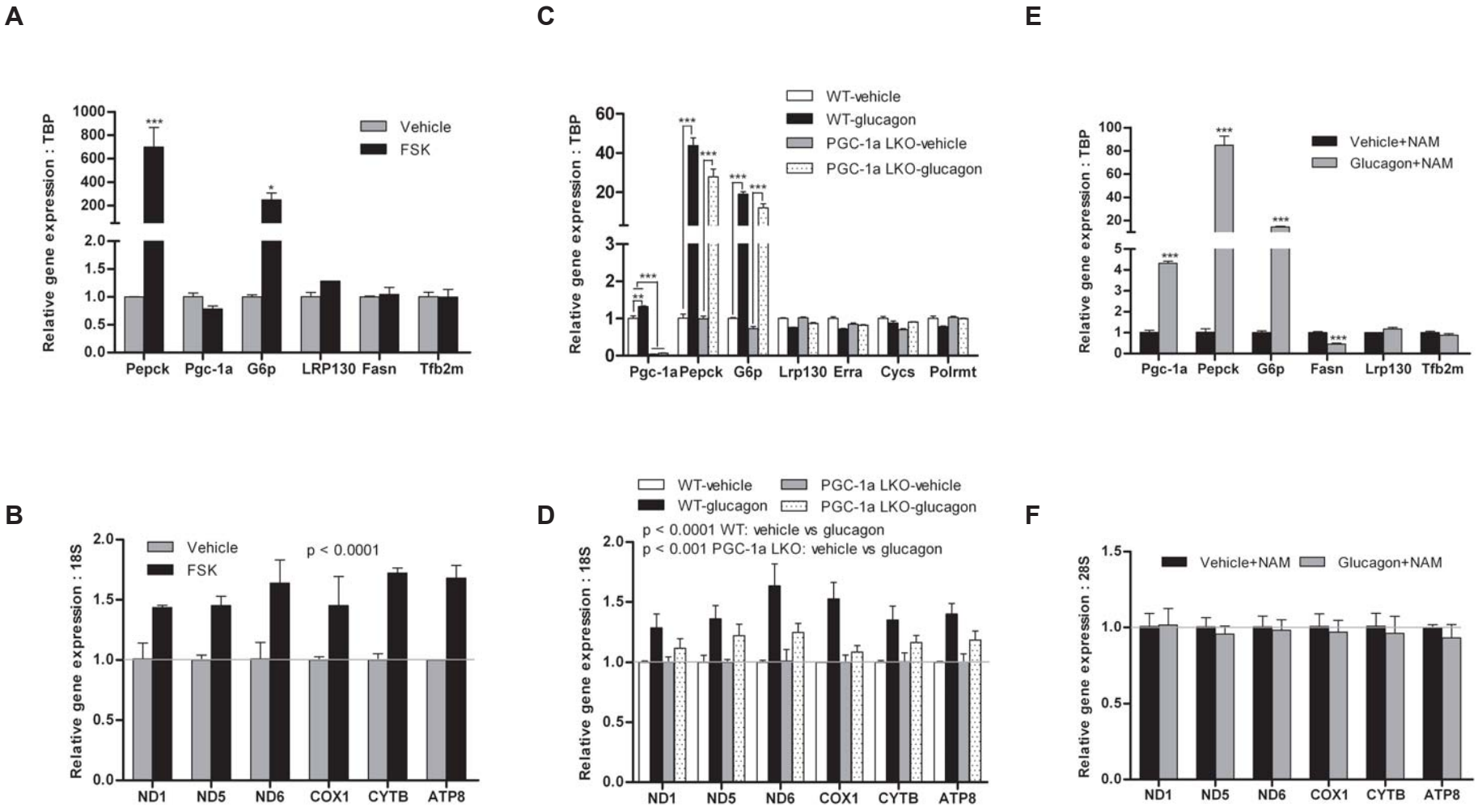
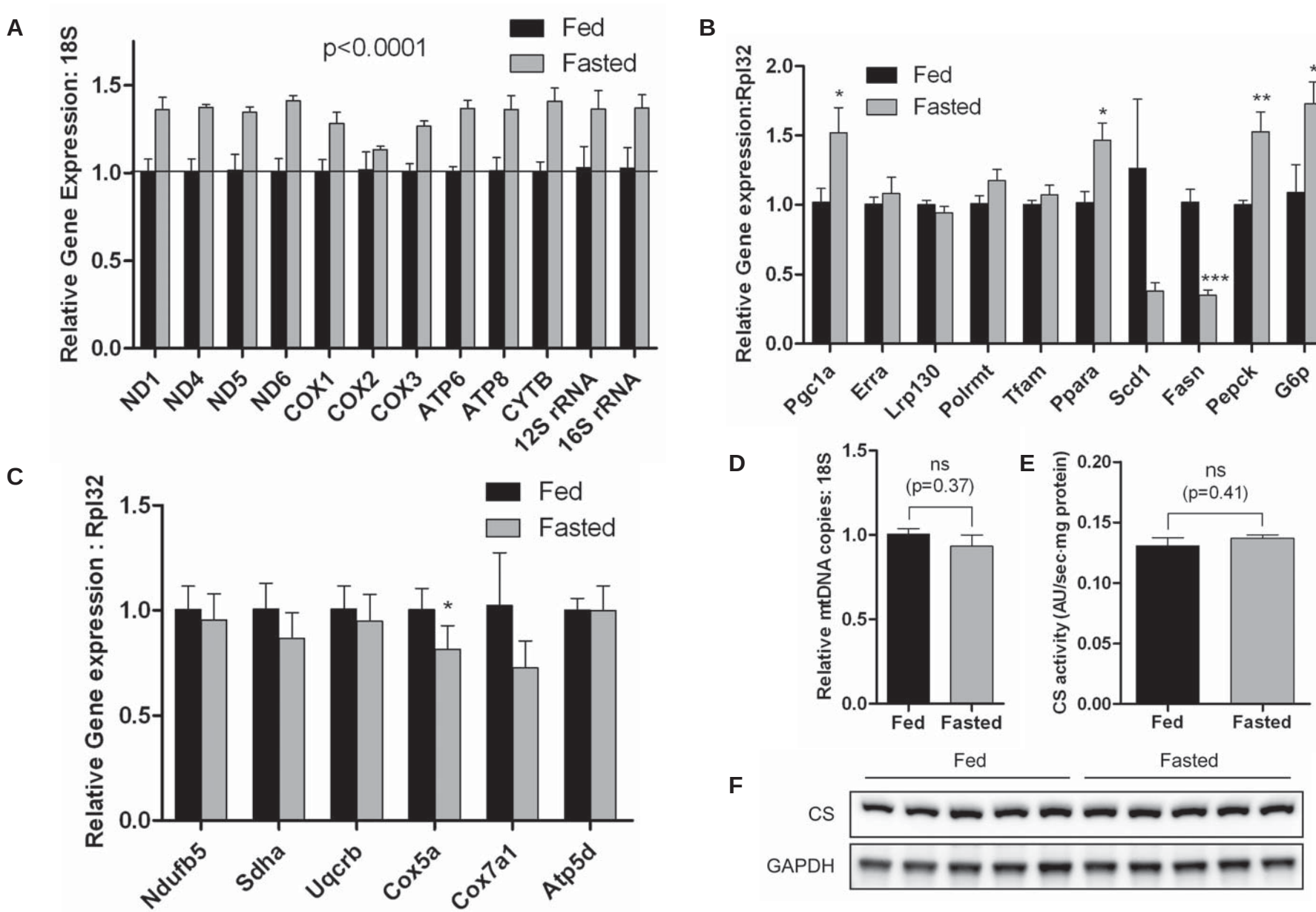
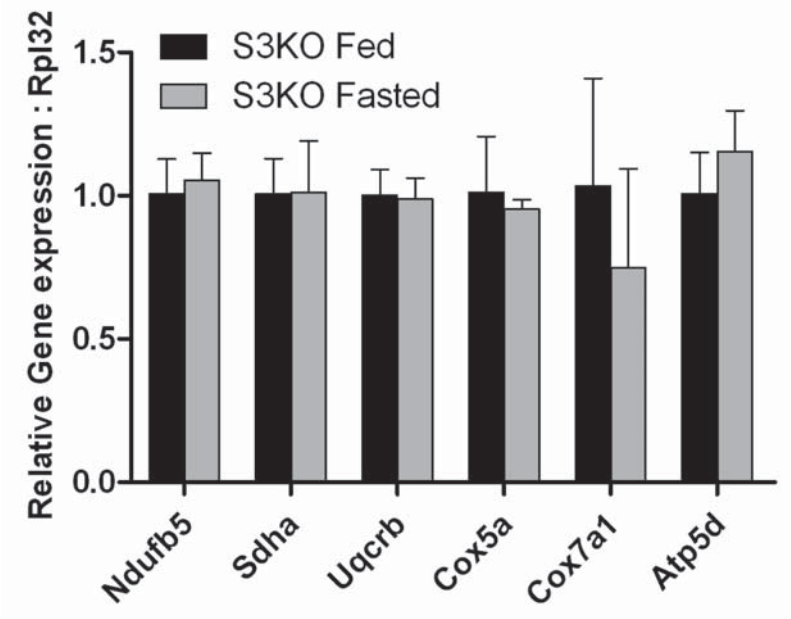


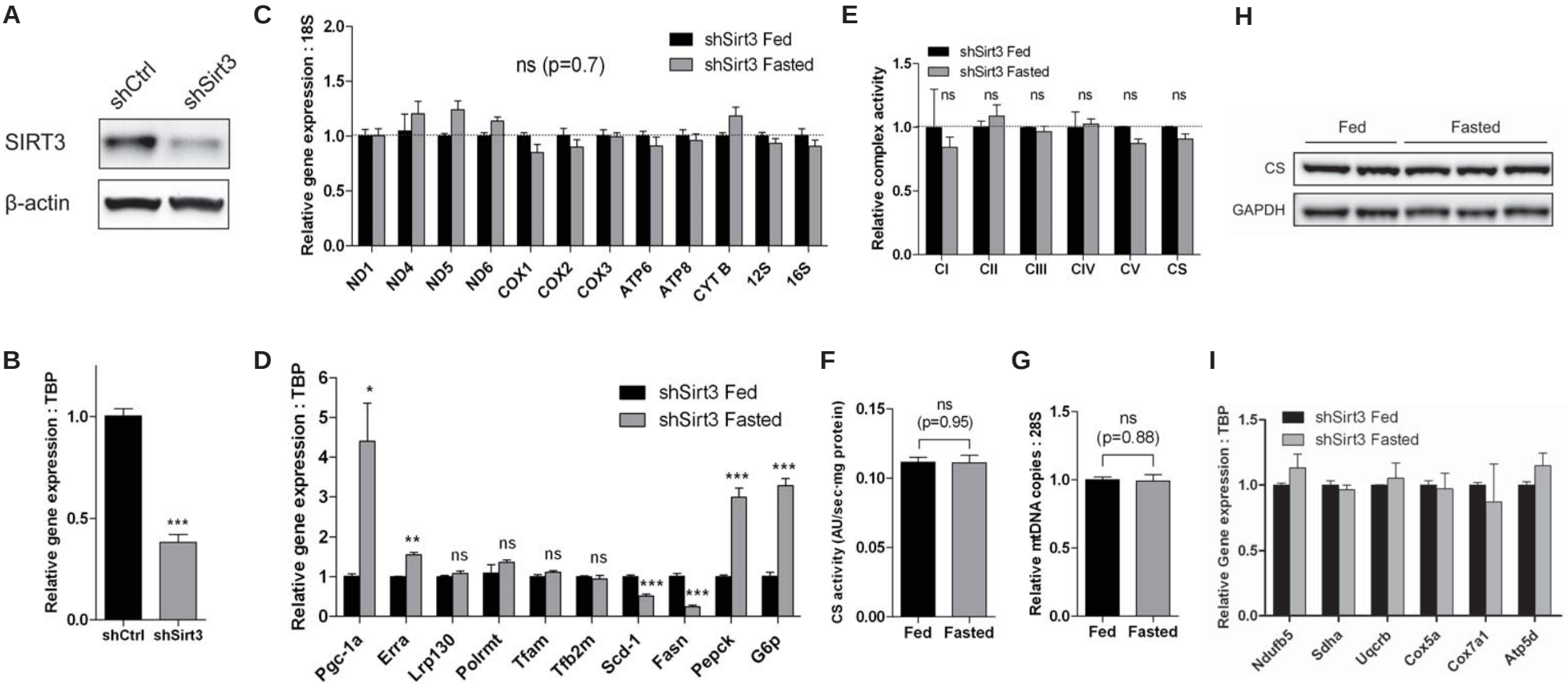
Supplementary Figure 1. cAMP signaling mediates induction of mitochondrially encoded genes, Pgc-1α is not required for induction of mitochondrially encoded gene expression but NAD+-dependent pathways are required. A) Following an 18 hour treatment with forskolin, which increases intra-cellular cAMP levels, Pepck and G6p, both of which are fasting responsive genes, were induced in primary hepatocytes. B) Treatment of primary hepatocytes with forskolin also induced mitochondrially encoded gene expression. C) In Pgc-1α null hepatocytes, glucagon induces fasting responsive genes similar to wild-type cells. D) In Pgc-1α null hepatocytes, glucagon still induces mitochondrially encoded gene expression; but, the induction is modestly blunted. Note: induction of mitochondrially encoded gene expression by forskolin was normal in primary hepatocytes in which Pgc-1α was knocked down more than 75% (data not shown). E) Nicotinamide an inhibitor of NAD+-dependent pathways did not alter glucagon mediated induction of fasting responsive genes; however, F) induction of mitochondrially encoded gene expression was completely abrogated (n=3). Two-way ANOVA for all studies. For nuclear encoded genes, a Bonferroni post test was also performed. *p<0.05, **p<0.01, ***p<0.001 (n=3).



Supplementary Figure 2. Fasting induces mitochondrially encoded genes in 129S mice. (A) Hepatic gene expression of mitochondrially encoded transcripts in 129S mice fasted for 24 hours (n=5). (B) Expression of genes that regulate mitochondrial biogenesis, mitochondrial transcription, lipogenesis and gluconeogenesis (n=5). (C) Expression of several nuclear encoded ETC genes. (D) Genetic assessment of mitochondrial content using mitochondrial DNA content (n=5). (E) Biochemical assessment of mitochondrial content using citrate synthase (CS) activity in whole liver homogenate (n=5). (F) Assessment of mitochondrial content using citrate synthase (CS) protein in whole liver homogenate (n=5). For gene expression, 2-way ANOVA with Bonferroni post test where indicated. (mean+s.e.m, *p<0.05, **p<0.01, ***p<0.001).

