gene trap alleles and Tg-BAC rescue. a-d, Images of E18.5 brains and (**e-g**) adult pigmentation patterns from indicated genotypes. Scale bars=1 mm. **h,** Graph representing length (blue) and width (red) measurements of whole mount E18.5 brains. Shown are the average values for all embryos (n=5-8 per genotype). **, P<0.005; Error bars, s.d.

Supplementary Figure 3



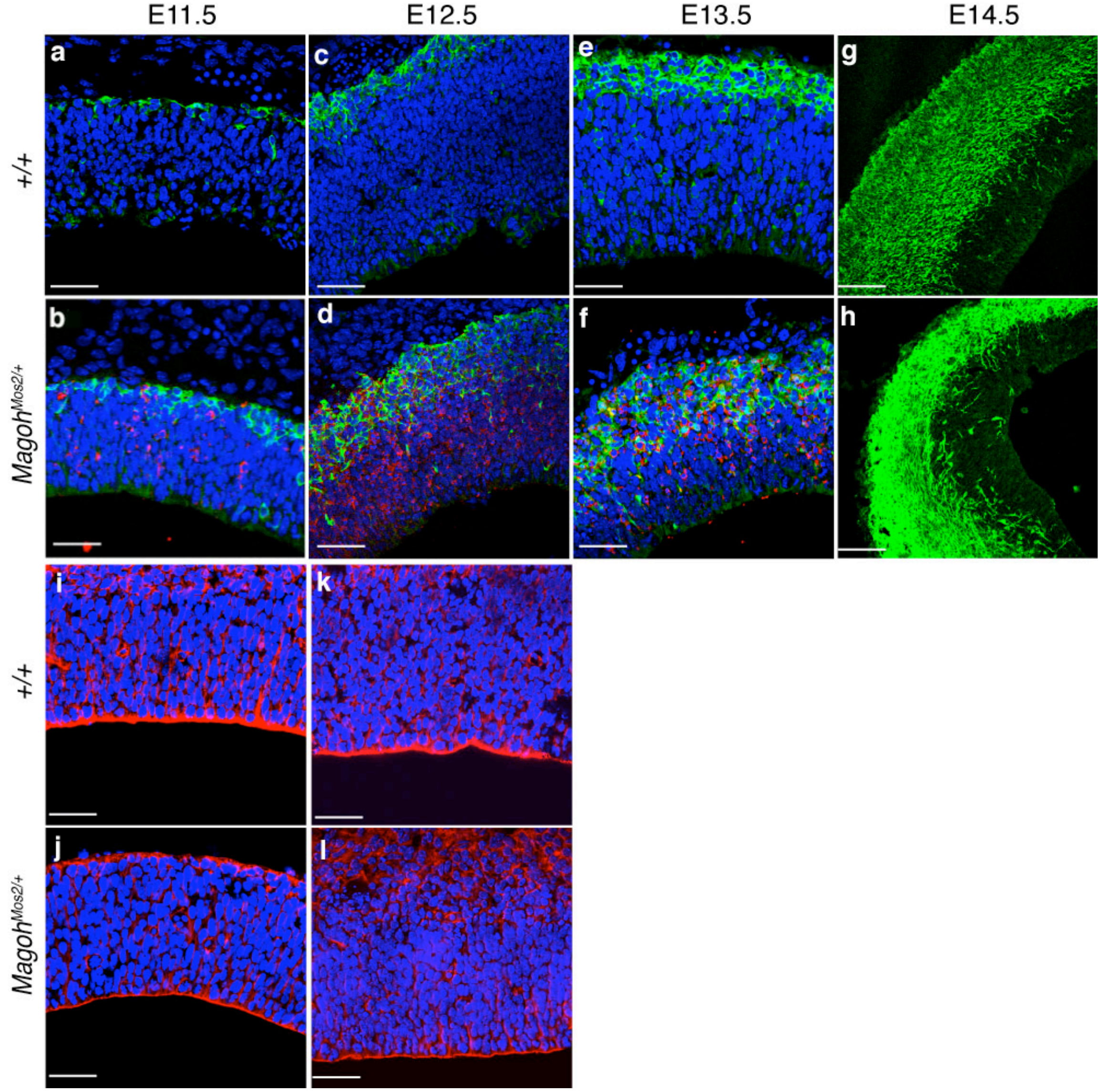
Supplementary Figure 3 Thickness of neuronal layers and cortex, and total number of neurons is reduced in *Magoh*$^{Mos2/+}$ mice. a, Graph representing the thickness of the neuronal layers III-VI, marked by antibodies against Foxp1, Foxp2, and Tbr1, as a percentage of total cortical thickness at E18.5. Shown are the average values for all embryos (n=2-4 per genotype, n=2-3 sections per embryo). **b,** Graph representing the average total number of Foxp1 (red), Foxp2 (blue), and Tbr1 (green) positive neurons within 450 μm^2 fields (n=3-5 sections per genotype). **c,** Graph representing cortical thickness of control (grey) and *Magoh*$^{Mos2/+}$ (black) brain sections at indicated ages. Shown are the average values for all embryos (n=2-4 per genotype, average 10 sections each) measured within a 318 μm^2 field. *, $P<0.05$, **, $P<0.005$; Error bars, s.d.

