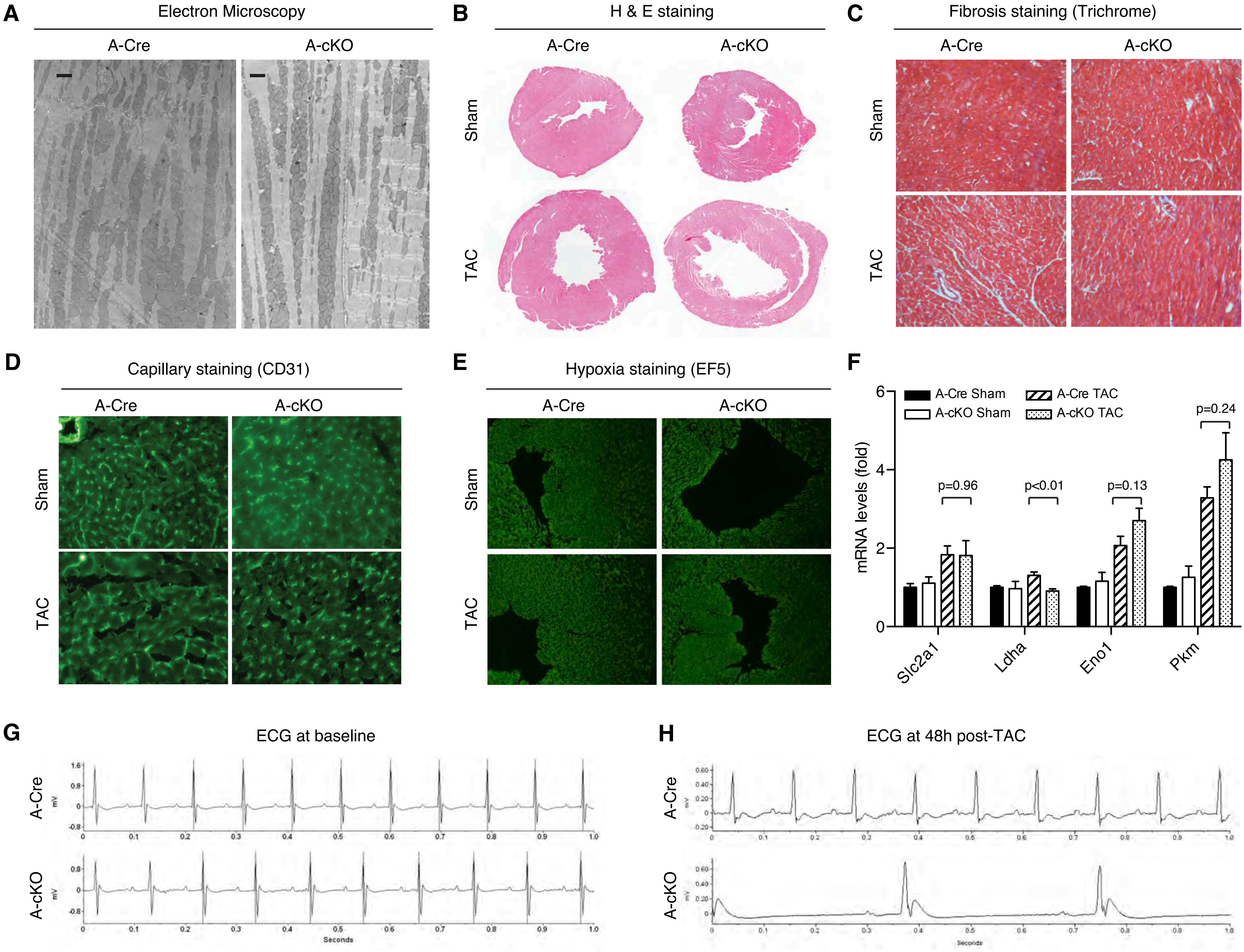
Supplementary Figure 1. Normal structure of A-cKO heart at baseline.

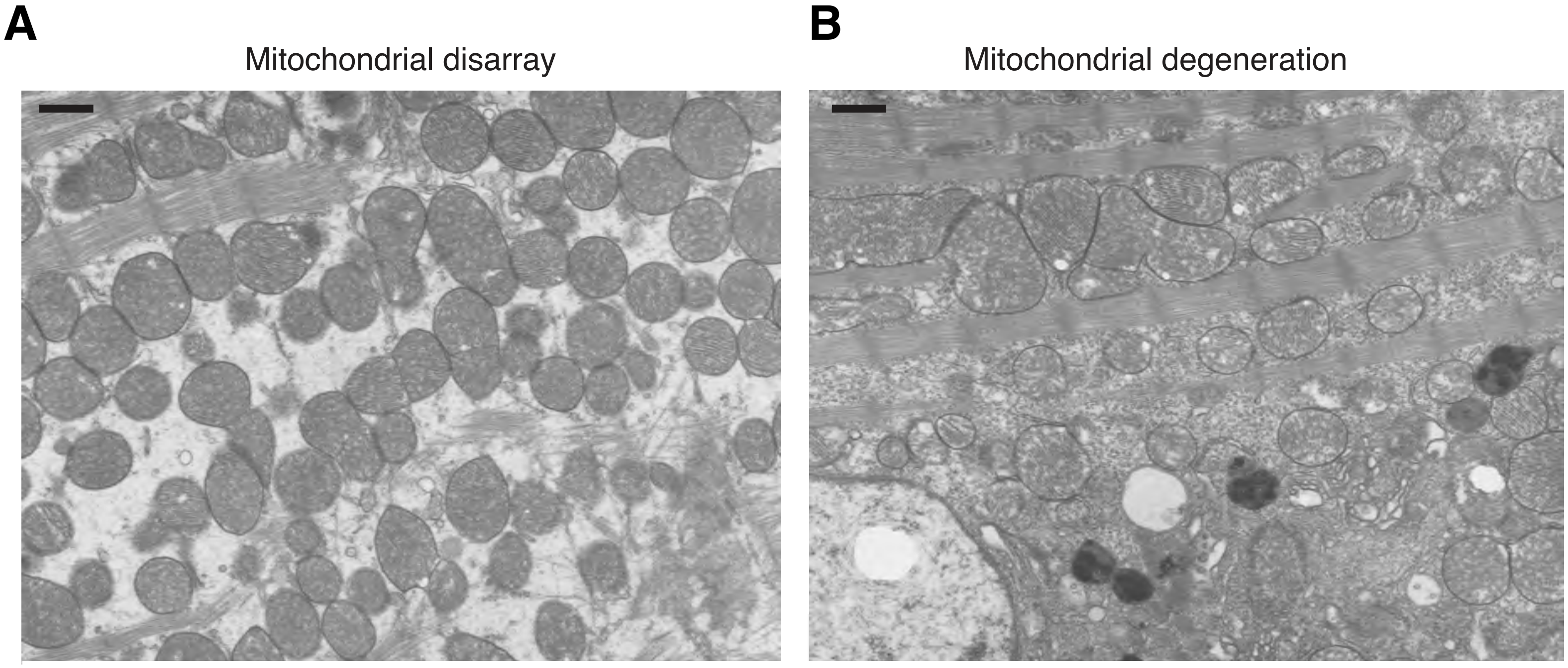
(A) Ultrastructure of myocardium by TEM. Scale bars indicate 1 μm. (B) Hematoxylin & Eosin (H&E) staining of heart tissue. (C) Trichrome staining for fibrosis. (D) Endothelial marker CD31 staining for myocardial capillary density. (E) EF5 staining for hypoxia stress. (F) Expression of hypoxia-inducible genes by qPCR. (G,H) ECG recording by telemetry.



Supplementary Figure 1

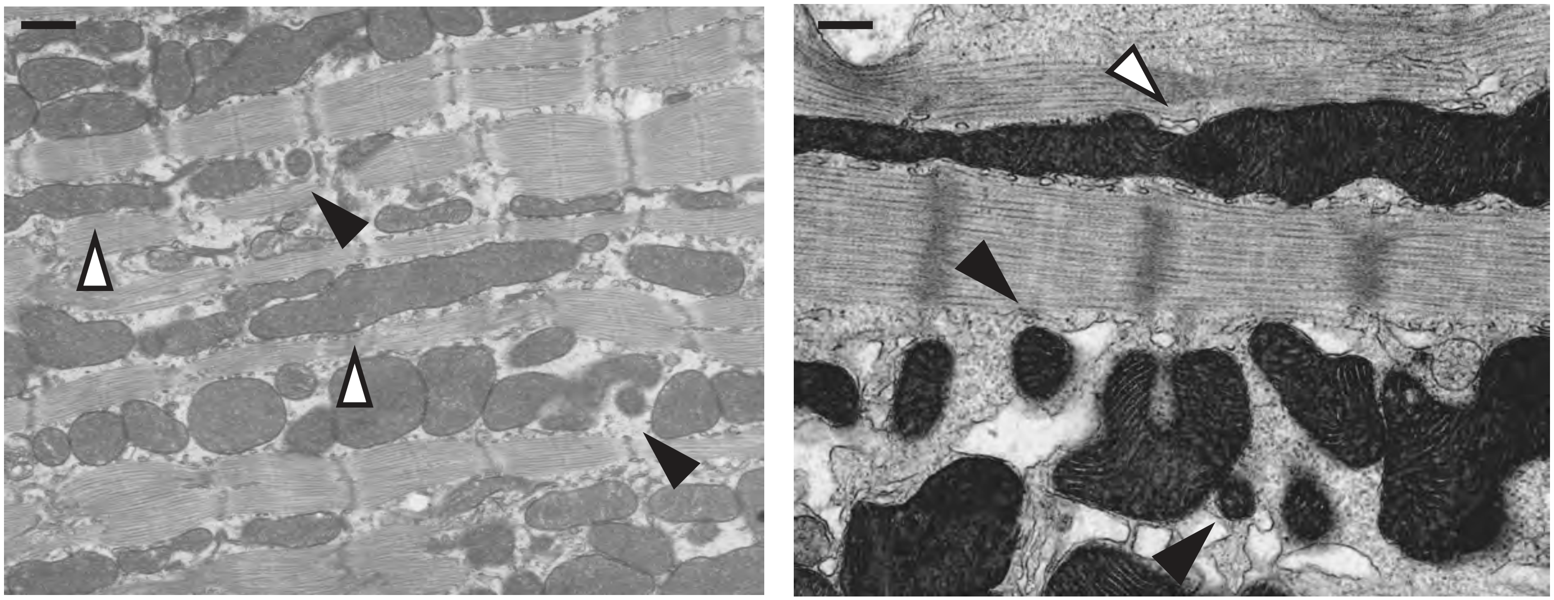
Supplementary Figure 2. TAC-induced severe mitochondrial damage in A-cKO heart.

(A) Mitochondrial disarray. (B) Mitochondrial degeneration. (C,D) Altered size and shape of mitochondria. Black arrowheads: fragmented mitochondria. White arrowheads: giant mitochondria. Scale bars indicate 1 μm.



C

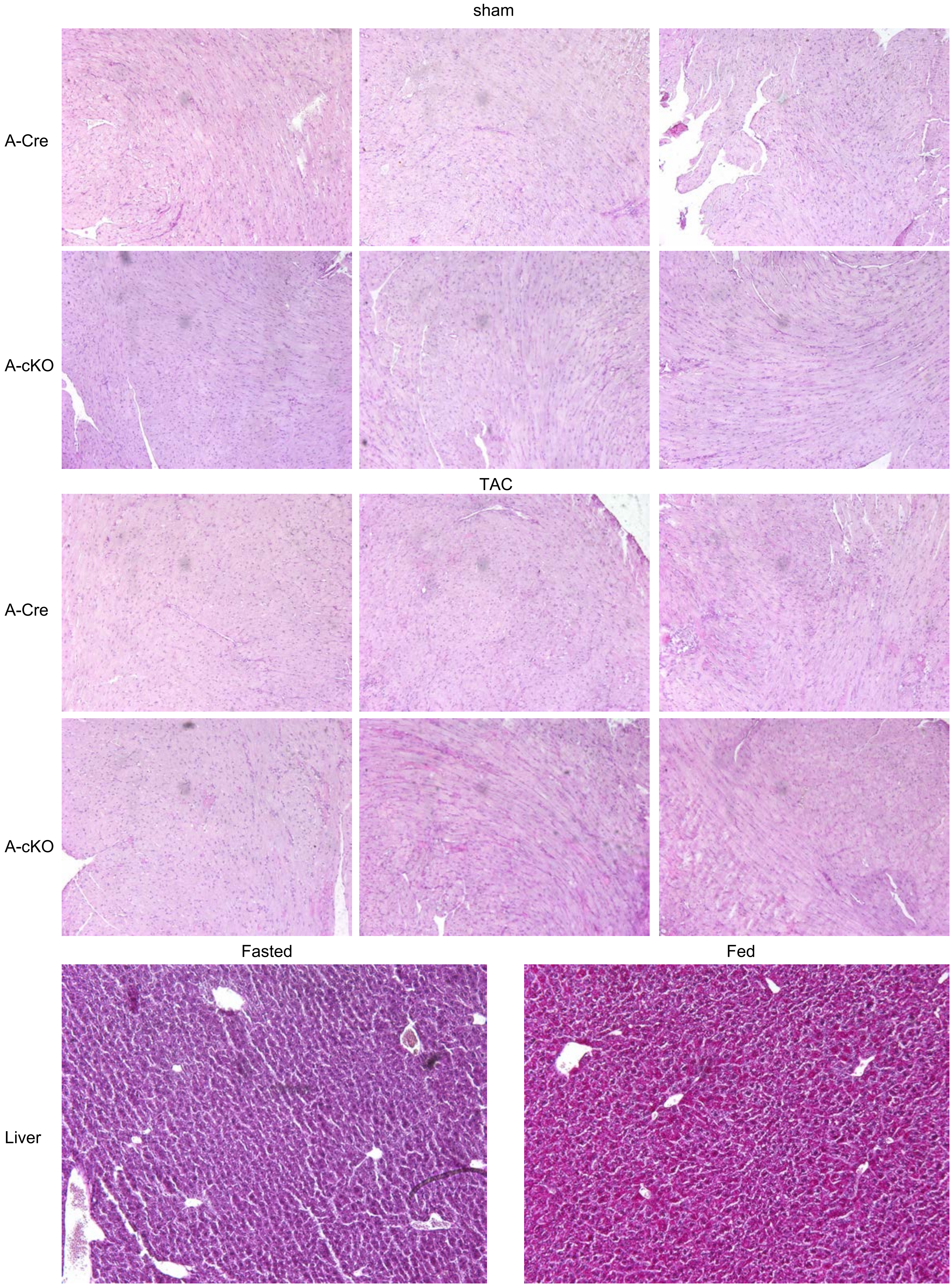
Mitochondrial fragmentation and formation of giant mitochondria



Supplementary Figure 2

Supplementary Figure 3. Myocardial glycogen content before and after 3-day of TAC.

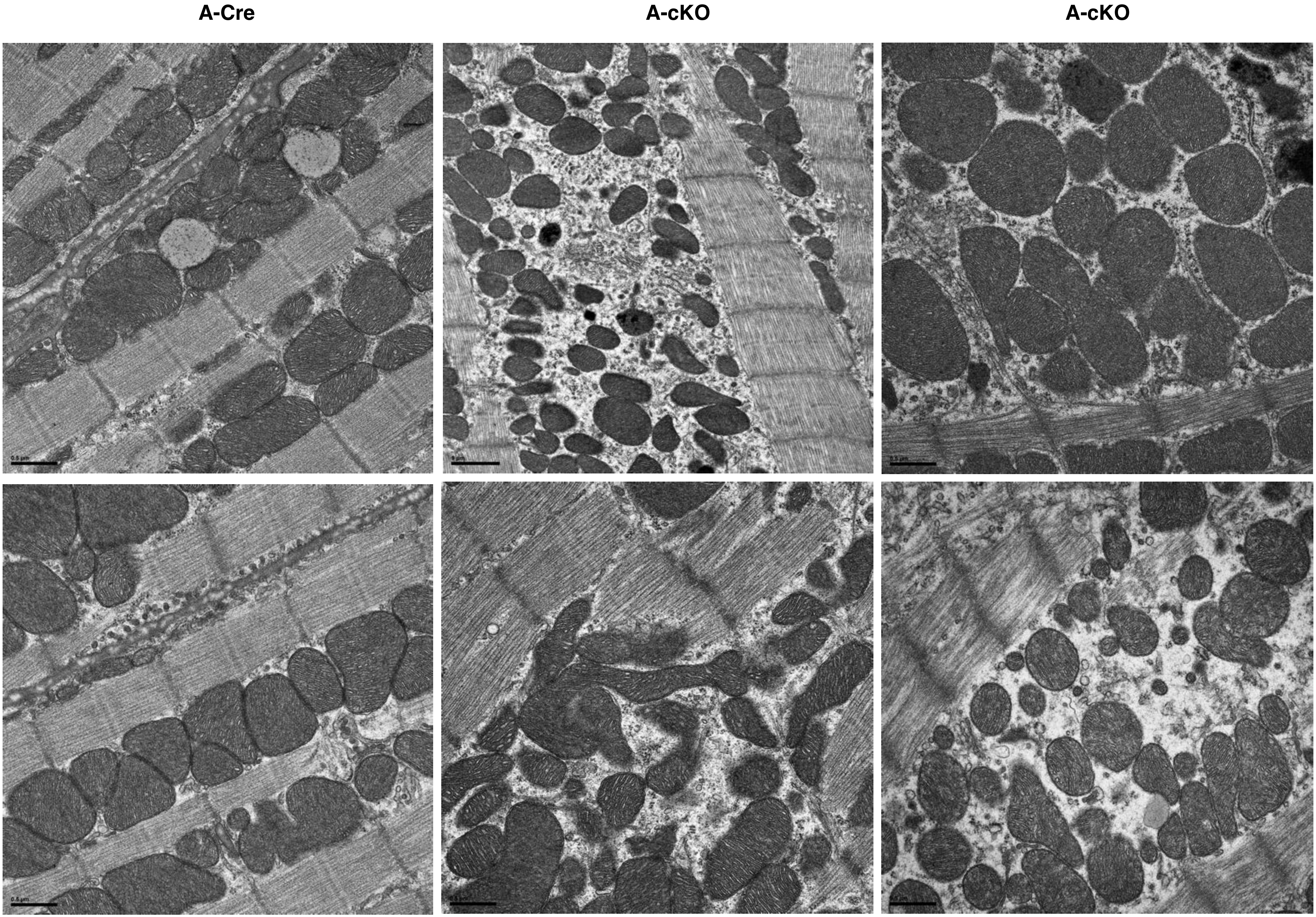
Glycogen deposition was assessed by PAS staining. n=3 in each group. Liver sections from normally fed (Fed) and 24-hour fasted (Fasted) mice were included as controls. Glycogen deposits stained in red.



Supplementary Figure 3

Supplementary Figure 4. Mitochondrial dysfunction in aged KLF4-deficient hearts.

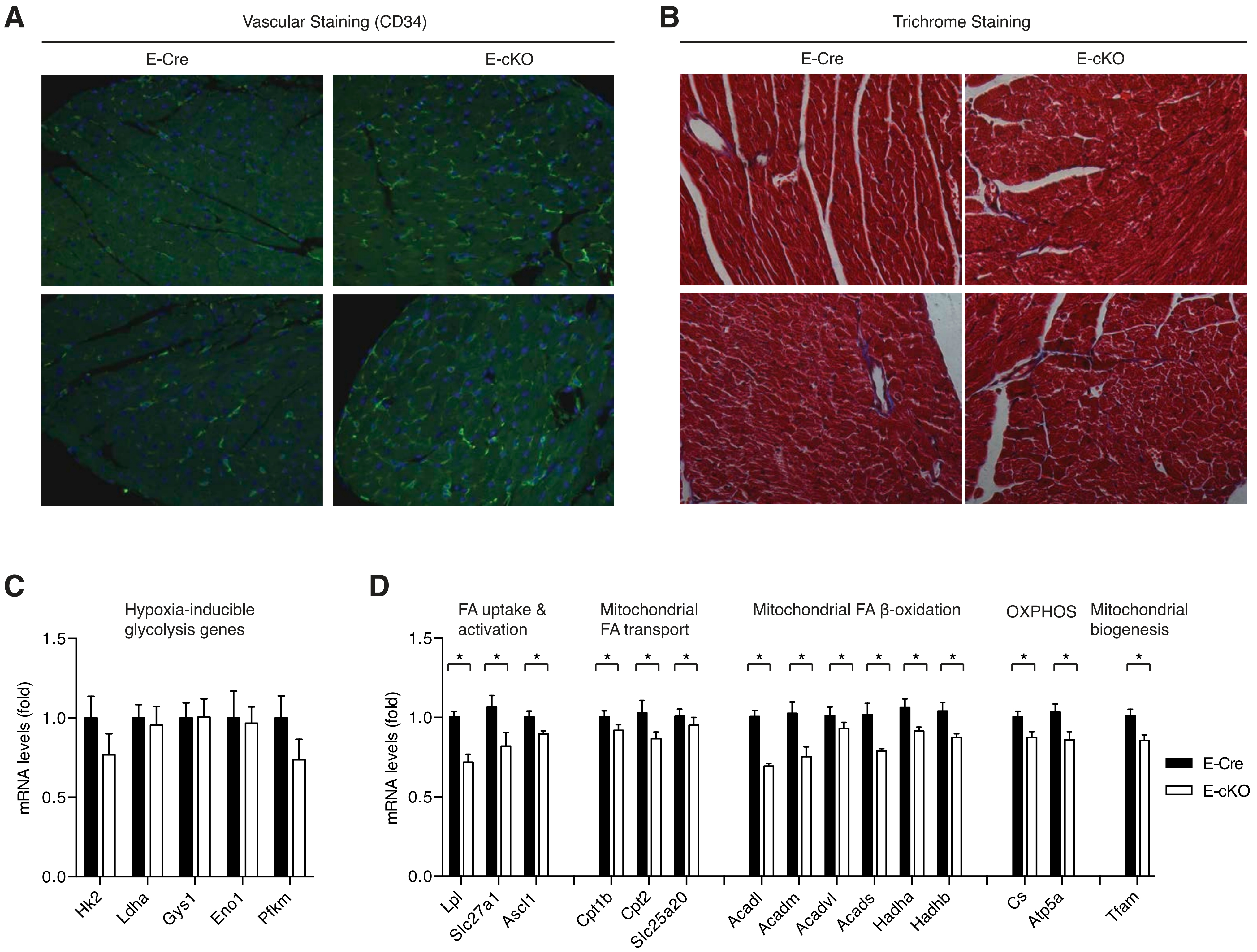
Mice were 9-month old. Scale bars indicate 0.5 μm. Representative images from 3 animals in each group were shown.



Supplementary Figure 4

Supplementary Figure 5. Normal vascular development and gross structure of E-cKO heart.

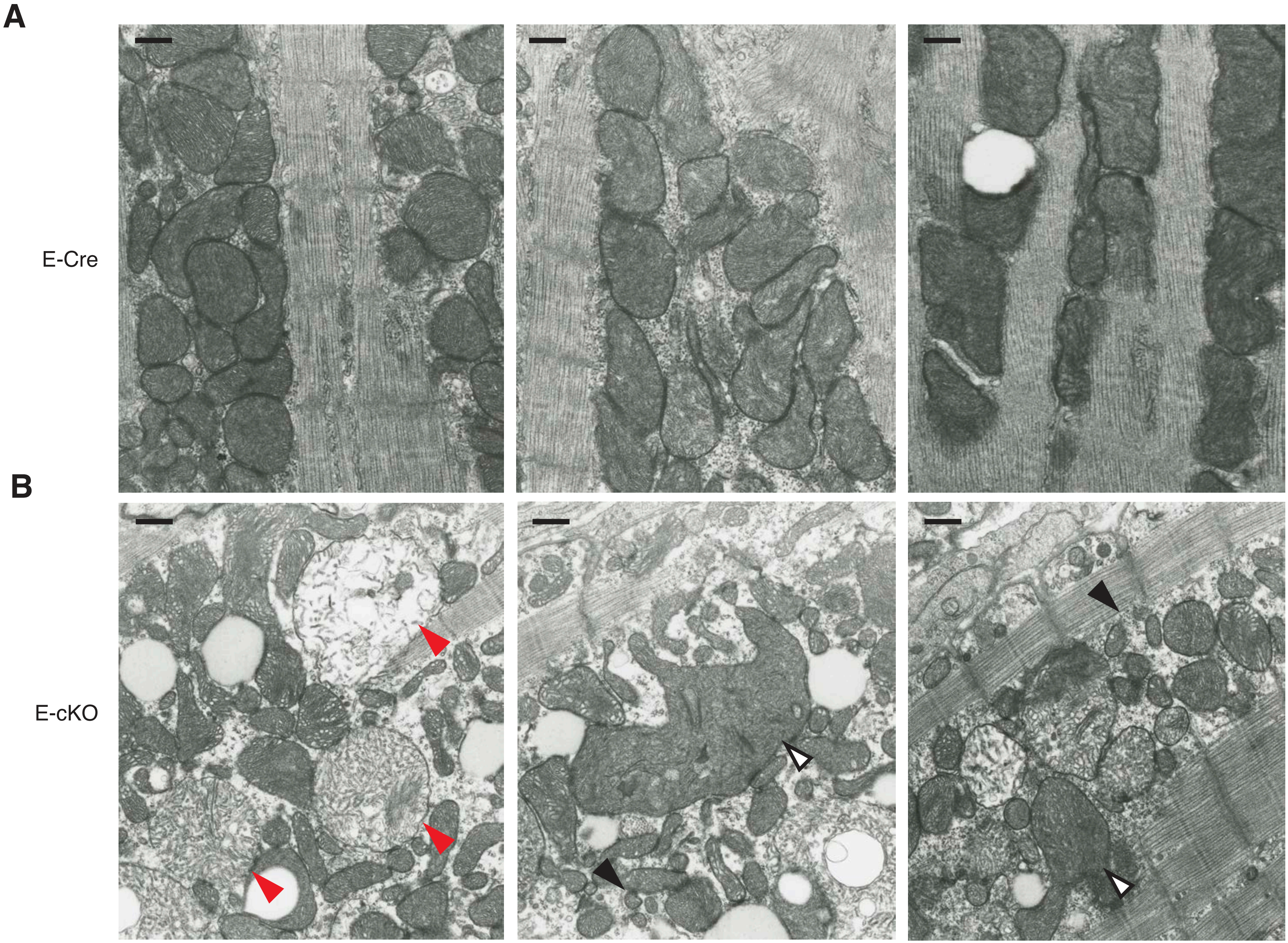
(A) Capillary density revealed by CD34 staining. (B) Trichrome staining to reveal fibrosis. Representative images from 3 pairs of animals were shown. (C) Expression of hypoxia-inducible glycolysis genes. (D) Expression of metabolic and mitochondrial genes. Genes expression was determined in the heart at 2-week of age. n=10 in each group. *$p<0.05$.



Supplementary Figure 5

Supplementary Figure 6. Mitochondrial abnormality in E-cKO hearts at 2-week after birth.

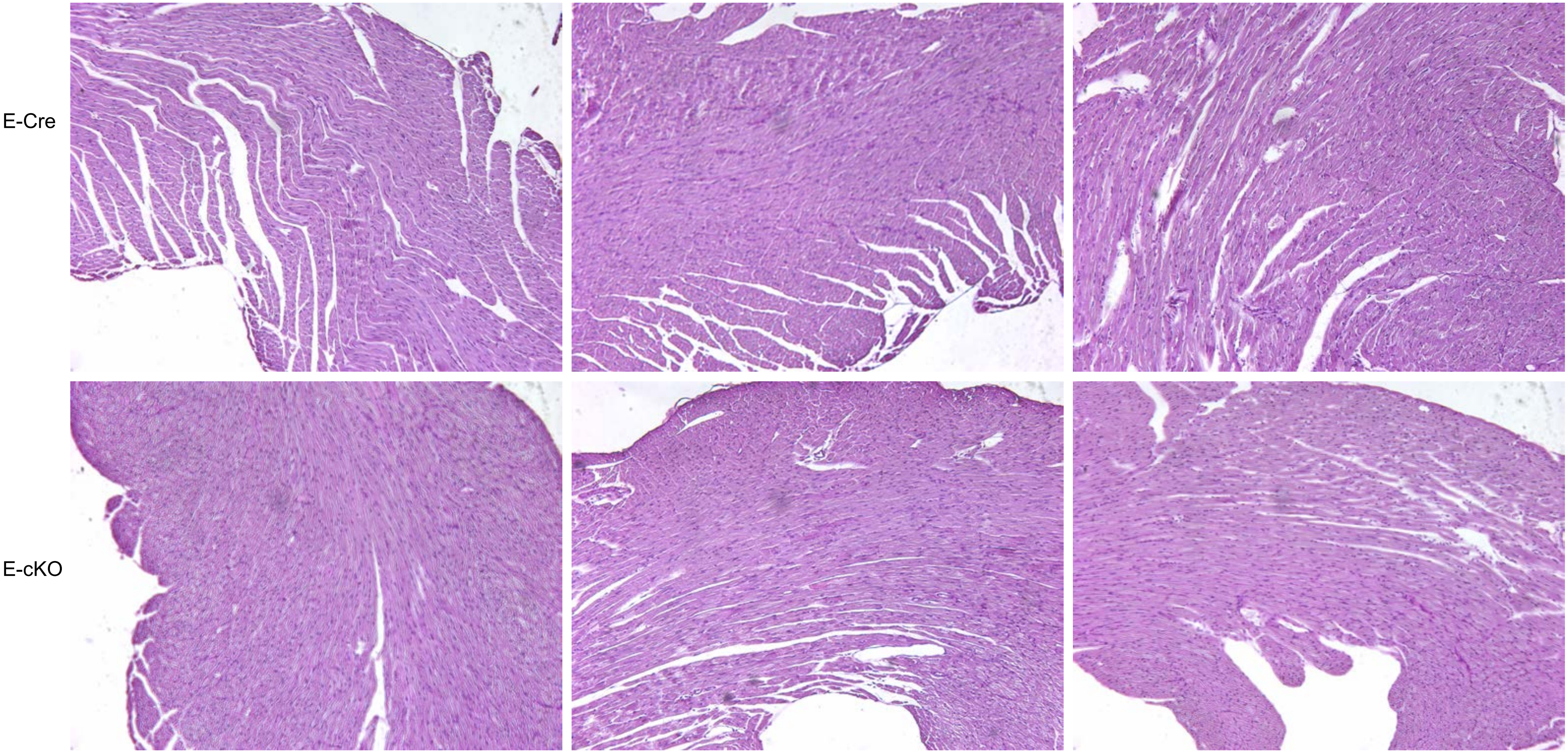
(A) Normal ultrastructure of E-Cre hearts. (B) Abnormality of myocardial ultrastructure in E-cKO hearts showing mitochondrial disarray, degeneration, and altered size and shape of mitochondria. Red arrowheads: degenerated mitochondria. Black arrowheads: fragmented mitochondria. White arrowheads: giant mitochondria. Scale bars indicate 500 nm.



Supplementary Figure 6

Supplementary Figure 7. Myocardial glycogen content in 3-week-old mice.

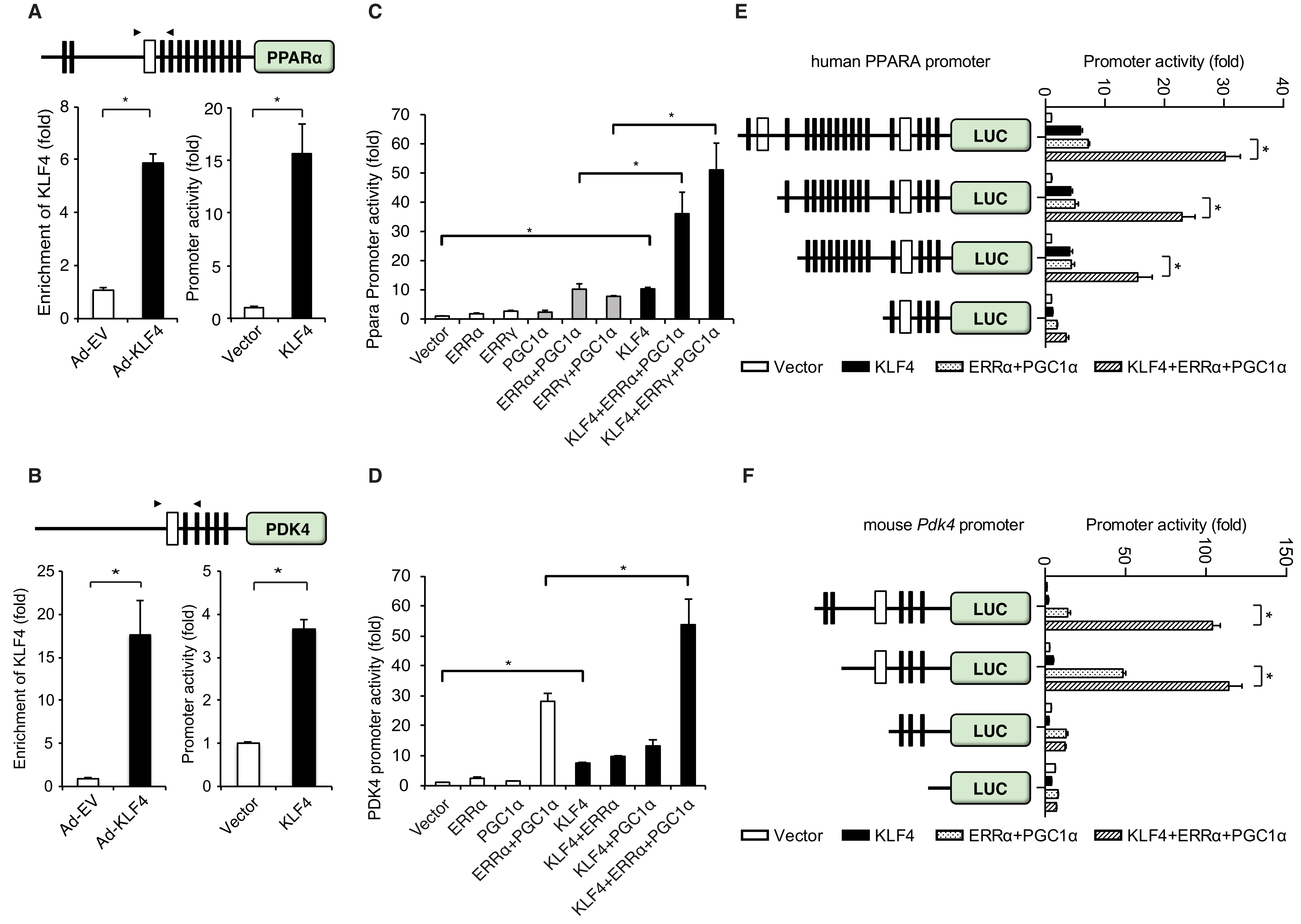
Glycogen deposition was assessed by PAS staining. n=3 in each group. Glycogen deposits stained in red.