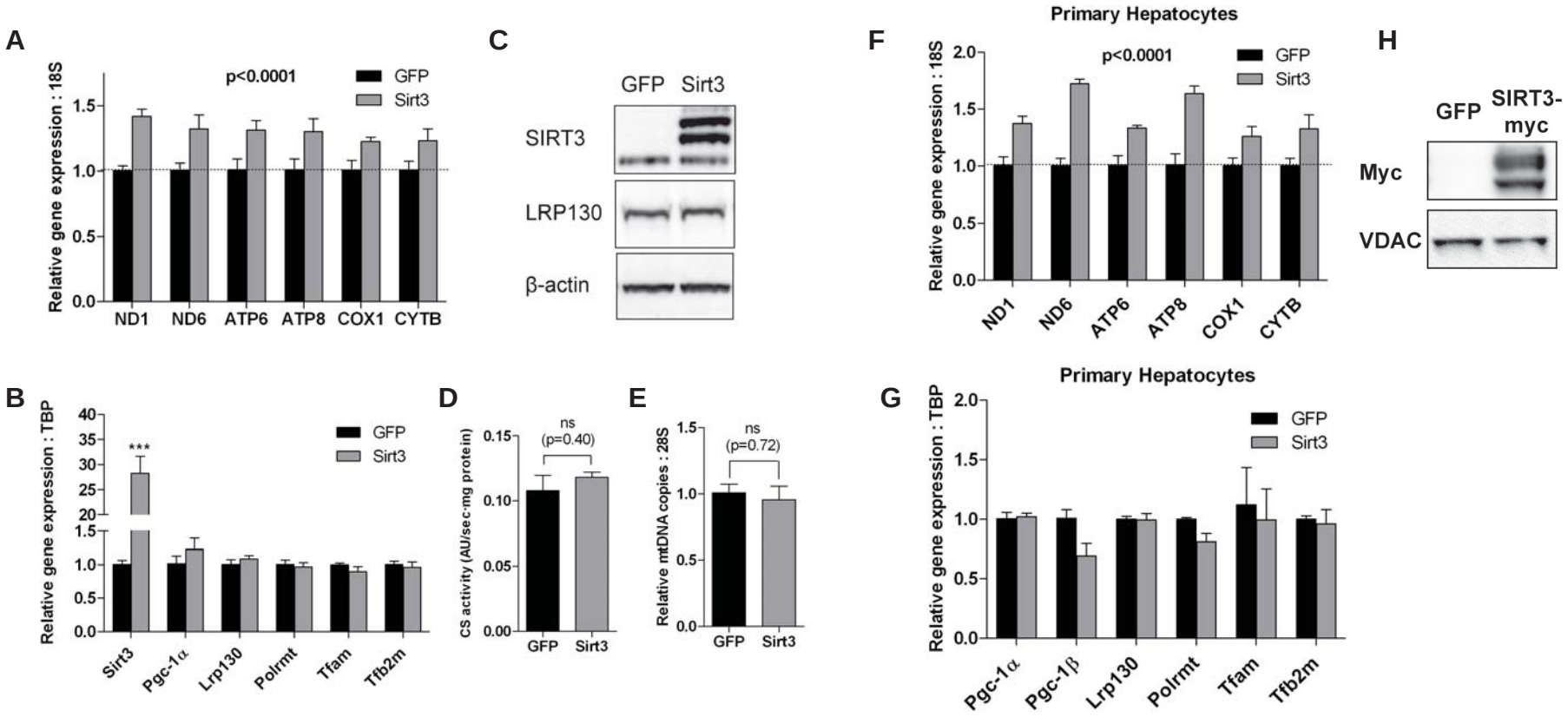


Supplementary Figure 3. Effect of fasting in Sirtuin 3 knockout mouse liver (S3KO) on a 129S mice background. Gene expression of several nuclear encoded mitochondrially encoded genes in sirtuin 3 knockout mouse liver (S3KO) in the fed or fasted state (n=3). For gene expression, 2-way ANOVA with Bonferroni post test (p=ns for all comparisons). Error bars represent mean±s.e.m.



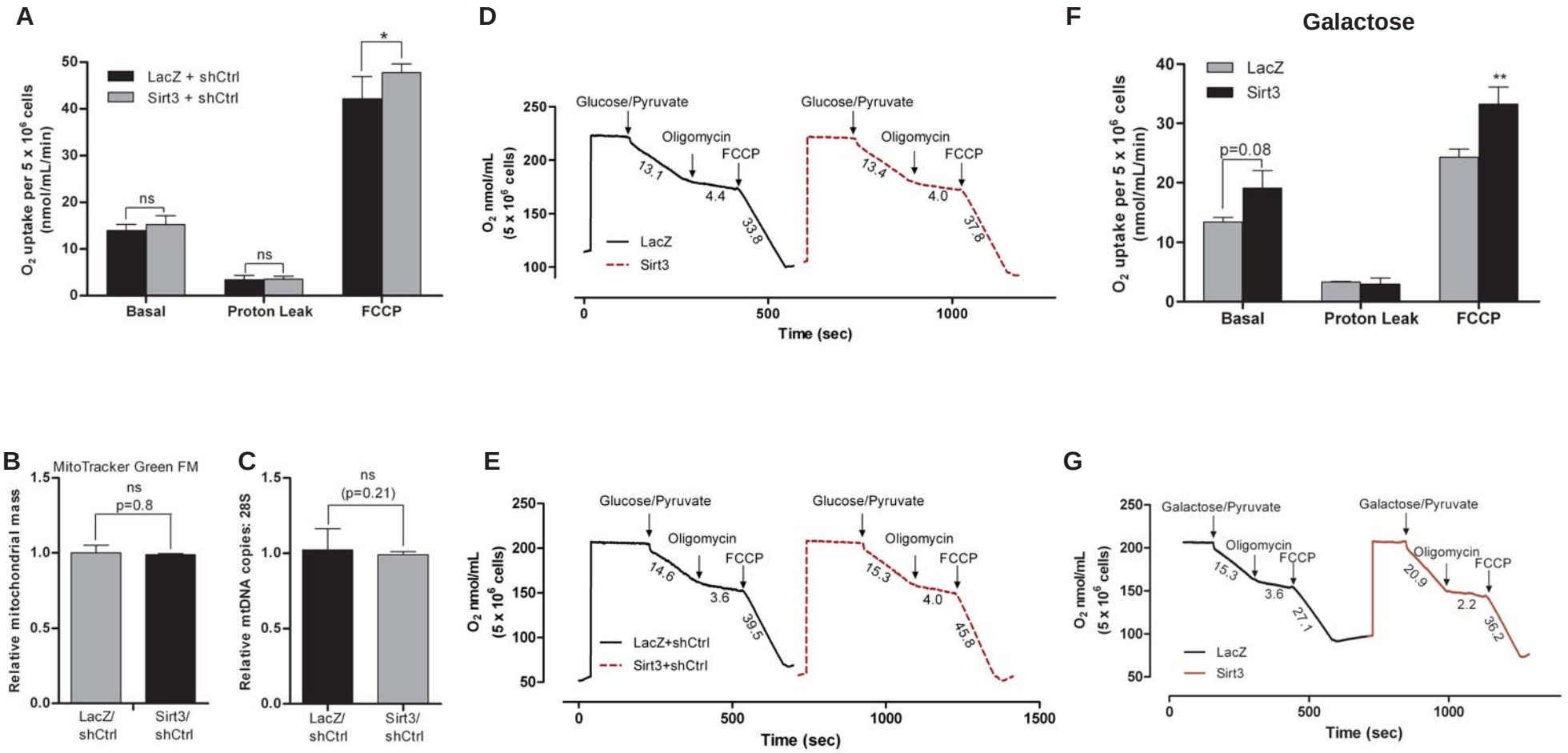
Supplementary Figure 4: In liver, knockdown of *Sirt3* in C57BL6 mouse liver impairs fasting-mediated induction of mitochondrially encoded genes and OXPHOS.

A, Protein expression in *Sirt3* deficient mouse liver. *Sirt3* knockdown was achieved by tail vein injecting adenovirus encoding shSirt3. Knockdown of SIRT3 protein in liver was confirmed by comparison with a control shRNA (shCtrl) (n=4). B, Gene expression of *Sirt3* following its knockdown in mouse liver (n=3). C, Hepatic gene expression of mitochondrially encoded transcripts in liver deficient for SIRT3. Mice were either in the fed state or fasted for 24 hours (n=3). D, Expression of genes that regulate mitochondrial biogenesis, mitochondrial transcription, lipogenesis and gluconeogenesis in liver deficient for SIRT3 (n=3). E, Complex activity of mitochondria isolated from shSirt3 mouse liver either in the fed state or after fasting for 24 hours (n=3). CI through CV denotes activities for complexes I through V. CS denotes citrate synthase . F, Biochemical assessment of mitochondrial content using citrate synthase activity in whole liver homogenate (n=3). G, Genetic assessment of mitochondrial content using mitochondrial DNA content (n=3). H, Citrate synthase (CS) immunoblot. I, Gene expression of several nuclear encoded electron transport chain subunits (n=3). For gene expression, 2-way ANOVA with Bonferroni post test where indicated. For complex activity and mitochondrial content two-tailed unpaired Student's t test. (mean+s.e.m, *p<0.05, **p<0.01, ***p<0.001)



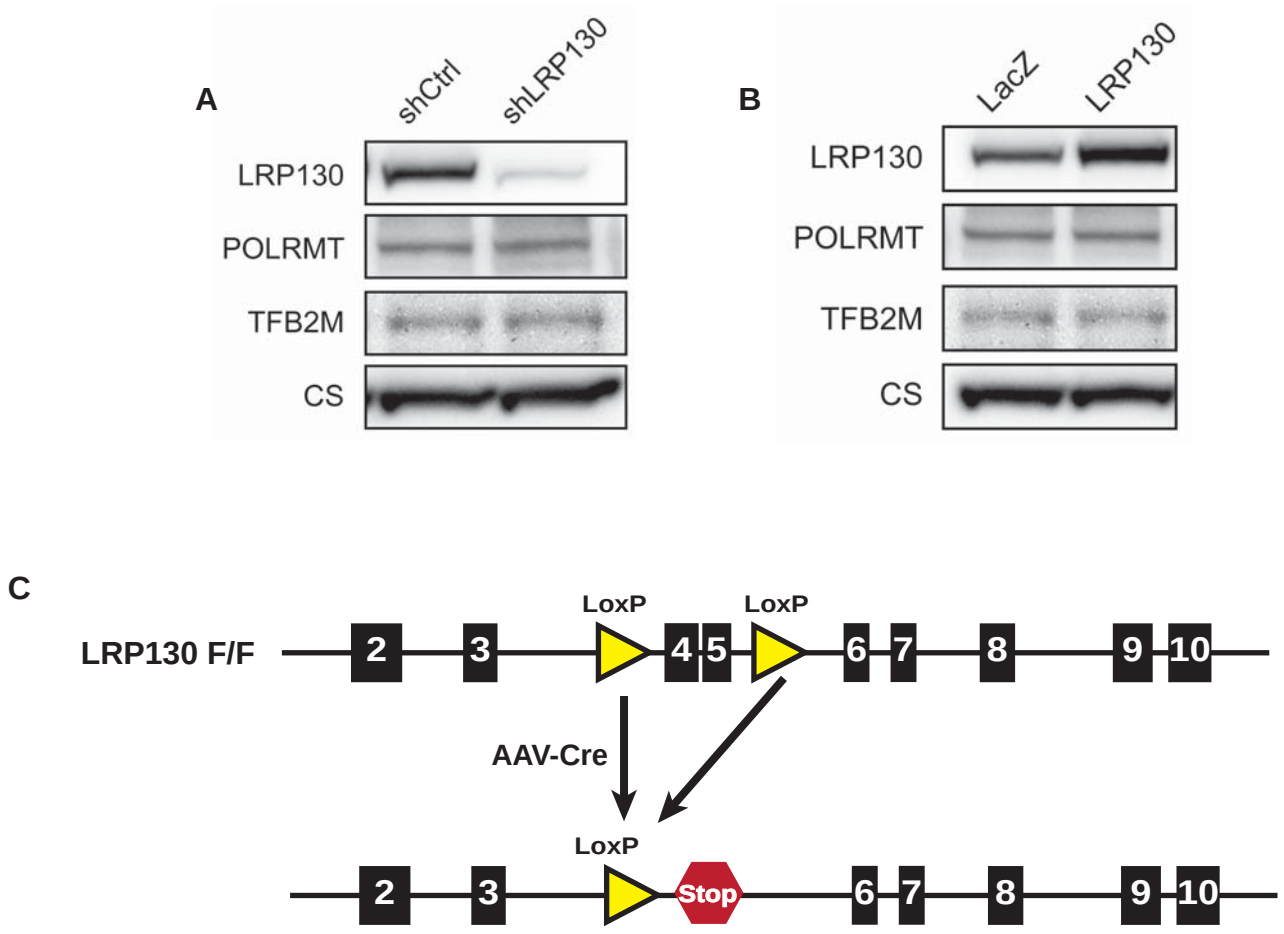
Supplementary Figure 5: Ectopic expression of SIRT3 in mouse liver and primary hepatocytes induces mitochondrially encoded transcripts.

A, Hepatic gene expression of mitochondrially encoded transcripts in mouse liver transduced with adenovirus encoding either GFP or Sirt3 (n=4). B, Expression of genes that influence mitochondrial biogenesis and mitochondrial transcription (n=4). C, Immunoblot showing expression of ectopically expressed myc-tagged SIRT3 protein, following transduction of C57BL6 mouse liver with adenovirus. Note, ectopically expressed SIRT3 is myc-tagged, and thus, migrates at a slightly higher molecular weight. D, Biochemical assessment of mitochondrial content using citrate synthase activity of whole liver homogenate (n=4). E, Genetic assessment of mitochondrial content using mitochondrial DNA content (n=3). F, Gene expression of mitochondrially encoded transcripts in primary hepatocytes transduced with adenovirus encoding either GFP or Sirt3 (n=3). G, Expression of genes that influence mitochondrial biogenesis and mitochondrial transcription in primary hepatocytes (n=3). H, Immunoblot showing expression of ectopically expressed myc-tagged SIRT3 protein in primary hepatocytes. For gene expression, 2-way ANOVA with Bonferroni post test where indicated. For mitochondrial content, two-tailed unpaired Student's t test. (mean+s.e.m, ***p<0.001).