Supplementary Figure 4



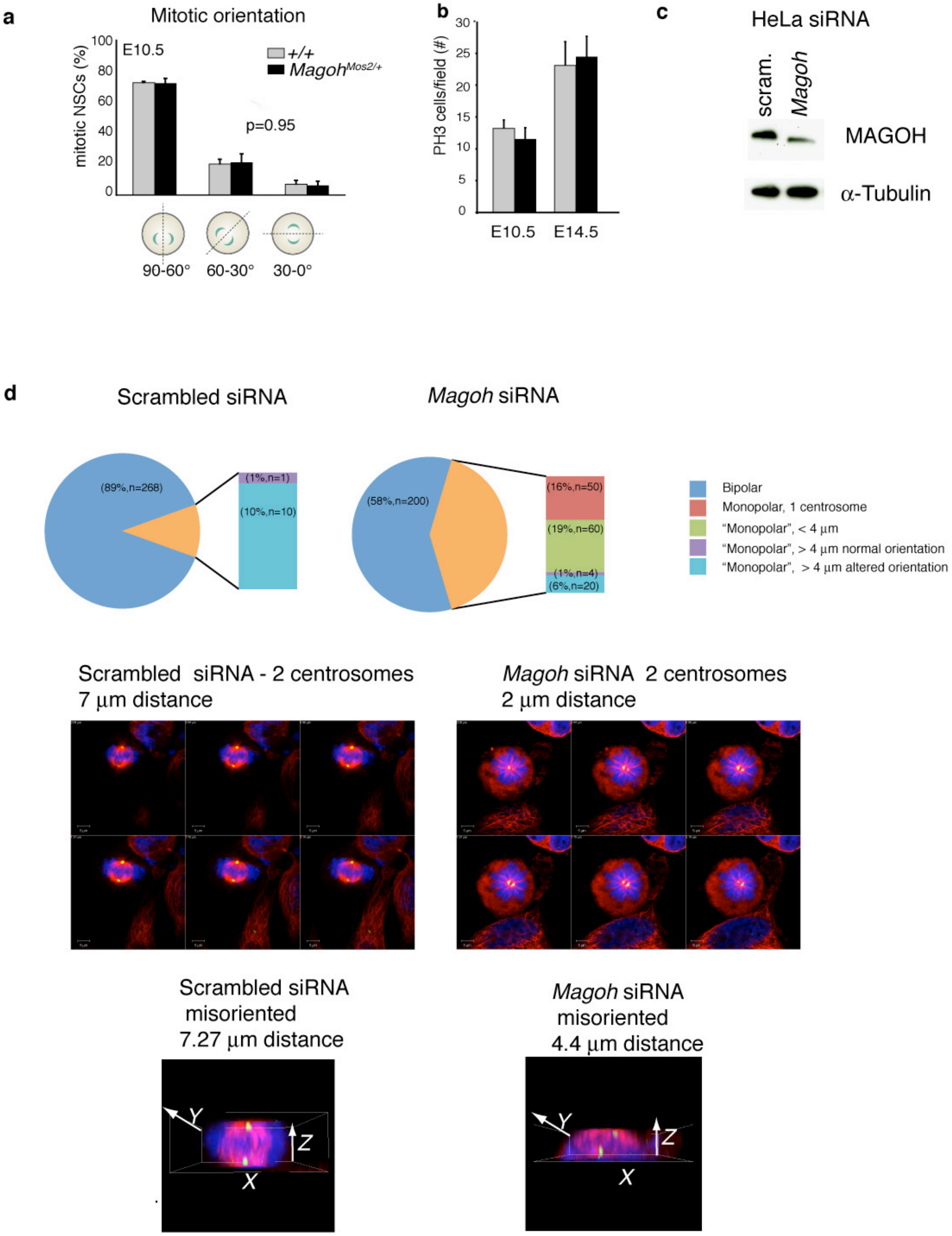
Supplementary Figure 4 Analysis of NSC and IPC populations. a, Confocal micrographs of coronal sections from indicated genotypes at E16.5, stained for BrdU (red). Pregnant females were dissected 1 hour after injection with BrdU. Scale bars= 50 μm. **b,** Graph representing the average number of BrdU positive cells in the SVZ/IZ/CP layers as measured within a 150 μm X 300 μm wide field. **c,** Graph depicting the percentage of total DAPI cells that are BrdU positive measured within a 318 μm^2 field. Graphs in **(b,c)** indicate the average values for all embryos (n=2-4 per genotype, 10 sections per embryo). **d,** Graph representing quantitative gene expression of *Pax6* and *Tbr2* averaged from 4 replicates each of control (n=4) and *Magoh*$^{Mos2/+}$ (n=5) E12.5 cortices, as measured by quantitative real-time PCR (P=0.73 and P<0.005, respectively). Expression was normalized to *Gapdh* and wild-type levels were set to 1.0. *, P<0.05, **, P<0.005; Error bars, s.d.

Supplementary Figure 5



Supplementary Figure 5 Apoptosis of new neurons in *Magoh*$^{Mos2/+}$ embryos beginning at E11.5. **a-h,** Confocal micrographs of coronal sections from indicated ages and genotypes and stained for Tuj1 (green), DAPI (blue), and CC3 (red) **(a-f)**, and Tuj1 (green) **(g-h)**. **i-l**, Confocal micrographs of coronal sections from indicated ages and genotypes and stained for Phalloidin (red) and DAPI (blue). Note the apical membrane is intact, as seen with Phalloidin staining. Scale bars, 40 μm (**a-f, i-l),** 80 μm **(g, h).**

