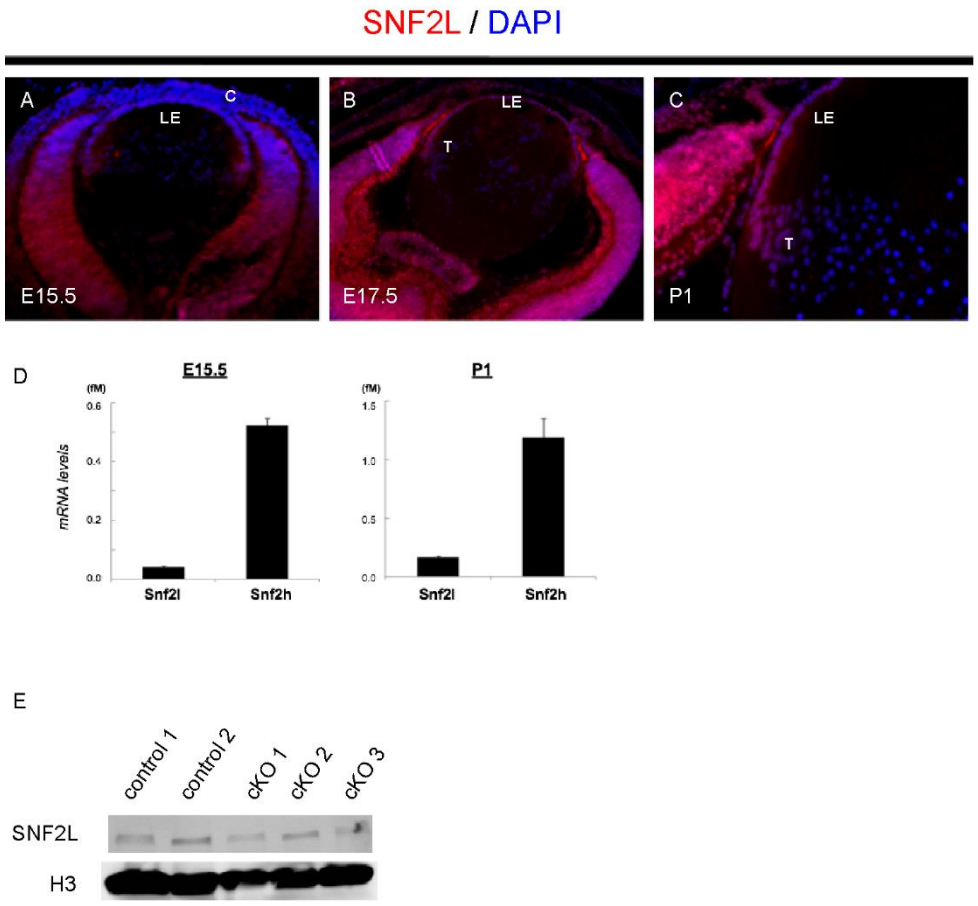
Supplementary Table S1. Classification of transcriptional changes of genes in major biological functions by gene ontology (GO) in the Snf2h mutants.