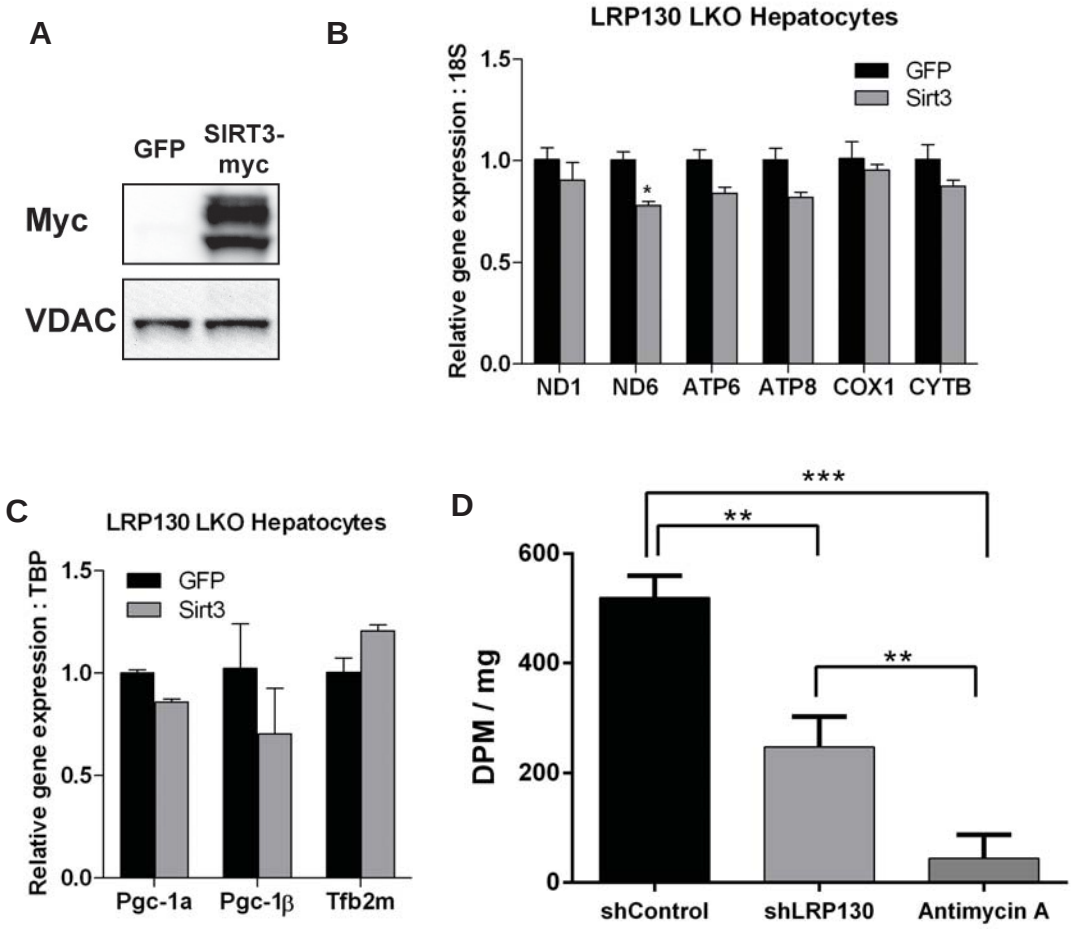


Supplementary Figure 6: Respiration and mitochondrial content in H2.35 hepatoma cells with ectopic expression of *Sirt3*.

A, Cellular respiration in shControl H2.35 hepatoma cells replete with sirtuin 3 (Sirt3). Two-tailed unpaired Student's t test. (n=3-4, mean±std, *p < 0.05). B, MitoTracker Green, a measure of mitochondrial biogenesis, was assessed in H2.35 hepatoma cells replete with sirtuin 3 (Sirt3) that co-express shControl RNA (shCtrl). (n=3, mean±s.e.m.). C, Mitochondrial DNA content, a measure of mitochondrial content, was quantified in H2.35 hepatoma cells replete with sirtuin 3 (Sirt3) that co-express shControl RNA (shCtrl). Two-tailed unpaired Student's t test. (mean±s.e.m, *p<0.05). Representative oxygen consumption curves for (D) H2.35 heptoma cells expressing LacZ or Sirt3 as shown in Figure 3J and (E) those that co-express shControl RNA (shCtrl) as shown here in Fig. S6A. (F) Cellular respiration using galactose in H2.35 hepatoma cells that ectopically express LacZ or sirtuin 3 (Sirt3). Two-tailed unpaired Student's t test. (n=3-4, mean±std, *p < 0.05). Two hours prior to cell collection, medium was changed to galactose containing medium. Respiration was performed as described in materials and methods but galactose was used in *in lieu* of glucose. (G) Representative oxygen consumption curves for galactose respiration studies.



Supplementary Figure 7. Effect of LRP130 protein level on the basal transcription machinery and a schematic of the LRP130 floxed allele. A) Immunoblot of mitochondria isolated from H2.35 hepatoma cells, showing that deficiency of LRP130 does not alter the level of POLRMT or TFB2M protein. B) Immunoblot of mitochondria isolated from H2.35 hepatoma cells, showing that ectopic expression of LRP130 does not alter the level of POLRMT or TFB2M protein. C) Schematic of the floxed allele in LRP130 flox/flox (F/F) mice. To generate LRP130 liver-specific KO mice (LRP130 LKO), liver specific adeno-associated virus that expresses Cre recombinase (AAV-Cre) was tail vein injected into adult male LRP130 flox/flox mice of 8-12 weeks of age. Littermate control male wild-type mice were also injected with AAV-Cre.1 x 10(11) GC viral particles were tail vein injected per mouse. After 3 weeks, liver was harvested in either the fed or fasted state (Fig. 5H-K).



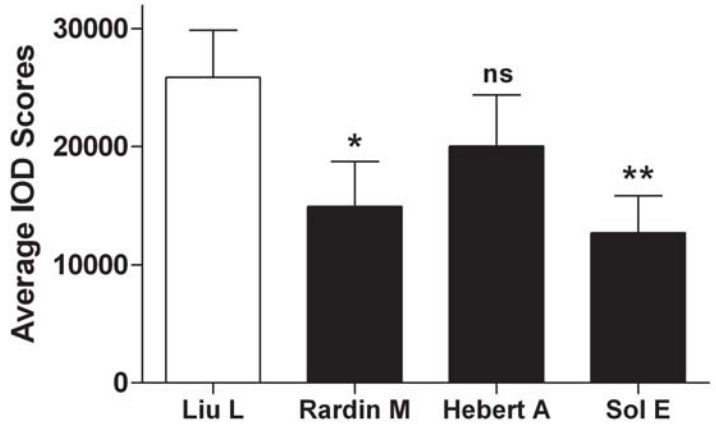
Supplementary Figure 8: Effect of ectopic expression of SIRT3 in LRP130 deficient cells.

A, Immunoblot showing expression of ectopically expressed myc-tagged SIRT3 protein in LRP130 KO hepatocytes. B, Gene expression of mitochondrially encoded transcripts in LRP130 KO hepatocytes transduced with adenovirus encoding either GFP or *Sirt3* (n=4). Note, in LRP130 KO hepatocytes, SIRT3 is no longer sufficient to induce mitochondrially encoded genes. C, Expression of genes that influence mitochondrial biogenesis and mitochondrial transcription (n=4). D, Fatty acid oxidation of radiolabeled ^{14}C-palmitate to CO_2 in H2.35 cells stably expressing sirtuin 3 and treated with NAD+ as describe in the methods section. Deficiency of LRP130 was associated with reduced fatty acid oxidation. Antimycin A, which inhibits the electron transport chain at complex III, serves as a positive control, showing nearly complete inhibition of fatty acid oxidation (n=3). In cells treated with niocotinamide there was no longer a difference between shControl (shCtrl) and shLRP130 cells (data not shown), suggesting strong interplay between sirtuin 3 and LRP130. Two-way ANOVA with Bonferroni post test where indicated. (mean±s.e.m, *p<0.05).

A

	Liu L	Rardin M	Hebert A	Sol E
Liu L	17*†			
Rardin M	2†	8		
Hebert A	3*	3	10	
Sol E	3*†	2	2	11

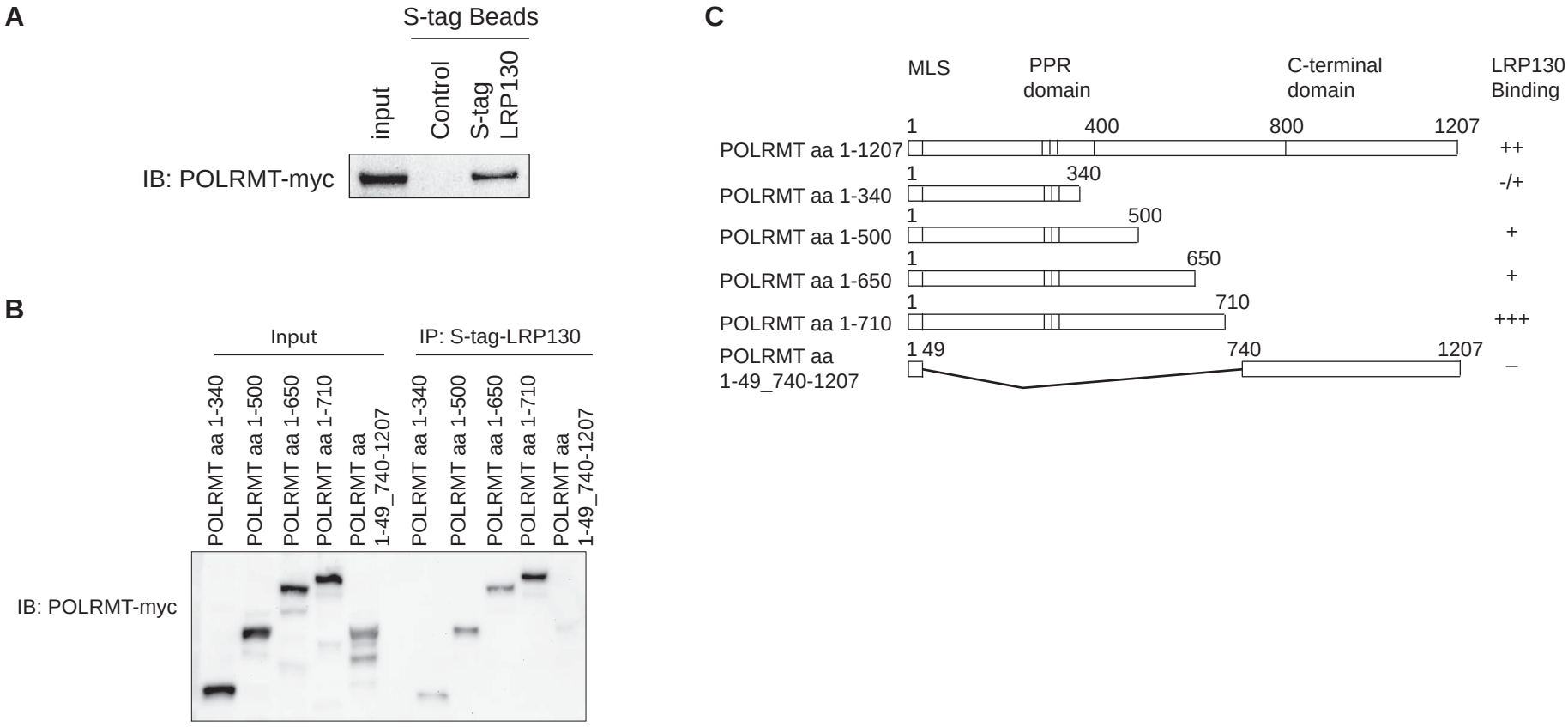
C



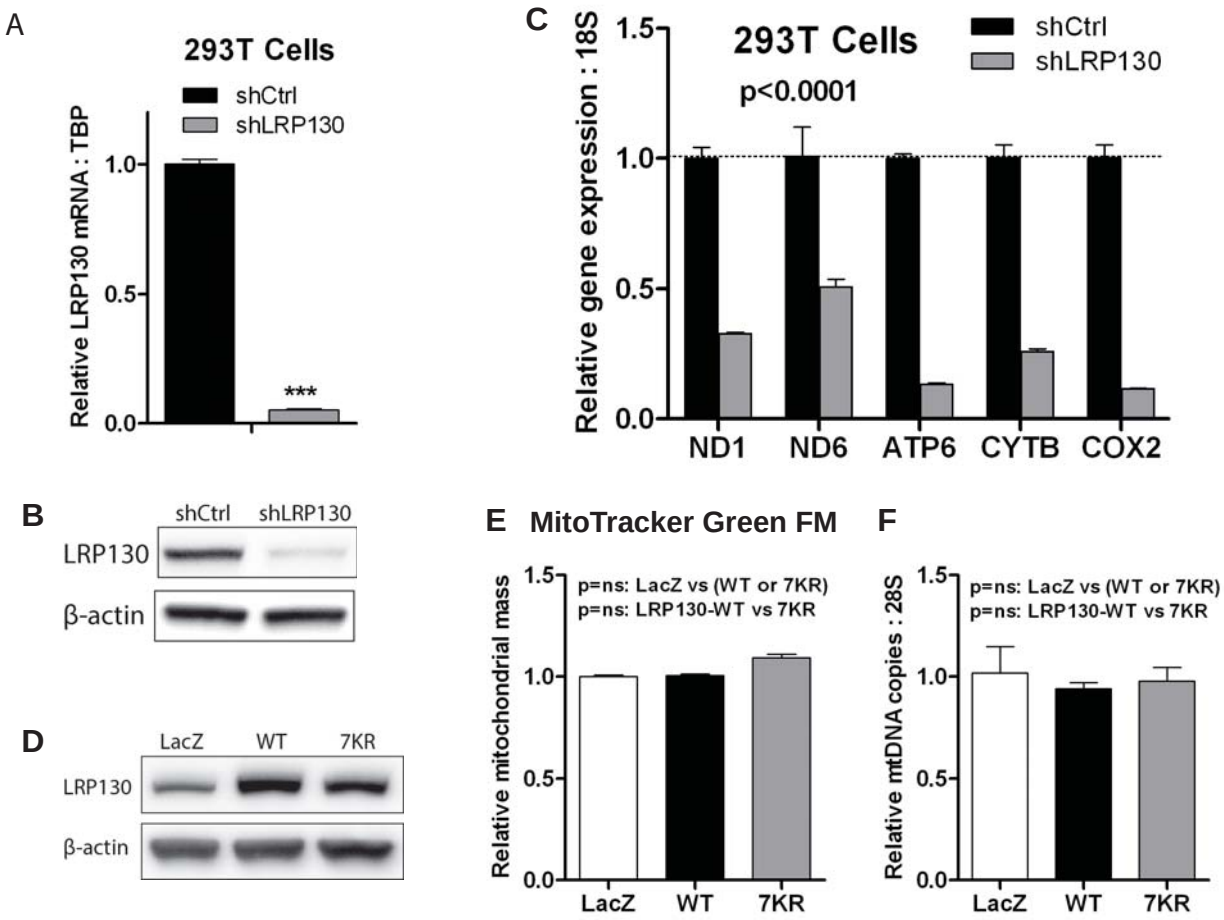
B

	Liu L	Rardin M	Hebert A	Sol E
Liu L	**17**			
Rardin M	**225, 749**	**8**		
Hebert A	**867, 1036, 1048**	**186, 291, 462**	**10**	
Sol E	**749, 867**	**291, 749**	**291, 867**	**11**

Supplementary Figure 9. Comparison of acetylated lysines in LRP130 (LRPPRC) across various studies. A) Pair wise overlap of acetylated lysine sites in this study (Liu L) compared with other studies that ablated sirtuin 3 in cells or mouse liver. Gray indicates the number of unique acetylated lysine peptides of LRP130 (LRPPRC) identified in a particular study. Blue represents the number of peptides common between two studies. *Indicates a unique site identified across three separate studies. †indicates another unique site shared across three separate studies. Using a hypergeometric distribution, the probability that shared acetylated sites between two or more studies arose from a non-random (biological) process was greater than 80% across all studies (see materials and methods for mathematical formula and derivation used). B) Acetylated lysine residues shared across studies shown in panel A. For simplicity, mouse residues are reported for all studies, irrespective of whether or not the study was performed using mouse or human samples.C) Average IOD (integrated optical density) binding scores established by Smith BC et al 2011 (ACS Chem. Biol.) was compared across studies. A high score indicates greater affinity for SIRT3.