Supplementary Figure 7

Supplementary Figure 8. Interaction and cooperativity between KLF4 and the ERR/PGC-1 module.

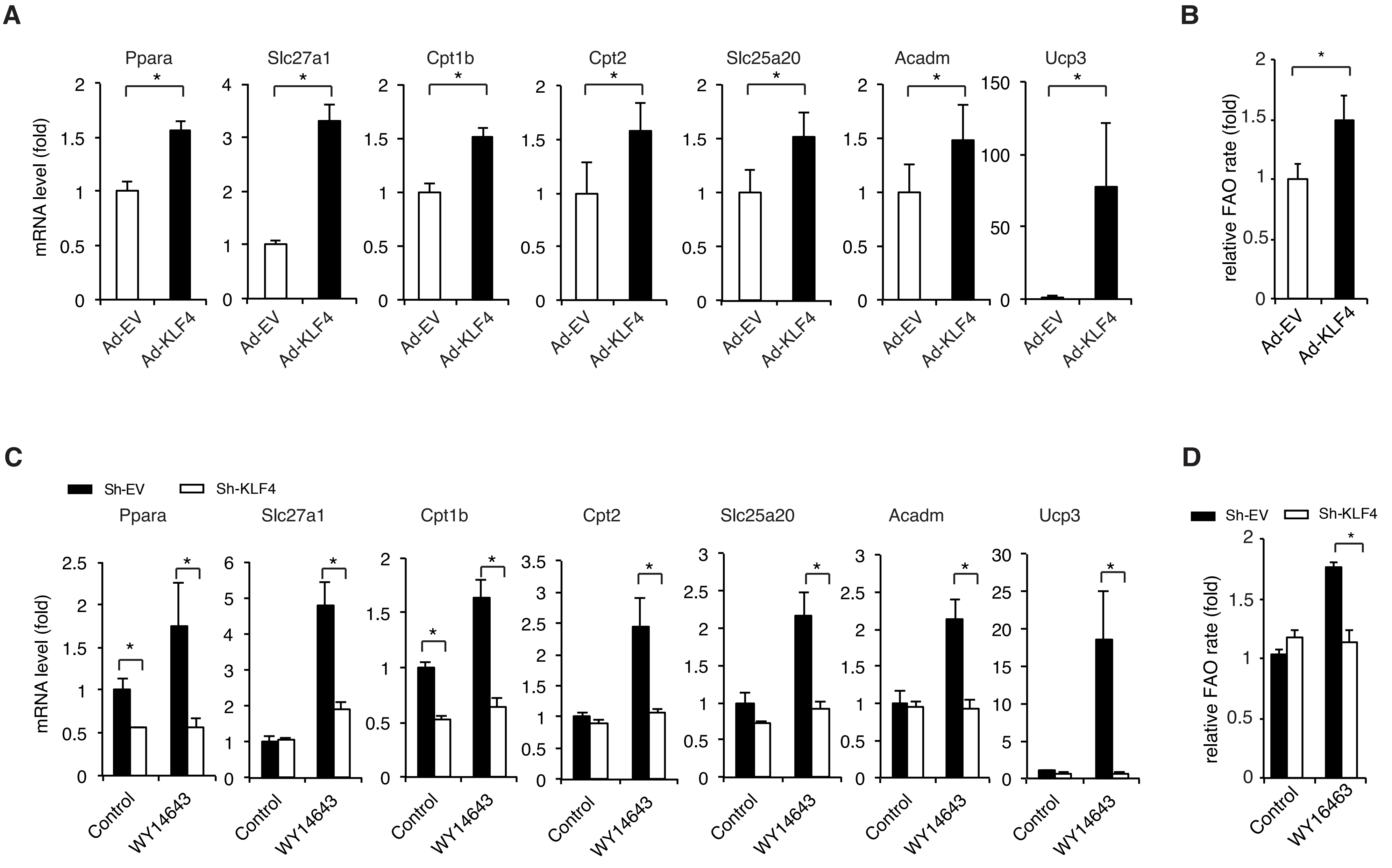
(A, D) Recruitment of KLF4 onto endogenous *Ppara* (A) and *Pdk4* (D) promoters and activation of the promoter reporter. Solid bars indicate KRE and open bar indicates NRRE. Arrow heads indicate PCR regions in ChIP assays. (B, E) Synergistic cooperativity between KLF4 and the ERR/PGC-1 complex on target promoters. (C, F) Promoter truncation analysis. n=3. $*p<0.05$.



Supplementary Figure 8

Supplementary Figure 9. KLF4 positively regulates and is requisite for PPARα signaling.

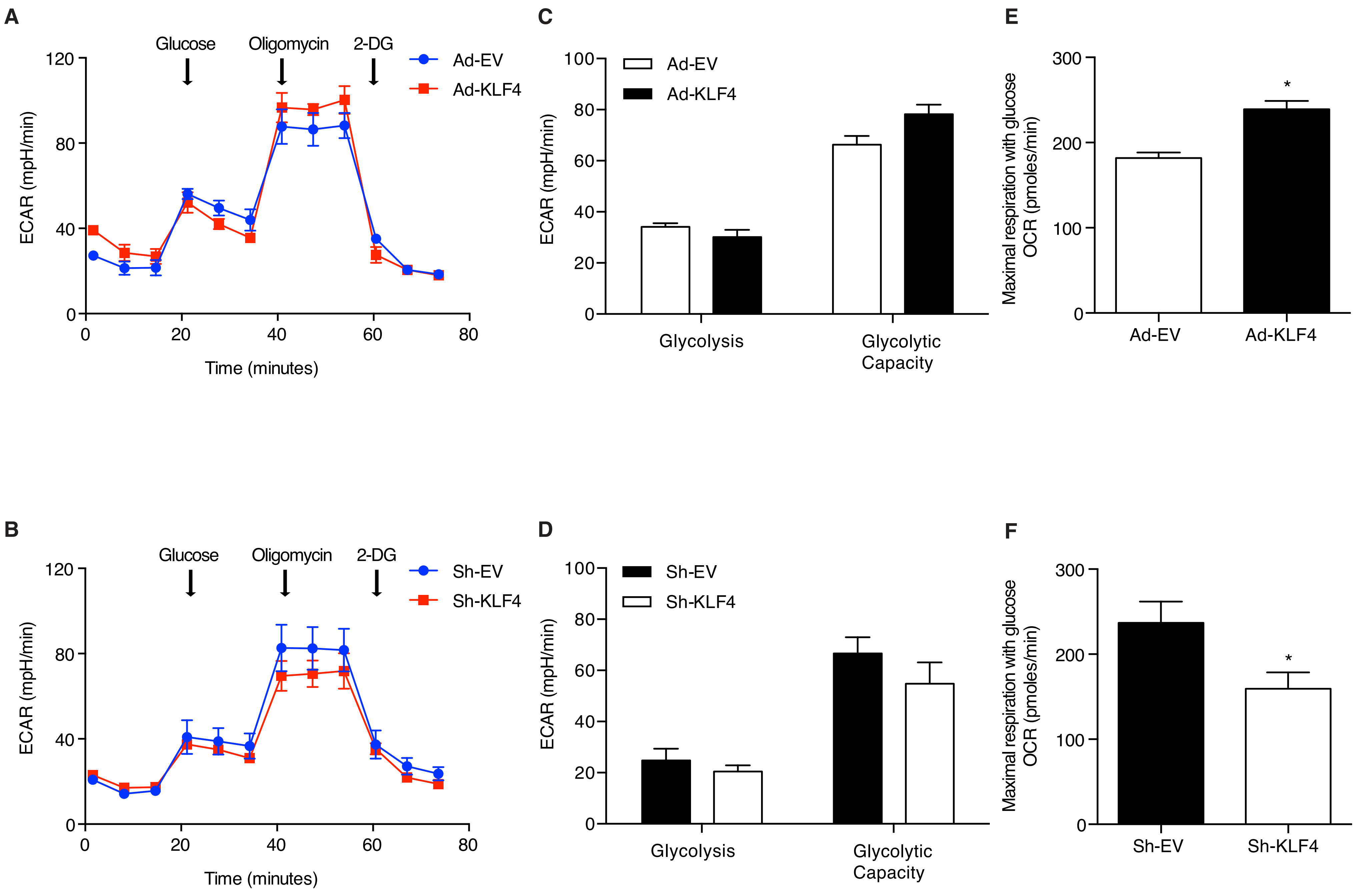
(A, B) Adenoviral overexpression of KLF4 in NRVM induced PPARα target genes (A) and enhanced FAO (B). (C, D) Adenoviral knockdown of KLF4 in NRVM impaired PPARα ligand WY14643-induced target genes expression and induction of FAO. NRVM were infected with adenovirus for 48 h before treatment with WY14643 for 16 h. n=3 in each group. $^*p<0.05$.



Supplementary Figure 9

Supplementary Figure 10. Effects of KLF4 on cardiac glucose metabolism.

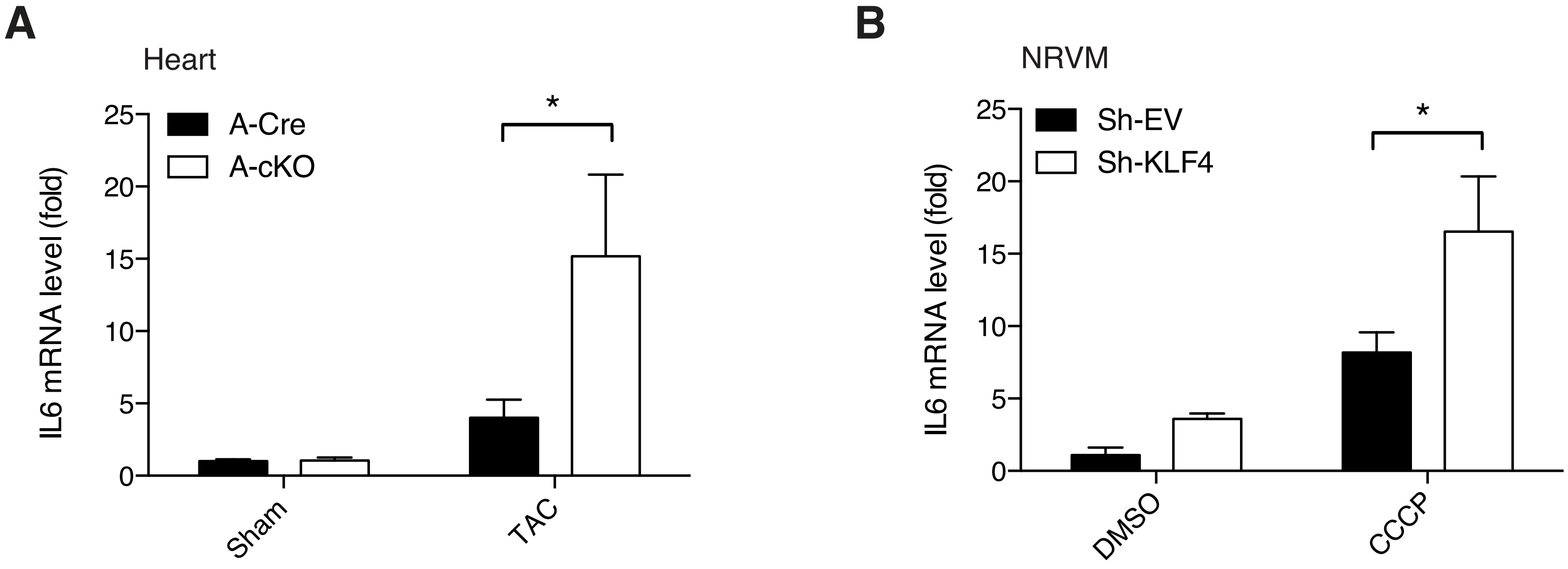
(A, B) Glycolysis assays using the Seahorse glycolysis stress test in NRVM with acute overexpression (A) or knockdown (B) of KLF4. (C, D) Glycolysis rate shown as extracellular acidification rate (ECAR). Basal glycolysis rate was calculated as $\Delta(\text{ECAR}_{\text{glucose}}\text{-ECAR}_{\text{basal}})$. Glycolysis capacity was calculated as $\Delta(\text{ECAR}_{\text{Oligomycin}}\text{-ECAR}_{\text{basal}})$. (E, F) Maximal glucose oxidation rate was calculated from FCCP-induced oxygen consumption rate (OCR) with glucose (25 mmol/L) as the sole substrate using the Seahorse cell mito stress test. n=3 in each group. *$p<0.05$.



Supplementary Figure 10

Supplementary Figure 11. Impaired mitophagy was associated with inflammation.

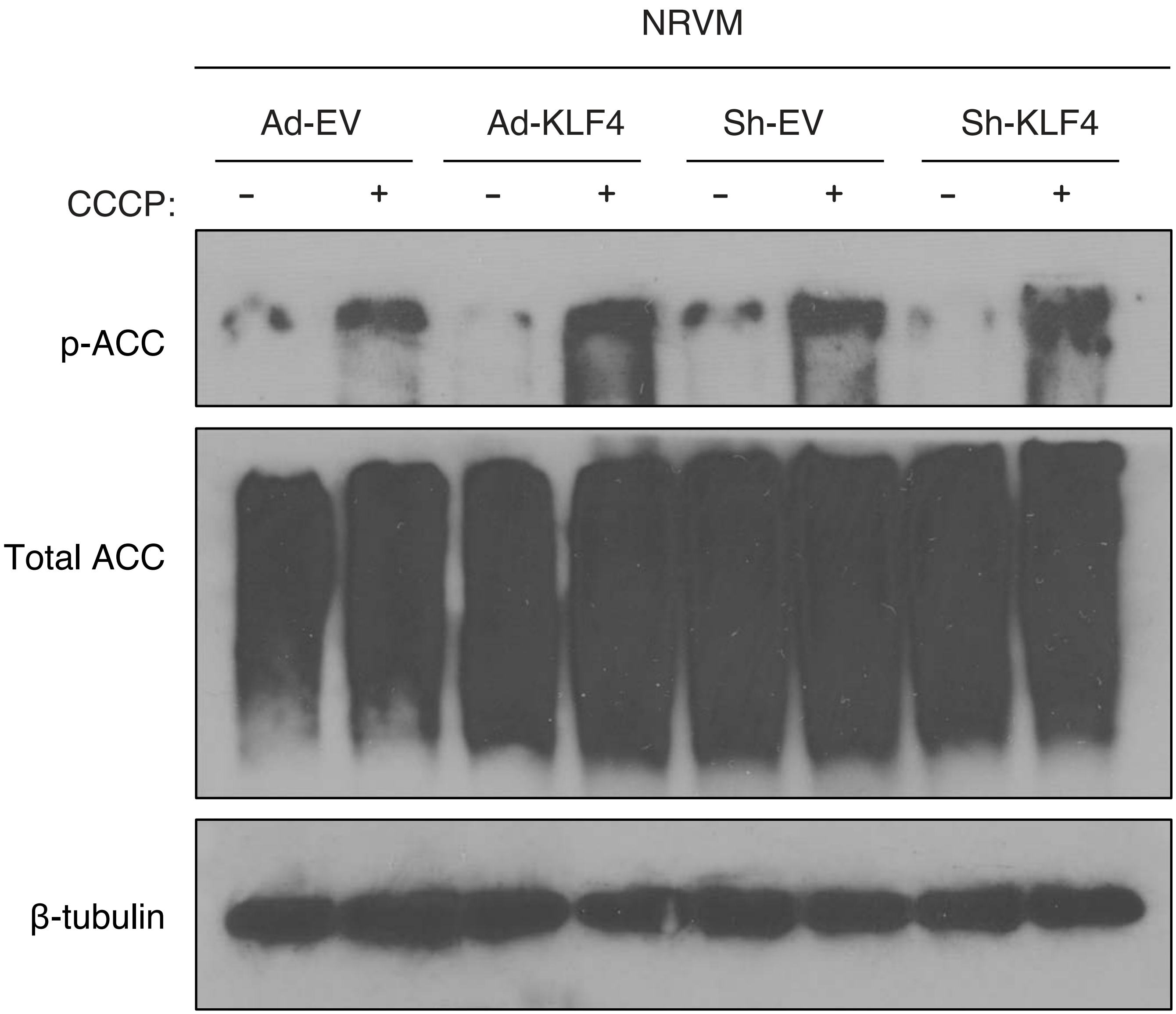
(A) IL6 mRNA expression in KLF4-deficient myocardium. (B) IL6 mRNA expression in KLF4-deficient cardiomyocytes. n=3 in each group. *$p<0.05$.



Supplementary Figure 11

Supplementary Figure 12. KLF4 does not affect AMPK-mediated phosphorylation of ACC in NRVM.

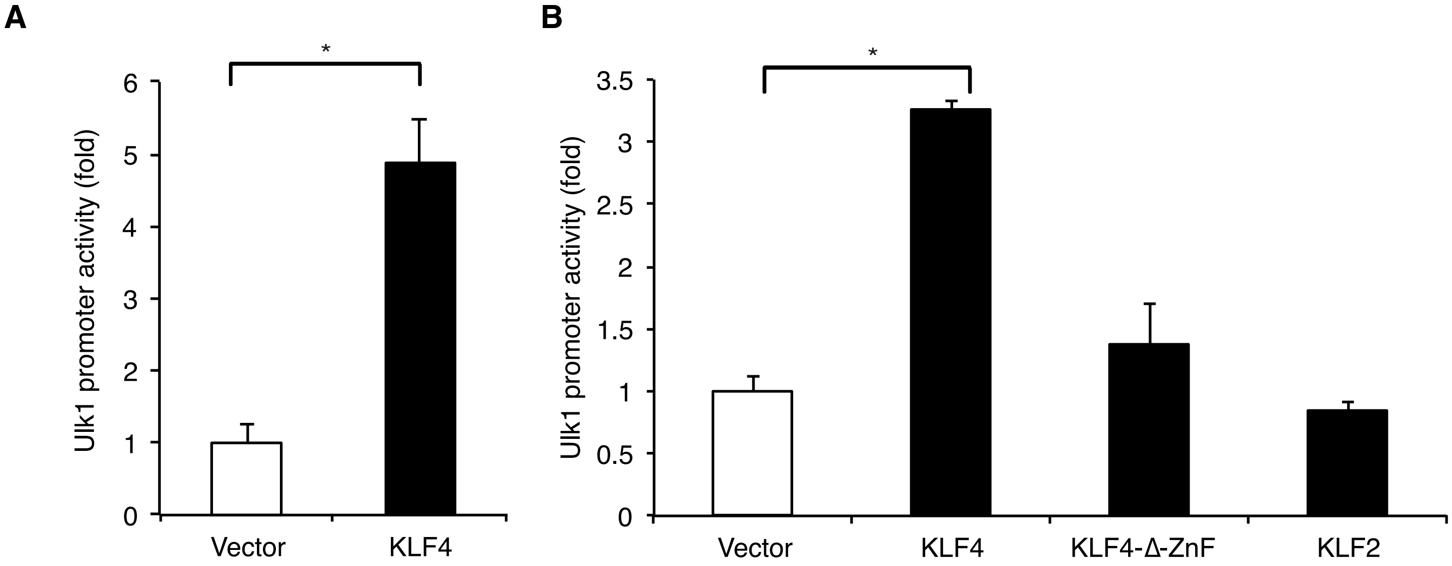
Western blot for total protein of Acetyl-CoA Carboxylase (ACC) and its Ser79-phosphorylated form in NRVM. ACC is a confirmed direct target of AMPK.



Supplementary Figure 12

Supplementary Figure 13. KLF4 directly activates ULK1 promoter.

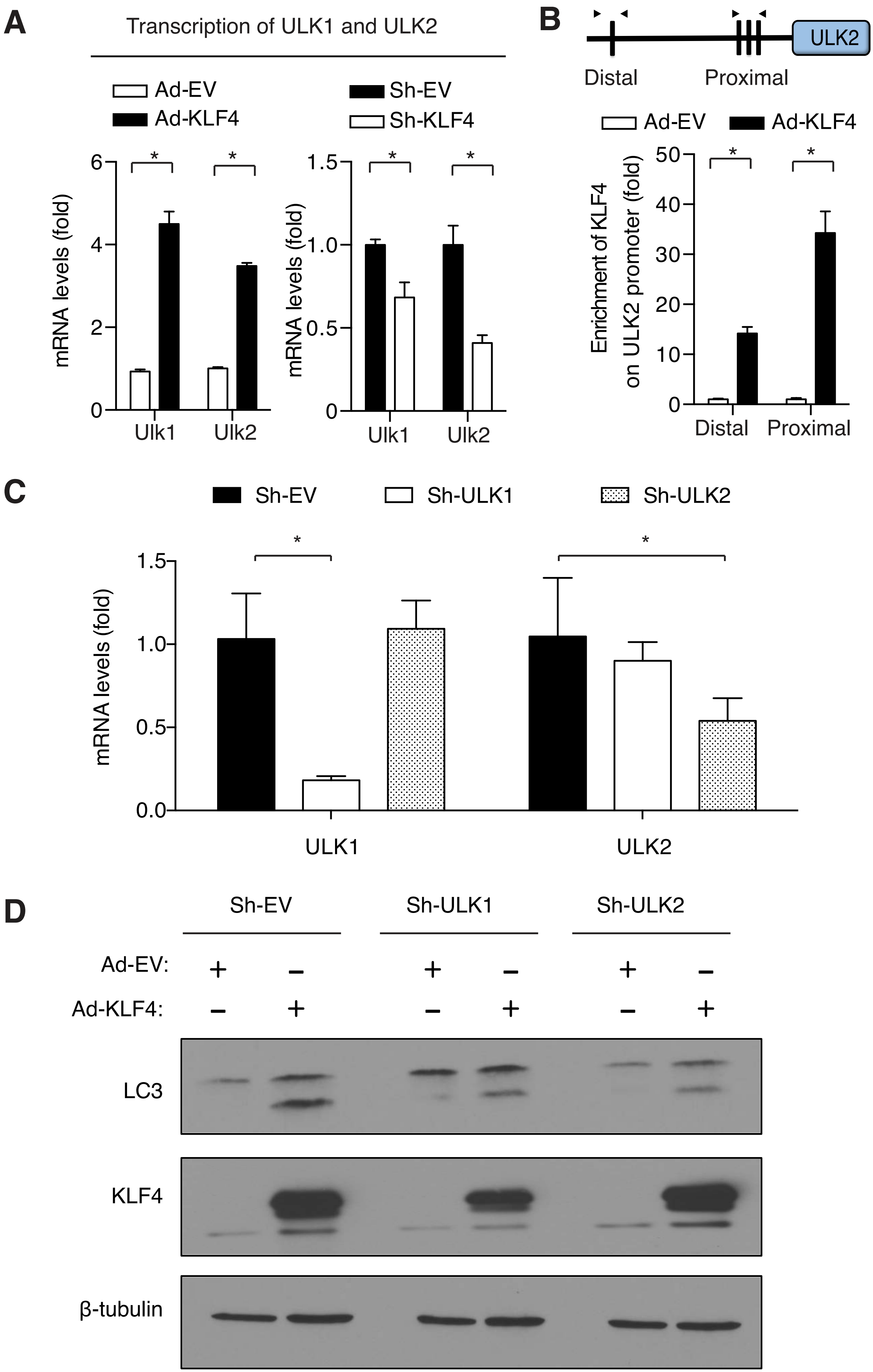
(A) KLF4 activated ULK1 promoter in NRVM. (B) The KLF4-mediated activation of ULK1 promoter requires the DNA binding domain (ZnF) and it is specific to KLF4. Luciferase reporter activity was assayed 24h post transfection. n=3 in each group. *$p<0.05$.



Supplementary Figure 13

Supplementary Figure 14. KLF4-induced LC3 activation is dependent on ULK1 and ULK2.

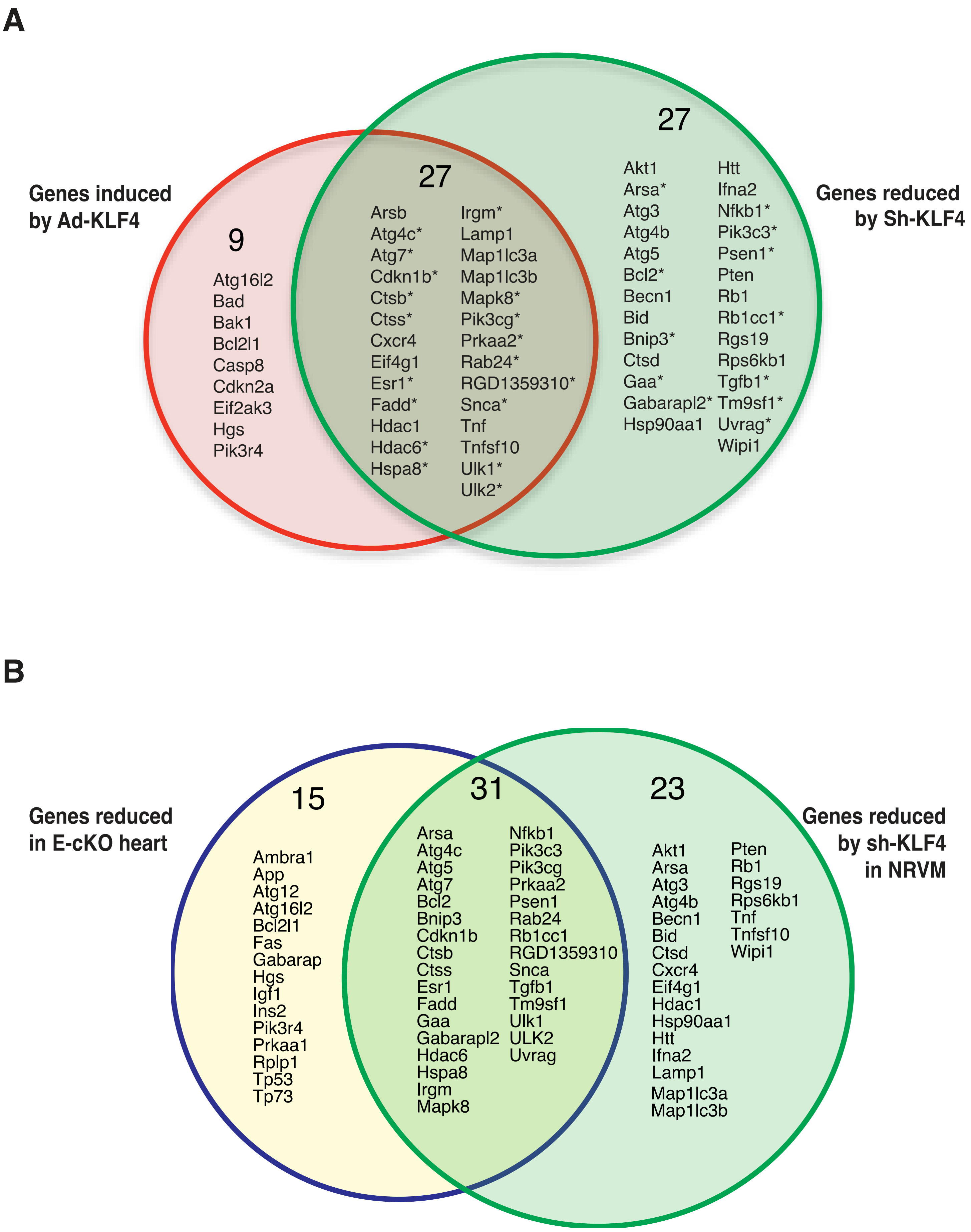
(A) KLF4 regulates transcription of ULK1 and ULK2. (B) KLF4 binds to ULK2 proximal promoter. (C) Adenoviral knockdown of ULK1 and ULK2 in NRVM. (D) Deficiency of ULK1 or ULK2 attenuated KLF4-mediated LC3 activation. NRVMs were infected with scramble shRNA (Sh-EV) or Sh-ULK1, Sh-ULK2 adenovirus for 48 h before secondary infection with adenoviral KLF4. Cells were cultured for another 24 h before harvested for Western blot analysis. $^*p<0.05$, n=6 in each group.



Supplementary Figure 14

Supplementary Figure 15. KLF4 regulates autophagy signaling in cardiomyocytes.

(A) Venn diagram showing genes that were significantly induced by KLF4 overexpression or reduced by KLF4 knockdown (difference over ±1.5 fold and $p<0.05$). NRVMs were infected with adenovirus expressing KLF4 mRNA or KLF4-targeting shRNA for 72 h. Corresponding empty viruses (Ad-EV, Sh-EV) were used as control. (B) Venn diagram showing genes that were significantly reduced in KLF4-silencing NRVM *in vitro* and in KLF4 deficient heart *in vivo* (difference over -1.5 fold and $p<0.05$). *Asterisks indicate genes that are recapitulated *in vivo*. Total RNA was extracted, purified, reverse transcribed into cDNA and subjected to qPCR analysis with the RT^2 Profiler PCR Array targeting autophagy pathway (Qiagen, PAMM-084Z, PARN-084Z).



Supplementary Figure 15

Supplementary Table I. Substrates used for mitochondrial respiration assays.

Substrate	Check point(s)
Palmitoyl-CoA	Palmitoyl-CoA (+carnitine+Malate): requires all steps of mitochondrial fatty acid transport and oxidation (FAO), TCA and ETC.
Palmitoyl-carnitine	Palmitoyl-carnitine (+Malate): bypasses mitochondrial carnitine palmitoyl transferase 1 (CPT1) as the limiting step of fatty acid mitochondrial transport, uses long-chain acyl dehydrogenase (LCAD), and requires TCA, ETC.
Octanoyl-carnitine	Octanoylcarnitine (+Malate): bypasses CPT1, uses medium-chain acyl dehydrogenase (MCAD), and requires TCA, ETC.
Acetyl-carnitine	Acetylcarnitine (+Malate): bypasses FAO, CPT1, uses carnitine acylcarnitine translocase (CACT) and requires TCA, ETC.
Pyruvate	Pyruvate (+Malate): uses pyruvate transporter and dehydrogenase, produces NADH from TCA, and NADH is oxidized through ETC.

