

**Figure S1**

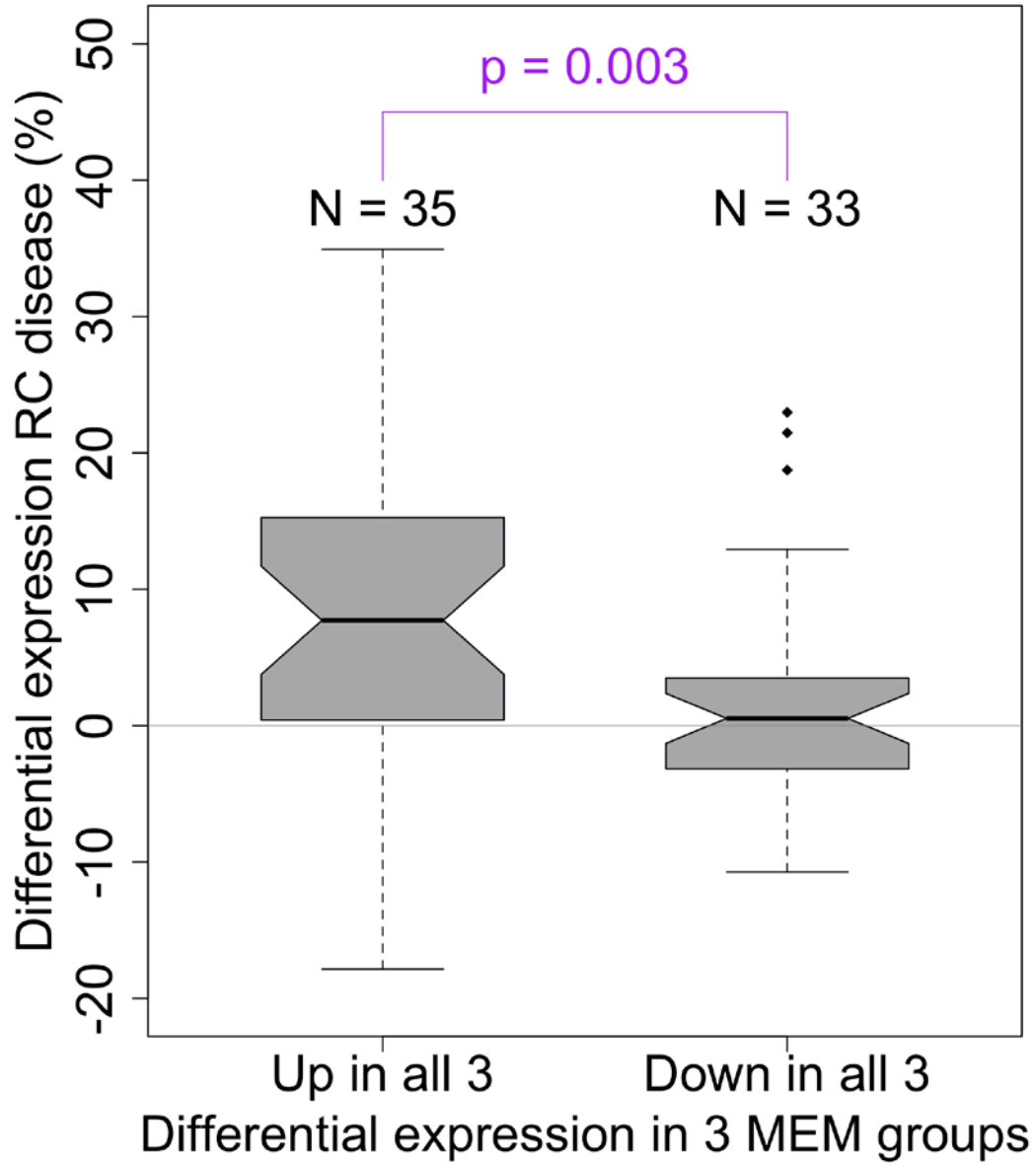


Figure S2

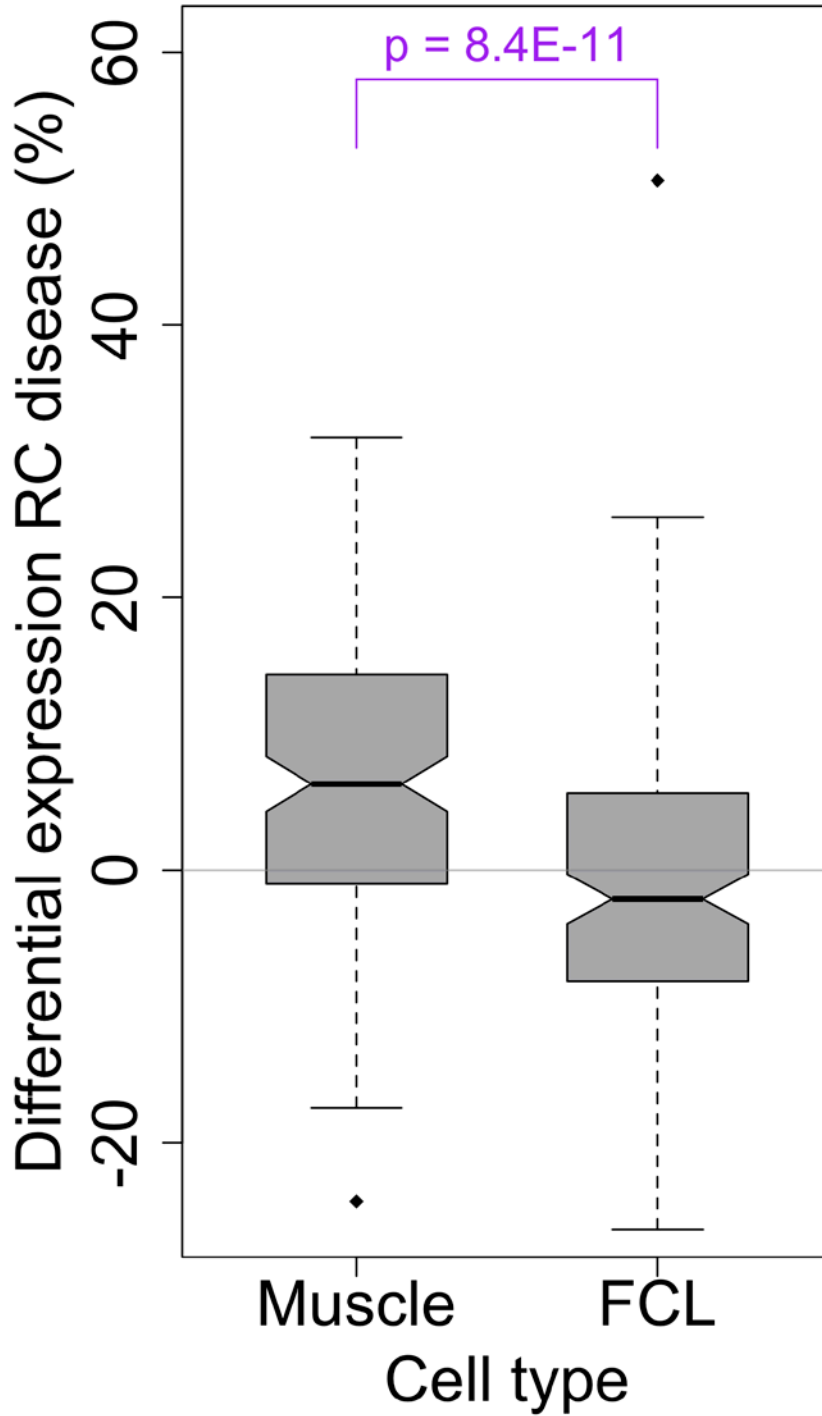