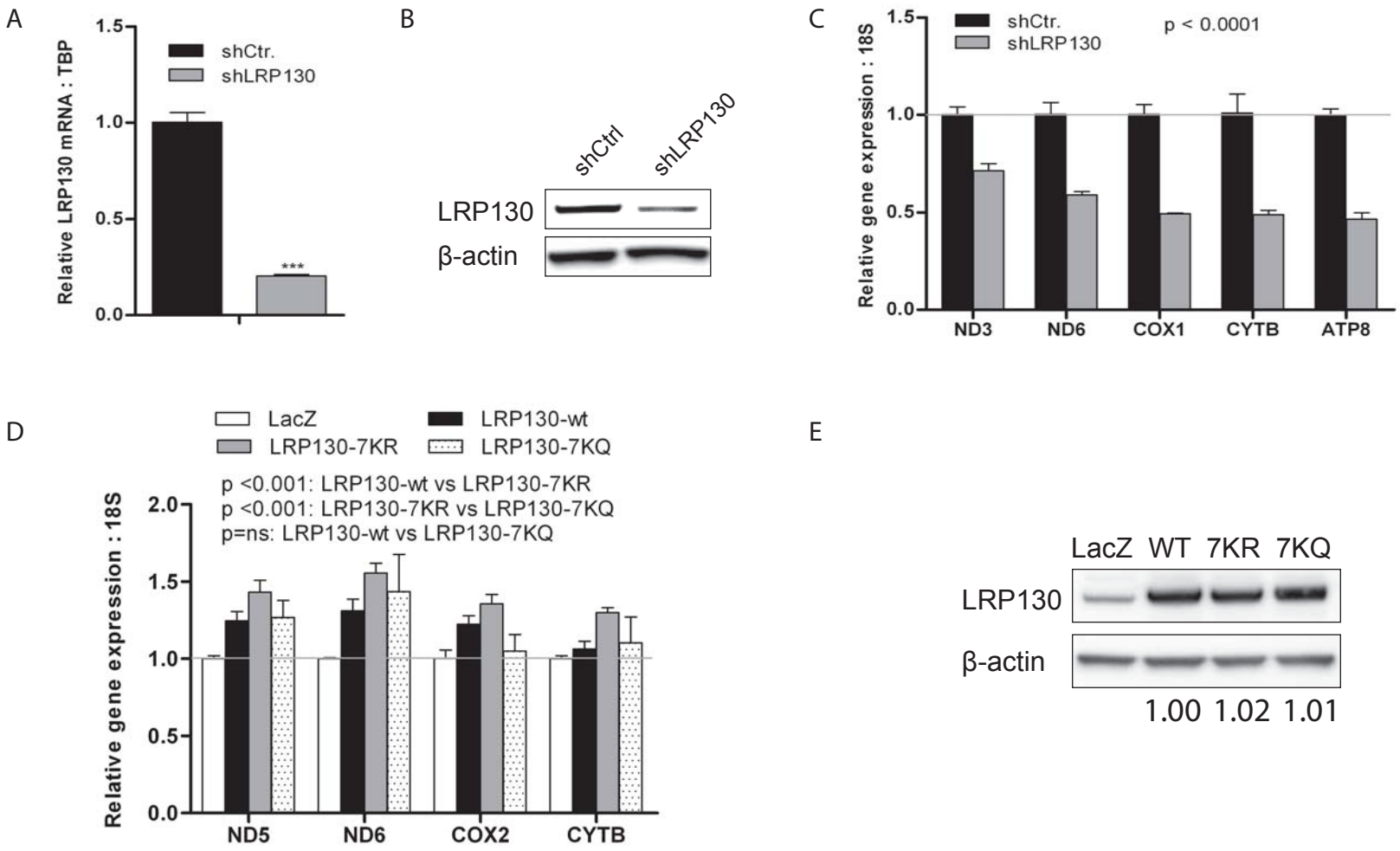


Supplementary Figure 10. Mapping of the interaction between POLRMT and LRP130 (LRPPRC). A) Immunoblot showing the interaction between *in vitro* translated POLRMT bearing a C-terminal myc tag and purified LRP130 protein containing an S-Tag. B) Immunoblot of various fragments of POLRMT and their level of interaction with S-tagged full length purified LRP130 protein. C) Schematic summarizing the interactions shown in (B).



Supplementary Figure 11: Knock-down of human LRP130 in 293T cells and reconstitution with mouse wild-type LRP130 or the LRP130 7KR mutant.

A, Using retrovirus, human LRP130 was stably knocked-down in 293T cells. The shRNA construct targeting human LRP130 does not affect murine LRP130 (data not shown). B, Immunoblot confirming greater than 95% knock down of human *LRP130*. C, As expected, 293T cells deficient for LRP130 have reduced expression of mitochondrially encoded genes. D, Transient transfection of LacZ, murine wild-type LRP130 or the 7KR into 293T cells lacking human LRP130. A long exposure permitted comparison of the level of ectopically expressed murine LRP130 compared with the remaining endogenous human LRP130. Based on the knock-down of human LRP130, reconstitution with murine LRP130 is within a physiological range. E, Fluorescent assessment of mitochondrial content using MitoTracker Green FM (n=3). F, Genetic assessment of mitochondrial content using mitochondrial DNA content (n=3). For gene expression, Two-way ANOVA. For mitochondrial content, two-tailed unpaired Student's t test. (mean+s.e.m, ***p<0.001).



Supplementary Figure 12: Knock-down of human LRP130 in 293T cells and reconstitution with mouse wild-type LRP130 or the LRP130 7KQ mutant.

A, Using transient transfection of a plasmid bearing an shRNA construct targeted to human *LRP130*, human *LRP130* was knocked down in 293T cells. The shRNA construct targeting human *LRP130* does not affect murine *Lrp130* (data not shown). B, Immunoblot confirming knock-down of human LRP130. C, As expected, 293T cells deficient for LRP130 have reduced expression of mitochondrially encoded genes (n=3). D, Gene expression following transient transfection of LacZ, murine wild-type LRP130, 7KR mutant and the 7KQ mutant into 293T cells deficient for human LRP130 (n=3). E, A long exposure immunoblot permitted comparison of the level of ectopically expressed murine LRP130 compared with remaining endogenous human LRP130.

Supplementary Table 1. Mass spectrometry intensities for lysines in murine LRP130 sensitive to deacetylation by SIRT3.

Lysine	Ac-Ctrl	SIRT3	Rel Ac	Sequence	Species
225	148,400	37,700	0.25	G F M K T K D L P I T	Mouse
				G F M K T K D L P V T	Human
				G F M K T K D L P V T	Bovine
				G F M K T K D L P I T	Pig
				G F M K S K D L P I T	Chicken
452	58,790	9,759	0.17	G H Q K T K N V Q G I	Mouse
				G R R K E K N V Q G I	Human
				G H Q K E K N V Q G I	Bovine
				G Y Q K E K N V Q G I	Pig
				G F Q K E K N L K G V	Chicken
671	341,300	29,490	0.09	T L E K L K A E G Q P	Mouse
				T L E T L K A E N Q P	Human
				K L E K L K A E N Q P	Bovine
				K L E K L K S E N Q P	Pig
				K L E K R K A E N Q P	Chicken
749	131,800	8,111	0.06	I L D T A K Y V A L V	Mouse
				V L D T G K Y V G L V	Human
				V L D T G K Y V R L V	Bovine
				V L D T G K Y L G L V	Pig
				A L D S G K Y I A L V	Chicken
867	202,000	29,620	0.15	C K L V E K G E T D L	Mouse
				C K L V E K G E T D L	Human
				C K L I E K G E T E L	Bovine
				C R L I E K G K T E L	Pig
				C R L I E K G D T E L	Chicken
979	568,100	92,830	0.16	D A A W T K M Q E E N	Mouse
				D A V W N K I Q E E N	Human
				D A V W N K M Q E E N	Bovine
				D A V W N K M Q E E N	Pig
				E A V W T K I Q E E N	Chicken
1000	291,200	22,170	0.08	L A E I L K T S N Q E	Mouse
				L A E I L R E G N Q E	Human
				L A E I L R N N N Q D	Bovine
				L A E I L R N S N Q E	Pig
				L A D I F E K N G Q V	Chicken
1036	1,160,000	25,000	0.02	E D V T E K T L L S N	Mouse
				E P D F Q K D I L I A	Human
				E V N L Q K E L L N A	Bovine
				Q G N L Q K E L L K A	Pig
				E - - - E R K I R M L	Chicken
1048	2,007,000	165,000	0.08	K L K K S K D A Y N I	Mouse
				R L N Q K K G A Y D I	Human
				R T R R N K D A F N I	Bovine
				R K R K N R D A F N I	Pig
				K K N S A R E A Y N V	Chicken

Lysine	Ac-Ctrl	SIRT3	Rel Ac	Sequence	Species
1059	94,900	11,700	0.12	F L K A E K Q N V V F	Mouse
				F L N A K E Q N I V F	Human
				F L T A K K Q N I V F	Bovine
				F L K A K R Q N I V F	Pig
				F L K N Q G K - S D Y	Chicken
1174	4,216,000	567,300	0.13	- I G L S K M V F I N	Mouse
				S I G L S K M V F I N	Human
				S I G L S R M V F I N	Bovine
				S I G L S R M V F I N	Pig
				S I G L S P S L I S N	Chicken
1187	767,100	116,000	0.15	A L A Q M K N N K L D	Mouse
				A L A Q I K N N N I D	Human
				A L A Q I K N N N I D	Bovine
				A L A Q I K N N D I D	Pig
				A L A H T N N N D L D	Chicken
1250	373,700	11,900	0.03	Q F A L Y K P V T D L	Mouse
				Q F A I Y K P V T D F	Human
				Q F A V Y K P V T D L	Bovine
				Q F A V Y K P V T D L	Pig
				Q F G I Y R P V T D L	Chicken
1336	72,222,000	32,967,000	0.46	D V A S A K A L Y E Y	Mouse
				D V T S A K A L Y E H	Human
				D V A S A K A L Y E S	Bovine
				D V T S A K E L Y E N	Pig
				D V A S V K A V Y E K	Chicken
1348	1,950,000	39,600	0.02	T A K N L K L D D L F	Mouse
				T A K N T K L D D L F	Human
				T A K N V K L N D L F	Bovine
				T A K D T K L N D L F	Pig
				K E K N I Q L P E L S	Chicken
1355	1,334,000	84,900	0.06	D D L F L K R Y A A L	Mouse
				D D L F L K R Y A S L	Human
				N D L F L K R Y A V L	Bovine
				N D L F L K R Y A V L	Pig
				P E L S L K S L A A F	Chicken
1385	1,788,000	28,000	0.02	Y I K Q L K E A R E S	Mouse
				Y A Q Q L R K L R E N	Human
				Y A K Q L K E S K E T	Bovine
				Y A K Q L K E S K E N	Pig
				Y V E E W R K R R L E	Chicken

Shown in columns 2 and 3 are mass spectrometry intensities for lysines in murine LRP130 sensitive to deacetylation by SIRT3, that is, those sites showing less than 50% acetylation when treated with SIRT3 and NAD^+. 'Rel Ac' denotes relative acetylation, derived by dividing the intensity of the SIRT3 sample by the acetylated control sample (Ac-Ctrl). Bolded lysine positions in column 1 were mutated in this study, generating a 7KR LRP130 mutatnt. Highlighted in light gray are lysine residues in mouse and various other species. In some species, lysine residues were replaced with arginine residues, which mimic deacetylation and are highlighted in dark gray.

Supplementary Table 2. Murine primers used for RT-qPCR.