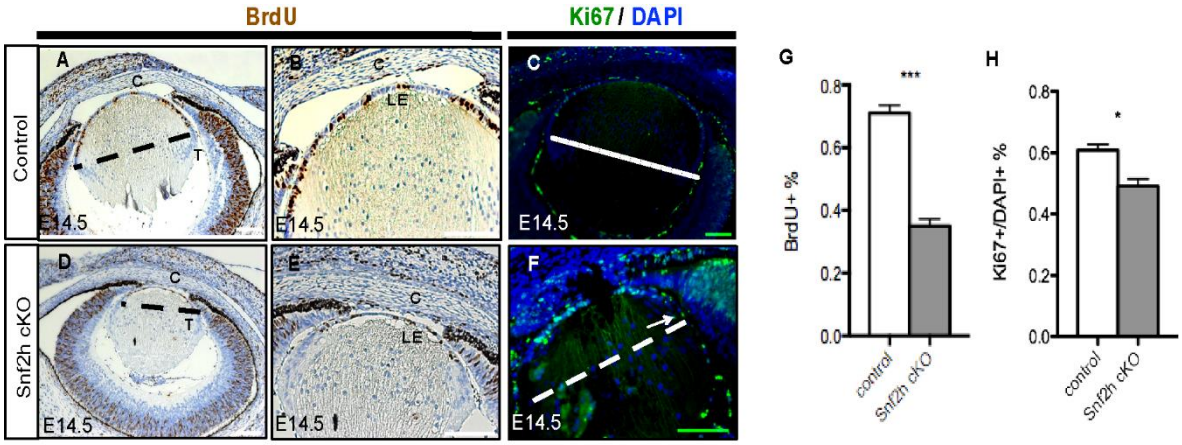
Terms	Catagories	Genes(Red=Upregulated; Blue=Downregulated)
GO: 0006325	~chromatin organization	HIST2H2AA2, EZH1, HIST1H2AD, ARID4B, CTCF, HIST2H3C1, LOC100047441, CBX8, HIST2H2AA1, MLL5, HIST2H2AC, SMARCD1, PBRM1, MLL3, KDM5A, HIST3H2BA, BAZ2A, DNMT3B, KDM5B, MLL1, CHD4, DNMT3A, SATB1, HIST1H1C, MTA2, HMG20A, BANP, ARID1A, MBD3, SUV420H2, HDAC3, PRDM9, SMARCE1, BAZ1B, BPTF, JMJD6, MSL1, SMARCC1, ASH1L, PHF21A, SMARCA2, APBB1, NCOR1, RNF20, HIST1H2AN, SMARCA4
GO: 0045449	~regulation of transcription	THRA, LOC100044968, CNOT3, BBX, NR2E3, RORA, CBX8, CNOT4, PNN, IGHMBP2, MAGED1, MLL5, SIN3A, LOC100047138, MED27, PQBP1, MLL3, MLL1, SATB1, TCFAP2B, RCOR2, MTA2, TCFAP2A, HMG20A, TAF6L, PPARGC1A, DDIT3, SUV420H2, PRDM9, HIF1A, PIAS4, RFC1, BAZ1B, VEGFA, MGA, ZFP260, VGLL4, SMARCA2, SMARCA4, FUS, HMGB1, HMGB2, SOX4, NFKBIA, SOX9, NR2C2, LHX1, ELK4, PBRM1, TCF4, LHX9, DNMT3B, TCF25, HIP1, PLAGL2, KLF6, DNMT3A, TESC, TAF7, CELSR2, SNW1, ZFP148, SMAD1, ZFP445, ZFP444, USF1, SAFB2, NRF1, RNF6, HDAC3, MLX, SMARCC1, ATF7, SUPT16H, RFX2, NCOR1, NCOR2, KLF3, NKAP, LOC100046855, BACH1, ELF2, EZH1, CCNT1, ARID4B, CTCF, PHF20, ZKSCAN3, BZW1, LBH, POU5F1, ANP32A, LRRFIP1, KDM5A, KDM5B, SERTAD2, SSBP3, SSBP2, ARID5B, ZFX, RUNX1T1, GTF2H4, BANP, TLE1, SPEN, TOPORS, MBD3, PURB, PCGF1, JMY, PURA, NCOA1, BRWD1, BPTF, HMG1L1, BTG2, GTF2I, ASH1L, HIPK2, LOC637733, MDM4, RBM39, MED1, ZFP395, MTDH, UBE3A, NFIX, ZFP318, ZFP316, 5730403M16RIK, ZFP191, CENPB, RB1CC1, GATAD2B, ZFP219, BCL9L, NFATC2, ING1, ETV5, BAZ2A, CHD4, IL4, NLK, HMBOX1, ILF3, DACH1, ATRX, PKNOX1, GMCL1, ID2, UBTF, JMJD6, THRAP3, PHF21A, ZBTB3, ID3, TBL1X, NFIC, APBB1