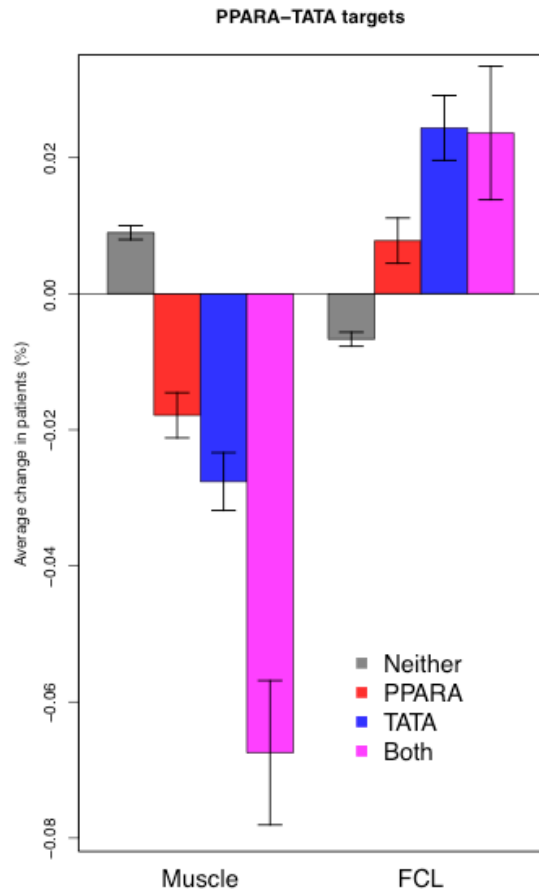
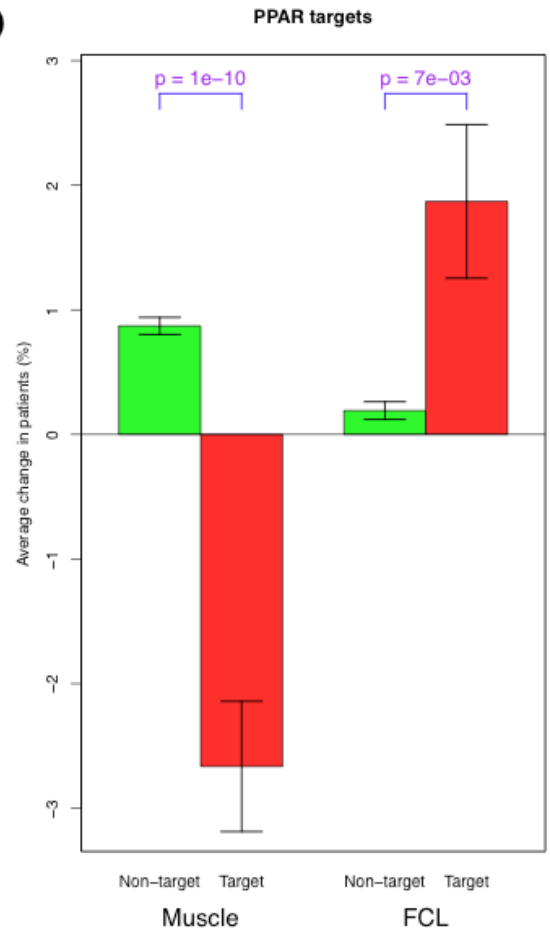


