

### **Supplementary Figure 1**

MrBayes tree of STRAD gene in Metazoan using *Hydra magnipapillata* as the outgroup (46,47). The taxon name is composed of the species name, gene name (STRAD, STRAD $\alpha$ , or STRAD $\beta$ ), and gene ID (NCBI GI numbers and one Ensembl protein ID for *Equus caballus* STRAD $\alpha$ ). Scale bar represents amino acid replacements/site/unit evolutionary time.

Veleva-Rotse\_FigS2









Supplementary Figure 2 - STRAD splicing is developmentally regulated (A) Amplicon sequencing indicates that at least five variants arise in the amino terminal domain of STRADa. Arrows indicate RT-PCR primer placement. (B) RT-PCR of C-terminal STRADa splicing (primers span exons 9-12) of STRAD in multiple tissues. (C) STRAD $\beta$  splicing diagram in which arrows denote primers. Exon 8 is skipped in STRAD $\beta$ -2 creating a premature stop codon and truncated mRNA. (D-F) STRAD $\beta$  RT-PCR (D) the only reported splicing variant for STRAD $\beta$  indicates that this splicing event occurs in all tissues except skeletal and cardiac muscle. (E) STRAD $\beta$  splicing across developmental time in E14.5-E18.5 cortex. (F) STRAD $\beta$  splice variant expression in primary cultured interneurons, astrocytes and oligodendrocytes.



#### Veleva-Rotse\_FigS3

# Supplemental Figure 3 -STRAD Gene Structure, Mutant and Conditional Alleles

(A) The human and mouse STRAD $\alpha$  genes consist of 13 exons and STRAD $\beta$  has 12. Schematic of the human PMSE Syndrome deletion eliminating exons 9-13. Schematic of the mouse STRADα locus disrupted via insertional mutagenesis of a splice trap construct that eliminates gene expression and the conditional allele in which exons 7 and 8 are flanked by loxP sites. Schematic of the STRAD<sub>β</sub> conditional allele in which exon 2 (which includes the start codon) is flanked by loxP sites. Black boxes indicate untranslated regions of exons and white boxes indicate the open reading frame. (B) Western blot demonstrating a loss of STRAD $\alpha$  expression in a STRAD $\alpha^{--}$  E16.5 cortex, while

protein level is unchanged in STRAD $\alpha^{+/-}$  cortex. (C) STRAD $\alpha^{-/-}$  mice are not viable postnatally, while almost normal Mendelian ratios exist prenatally. (D) Western blot indicating loss of STRAD $\alpha$  protein in the P30 STRAD $\alpha^{\text{ff}}$ ; Nes-cre<sup>+</sup> cortex compared with STRAD $\alpha^{\text{f+}}$ ; Nes-cre<sup>+</sup> littermate. (E-G) Primary culture cortical neurons from embryonic day 16.5 mouse cortex grown for 5 days *in vitro* and immunolabeled for MAP2/Tau. Indeterminate neurites are seen in (F-G) STRAD $\alpha^{-/-}$ ;STRAD $\beta^{\text{fl/fl}}$ ;Emx1-cre<sup>+</sup> neurons but not in (E) STRAD $\alpha^{+/-}$ ;STRAD $\beta^{\text{fl/fl}}$ ;Emx1-cre<sup>+</sup>. Scale bar=20um.



Veleva-Rotse FigS4

4<sup>1</sup>

+

-50kD

37kD

50kD

37kD

-50kD

37kD

50kD

37kD

## Supplemental Figure 4 – LKB1 Stability

(A) Up-regulation of LKB1 mRNA in STRAD<sup>-/-</sup> (KO) E16.5 cortex relative to STRAD<sup>+/+</sup>(WT) as assessed by gRT-PCR. WT N=3, KO N=4 from 2 different litters. Quantification of Western blot replicates: (B) Significant destabilization of LKB1 in  $STRAD\alpha$ KO protein E16.5 embryonic hearts. WT N=2, KO N=4 (C) MO25 levels are unchanged in STRAD $\alpha$  KO E16.5 cortex compared with WT. WT N=2, KO N=4. (D) STRAD $\alpha$  protein is destabilized in LKB1<sup>ff</sup>: Emx1-Cre⁺ E16.5 cortex compared with littermate controls. N  $\geq$  10 cortices of each genotype from at least 3 litters. (A-D) Error bars represent SEM; \*p<0.05, \*\*\*p<0.001 by Student's T-test. (E) Quantification of western blot analysis of the levels of LKB1 phosphorylated at serine 428/431 in primary cultures derived from either control or STRAD $\alpha$ -null

mice. (F) HEK293 cells were transfected with HA-tagged LKB1 and STRAD constructs. Representative Western blot anti-HA of untreated and 4hrs 50µg/mL cycloheximide treated cells, with actin as a loading control. (G) Quantification and comparison of LKB1 stability following 50 µg/ml cycloheximide treatment when co-transfected with STRAD $\alpha$  splice variants STRAD $\alpha$ -2, -1 or -7.



Supplemental Figure 5 – Subcellular localization of epitope-tagged LKB1 and STRAD Variants

Verification of subcellular localization for epitope-tagged LKB1 and STRAD constructs transiently transfected in HEK293 cells. (A-A'''') LKB1+GFP-expressing empty vector, (B-B'''') LKB1+STRADα-2. (C-C'''') LKB1+STRADβ-1, (D-D'''') The LKB1+STRADα-2 YHF (LKB1 binding mutant), (E-E'''') LKB1ΔNLS+GFP-expressing empty vector (F-F'''') LKB1ΔNLS+STRADα-2.

# Table S1

Target Protein	Species	Company	Concentration Used
Actin	Mouse	Millipore	1:10,000 (WB)
Cleaved Caspase3	Rabbit	Cell Signaling	1:1000 (IF)
GFP	Chicken	Aves	1:1000 (IF)
LKB1 D60C5	Rabbit	Cell Signaling	1:1000 (WB)
MAP2	Rabbit	Chemicon	1:10,000 (IF)
MAP2	Chicken	Covance	1:10,000 (IF)
Μ025α	Rabbit	Cell Signaling	1:1000 (WB)
STRADa	Rabbit	Sigma	1:1,000 (WB)
Tag1	Mouse IgM	DSHB	1:50 (IF)
Tau-1 Clone PC1C6	Mouse	Millipore	1:1,000 (IF)
Tubulin (βIII)	Mouse	BD	1:1000 (IF)

Table of antibodies used.