

Supplementary Data S1

TRPV4 acetylation in prenatal liver prevents low glucose-induced inhibition of mTORC1 and safeguards fetal development

This file includes:

Full sequence of TRPV4-WT, TRPV4-K608R, GCaMP6s

The details of constructing gene knock-in mouse models

Rosa26-LSL-TRPV4-WT-HA Genotyping Protocol

Rosa26-LSL-TRPV4-K608R-HA Genotyping Protocol

Gel source data

Full sequence: TRPV4-WT Homo sapiens CCDS9134.1

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Full sequence: TRPV4-K608R Homo sapiens

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Full sequence: GCaMP6s

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SMOC-Report for Rosa26 knock-in mouse model (TRPV4-WT)

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1. Background and Objective

1.1 Objective

Generation of the CAG-LSL-TRPV4-WT-HA-WPRE-pA cassette knock-in mouse model at Rosa26 gene locus via CRISPR/Cas9 technology.

1.2 Background

Gene Name (MGI Number): Gt(ROSA)26Sor (104735)

Gene URL Link (MGI) : <http://www.informatics.jax.org/marker/MGI:104735>

Gene URL Link (Ensembl) :

http://asia.ensembl.org/Mus_musculus/Gene/Summary?g=ENSMUSG00000086429;r=6:113067428-113077333

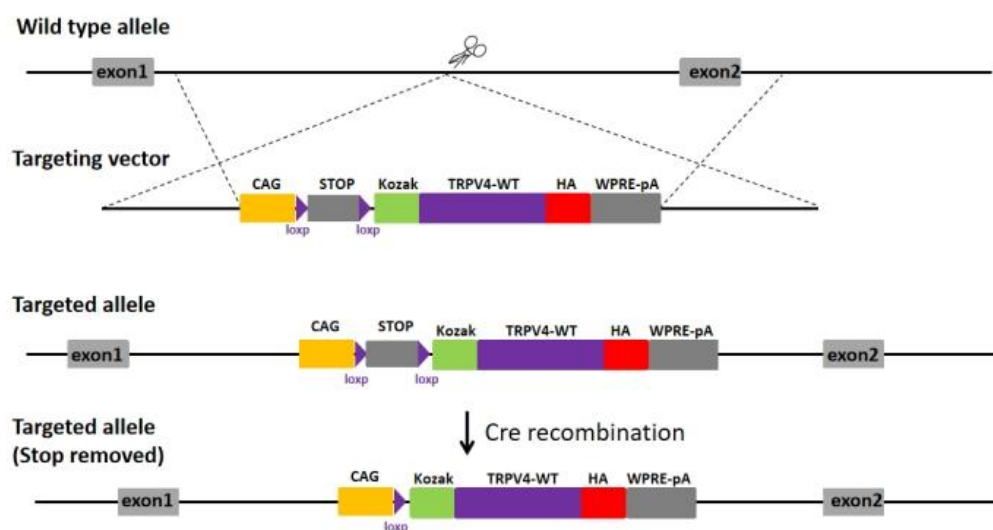
Knockin Cassette: CAG-LSL-TRPV4-WT-HA-WPRE-pA

2. Abstract

The project process was as follows: 1) Cas9 mRNA and gRNA were produced by in vitro transcription; 2) donor vectors were constructed by in-fusion. The plasmid structure contains 5'homologous arm (3.3 kb), Knock-in, 3'homologous arm (3.3 kb) ; 3) the mixture of Cas9 mRNA,gRNA and donor vector was micro-injected into fertilized eggs (C57BL/6J), then 1 F0 mouse that identified by PCR and sequencing was generated; 4) F0 positive mouse was crossed with wild-type C57BL/6J mice to generate 6 F1 mice.

3. Recombinant strategy

3.1 Strategy figure :



Strategy figure

3.2 Sequence of sgRNAs

gRNAs	Sequence (5'-3')
gRNA1	GGGGACACACTAAGGGAGCT TGG

4. Acquisition and genotypic identification of mice

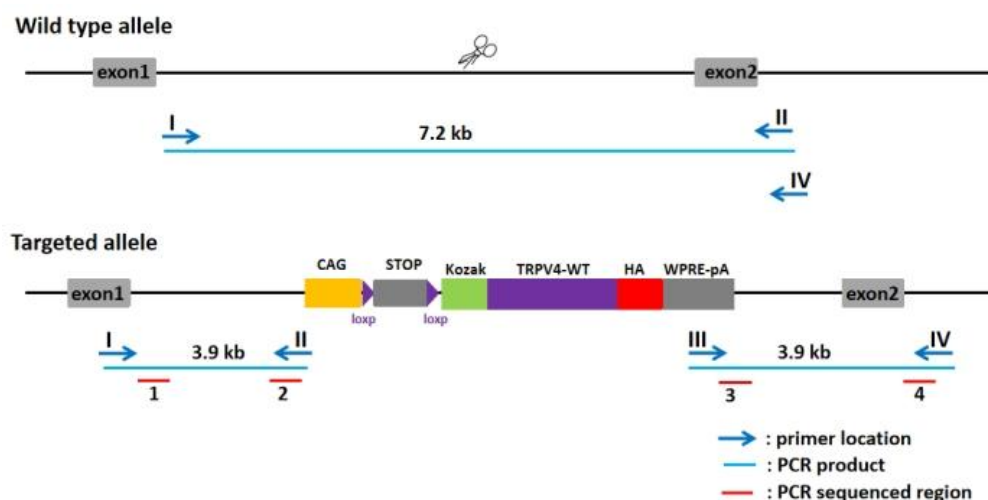
4.1 F0 mice genotyping

The injected fertilized eggs were transplanted into pseudo-pregnant mice, and the mice born about 20 days were F0 generation mice. The genotype were identified by PCR amplification and sequencing. Because the early cleavage rate of fertilized eggs is very fast, the F0 generation mice obtained are chimera and do not necessarily have the ability of stable inheritance. It is necessary to pass the positive F0 generation mice to obtain stable heritable F1 generation mice.

4.2 F1 mice genotyping

F0 generation positive mice were mated with wild type C57BL/6J mice to obtain F1 generation mice. The genotype of F1 generation mice were identified by PCR method and sequencing.

4.2.1 Genotyping strategy of F1 mice



Strategy of F1 mice genotyping

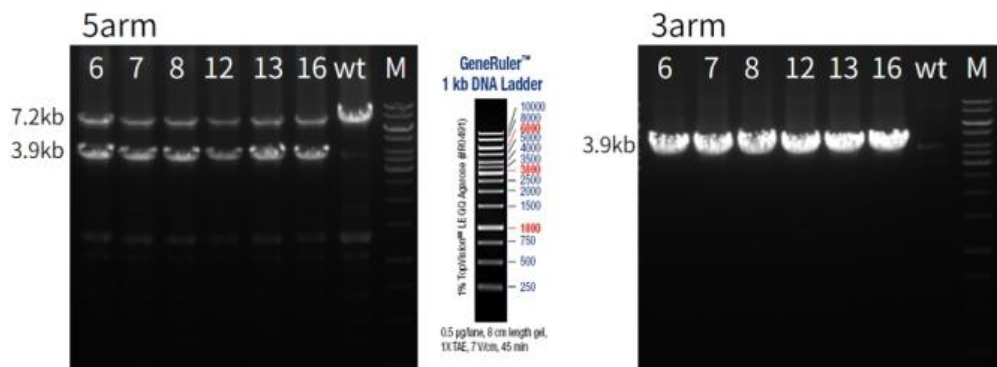
Genotyping method:

5'homologous arm: 3.9 kb fragment should be amplified in the homologous recombinant DNA, and 7.2 kb fragment can be amplified in the negative DNA.

3'homologous arm: 3.9 kb fragment should be amplified in the homologous recombinant DNA, and none of fragments can be amplified in the negative DNA.

4.2.2 PCR genotyping of homologous recombinant F1 mice

The number of homologous recombinant F1 mice were 6,7,8,12,13,16. The agarose gel electrophoresis of PCR results were shown in Figure 3. All positive PCR products were confirmed by sequencing.



Agarose gel electrophoresis of PCR results.

(number: the number of F1 mice; M: 1kb DNA ladder)

4.2.3 Method for identifying 5'homologous recombinant F1 mice

Primers:

Primer	Sequence 5' --> 3'	Primer Type
I	TTCTGTGAGACAGCCGGGTA	Forward
II	TTTTTGGGGGTGATGGTGGTC	Reverse

Reaction system:

Reaction Component	Volume (μ l)
ddH ₂ O	8.05
2xPCR Buffer	10
Primer I (20pmol/ μ l)	0.3
Primer II (20pmol/ μ l)	0.3
KOD-Multi&Epi-*	0.35
Genomic DNA	1
Total	20

* KOD-Multi&Epi- (TOYOBO, Code No: KME-101)

PCR program:

Step #	Temp (°C)	Time	Note
1	94	3 min	-
2	98	20 sec	-
3	63	20 sec	-
4	68	4 min	repeat steps 2-4 for 35cycles
5	68	5 min	-
6	12	-	hold

4.2.4 Method for identifying 3'homologous recombinant F1 mice

Primers:

Primer	Sequence 5' --> 3'	Primer Type
III	TTGCCAGCCATCTGTTGTT	Forward
IV	TGCCACCTTTCAGTTAGTTTGT	Reverse

Reaction system:

Reaction Component	Volume (µl)
ddH ₂ O	8.05
2xPCR Buffer	10
Primer III (20pmol/µl)	0.3
Primer IV (20pmol/µl)	0.3
KOD-Multi&Epi-*	0.35
Genomic DNA	1
Total	20

* KOD-Multi&Epi- (TOYOBO, Code No: KME-101)

PCR program:

Step #	Temp (°C)	Time	Note
1	94	3 min	-
2	98	20 sec	-
3	63	20 sec	-
4	68	4 min	repeat steps 2-4 for 35cycles
5	68	5 min	-
6	12	-	hold

4.2.5 Information of homologous recombinant F1 mice

Table: The information of positive F1 mice

Mice ID	DOB	Generations	Sex	Type	Genotype	Father	Mother
6	2023/9/11	F1	♂	KI	He	9F0	6J
7	2023/9/11	F1	♂	KI	He	9F0	6J
8	2023/9/11	F1	♂	KI	He	9F0	6J
12	2023/9/11	F1	♂	KI	He	9F0	6J
13	2023/9/11	F1	♀	KI	He	9F0	6J
16	2023/9/11	F1	♀	KI	He	9F0	6J

SMOC-Report for Rosa26 knock-in mouse model (TRPV4-K608R)

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8.1 F0 mice genotyping

8.2 F1 mice genotyping

8.2.1 Genotyping strategy of F1 mice

8.2.2 PCR genotyping of homologous recombinant F1 mice

8.2.3 Method for identifying 5'homologous recombinant F1 mice

8.2.4 Method for identifying 3'homologous recombinant F1 mice

8.2.5 Information of homologous recombinant F1 mice

5. Background and Objective

5.1 Objective

Generation of the CAG-LSL-TRPV4-K608R-HA-WPRE-pA cassette knock-in mouse model at Rosa26 gene locus via CRISPR/Cas9 technology.

5.2 Background

Gene Name (MGI Number): Gt(ROSA)26Sor (104735)

Gene URL Link (MGI) : <http://www.informatics.jax.org/marker/MGI:104735>

Gene URL Link (Ensembl) :

http://asia.ensembl.org/Mus_musculus/Gene/Summary?g=ENSMUSG00000086429;r=6:113067428-113077333

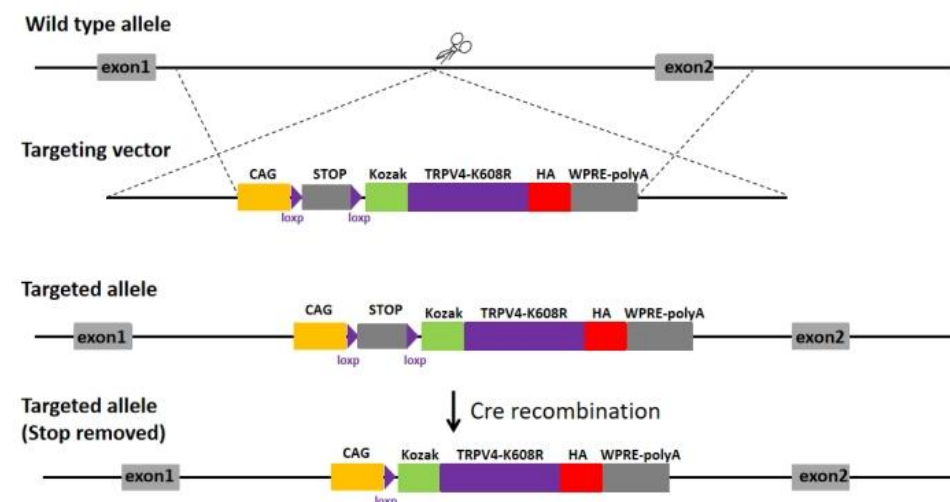
Knockin Cassette: CAG-LSL-TRPV4-K608R-HA-WPRE-pA

6. Abstract

The project process was as follows: 1) Cas9 mRNA and gRNA were produced by in vitro transcription; 2) donor vectors were constructed by in-fusion. The plasmid structure contains 5'homologous arm (3.3 kb), Knock-in, 3'homologous arm (3.3 kb) ; 3) the mixture of Cas9 mRNA,gRNA and donor vector was micro-injected into fertilized eggs (C57BL/6J), then 1 F0 mouse that identified by PCR and sequencing was generated; 4) F0 positive mouse was crossed with wild-type C57BL/6J mice to generate 9 F1 mice.

7. Recombinant strategy

7.1 Strategy figure :



Strategy figure

7.2 Sequence of sgRNAs

gRNAs	Sequence (5'-3')
gRNA1	GGGGACACACTAAGGGAGCT TGG

8. Acquisition and genotypic identification of mice

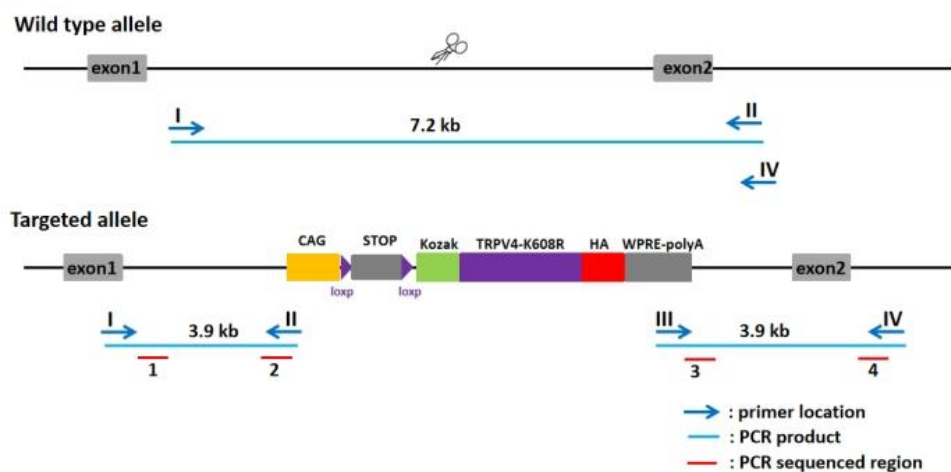
8.1 F0 mice genotyping

The injected fertilized eggs were transplanted into pseudo-pregnant mice, and the mice born about 20 days were F0 generation mice. The genotype were identified by PCR amplification and sequencing. Because the early cleavage rate of fertilized eggs is very fast, the F0 generation mice obtained are chimera and do not necessarily have the ability of stable inheritance. It is necessary to pass the positive F0 generation mice to obtain stable heritable F1 generation mice.

8.2 F1 mice genotyping

F0 generation positive mice were mated with wild type C57BL/6J mice to obtain F1 generation mice. The genotype of F1 generation mice were identified by PCR method and sequencing.

8.2.1 Genotyping strategy of F1 mice



Strategy of F1 mice genotyping

Genotyping method:

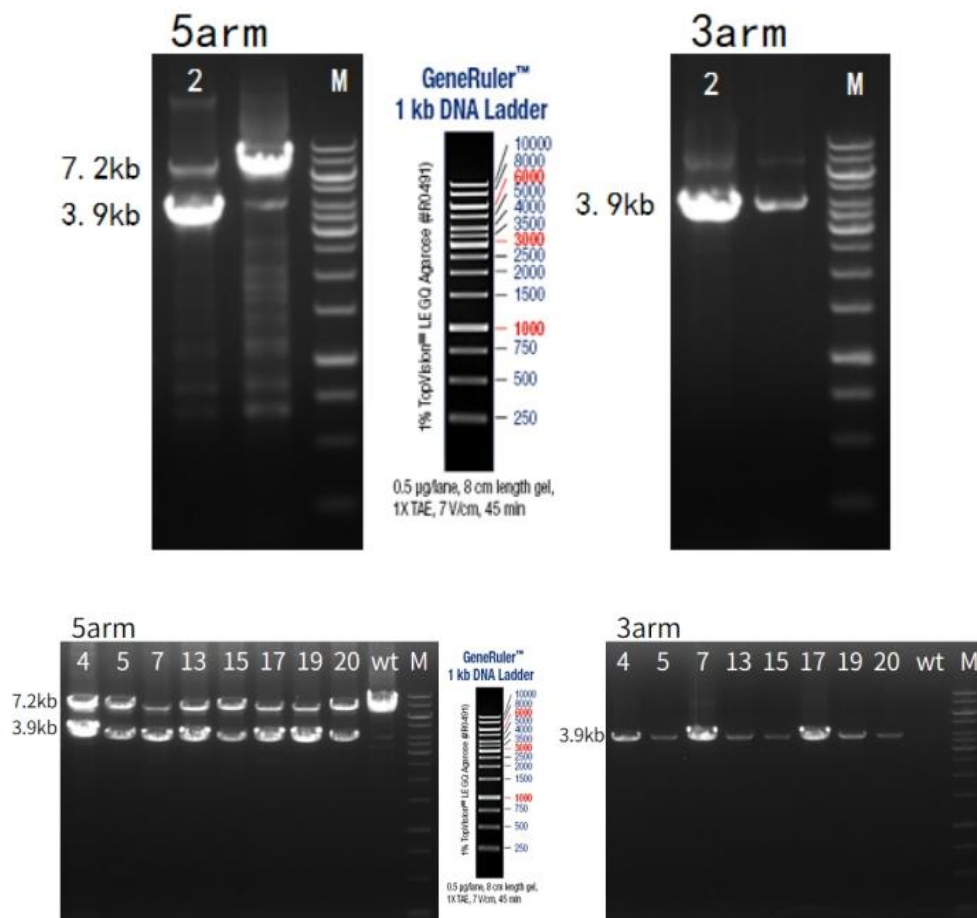
5'homologous arm: 3.9 kb fragment should be amplified in the homologous recombinant DNA, and 7.2 kb fragment can be amplified in the negative DNA.