Figure S3

**A**



**B**



# Figure S4

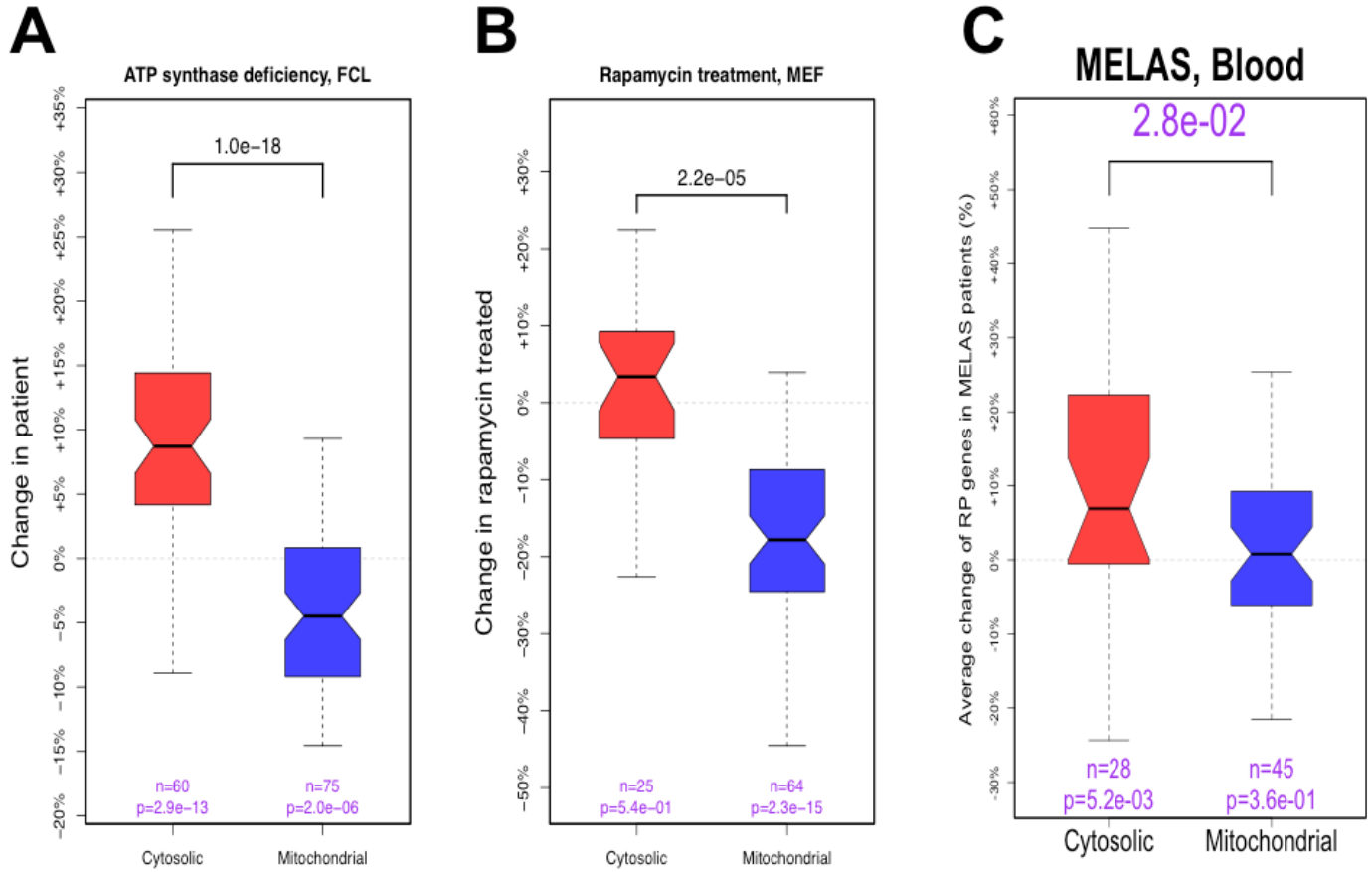
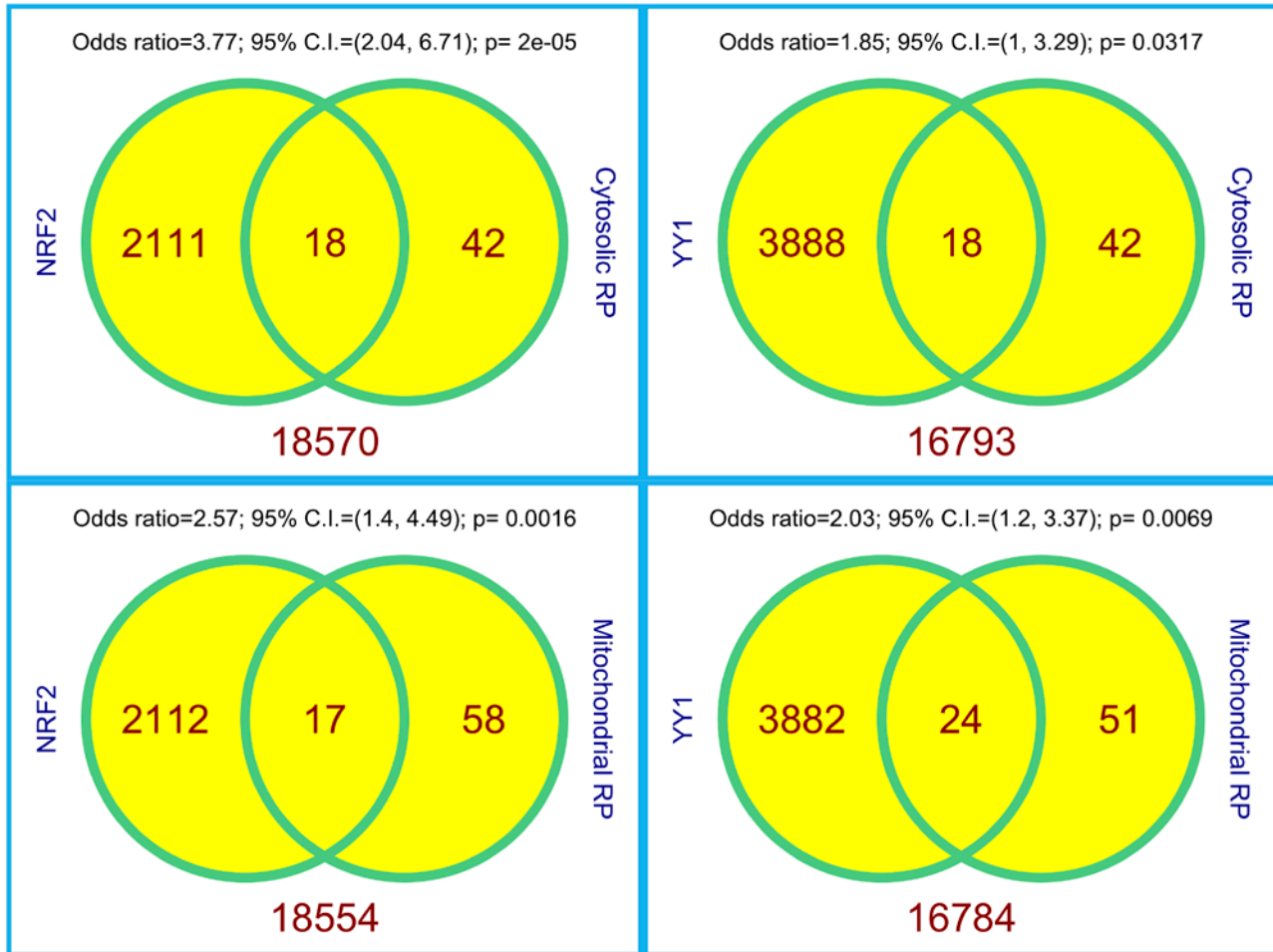