Supplementary Table II. Primer sequences for quantitative real-time PCR.

qPCR primers for mouse genes

Gene	Official symbol	Forward primer 5'-3'	Reverse primer 5'-3'	Official Full Name
MCAD	Acadm	cgaacacaacactcgaaagc	ctgctgttccgtcaactcaa	acyl-Coenzyme A dehydrogenase, medium chain
VLCAD	Acadvl	ggtggtttgggcctctcta	gggtaacgctaacaccaagg	acyl-CoA dehydrogenase, very long chain
ACSL1	Acsl1	aaagatggctggttacacacg	cgataatcttcaaggtgccatt	acyl-CoA synthetase long-chain family member 1
sk-actin	Acta1	aatgagcgtttccgttgc	atccccgcagactccatac	actin, alpha 1, skeletal muscle
CKMT2	Ckmt2	gcaggatctggatacgacaga	ggccatccttcttcttggtt	creatine kinase, mitochondrial 2
CPT1b	Cpt1b	tgcctttacatcgtctccaa	ggctccagggttcagaaagt	carnitine palmitoyltransferase 1b, muscle
CPT2	Cpt2	ccaaagaagcagcgatgg	tagagctcaggcagggtga	carnitine palmitoyltransferase 2
CS	Cs	ggaaggctaagaacccttgg	tcatctccgtcatgccatagt	citrate synthase
CYCS	Cycs	gctgctgtatttatggcattga	gattctcagaaggcaagtgctta	cytochrome c, somatic
DRP1	Dnm1	tgcagctagtccacgtttca	cccattcttctgcttcaactct	dynamin 1-like
ERRalpha	Esrra	ccttccctgctggacctc	cgacaccagagcgttcact	estrogen related receptor, alpha
FIS1	Fis1	tggtgtctgtggaggatctg	attgcgtgctcttggacac	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)
GATA4	Gata4	ggaagacaccccaatctcg	catggccccacaattgac	GATA binding protein 4
HADHB	Hadhb	tgaaaacaagcaatgtggcta	tgaagagatacaagccatggtg	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
KLF4	Klf4	cgggaagggagaagacact	gagttcctcacgccaacg	Kruppel-like factor 4 (gut)
LPL	Lpl	gctggtgggaaatgatgtg	tggacgttgtctagggggta	ipoprotein lipase
MFN1	Mfn1	aagcataaagctcaggggatg	tgcttgaaatccttctgcaa	mitofusin 1
MFN2	Mfn2	cacagtgggtcacgtgaaaa	cccccagaaagaacacaaca	mitofusin 2
ATP6	mt-Atp6	ccataaatctaagtatagccattccac	agctttttagtttgtgtcggaag	ATP synthase 6, mitochondrial
CO1	mt-Co1	cagaccgcaacctaaacaca	ttctgggtgcccaaagaat	cytochrome c oxidase I, mitochondrial
CO2	mt-Co2	gccgactaaatcaagcaaca	caatgggcataaagctatgg	cytochrome c oxidase II, mitochondrial
CYTB	mt-Cytb	gaggttggttcggttttgg	gttttgaaagggtgggtgac	cytochrome b, mitochondrial
ND1	mt-Nd1	acacttattacaacccaagaacacat	tcatattatggctatgggtcagg	NADH dehydrogenase 1, mitochondrial
ND2	mt-Nd2	ccatcaactcaatctcacttctatg	gaatcctgttagtggtggaagg	NADH dehydrogenase 2, mitochondrial
ND5	mt-Nd5	gccaacaacatatttcaacttttc	accatcatccaattagtagaaagga	NADH dehydrogenase 5, mitochondrial
NDUFB3	Ndufb3	cgggaggtcagattgctg	tttccactgtctgtaatctggaag	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3
NDUFB5	Ndufb5	cctggctatcctccagattg	cgcatcagccttcgaact	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5
NDUFB7	Ndufb7	cccgagaagatacccagctt	ggcatccatcatctcttgttg	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 7
ANP	Nppa	cacagatctgatggatttcaaga	cctcatcttctaccggcatc	natriuretic peptide A
BNP	Nppb	gtcagtcgtttgggctgtaac	agacccaggcagagtcagaa	natriuretic peptide B
OPA1	Opa1	accaggagaagtagactgtgtcaa	tcttcaaataaacgcagaggtg	optic atrophy 1
POLRM	Polrmt	ccatgctgaactgctgga	ctcaggtgtgccctctgc	polymerase (RNA) mitochondrial (DNA directed)
PPARalpha	Ppara	ctgagaccctcggggaac	aaacgtcagttcacagggaag	peroxisome proliferator activated receptor alpha
PPARdelta	Ppard	gtatgcgcatgggactcac	gtctgagcgcagatggact	peroxisome proliferator activator receptor delta
PGC1alpha	Ppargc1a	gaaagggccaaacagagaga	gtaaatcacacggcgctctt	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
PGC1beta	Ppargc1b	gacgtggacgagctttcact	ctgctgttccgtcaactcaa	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
CACT	Slc25a20	atccgcggcttctacaaag	tacatcccactggcaggaac	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20
FATP1	Slc27a1	gacaagctggatcaggcaag	gaggccacagaggctgttc	solute carrier family 27 (fatty acid transporter), member 1
TFAM	Tfam	caaaggatgattcggctcag	aagctgaatatatgcctgcttttc	transcription factor A, mitochondrial
TFB2M	Tfb2m	aaacccatcccgtcaaatta	taatgccccagtcaggattc	transcription factor B2, mitochondrial
ULK1	Ulk1	ggatccatggtgtcactgc	caagggcagctgattgtacc	unc-51 like kinase 1
GLUT1	Slc2a1	atggatcccagcagcaag	ccagtgttatagccgaactgc	solute carrier family 2 (facilitated glucose transporter), member 1
LDHA	Ldha	ggcactgacgcagacaag	tgatcacctcgtaggcactg	lactate dehydrogenase A
ENO1	Eno1	gaggcgcttagtgctgct	agaatagacatggcgaatttctg	enolase 1, alpha non-neuron
PKM2	Pkm	aagggggactaccctctgg	cctcgaatagctgcaagtgg	pyruvate kinase, muscle
Gapdh	Gapdh	tggcaaagtggagattgttgcc	aagatggtgatgggcttcccg	glyceraldehyde-3-phosphate dehydrogenase
Chr6		atggaaagcctgccatcatg	tccttgttgttcagcatcac	mouse chromosome 6

qPCR primers for rat genes

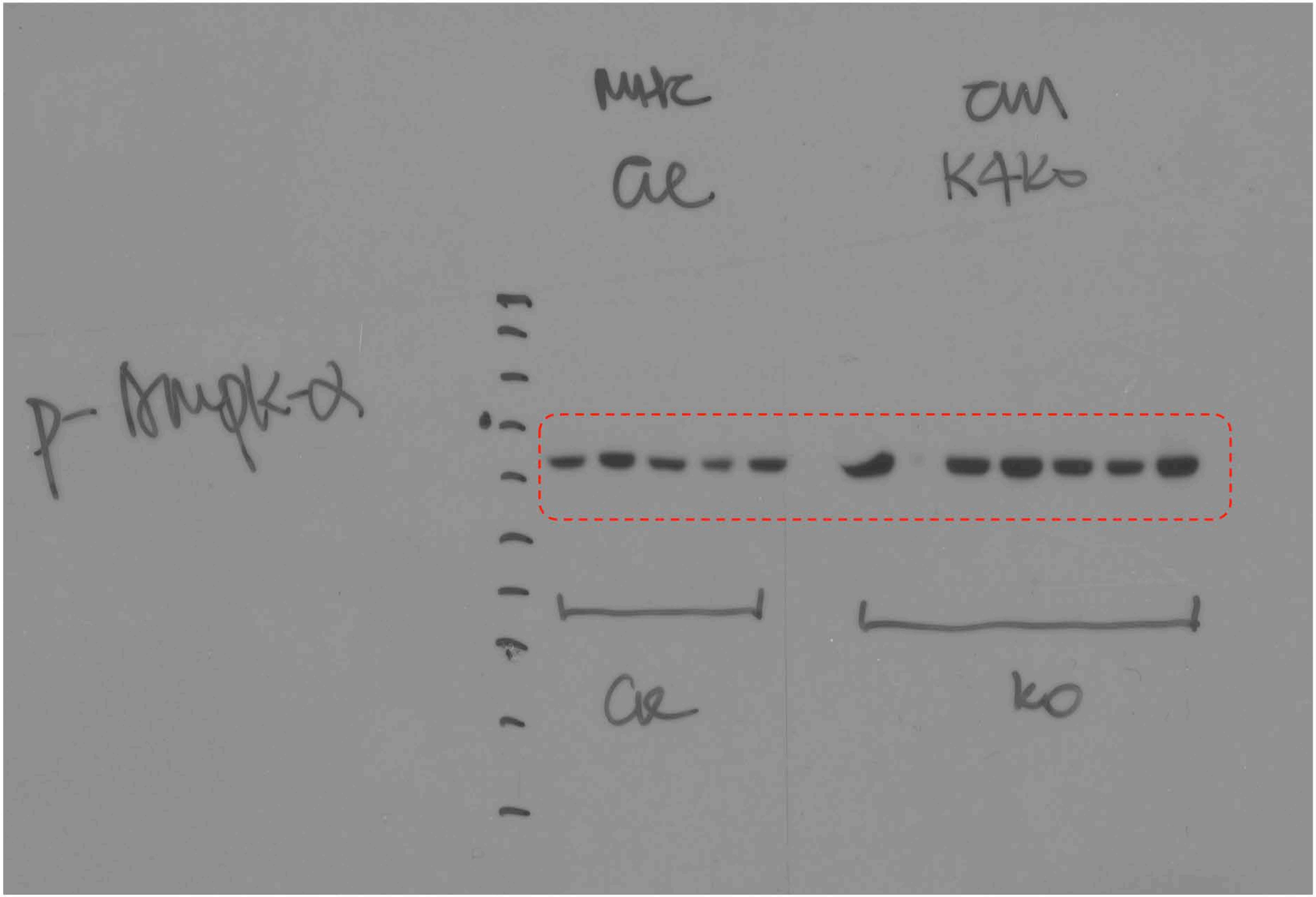
Gene	Official Symbol	Forward primer 5'-3'	Reverse primer 5'-3'	Official Full Name
Acox1	Acox1	caccttcgagggagagaaca	cgcacctggtcgtagatttt	acyl-CoA oxidase 1, palmitoyl
ACSL1	Acsl1	ttacacacgggggacattg	tcctgtcgataatcttcaaggtg	acyl-CoA synthetase long-chain family member 1
ATP6	mt-Atp6	taagcatagccatcccccta	ttagtttgtgtcggaagcctaga	ATP synthase 6, mitochondrial
CO3	mt-Co3	taaacccaagcccatgacc	agccggatgtaagtagaagagc	cytochrome c oxidase III, mitochondrial
COX5b	Cox5b	gaatagtgggctgcatctgtg	gggcaccaacttgtaatgtgt	cytochrome c oxidase subunit Vb
CPT1b	Cpt1b	gtgactggtgggaagagtacg	ctgcttgttggctcgtgtt	carnitine palmitoyltransferase 1b, muscle
CPT2	Cpt2	agcctctcttggatgacagc	cttcccaacgccagtctc	carnitine palmitoyltransferase 2
CS	Cs	cgtttgtaccttaccatccaca	tgctgcaaaggacaggtaag	citrate synthase
CYCS	Cycs	gatgccaacaagaacaaaggt	tgggattttccaaatactccat	cytochrome c, somatic
CYTB	mt-Cytb	ccctagtactattcttcccagacct	agggggttagcgggtgtat	cytochrome b, mitochondrial
ERRalpha	Esrra	cttccctgctggtcctctg	caccagggcgttaactgg	estrogen related receptor, alpha
FATP1	Slc27a1	gggtttgcaagccagaga	caaagcagccccaatgag	solute carrier family 27 (fatty acid transporter), member 1
HadhA	Hadha	ggcagtctcagtcgcttctc	aaagctgtggcaaatgcag	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
HadhB	Hadhb	ctttagtggctgcctgtgc	ttgggtaggcttccacaatc	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit
KLF4	Klf4	ccgtccttctccacgttc	gagttcctctcgccaacg	Kruppel-like factor 4 (gut)
LCAD	Acadl	gcagttacttgggaagagcaa	ggcatgacaatatctgaatgga	acyl-CoA dehydrogenase, long chain
MCAD	Acadm	gggactagggtttagcttcgag	ccgagcaattgtttgaaactc	acyl-Coenzyme A dehydrogenase, medium chain
MFN1	Mfn1	caaactgcagccaccaagt	gttggcacagtcgagcaa	mitofusin 1
ND1	mt-Nd1	cctcaacctaggcataccattt	aggctcatcccgatcataga	NADH dehydrogenase 1, mitochondrial
ND2	mt-Nd2	ccattctcgcaatttcatca	tttcgtgtttgggtctggtt	NADH dehydrogenase 2, mitochondrial
ND4	mt-Nd4	catcagtaagccatatagccctagtc	aagcttcatggtgtctggattat	NADH dehydrogenase 4, mitochondrial
OPA1	Opa1	accaggagaagtagacggtgtc	ttcttcaaatgtatgcagaggtg	optic atrophy 1
PGC1alpha	Ppargc1a	aaagggccaagcagagaga	gtaaatcacacggcgctctt	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
PGC1beta	Ppargc1b	cttcgaggtgtttggtgagat	cgtgcttctggcctctct	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
POLRM	Polrmt	cgtgctgctcaaggacttct	gcagctgctggtagaaaagg	polymerase (RNA) mitochondrial (DNA directed)
PPARalpha	Ppara	tgcggactaccagtacttaggg	gctggagagagggtgtctgt	peroxisome proliferator activated receptor alpha
TFB2M	Tfb2m	caaaacccatcccatcaact	aatgccccagtcaggattc	transcription factor B2, mitochondrial
UCP3	Ucp3	cccctacactgtatgctgagg	agaaaggagggcatgaatcc	ncoupling protein 3 (mitochondrial, proton carrier)
ULK1	Ulk1	ccagtgtctgacagggaagg	cataaaacaggcgcaaatcc	unc-51 like kinase 1
ULK2	Ulk2	cacagaacgaccaatggatg	ggcaatgccaacacacaaca	unc-51 like kinase 2
GAPDH	Gapdh	gctggcattgctctcaatgaca	tccaccaccctgttgctgta	glyceraldehyde-3-phosphate dehydrogenase
Chr4		ctgcagcaagatgtacaccaa	tcatctgagcgtgaaaacctc	rat chromosome 4

qPCR primers for ChIP

proximal	Ppara	tcagccatctccagggtctcag	actatgctatttgtggcgatgagc
proximal	Cycs	cggcggtcttagcactacc	ggtaacaccggctcttaggac
proximal	Ulk1	agccacatcgtctgttaggac	gtcggaactcactccgactc
Distal	Ulk1	catagctagagatagttcagaccttgg	gccttatagtgggcggaact
proximal	Ulk2	cgacggctgcttaggaac	gagggtggcttcaggtcag
Distal	Ulk2	cagaggacttgggtttgatttc	gtcgatctcctgagactggaat
non-targeting		ctgcagcaagatgtacaccaa	tcatctgagcgtgaaaacctc

Full Unedited Gel Images

Full unedited gel for Figure 2C



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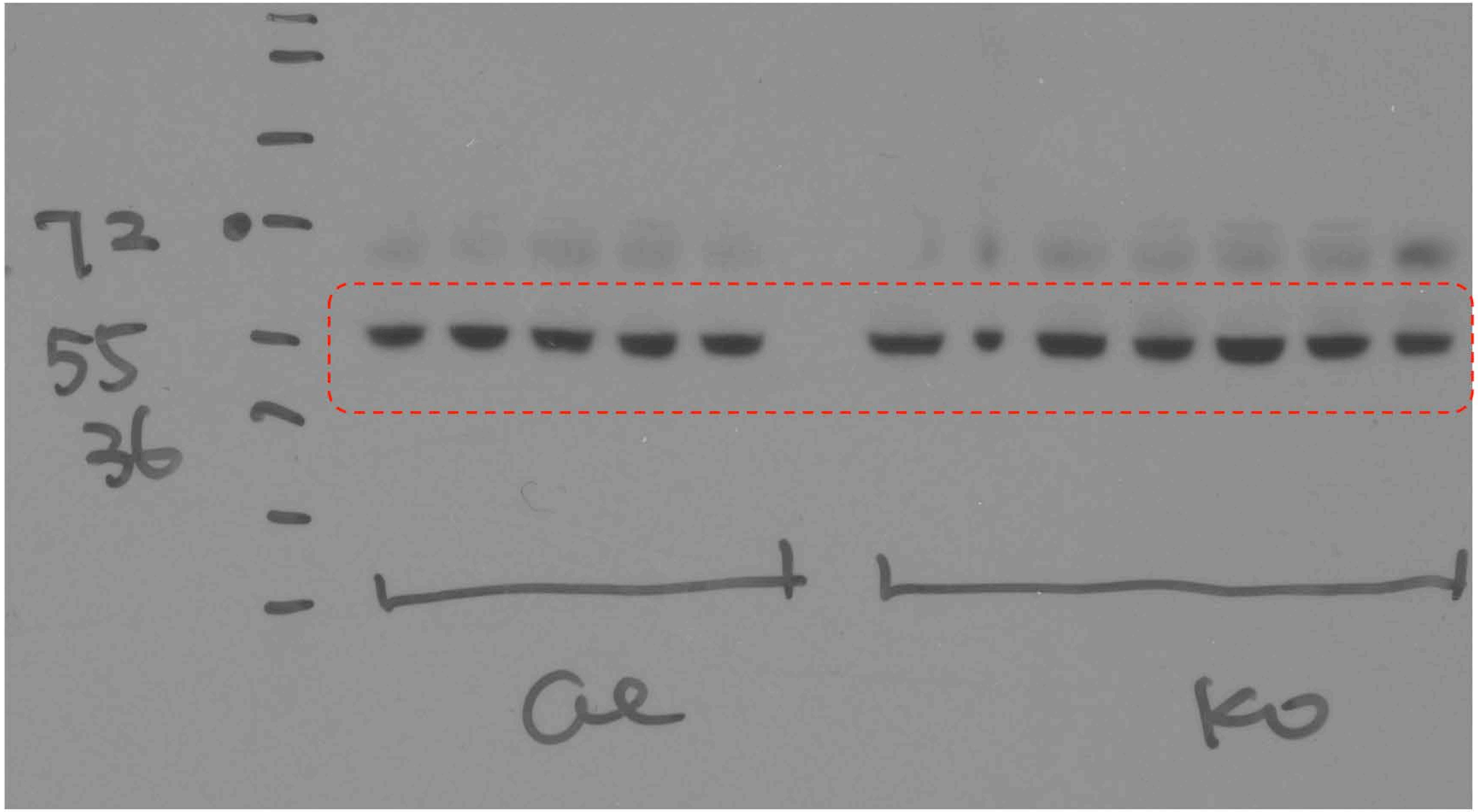

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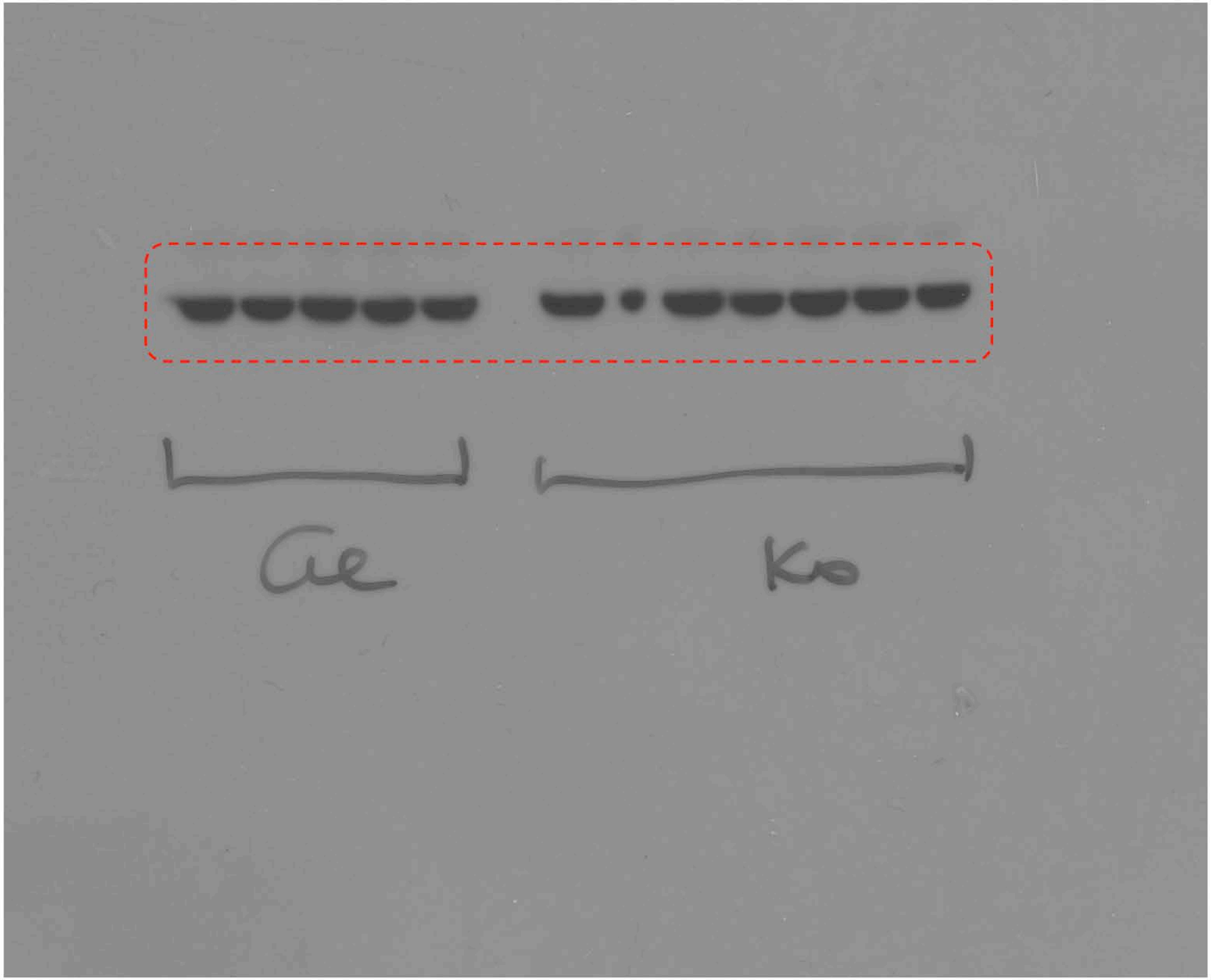

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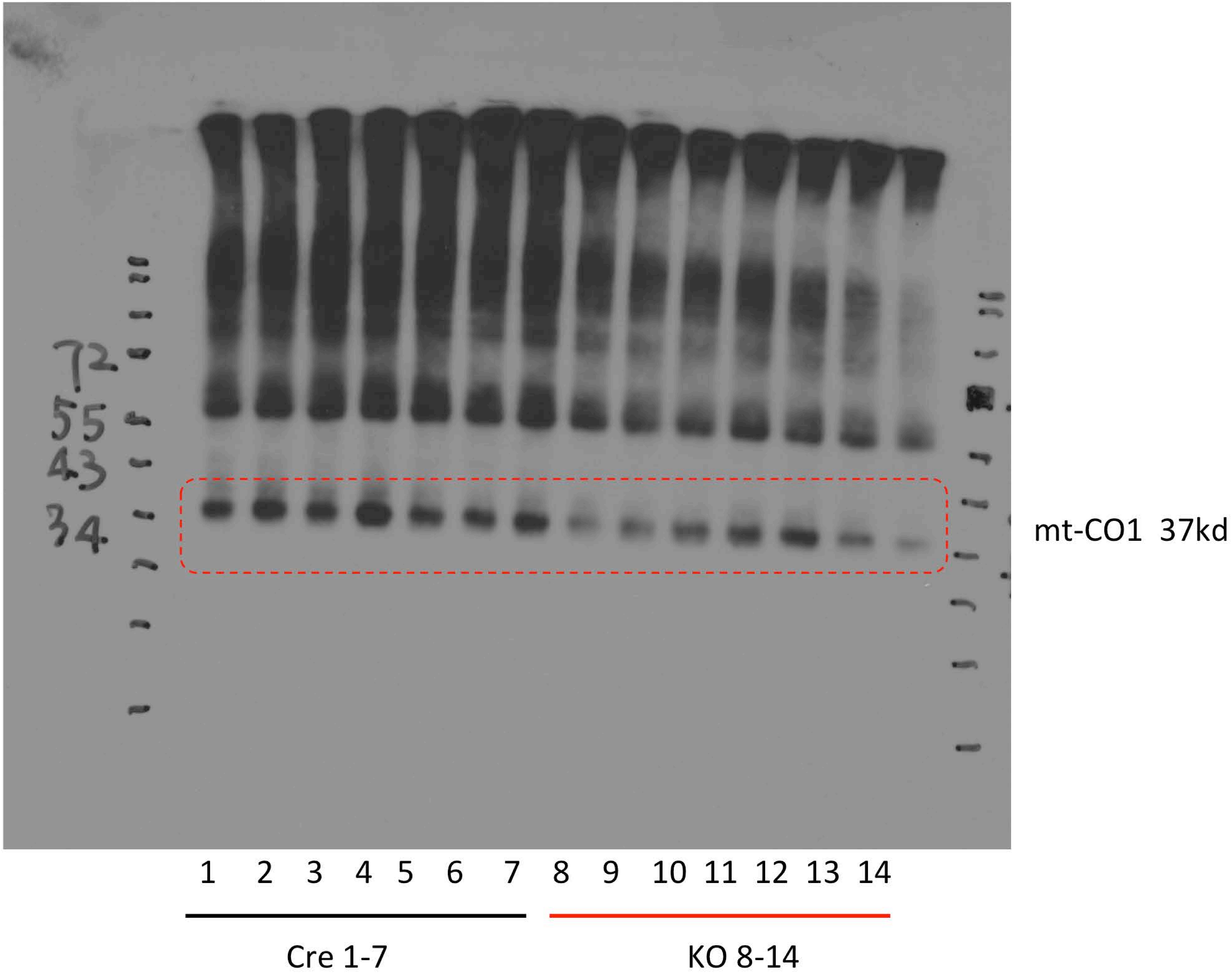

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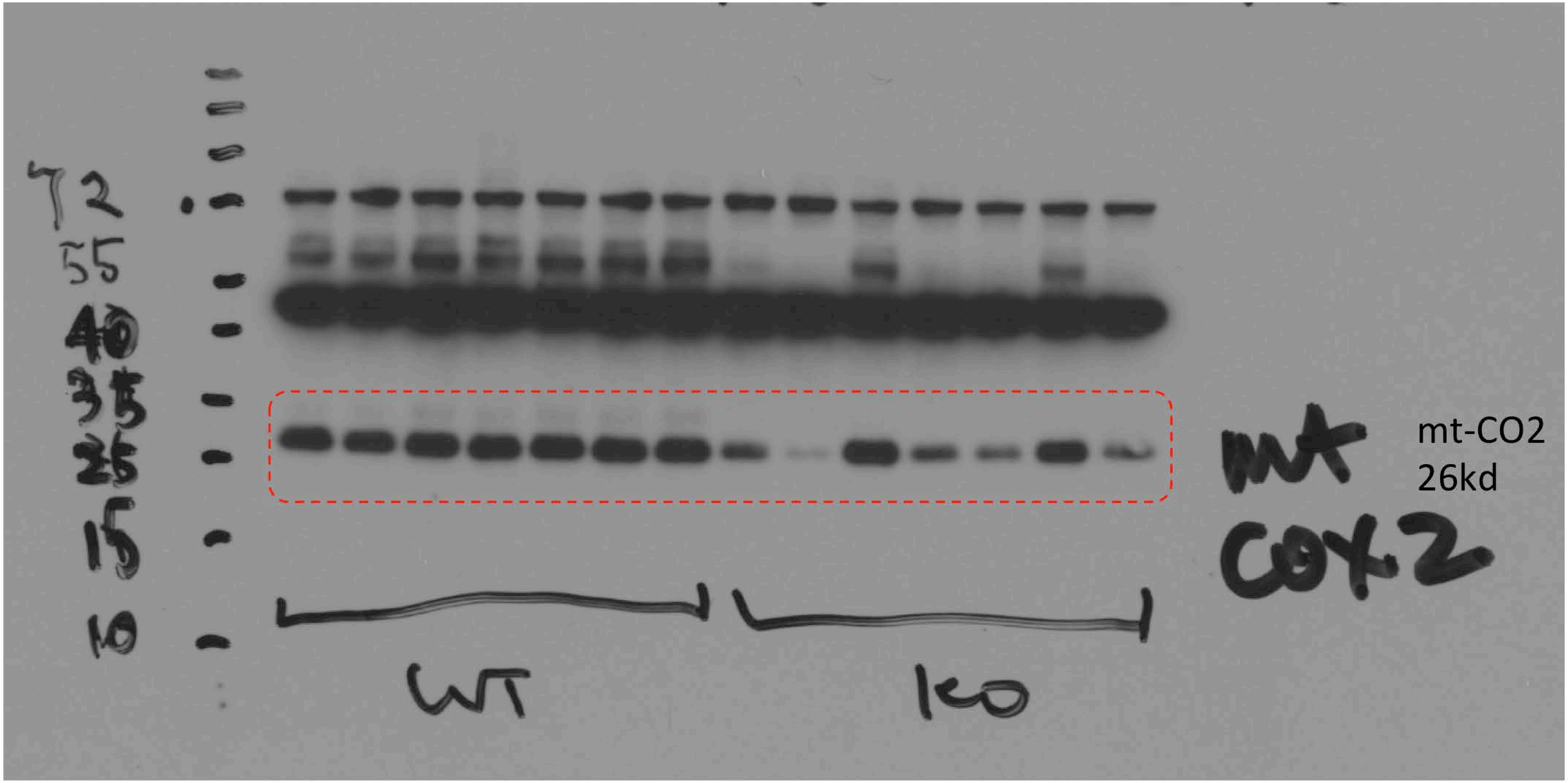

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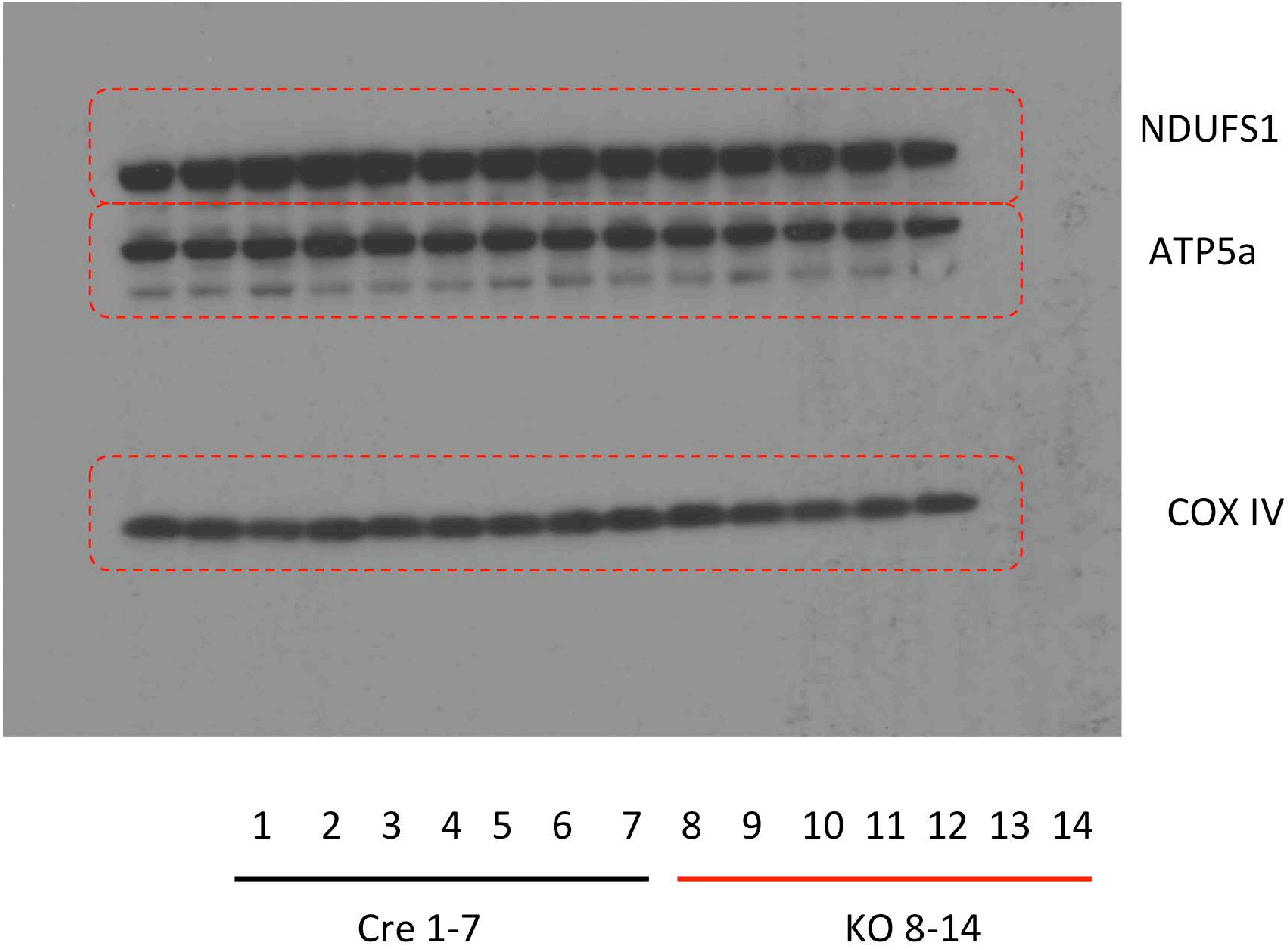