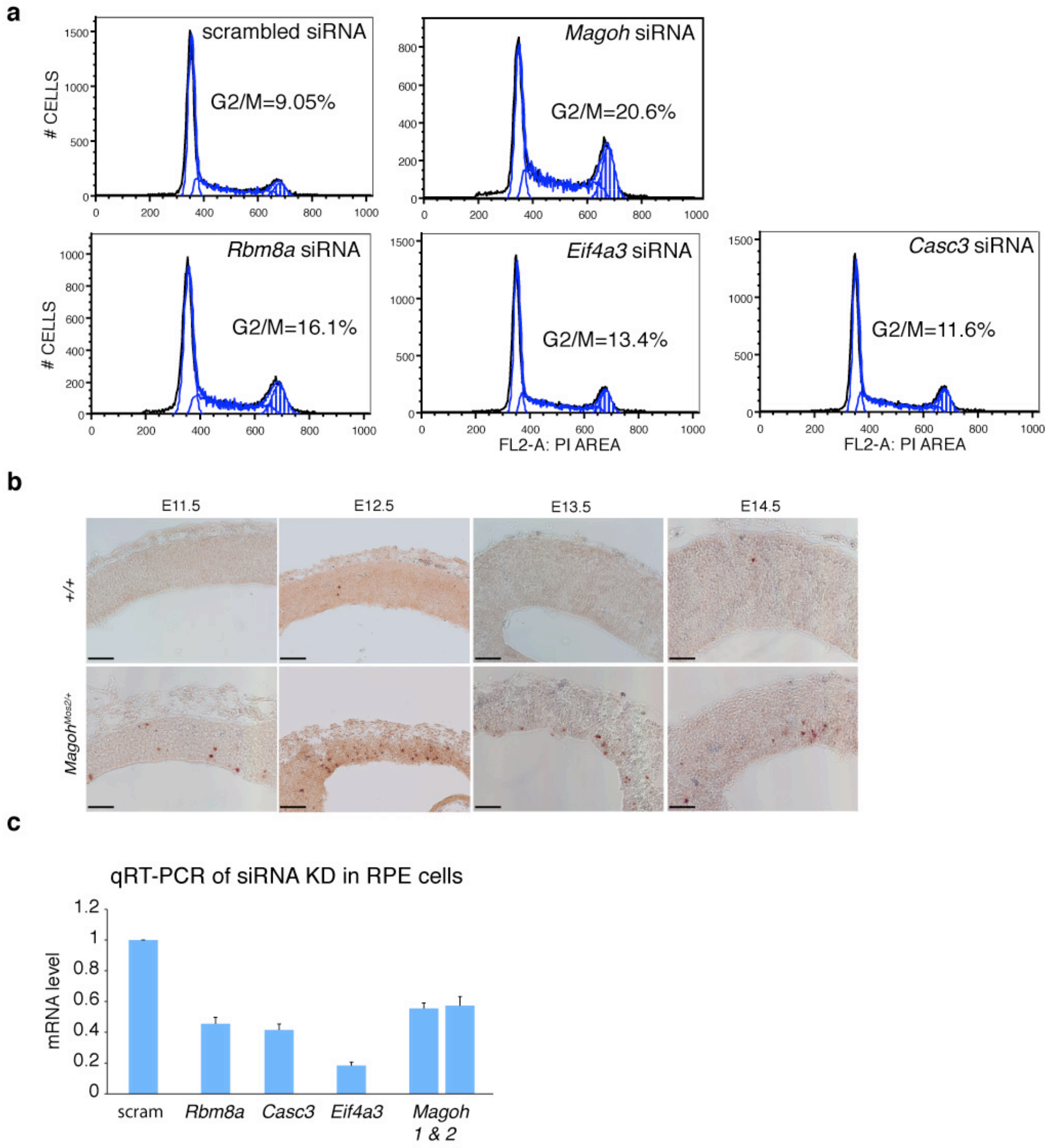
Supplementary Figure 6



Supplementary Figure 6 Requirement of *Magoh* for mitosis *in vitro* and *in vivo*. a, Graph depicting mitotic orientation of NSCs from control (grey) and *Magoh*$^{Mos2/+}$ (black)