GO: 0032259	~methylation	SATB1, DNMT3A, ILF3, CTCF, SUV420H2, MLL5, PRMT1, PRDM9, BTG2, MLL3, BAZ2A, DNMT3B, MLL1
GO: 0007049	~cell cycle	CCNT1, MLL5, SIN3A, EVI5, CEP250, CDKN2D, RANBP1, PARD3B, TUBB3, ASPM, ESCO1, ZC3HC1, CEP110, SKP2, BANP, DDIT3, JMY, LOC100045547, PRDM9, SPAG5, MDM2, PDCD6IP, MDM4, SEPT6, PPP2R3A, RABGAP1, NEK1, CAMK2G, CEP164, CEP55, ZFP318, SPC25, GADD45GIP1, RB1CC1, CLASP1, ING1, APC, EXO1, PDS5A, CENPE, CDC20, 9130404D08RIK, ATM,
GO: 0000280	~nuclear division	ZC3HC1, PDS5A, NEK1, CENPE, CDC20, CEP164, CEP55, 9130404D08RIK, SPC25, RPS6KA2, SPAG5, CLASP1, SMC1A, CIT, TUBB3, ASPM, APC
GO: 0042127	~regulation of cell proliferation	WNT5A, APOBEC1, FGFR3, IL18, BTC, PAX3, PMAIP1, SKAP2, SOX9, MSX2, ARX, PRL2C3, PRL2C4, HOXA3, GATA3, TDGF1, TRP63, LHX5, HSF4, CALCRL, TFF1, FIGF, FANCA, PRL2C2, TES, CLEC2I, NOX4, KLF5, AR, ICOSL, NANOG, CD3E, IGH-6, DBH, LEFTY1, SHOX2, SMO, MSX1, EREG, SERPINB5, CCND2, NOTCH4, NR5A2, KLF4, AY074887
GO: 0002009	~morphogenesis of an epithelium	WNT5A, KRT6A, AR, FGFR3, BTRC, CELSR1, PAX3, SOX9, ALDH1A1, SFRP1, SERPINB5, HOXA5, TRP63, FOXD1
GO: 0006355	~regulation of transcription, DNA-dependent	ZFP46, HTATIP2, LOC100047651, ANKRD1, PAX3, HOXD10, HOXC8, FLI1, PAX9, GATA3, TDGF1, TRP63, SOX15, HSF4, PITX3, TBL1XR1, AR, NANOG, PPARGC1A, HOXD9, INHBA, SMO, MSX1, HOXD8, MNDA, FOXC1, ZFPM1, MTDH, EHF, SOX9, TCFCP2L1, ARX, MSX2, TAL1, FOXQ1, HOXA3, HOXA5, NFAT5, HOXA10, LHX5, LHX8, FOXD1, NKX2-2, PRL2C2, KLF5, REX2, ZFP386, CDKN1C, SHOX2, HOXB1, SALL4, NR5A2, NFIA, KLF4

