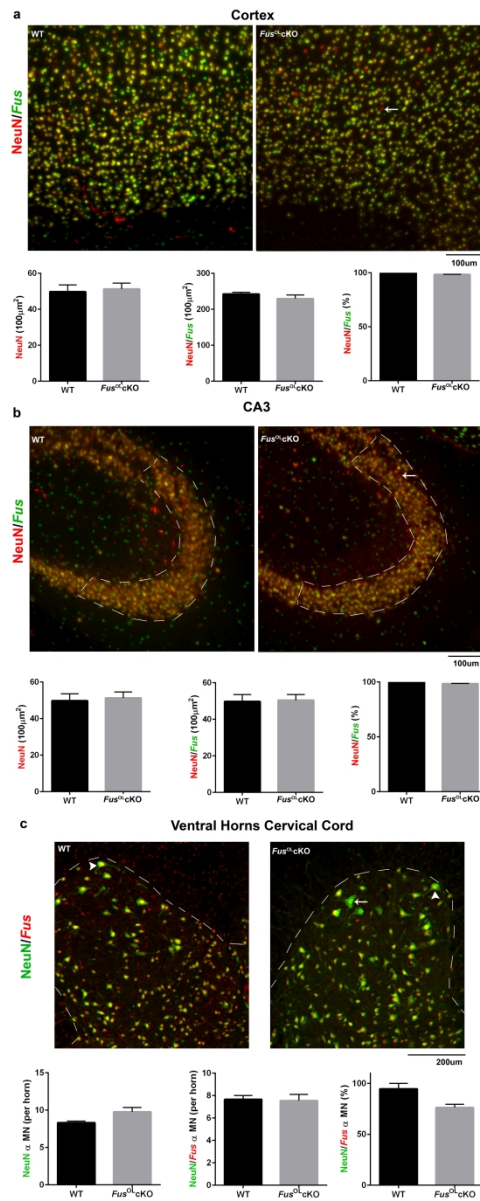


169x77mm (300 x 300 DPI)



218x539mm (300 x 300 DPI)

Table S1

List of primary Antibodies used for WB

1° Antibody	Company	Catalog No.	Source	Target Size	W.B.
Akt (pan)	Cell Signaling	4691	Rabbit	60	1/1000
p-Akt	Cell Signaling	9271	Rabbit	60	1/1000
HMGCR	Abcam	ab174830	Rabbit	96	1/1000
p44/42 (Erk1/2)	Cell Signaling	4696	Mouse	42, 44	1/1000
P-44/42 (p-Erk1/2)	Cell Signaling	4377	Rabbit	42, 44	1/500
Mtor	Cell Signaling	2983	Rabbit	289	1/1000
p-mTOR	Cell Signaling	2974	Rabbit	289	1/500
p-S6 RP	Cell Signaling	5364	Rabbit	32	1/1000
GAPDH	Thermo	MA5-15738	Mouse	37	1/3000
GAPDH	Abcam	Ab9485	Rabbit	37	1/2500
U1A	Abcam	Ab55751	Mouse	34	1/2500
MAG	Santa Cruz	Sc-9544	Goat	115	1/1000
MBP	Abcam	Ab40390	Rabbit	14-21	1/1000
MBP	Biologend	Ab808401	Mouse	14-21	1/1000
FUS	Bethyl Labs	A300-302A	Rabbit	70	1/1000
PLP	Dr. Wendy Macklin	AA3	Rat	18-25	1/1000

Motif sequence for FUS target genes	Note	Reference
5'-CAGVACDGCCWG-3'	V=(A, C or G), D=(A, G, or T), W=(A or T)	ref. 42

FIMO report

Column name	Note	Reference
Gene name		
Chr ID	The chromosome ID	
Gene start	The start coordinate of the gene	
Gene end	The end coordinate of the gene	
Gene strand	The strand information of the gene	NCBI
Motif start	The start position of the motif occurrence	
Motif stop	The end position of the motif occurrence	
Motif strand	Strand of the predicted motif	
Score	The score for the motif occurrence	
P-value	The p-value of the motif occurrence	FIMO

Total FIMO score by gene

Column name	Note	
Gene name	Gene name	
Total FIMO score	The sum of all FIMO scores per each gene	
PAR-CLIP		ref. 48