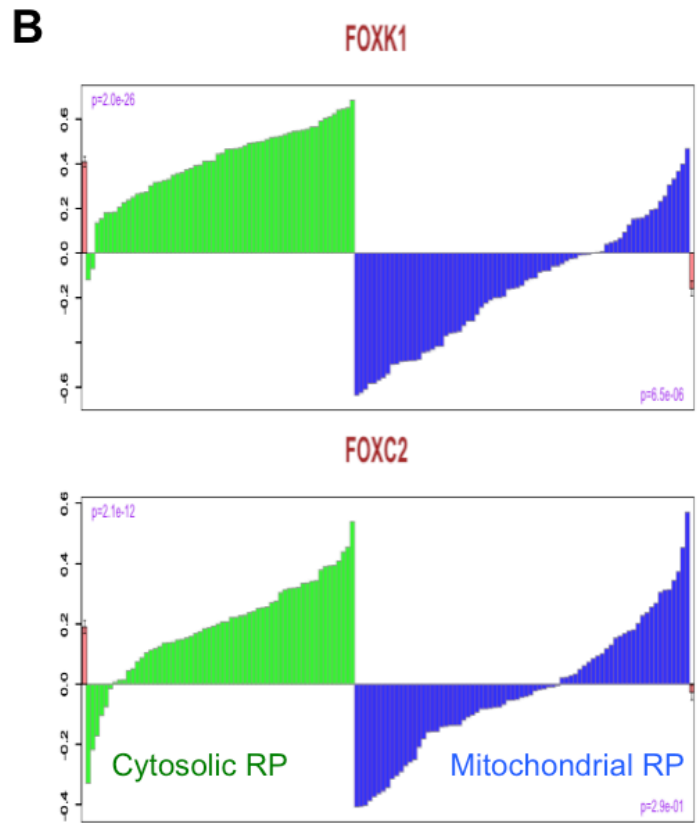
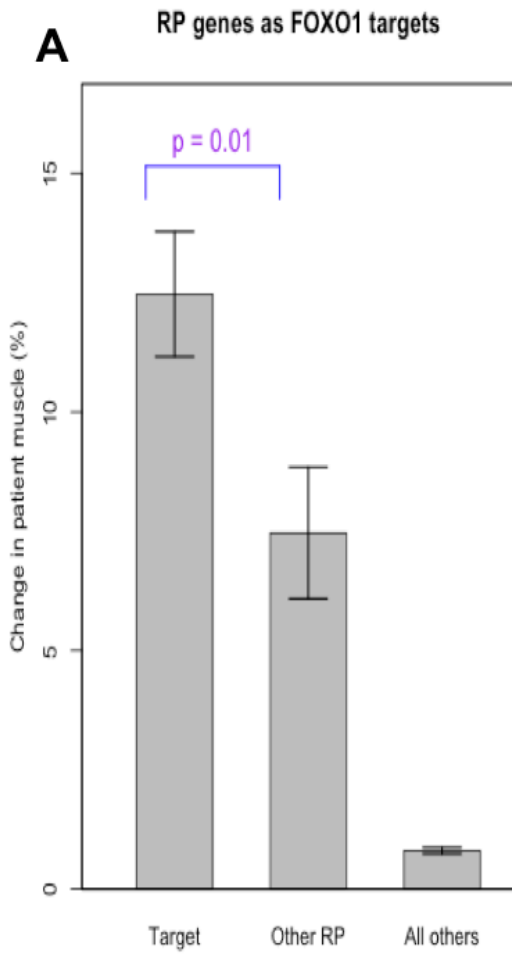