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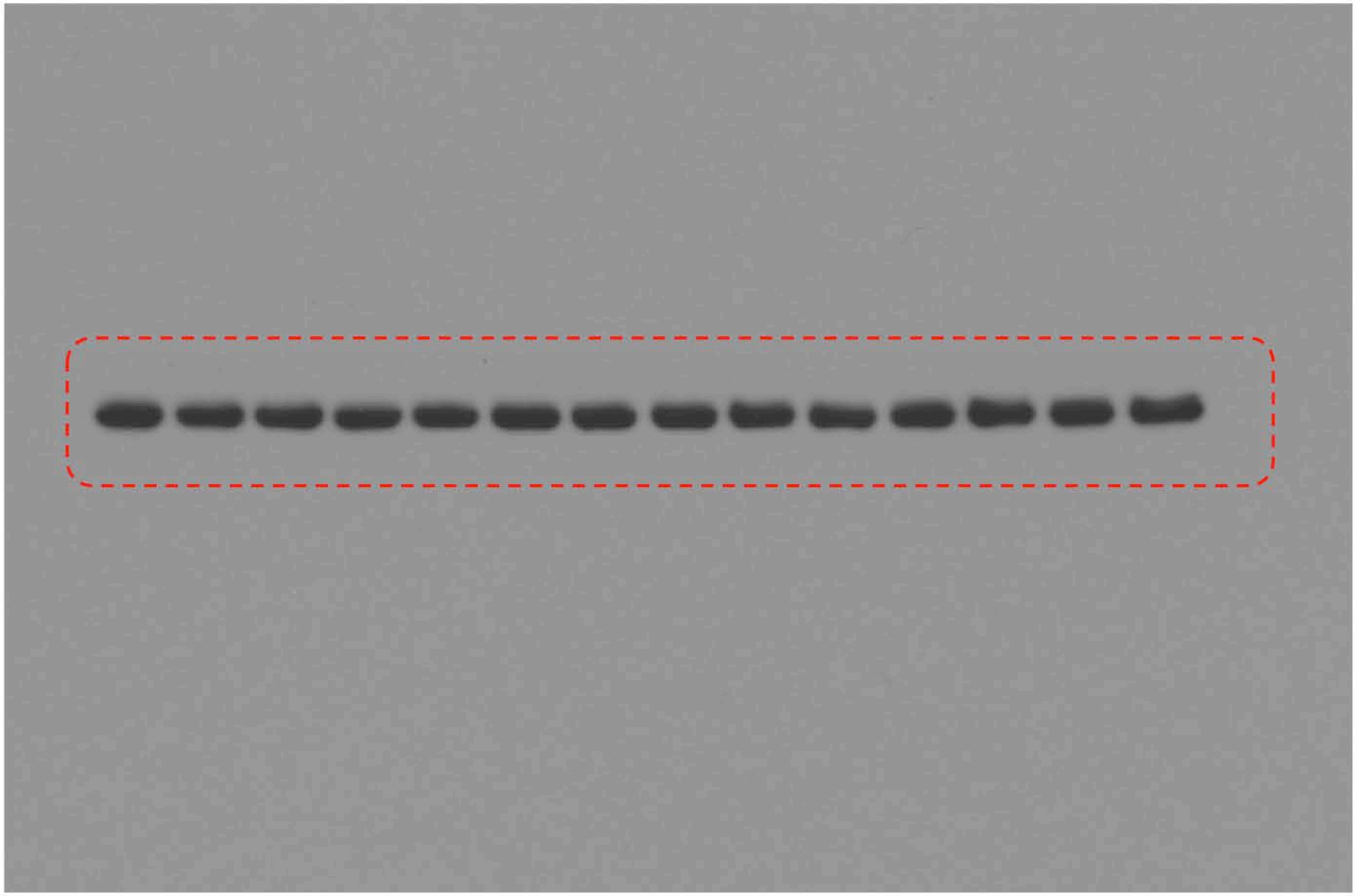