Gene name	Chr ID	Gene start	Gene end	Gene strand	Motif start	Motif stop	Motif strand	Score
INSIG2	chr1	1.21E+08	1.21E+08	-	19794	19805	-	14.1818
HSD17B7	chr1	1.7E+08	1.7E+08	-	353	364	-	13.903
HSD17B7	chr1	1.7E+08	1.7E+08	-	12467	12478	-	13.903
INSIG2	chr1	1.21E+08	1.21E+08	-	13002	13013	-	13.6364
INSIG2	chr1	1.21E+08	1.21E+08	-	4808	4819	-	10.4667
INSIG2	chr1	1.21E+08	1.21E+08	-	25323	25334	-	10.2
INSIG2	chr1	1.21E+08	1.21E+08	-	23884	23895	-	10.1879
HSD17B7	chr1	1.7E+08	1.7E+08	-	991	1002	-	8.95758
INSIG2	chr1	1.21E+08	1.21E+08	-	16899	16910	-	8.95758
INSIG2	chr1	1.21E+08	1.21E+08	-	23718	23729	-	8.94545
LSS	chr10	76531588	76557138	+	24967	24978	+	19.4061
LSS	chr10	76531588	76557138	+	5777	5788	+	10.1879
LSS	chr10	76531588	76557138	+	12905	12916	+	8.95758
LSS	chr10	76531588	76557138	+	13017	13028	+	8.95758
LSS	chr10	76531588	76557138	+	13255	13266	+	8.95758
LSS	chr10	76531588	76557138	+	19434	19445	+	8.94545
SREBF1	chr11	60199089	60222581	-	1167	1178	-	19.4061
SREBF1	chr11	60199089	60222581	-	8094	8105	-	19.4061
SEC14L2	chr11	4097039	4123415	-	8487	8498	-	19.4061
NPC1L1	chr11	6211013	6230143	-	13547	13558	-	19.4061
NPC1L1	chr11	6211013	6230143	-	14328	14339	-	19.4061
SEC14L2	chr11	4097039	4123415	-	16967	16978	-	19.4061
SEC14L2	chr11	4097039	4123415	-	6675	6686	-	14.1697
SEC14L2	chr11	4097039	4123415	-	4181	4192	-	13.903
NPC1L1	chr11	6211013	6230143	-	6925	6936	-	13.903
SEC14L2	chr11	4097039	4123415	-	17351	17362	-	13.903
SREBF1	chr11	60199089	60222581	-	18385	18396	-	13.903
SEC14L2	chr11	4097039	4123415	-	5482	5493	-	13.6364
NPC1L1	chr11	6211013	6230143	-	7663	7674	-	13.6364
SREBF1	chr11	60199089	60222581	-	16269	16280	-	9.92121
SREBF1	chr11	60199089	60222581	-	3135	3146	-	9.63636
SREBF1	chr11	60199089	60222581	-	17494	17505	-	9.63636
SREBF1	chr11	60199089	60222581	-	21214	21225	-	9.63636
SREBF1	chr11	60199089	60222581	-	6629	6640	-	9.3697
SEC14L2	chr11	4097039	4123415	-	21534	21545	-	9.3697
SREBF1	chr11	60199089	60222581	-	2329	2340	-	9.22424
SREBF1	chr11	60199089	60222581	-	19122	19133	-	8.95758
SEC14L2	chr11	4097039	4123415	-	26129	26140	-	8.95758
SREBF1	chr11	60199089	60222581	-	822	833	-	8.94545
SREBF1	chr11	60199089	60222581	-	2081	2092	-	8.94545
SREBF1	chr11	60199089	60222581	-	3486	3497	-	8.94545
SREBF1	chr11	60199089	60222581	-	18725	18736	-	8.94545
SREBF1	chr11	60199089	60222581	-	21744	21755	-	8.94545
SEC14L2	chr11	4097039	4123415	-	9743	9754	-	8.69091
SEC14L2	chr11	4097039	4123415	-	18485	18496	-	8.69091
APOB	chr12	7977648	8016835	+	23756	23767	+	19.4061
APOB	chr12	7977648	8016835	+	26487	26498	+	14.8727
APOB	chr12	7977648	8016835	+	36325	36336	+	13.903
APOB	chr12	7977648	8016835	+	37689	37700	+	13.6364
APOB	chr12	7977648	8016835	+	7681	7692	+	9.92121
IDI2	chr13	8952863	8960945	+	883	894	+	19.4061