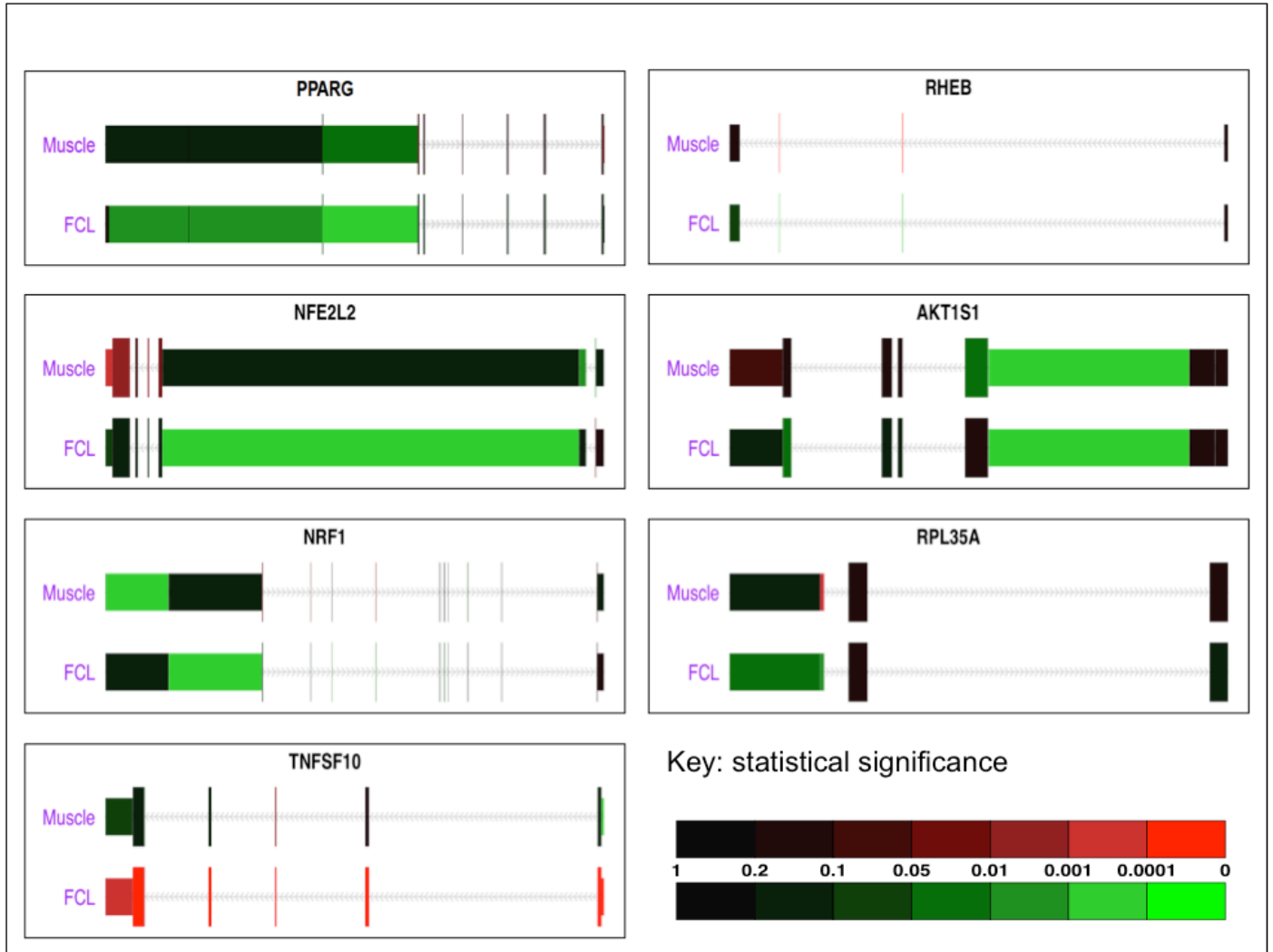
Figure S5



# Figure S6



# Figure S7



# Figure S8