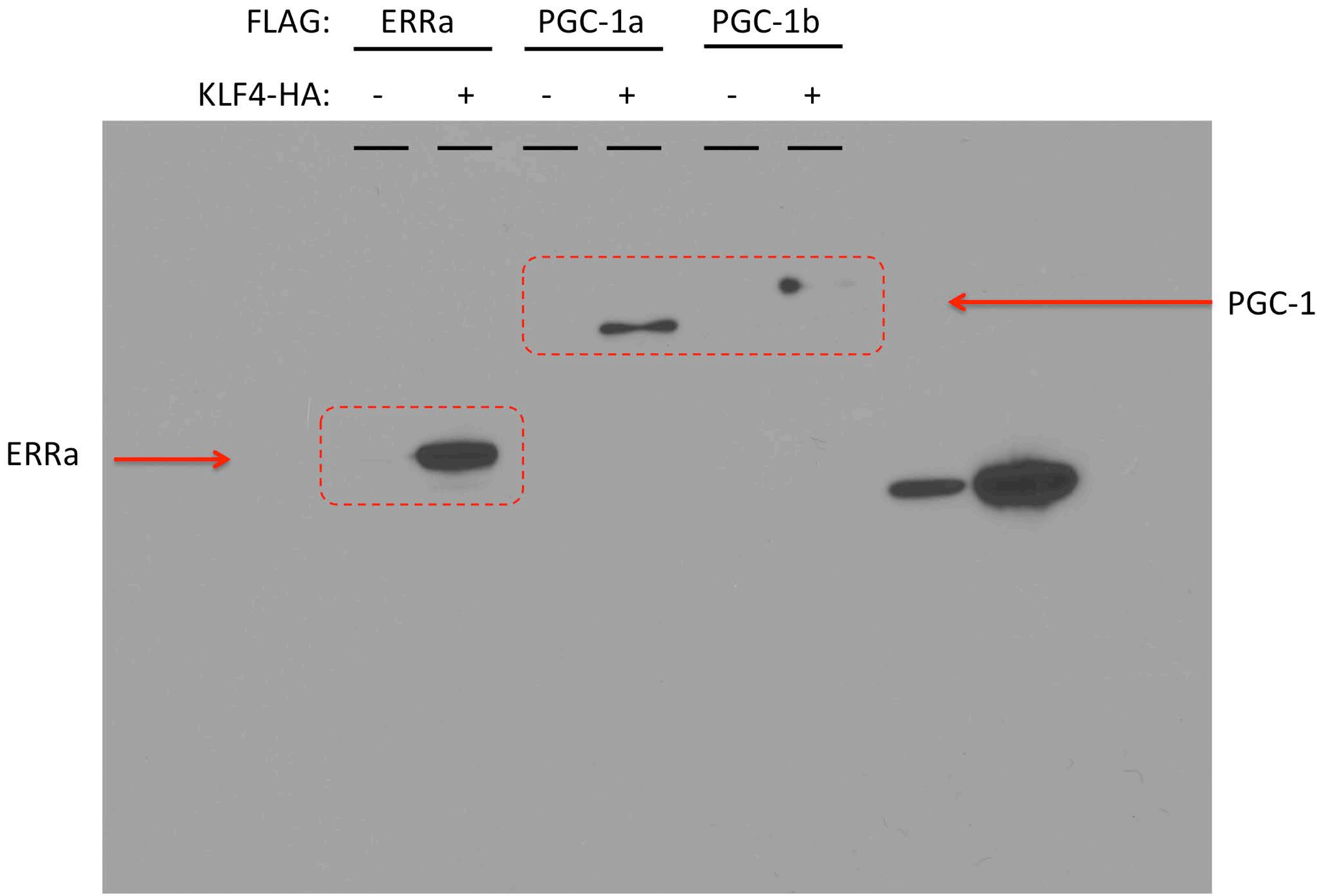
beta-tubulin

1 2 3 4 5 6 7 8 9 10 11 12 13 14

Cre 1-7

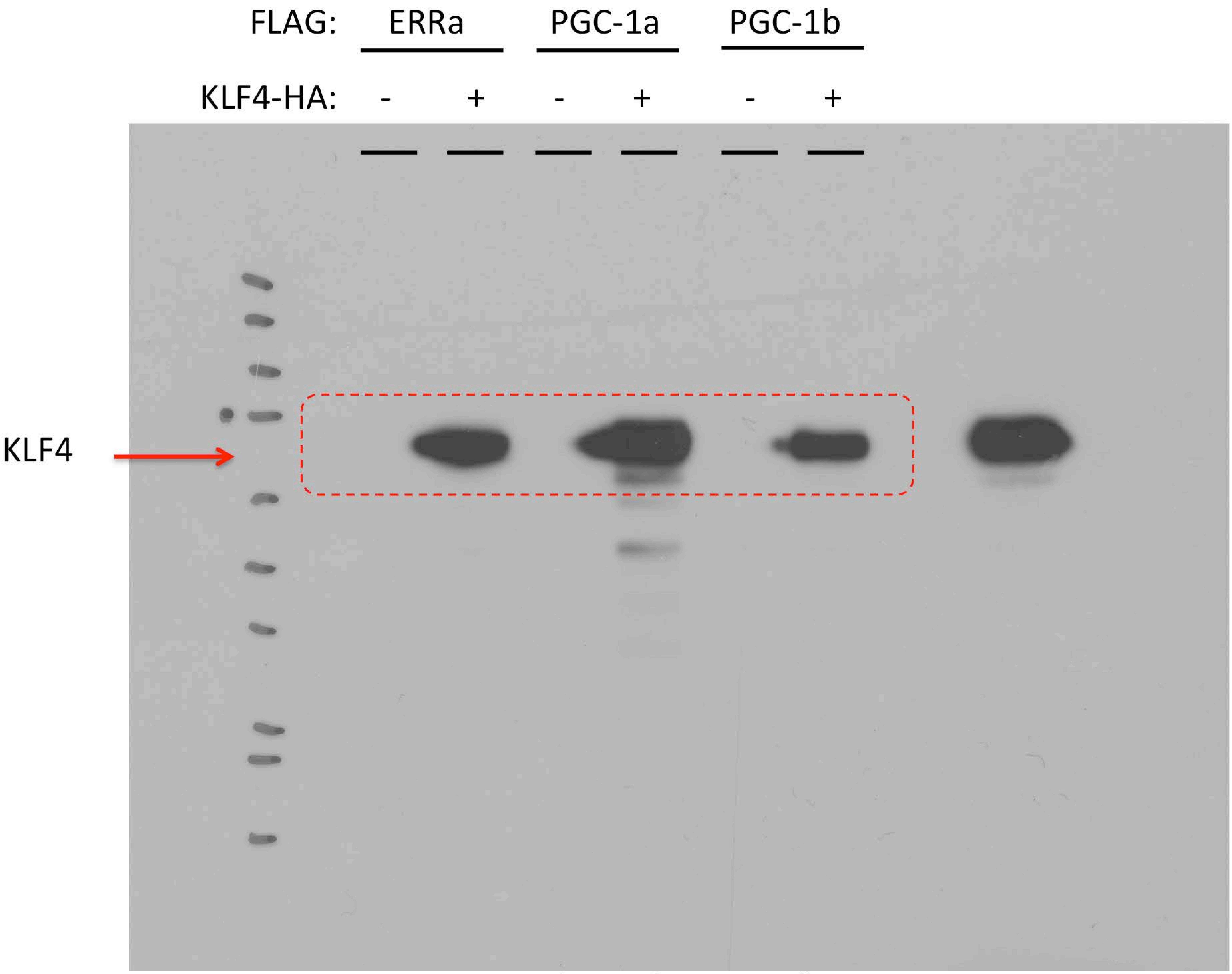
KO 8-14

Full unedited gel for Figure 5F



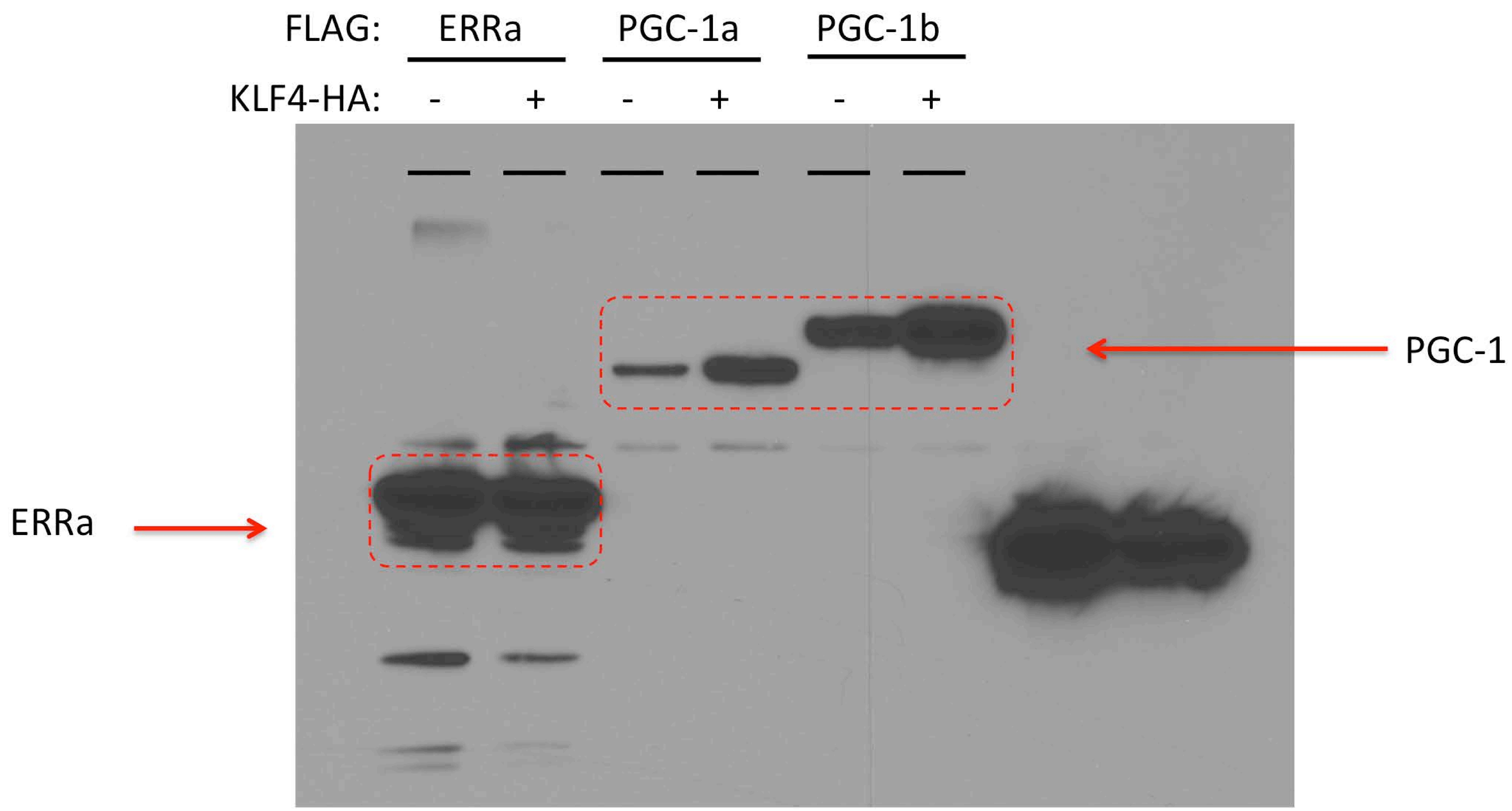
IP by anti-HA, WB for FLAG

Full unedited gel for Figure 5F



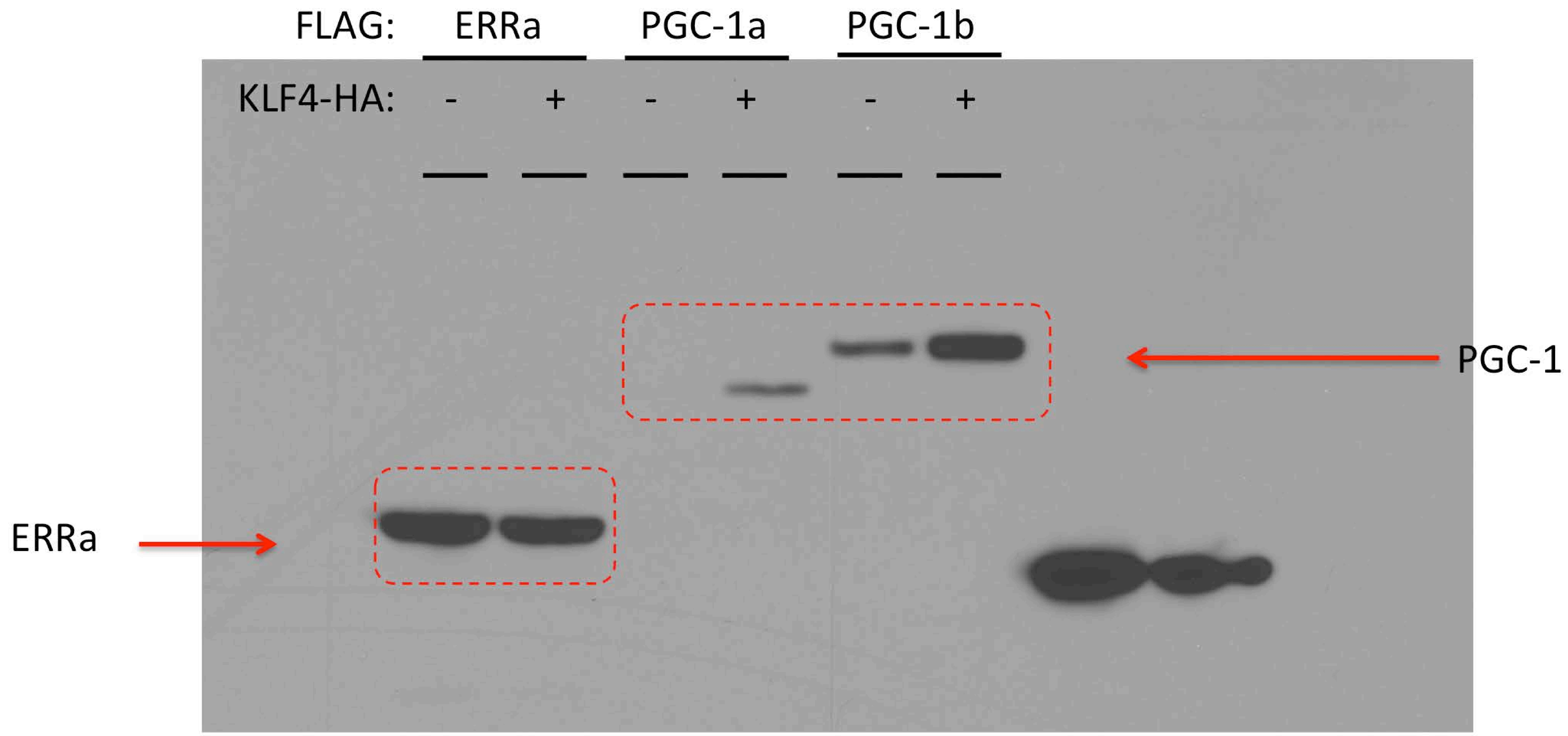
IP by anti-HA, WB for HA

Full unedited gel for Figure 5F



Cell lysate/input of IP
WB for FLAG

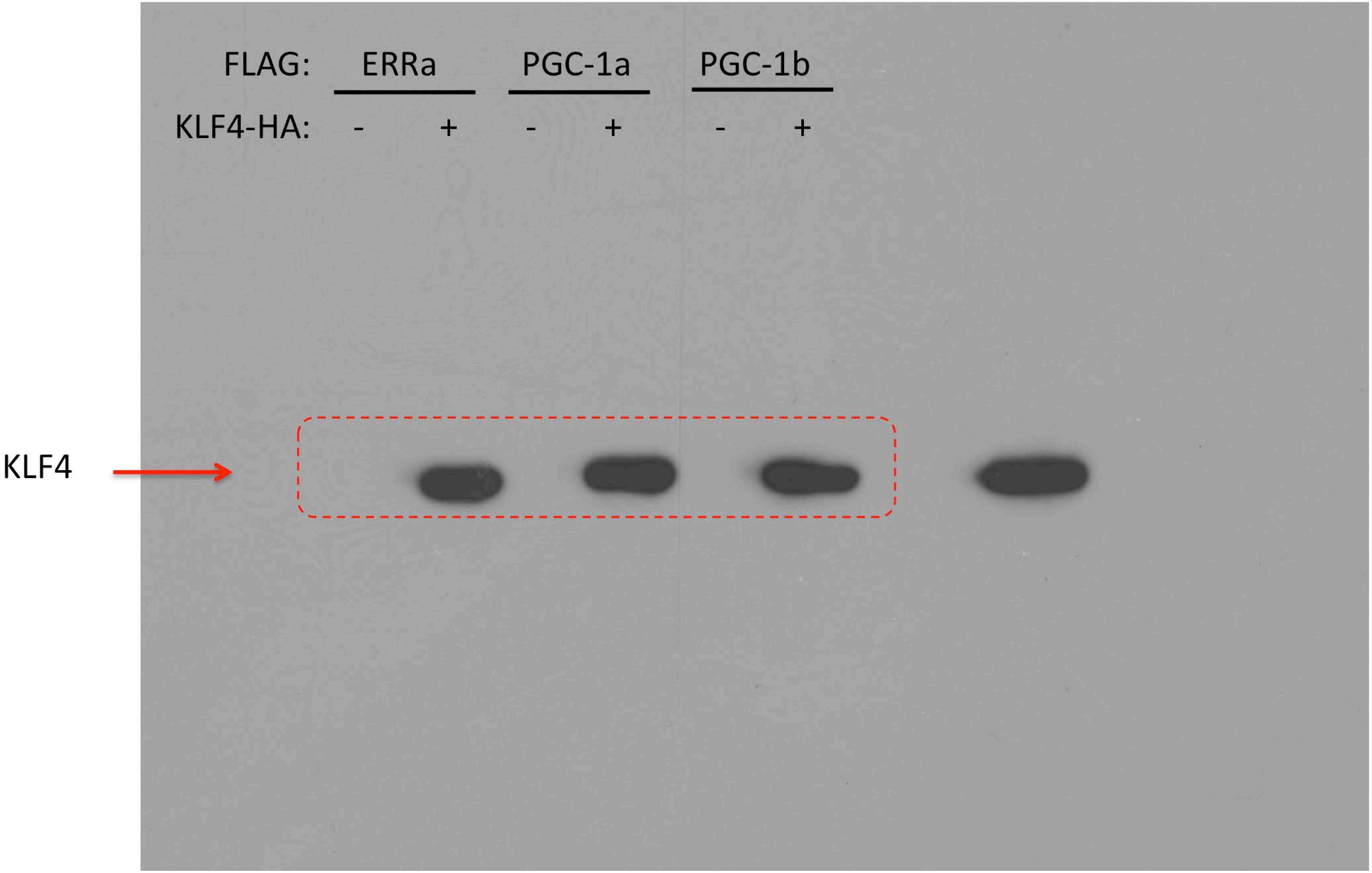
Full unedited gel for Figure 5F



Cell lysate/input of IP

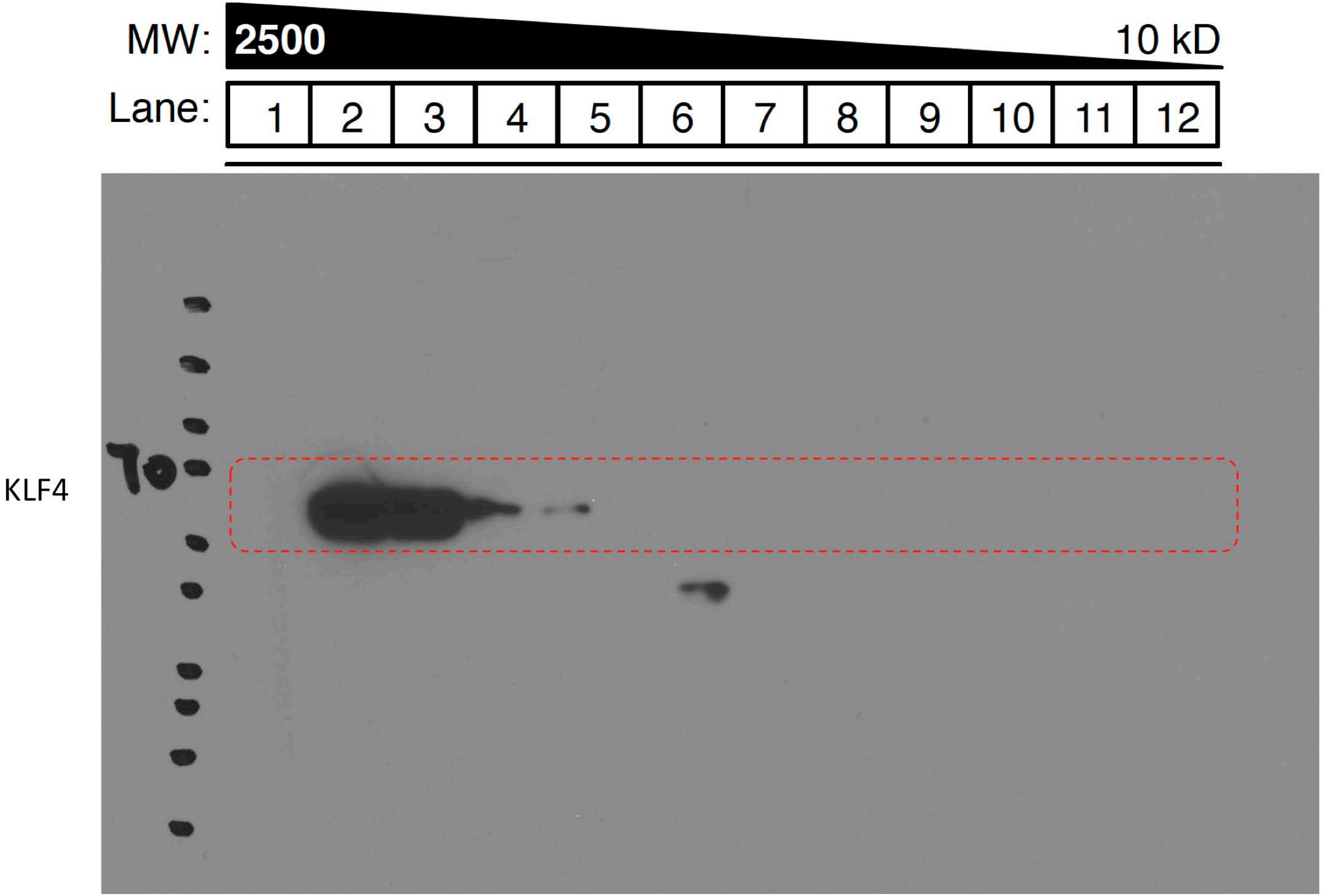
Lighter exposure

Full unedited gel for Figure 5F

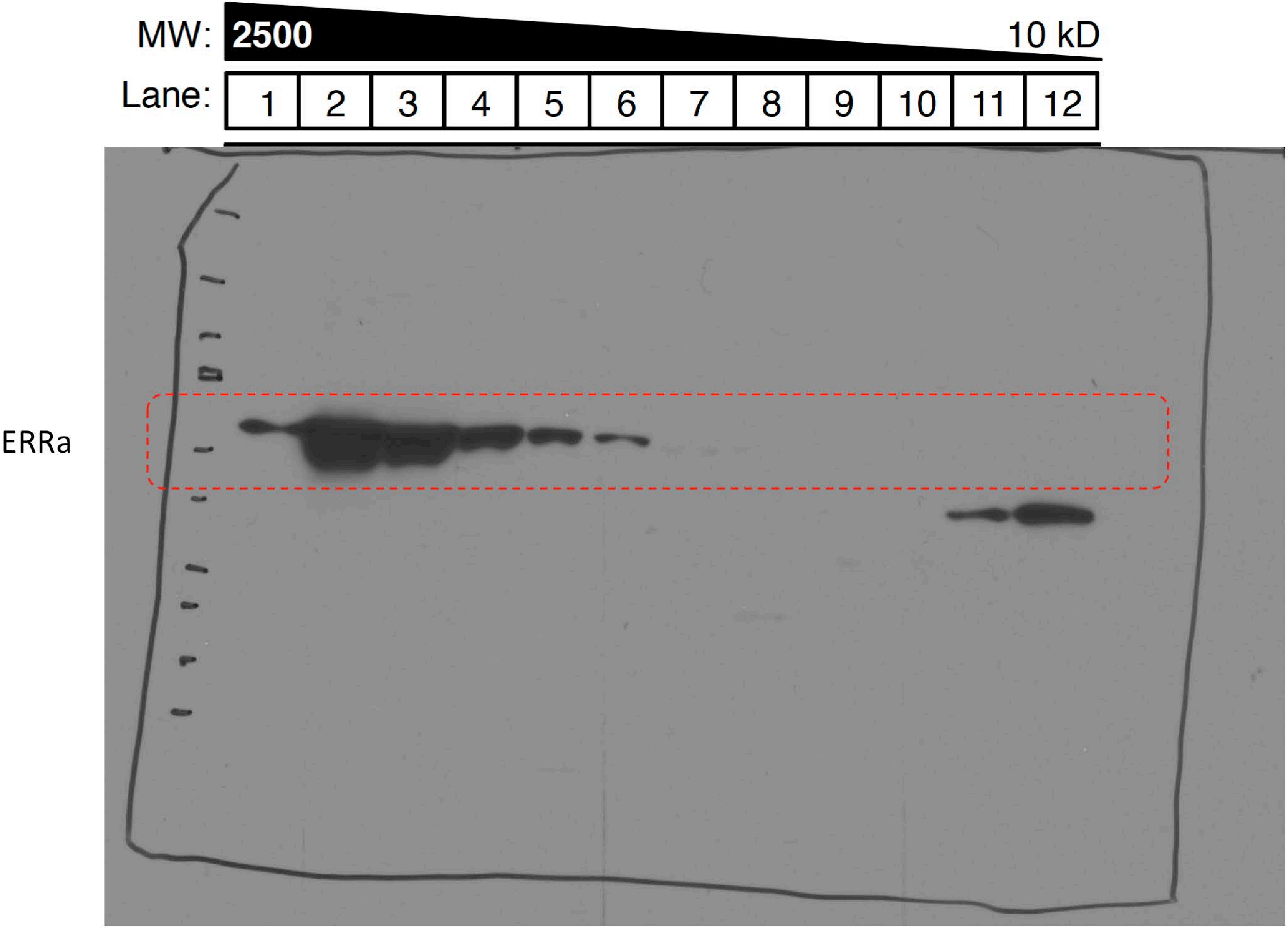


Cell lysate/input of IP

Full unedited gel for Figure 5G

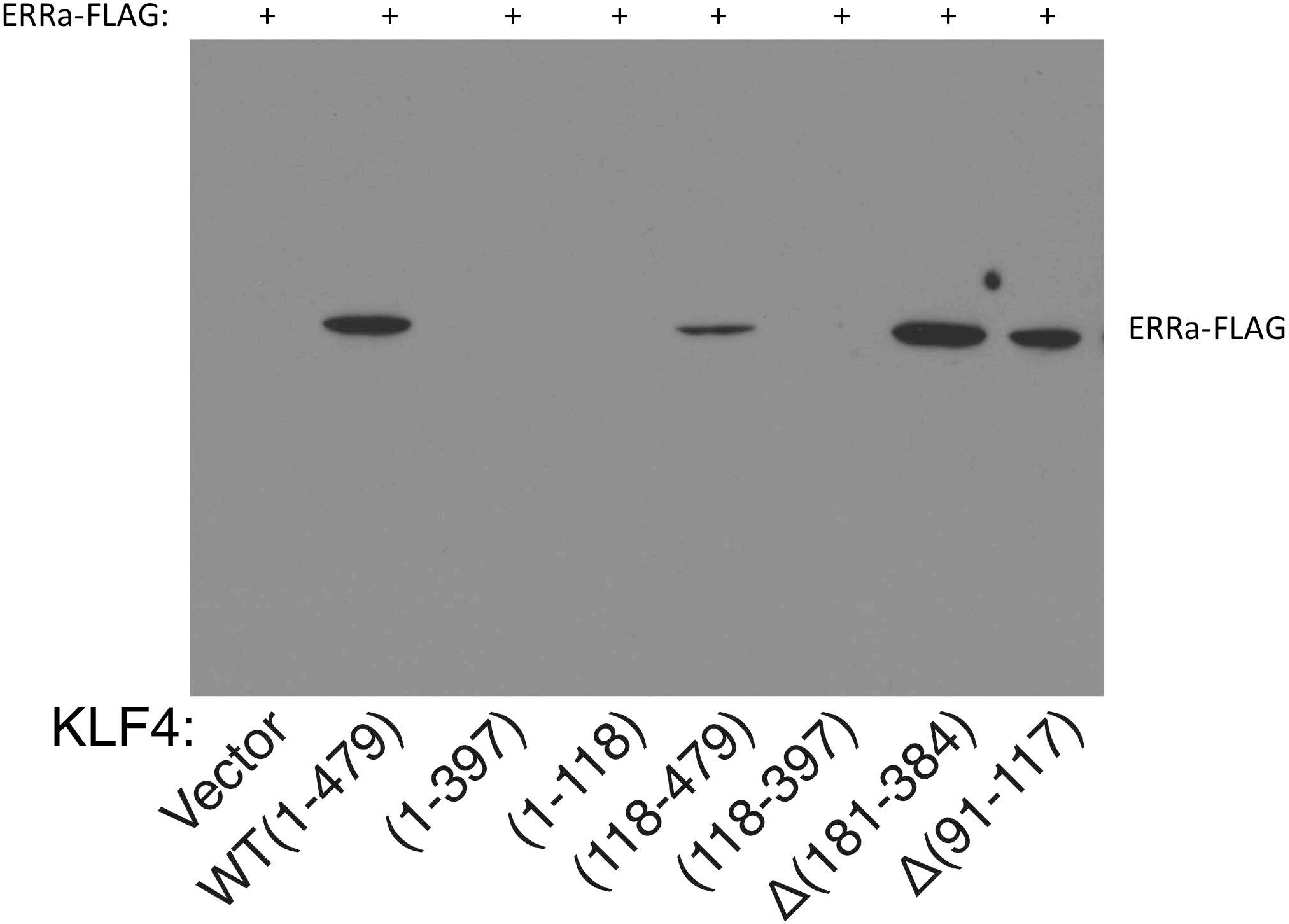


Full unedited gel for Figure 5G



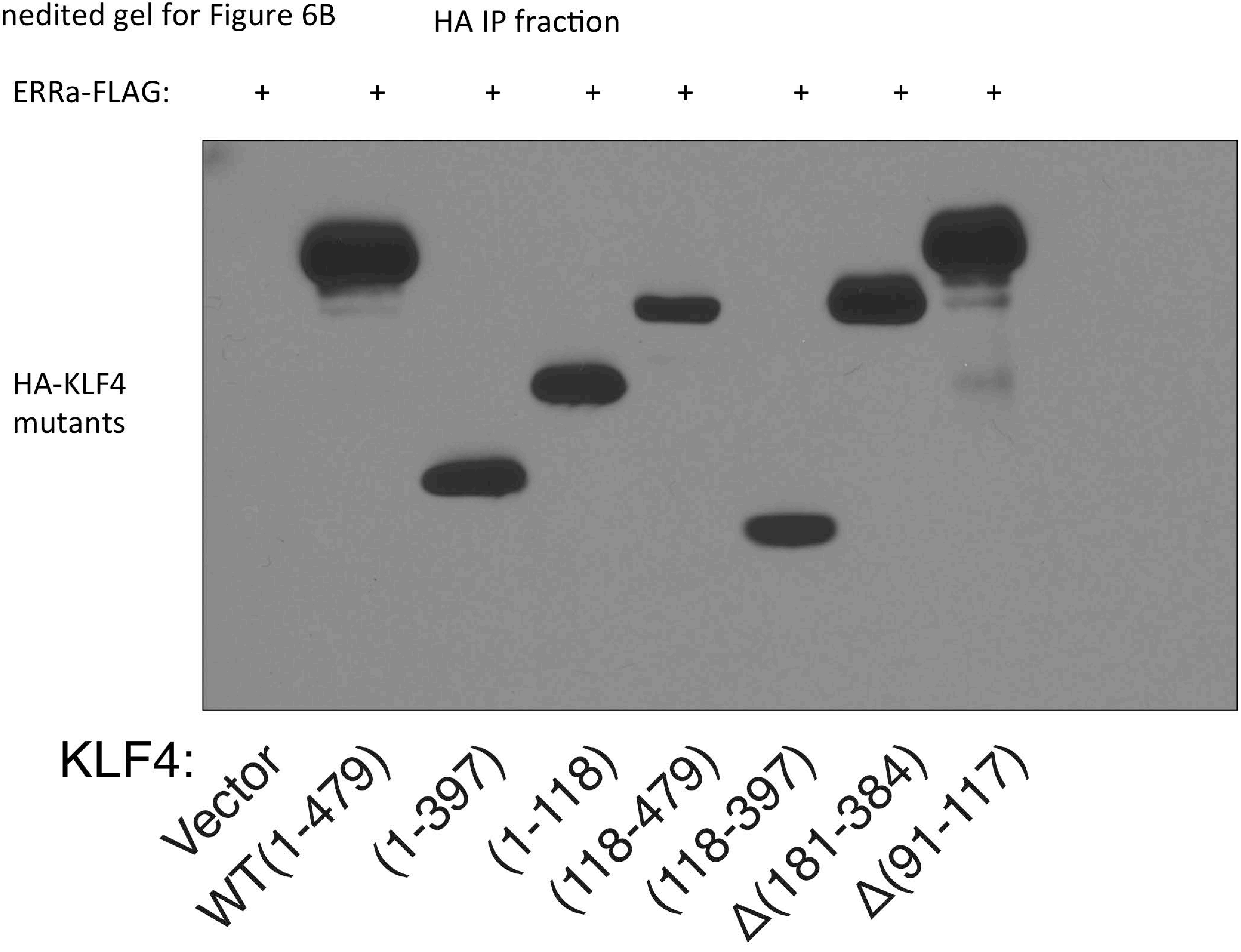
Full unedited gel for Figure 5G

Full unedited gel for Figure 6B



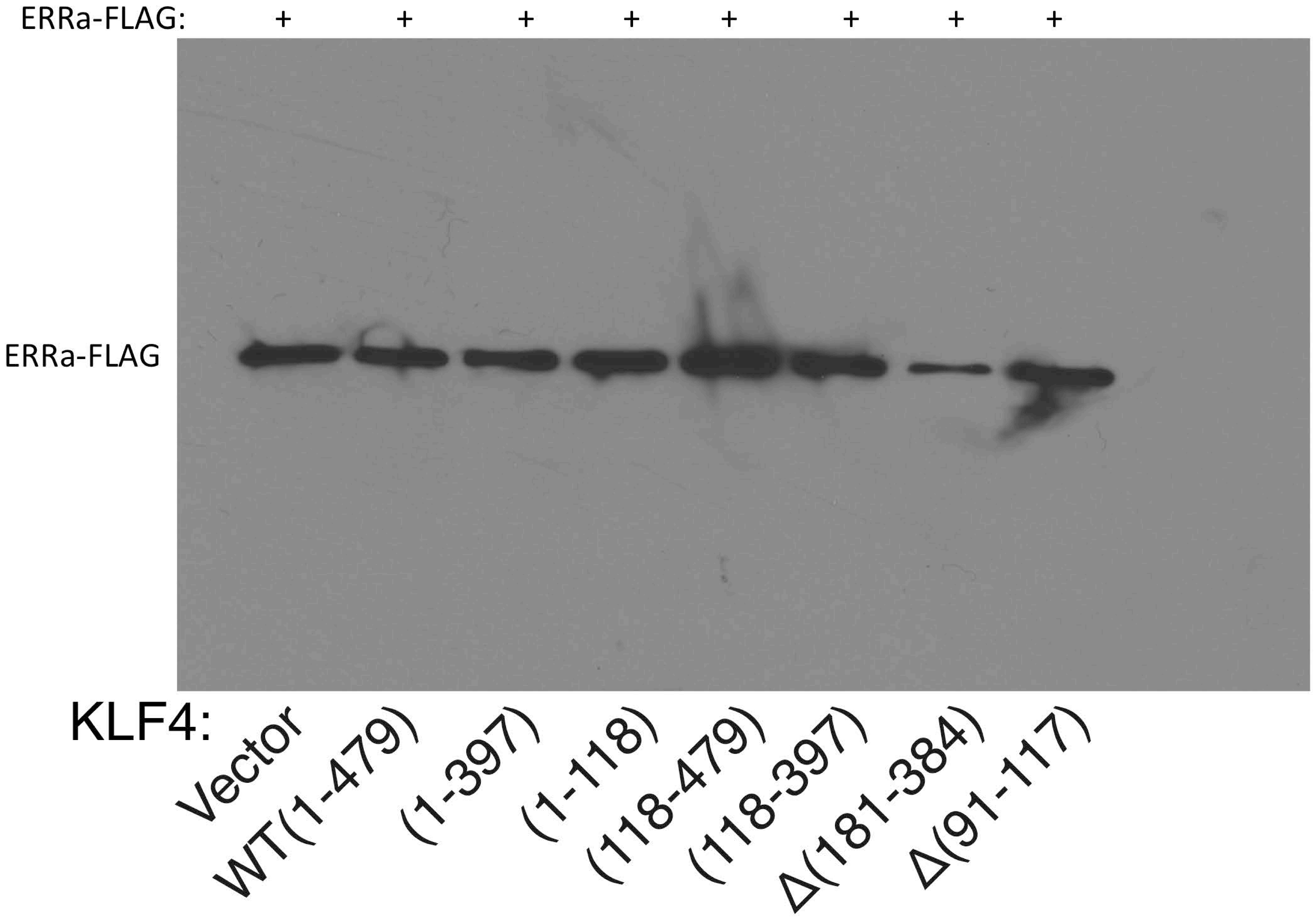
HA IP fraction

Full unedited gel for Figure 6B

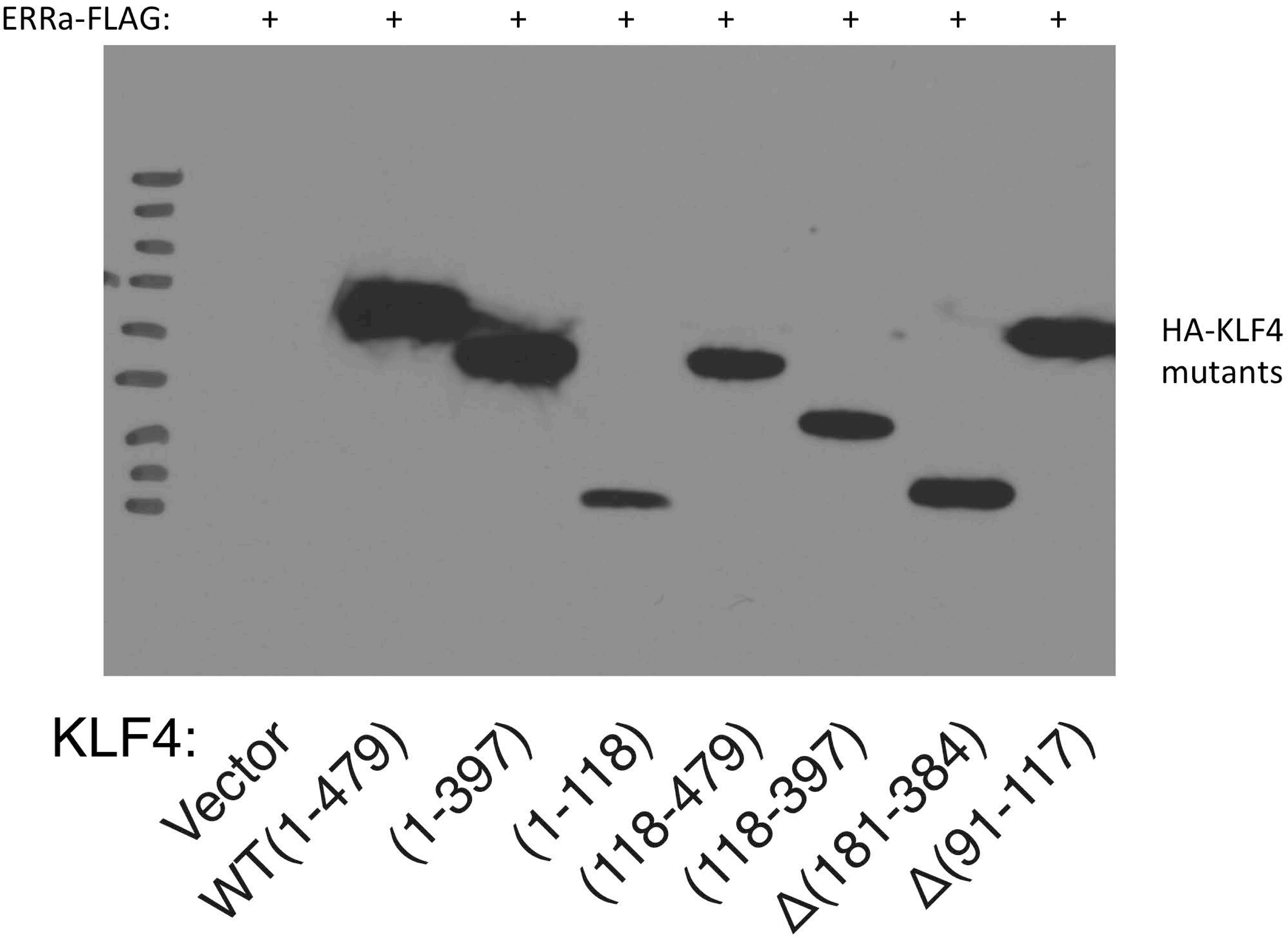


Full unedited gel for Figure 6C

Cell lysate/IP input

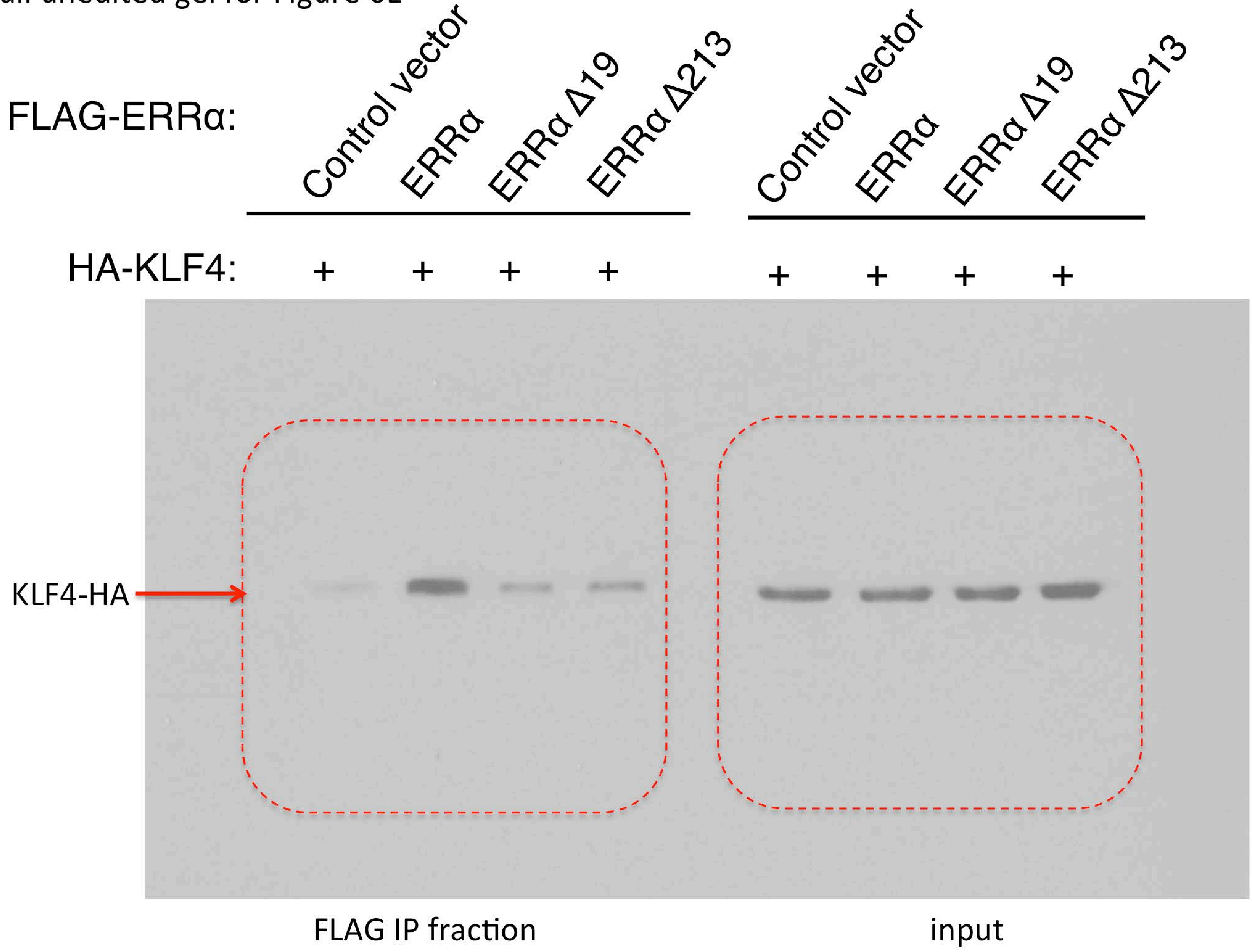