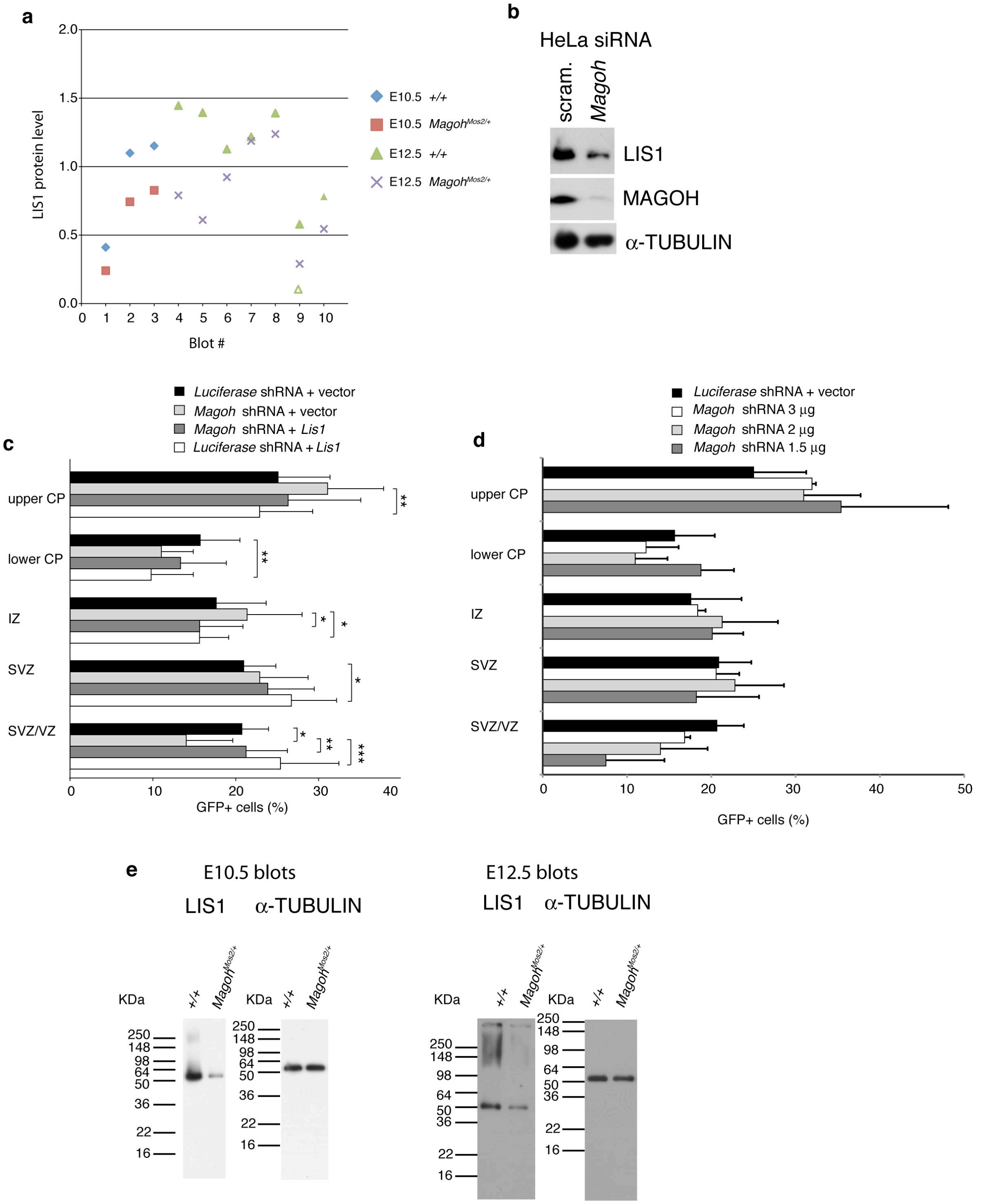
E10.5 embryos (*P*=0.95). **b,** Graph depicting the number of PH3 cells at E10.5 and E12.5 (*P*=0.2642 and *P*=0.4022, respectively). Error bars, s.d. **c,** Representative Western blot analyses of lysates of siRNA-treated cells probed with antibodies against Magoh (17 kDa), α-Tubulin (55 kDa). MAGOH was reduced on average by 60-70%. **d,** Pie graphs and bar charts representing the distribution of indicated phenotypic classes of knockdown cells. Beneath them are confocal micrographs of 4 representative HeLa cells treated with indicated siRNAs and stained with anti-α-Tubulin (red), anti-γ-Tubulin (green) and DAPI. Consecutive optical slices, with μm pole to pole distance indicated, demonstrate that centrosomes were in the same optical plane, and therefore not misoriented. Also shown are Z stacks with representative images of misoriented cells.

Supplementary Figure 7

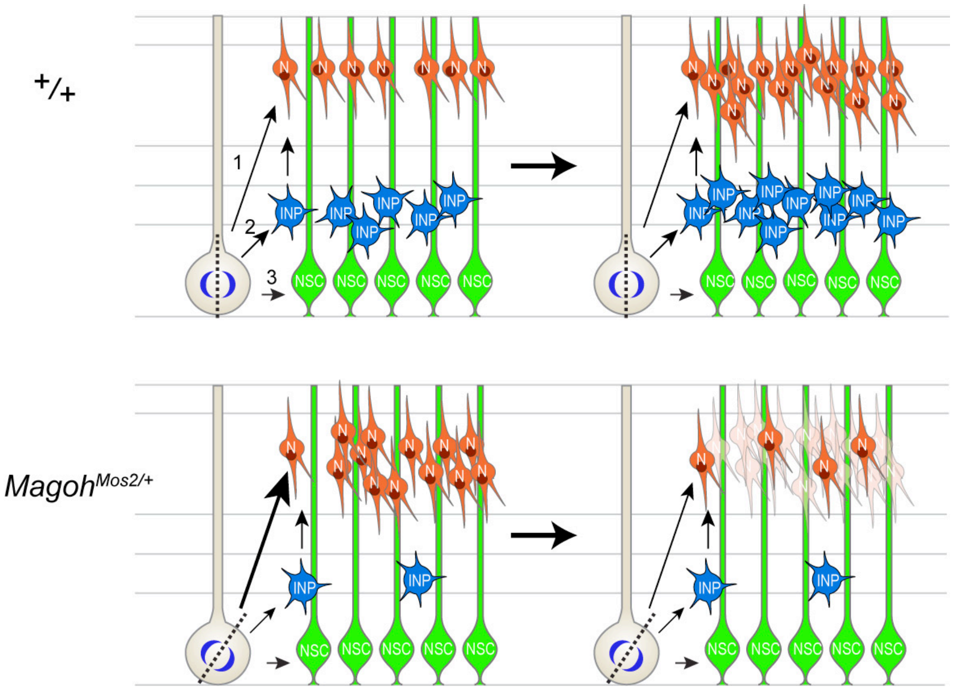


Supplementary Figure 7 Analysis of siRNA treated cells. a, FACS analysis of HeLa cells treated with indicated siRNAs with the percentage of G2/M cells shown. **b,** Images of coronal sections of indicated ages and genotypes stained for γ-H2AX (brown cells) to identify cells exhibiting spontaneous double strand DNA breaks, which are dramatically increased in *Magoh*$^{Mos2/+}$ embryos. Scale bars, 50 μm. **c,** Graph depicting qRT-PCR analysis of siRNA treated RPE cells. Error bars, s.d.