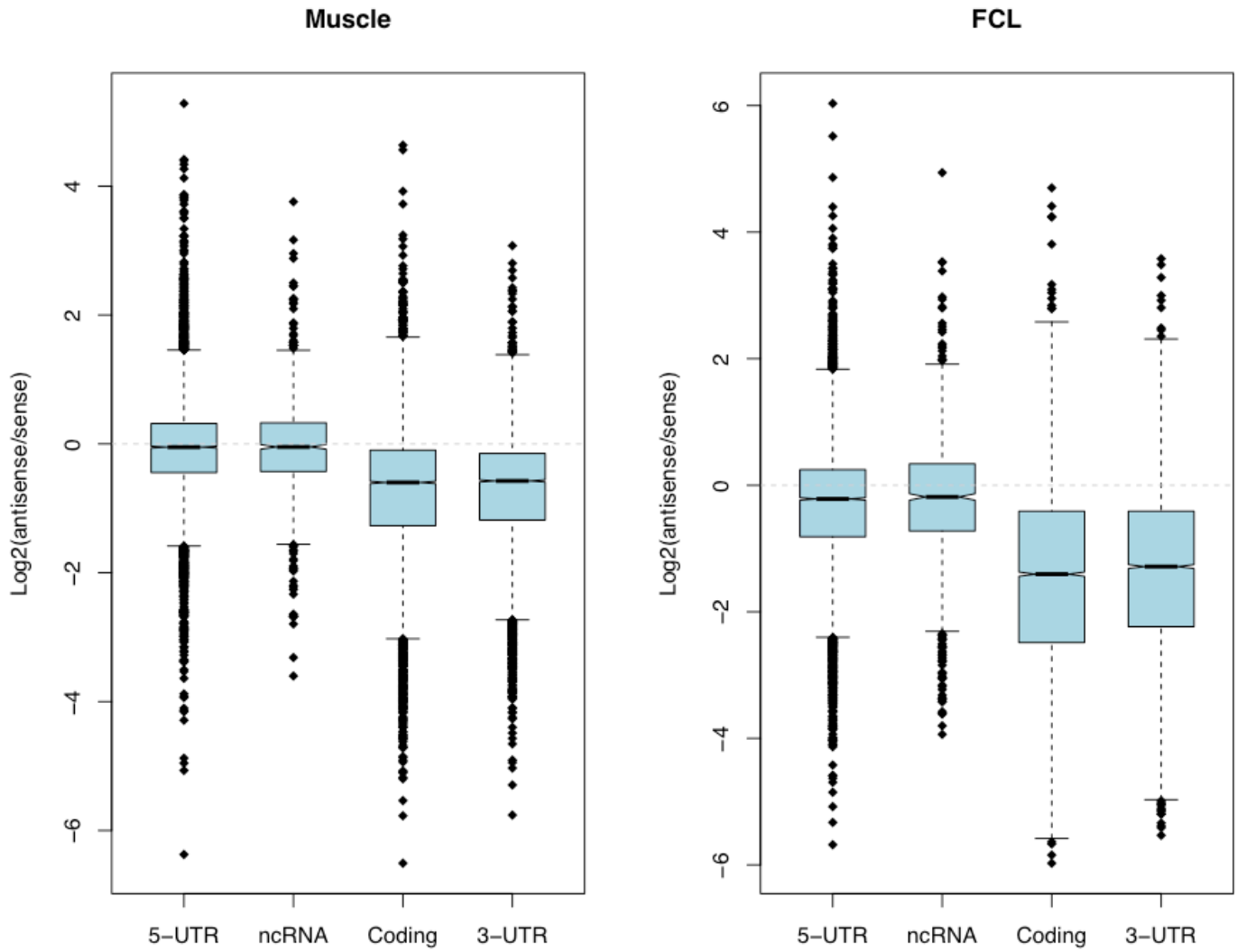
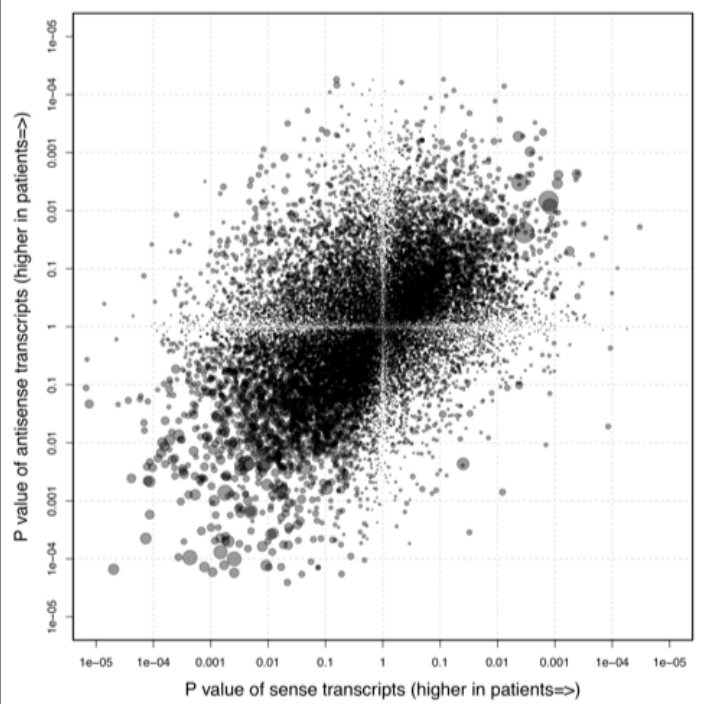
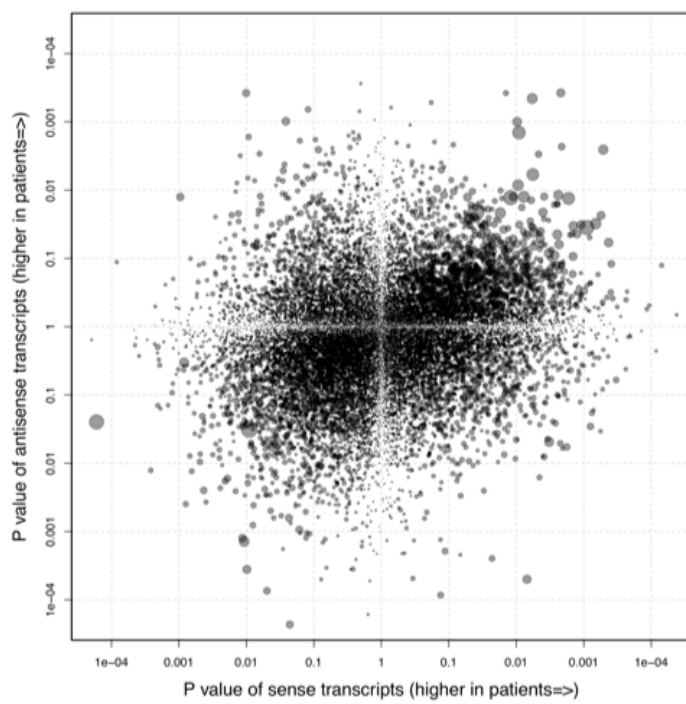