IDI2	chr13	8952863	8960945 +	3344	3355 +	19.4061
HMGCS1	chr13	1.2E+08	1.2E+08 +	11294	11305 +	19.4061
HMGCS1	chr13	1.2E+08	1.2E+08 +	13764	13775 +	19.4061
HMGCS1	chr13	1.2E+08	1.2E+08 +	2930	2941 +	14.1818
IDI2	chr13	8952863	8960945 +	2137	2148 +	13.903
IDI2	chr13	8952863	8960945 +	3687	3698 +	13.903
HMGCS1	chr13	1.2E+08	1.2E+08 +	12485	12496 +	13.903
HMGCR	chr13	96648967	96670936 -	14570	14581 -	13.903
IDI2	chr13	8952863	8960945 +	7046	7057 +	13.6364
HMGCR	chr13	96648967	96670936 -	10539	10550 -	10.2
HMGCR	chr13	96648967	96670936 -	11758	11769 -	9.63636
FDFT1	chr14	63145150	63179578 -	4634	4645 -	19.4061
FDFT1	chr14	63145150	63179578 -	8009	8020 -	19.4061
FDFT1	chr14	63145150	63179578 -	33528	33539 -	14.1818
FDFT1	chr14	63145150	63179578 -	3092	3103 -	13.903
FDFT1	chr14	63145150	63179578 -	20179	20190 -	9.92121
FDFT1	chr14	63145150	63179578 -	21848	21859 -	9.92121
FDFT1	chr14	63145150	63179578 -	27133	27144 -	8.94545
PRKAA1	chr15	5143861	5181899 +	6808	6819 +	19.4061
CYB5R3	chr15	83153494	83172592 -	8945	8956 -	19.4061
CYB5R3	chr15	83153494	83172592 -	3504	3515 -	13.903
PRKAA1	chr15	5143861	5181899 +	4016	4027 +	13.903
CYB5R3	chr15	83153494	83172592 -	5756	5767 -	13.903
CYB5R3	chr15	83153494	83172592 -	8428	8439 -	13.903
CYB5R3	chr15	83153494	83172592 -	9578	9589 -	13.903
CYB5R3	chr15	83153494	83172592 -	11930	11941 -	13.903
CYB5R3	chr15	83153494	83172592 -	16129	16140 -	13.903
PRKAA1	chr15	5143861	5181899 +	31520	31531 +	13.903
PRKAA1	chr15	5143861	5181899 +	31211	31222 +	9.92121
CYB5R3	chr15	83153494	83172592 -	12430	12441 -	9.90303
CYB5R3	chr15	83153494	83172592 -	12104	12115 -	9.63636
CYB5R3	chr15	83153494	83172592 -	10421	10432 -	8.94545
SOD1	chr16	90220754	90226329 +	3734	3745 +	13.6364
SOD1	chr16	90220754	90226329 +	3940	3951 +	9.92121
SOD1	chr16	90220754	90226329 +	246	257 +	8.94545
ABCG1	chr17	31057675	31117988 +	4340	4351 +	19.4061
ABCG1	chr17	31057675	31117988 +	12024	12035 +	19.4061
ABCG1	chr17	31057675	31117988 +	12053	12064 +	19.4061
ABCG1	chr17	31057675	31117988 +	38413	38424 +	19.4061
ABCG1	chr17	31057675	31117988 +	38132	38143 +	19.1394
ABCG1	chr17	31057675	31117988 +	52452	52463 +	14.4485
ABCG1	chr17	31057675	31117988 +	10256	10267 +	13.903
ABCG1	chr17	31057675	31117988 +	42489	42500 +	13.903
ABCG1	chr17	31057675	31117988 +	52862	52873 +	13.903
ABCG1	chr17	31057675	31117988 +	30368	30379 +	9.91515
ABCG1	chr17	31057675	31117988 +	14614	14625 +	9.63636
ABCG1	chr17	31057675	31117988 +	56339	56350 +	8.94545
FGF1	chr18	38838673	38929472 -	11818	11829 -	19.4061
FGF1	chr18	38838673	38929472 -	24448	24459 -	19.4061
FGF1	chr18	38838673	38929472 -	86541	86552 -	19.4061
FGF1	chr18	38838673	38929472 -	4991	5002 -	19.1394
FGF1	chr18	38838673	38929472 -	5614	5625 -	14.1818