3'homologous arm: 3.9 kb fragment should be amplified in the homologous recombinant DNA, none of fragments can be amplified in the negative DNA.

8.2.2 PCR genotyping of homologous recombinant F1 mice

The number of homologous recombinant F1 mice were 2,4,5,7,13,15,17,19,20. The agarose

gel electrophoresis of PCR results were shown in Figure 3. All positive PCR products were confirmed by sequencing.



Agarose gel electrophoresis of PCR results.

(number: the number of F1 mice; M: 1kb DNA ladder)

8.2.3 Method for identifying 5'homologous recombinant F1 mice

Primers:

Primer	Sequence 5' --> 3'	Primer Type
I	TTCTGTGAGACAGCCGGGTA	Forward
II	TTTTTGGGGGTGATGGTGGTC	Reverse

Reaction system:

Reaction Component	Volume (μl)
ddH2O	8.05
2xPCR Buffer	10
Primer I (20pmol/μl)	0.3
Primer II (20pmol/μl)	0.3
KOD-Multi&Epi-*	0.35
Genomic DNA	1
Total	20

* KOD-Multi&Epi- (TOYOBO, Code No: KME-101)

PCR program:

Step #	Temp (°C)	Time	Note
1	94	3 min	-
2	98	20 sec	-
3	63	20 sec	-
4	68	4 min	repeat steps 2-4 for 35cycles
5	68	5 min	-
6	12	-	hold

8.2.4 Method for identifying 3'homologous recombinant F1 mice

Primers:

Primer	Sequence 5' --> 3'	Primer Type
III	TTGCCAGCCATCTGTTGTT	Forward
IV	TGCCACCTTTCACCTTAGTTTGT	Reverse

Reaction system:

Reaction Component	Volume (μl)
ddH ₂ O	8.05
2xPCR Buffer	10
Primer III (20pmol/μl)	0.3
Primer IV (20pmol/μl)	0.3
KOD-Multi&Epi-*	0.35
Genomic DNA	1
Total	20

* KOD-Multi&Epi- (TOYOBO, Code No: KME-101)

PCR program:

Step #	Temp (°C)	Time	Note
1	94	3 min	-
2	98	20 sec	-
3	63	20 sec	-
4	68	4 min	repeat steps 2-4 for 35cycles
5	68	5 min	-
6	12	-	hold

8.2.5 Information of homologous recombinant F1 mice

Table: The information of positive F1 mice

Mice ID	DOB	Generations	Sex	Type	Genotype	Father	Mother
---------	-----	-------------	-----	------	----------	--------	--------

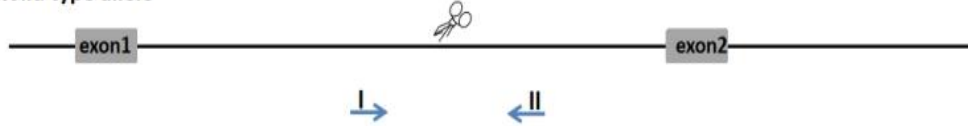
2	2023/8/7	F1	♀	KI	He	3F0	6J
4	2023/8/14	F1	♂	KI	He	3F0	6J
5	2023/8/14	F1	♂	KI	He	3F0	6J
7	2023/8/14	F1	♂	KI	He	3F0	6J
13	2023/8/14	F1	♂	KI	He	3F0	6J
15	2023/8/14	F1	♀	KI	He	3F0	6J
17	2023/8/14	F1	♀	KI	He	3F0	6J
19	2023/8/14	F1	♀	KI	He	3F0	6J
20	2023/8/14	F1	♀	KI	He	3F0	6J

Rosa26-LSL-TRPV4-WT-HA Genotyping Protocol

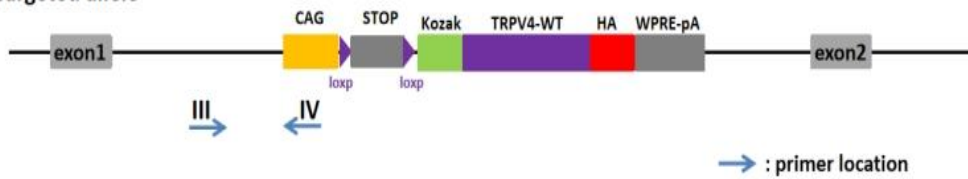
Common Name	Rosa26-LSL-TRPV4-WT-HA	Cat. NO.	
Strain of Origin	C57BL/6J	Version	V1

Genotyping strategy

Wild type allele



Targeted allele



Primers

Primer	Sequence (5'→3')	Primer type
P1	TCAGATTCTTTTATAGGGGACACA	Forward
P2	TAAAGGCCACTCAATGCTCACTAA	Reverse
P3	GGGTGGGGTTGGGAAATCTT	Forward
P4	TAGGGGGCGTACTTGGCATA	Reverse

Expected results

Results	
Genotype	<p>Wild type: P1P2 =967 bp;</p> <p>Heterozygote: P1P2 =967 bp; P3P4=737 bp</p> <p>Homozygote: P3P4 =737 bp</p>

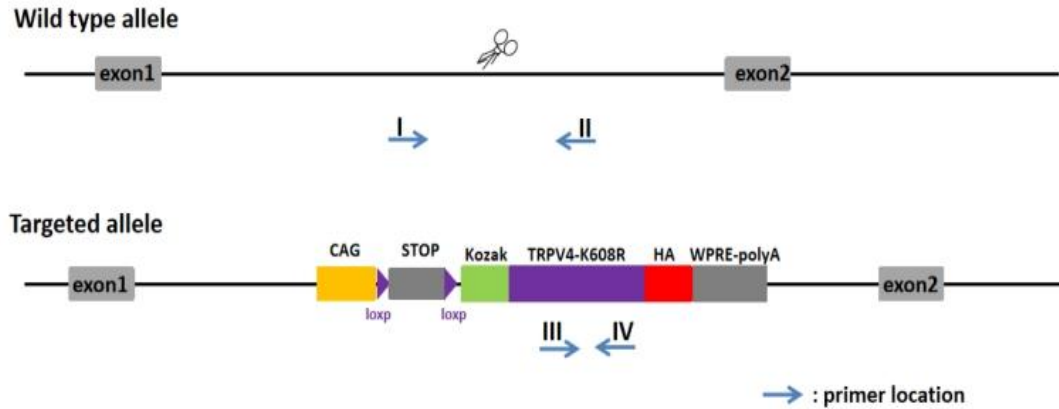
Reaction & Cycling

PCR Reaction System	Reaction Component			Volume (μl)
	ddH ₂ O			8.0
	2×Taq Plus Master Mix			10.0
	P1(10 pmol/μl) or P3(10 pmol/μl)			0.5
	P2(10 pmol/μl) or P4(10 pmol/μl)			0.5
	Genomic DNA			1.0
	Total			20
	2×Taq Plus Master Mix from Vazyme(Code Number: P222-1)			
Cycling Reaction	Step	Temp	Time	Note
	1	95°C	5 min	
	2	95°C	30 sec	
	3	60°C	30 sec	
	4	72°C	30 sec	35 repeats to 2
	5	72°C	5 min	
	6	12°C	Hold	

Rosa26-LSL-TRPV4-K608R-HA Genotyping Protocol

Common Name	Rosa26-LSL-TRPV4-K608R-HA	Cat. NO.	CM-KI-231843
Strain of Origin	C57BL/6J	Version	V1

Genotyping strategy



Primers

Primer	Sequence (5'→3')	Primer type
P1	TCAGATTCTTTTATAGGGGACACA	Forward
P2	TAAAGGCCACTCAATGCTCACTAA	Reverse
P3	CCTGTGTGCCATGGTCATCT	Forward
P4	CAGGAGGAAGGTGCTGAAGG	Reverse

Expected results

Results	
Genotype	<p>Wild type: P1P2 =967 bp; Heterozygote: P1P2 =967 bp; P3P4=580 bp Homozygote: P3P4 =580 bp</p>

Reaction & Cycling

PCR Reaction System	Reaction Component			Volume (μl)
	ddH ₂ O			8.0
	2×Taq Plus Master Mix			10.0
	P1(10 pmol/μl) or P3(10 pmol/μl)			0.5
	P2(10 pmol/μl) or P4(10 pmol/μl)			0.5
	Genomic DNA			1.0
	Total			20
	2×Taq Plus Master Mix from Vazyme(Code Number: P222-1)			
Cycling Reaction	Step	Temp	Time	Note
	1	95°C	5 min	
	2	95°C	30 sec	
	3	60°C	30 sec	
	4	72°C	30 sec	35 repeats to 2
	5	72°C	5 min	
	6	12°C	Hold	

Uncropped gels for Fig. 1 to 5 and Fig. S1, 4, 9 to 12, 15 to 18. After electrophoretic transfer of proteins, the PVDF membranes were cut into strips containing sets of samples, and were then subjected to immunoblotting. Show here are films that had been exposed and developed to the membrane strips. The Pierce Prestained Protein MW Marker (Cat. 26612, ThermoFisher Scientific) was used as the protein markers.