Primer	Forward (5' -> 3')	Reverse (5' -> 3')
12S (Rnr1)	CCCCGCTCTACCTCACCAT	AATACCTTTTTAGGGTTTGCTGAAGA
16S (Rnr2)	GCCTGCCCAGTGACTAAAGTTT	AACAAGTGATTATGCTACCTTTGCA
18S (Rn18s)	AGTCCCTGCCCTTTGTACACA	CGATCCGAGGGCCTCACTA
28S (Rn28s1)	GAATCCGCTAAGGAGTGTGTAACA	CTCCAGCGCCATCCATTT
36B4 (Rplp0)	TGCAGATCGGGTACCCAACT	ACGCGCTTGTACCCATTGA
ATP6	AATTACAGGCTTCCGACACAAAC	TGGAATTAGTGAAATTGGAGTTCCT
ATP8	GCCACAACTAGATACATCAACATGATT	GGTTGTTAGTGATTTTGGTGAAGGT
COX1	TTTTCAGGCTTCACCCTAGATGA	CCTACGAATATGATGGCGAAGTG
COX2	TGAAGACGTCCTCCACTCATGA	GCCTGGGATGGCATCAGTT
COX3	GCAGGATTCTTCTGAGCGTTCT	GTCAGCAGCCTCCTAGATCATGT
CYTB	AGACAACTACATACCAGCTAATCCACTAA	GAATGGCGTATGCAAATAGGAAA
Erra (Esrra)	GCAGGGCAGTGGGAAGCTA	CCTCTTGAAGAAGGCTTTGCA
Fasn	CGGGTTCGTGAAACTGATAAA	CATGGTTGACAGCAAAATGG
G6p (G6pc)	ATGACTTTGGGATCCAGTCG	TGGAACCAGATGGGAAAGAG
Hprt	TGGCCATCTGCCTAGTAAAGC	GGCTCATAGTGCAAATCAAAAGTC
Lrp130 (Lrpprc)	TTCAGTGCTCTCGTCACAGG	GTCGCGGTCCATGAAGTAAT
ND1	CCCCTTCGACCTGACAGAAG	GGGCCGGCTGCGTATT
ND4	ATCACTCCTATTCTGCCTAGCAAAC	GAAGTCCTCGGGCCATAATTATAGT
ND5	CGGACGAACAGACGCAAATA	CAAACTATAGCTAAAATGAATCCGATGT
ND6	ACAAAGATCACCCAGCTACTACCAT	TTGATGATGTTGGAGTTATGTTGGA
Pepck (Pck1)	CATATGCTGATCCTGGGCATAAC	CAAACTTCATCCAGGCAATGTC
Pgc-1a (Ppargc1a)	GCCGTGTGATTTACGTTGGTAA	AAAACTTCAAAGCGGTCTCTCAA
Pgc-1b (Ppargc1b)	GCCTCTCCAGGCAGGTTCA	TAGAGAACTCAGTCCAGAAGGCTTT
Polrmt	TCTTCAAAAGTCTACAGGAGATGTTCAC	TGAGGTTGGCACTCTCAGTCA
Rpl32	CGCAAGTTCCTGGTCCACAATGTC	GCTCTTTCTACGATGGCTTTTCGG
Sirt3	TACAGGCCCAATGTCACTCA	ACAGACCGTGCATGTAGCTG
Tbp	ACCCTTCACCAATGACTCCTATG	TGACTGCAGCAAATCGCTTGG
Tfam	CCGAAGTGTTTTTCCAGCAT	GGCTGCAATTTTCCTAACCA
Tfb2m	AGAGCCGTTGCCTGATTCTG	CCGATCGATTCCTGGATGTC

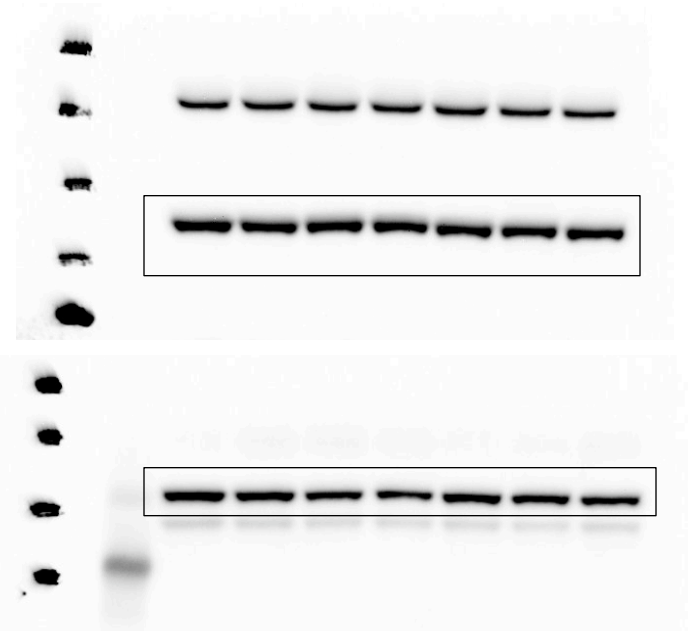
Where indicated official gene symbols are shown in brackets.

Supplementary Table 3. Human primers used for RT-qPCR

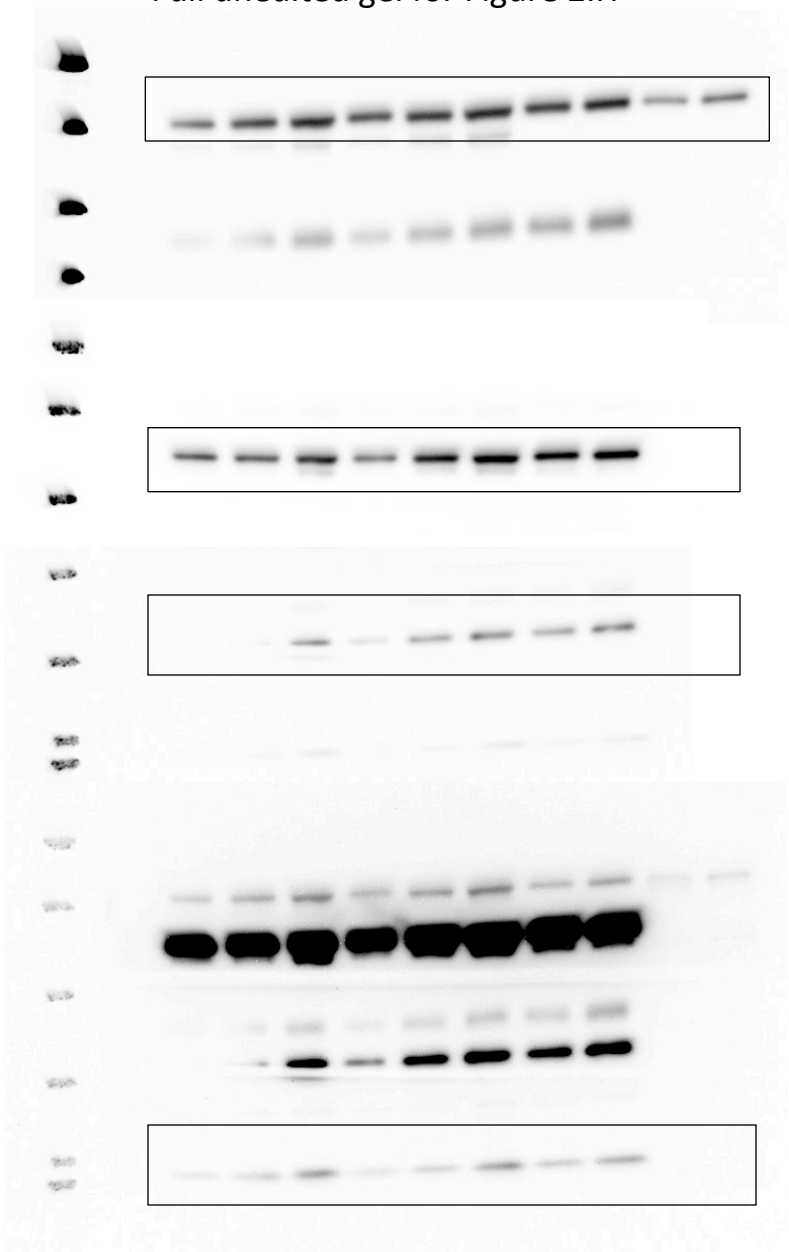
Primer	Forward (5' -> 3')	Reverse (5' -> 3')
ND1	CCCTAAAACCCGCCACATCT	GAGCGATGGTGAGAGCTAAGGT
ND2	GACATCCGGCCTGCTTCTT	TACGTTTAGTGAGGGAGAGATTTGG
ND6	CCCCGAGCAATCTCAATTACA	TGATTATGGGCGTTGATTAGTAGTAGTT
COX2	CCGACTACGGCGGACTAATC	CGCCTGGTTCTAGGAATAATGG
ATP8	CCCTCACCAAAGCCCATAAA	GAATGAAGCGAACAGATTTTCGT
CYTB	AACCGCCTTTTCATCAATCG	AGCGGATGATTCAGCCATAATT
TBP	GCACAGGAGCCAAGAGTGAA	TCACAGCTCCCCACCATGTT
18S (RNA18S5)	CGCAGCTAGGAATAATGGAATAGG	CATGGCCTCAGTTCCGAAA
28S (RNA28S5)	CCCAGTGCTCTGAATGTCAA	ATGACGAGGCATTTGGCTAC
36B4 (RPLP0)	GCGACCTGGAAGTCCAACTA	TGTCTGCTCCCACAATGAAA
LRP130 (LRPPRC)	CGAGGACCGACGGAAGCT	AATGCTCCTCCTTGGCCTGTA

Where indicated official gene symbols are shown in brackets.