Full unedited gel for Figure 6C

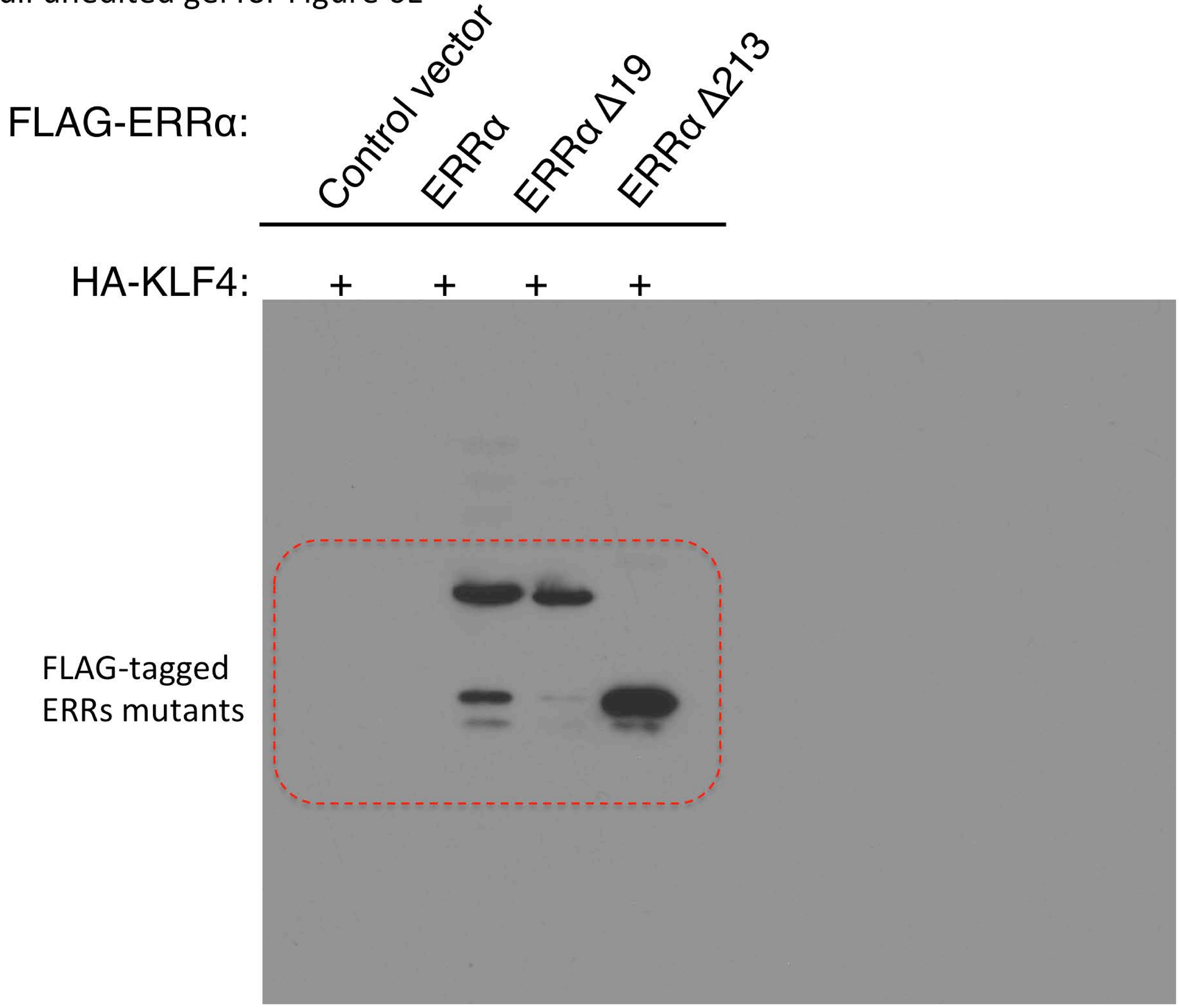


Cell lysate/IP input

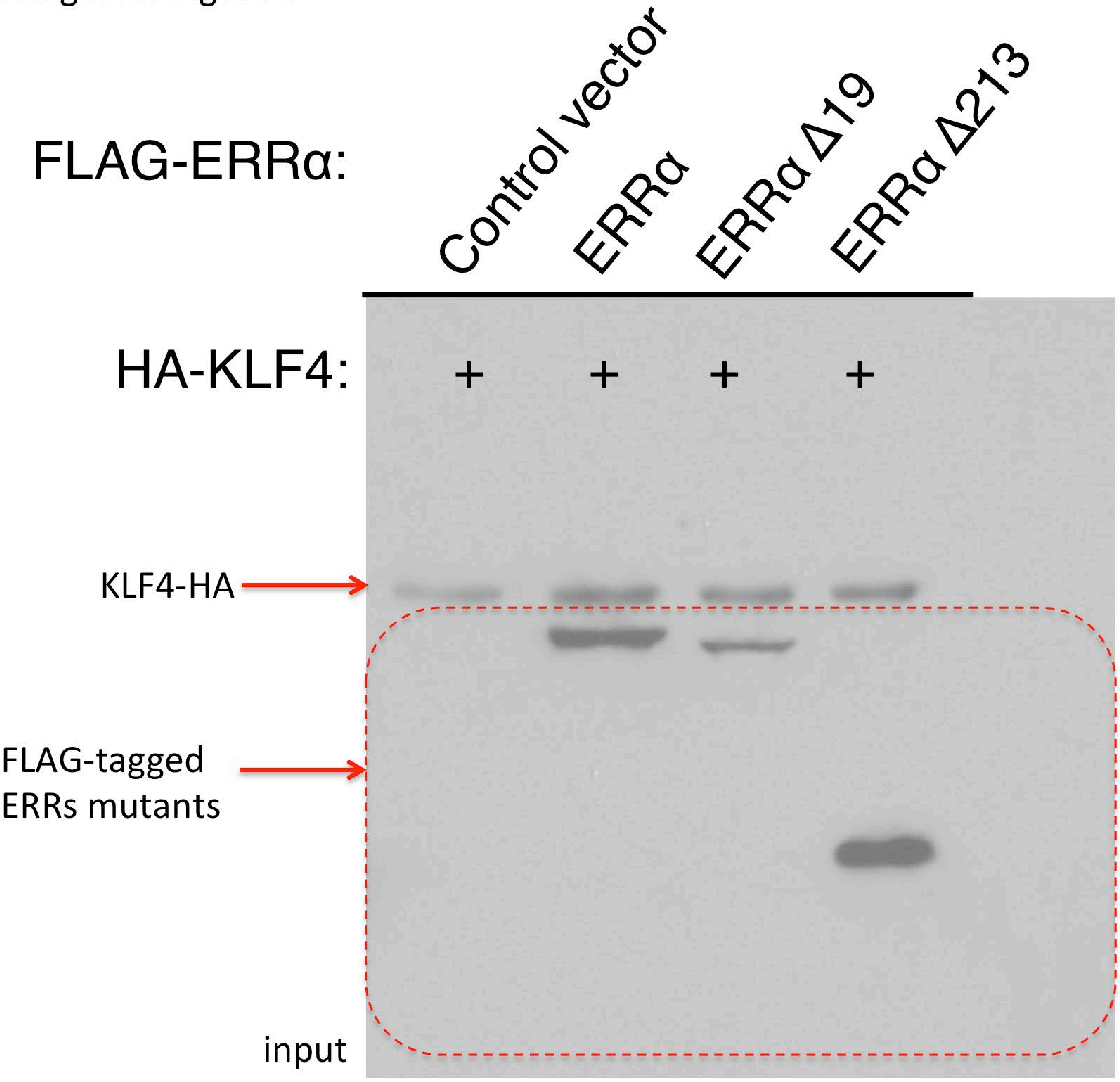
Full unedited gel for Figure 6E



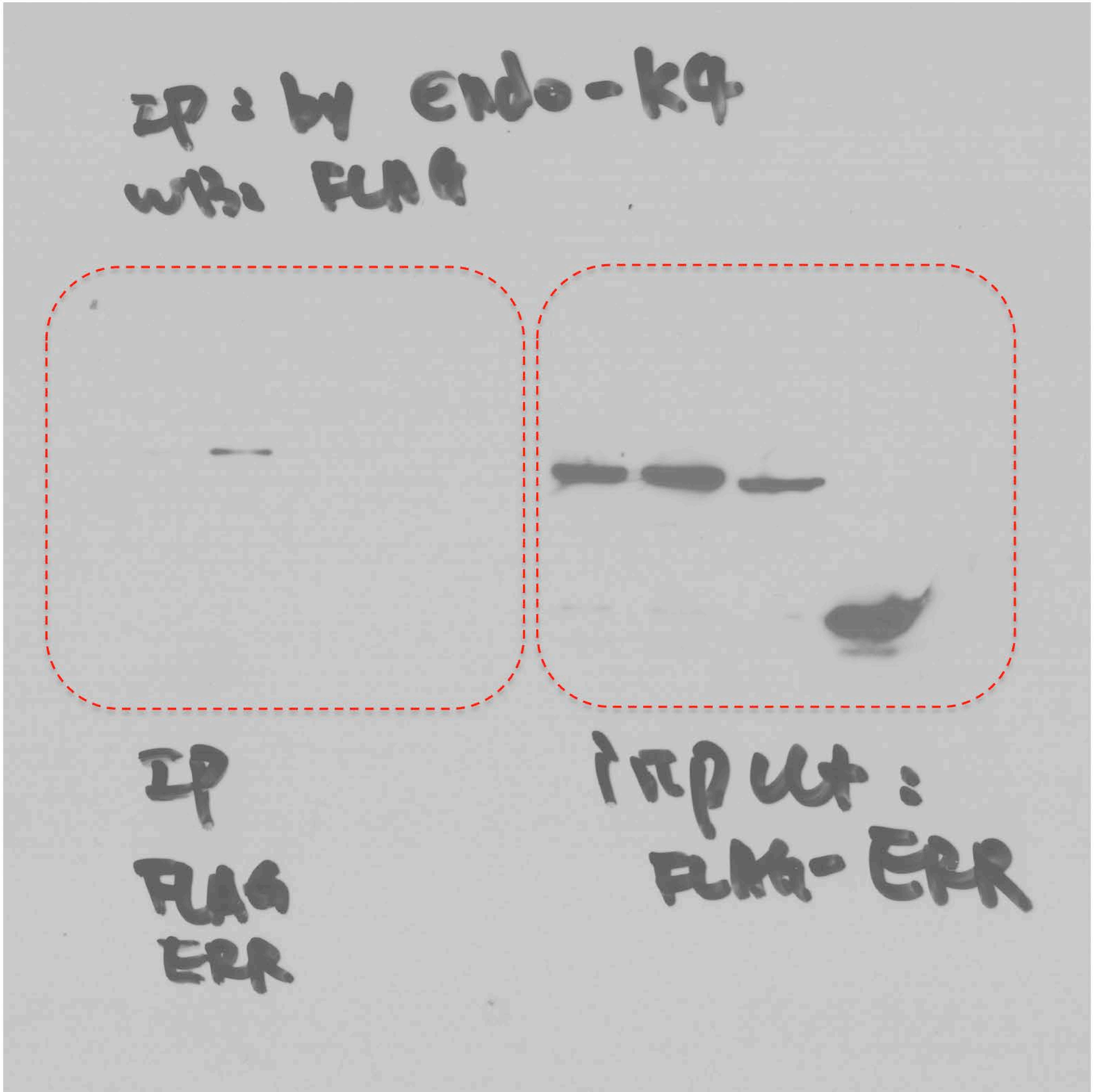
Full unedited gel for Figure 6E



Full unedited gel for Figure 6E



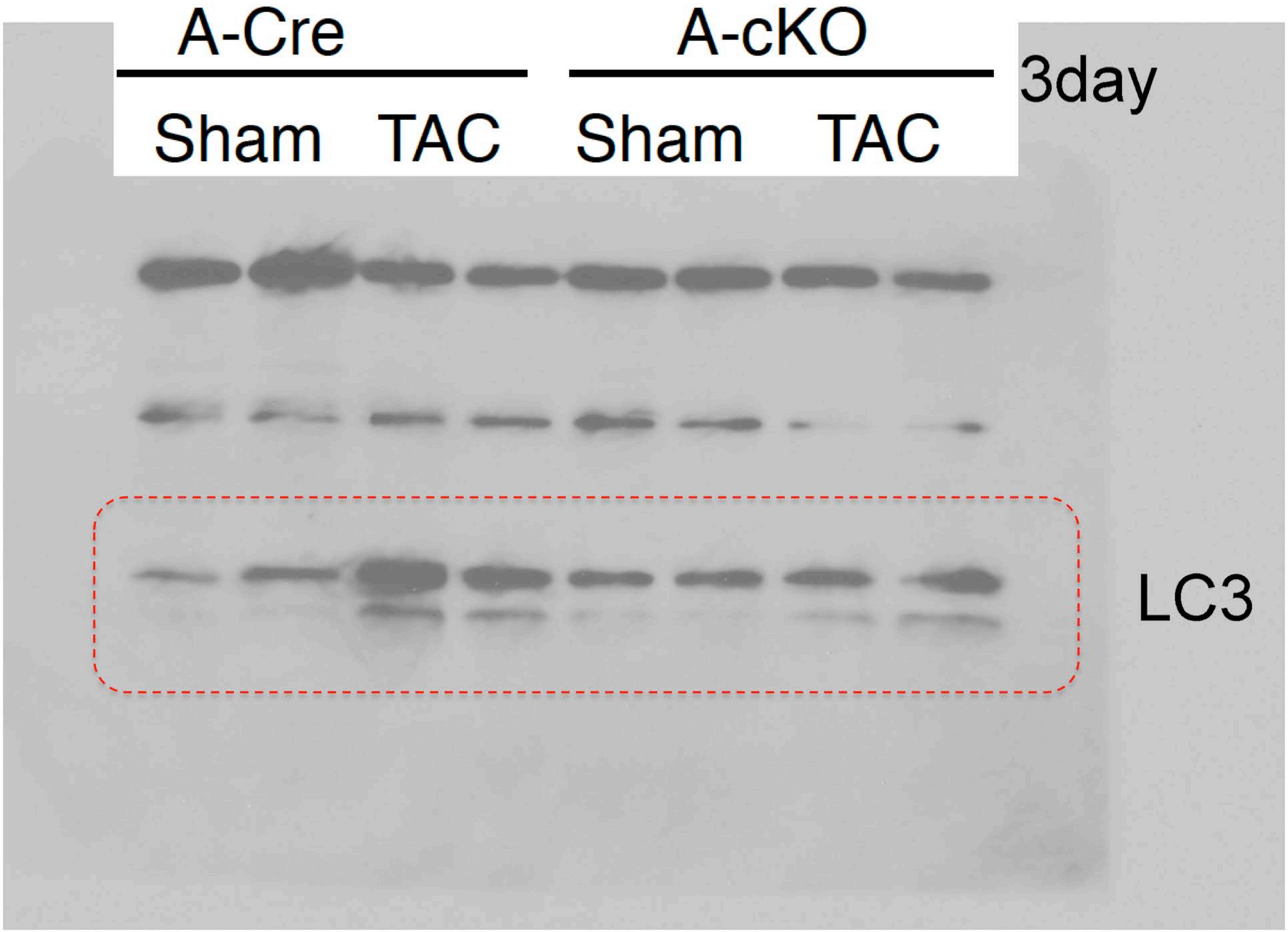
Full unedited gel for Figure 6F



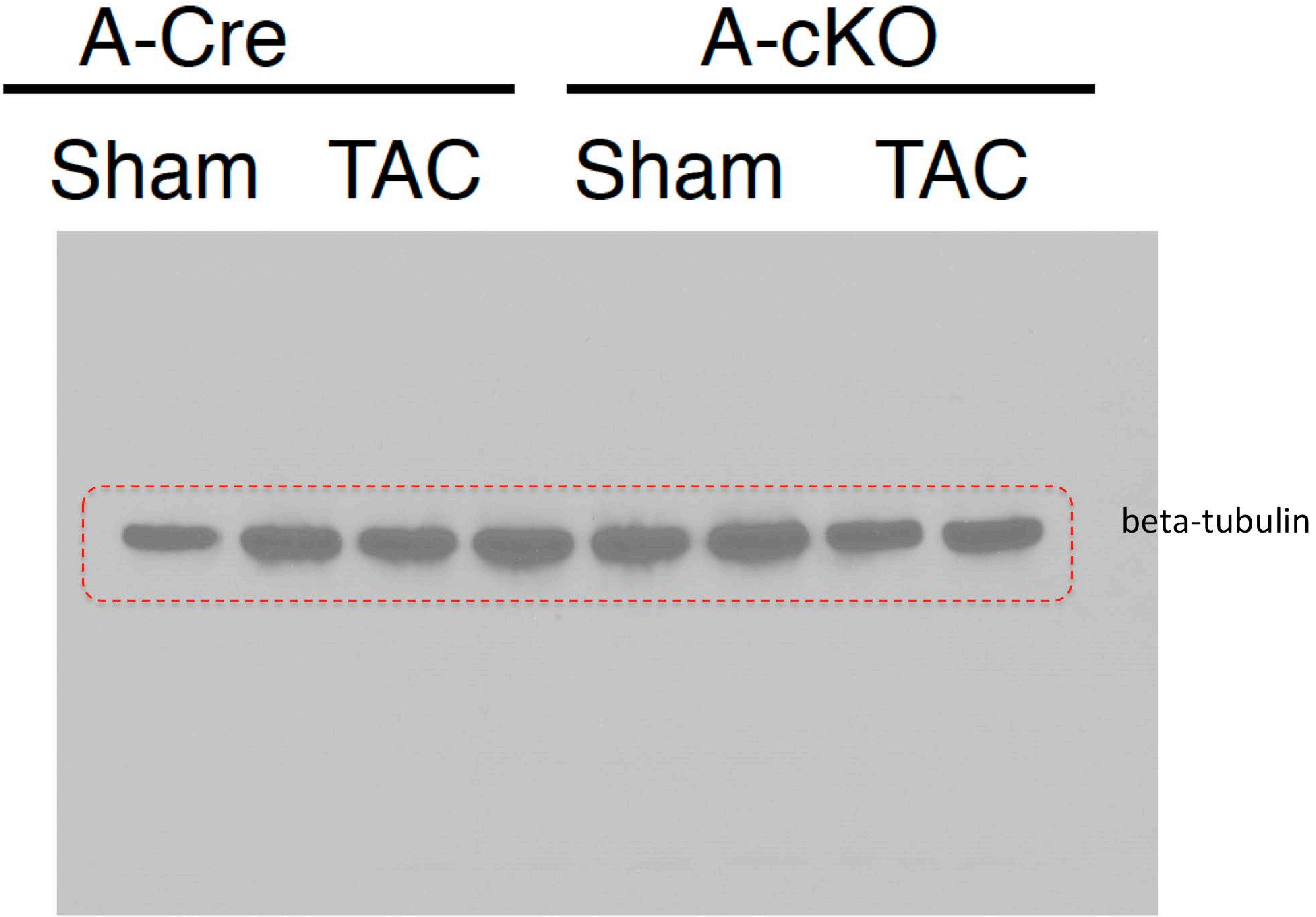
Full unedited gel for Figure 6F

Full unedited gel for Figure 6F

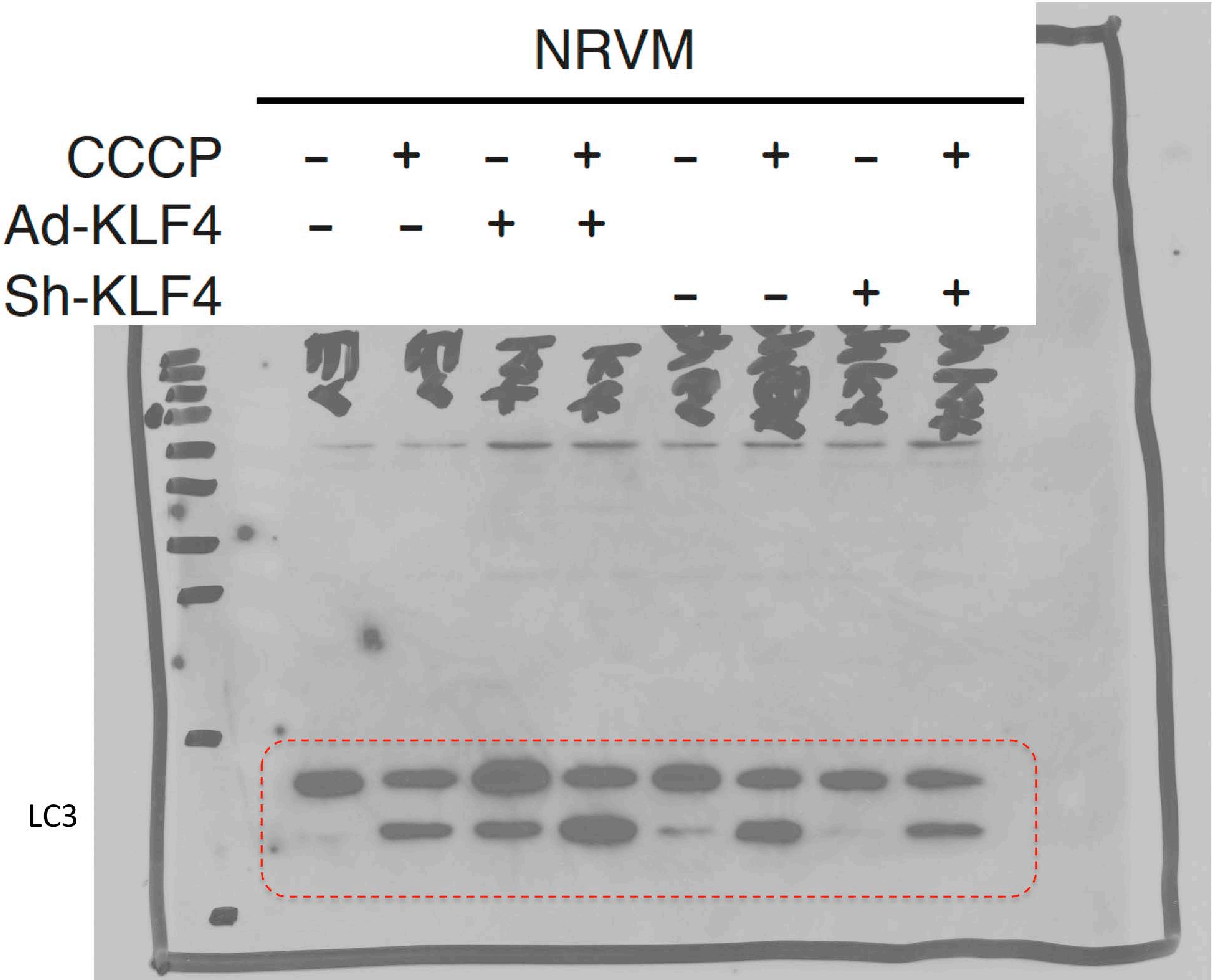
Full unedited gel for Figure 8A-top



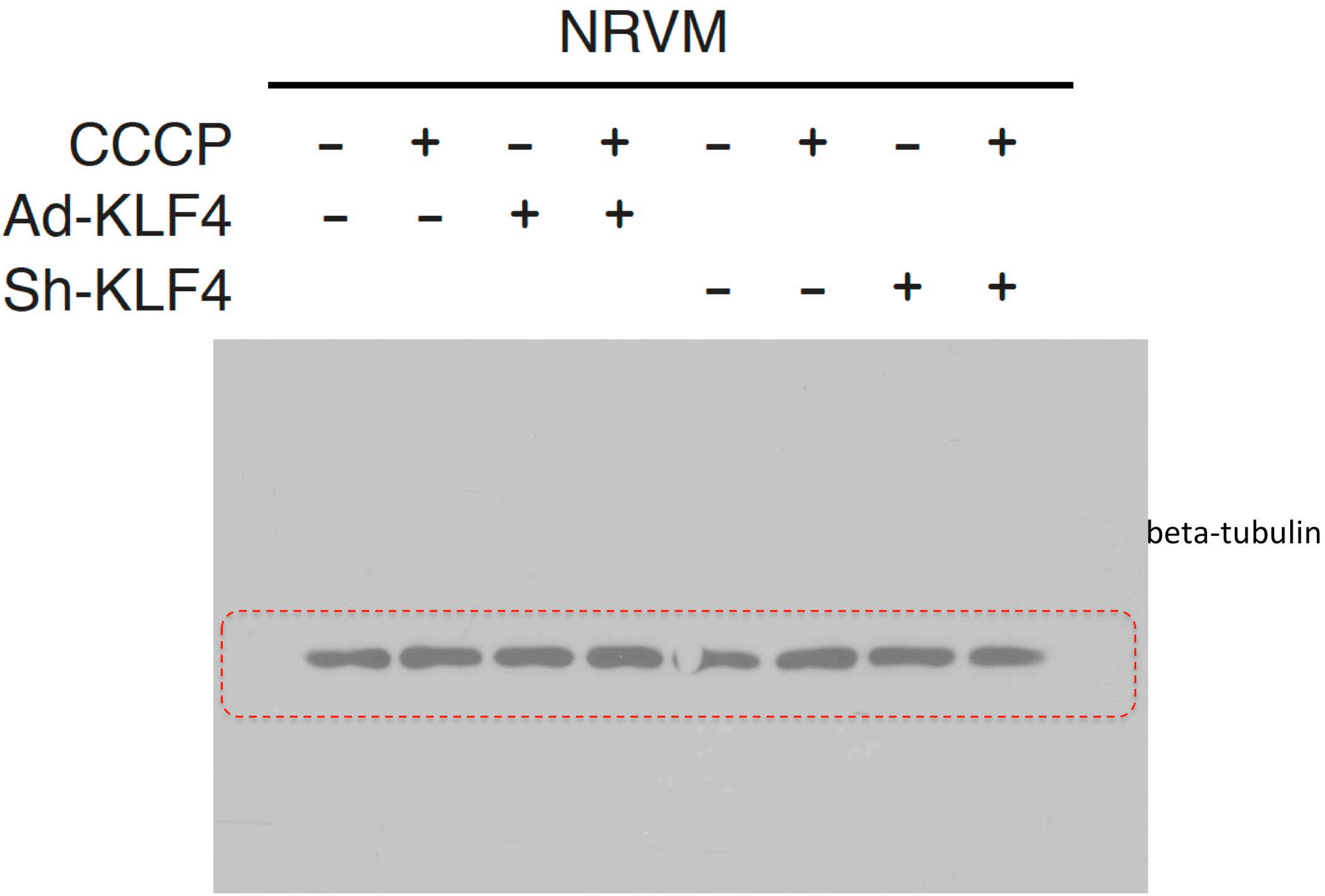
Full unedited gel for Figure 8A-top



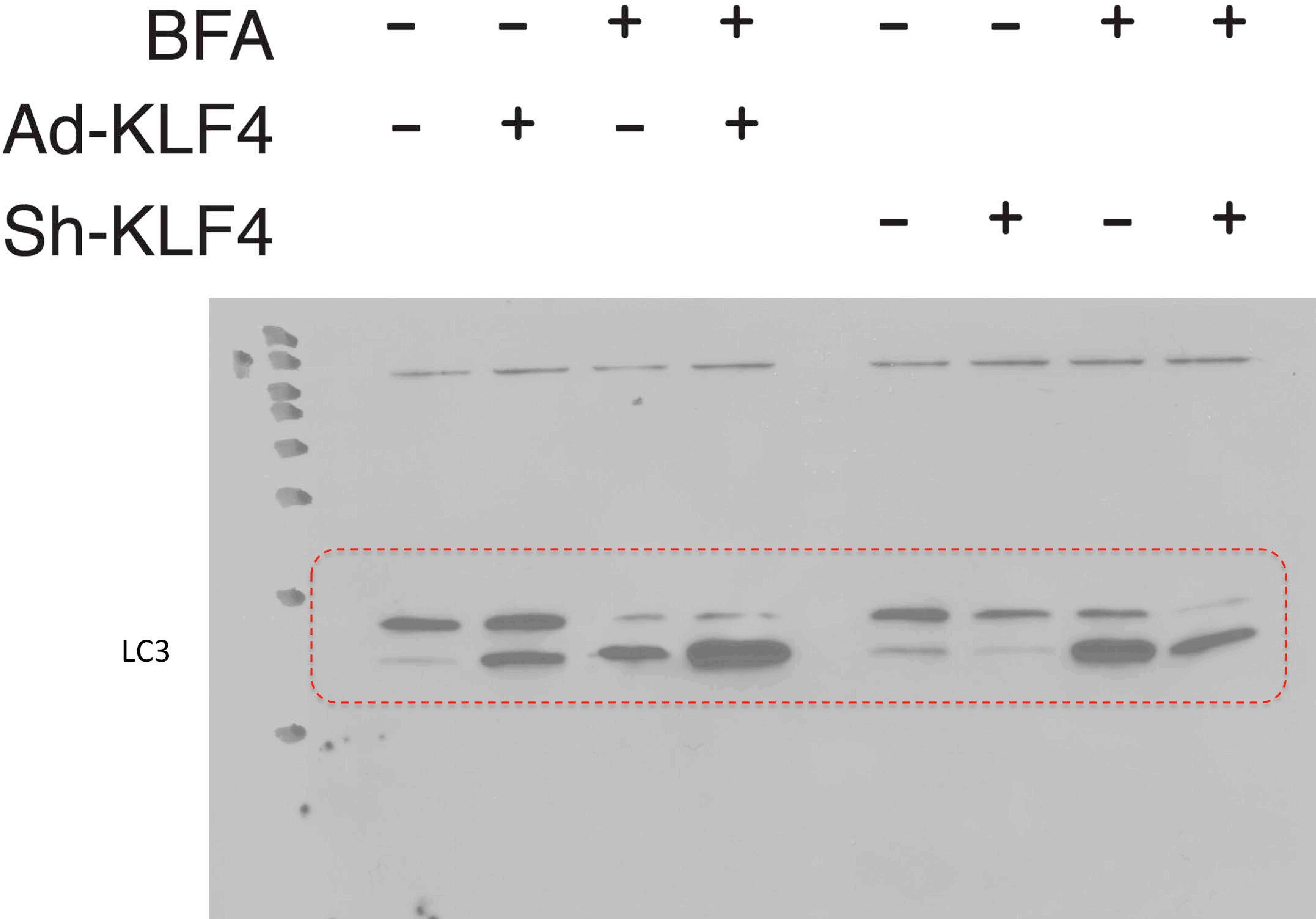
Full unedited gel for Figure 8A-middle



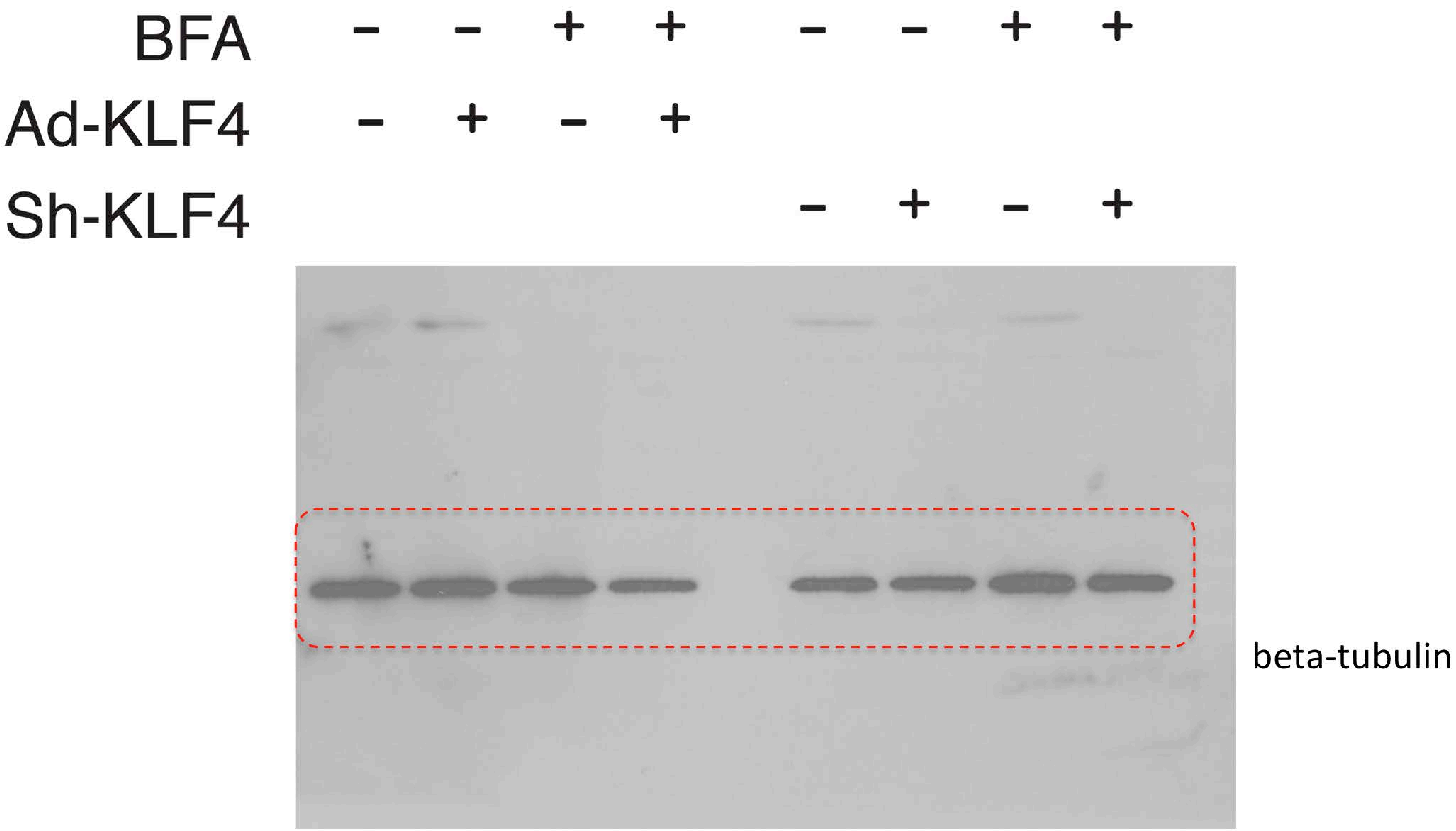
Full unedited gel for Figure 8A-middle



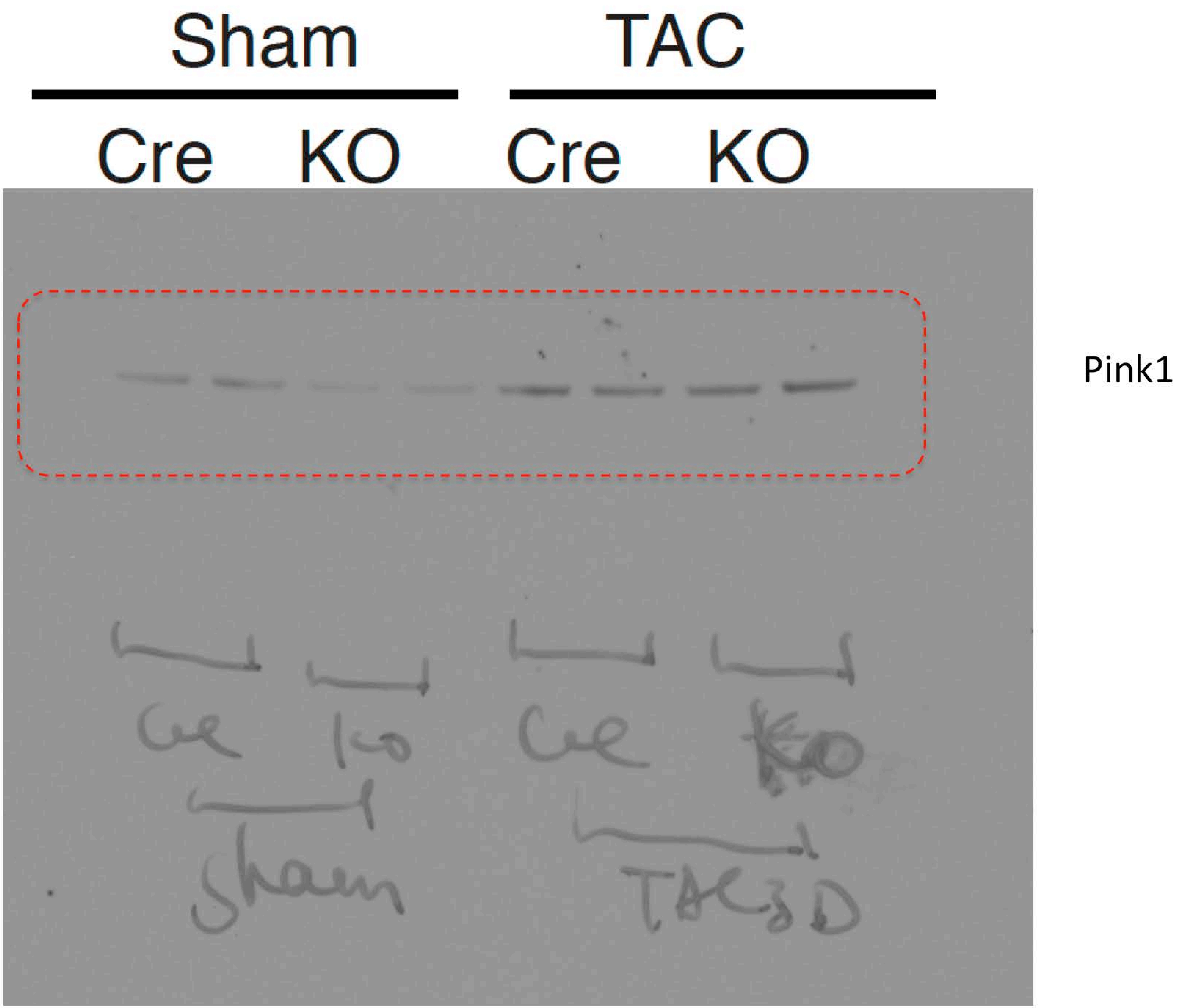
Full unedited gel for Figure 8A-bottom



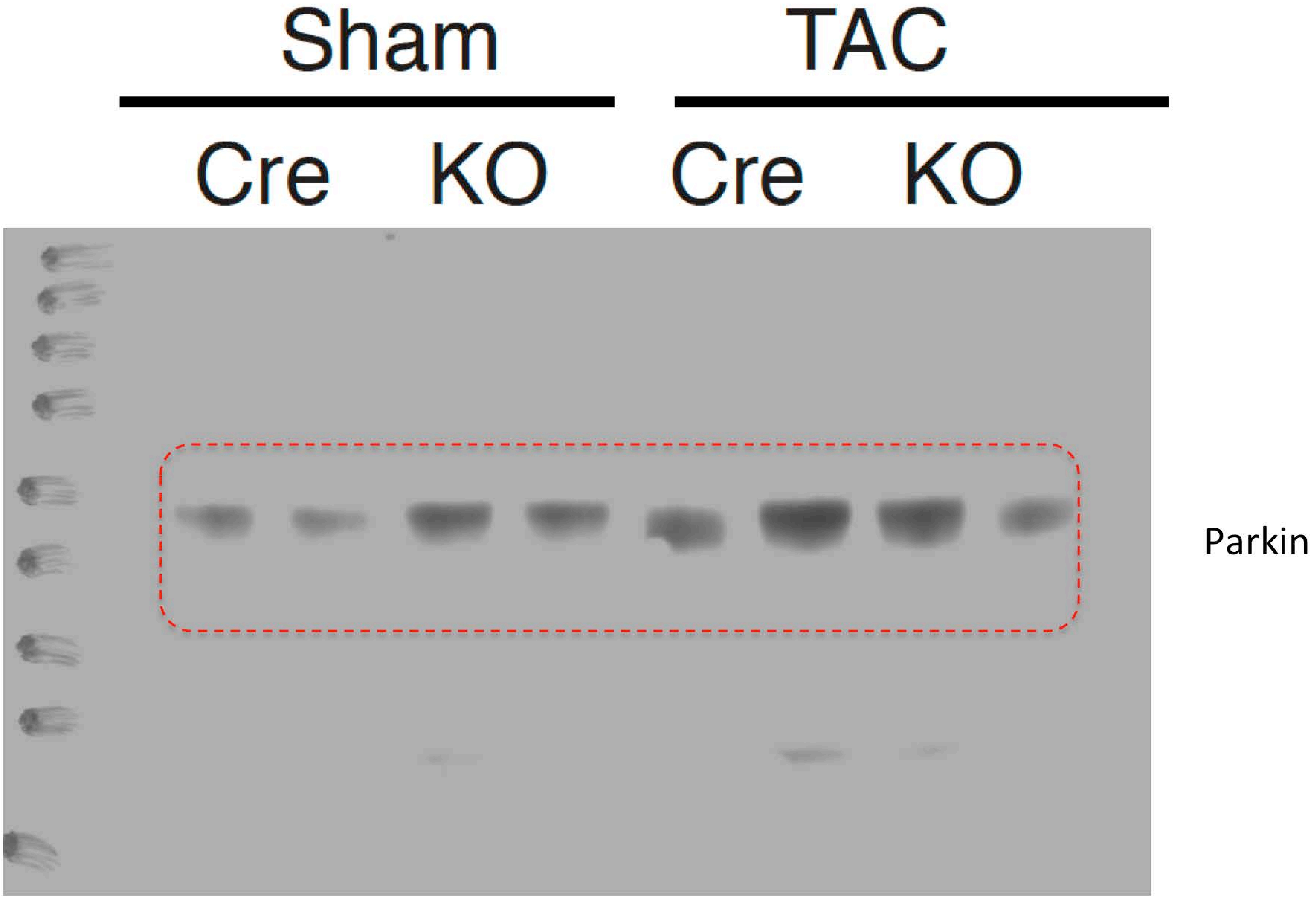
Full unedited gel for Figure 8A-bottom



Full unedited gel for Figure 8B-top



Full unedited gel for Figure 8B-top



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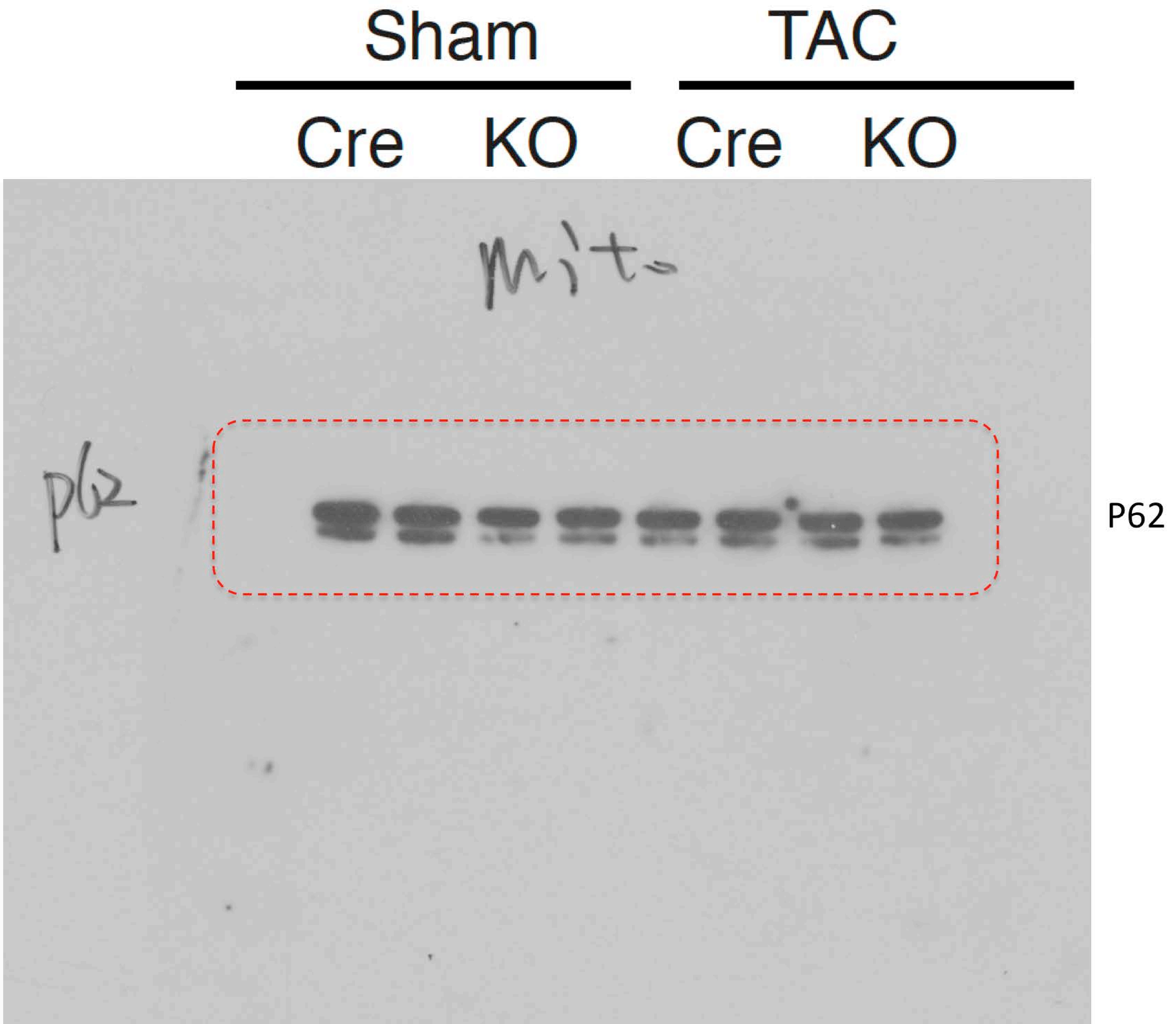