Supplementary Figure 8



Supplementary Figure 8 Analyses of LIS1 expression and *In utero* electroporations. **a,** Graph representing LIS1 protein levels, normalized for loading. Average measurements from 10 different blots which each include 4 pairs of mutant and control are shown. Note that in all experiments, LIS1 levels are lower in *Magoh*$^{Mos2/+}$. **b,** Western analysis of LIS1 and Magoh protein on scrambled and *Magoh* siRNA-treated HeLa cells. **c,** Graph representing distribution of GFP-positive cells in different layers of the cortex from *in utero* electroporated brains, as shown. **d,** Graph representing distribution of GFP-positive cells in different layers of the cortex from brains electroporated with various dosages of *Magoh* shRNA, as shown. **e**, Full-length Western blots of data shown in Figure 6b. *, $P<0.05$, **, $P<0.005$, ***, $P<0.0005$; Error bars, s.d.



Supplementary Figure 9 Model of *Magoh*$^{Mos2/+}$ phenotype. Graphic representation of neurogenesis in control (top) and *Magoh*$^{Mos2/+}$ brains (bottom). In control brains, apically dividing neural stem cells (NSCs) undergo three types of divisions: (1) neurogenic asymmetric divisions to directly produce neurons (N) and NSCs, (2) proliferative asymmetric divisions to produce NSCs and intermediate neural progenitors (INPs) which then generate neurons, (3) proliferative symmetric divisions to self-renew (3). In *Magoh*$^{Mos2/+}$ brains, NSCs are not reduced, but INPs are depleted, and neurons are increased but subsequently undergo apoptosis. In the proposed model, a shift in asymmetric divisions (increased type 1 and decreased type 2) produces ectopic neurons and fewer INPs, without affecting NSC number. Another possible mechanism (not shown) is that in *Magoh*$^{Mos2/+}$ brains INPs are produced but prematurely differentiate into neurons. We propose that in *Magoh*$^{Mos2/+}$ mice, alterations in mitotic spindle integrity and cell division of NSCs (either through misoriented or dysfunctional mitotic spindles, as shown) influences cell fates of neurons and INPs.

Body part	**Control (avg. g)**	***Magoh*$^{Mos2/+}$ (avg. g)**	**Normalized %change**	***P* value**
Body	39.48 g	25.96 g	33 % lower	0.046*
Brain	0.509 g	0.234 g	28 % lower	0.045*
Thymus	0.032 g	0.023 g	1.1% higher	0.532
Heart	0.191 g	0.139 g	1.1 % higher	0.456
Spleen	0.098 g	0.062 g	3 % lower	0.892
Liver	1.585 g	1.206 g	1.2 % higher	0.290
Kidney	0.464 g	0.392 g	1.3 % higher	0.131

Supplementary Table 1. Body and organ weights of control and *Magoh*$^{Mos2/+}$ animals. Measured average (avg.) organ weights (g) and percentage difference (*Magoh*$^{Mos2/+}$ value/control value). For all except body weight, percentage difference was calculated after normalization for body weight, and *P* values indicate differences in normalized values. For each genotype, three age and gender matched animals were analyzed.

mutant /wt	*P* value	Gene Name	Gene ID	AFFY cluster ID
0.46	0.0475	PREDICTED: Mus musculus similar to Sycp3 like Y-linked (LOC621831), misc RNA.	-	10608382
0.48	0.0122	T-box brain gene 1	*Tbr1*	10472313
0.51	0.0085	Solute carrier family 17	*Slc17a6*	10553501
0.52	0.0007		-	10354229
0.53	0.0022	Fatty acid binding protein 7, brain	*Fabp7*	10363224
0.53	0.0442	ncrna:snoRNA chromosome:NCBIM36:7:59750814:59750907:-1 gene:ENSMUSG00000075807	-	10564183
0.56	0.0009	Mago-nashi homolog, proliferation-associated (Drosophila)	*Magoh*	10506736
0.57	0.0246	Vomeronasal 1 receptor, D21	*V1rd21*	10550770
0.57	0.0057	Tbr2	*Eomes*	10589994
0.58	0.0213	Ornithine decarboxylase antizyme 1	*Oaz1*	10364909
0.60	0.0055	RAS guanyl releasing protein 1	*Rasgrp1*	10486061
0.60	0.0217	Doublecortin (Dcx), transcript variant 4	*Dcx*	10607156
0.61	0.0053	Protein tyrosine phosphatase, receptor type Z, polypeptide 1	*Ptprz1*	10536667
0.62	0.0185	Mus musculus R38c snoRNA	-	10386093
0.63	0.0038	Glycoprotein m6b	*Gpm6b*	10603151
0.63	0.0063	CDNA clone IMAGE:6819393	-	10406461
0.64	0.0096	Hydroxyprostaglandin dehydrogenase 15 (NAD)	*Hpgd*	10571840
0.65	0.0138	Neural zinc finger protein NZF-2b	*Myt1*	10479698
0.65	0.0127	Distal-less homeobox 1	*Dlx1*	10472809
0.65	0.0020	Tubulin, beta 3	*Tubb3*	10576332
0.65	0.0046	Crystallin, mu	*Crym*	10567546
0.66	0.0066	Insulin-like growth factor binding protein-like 1	*Igfbpl1*	10512721
0.67	0.0304	similar to Ina protein	-	10463737
0.67	0.0377		-	10550320
0.67	0.0131	Tweety homolog 1 (Drosophila)	*Ttyh1*	10549594
0.67	0.0047	Endothelin receptor type B	*Ednrb*	10422164
0.68	0.0050	Guanine nucleotide binding protein (G protein), gamma 3	*Gng3*	10465820
0.68	0.0434		-	10582572
0.68	0.0371		-	10439889
0.68	0.0018	Junction adhesion molecule 2	*Jam2*	10436666
0.68	0.0177	Strain C57BL/6J nuclear factor I/B	*Nfib*	10514049
0.68	0.0118		-	10562546