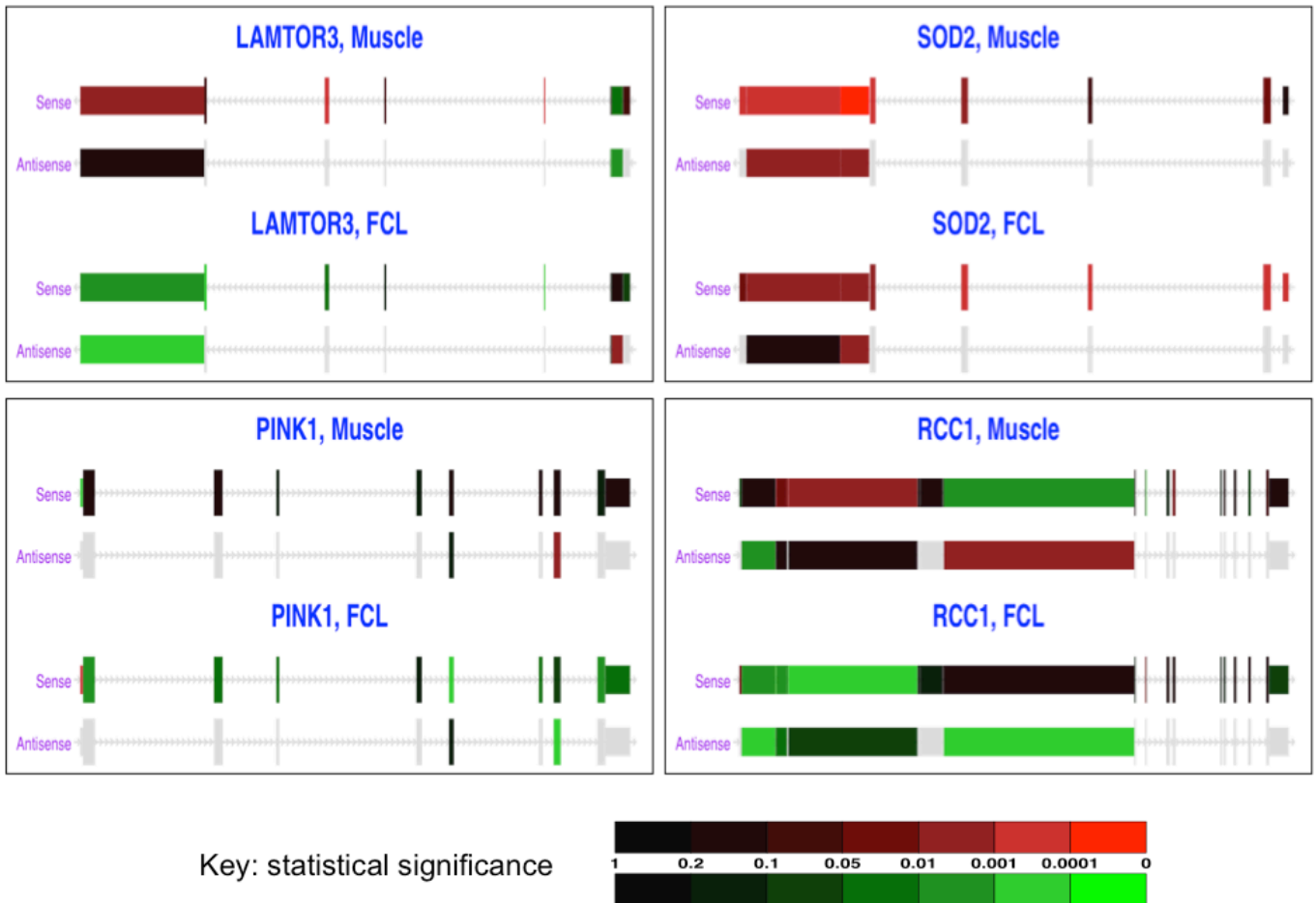
Figure S9

Muscle