FGF1	chr18	38838673	38929472 -	86567	86578 -	14.1818
FGF1	chr18	38838673	38929472 -	8611	8622 -	13.903
FGF1	chr18	38838673	38929472 -	23833	23844 -	10.2
FGF1	chr18	38838673	38929472 -	15754	15765 -	10.1879
FGF1	chr18	38838673	38929472 -	40801	40812 -	10.1879
FGF1	chr18	38838673	38929472 -	82249	82260 -	10.1818
FGF1	chr18	38838673	38929472 -	47493	47504 -	9.91515
FGF1	chr18	38838673	38929472 -	17785	17796 -	8.95758
FGF1	chr18	38838673	38929472 -	87746	87757 -	8.95758
FGF1	chr18	38838673	38929472 -	9070	9081 -	8.94545
TM7SF2	chr19	6062821	6068373 -	4188	4199 -	14.1697
TM7SF2	chr19	6062821	6068373 -	3140	3151 -	13.903
FDPS	chr3	89093588	89101959 -	4536	4547 -	19.4061
PMVK	chr3	89454541	89469013 +	11684	11695 +	19.4061
PMVK	chr3	89454541	89469013 +	886	897 +	14.4485
PMVK	chr3	89454541	89469013 +	8537	8548 +	14.1818
HMGCS2	chr3	98280435	98310738 +	11554	11565 +	14.1818
PMVK	chr3	89454541	89469013 +	13582	13593 +	14.1818
FDPS	chr3	89093588	89101959 -	3187	3198 -	14.1818
HMGCS2	chr3	98280435	98310738 +	539	550 +	13.903
HMGCS2	chr3	98280435	98310738 +	11583	11594 +	13.903
HMGCS2	chr3	98280435	98310738 +	20462	20473 +	13.903
FDPS	chr3	89093588	89101959 -	4640	4651 -	13.6364
PMVK	chr3	89454541	89469013 +	5301	5312 +	13.6364
HMGCS2	chr3	98280435	98310738 +	1475	1486 +	10.1879
HMGCS2	chr3	98280435	98310738 +	14055	14066 +	10.1879
PMVK	chr3	89454541	89469013 +	9840	9851 +	9.92121
PMVK	chr3	89454541	89469013 +	6338	6349 +	9.3697
PMVK	chr3	89454541	89469013 +	5727	5738 +	8.95758
HMGCS2	chr3	98280435	98310738 +	18870	18881 +	8.95758
HMGCS2	chr3	98280435	98310738 +	18907	18918 +	8.95758
HMGCS2	chr3	98280435	98310738 +	21508	21519 +	8.95758
PEX2	chr3	5560188	5576239 -	289	300 -	8.94545
PMVK	chr3	89454541	89469013 +	3474	3485 +	8.94545
HMGCS2	chr3	98280435	98310738 +	3562	3573 +	8.94545
PMVK	chr3	89454541	89469013 +	5692	5703 +	8.94545
PMVK	chr3	89454541	89469013 +	13176	13187 +	8.94545
HMGCS2	chr3	98280435	98310738 +	25667	25678 +	8.94545
PRKAA2	chr4	1.05E+08	1.05E+08 -	4561	4572 -	19.4061
PRKAA2	chr4	1.05E+08	1.05E+08 -	5826	5837 -	19.4061
DHCR24	chr4	1.07E+08	1.07E+08 +	7142	7153 +	19.4061
PRKAA2	chr4	1.05E+08	1.05E+08 -	7342	7353 -	19.4061
DHCR24	chr4	1.07E+08	1.07E+08 +	7455	7466 +	19.4061
PRKAA2	chr4	1.05E+08	1.05E+08 -	15952	15963 -	19.4061
DHCR24	chr4	1.07E+08	1.07E+08 +	19096	19107 +	19.4061
DHCR24	chr4	1.07E+08	1.07E+08 +	26809	26820 +	19.1394
PRKAA2	chr4	1.05E+08	1.05E+08 -	19370	19381 -	14.1818
PRKAA2	chr4	1.05E+08	1.05E+08 -	8788	8799 -	13.903
PRKAA2	chr4	1.05E+08	1.05E+08 -	16248	16259 -	13.903
DHCR24	chr4	1.07E+08	1.07E+08 +	19352	19363 +	13.903
PRKAA2	chr4	1.05E+08	1.05E+08 -	28060	28071 -	13.903
PRKAA2	chr4	1.05E+08	1.05E+08 -	36150	36161 -	13.903

PRKAA2	chr4	1.05E+08	1.05E+08	-	10459	10470	-	13.6364
DHCR24	chr4	1.07E+08	1.07E+08	+	24033	24044	+	13.6364
PRKAA2	chr4	1.05E+08	1.05E+08	-	44627	44638	-	13.6364
PRKAA2	chr4	1.05E+08	1.05E+08	-	55477	55488	-	13.6364
PRKAA2	chr4	1.05E+08	1.05E+08	-	58194	58205	-	13.6364
DHCR24	chr4	1.07E+08	1.07E+08	+	20712	20723	+	10.2
DHCR24	chr4	1.07E+08	1.07E+08	+	24024	24035	+	10.1879
PRKAA2	chr4	1.05E+08	1.05E+08	-	16856	16867	-	9.92121
DHCR24	chr4	1.07E+08	1.07E+08	+	17694	17705	+	9.92121
DHCR24	chr4	1.07E+08	1.07E+08	+	28058	28069	+	9.92121
DHCR24	chr4	1.07E+08	1.07E+08	+	3677	3688	+	9.63636
PRKAA2	chr4	1.05E+08	1.05E+08	-	74575	74586	-	9.63636
DHCR24	chr4	1.07E+08	1.07E+08	+	25338	25349	+	8.95758
DHCR24	chr4	1.07E+08	1.07E+08	+	25666	25677	+	8.95758
PRKAA2	chr4	1.05E+08	1.05E+08	-	14615	14626	-	8.95758
PRKAA2	chr4	1.05E+08	1.05E+08	-	51591	51602	-	8.95758
PRKAA2	chr4	1.05E+08	1.05E+08	-	2282	2293	-	8.94545
PRKAA2	chr4	1.05E+08	1.05E+08	-	11157	11168	-	8.94545
PRKAA2	chr4	1.05E+08	1.05E+08	-	70417	70428	-	8.94545
POR	chr5	1.36E+08	1.36E+08	+	9504	9515	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	10540	10551	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	12350	12361	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	14315	14326	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	21913	21924	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	27473	27484	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	39062	39073	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	48003	48014	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	51746	51757	+	19.4061
POR	chr5	1.36E+08	1.36E+08	+	52453	52464	+	19.4061
MVK	chr5	1.14E+08	1.14E+08	+	1303	1314	+	19.1394
POR	chr5	1.36E+08	1.36E+08	+	63902	63913	+	14.1818
POR	chr5	1.36E+08	1.36E+08	+	37137	37148	+	14.1697
POR	chr5	1.36E+08	1.36E+08	+	58084	58095	+	14.1697
POR	chr5	1.36E+08	1.36E+08	+	8498	8509	+	13.903
MVK	chr5	1.14E+08	1.14E+08	+	10356	10367	+	13.903
POR	chr5	1.36E+08	1.36E+08	+	16995	17006	+	13.903
POR	chr5	1.36E+08	1.36E+08	+	53534	53545	+	13.903
CYP51	chr5	4081145	4104746	-	16381	16392	-	13.6364
MVK	chr5	1.14E+08	1.14E+08	+	9366	9377	+	10.2
POR	chr5	1.36E+08	1.36E+08	+	31149	31160	+	9.92121
CYP51	chr5	4081145	4104746	-	782	793	-	9.63636
INSIG1	chr5	28071363	28078662	+	1150	1161	+	9.63636
POR	chr5	1.36E+08	1.36E+08	+	8308	8319	+	8.95758
POR	chr5	1.36E+08	1.36E+08	+	65004	65015	+	8.95758
POR	chr5	1.36E+08	1.36E+08	+	60203	60214	+	8.69091
CFTR	chr6	18170687	18322768	+	45709	45720	+	19.4061
CFTR	chr6	18170687	18322768	+	73262	73273	+	19.4061
CFTR	chr6	18170687	18322768	+	53218	53229	+	14.1818
CFTR	chr6	18170687	18322768	+	17967	17978	+	14.1697
CFTR	chr6	18170687	18322768	+	26198	26209	+	13.903
CFTR	chr6	18170687	18322768	+	67658	67669	+	13.903
CFTR	chr6	18170687	18322768	+	130856	130867	+	13.903