0.69	0.0207	SPARC-like 1	*Sparcl1*	10531931
0.69	0.0020	Microtubule-associated protein 2	*Mtap2*	10347036
0.69	0.0134	POU domain, class 3, transcription factor 4	*Pou3f4*	10601459
0.69	0.0425	cdna:known chromosome:NCBIM36:10:21756008:21757495:-1 gene:ENSMUSG00000069712	-	10368222
0.69	0.0477	Secretogranin III	*Scg3*	10595033
0.69	0.0009	Fasciculation and elongation protein zeta 1 (zygin I)	*Fez1*	10584259
0.70	0.0436		-	10582584
0.70	0.0057	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) transcript variant 1	*Elavl4*	10515095
0.70	0.0431	B-cell CLL/lymphoma 11A (zinc finger protein)	*Bcl11a*	10374727
0.70	0.0289	Immunoglobulin superfamily containing leucine-rich repeat 2	*Islr2*	10594048
0.70	0.0057	Cysteine dioxygenase 1, cytosolic	*Cdo1*	10458828
0.70	0.0097	Calcium channel, voltage-dependent, alpha2/delta subunit 1 transcript variant e	*Cacna2d1*	10519815
0.71	0.0177	similar to spermiogenesis specific transcript on the Y 1	-	10608613
0.71	0.0335	cdna:known chromosome:NCBIM36:16:77479609:77479770:1 gene:ENSMUSG00000074941	-	10436598
0.71	0.0053	T-box 22	*Tbx22*	10601433
0.71	0.0371	Deleted in colorectal carcinoma	*Dcc*	10459671
0.71	0.0010	Secernin 1	*Scrn1*	10544875
0.71	0.0382	Scot mRNA for succinyl CoA transferase	*Oxct1*	10422608
0.71	0.0134	Rho, GDP dissociation inhibitor (GDI) beta	*Arhgdib*	10548892
0.71	0.0153	ATP-binding cassette, sub-family D (ALD), member 2	*Abcd2*	10431697
0.71	0.0202	ncrna:snoRNA chromosome:NCBIM36:2:129969457:129969528:1 gene:ENSMUSG00000065272	-	10476106
0.72	0.0192	Transmembrane protein 35	*Tmem35*	10601701
0.72	0.0122	RNA-binding protein mHuC-S	*Elavl3*	10591706
0.72	0.0059	Eph-related receptor tyrosine kinase (Mek4) secreted	*Epha3*	10440258
0.72	0.0018	Ca2+-dependent secretion activator (Cadps), transcript variant 1	*Cadps*	10417628
0.73	0.0086	Potassium channel, subfamily K, member 10	*Kcnk10*	10401987
0.73	0.0122	Dihydropyrimidinase-like 4	*Dpysl4*	10558481

0.73	0.0191		-	10584600
0.73	0.0114	Suppression of tumorigenicity 18	*St18*	10344679
0.73	0.0048	Transgelin 3 (Tagln3)	*Tagln3*	10439695
0.73	0.0115	Rho family GTPase 2	*Rnd2*	10381416
0.74	0.0443	Lysozyme 2	*Lyz2*	10372648
0.74	0.0099	Neurogenin 2	*Neurog2*	10495964
0.74	0.0436	ncrna:snoRNA chromosome:NCBIM36:5:130104248:130104382:1 gene:ENSMUSG00000065304	-	10526085
0.74	0.0088	Thymosin, beta 4, X chromosome	*Tmsb4x*	10607865
0.74	0.0425	Delta-like 3 (Drosophila)	*Dll3*	10561376
0.74	0.0125	RIKEN cDNA 6330403K07 gene	*6330403K07Rik*	10388042
0.74	0.0246	LIM-homeodomain protein	*Lhx8*	10502961
0.74	0.0190	Ectonucleoside triphosphate diphosphohydrolase 1	*Entpd1*	10463070
0.74	0.0016	cdna:known chromosome:NCBIM36:12:54991829:54993367:1 gene:ENSMUSG00000073093	-	10395733
0.74	0.0138	Zinc finger, CCHC domain containing 12	*Zcchc12*	10599187
0.74	0.0138	Tubulin, beta 2B	*Tubb2b*	10399419
0.74	0.0488	Interferon-induced protein with tetratricopeptide repeats 2	*Ifit2*	10462613
0.74	0.0138	Glycoprotein m6a	*Gpm6a*	10571815
0.74	0.0205	Homeobox, msh-like 2	*Msx2*	10409314
0.74	0.0378	Coagulation factor XIII, A1 subunit	*F13a1*	10408693
0.75	0.0011	Neuron specific gene family member 1	*Nsg1*	10529656
0.75	0.0141	Cyclin-dependent kinase inhibitor 1C (P57)	*Cdkn1c*	10569429
0.75	0.0417	Distal-less homeobox 2	*Dlx2*	10483626
0.75	0.0425	Chemokine (C-X-C motif) ligand 13	*Cxcl13*	10523359
0.75	0.0151		-	10602733
0.75	0.0010	P21-activated kinase 3	*Pak3*	10602198
1.34	0.0473	cdna:known chromosome:NCBIM36:11:9875883:9876050:-1 gene:ENSMUSG00000069964	-	10598794
1.34	0.0306	Carbonic anhydrase 4	*Car4*	10379866
1.34	0.0292	Phospholipase C, gamma 2	*Plcg2*	10575799
1.34	0.0138	Arrestin domain containing 3	*Arrdc3*	10406407
1.34	0.0182	cdna:known chromosome:NCBIM36:5:62890685:63037911:-1 gene:ENSMUSG00000037999	-	10530100
1.34	0.0027	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	*Adamts3*	10531201