Fig. 1A

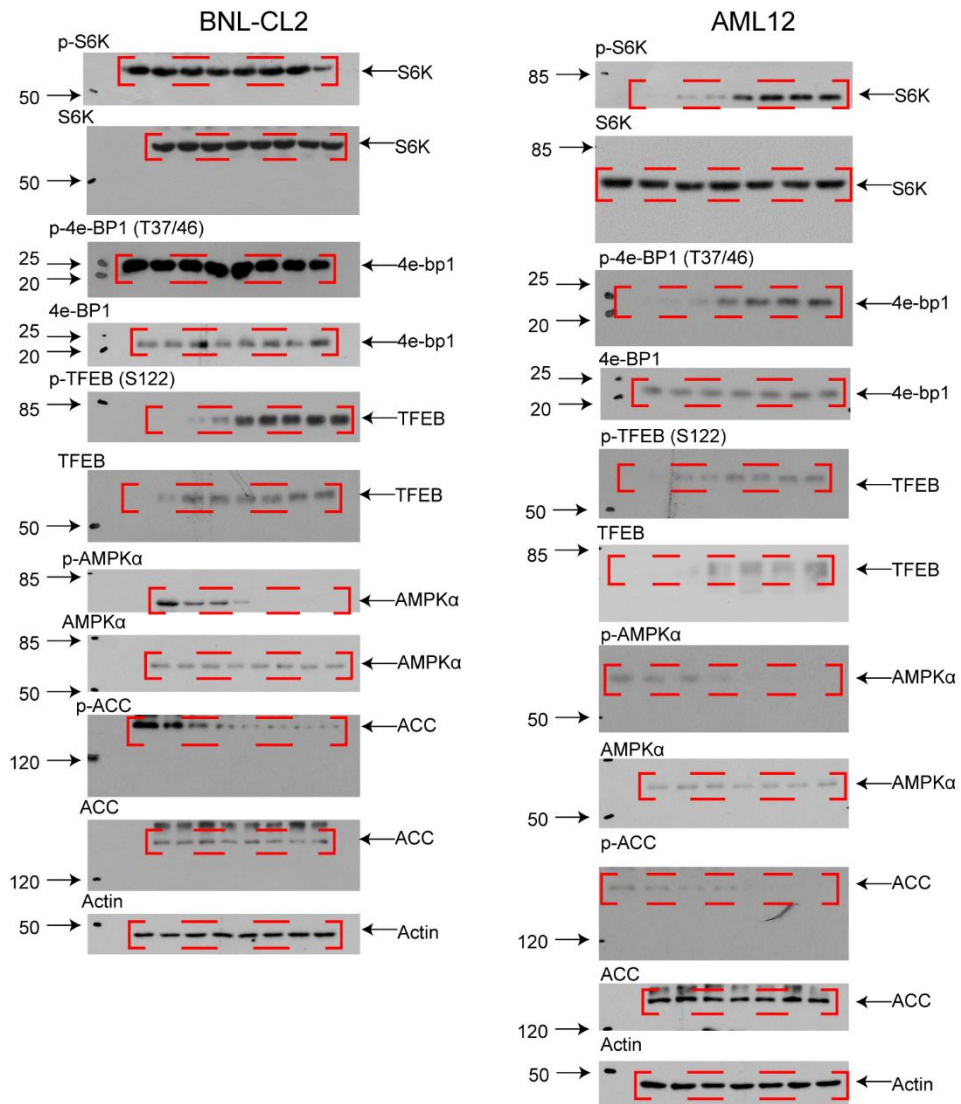


Fig. 1A

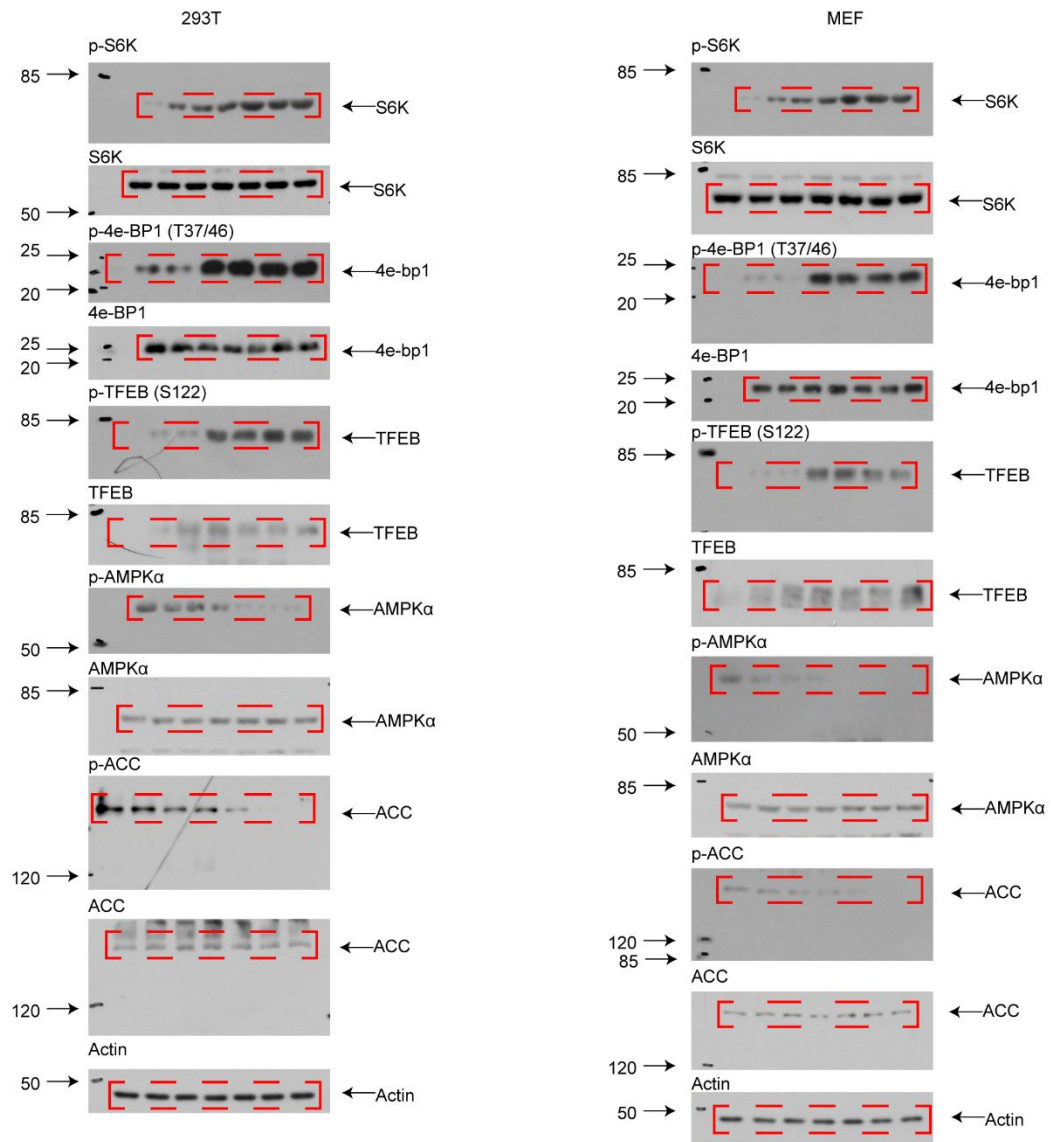


Fig. 1B

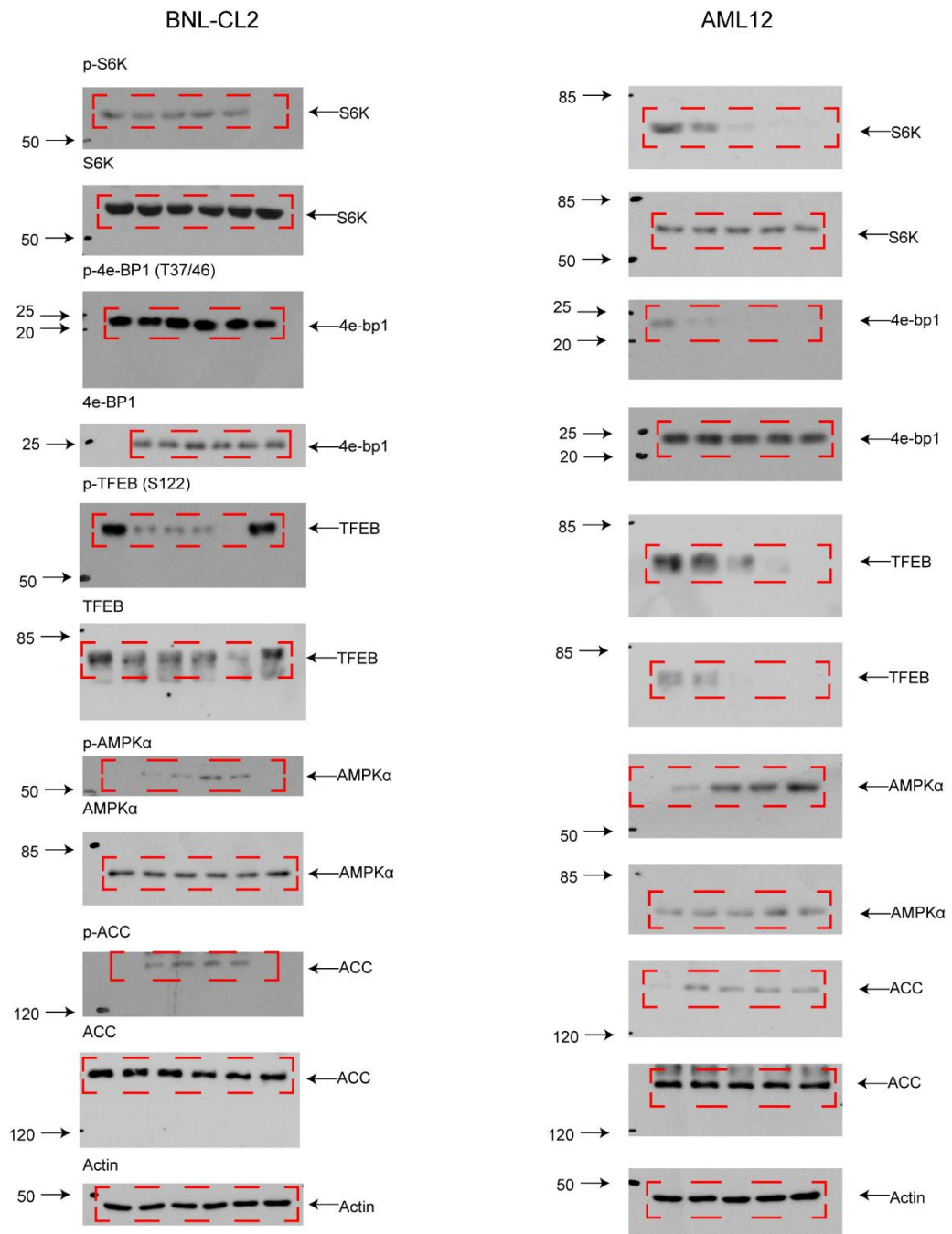


Fig. 1B

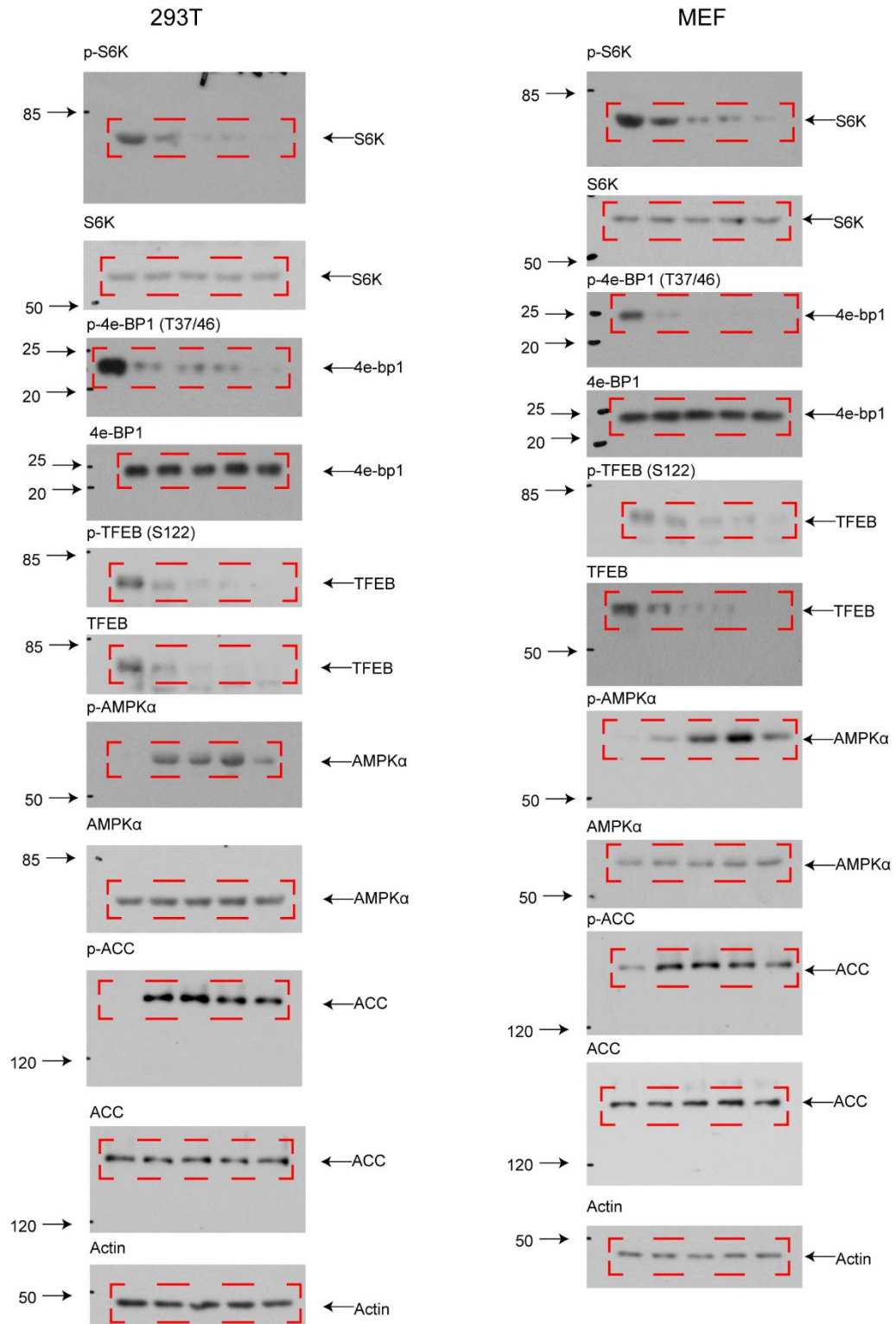


Fig. 1C

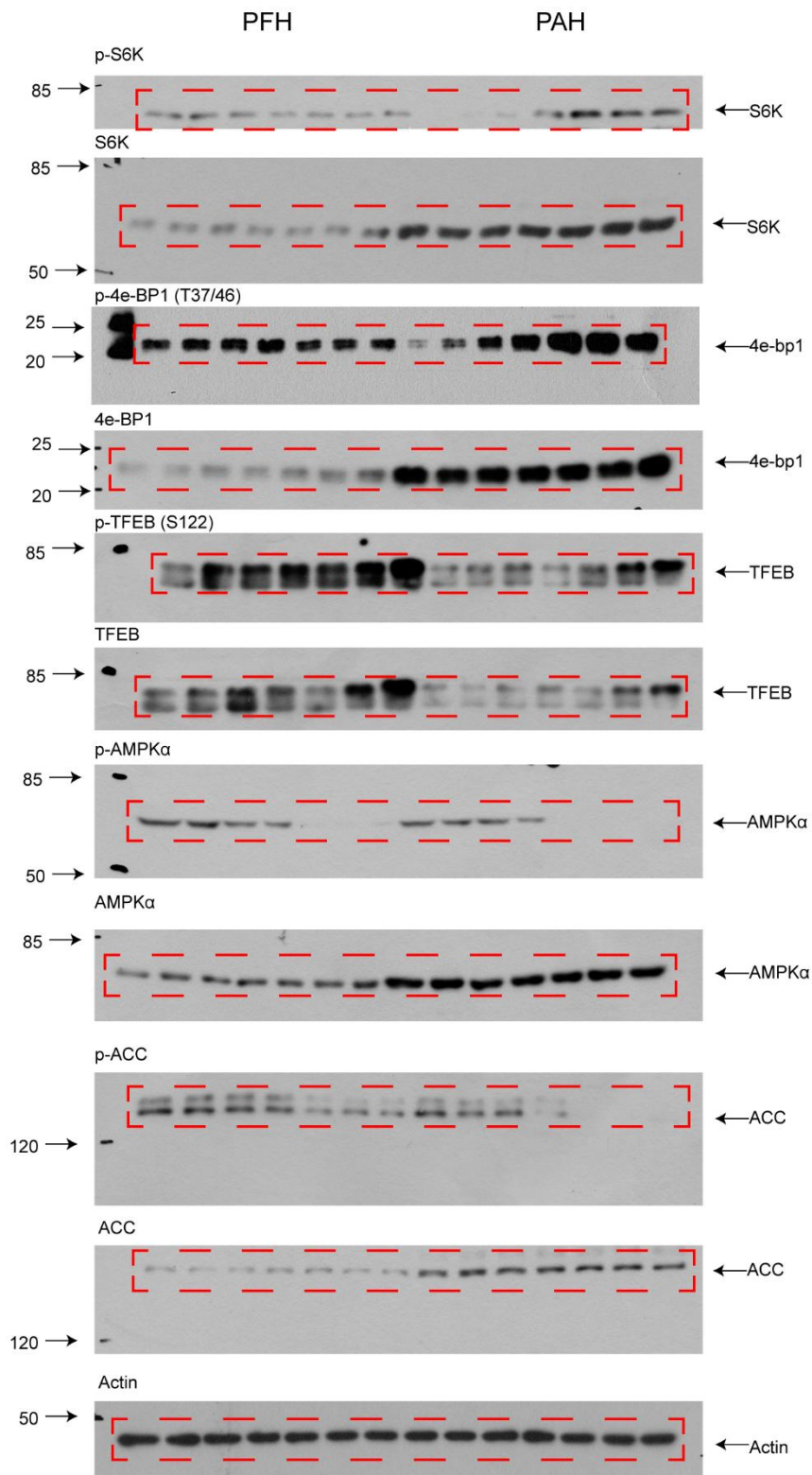


Fig. 1D

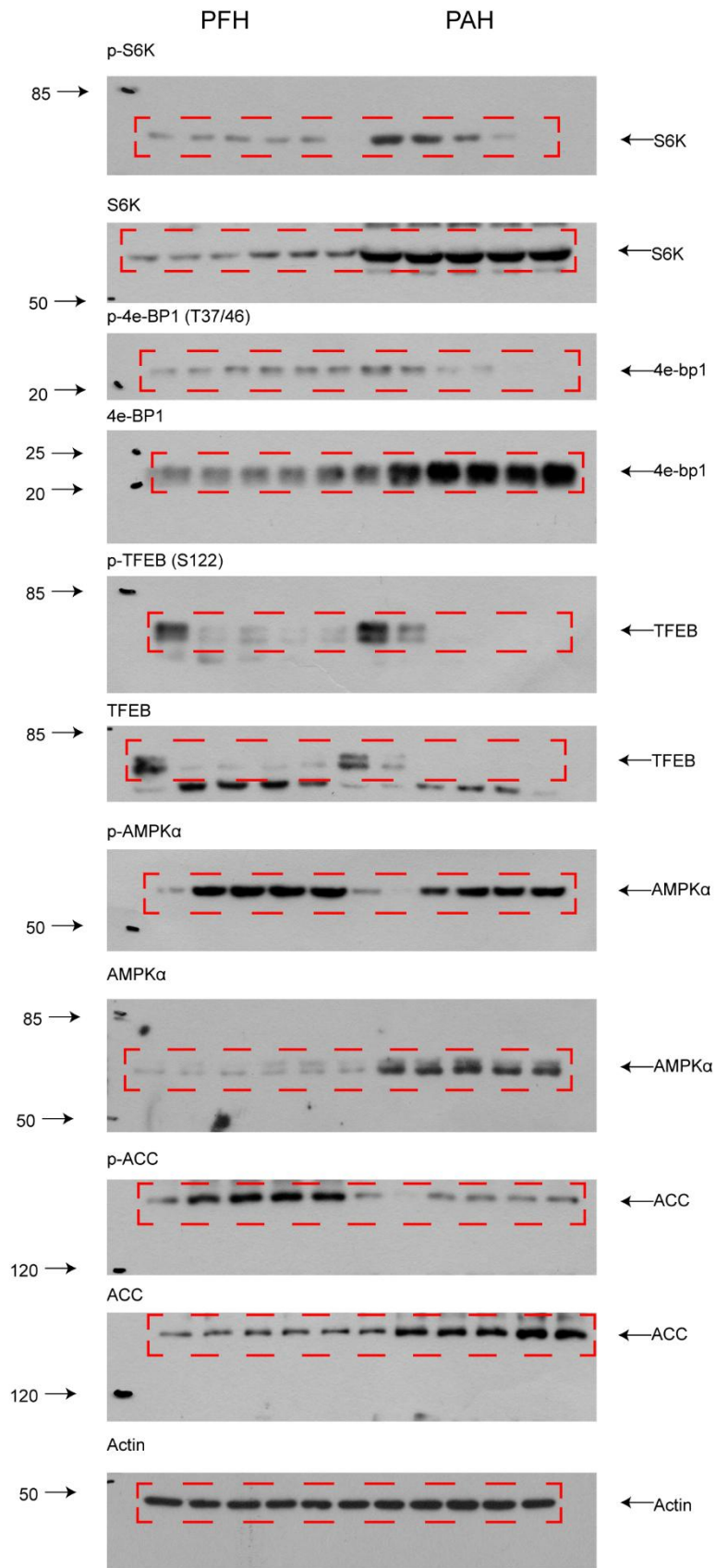


Fig. 1E

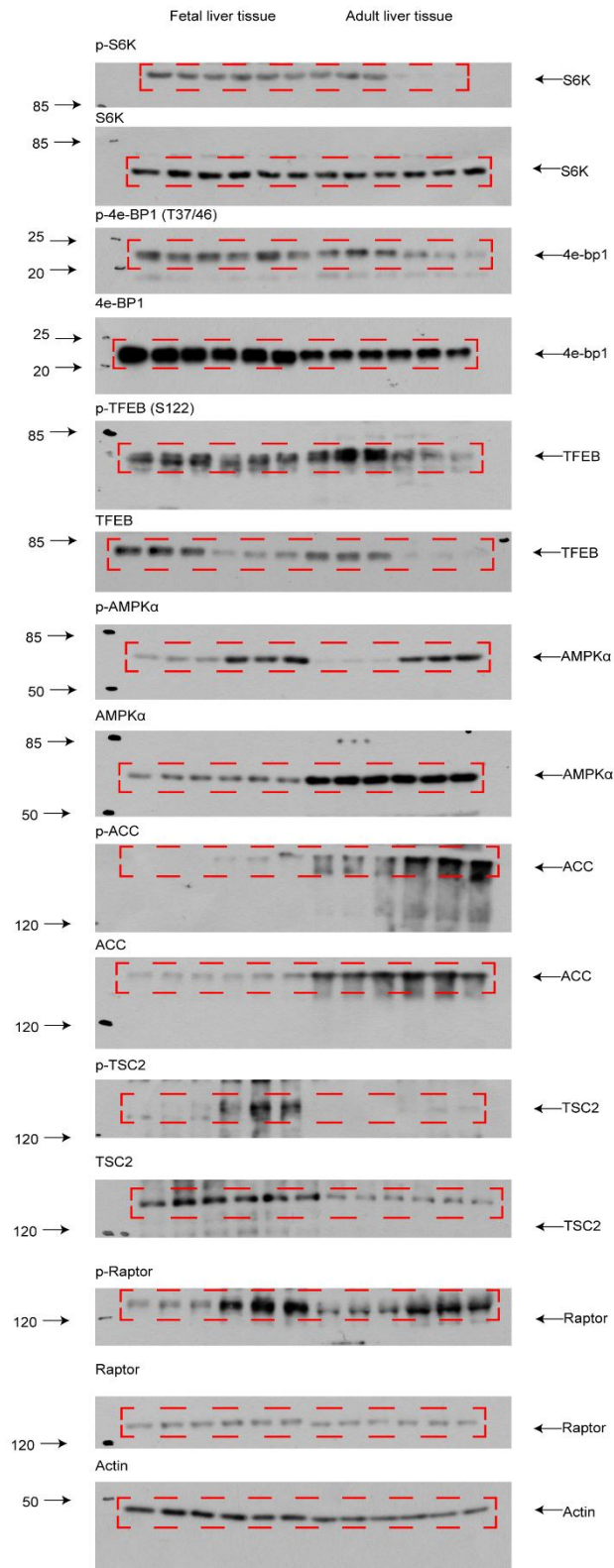


Fig. 1F

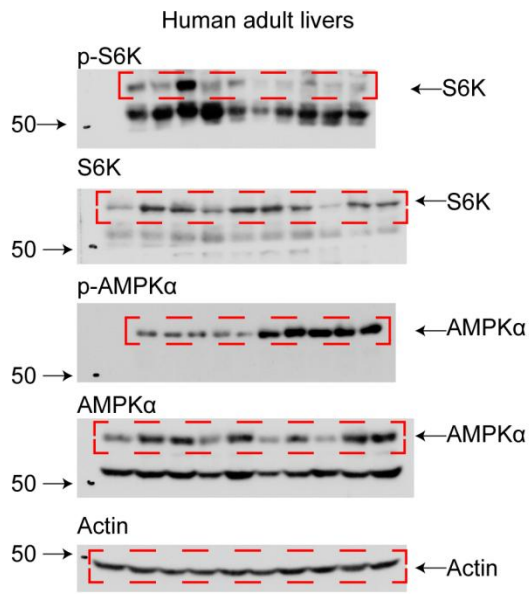