Supplementary Table S2. A list of primers (Dnase2b, Foxe3, Hsf4, Snf2l and three control genes: B2M, SDHA, and HPRT).

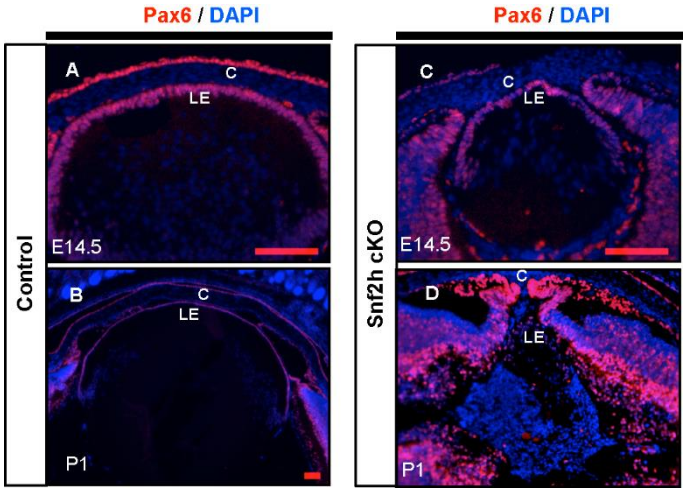
Gene	Primer direction	Sequence 5' →3'
B2m	Forward	TGGTGCTTGTCTCACTGACC
B2m	Reverse	TATGTTCGGCTTCCCATTCT
Bcl2	Forward	GGGAAACACCAGAATCAAGT
Bcl2	Reverse	AGCCAGGAGAAATCAAACAG
Bfsp	Forward	GTTACTGGGATGAGGGAGGAG
Bfsp	Reverse	CTGCAGCTCAGCTTTCTGTG
Cdh1	Forward	CAAAGTGACGCTGAAGTCCA
Cdh1	Reverse	TACACGCTGGGAAACATGAG
Cdkn1b (P27)	Forward	TCAAACGTGAGAGTGTCTAACG
Cdkn1b (P27)	Reverse	CCGGGCCGAAGAGATTTCTG
Cdkn1c (P57)	Forward	TCCTGCACCCGGGACT
Cdkn1c (P57)	Reverse	GTTCGACGCCTTGTTCTCC
Dnase2b	Forward	GCCCAGGGTCTAAACTTCGT
Dnase2b	Reverse	TTCTGCCAGGTTTGTGCTAA
Dnmt3a	Forward	GTGCAGAAACATCGAGGACA
Dnmt3a	Reverse	ATGCCTCCAATGAAGAGTGG
Fgfr1	Forward	GTTTAAGCCTGACCACCGAA
Fgfr1	Reverse	GAAGGCACCACAGAATCCAT
Fgfr3	Forward	GCCTGCGTGCTAGTGTTCT
Fgfr3	Reverse	CCTGTACCATCCTTAGCCCAG
Foxe3	Forward	GGTGGCTGATTATGGTATGGATTCC
Foxe3	Reverse	ATCAAGAAGGAAGGCCAAAGCG
Gsn	Forward	TCCGGCTACTTCAAGTCTGG
Gsn	Reverse	CTCTGGACCACCACCTCATT
Hes1	Forward	CAACACGACACCGGACAA
Hes1	Reverse	CATTTATTCTTGCCCTTCGC
Hif1a	Forward	TTCTCAGTCGACACAGCCTC
Hif1a	Reverse	CCAAAAGTTCTTCCGGCTC
Hsf4	Forward	GGCACAAGTAGGAGCCAAGAGTC
Hsf4	Reverse	TTCCTGCATGGCGCAGTCT
Hod	Forward	CAACAAGGTCAACAAGCACC
Hod	Reverse	AACCATTTCTGCGTCTGCTC
Hprt	Forward	GTTGTTGGATATGCCCTTGA
Hprt	Reverse	GGCTTTGTATTTGGCTTTTCC
Jag1	Forward	GTCCCAAGCATGGGTCTTGT
Jag1	Reverse	TGCACTTGTCGCAGTACAGG
Mab21l1	Forward	CAGGAACCGCGTTTCATCAG
Mab21l1	Reverse	CAGGAACCGCGTTTCATCAG
Notch4	Forward	CCAGAATGCGAGACAGAACTG
Notch4	Reverse	GGTCAACCCCATGTAGCCTG
Pax6	Forward	GCACATGCAAACACACATGA
Pax6	Reverse	ACTTGGACGGGAACTGACAC
Pitpnm2	Forward	GCTAGTCCTAGCCTTGAGGAAA
Pitpnm2	Reverse	TTGTACACTTGCTGACACGCT
Prox1	Forward	CAGCGGACTCTCTAGCACAG
Prox1	Reverse	GCCTGCCAAAAGGGGAAAGA
Rbpj	Forward	TGCGGTTACATGGGACTGG
Rbpj	Reverse	GGTCTTGGCACAACCAAATTC
Sdha	Forward	GAGGAAGCACACCCTCTCATA
Sdha	Reverse	GCACAGTCAGCCTCATTCAA
Six3	Forward	CCCGGCTTCTCTTACCTTTCT
Six3	Reverse	GAATCGGCGAAGTTTGGCAAC
Smarca2	Forward	CCACCAAGTCTGAAGATCGTG
Smarca2	Reverse	CCGCCTGAAGATTTAAGCCCA
Smarca4	Forward	TGCTGAAGGACAGACACCTG
Smarca4	Reverse	GAGGATCTTGCCACTCTCCA
Smarca5	Forward	AGAGCTGTTCGCACATTTCAT
Smarca5	Reverse	CCCTGGTTTCATCTTCAAGGGT
Smarcd1	Forward	GACGATGACTGATGTGGTGGG
Smarcd1	Reverse	ACCTTGGAGTAGAAGTATCGGC
Smarce1	Forward	AAAAGACCATCTTATGCCCCAC
Smarce1	Reverse	CCTGTAGTTGTTGTAGGCGAG
Spg5	Forward	CTGGAAGGCCAGCTAGATCC
Spg5	Reverse	TAACCCTCAGCTTGCTCACC
Vim	Forward	GTGCGCCAGCAGTATGAAAG
Vim	Reverse	GCATCGTTGTTCCGGTTGG
Wnt7b	Forward	CTTCACCTATGCCATCACGG
Wnt7b	Reverse	TGGTTGTAGTAGCCTTGCTTCT