1.35	0.0138	Solute carrier family 2 (facilitated glucose transporter), member 3	*Slc2a3*	10547641
1.35	0.0018	Proline/serine-rich coiled-coil 1	*Psrc1*	10495316
1.35	0.0246	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	*Adamts3*	10531197
1.35	0.0225	Solute carrier family 4 (anion exchanger), member 1	*Slc4a1*	10391649
1.35	0.0019	BCL2-associated X protein	*Bax*	10563303
1.35	0.0304	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	*Adamts3*	10531177
1.36	0.0122	Mitogen-activated protein kinase-activated protein kinase 3	*Mapkapk3*	10596637
1.36	0.0213	Premature mRNA for mKIAA0233 protein	*Fam38a*	10582337
1.36	0.0293	Polymerase (DNA directed), kappa	*Polk*	10411306
1.36	0.0334	cdna:Genscan chromosome:NCBIM36:6:92752350:92908659:-1	-	10546450
1.37	0.0425	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	*Adamts3*	10531175
1.38	0.0089	RIKEN cDNA 1700007K13 gene	*1700007K13Rik*	10481272
1.39	0.0038	cdna:known chromosome:NCBIM36:3:12838528:12838935:1 gene:ENSMUSG00000045699	-	10518346
1.40	0.0106	RIKEN cDNA 4933426M11 gene	*4933426M11Rik*	10396919
1.40	0.0064	MKIAA1991 protein	*Rnf169*	10565852
1.40	0.0377	Six6 opposite strand transcript 1	*Six6os1*	10400948
1.40	0.0138	Strain ILS glutamate receptor subunit 3	*Gria3*	10599348
1.41	0.0325		-	10528476
1.41	0.0192	RIKEN cDNA 2410018L13 gene	*2410018L13Rik*	10394833
1.42	0.0053	PLZF gene	*Zbtb16*	10593225
1.42	0.0304		-	10550181
1.42	0.0422	cDNA sequence BC039210	-	10582376
1.42	0.0126	Carnitine palmitoyltransferase 1c	*Cpt1c*	10562989
1.44	0.0114	Ras homolog gene family, member D	*Rhod*	10464754
1.45	0.0141	cdna:known chromosome:NCBIM36:15:61867652:62072228:1 gene:ENSMUSG00000072566	-	10424404
1.45	0.0169	MI0000687 miR-17 stem-loop	-	10416948
1.46	0.0138	S-adenosylhomocysteine hydrolase	*Ahcy*	10439762

1.46	0.0075	PTP36-D isoform	*Ptpn14*	10352661
1.46	0.0007	G two S phase expressed protein 1	*Gtse1*	10426016
1.47	0.0099	Cyclin-dependent kinase 6	*Cdk6*	10519324
1.47	0.0378	Sec61 beta subunit	*Sec61b*	10426889
1.47	0.0010	Apoptosis enhancing nuclease	*Aen*	10554233
1.50	0.0192	Stress-induced protein SIP18 (Sip)	*Trp53inp1*	10503259
1.50	0.0007	Germ cell nuclear factor protein	*Nr6a1*	10482249
1.51	0.0010	Zinc finger protein 365	*Zfp365*	10369783
1.51	0.0065	Lin-28 homolog (C. elegans)	*Lin28*	10517159
1.52	0.0031	Tripartite motif-containing 71	*Trim71*	10597427
1.54	0.0057	DNA-damage-inducible transcript 4-like,	*Ddit4l*	10496373
1.56	0.0032	RIKEN cDNA B230120H23 gene	*B230120H23Rik*	10472893
1.59	0.0046	Serine (or cysteine) peptidase inhibitor, clade E, member 2	*Serpine2*	10355984
1.61	0.0087	protogenin homolog (Gallus gallus)	*Prtg*	10586971
1.63	0.0165	Insulin receptor substrate 4 (Irs4	*Irs4*	10607059
1.63	0.0049	RIKEN cDNA 4632434I11 gene	4632434I11Rik	10565570
1.66	0.0018	Solute carrier family 19 (thiamine transporter), member 2	*Slc19a2*	10351259
1.66	0.0363	cdna:known chromosome:NCBIM36:1:87441024:87441395:-1 gene:ENSMUSG00000073628	-	10356291
1.68	0.0467	similar to Xlr-related, meiosis regulated (LOC664923), mRNA gene:ENSMUSG00000073255	-	10599064
1.75	0.0018	tumor necrosis factor receptor superfamily, member 10b	*Tnfrsf10b*	10416230
1.92	0.0044	Anoctamin 3, transcript variant 2	*Ano3*	10485718
1.93	0.0007	Sestrin 2	*Sesn2*	10516932
2.13	0.0020	Adenylate kinase 1	*Ak1*	10471474
2.16	0.0012	RIKEN cDNA 4930429B21 gene	*Zmat3*	10497673
2.17	0.0010	Pleckstrin homology-like domain, family A, member 3	*Phlda3*	10350146
2.49	0.0057	cdna:novel chromosome:NCBIM36:2:110458979:110459164:-1 gene:ENSMUSG00000074969	-	10485745
2.72	0.0325	Vomeronasal 2, receptor 50	*Vmn2r43*	10559883

2.87	0.0007	Cyclin G1	*Ccng1*	10385271
3.10	0.0007	Cyclin-dependent kinase inhibitor 1A(P21)	*Cdkn1a*	10443463
5.09	0.0007	Ectodysplasin A2 isoform receptor	*Eda2r*	10605874

Supplementary Table 2 Microarray analysis of E10.5 cortices. Shown are average transcript levels as a ratio of $Magoh^{Mos2/+}$/control, actual *P* values, gene name, gene symbol, and Affymetrix transcript cluster ID. Shown are those transcripts for which *P*<0.05 and with levels altered by at least 25%. Microarray data was generated from 5 biological replicates each of RNA from control and $Magoh^{Mos2/+}$ E10.5 cortices. *P* values were calculated using unpaired two-tailed t test. Data were corrected with Benjamini and Hochberg and are log transformed.