CFTR	chr6	18170687	18322768	+	139632	139643	+	13.903
CFTR	chr6	18170687	18322768	+	40486	40497	+	13.6364
CFTR	chr6	18170687	18322768	+	13868	13879	+	9.92121
CFTR	chr6	18170687	18322768	+	87392	87403	+	9.92121
CFTR	chr6	18170687	18322768	+	128615	128626	+	9.92121
CFTR	chr6	18170687	18322768	+	3254	3265	+	9.63636
CFTR	chr6	18170687	18322768	+	113604	113615	+	9.63636
APOE	chr7	19696109	19699188	-	2032	2043	-	13.903
DHCR7	chr7	1.44E+08	1.44E+08	+	21081	21092	+	13.6364
APOE	chr7	19696109	19699188	-	1095	1106	-	9.92121
APOE	chr7	19696109	19699188	-	971	982	-	9.90303
DHCR7	chr7	1.44E+08	1.44E+08	+	9246	9257	+	9.63636
DHCR7	chr7	1.44E+08	1.44E+08	+	22981	22992	+	8.94545
MVD	chr8	1.22E+08	1.22E+08	-	8149	8160	-	19.4061
MVD	chr8	1.22E+08	1.22E+08	-	871	882	-	13.9152
MVD	chr8	1.22E+08	1.22E+08	-	7635	7646	-	10.1879
MVD	chr8	1.22E+08	1.22E+08	-	2109	2120	-	9.63636
MVD	chr8	1.22E+08	1.22E+08	-	2847	2858	-	9.63636
MVD	chr8	1.22E+08	1.22E+08	-	6599	6610	-	9.3697
MVD	chr8	1.22E+08	1.22E+08	-	1858	1869	-	8.94545
MVD	chr8	1.22E+08	1.22E+08	-	3767	3778	-	8.94545
MVD	chr8	1.22E+08	1.22E+08	-	8560	8571	-	8.94545
SC5D	chr9	42251595	42264256	-	9646	9657	-	19.4061
SCAP	chr9	1.1E+08	1.1E+08	+	21457	21468	+	19.4061
SCAP	chr9	1.1E+08	1.1E+08	+	24564	24575	+	19.4061
SCAP	chr9	1.1E+08	1.1E+08	+	27874	27885	+	19.4061
SCAP	chr9	1.1E+08	1.1E+08	+	35779	35790	+	19.4061
SCAP	chr9	1.1E+08	1.1E+08	+	48120	48131	+	15.1394
SCAP	chr9	1.1E+08	1.1E+08	+	42709	42720	+	14.1818
SC5D	chr9	42251595	42264256	-	3646	3657	-	14.1697
SC5D	chr9	42251595	42264256	-	3194	3205	-	13.903
SC5D	chr9	42251595	42264256	-	4214	4225	-	13.903
SC5D	chr9	42251595	42264256	-	7355	7366	-	13.903
SCAP	chr9	1.1E+08	1.1E+08	+	8011	8022	+	13.903
SCAP	chr9	1.1E+08	1.1E+08	+	8937	8948	+	13.903
SCAP	chr9	1.1E+08	1.1E+08	+	17402	17413	+	13.6364
SCAP	chr9	1.1E+08	1.1E+08	+	42020	42031	+	10.1879
SCAP	chr9	1.1E+08	1.1E+08	+	23965	23976	+	9.92121
SC5D	chr9	42251595	42264256	-	9126	9137	-	9.91515
SCAP	chr9	1.1E+08	1.1E+08	+	32656	32667	+	8.95758
SCAP	chr9	1.1E+08	1.1E+08	+	42529	42540	+	8.95758
SCAP	chr9	1.1E+08	1.1E+08	+	45595	45606	+	8.95758
SC5D	chr9	42251595	42264256	-	4911	4922	-	8.95758
SC5D	chr9	42251595	42264256	-	6830	6841	-	8.95758
SCAP	chr9	1.1E+08	1.1E+08	+	29519	29530	+	8.94545
SCAP	chr9	1.1E+08	1.1E+08	+	29894	29905	+	8.94545
SCAP	chr9	1.1E+08	1.1E+08	+	432	443	+	8.69091
SC5D	chr9	42251595	42264256	-	8417	8428	-	8.69091
EBP	chrX	8185329	8193512	-	4374	4385	-	19.4061
EBP	chrX	8185329	8193512	-	4753	4764	-	19.4061
G6PDX	chrX	74409483	74429194	-	9600	9611	-	19.4061
G6PDX	chrX	74409483	74429194	-	10174	10185	-	19.4061