Fig. 1I

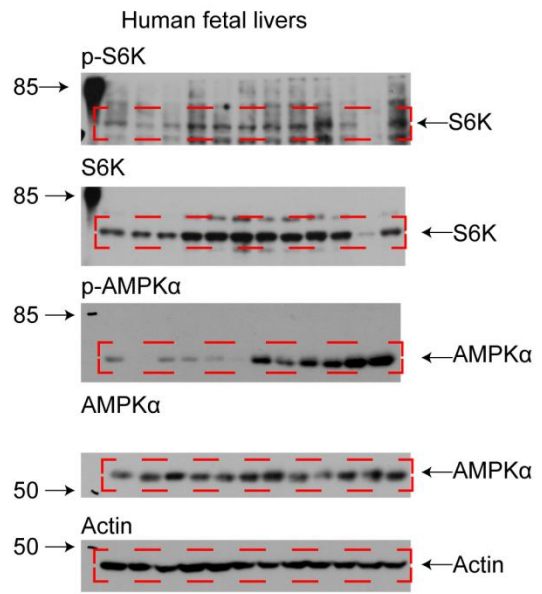


Fig. 1L

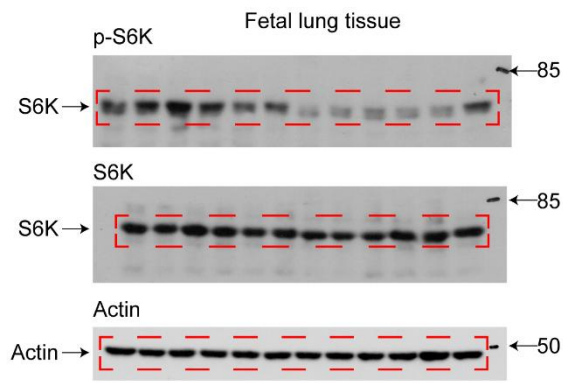


Fig. 1M

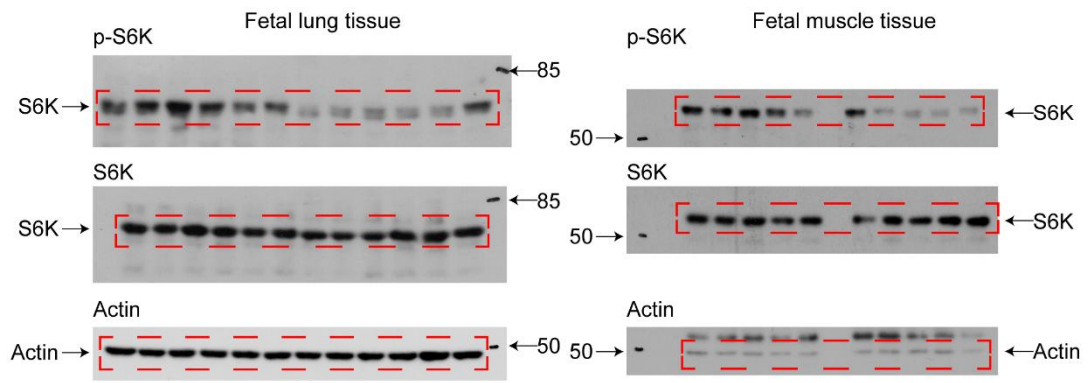


Fig. 1N

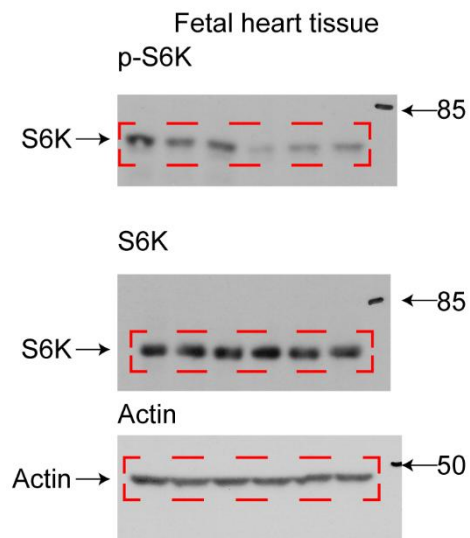


Fig. 2B

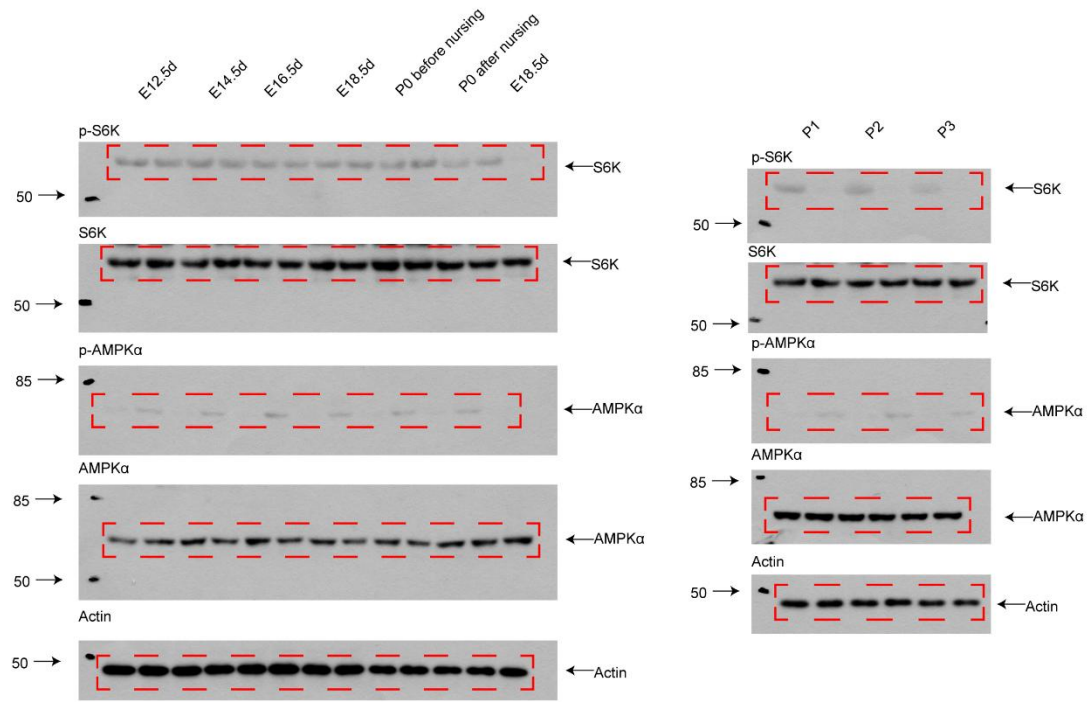


Fig. 2F

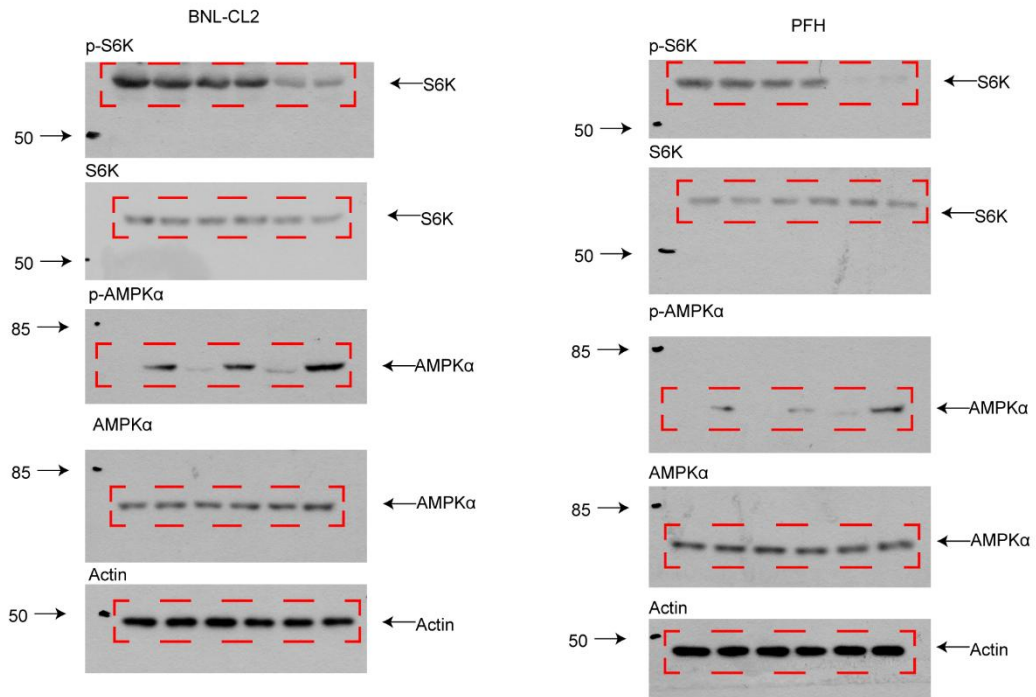


Fig. 2G

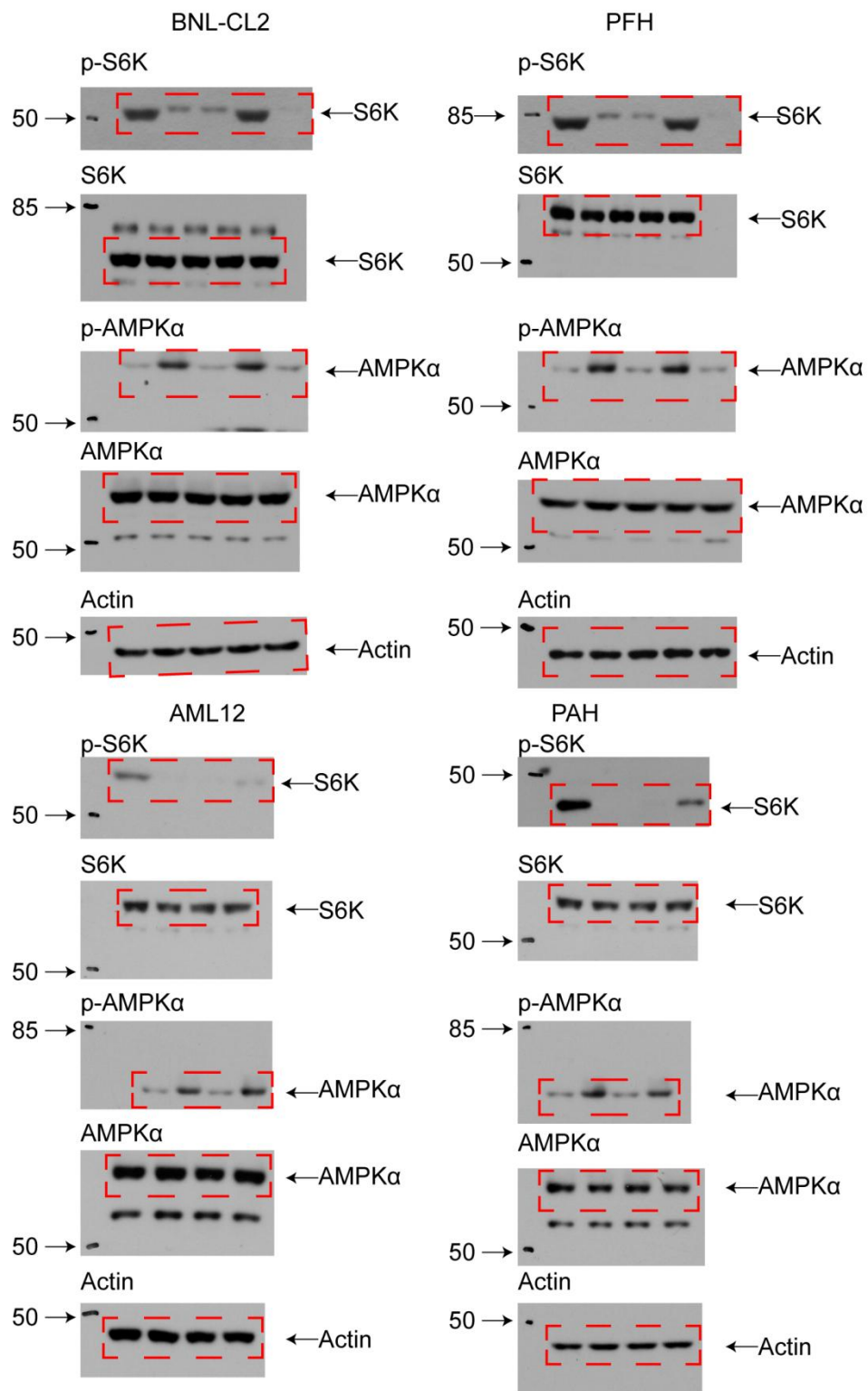


Fig. 2H

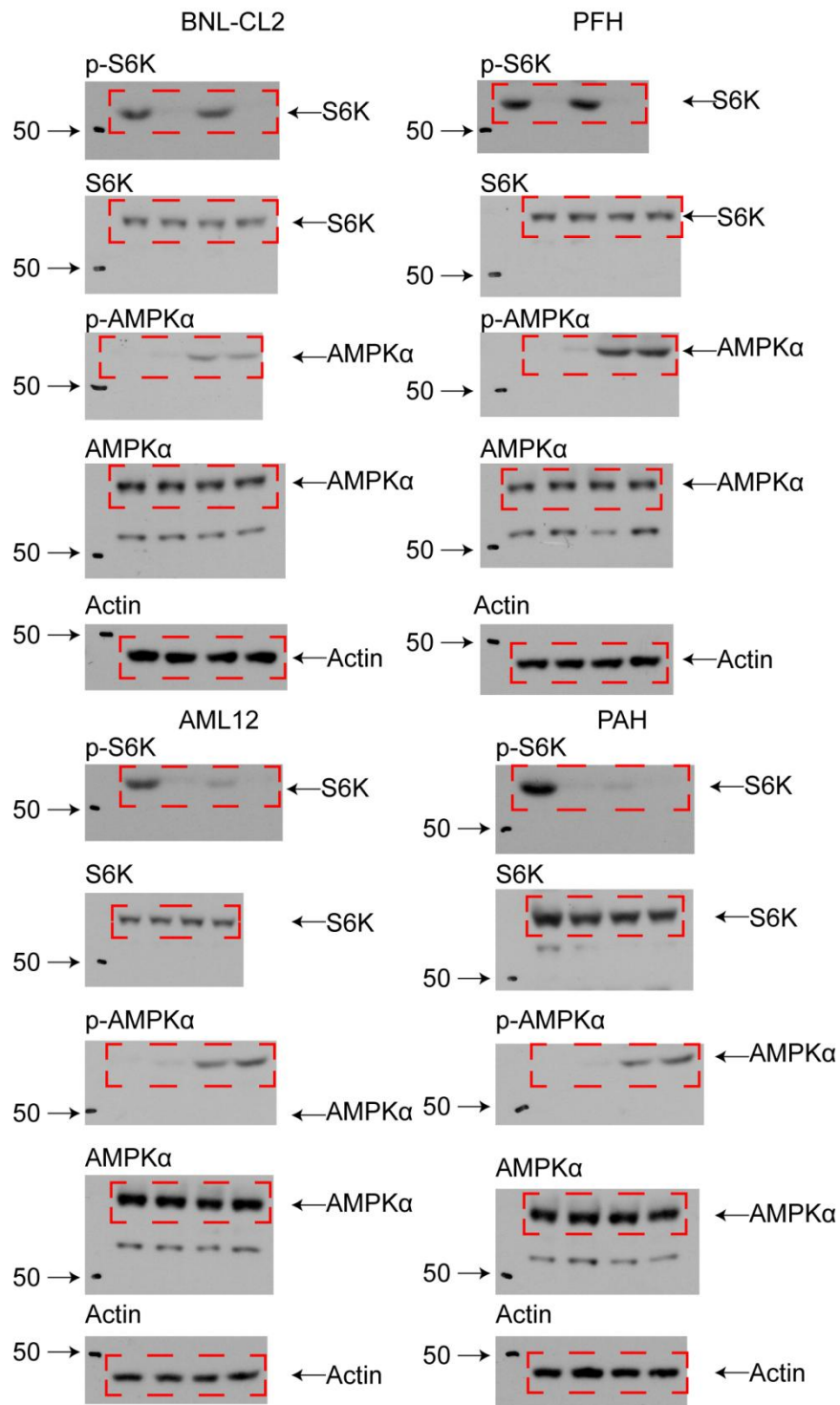