Figure #	**Statistical Test**	**Measurement**	**Actual *P* value**
1b	t test	**brain size/body size**	0.045
1e	t test	**gene expression**	
		magoh RNA 10.5	0.0001
		magoh RNA 12.5	0.0001
3o	t test	**Pax6 density**	
		E13.5	0.3401
		E14.5	0.0674
		E16.5	0.3416
3q	t test	**Tbr2 density**	
		E13.5	0.0016
		E14.5	0.0027
		E16.5	0.010961797
3p	t test	**VZ thickness**	
		E13.5	0.056569183
		E14.5	0.124822923
3r	t test	**BrdU+Tbr2+**	
		%Tbr2	0.113785335
		%BrdU	0.013072306
4o	fisher's test	**#TuJ1vs.nonTuJ1**	<0.0001
4p	t test	**IZ,CP thickness**	
		E13.5	0.002194927
		E14.5	0.00354797
S6A, 5b	chi square analysis	**mitotic orientation**	
		E10.5	0.97
		E11.5	0.001086296
		E12.5	0.011086495
5c	fisher's test	**%cells**	
		polyploidy	p=2.26E-9
		aneuloidy	p=0.00041
5i	t test	**avg.centrosome distance**	<0.0001
5j	t test	**%monopolar spindles relative to scrambled**	
		Magoh	0.002249217
		Rbm8a	0.000686706
		Eifa3	0.00683902
		Casc3	0.065469945
5k	t test	**#γ-H2AX cells**	
		E11.5	0.005203198
		E12.5	0.002324296
		E13.5	0.011882207

		E14.5	0.00171028
5n	chi square analysis	**γ-H2AXfoci relative to scrambled**	
		Magoh	<0.001
		Rbm8a	<0.001
		Casc3	<0.001
		Eif4a3	<0.001
S2h	t test	**brain dimensions**	
		length b6-or	3.26326E-06
		width b6-or	3.60682E-06
		length bac;or-or	2.63362E-06
		width bac;or-or	0.002378577
S3a	t test	**neuronal thickness**	
		Foxp1	0.004098614
		Foxp2	0.009130009
		Tbr1	0.010837506
S3b	t test	**total # neurons**	0.000708535
S3c	t test	**cortical thickness**	
		E11.5	0.327108122
		E12.5	0.043235011
		E13.5	1.84194E-05
		E14.5	1.47209E-05
S4b	t test	**BrdU in SVZ/IC/CP**	0.000749908
S4c	t test	**BrdU density**	0.110041523
S6b	t test	# PH3 cells	
		E10.5	0.264256403
		E14.5	0.402250288
		gene expression	
S8a	t test	lis1-10.5	0.0001
		lis1-12.5	0.9898
S4d	t test	pax6-12.6	0.733
S4d	t test	tbr2-12.5	0.001
S7c	t test	**gene expression**	
		rbm8a	0.042
		casc3	0.039
		ddx48	0.023
		magoh1	0.035
		magoh2	0.059
6f	t test	**electroporations**	t test lucif
		%Tbr2+cells/GFP	
		lucif	
		magoh vs lucif	0.04098
		magoh+lis vs lucif	0.813
		lis alone vs. lucif	0.041551015
		magoh+lis vs magoh	0.029204646

		lis alone vs. magoh	0.001054589
		lis alone vs. Magoh+lis	0.106835566
6d,s8c	t-test	**Electroporations**	
		Magoh shRNA vs.	
		Luciferase shRNA	
		outer cp	0.022855816
		cp	0.008822419
		iz	0.196402522
		svz	0.362332387
		lower svz/vz	0.001697782
		Magoh shRNA vs.	
		LIS1 rescue	
		outer cp	0.027018164
		cp	0.101226367
		iz	0.021996517
		svz	0.474832994
		lower svz/vz	0.000671697
		Magoh shRNA vs.	
		LIS1 alone	
		outer cp	0.001042953
		cp	0.428024035
		iz	0.013383953
		svz	0.052360689
		lower svz/vz	1.41685E-05
		Luciferase shRNA	
		Vs.LIS1 rescue	
		outer cp	0.944024334
		cp	0.214317145
		iz	0.349955854
		svz	0.051506021
		lower svz/vz	0.552206334
		Lis1 alone v.	
		Luciferase shRNA	
		outer cp	0.312030895
		cp	0.001619618
		iz	0.272431828
		svz	0.001009096
		lower svz/vz	0.012730874
		Lis1 alone v.	
		Lis1 rescue	
		outer cp	0.283458359
		cp	0.020204393
		iz	0.900414323
		svz	0.125486243
		lower svz/vz	0.045299940

Supplementary Table 3. Statistical analyses. All t-tests were unpaired, two-tailed. “s” refers to Supplementary Figure.

Supplementary Data 1. Serum chemistries, hematology, and organ weights of control and mutant animals. Excel spreadsheets reporting values measured for individual animals and average values for (1) hematological values measured in blood, (2) serum chemistries, (3) organ weights.