G6PDX	chrX	74409483	74429194 -	10980	10991 -	19.4061
NSDHL	chrX	72918557	72958514 +	10808	10819 +	14.1697
NSDHL	chrX	72918557	72958514 +	9757	9768 +	13.903
NSDHL	chrX	72918557	72958514 +	11441	11452 +	13.903
NSDHL	chrX	72918557	72958514 +	12620	12631 +	13.903
NSDHL	chrX	72918557	72958514 +	34301	34312 +	13.903
NSDHL	chrX	72918557	72958514 +	34970	34981 +	13.903
NSDHL	chrX	72918557	72958514 +	8668	8679 +	9.92121
G6PDX	chrX	74409483	74429194 -	10552	10563 -	8.94545
NSDHL	chrX	72918557	72958514 +	23530	23541 +	8.94545
NSDHL	chrX	72918557	72958514 +	30332	30343 +	8.94545

P-value

4.38E-06
1.75E-05
1.75E-05
2.19E-05
2.34E-05
2.48E-05
2.96E-05
5.60E-05
5.60E-05
7.18E-05
5.04E-07
2.96E-05
5.60E-05
5.60E-05
5.60E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
7.37E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
2.19E-05
2.19E-05
3.64E-05
4.88E-05
4.88E-05
4.88E-05
5.25E-05
5.25E-05
5.33E-05
5.60E-05
5.60E-05
7.18E-05
7.18E-05
7.18E-05
7.18E-05
7.18E-05
7.31E-05
7.31E-05
5.04E-07
1.71E-06
1.75E-05
2.19E-05
3.64E-05
5.04E-07

5.04E-07
5.04E-07
5.04E-07
4.38E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
2.19E-05
2.48E-05
4.88E-05
5.04E-07
5.04E-07
4.38E-06
1.75E-05
3.64E-05
3.64E-05
7.18E-05
5.04E-07
5.04E-07
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
3.64E-05
4.05E-05
4.88E-05
7.18E-05
2.19E-05
3.64E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07
6.88E-07
2.37E-06
1.75E-05
1.75E-05
1.75E-05
3.81E-05
4.88E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
6.88E-07
4.38E-06