Fig. 2I

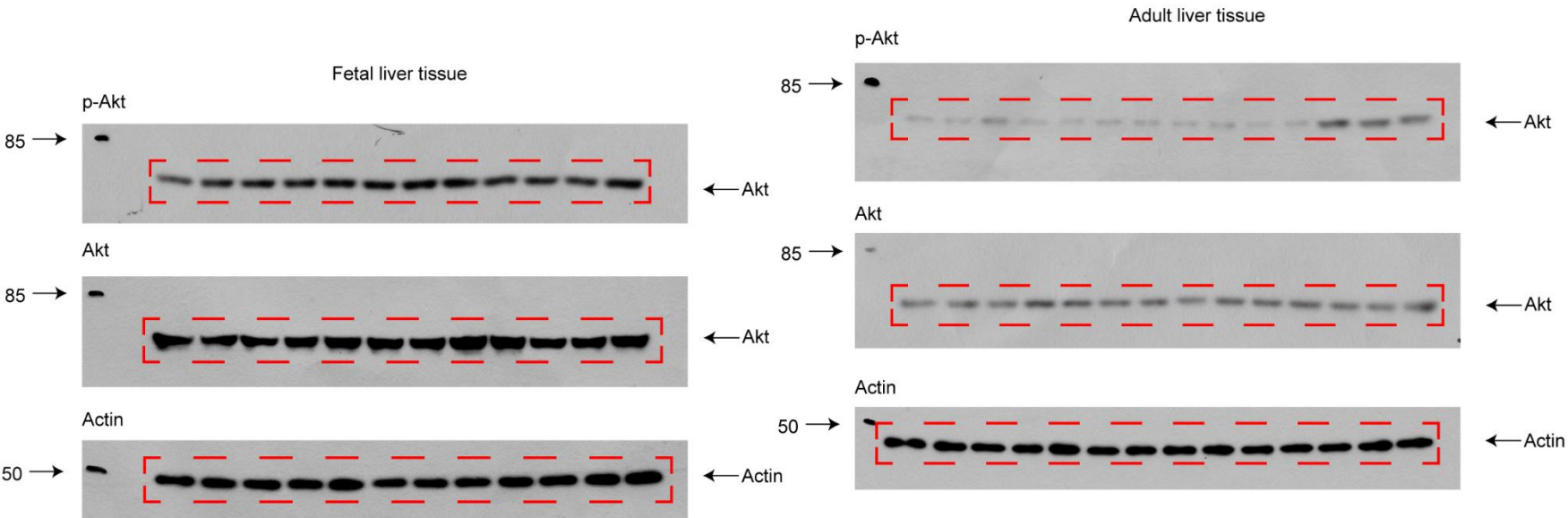


Fig. 3A

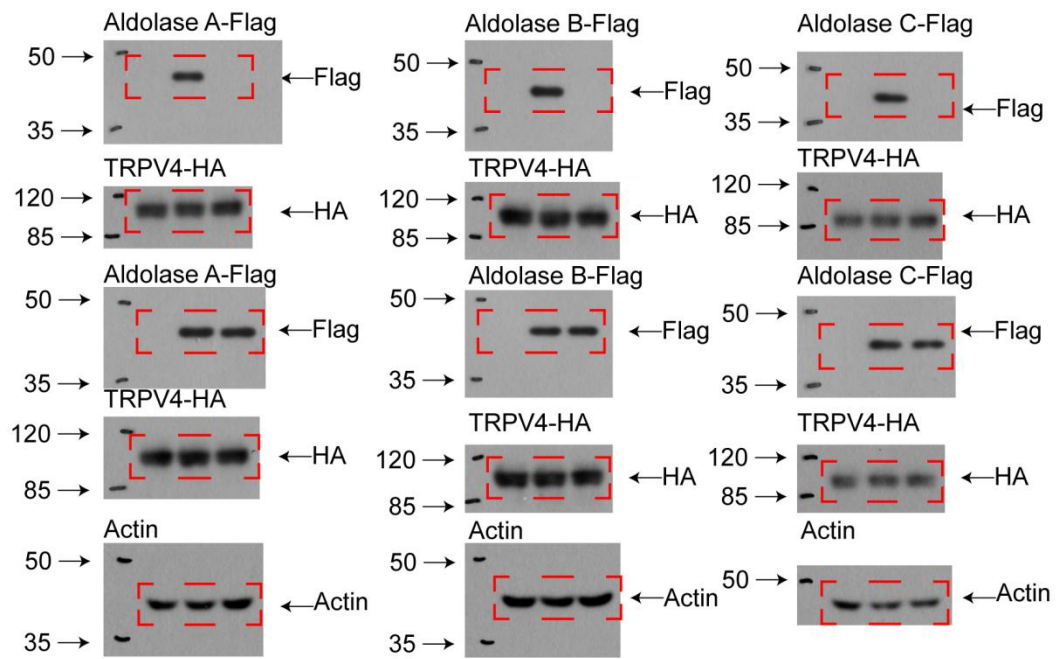


Fig. 3G

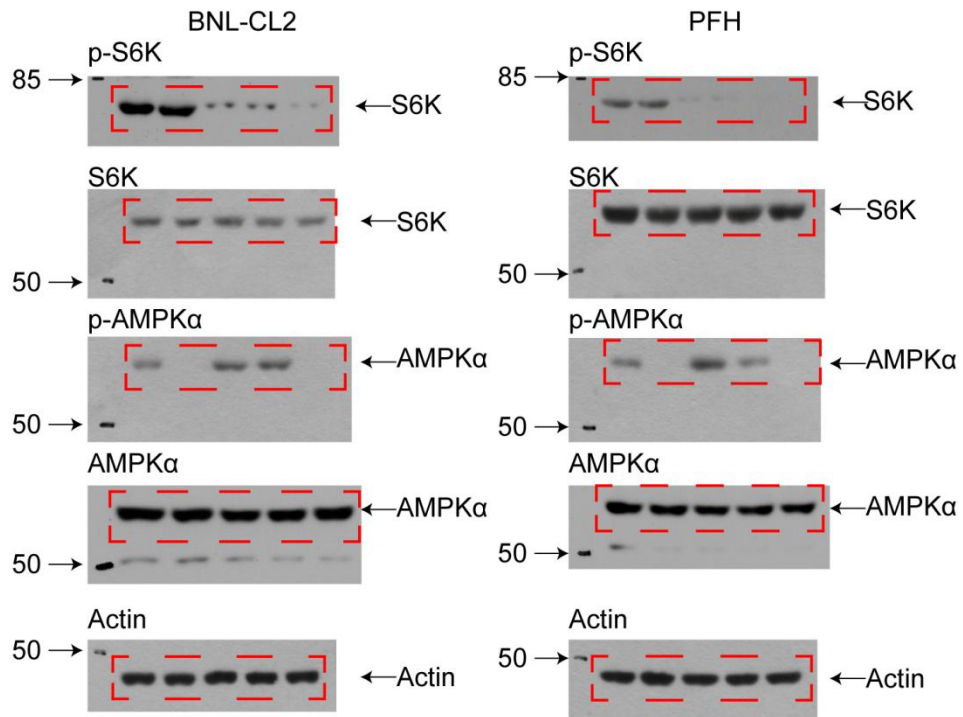


Fig. 3J

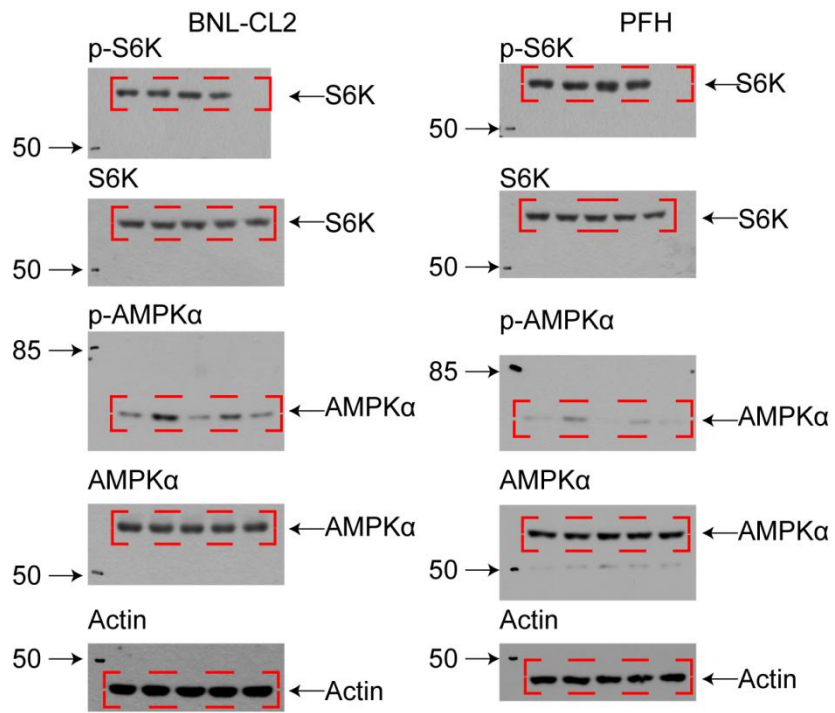


Fig. 3K

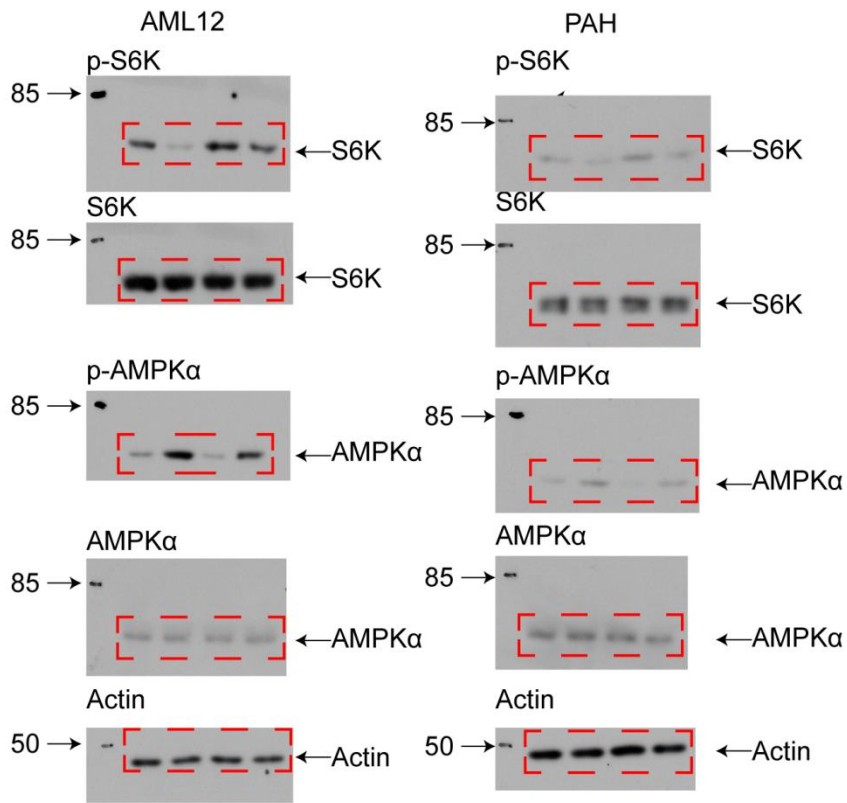


Fig.4A

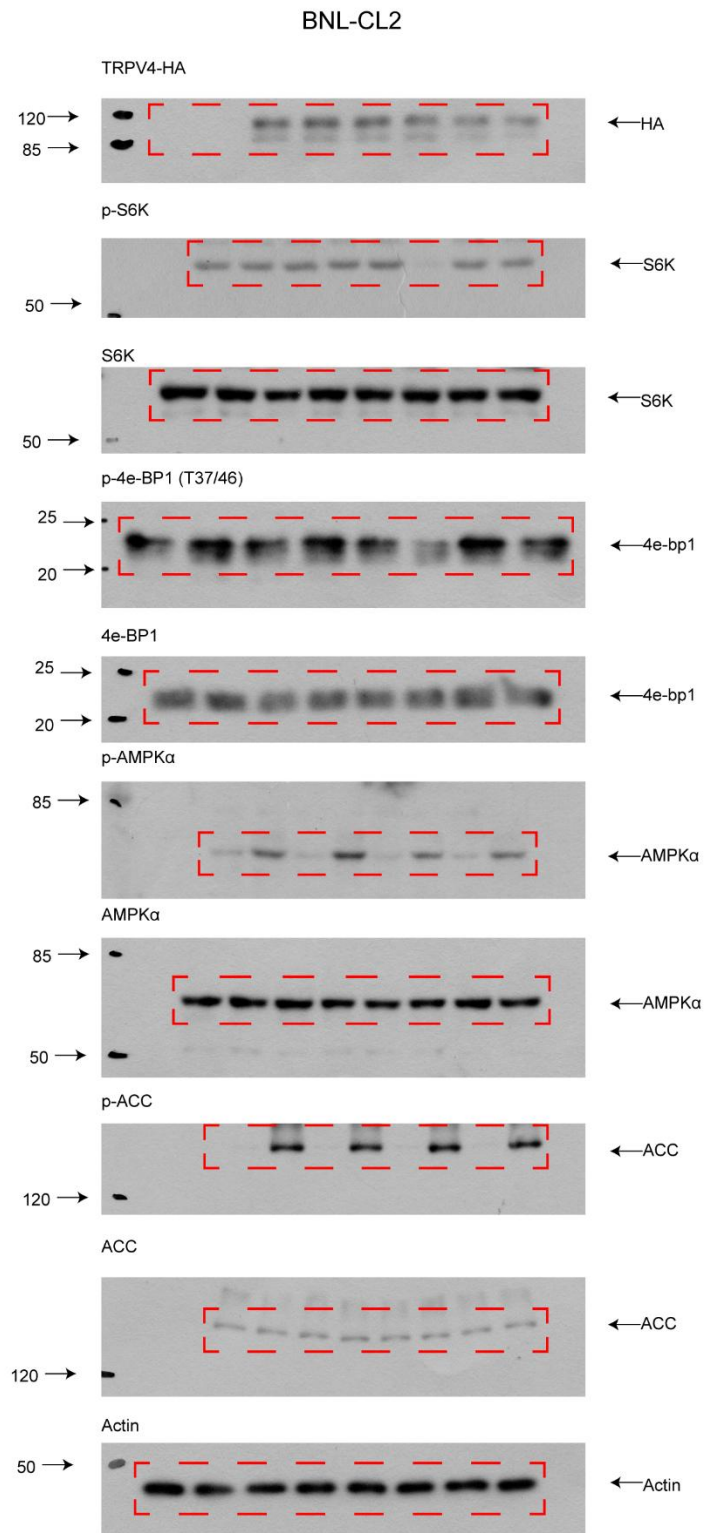


Fig. 4F

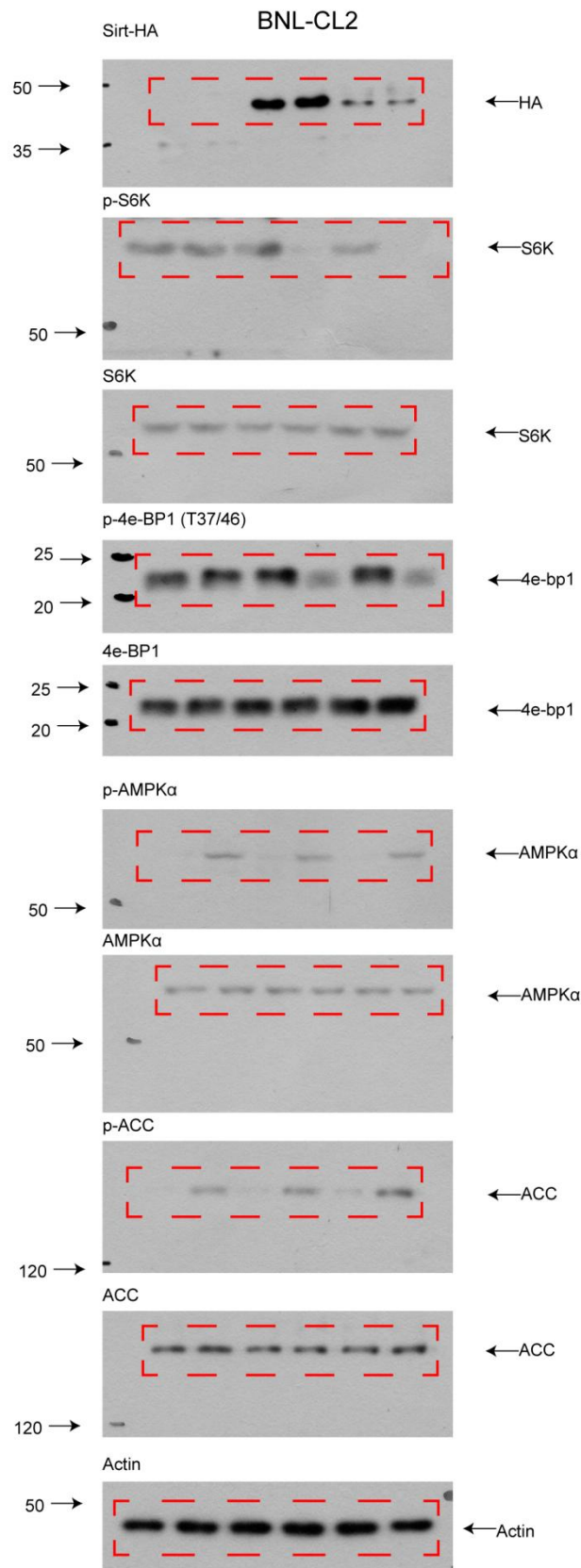


Fig. 4G