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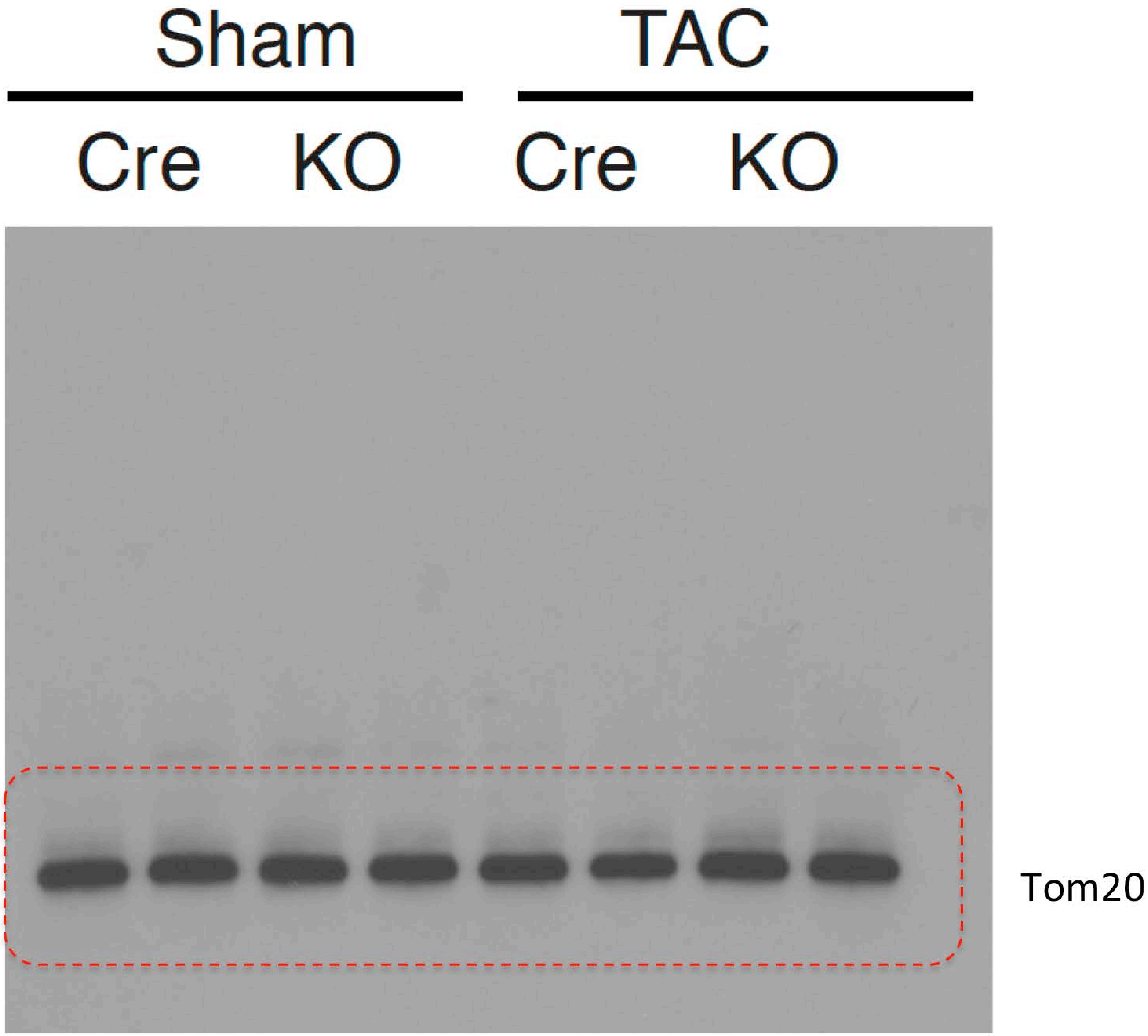
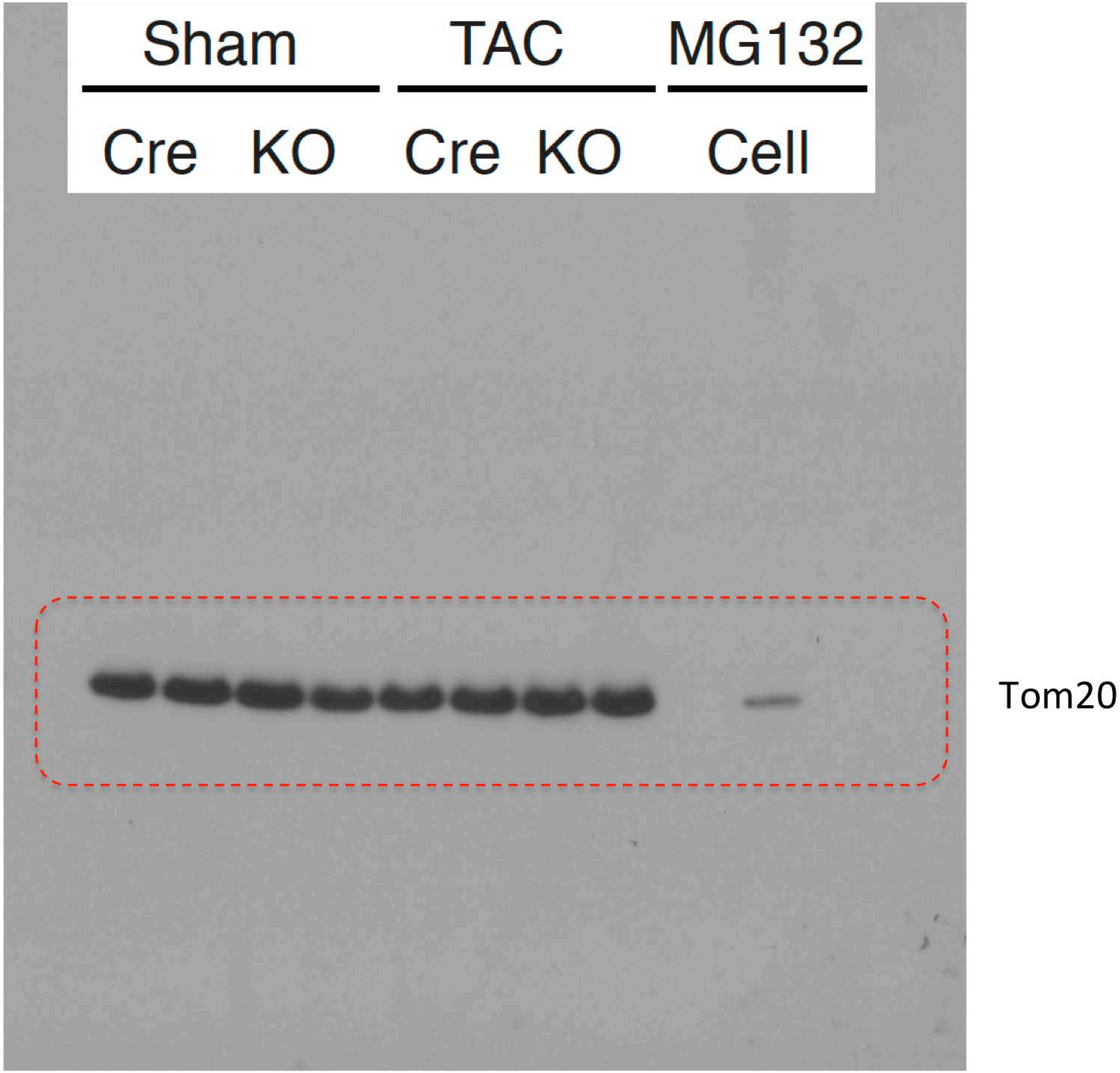
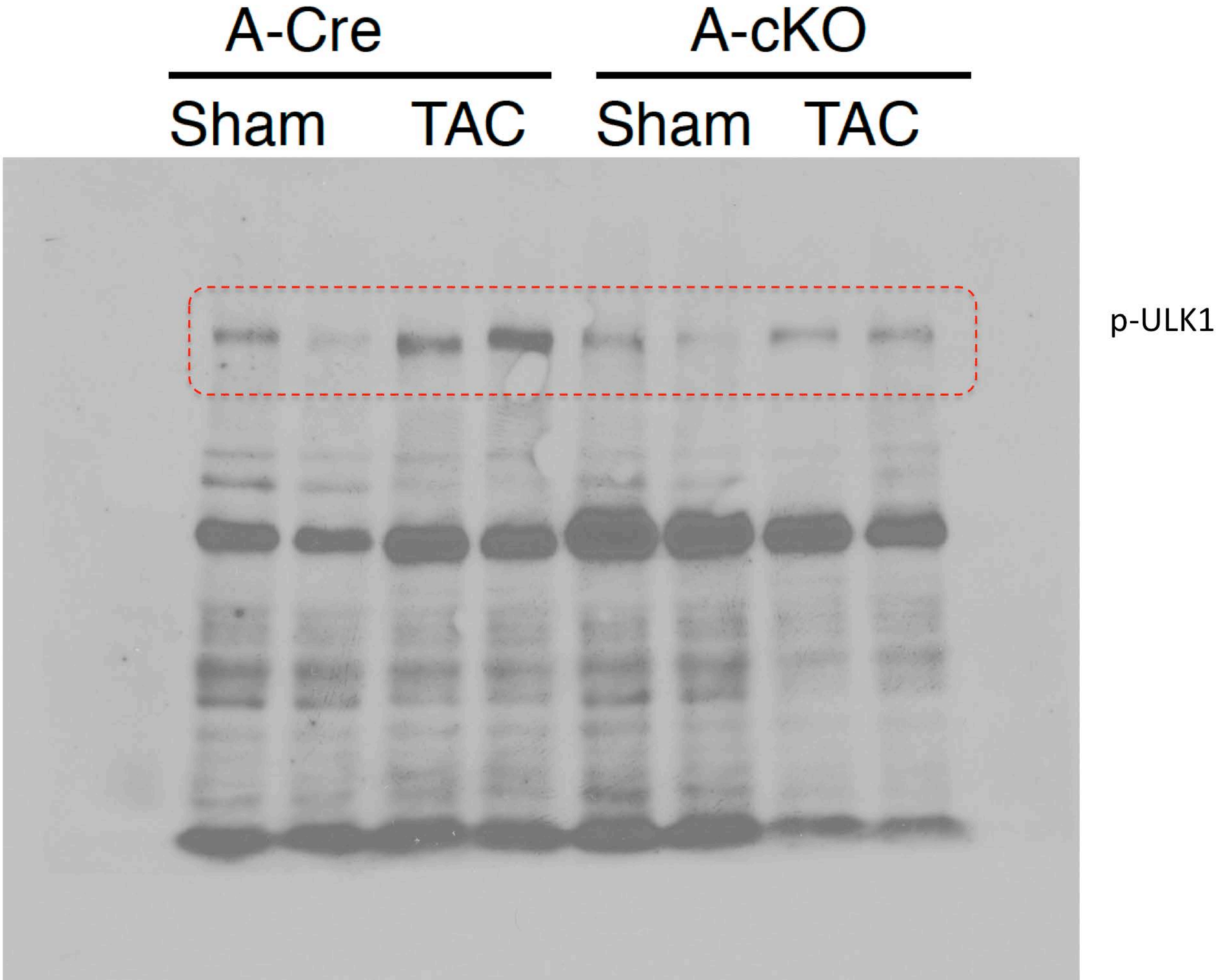


Full unedited gel for Figure 8B-bottom

Full unedited gel for Figure 8B-bottom



Full unedited gel for Figure 8C-top



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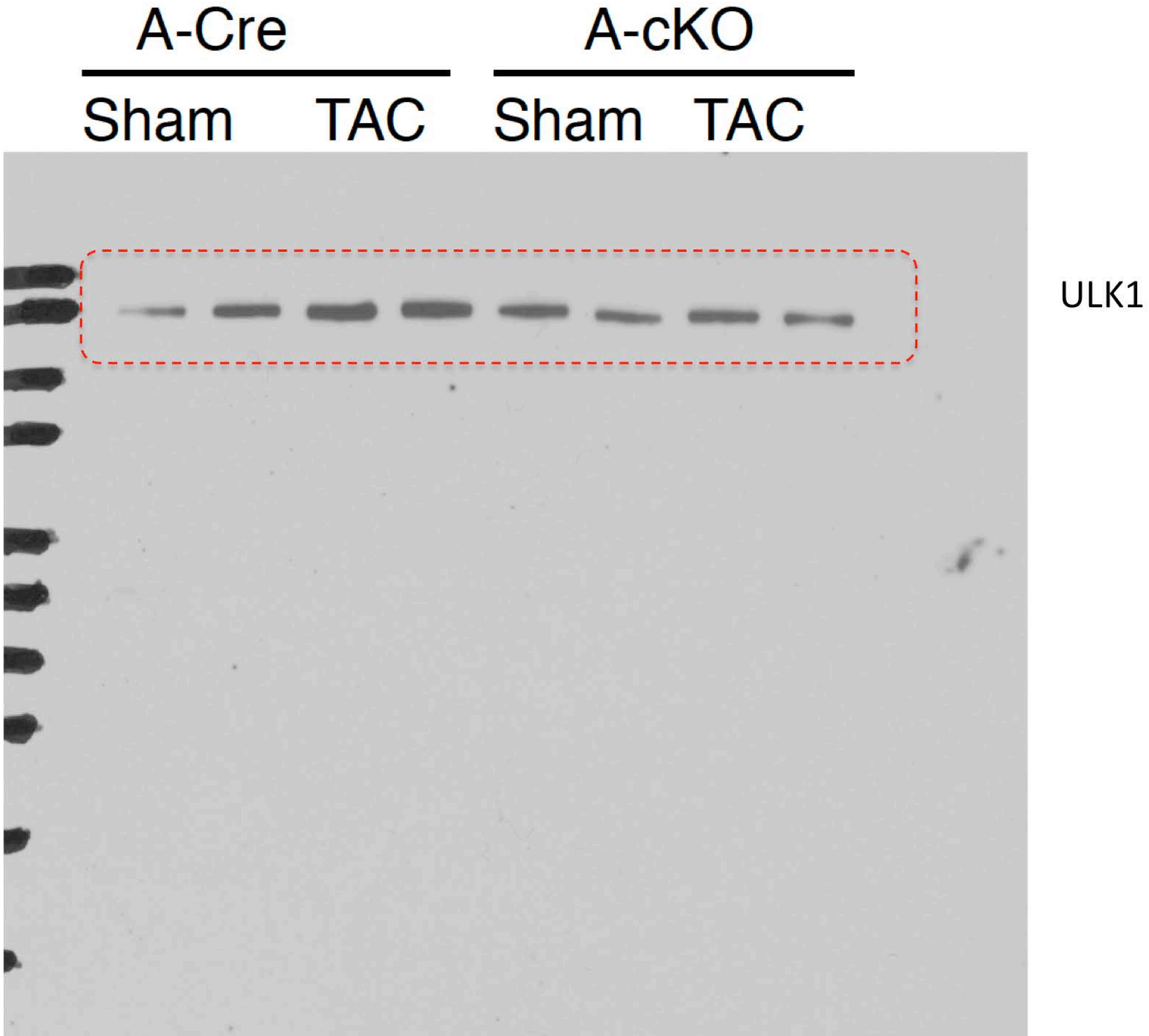

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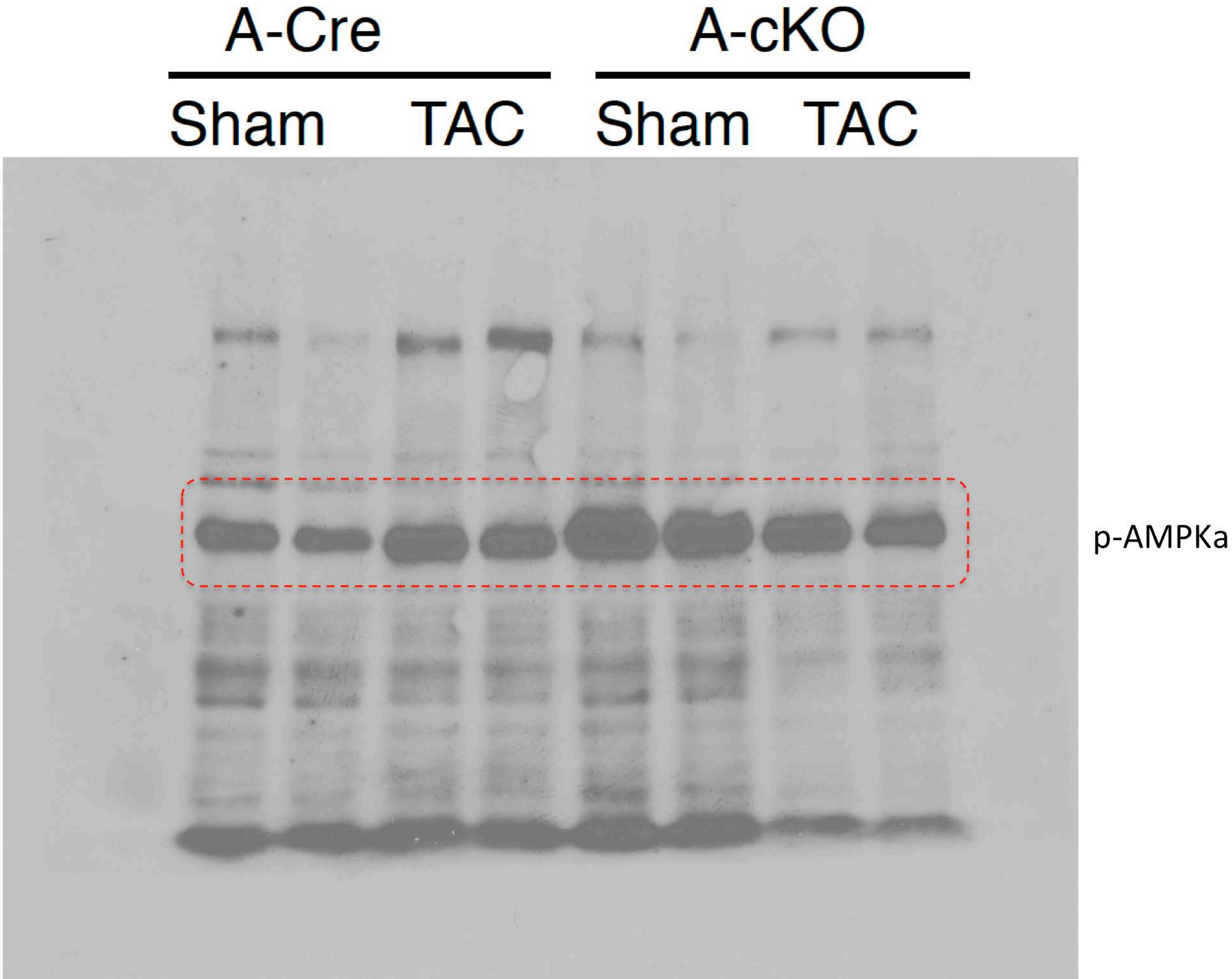

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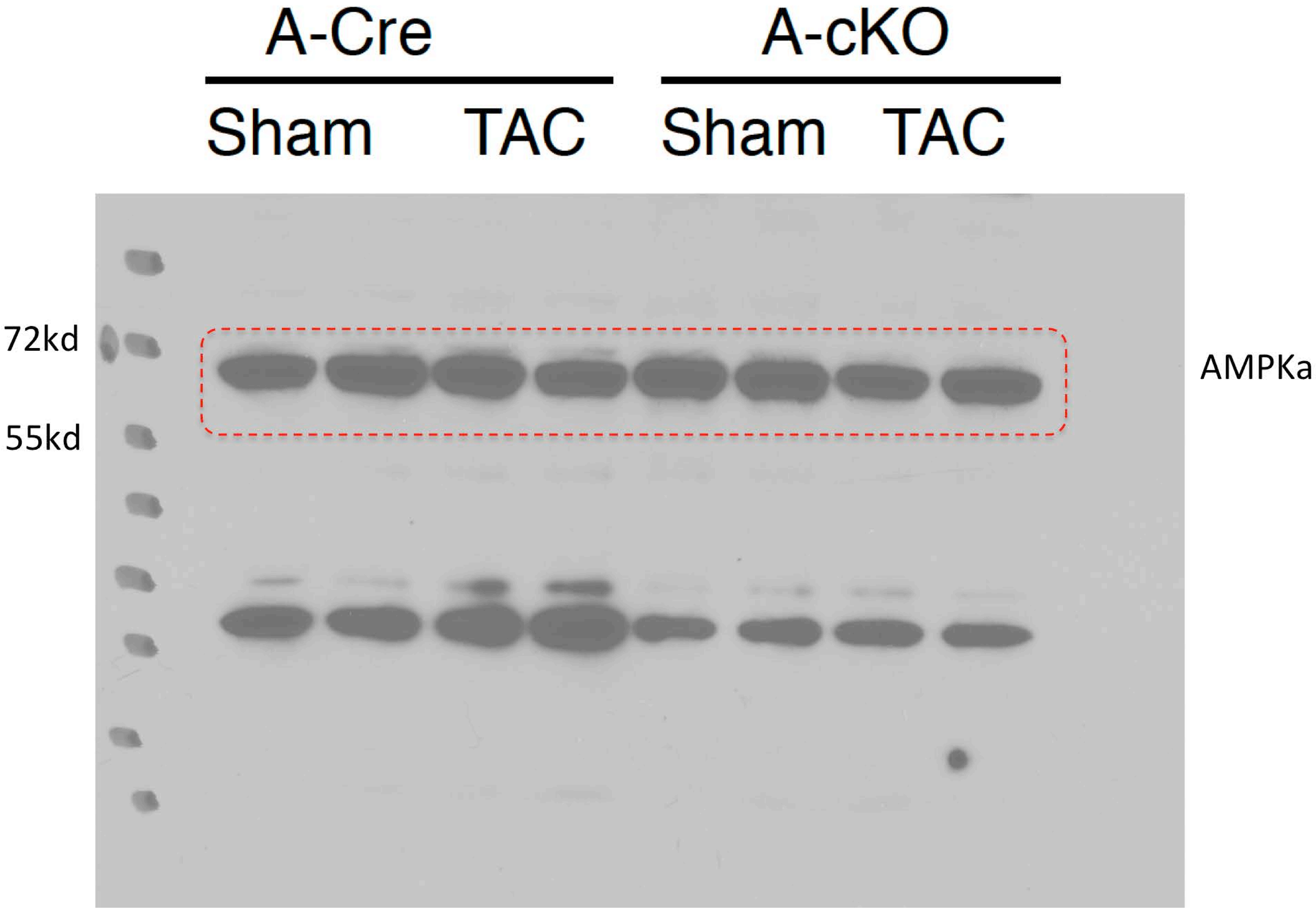

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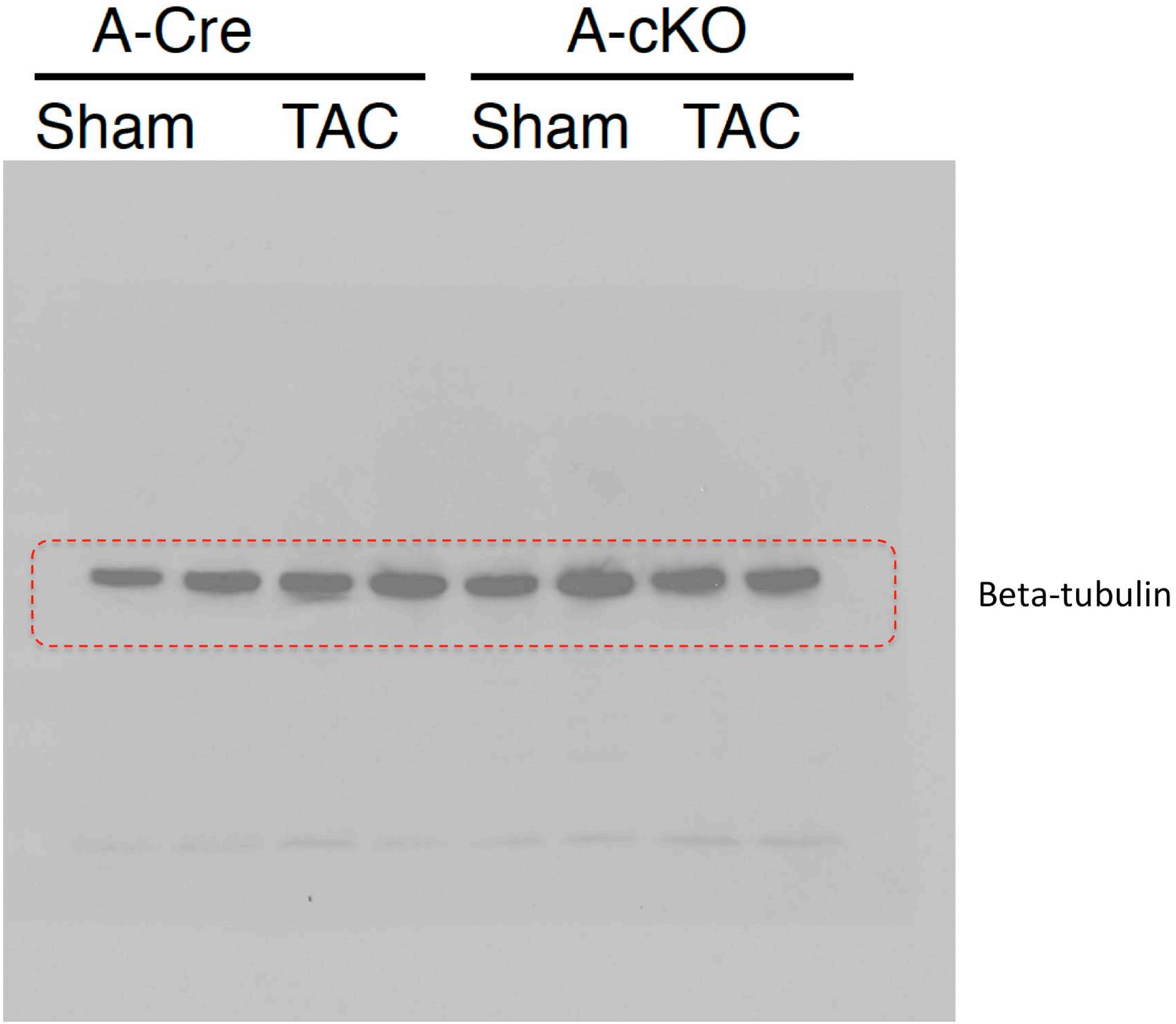

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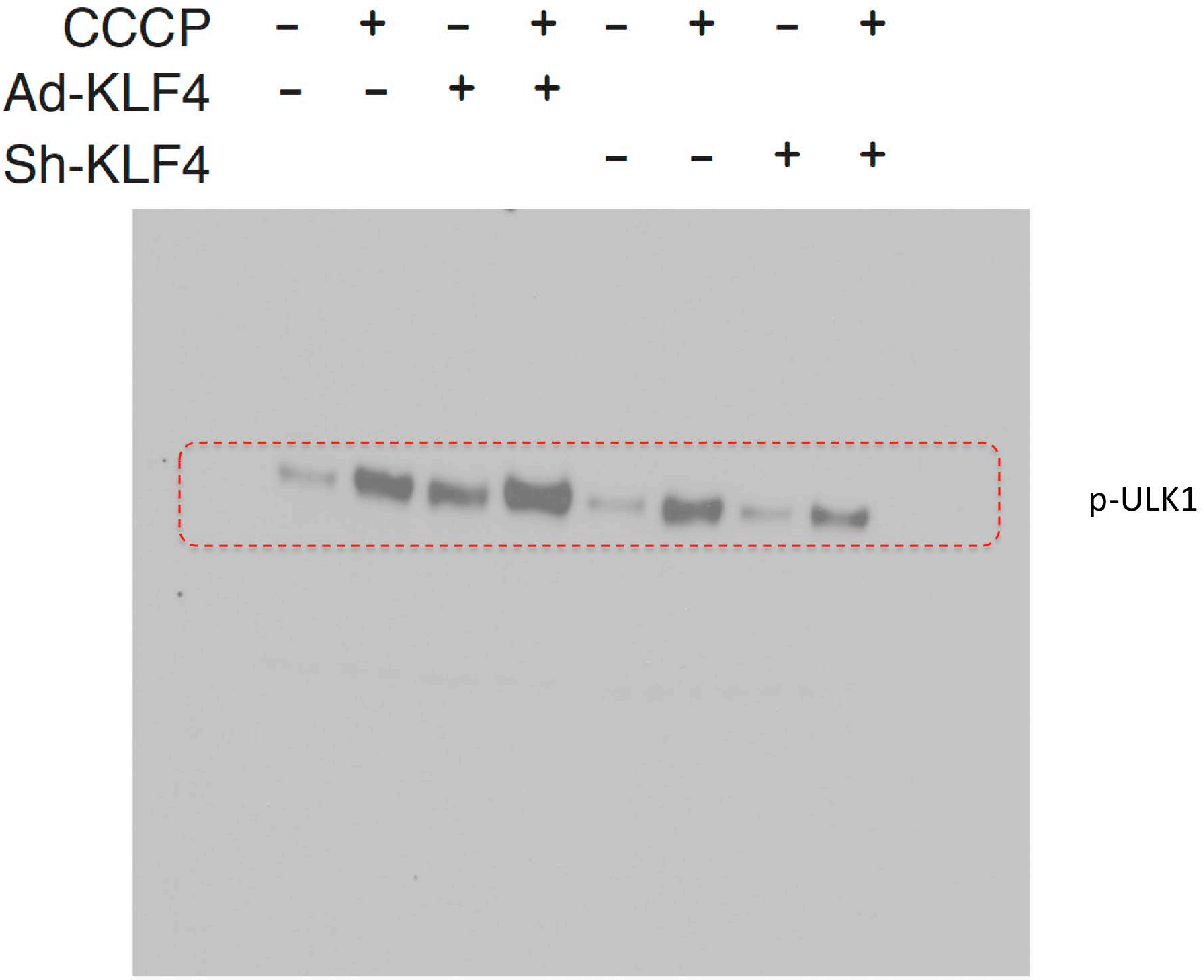

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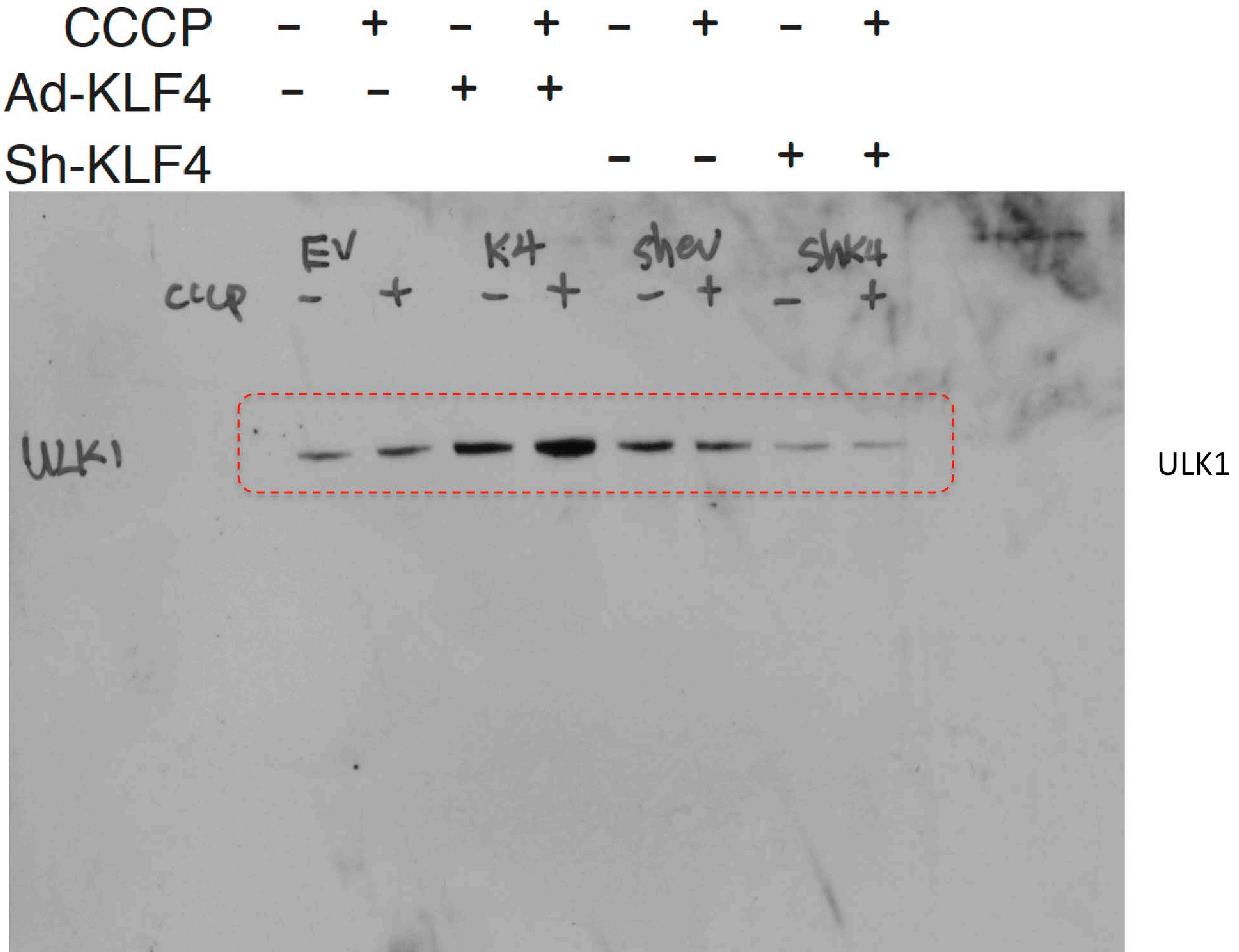

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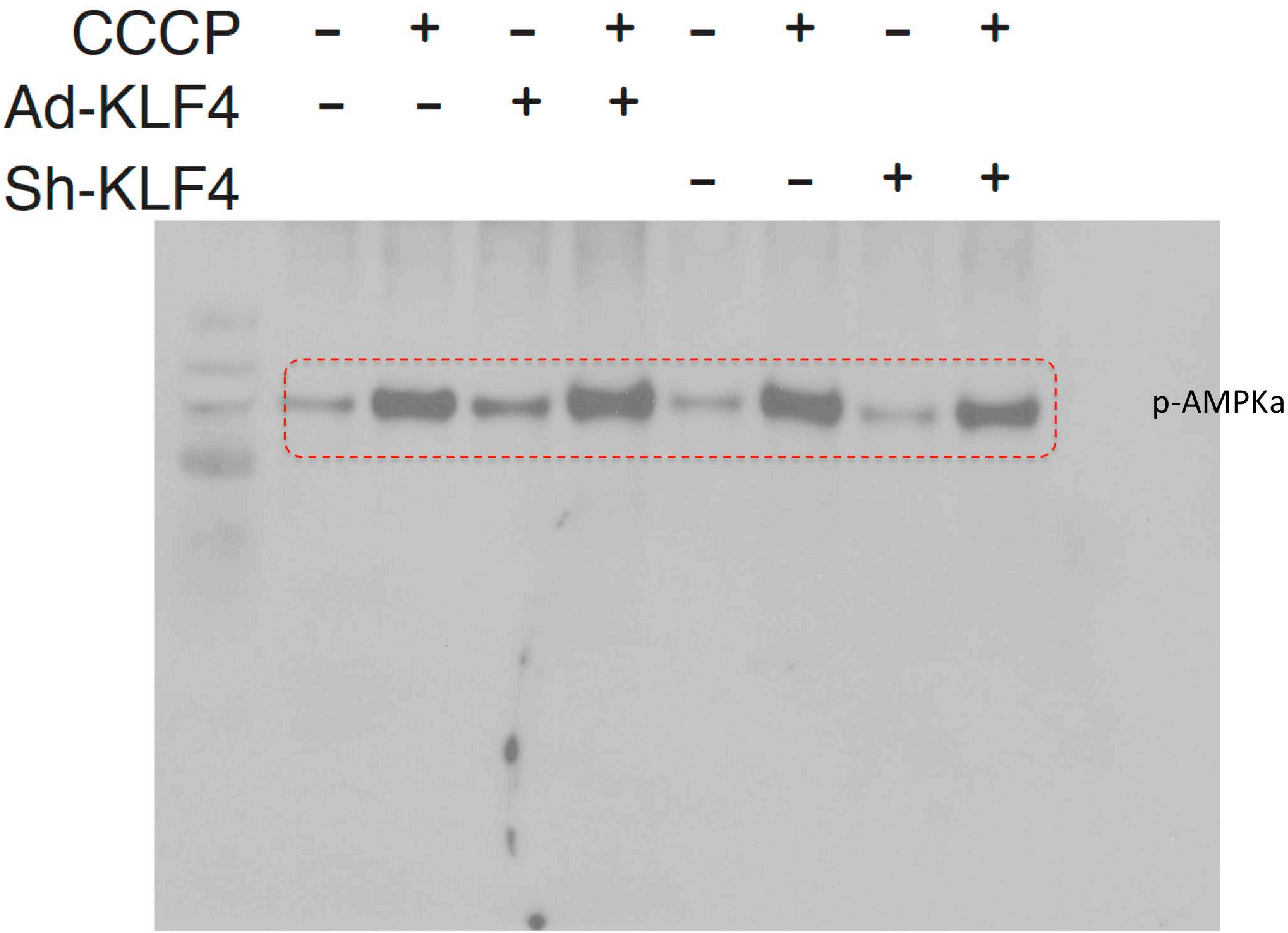