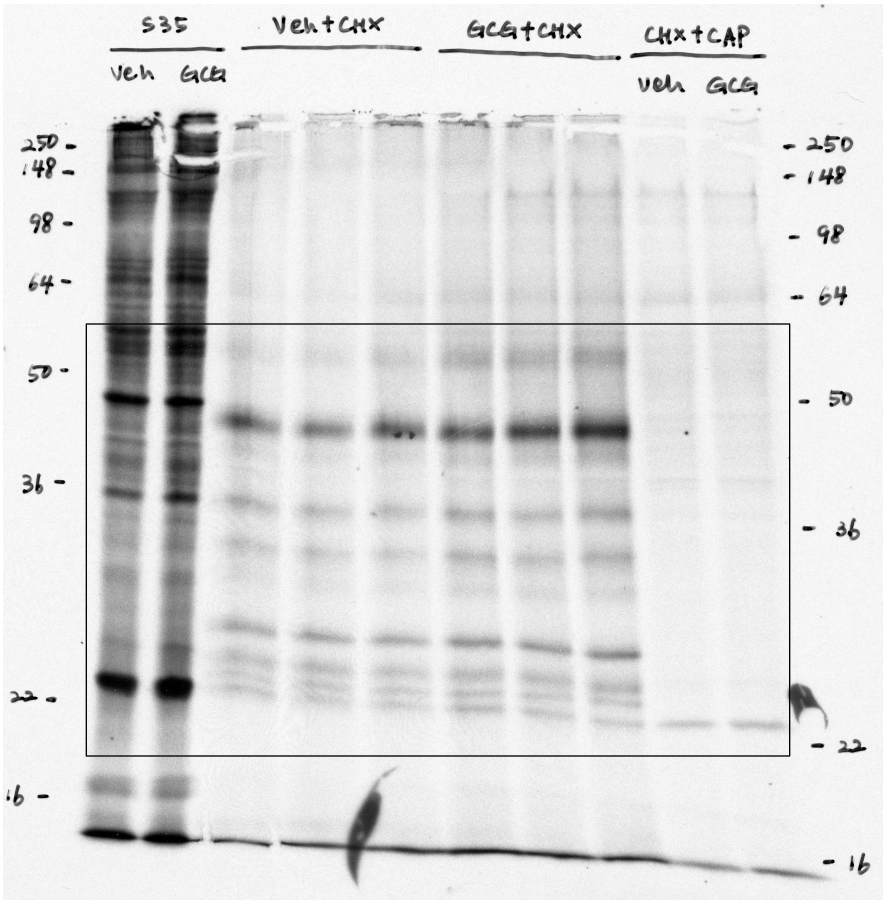
Full unedited gel for Figure 1.F



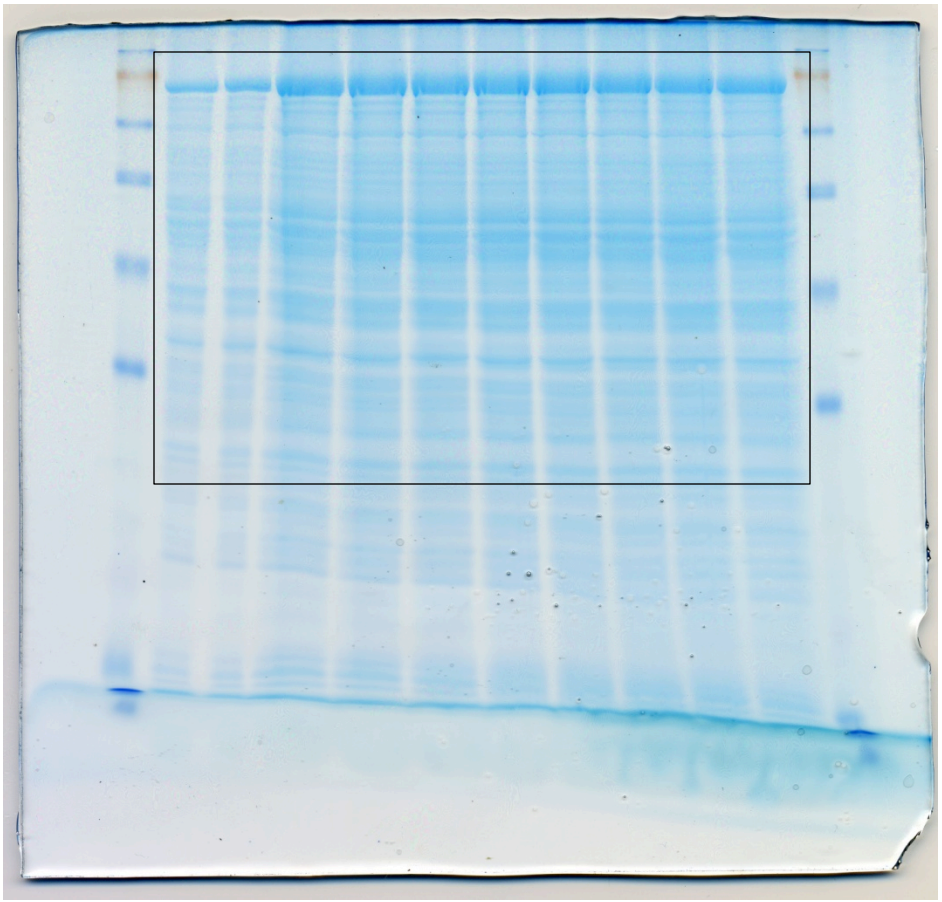
Full unedited gel for Figure 2.H



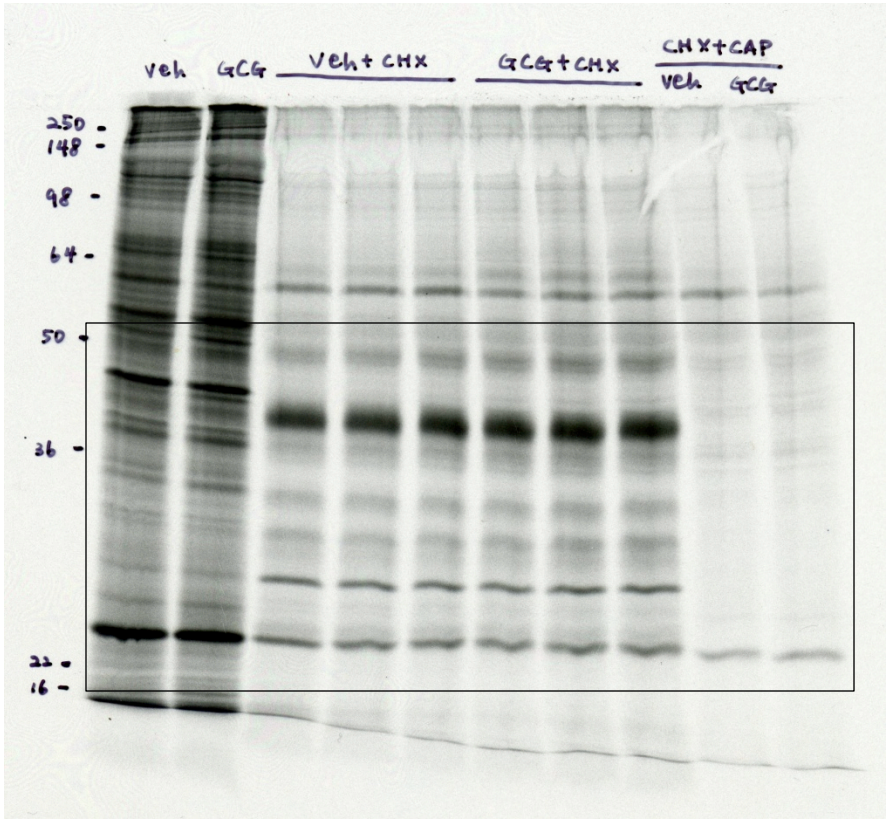
Full unedited gel for Figure 2.D



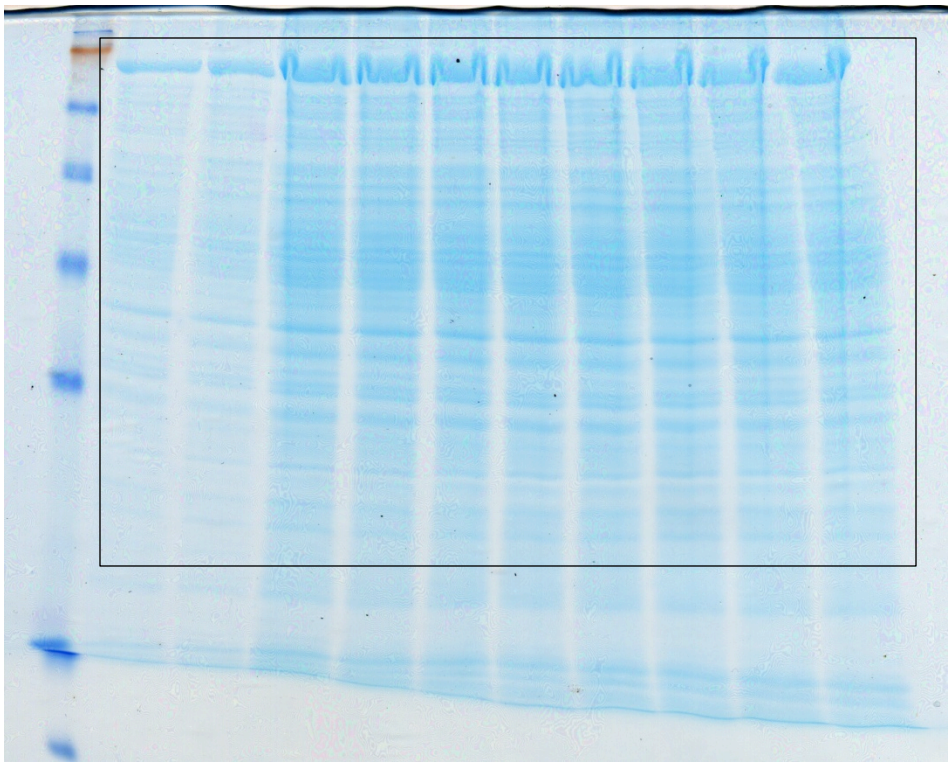
Full unedited gel for Figure 2.E



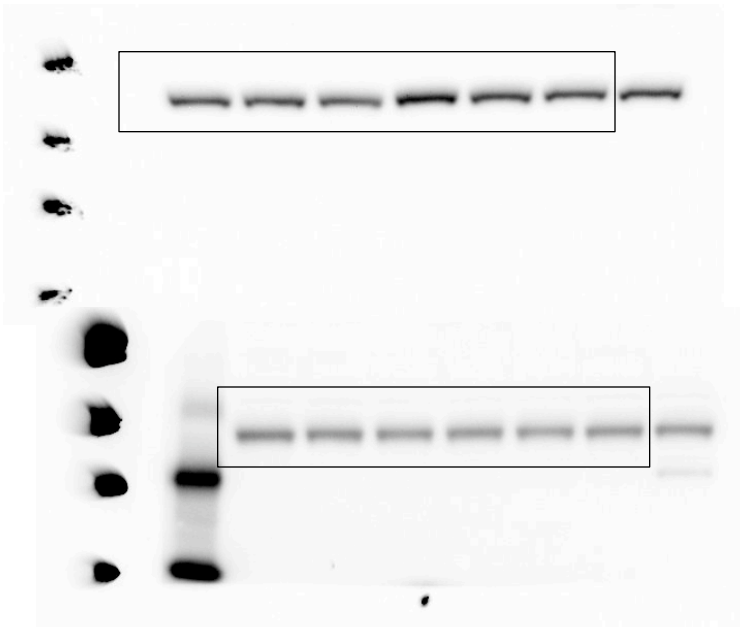
Full unedited gel for Figure 2.L



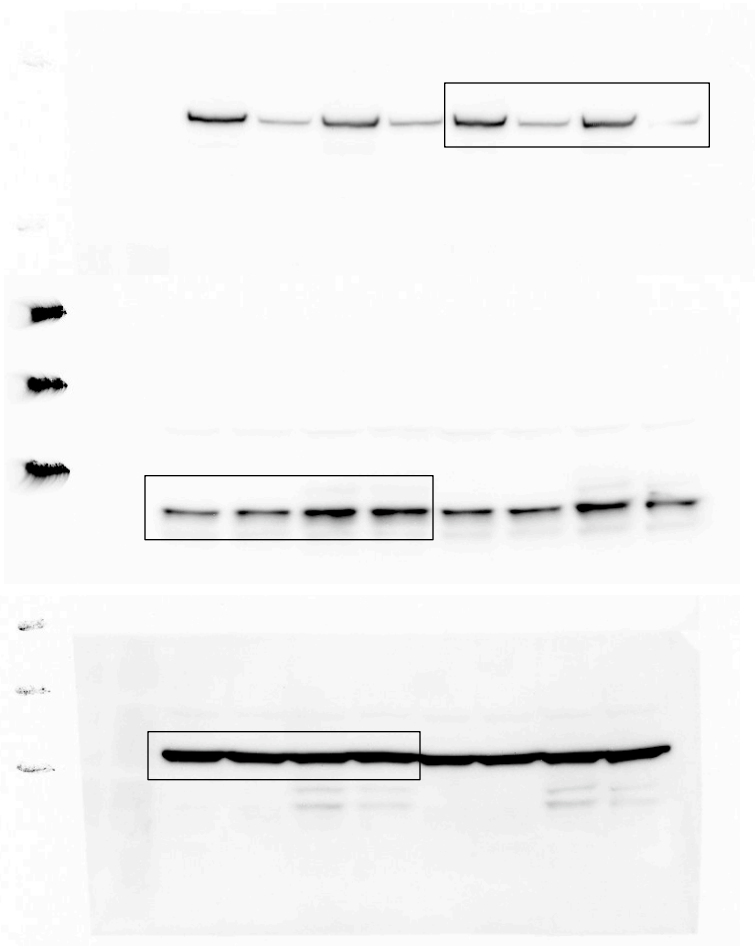
Full unedited gel for Figure 2.M



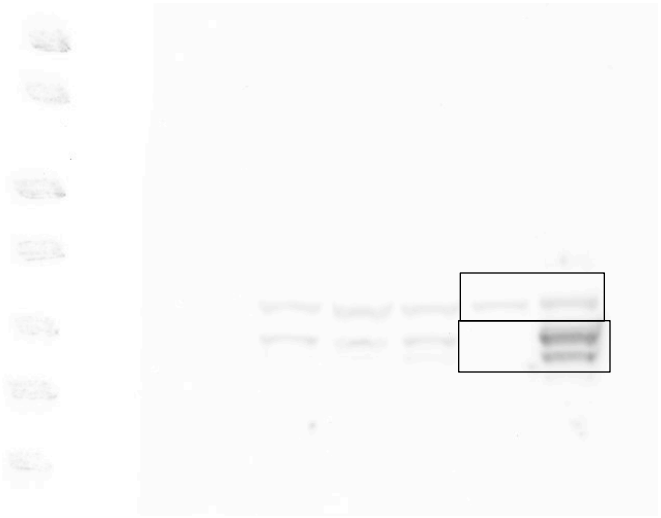
Full unedited gel for Figure 3.F



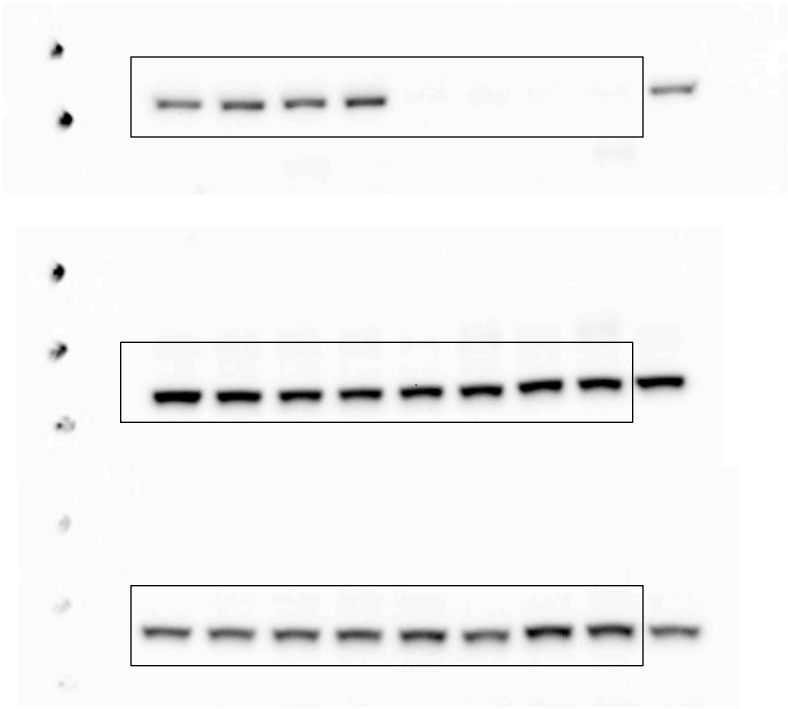
Full unedited gel for Figure 5.B



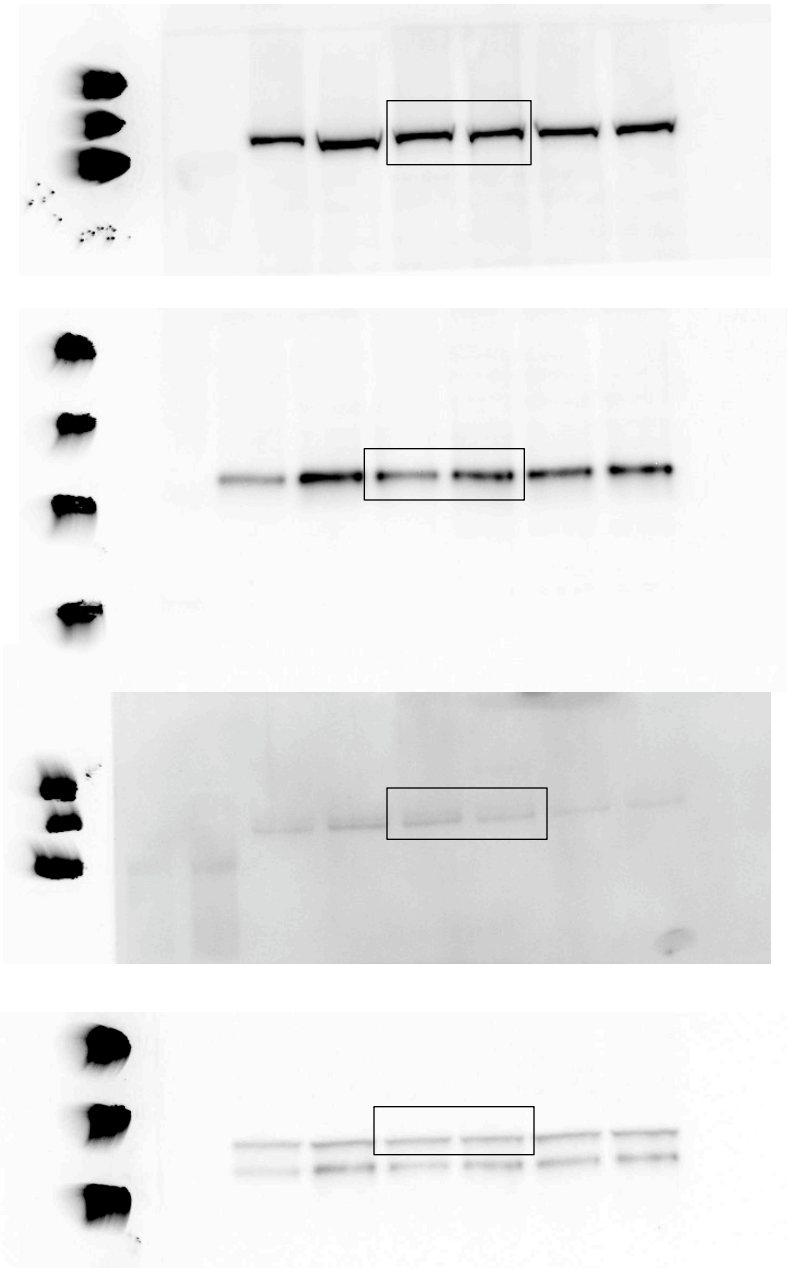
Full unedited gel for Figure 3.I



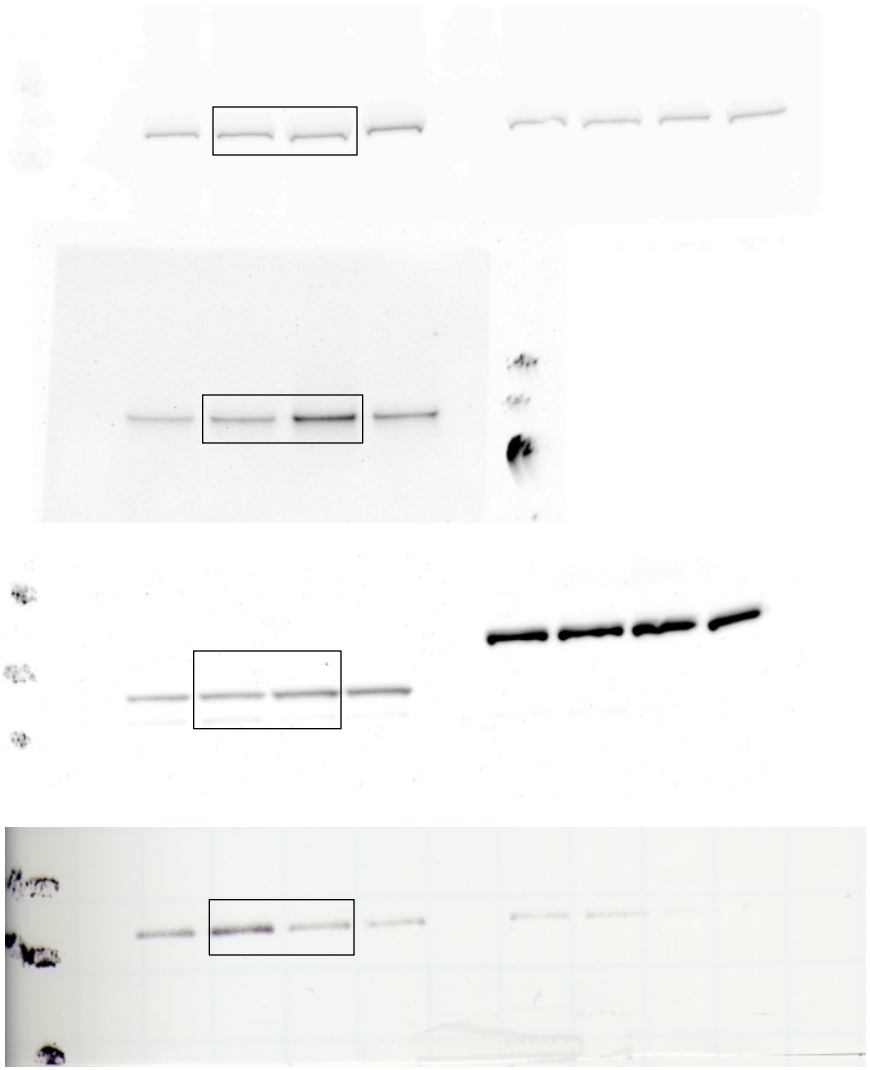
Full unedited gel for Figure 5.I



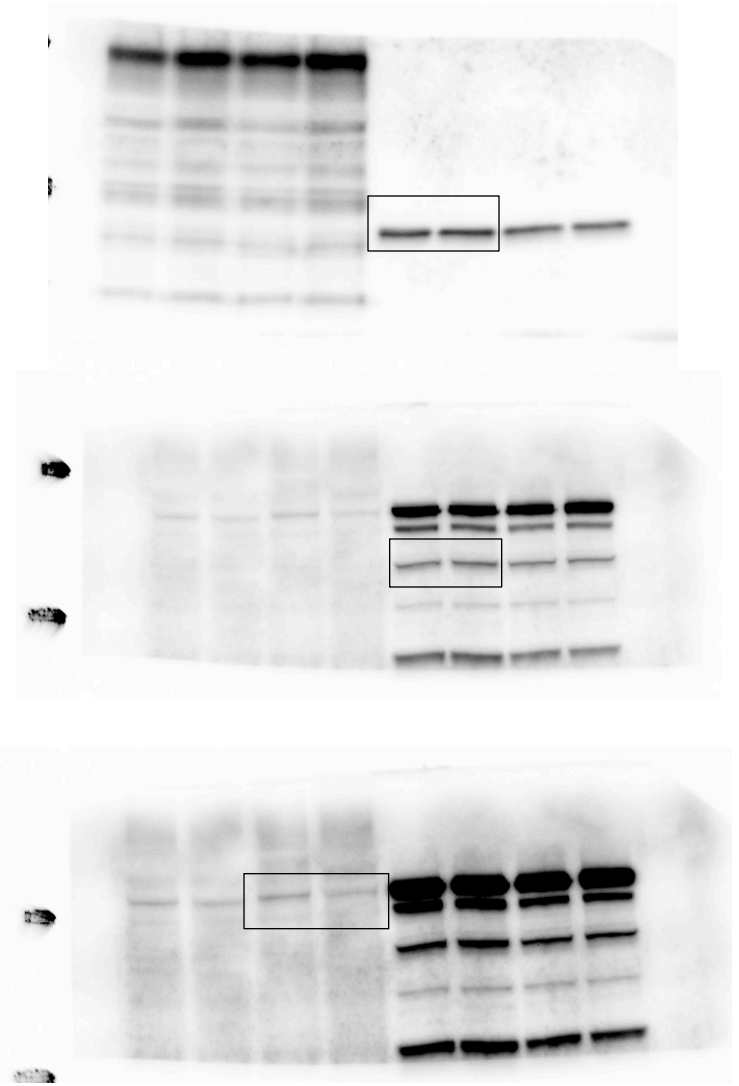