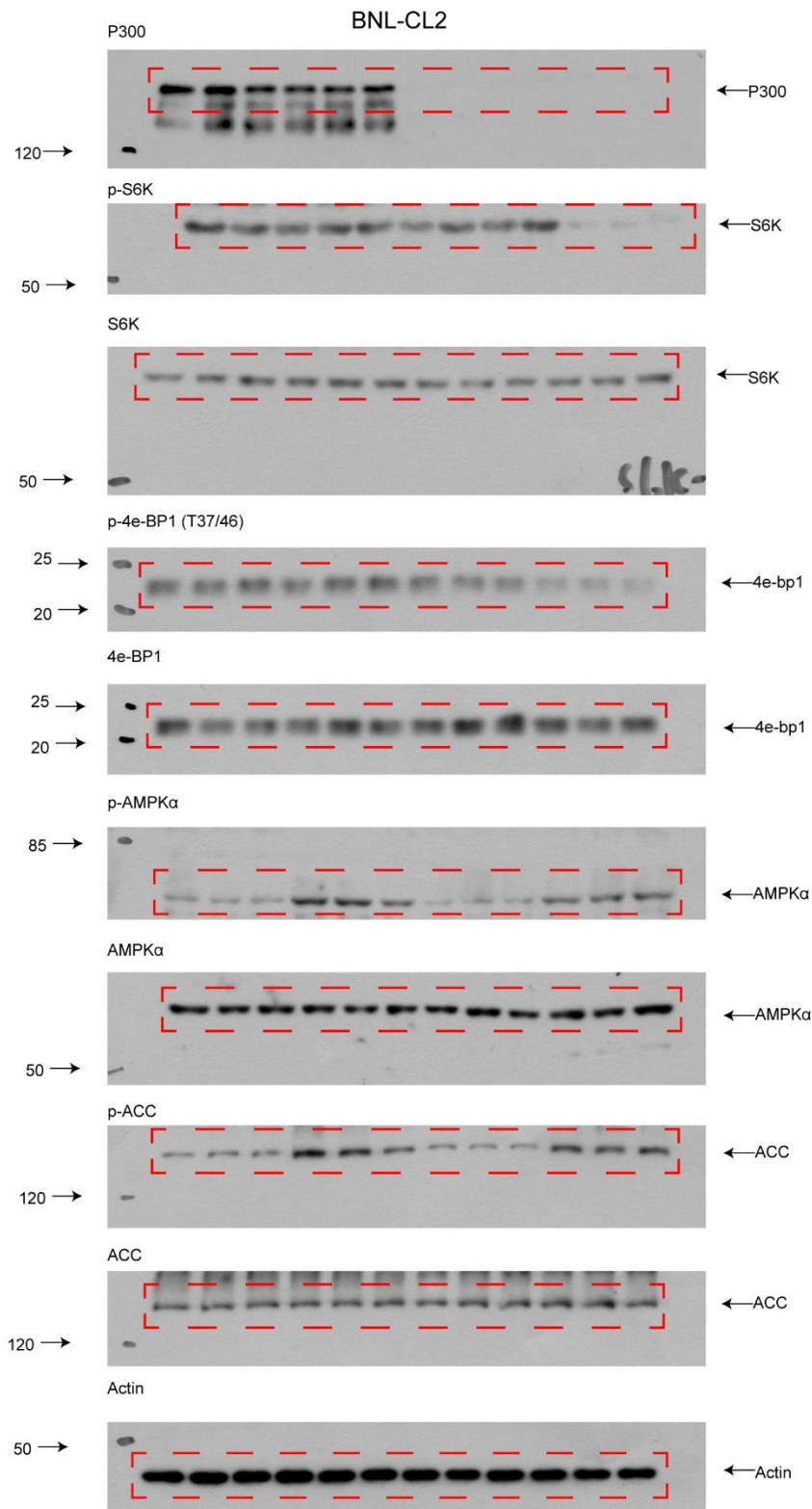


Fig. 4I

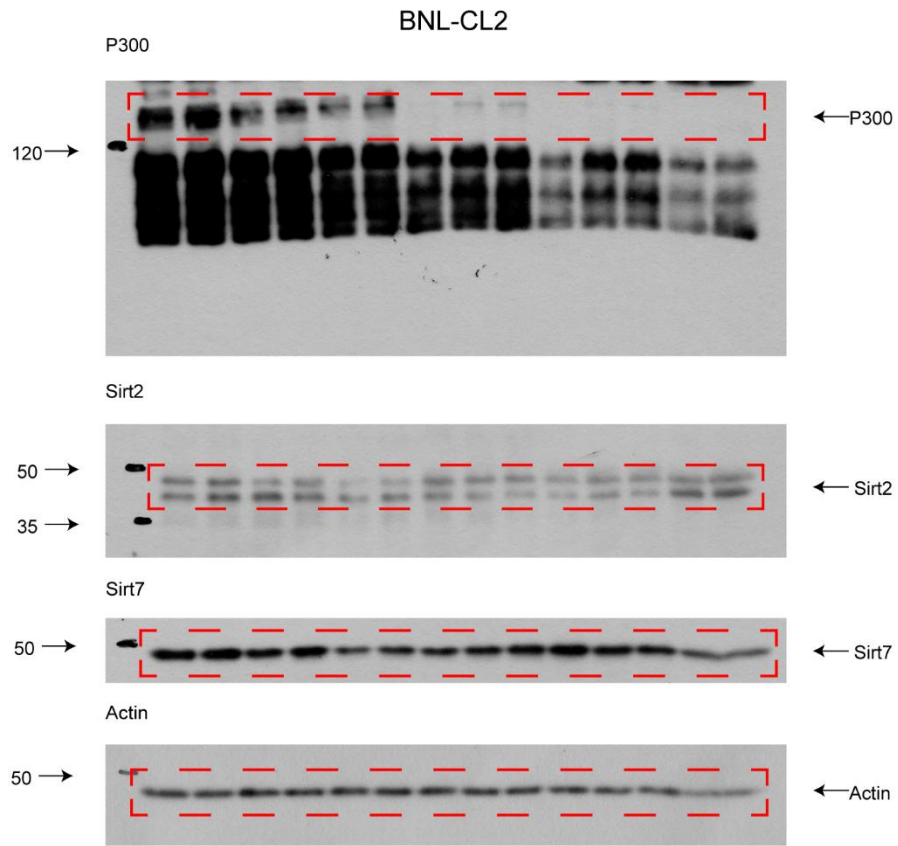


Fig. 5A

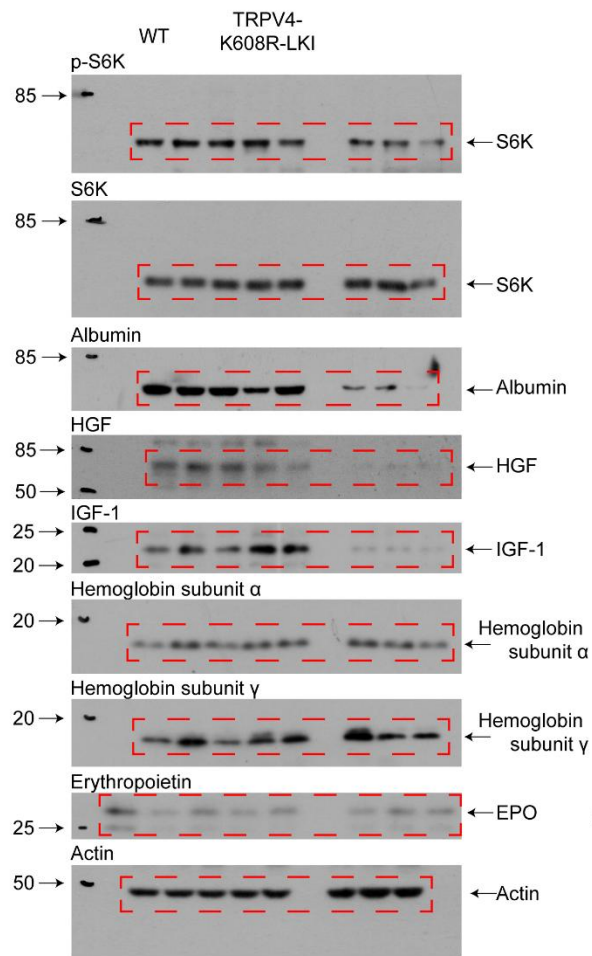


Fig. 5B

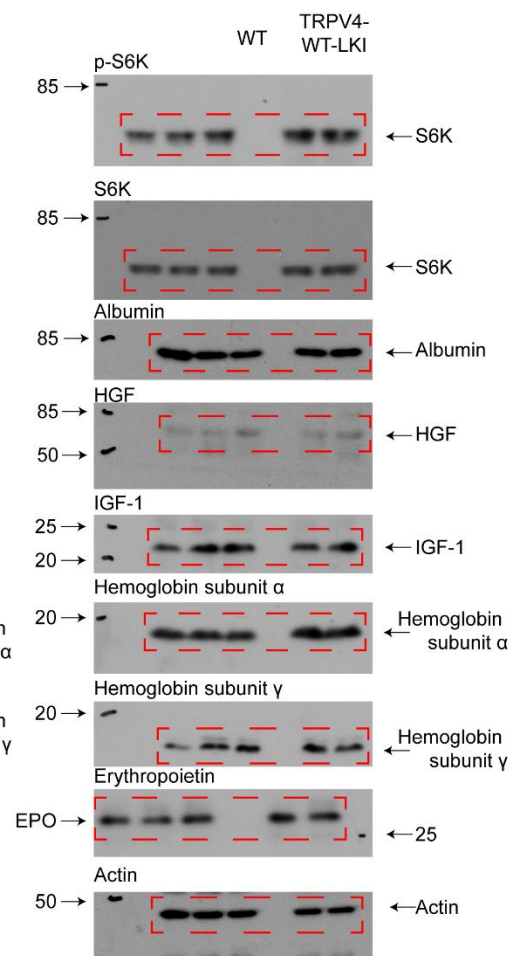


Fig. S1A

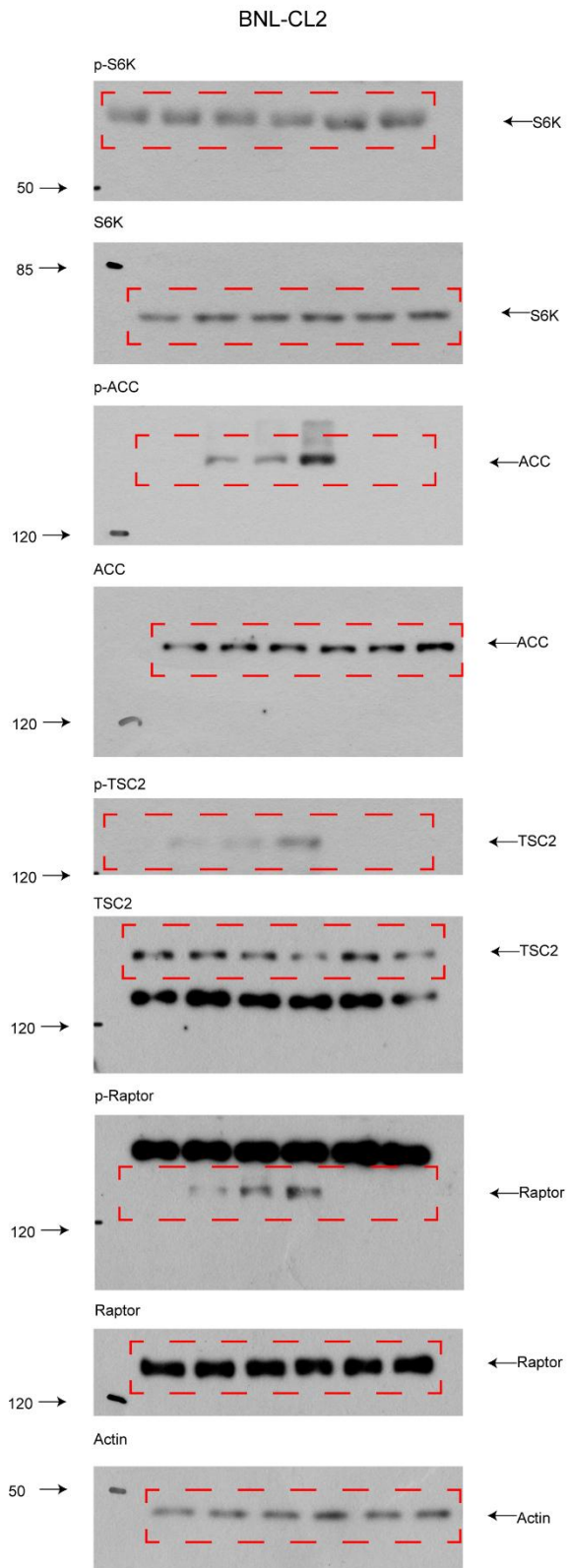


Fig. S1D

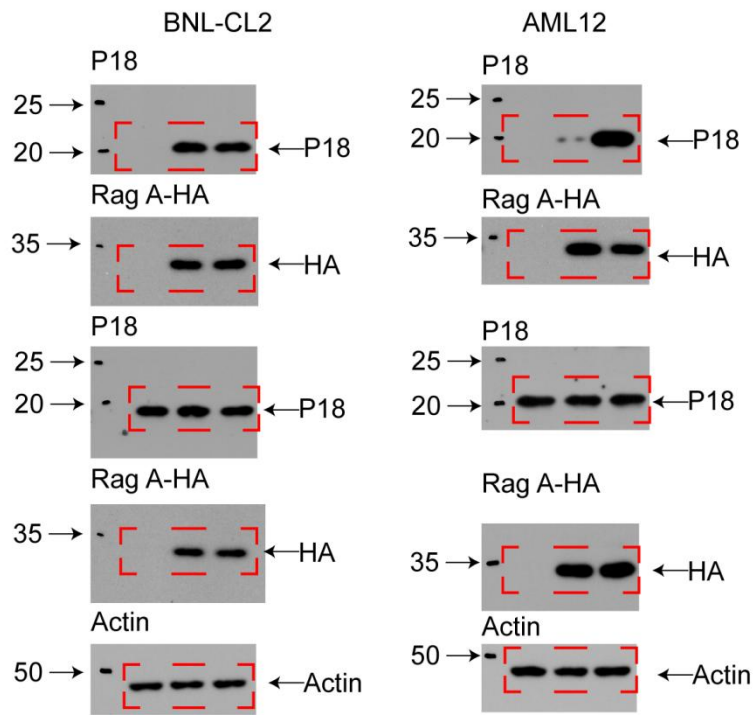


Fig. S4E

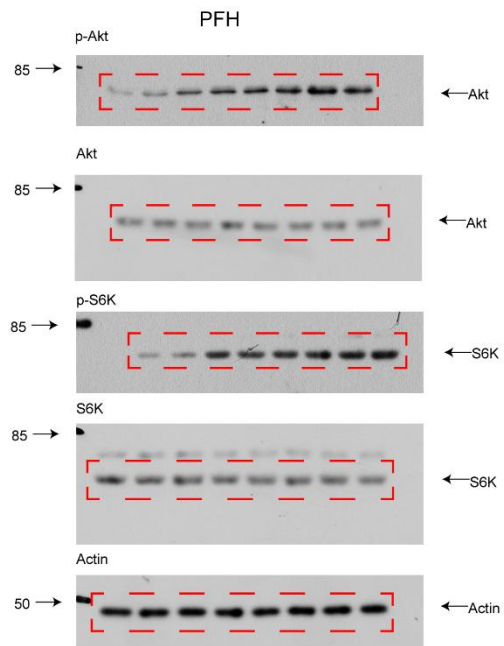


Fig. S4G

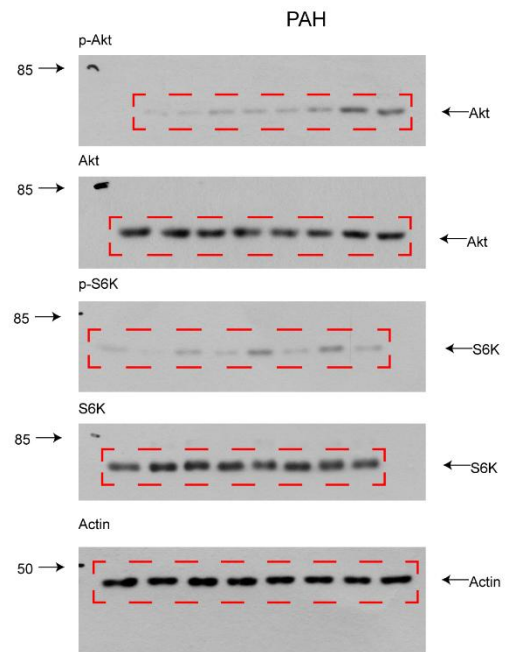


Fig. S4I