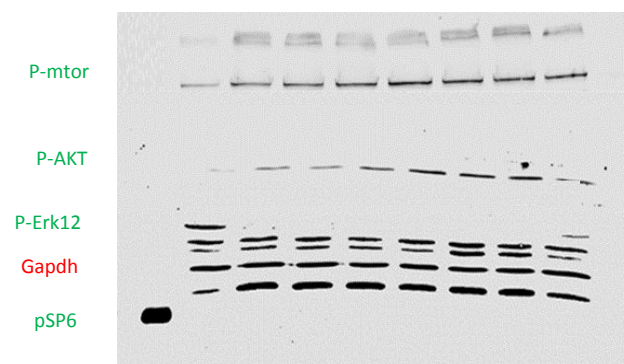
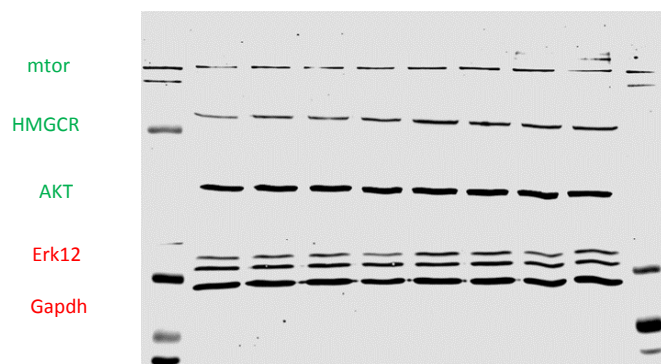
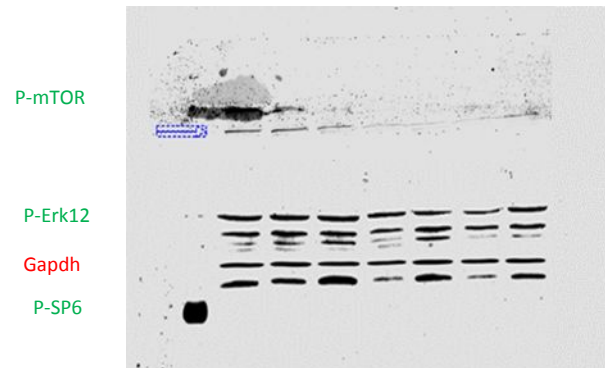
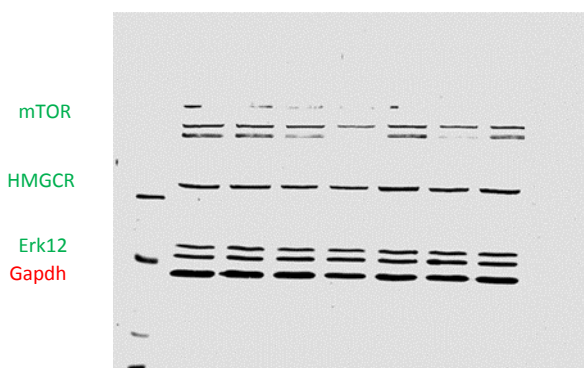
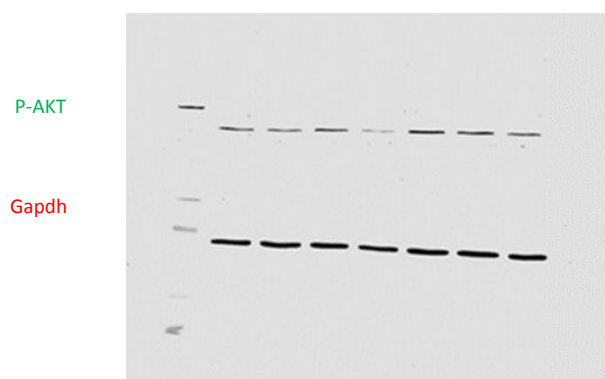
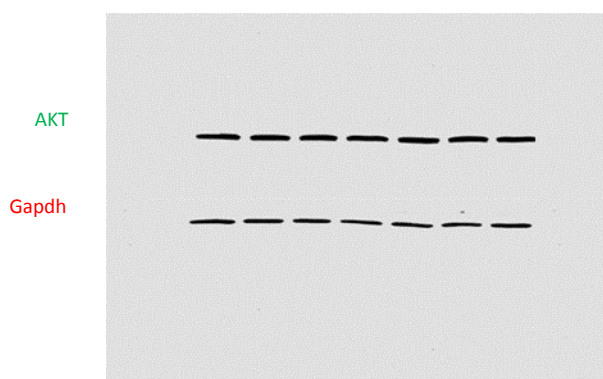
4.38E-06
1.75E-05
2.48E-05
2.96E-05
2.96E-05
3.02E-05
3.81E-05
5.60E-05
5.60E-05
7.18E-05
7.37E-06
1.75E-05
5.04E-07
5.04E-07
2.37E-06
4.38E-06
4.38E-06
4.38E-06
4.38E-06
1.75E-05
1.75E-05
1.75E-05
2.19E-05
2.19E-05
2.96E-05
2.96E-05
3.64E-05
5.25E-05
5.60E-05
5.60E-05
5.60E-05
5.60E-05
7.18E-05
7.18E-05
7.18E-05
7.18E-05
7.18E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
6.88E-07
4.38E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05