Supplementary Fig. S1. Expression of Snf2l in wild type mouse eye. (A-C) Immunofluorescence (red) detection of Snf2l in the E15.5, E17.5 and P1 eye. **(D)** Relative expression of Snf2h and Snf2l in wild type E15.5 and P1 lens. **(E)** Western immunoblotting analysis of Snf2l expression in extracts prepared from "control" and Snf2h$^{-/-}$ cKO newborn eye tissues.

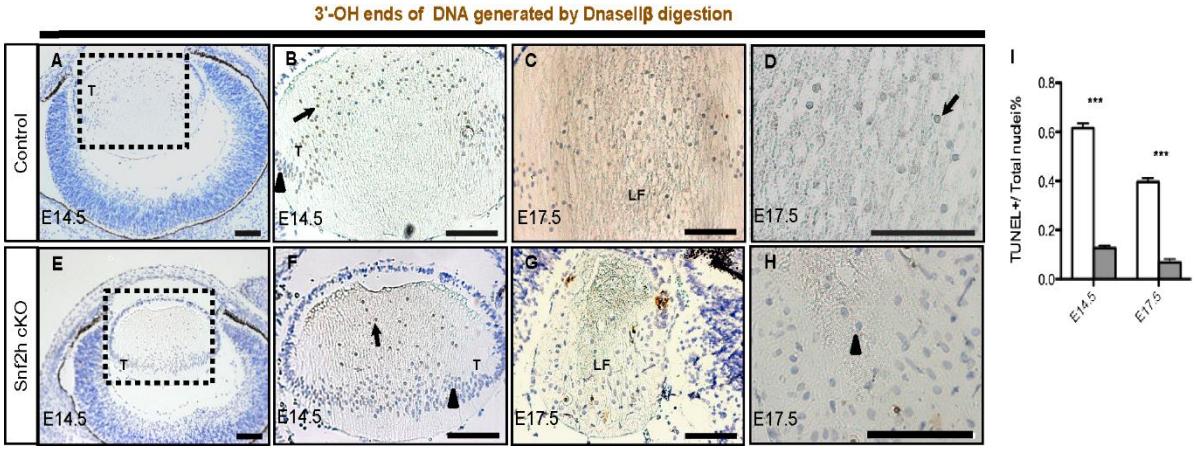


Supplementary Fig. S2: Depletion of Snf2h leads to a reduction of lens epithelial cell proliferation. (A-B) BrdU staining showed that the proliferating lens epithelial cells (brown) were present from the anterior of the lens epithelium to the lens equator. **(D-E)** In the Snf2h cKO lenses, the number of proliferating lens cells was markedly reduced, and the lens transitional zones were shifted forward. **(C-F)** The reduction of cell proliferation in the Snf2h cKO was observed by using the cell proliferation marker Ki67 (green). Nuclei were counterstained with DAPI (blue). **(G-H)** Quantification of BrdU and Ki67 positive cells versus the total number of lens epithelial cells. Scale bar = 100 μm. Pregnant females were injected with 5-bromo-2'-deoxyuridine (BrdU) (Sigma, St. Louis, MO) intraperitoneally (100 μg/g body weight). After two hours, the mice were sacrificed, and embryos were dissected and immediately fix with 4% paraformaldehyde. Sections were collected as described above. Monoclonal anti-BrdU was used and sections were counterstained with hematoxylin. Alternatively, embryo lens mid-sections were used to perform immunofluorescence with Ki67 antibody.