Full unedited gel for Figure 6.A



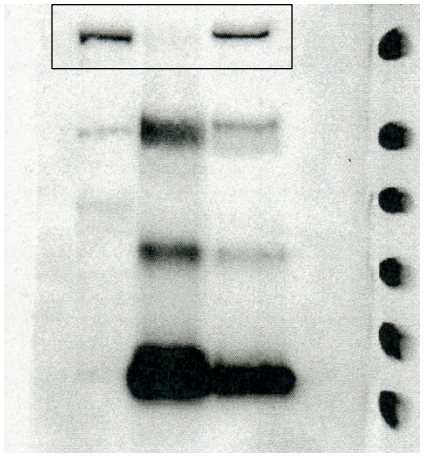
Full unedited gel for Figure 6.B



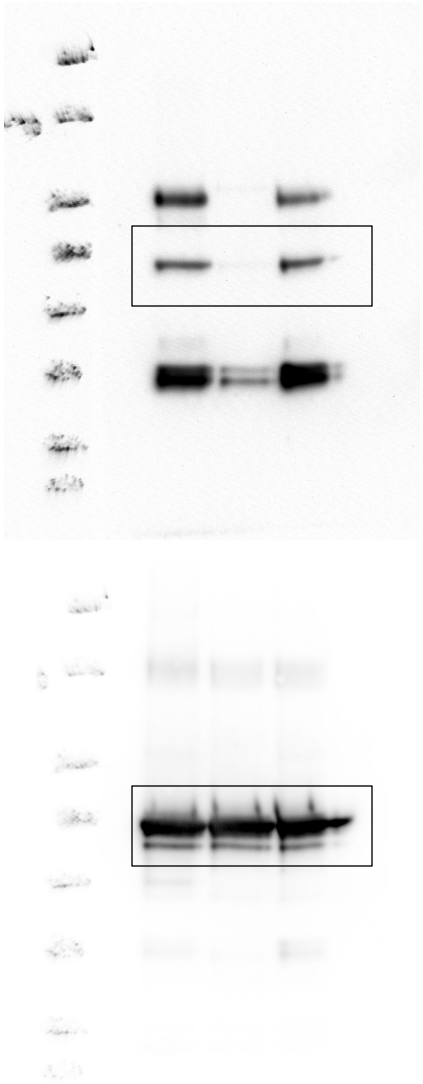
Full unedited gel for Figure 6.C



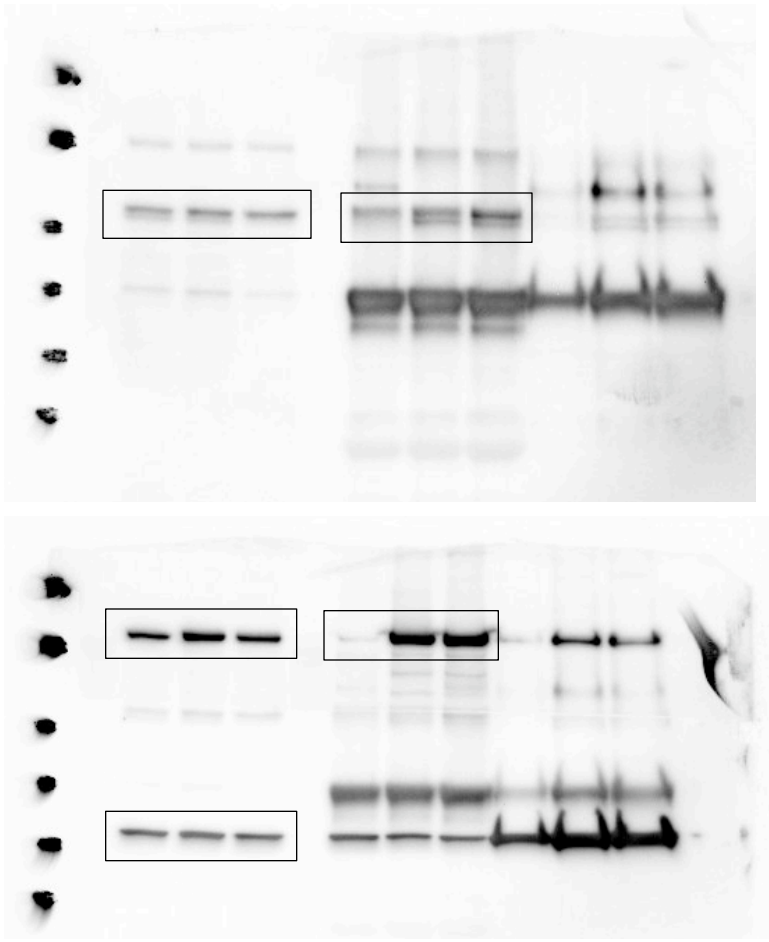
Full unedited gel for Figure 6.D



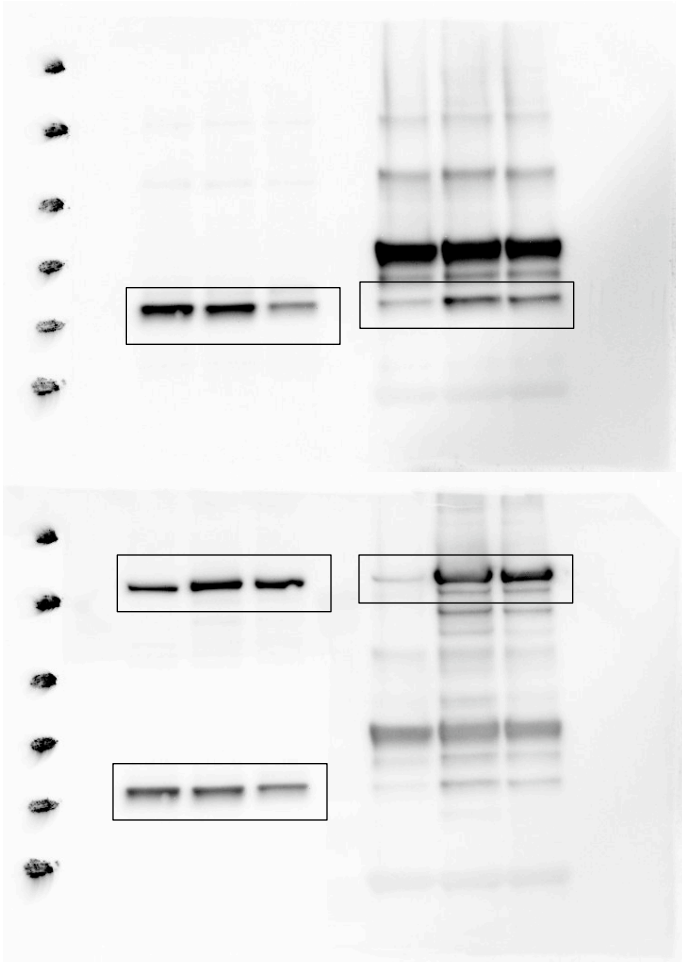
Full unedited gel for Figure 6.E



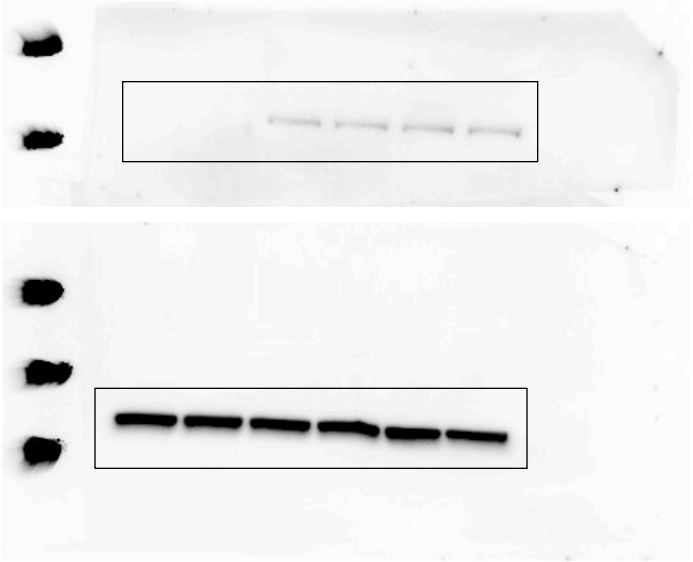
Full unedited gel for Figure 7.A



Full unedited gel for Figure 7.B

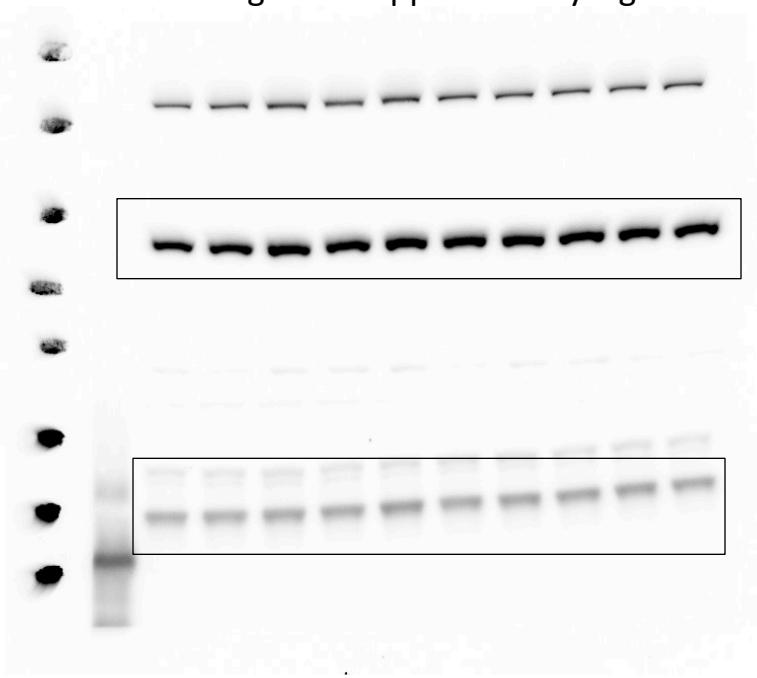


Full unedited gel for Figure 7.E

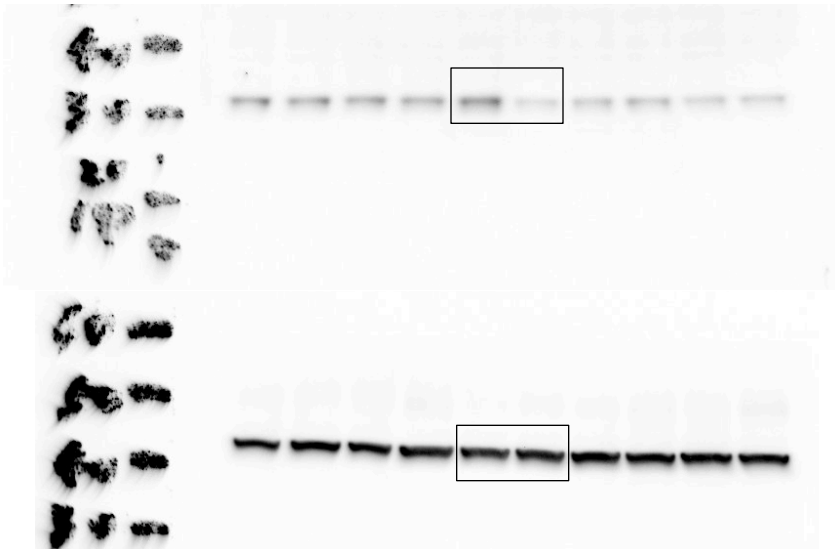


Supplementary Figure

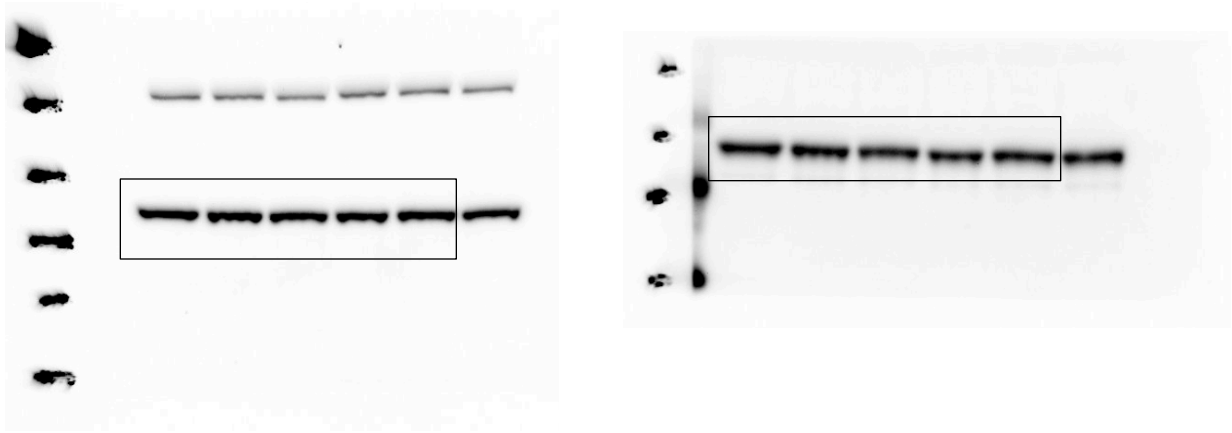
Full unedited gel for Supplementary Figure 2.F



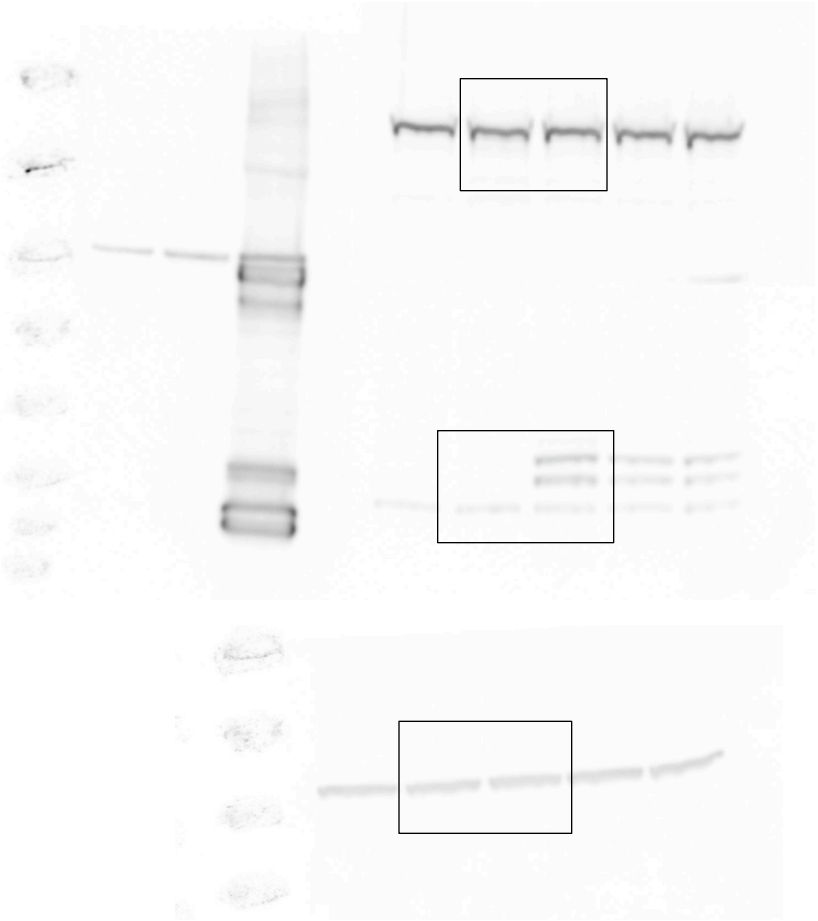
Full unedited gel for Supplementary Figure 4.A



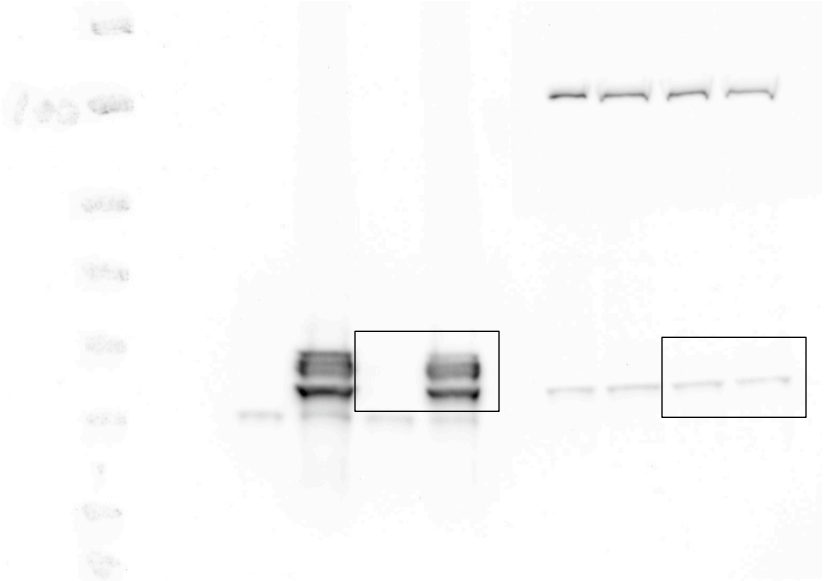