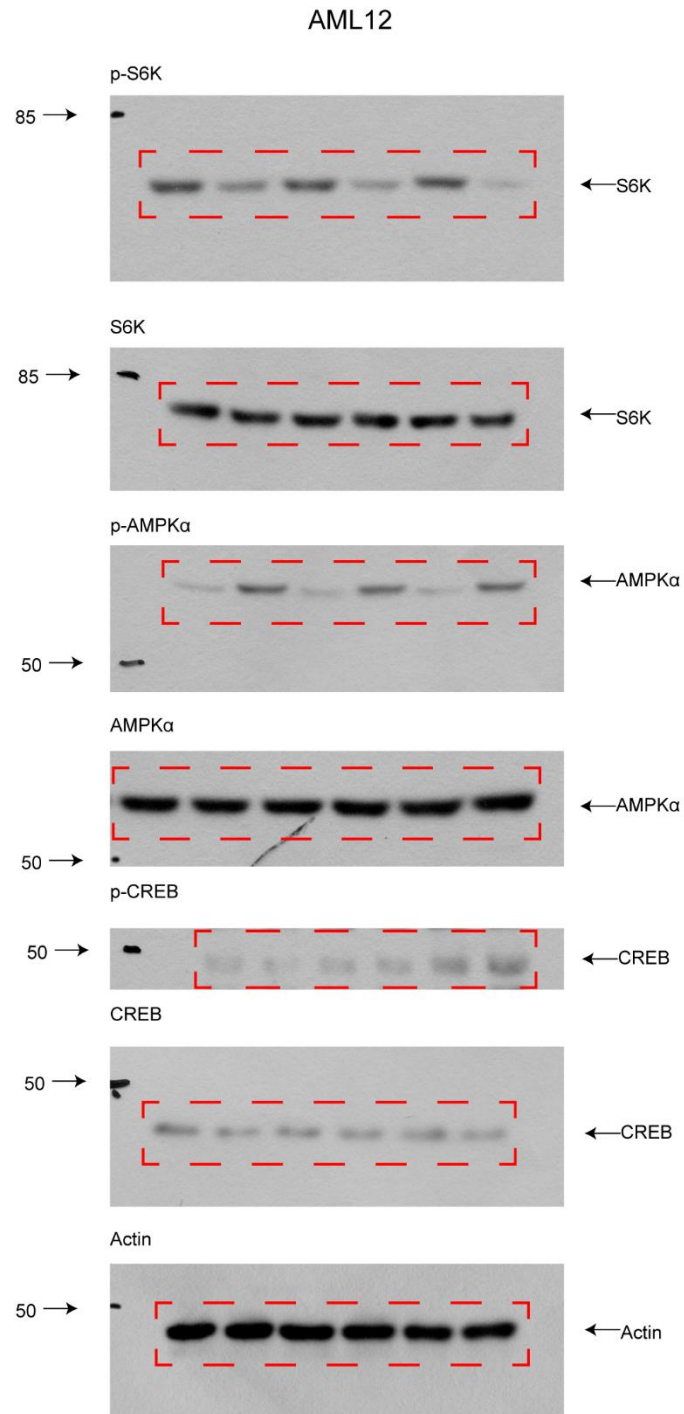


Fig. S9C

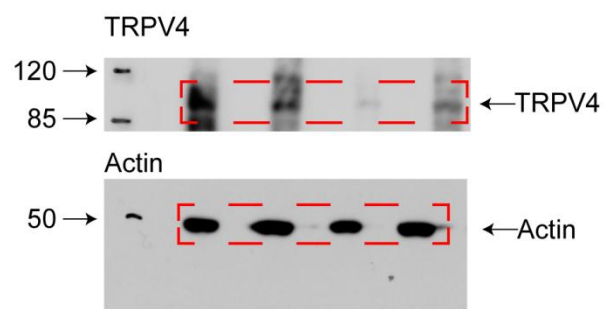


Fig. S10A

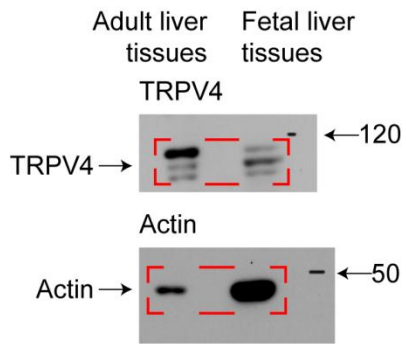


Fig. S10B

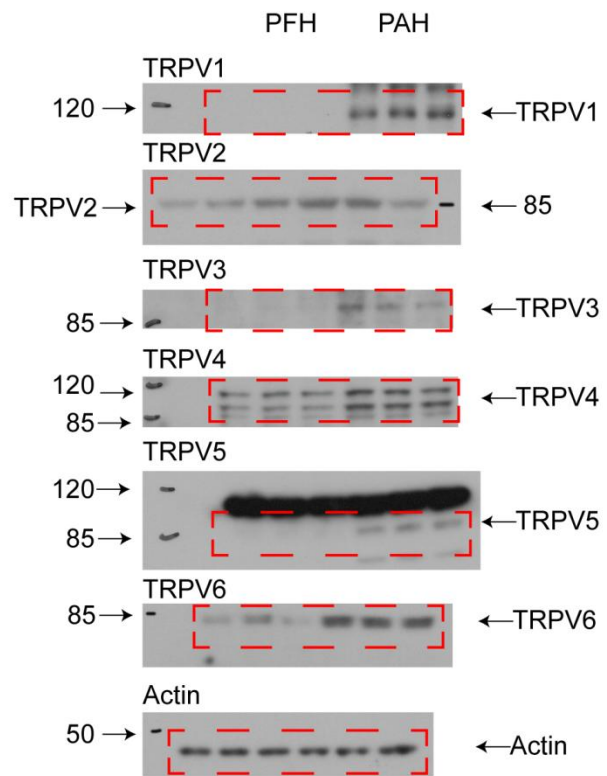


Fig. S11K

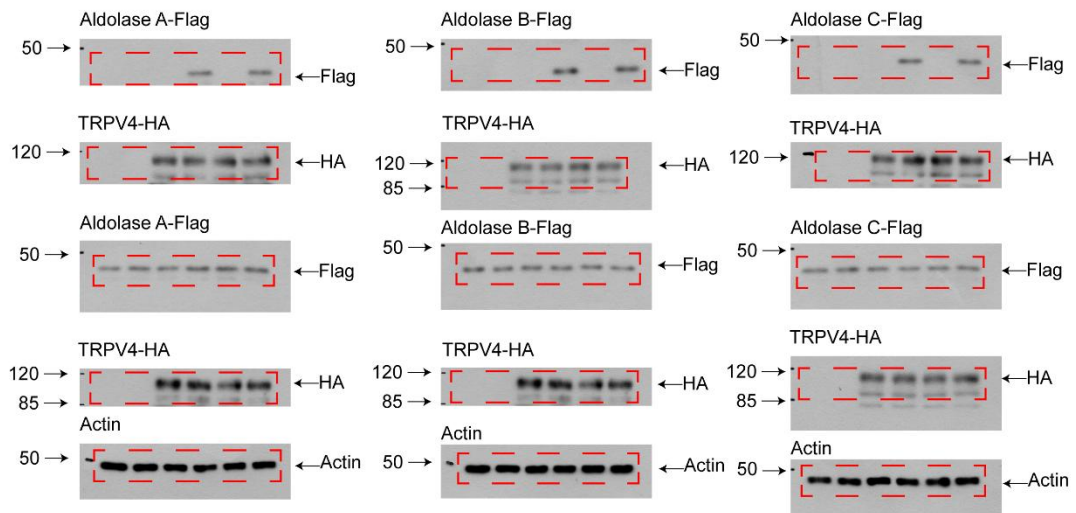


Fig. S12A, B

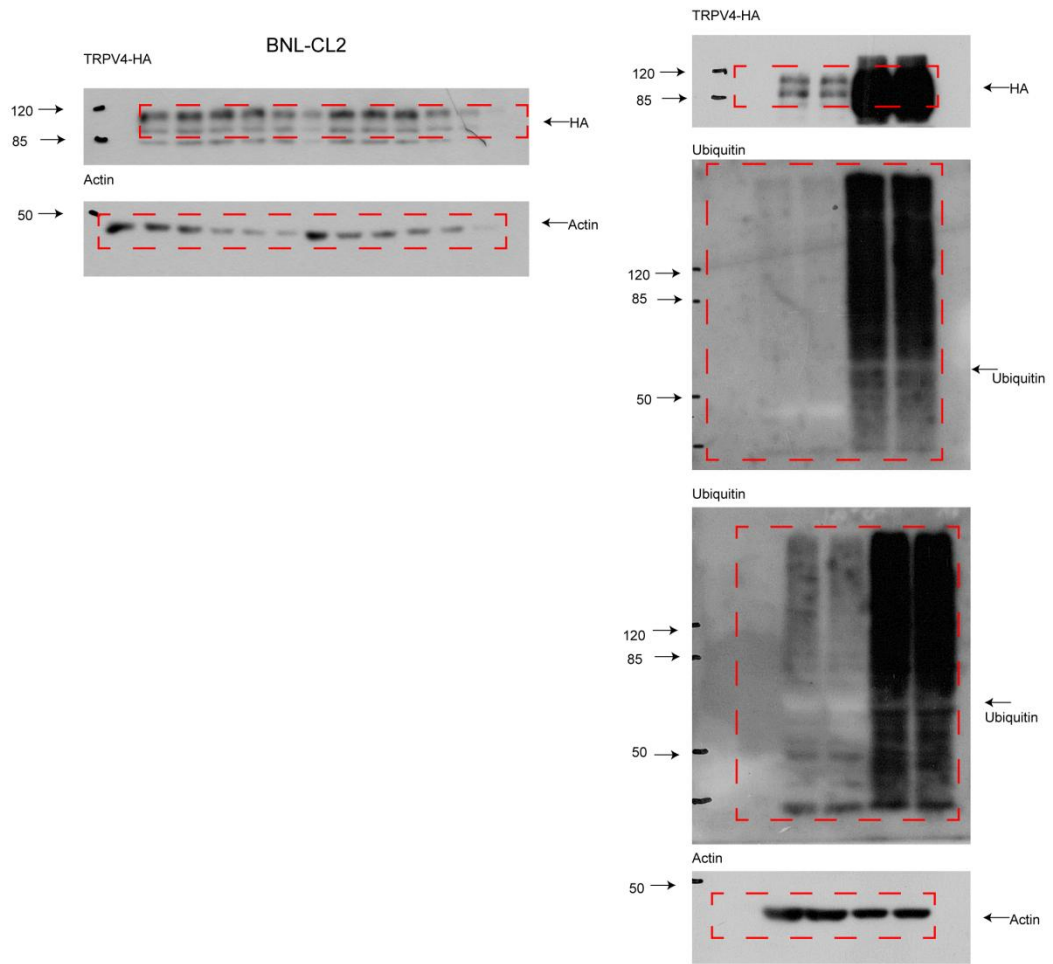


Fig. S12C

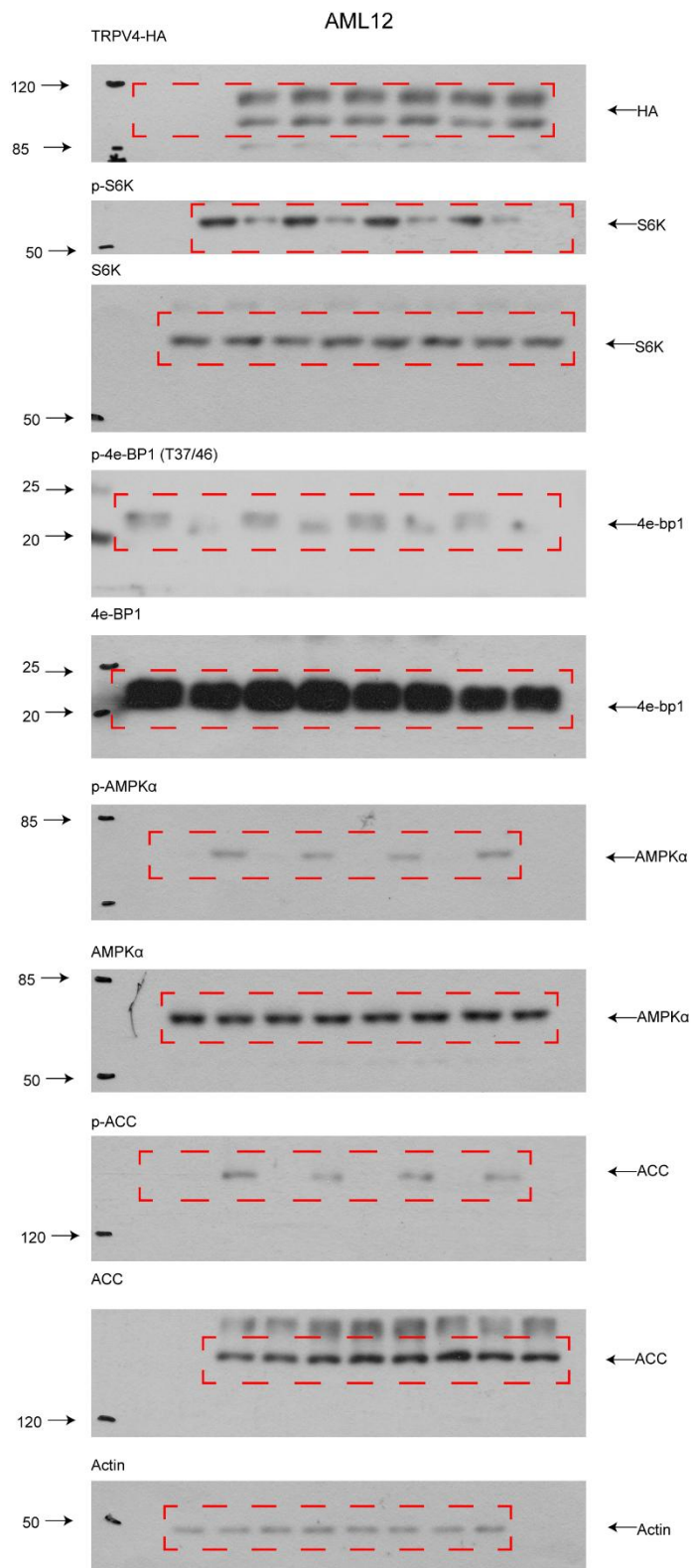


Fig. S13A-D

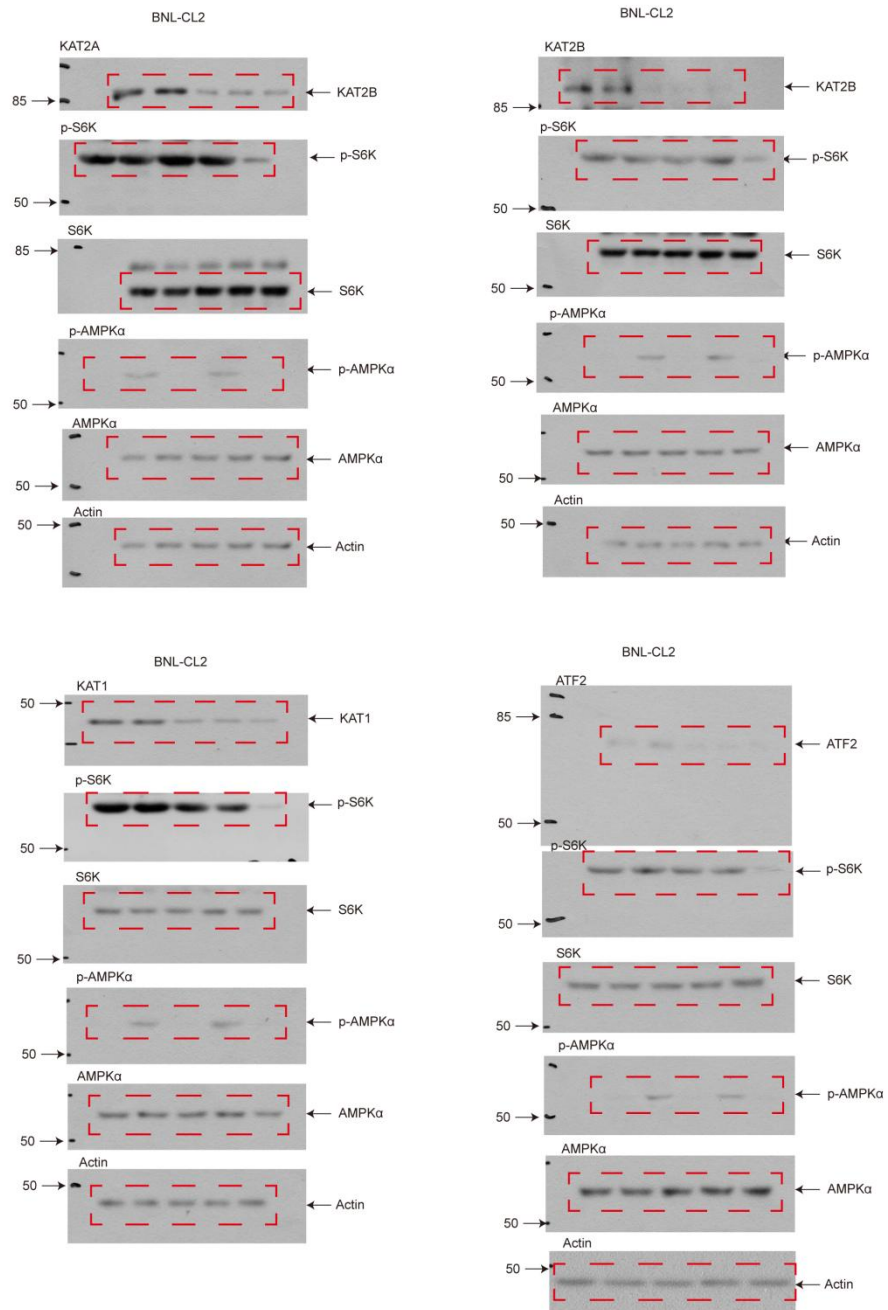