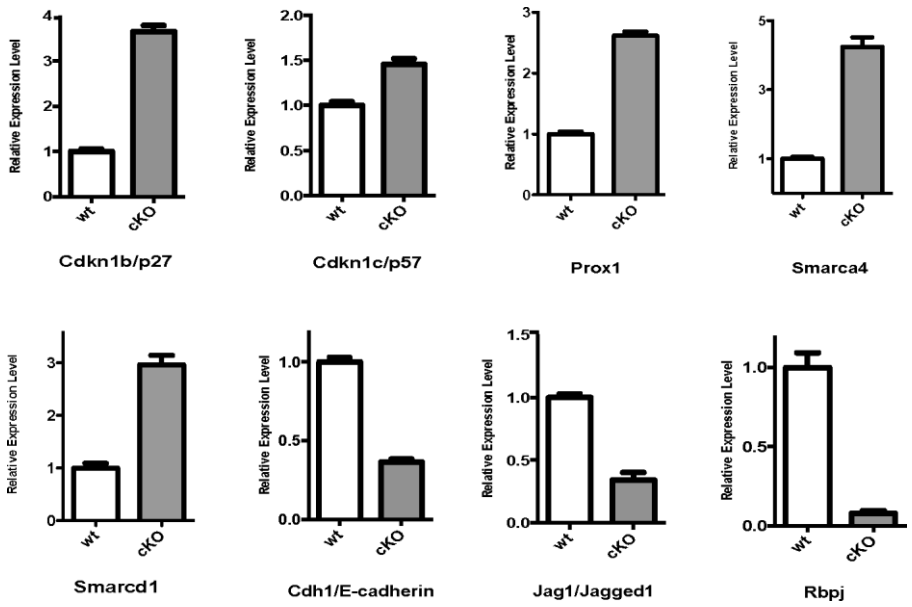
Supplementary Fig. S3. Expression of Pax6 in wild type and Snf2h mutated embryos.

(A-D) Attenuation of Pax6 expression (red) in Snf2h depleted lenses (E14.5 and P1). Lens epithelium, LE. The nuclei were counterstained with DAPI (blue). Scale bar = 100 μm.



Supplementary Fig. S4. Reduced formation of free 3'-OH ends in Snf2h mutated lens.

(A-H) The 3'-OH ends of DNA generated by DNase IIβ were evaluated by terminal deoxynucleotydyl transferase dUTP nick end labeling (TUNEL) staining (brown, source of kit) in E17.5 wild type and Snf2h depleted lenses. Panels B,D are higher magnification of panels A,C. Sections, prepared as described in Materials and Methods, were first deparaffinized and pretreated with proteinase K, followed by peroxidase blocking before TdT reaction. Sections were then incubated with Streptavidin-horse radish peroxidase (HRP) and counterstained with hematoxylin. Lens fiber cells, LF; Lens transitional zone, T. **(I)** Quantification of free 3'OH-ends of DNA. Quantification or cell counting was performed using NIH ImageJ or Axionvision software followed by data normalization ($n \geq 3$). To normalize pixel intensity, the mean value of least three immunoreactive negative regions from each staining section was subtracted from the examined region to score positive-stained cells. A minimum of three biological replicates (litter, embryos, and sections) were analyzed for all data sets. Histograms represent the mean ± the standard error of the mean (SEM). Samples and control groups were compared using a two-tailed, unpaired Student T-test to calculate p value. An asterisk (*) represents a statistically significant change ($p < 0.05$).



Supplementary Figure S5. Relative expression level of Cdkn1b/p27, Cdkn1c/p57, Prox1, Cdh1, Jag1, Rbpj, Smarca4 and Smarcd1 in the control and Snf2h$^{-/-}$ cKO eyes.