Full unedited gel for Supplementary Figure 4.H



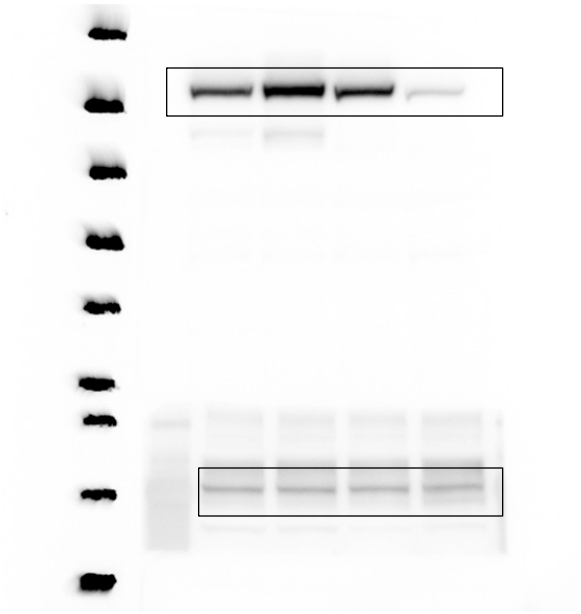
Full unedited gel for Supplementary Figure 5.C

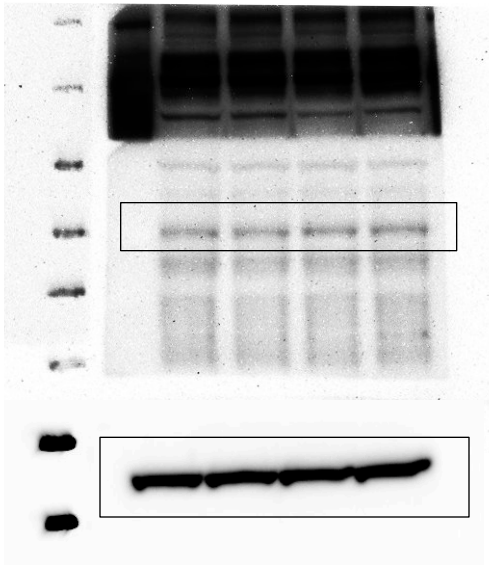


Full unedited gel for Supplementary Figure 5.H

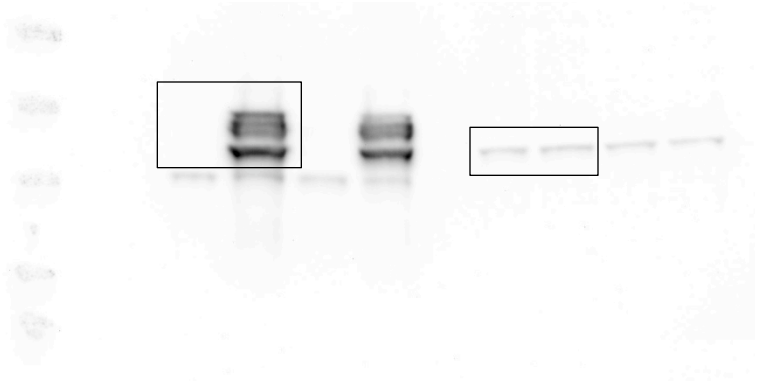


Full unedited gel for Supplementary Figure 7

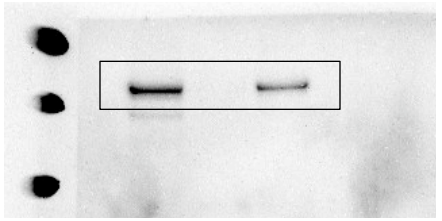




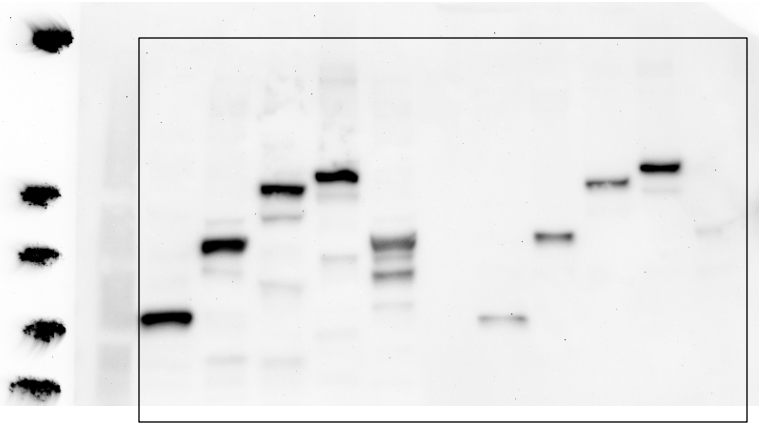
Full unedited gel for Supplementary Figure 8.A



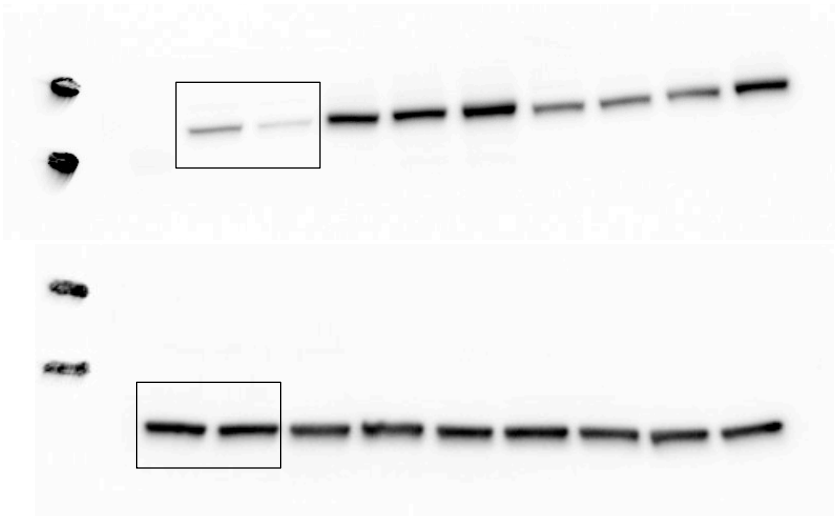
Full unedited gel for Supplementary Figure 10.A



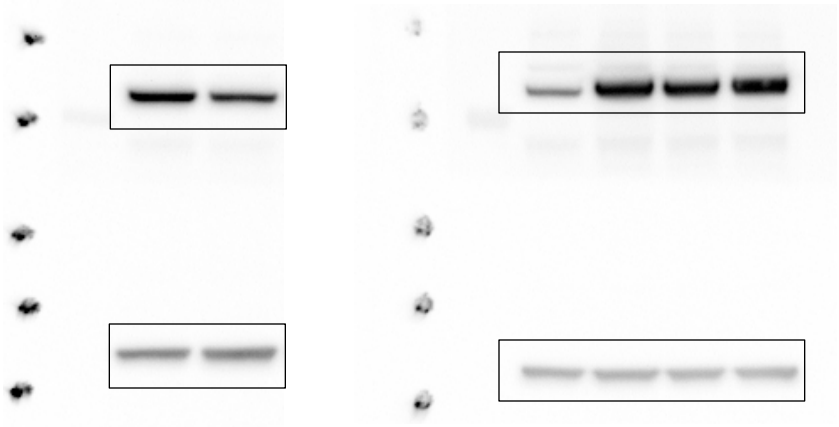
Full unedited gel for Supplementary Figure 10.B



Full unedited gel for Supplementary Figure 11.B



Full unedited gel for Supplementary Figure 12



Full unedited gel for Supplementary Figure 11.D