Fig. S13E-H

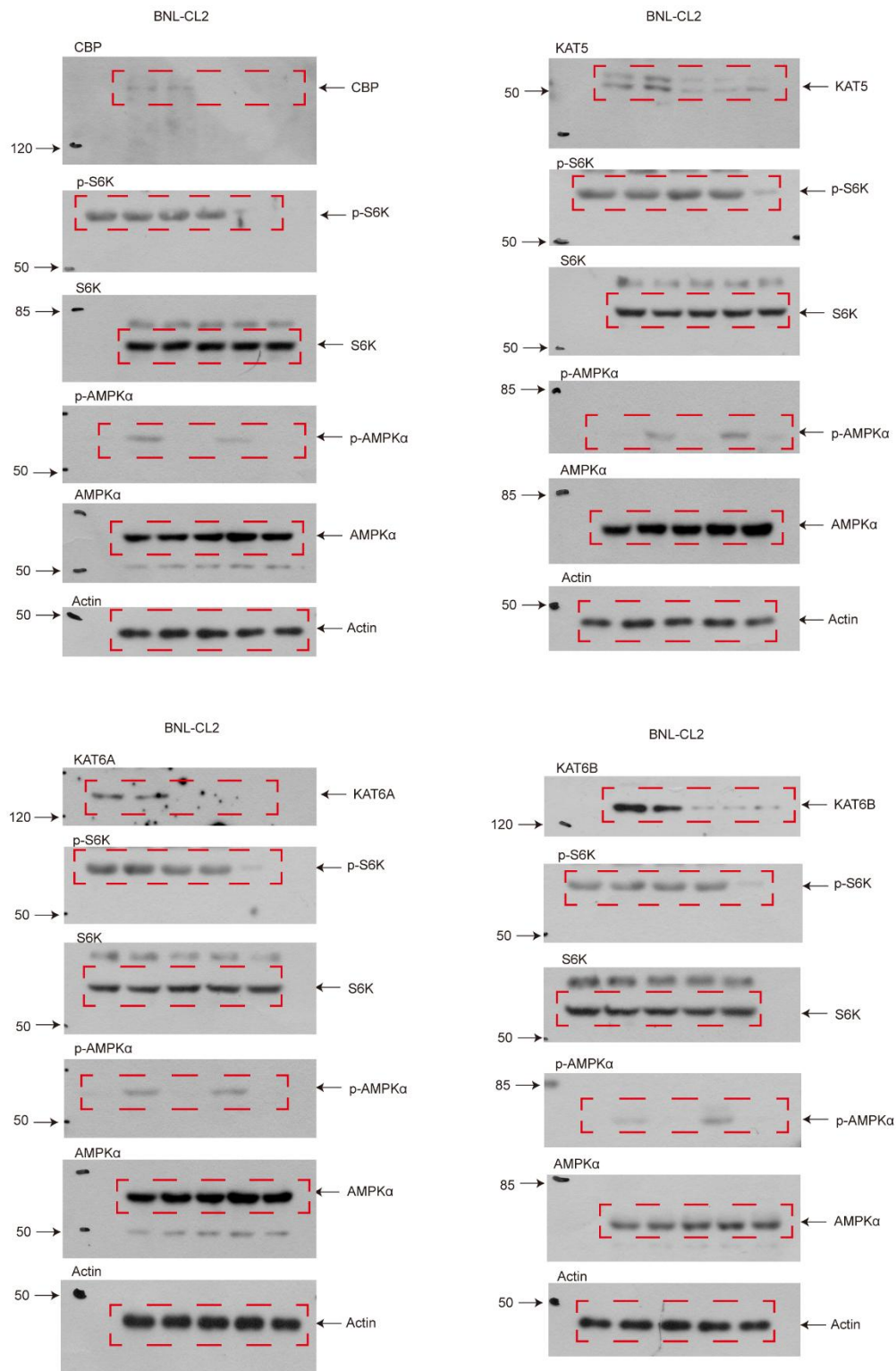


Fig. S13I-L

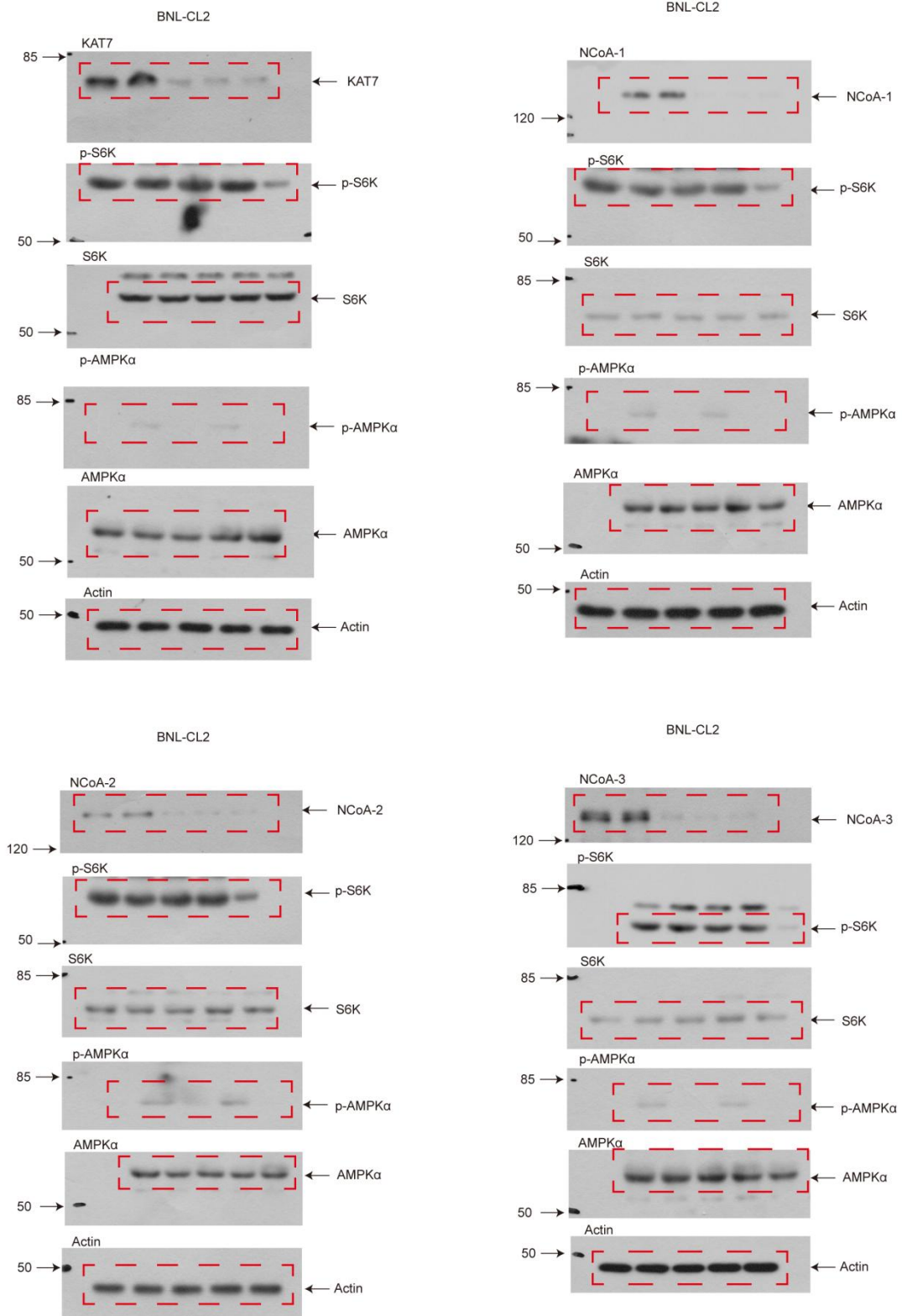


Fig. S13M-O

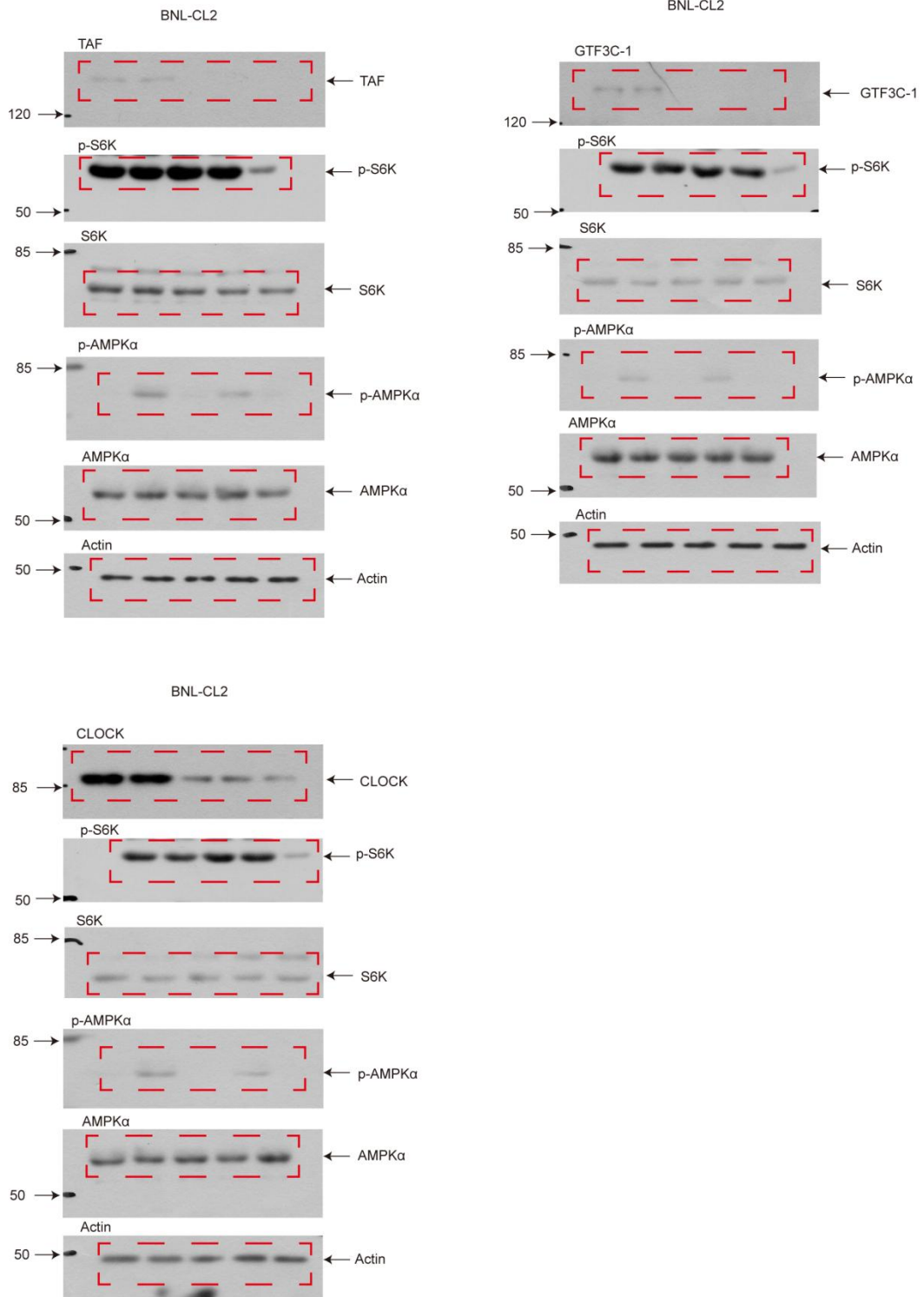


Fig. S14A-C

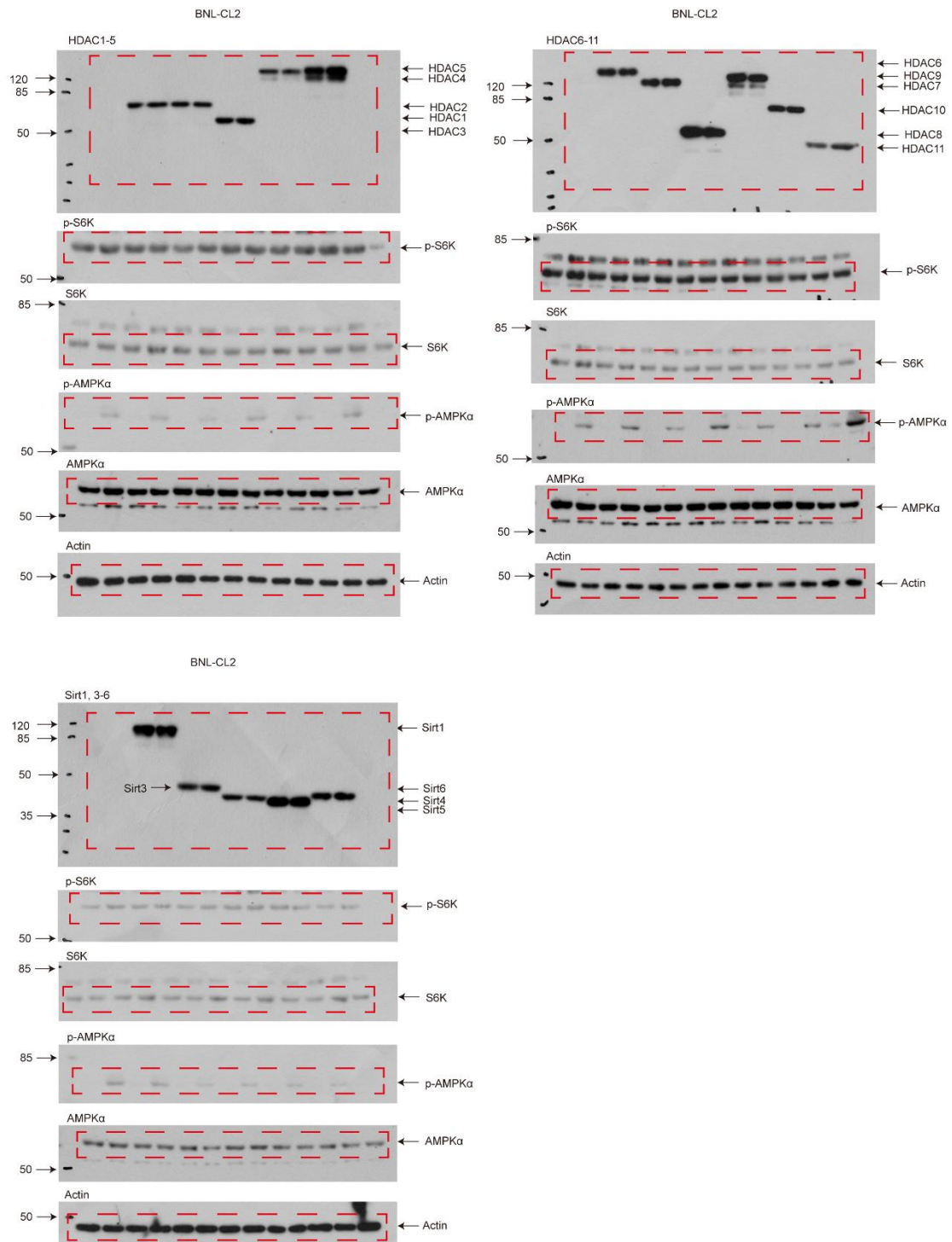


Fig. S17D

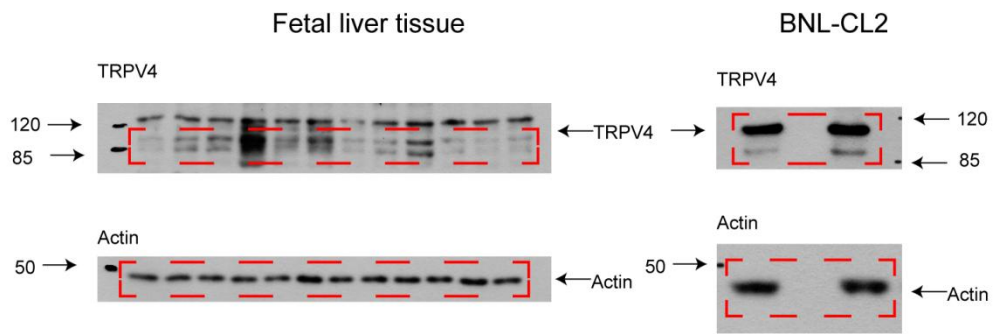


Fig. S19B

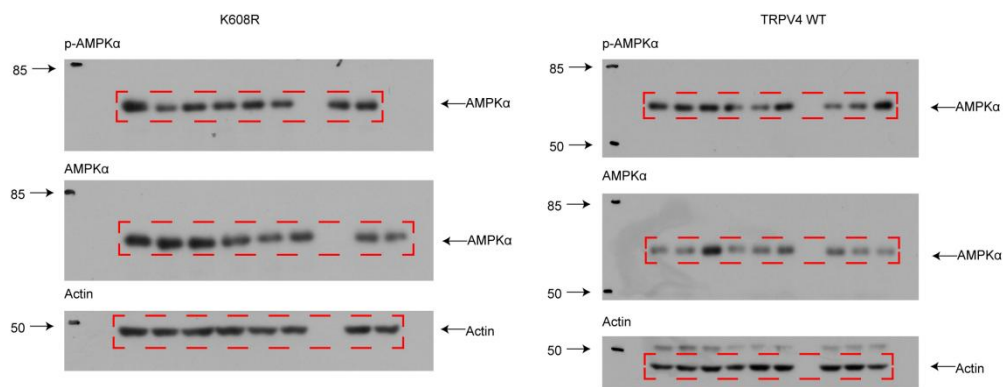


Fig. S21F

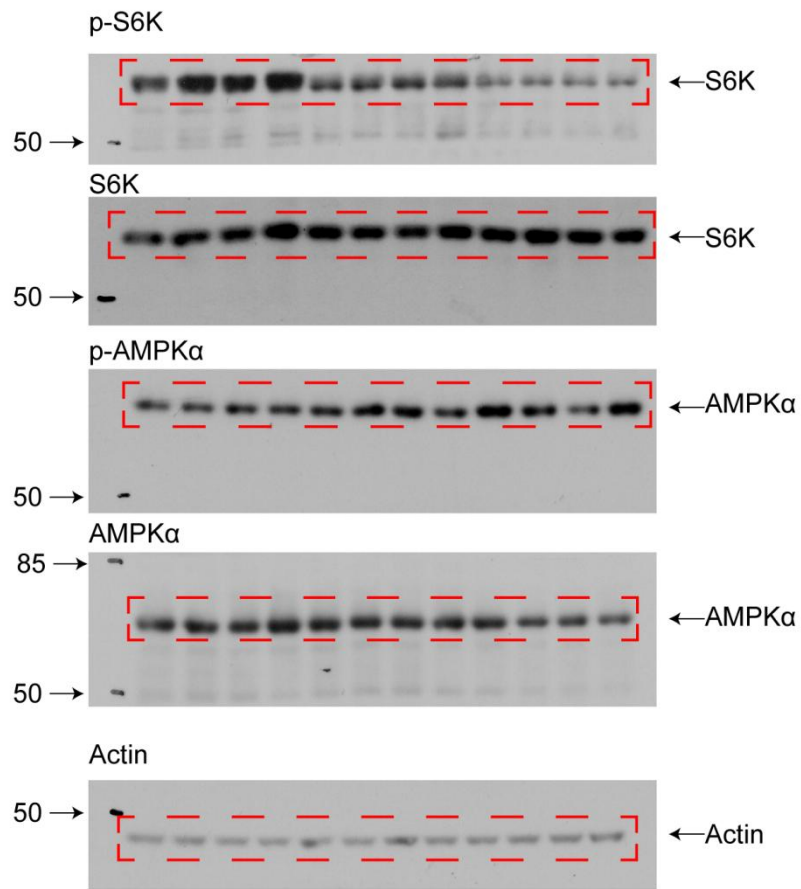


Fig. S21G

