Figure S1

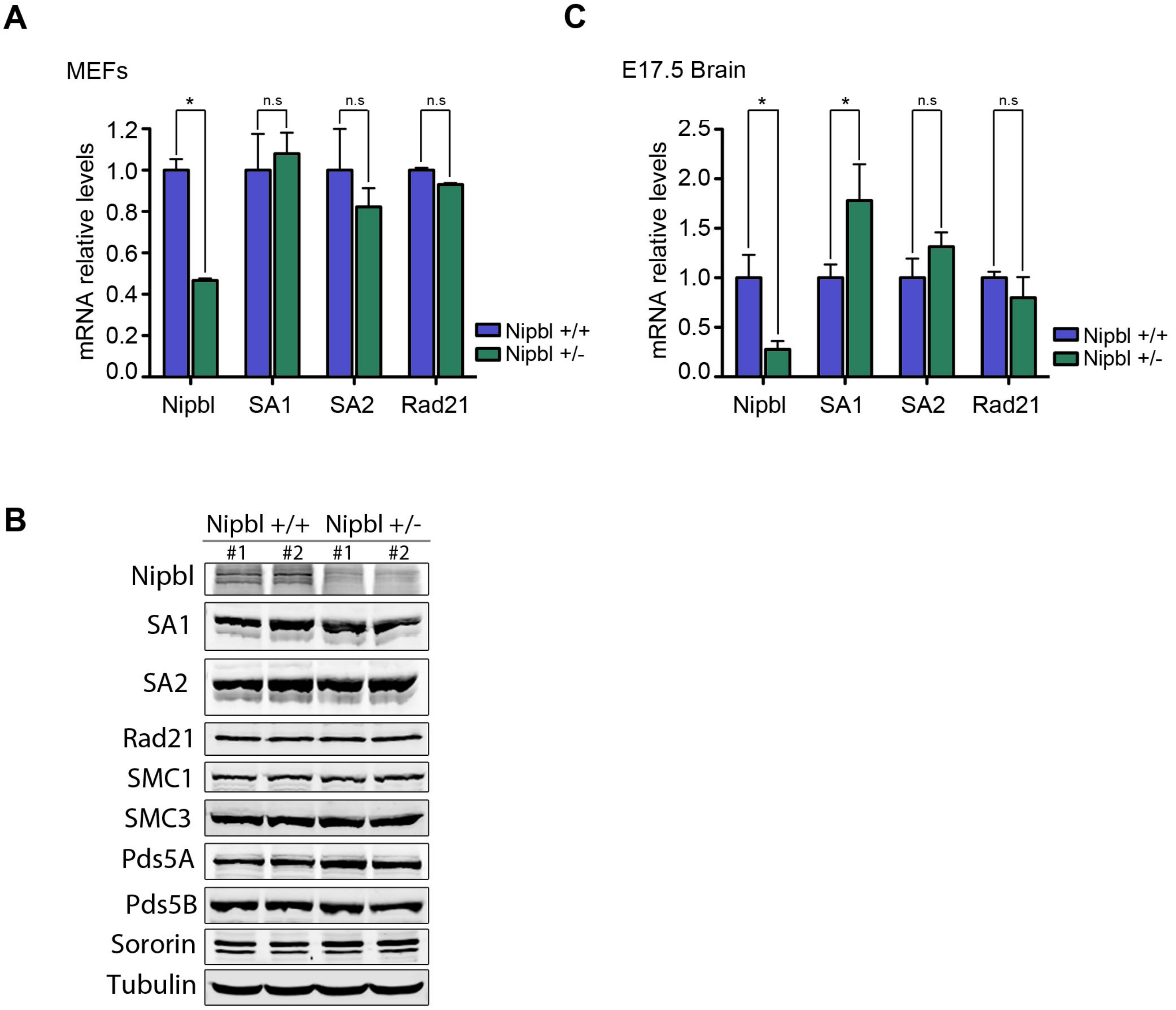

Figure S1. Changes in mRNA and protein levels in Nipbl heterozygous MEFs and brains. (A) mRNA levels of Nipbl and cohesin complex subunits in Nipbl heterozygous MEFs relative to wild-type controls (2 different clones per genotype and 3 independent qPCR reactions per condition). * *P* <0.05, ** *P* <0.01, n.s = not significant. (B) Western blot analysis of whole-cell extracts from wild-type and Nipbl +/- MEFs (2 clones each) with the indicated antibodies against cohesin subunits and its regulatory factors. Tubulin was used as loading control. (C) mRNA levels of Nipbl and cohesin subunits in brains from Nipbl heterozygous E17.5 embryos relative to the wild-type littermates (3 embryos per genotype and 3 independent qPCR reactions per condition). * *P* <0.05, ** *P* <0.01, n.s = not significant.