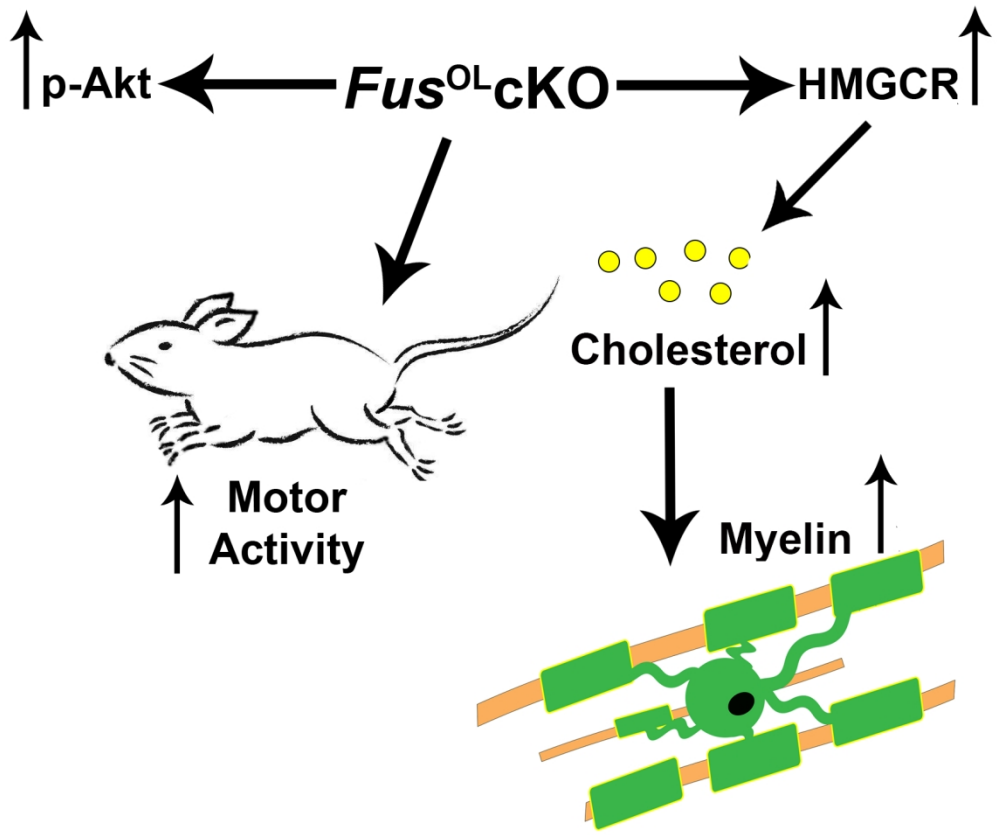
2.19E-05
2.19E-05
2.19E-05
2.19E-05
2.19E-05
2.48E-05
2.96E-05
3.64E-05
3.64E-05
3.64E-05
4.88E-05
4.88E-05
5.60E-05
5.60E-05
5.60E-05
5.60E-05
7.18E-05
7.18E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
6.88E-07
4.38E-06
7.37E-06
7.37E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
2.19E-05
2.48E-05
3.64E-05
4.88E-05
4.88E-05
5.60E-05
5.60E-05
7.31E-05
5.04E-07
5.04E-07
4.38E-06
7.37E-06
1.75E-05
1.75E-05
1.75E-05

1.75E-05
2.19E-05
3.64E-05
3.64E-05
3.64E-05
4.88E-05
4.88E-05
1.75E-05
2.19E-05
3.64E-05
4.05E-05
4.88E-05
7.18E-05
5.04E-07
8.35E-06
2.96E-05
4.88E-05
4.88E-05
5.25E-05
7.18E-05
7.18E-05
7.18E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07
5.04E-07
1.56E-06
4.38E-06
7.37E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
2.19E-05
2.96E-05
3.64E-05
3.81E-05
5.60E-05
5.60E-05
5.60E-05
5.60E-05
5.60E-05
7.18E-05
7.18E-05
7.31E-05
7.31E-05
5.04E-07
5.04E-07
5.04E-07
5.04E-07

5.04E-07
7.37E-06
1.75E-05
1.75E-05
1.75E-05
1.75E-05
1.75E-05
3.64E-05
7.18E-05
7.18E-05
7.18E-05

Gene name	Total FIMO score	PAR-CLIP
POR	314.81848	0
PRKAA2	266.27288	7
SCAP	221.95166	1
FGF1	197.15766	0
CFTR	185.44845	0
ABCG1	181.41826	1
DHCR24	172.67894	2
SREBF1	163.82426	0
CYB5R3	131.30894	0
PMVK	130.93944	1
SEC14L2	130.1334	0
HMGCS2	121.03024	0
SC5D	111.80602	0
NSDHL	111.49681	0
MVD	98.98797	0
FDFT1	95.68487	2
IDI2	80.2546	0
INSIG2	76.57583	0
APOB	71.73941	0
G6PDX	67.16375	0
HMGCS1	66.897	3
NPC1L1	66.3516	0
LSS	65.41219	2
PRKAA1	57.13331	0
FDPS	47.2243	0
MVK	43.2424	0
EBP	38.8122	0
HSD17B7	36.76358	0
HMGCR	33.73936	1
APOE	33.72724	0
SOD1	32.50306	1
DHCR7	32.21821	0
TM7SF2	28.0727	0
CYP51	23.27276	0
INSIG1	9.63636	1
PEX2	8.94545	2

6 weeks WB**28 weeks WB**



146x122mm (300 x 300 DPI)