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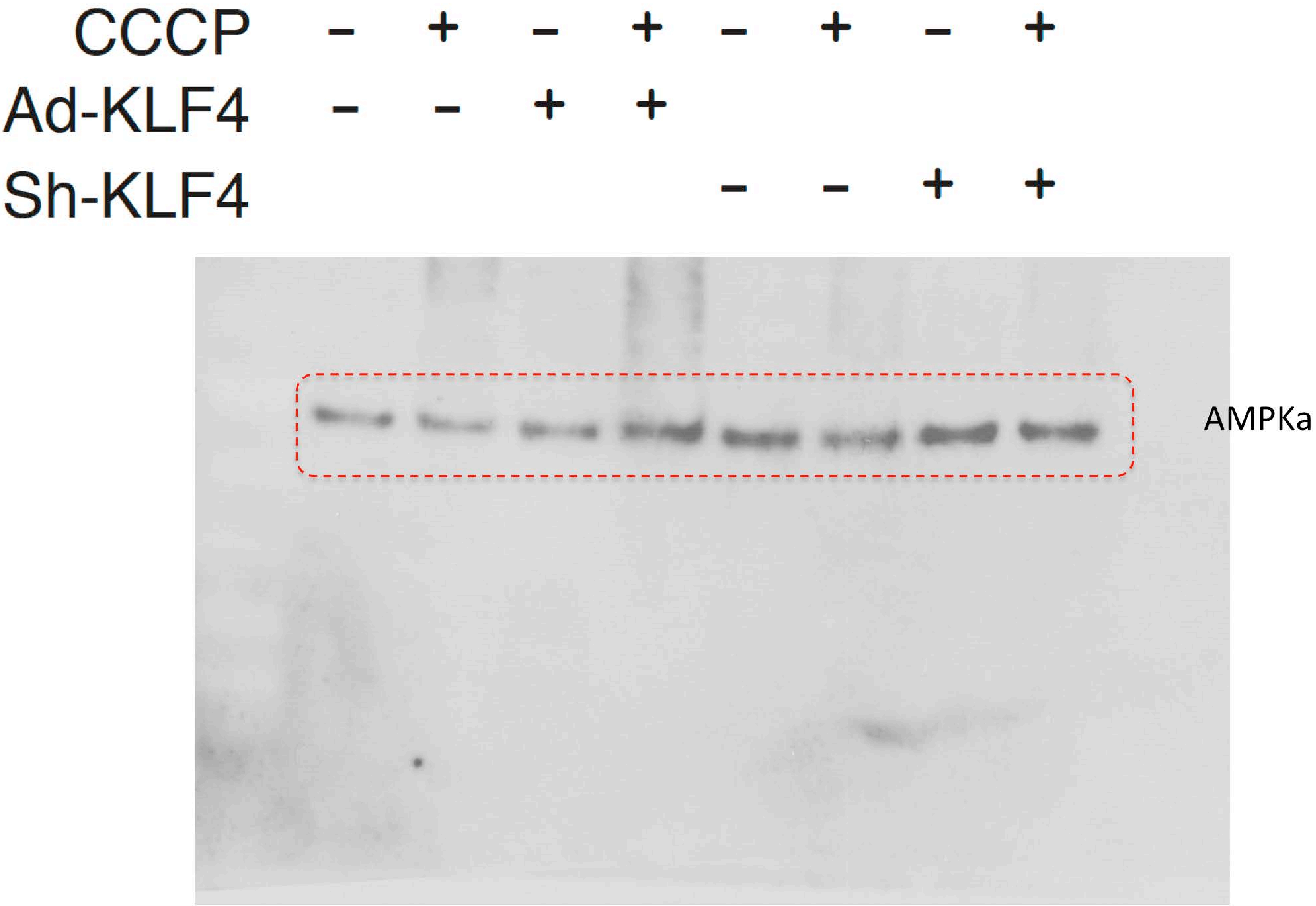

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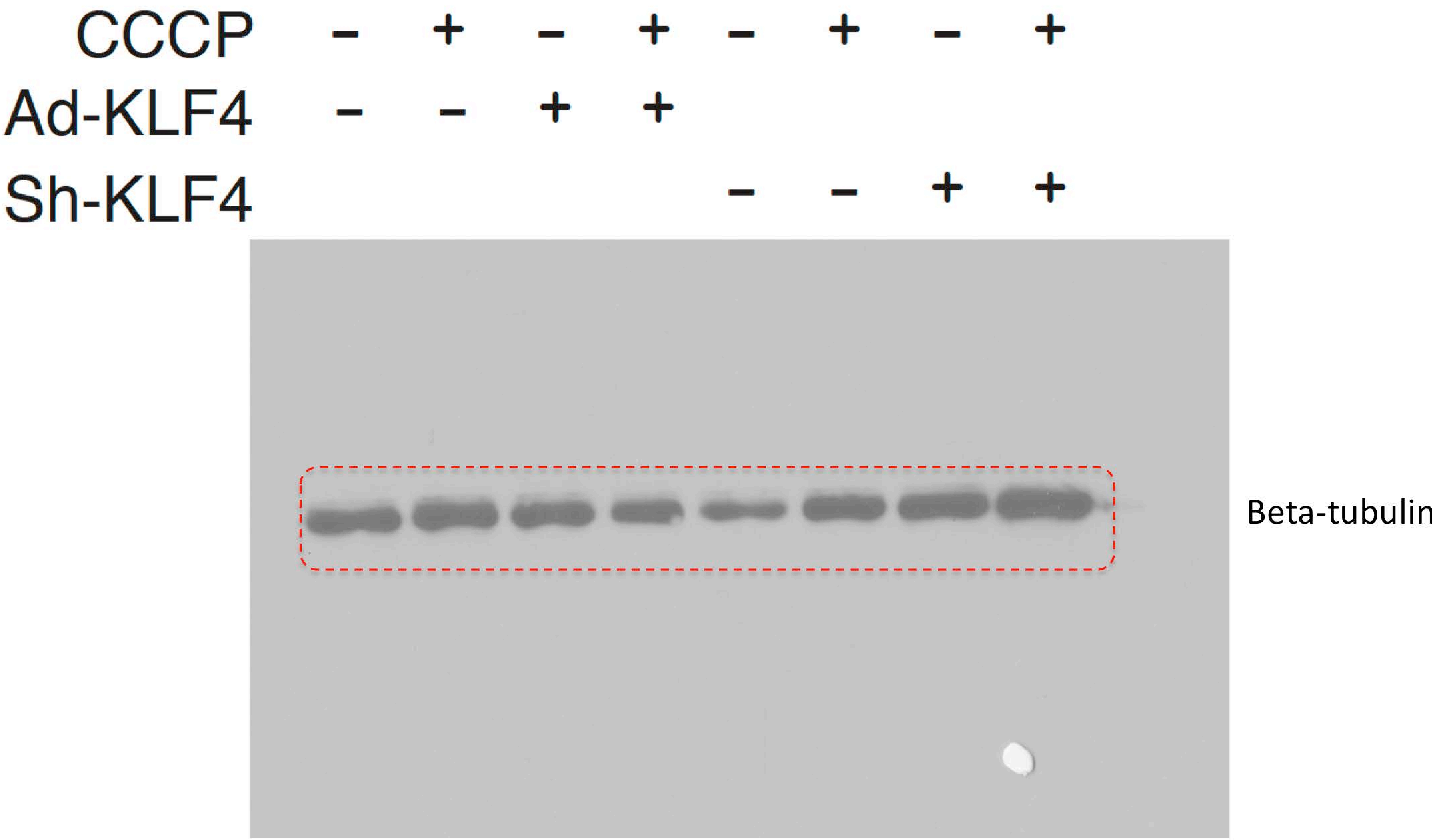
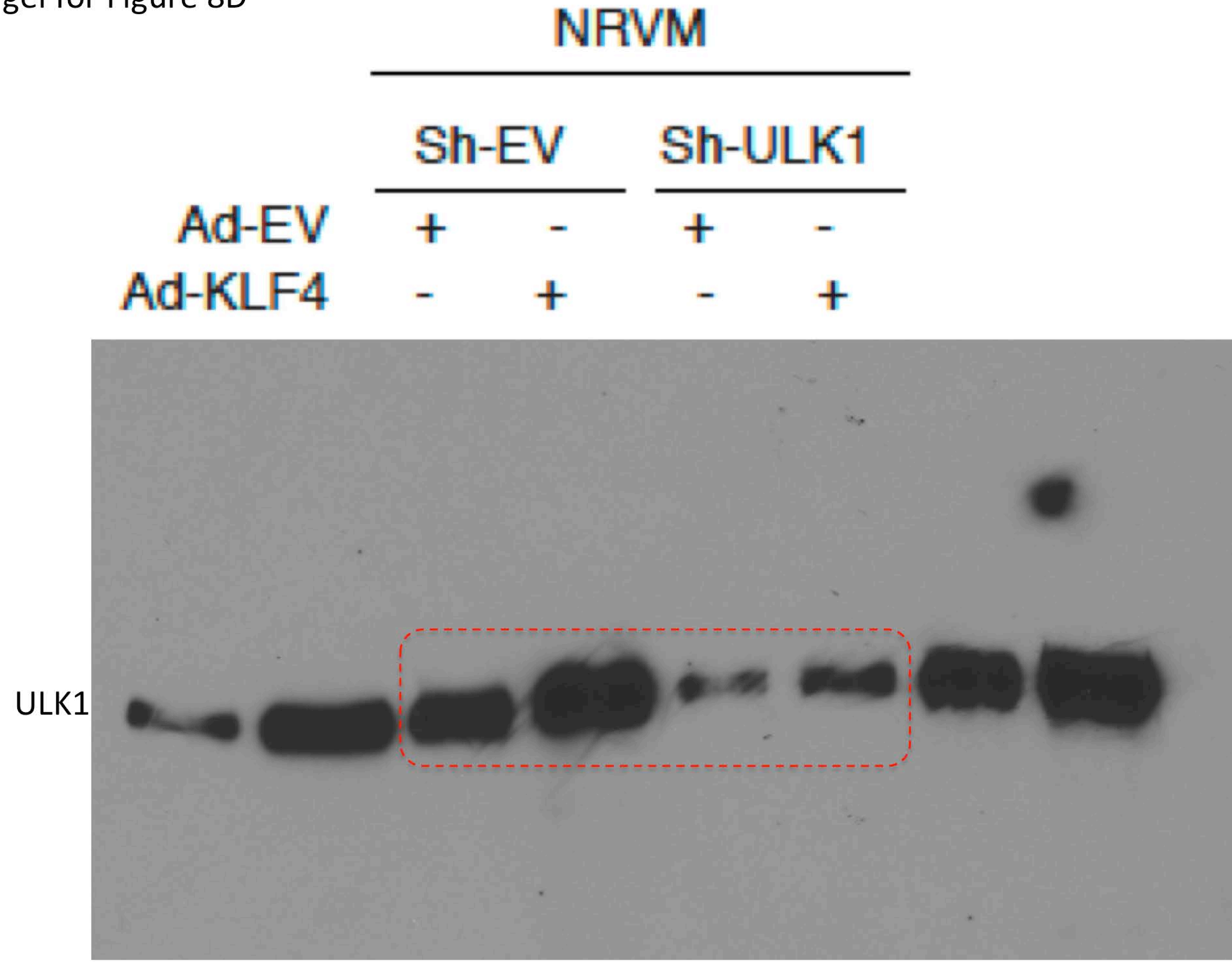
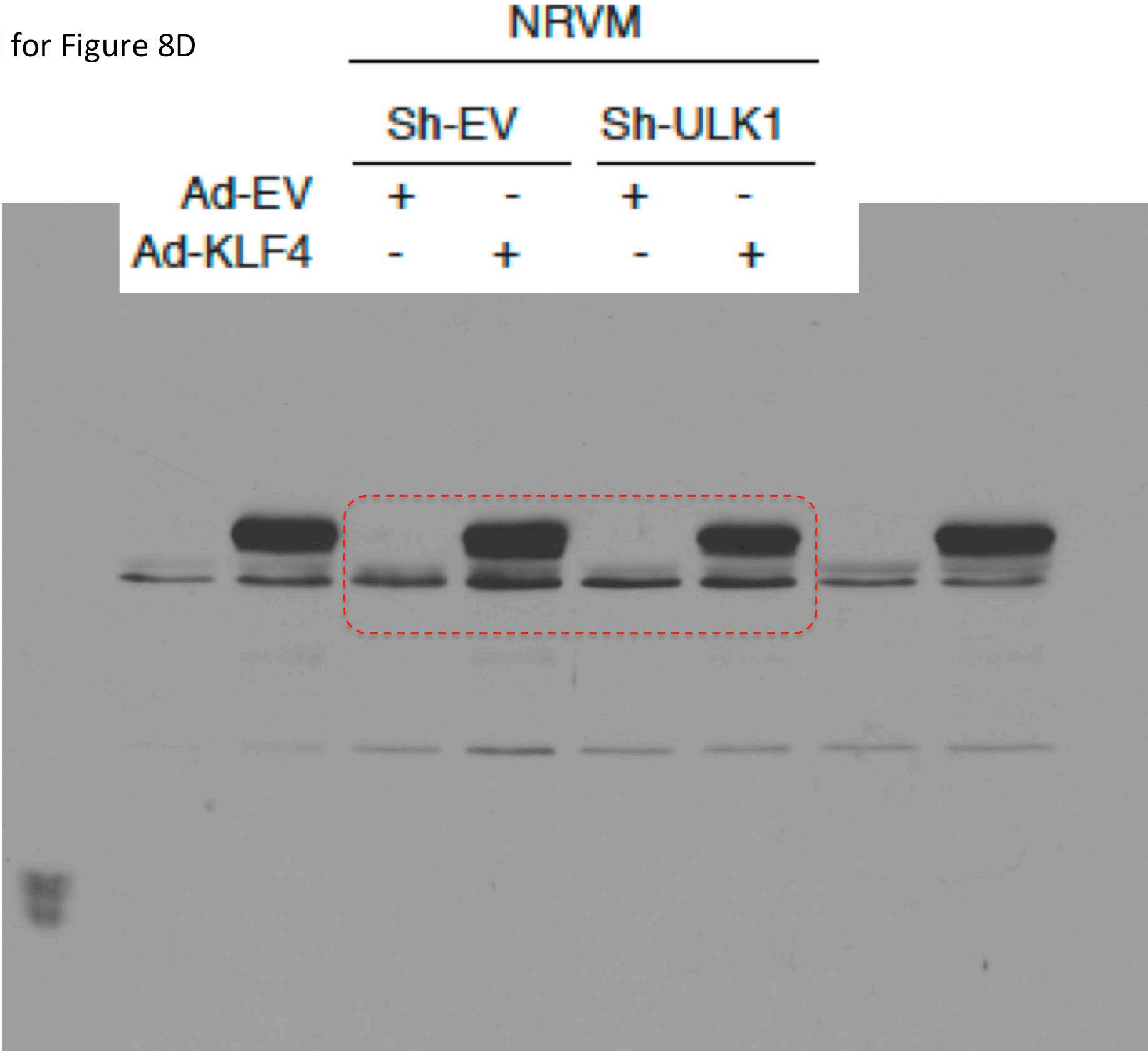


Full unedited gel for

Full unedited gel for Figure 8D

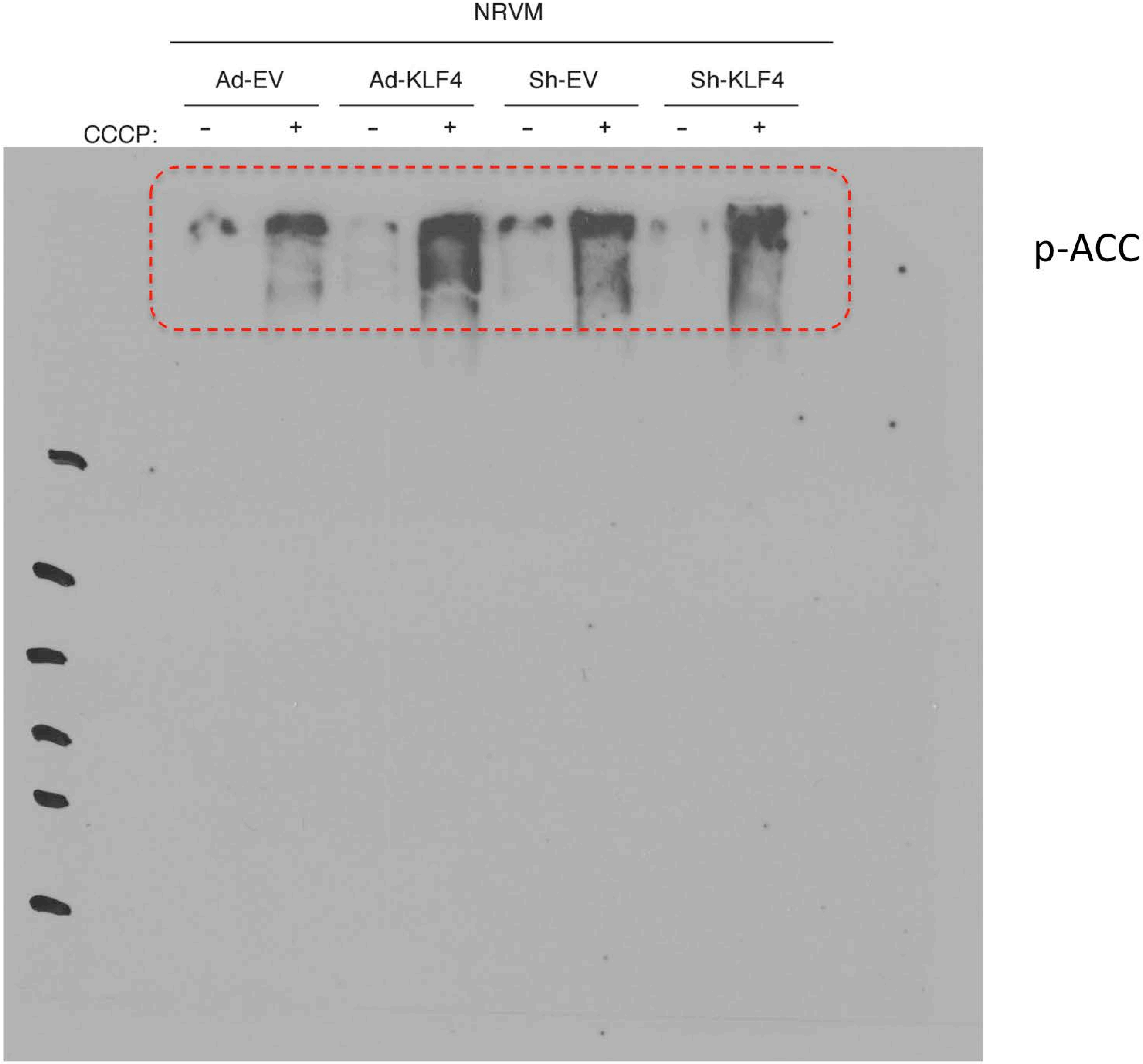


Full unedited gel for Figure 8D

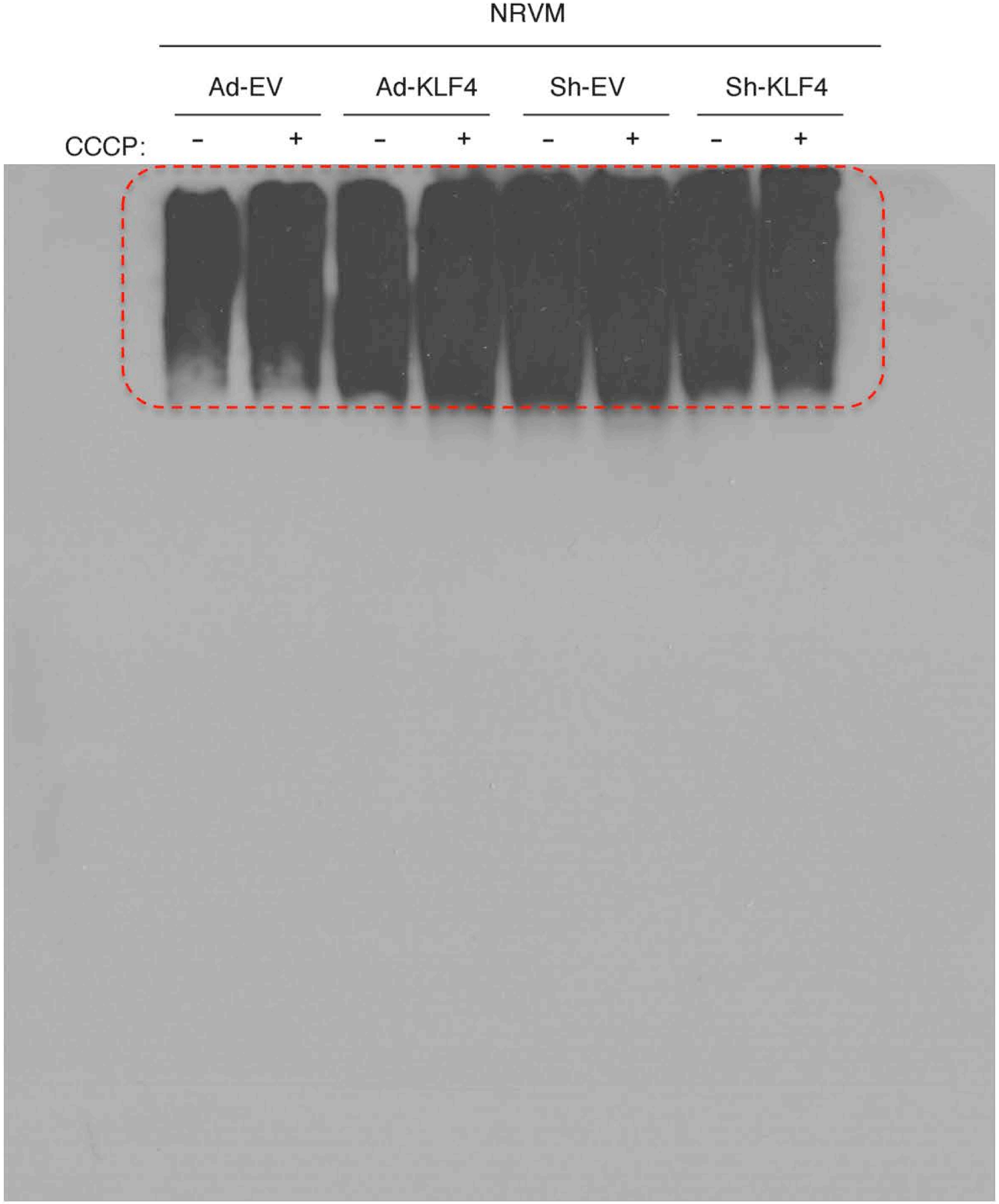


Full unedited gel for Figure 8D

Full unedited gel for Supplementary Figure 12

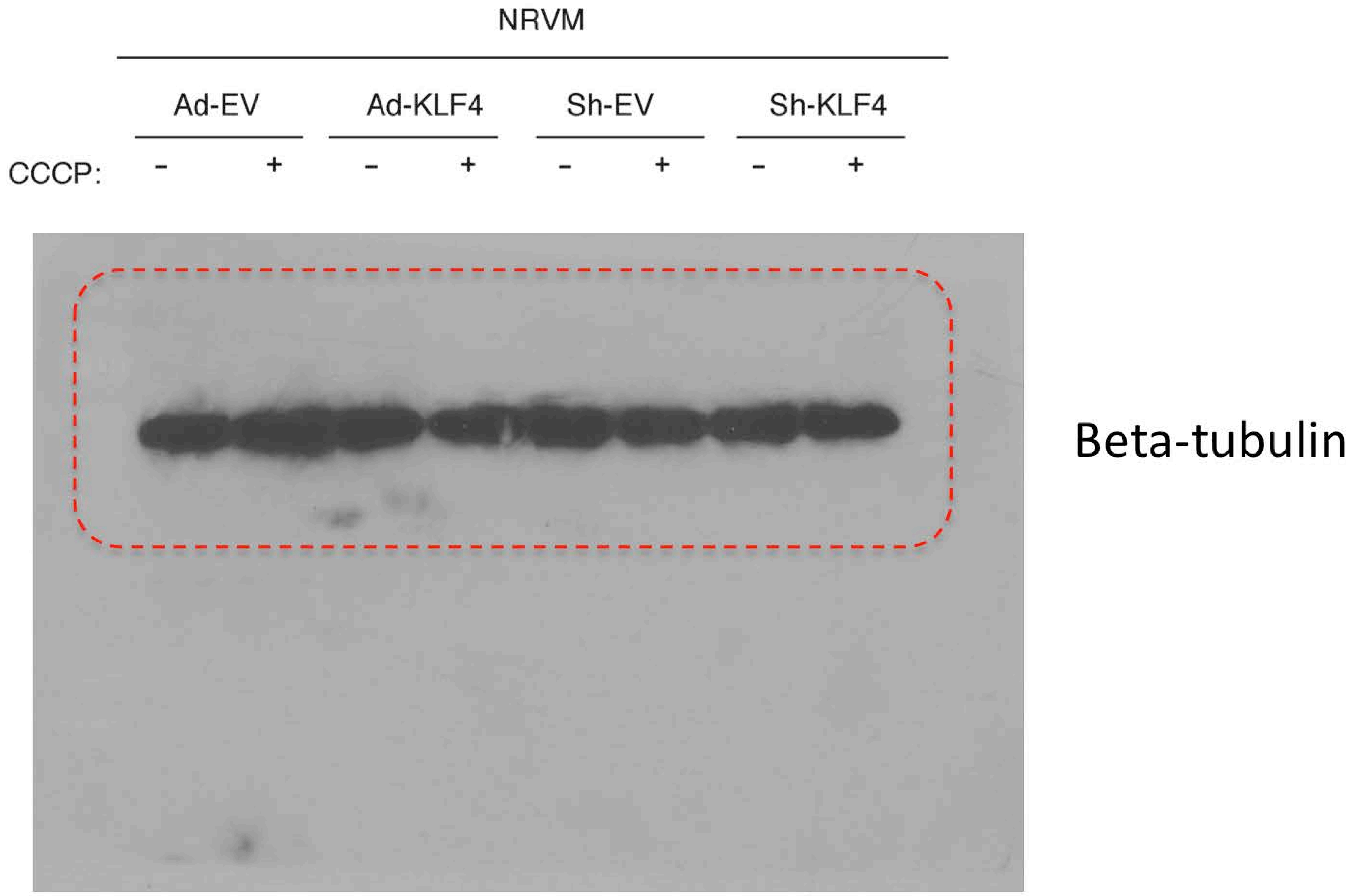


Full unedited gel for Supplementary Figure 12

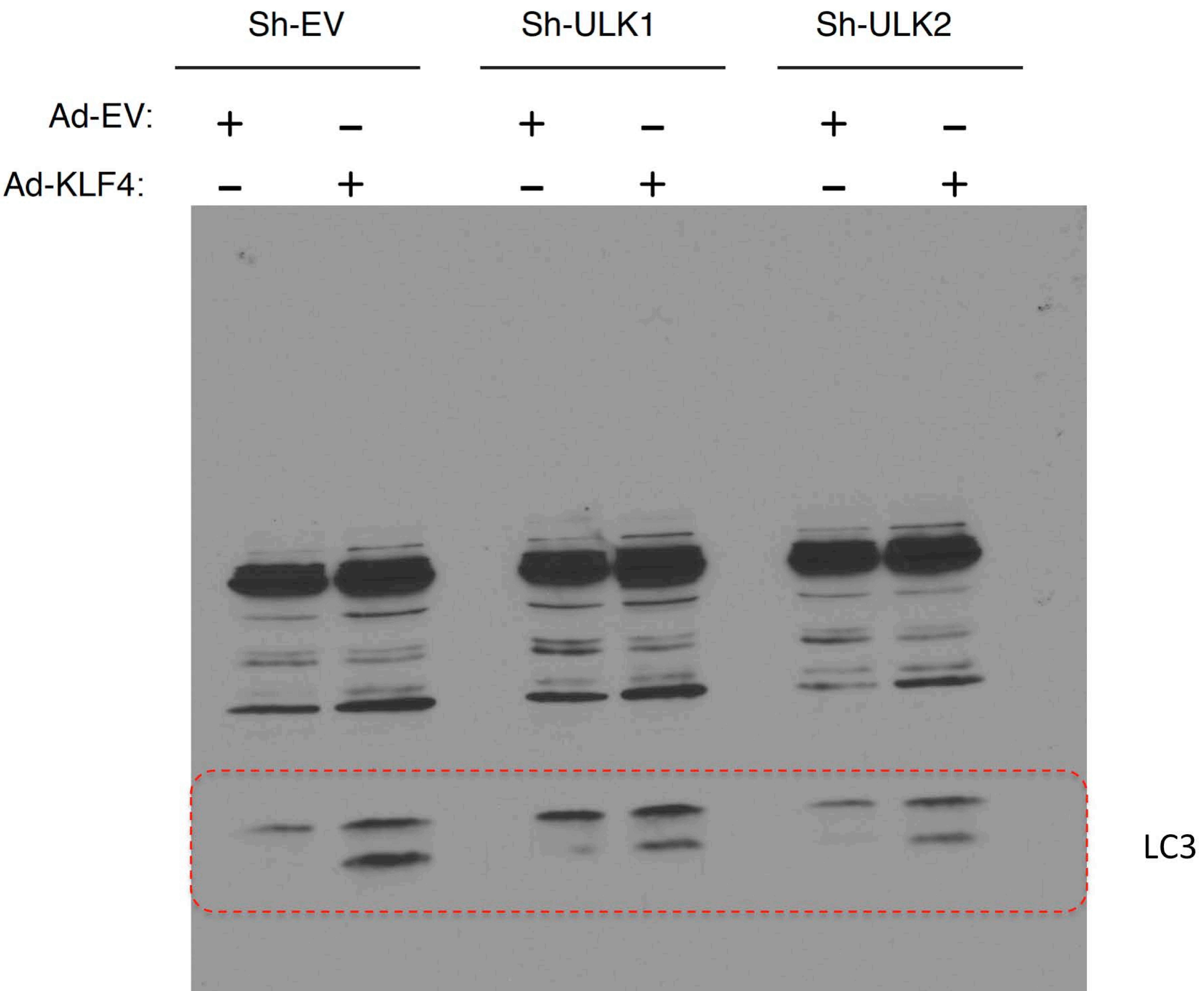


Total ACC

Full unedited gel for Supplementary Figure 12



Full unedited gel for Supplementary Figure 14D



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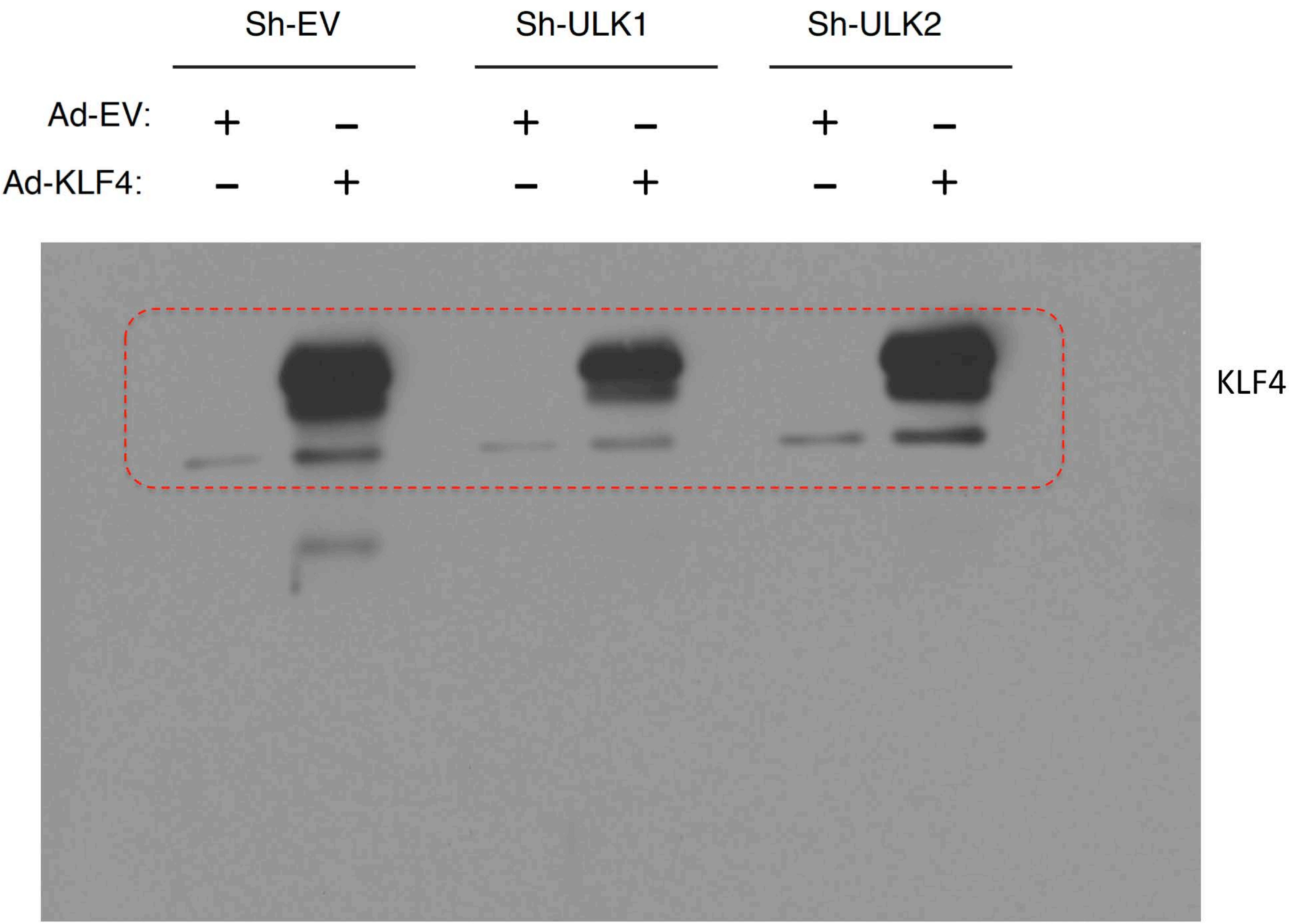

Full unedited gel for Supplementary Figure 14D