Figure S2

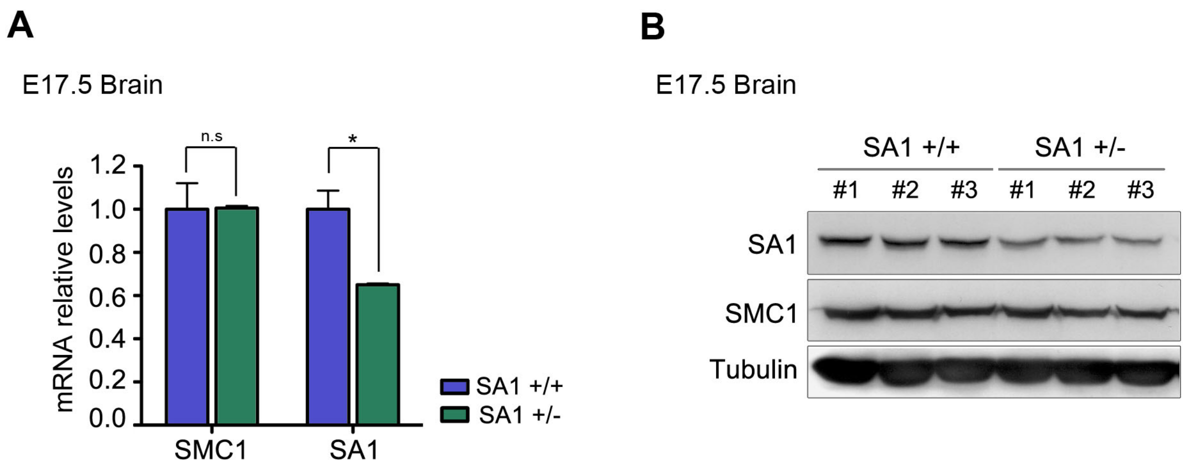

Figure S2. Changes in mRNA and protein levels in SA1 heterozygous brains.

(A) mRNA levels of cohesin complex subunits SMC1 and SA1 in brain tissue from SA1 heterozygous embryos relative to wild-type controls (3 embryos per genotype and 3 independent qPCR reactions per condition).). * *P* <0.05, n.s = not significant. (B) Western blot analysis of whole-cell extracts from SA1+/+ and SA1+/- embryonary brain tissue (3 embryos per genotype) with the indicated antibodies. Tubulin was used as loading control.

Supplementary Table S1: Primers used for Real Time-qPCR

Primer	***Sequence (5’-3’)***
Nipbl Fw	AGTCCATATGCCCCACAGAG
Nipbl Rev	ACCGGCAACAATAGGACTTG
SA1 Fw	AGGCTTTCATGCTGCTCTGT
SA1 Rev	TCCATGCTTTGGTTTTCCTC
SA2 Fw	GGGGGAGGAACTGTCTTTCT
SA2 Rev	CCTTCAATGTCTTCAAAATCTGTG
Rad21 Fw	CCCATTGGGACAAGAAGCTA
Rad21 Rev	GTCTGCGAGGAGGTATTTGG
Myc Fw	TCGCCTCACTCAGCTCCCCT
Myc Rev	ACCGTCCGCTCACTCCCTCT
Pcdh7 Fw	GACGGCTACTGCGCCTGGAT
Pcdh7 Rev	TGGGGGTGTCCACCAGGACA
Pcdh17 Fw	CCCAATAGGCTCTCGGCGCA
Pcdh17 Rev	AGCGGACTGCATCTCCGAGC
Pcdh11X Fw	CTGCGAGCTGTGGCGGTAGA
Pcdh11X Rev	TCTCCTGGGCGCCAGACTGA
Pcdhb16 Fw	AGGTCTCAGCCCTCGGAAAAGGA
Pcdhb16 Rev	GAATAGCGCCTCAGTTCCCCTGC
Pcdhb17 Fw	TGTGAAGCAAACGCCGAGGAAAGA
Pcdhb17 Rev	GGAAATGATCCGAGCCCTGCGAT
Pcdhb20 Fw	GGTATTACAGGAGCTTCACCGGCA
Pcdhb20 Rev	AGCACTCGCCTGAGACAATCCC
Pcdhb21 Fw	ACAAAGGTGGGGCACCCACAAG
Pcdhb21 Rev	TGGCAAGAACCGAGGACCCTTC
GAPDH Fw	TGCACCACCAACTGCTTAGC
GAPDH Rev	GAGGGGCCATCCACAGTCTTC

Supplementary Table S2: Primers used for ChIP-qpCR

Genomic Region	Primers	Sequence (5’-3’)
Chr 15: 61,814,801 - 61,815,300	**Myc**	Fw ACAAATCCGAGAGCCACAAC Rev TCGAGCTCATTGCACAATTC
Chr 5: 58,105,123 - 58,105,623	**Pcdh7**	Fw TTTGTCCCTTGGTGGAGTTC Rev AGGGTCGGGAGTCTTTCATT
Chr 14: 84,838,181 - 84,838,727	**Pcdh17**	Fw TTCCCGGTGTCAATCAATTT Rev TACATACTGG TCCCCCTTG
Chr X: 117,401,147 -117,401,603	**Pcdh11X**	Fw AGTCTGCTTTTGCCAGGTGT Rev ACCCTGAAAATCCTCCAAGG
Chr 18: 37,644,356 - 37,644,924	**Pcdhb17**	Fw GGCCAGTTTCTCACCACCTA Rev GCAGTCTCCATGGCTCTTTC
Chr 18: 37,672,967 - 37,673,448	**Pcdhb21**	Fw TGCAGGACAGGATGAGAGAA Rev GGCAGCTCAGAGAGTGGTTC