FCL

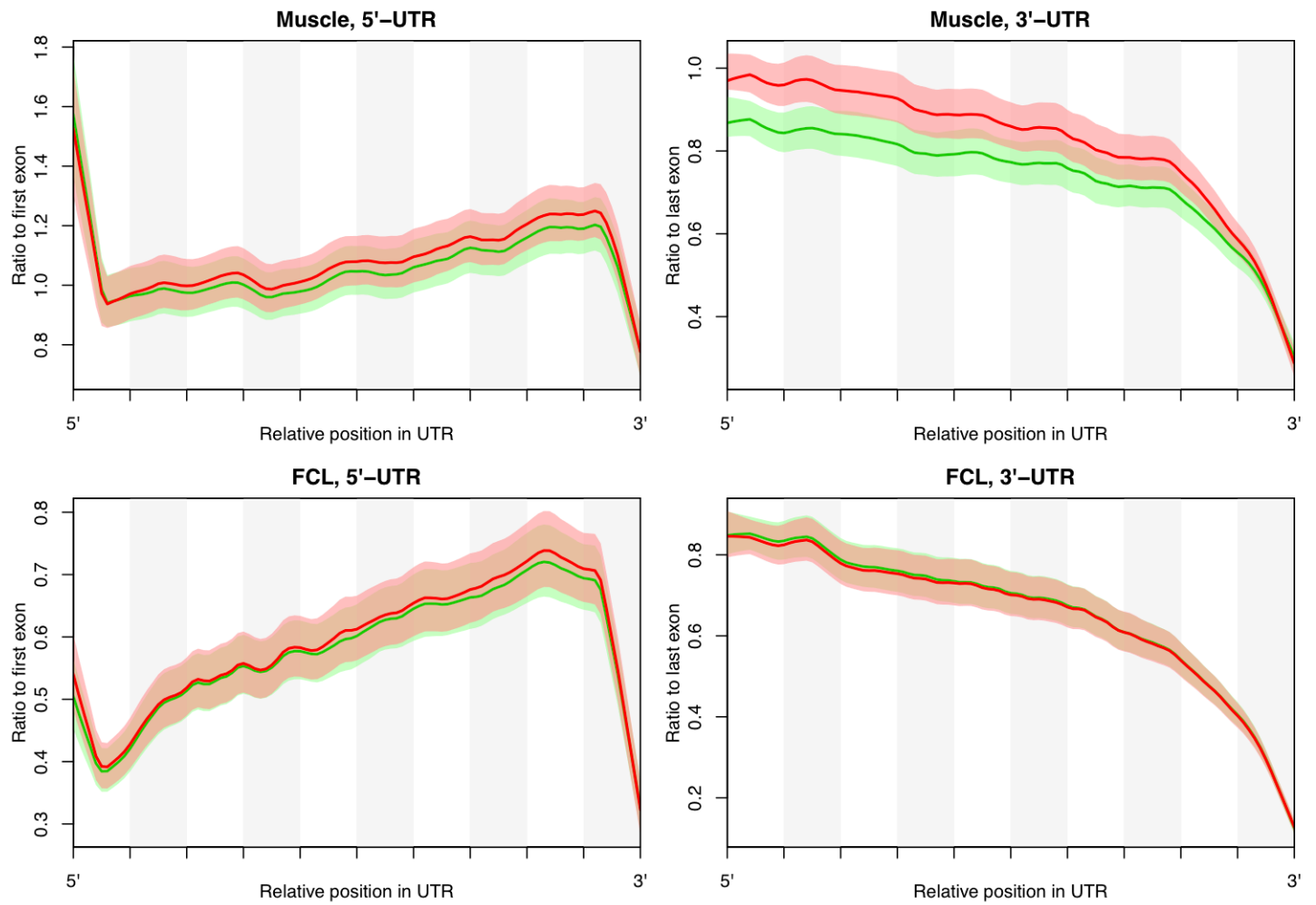


# Figure S10

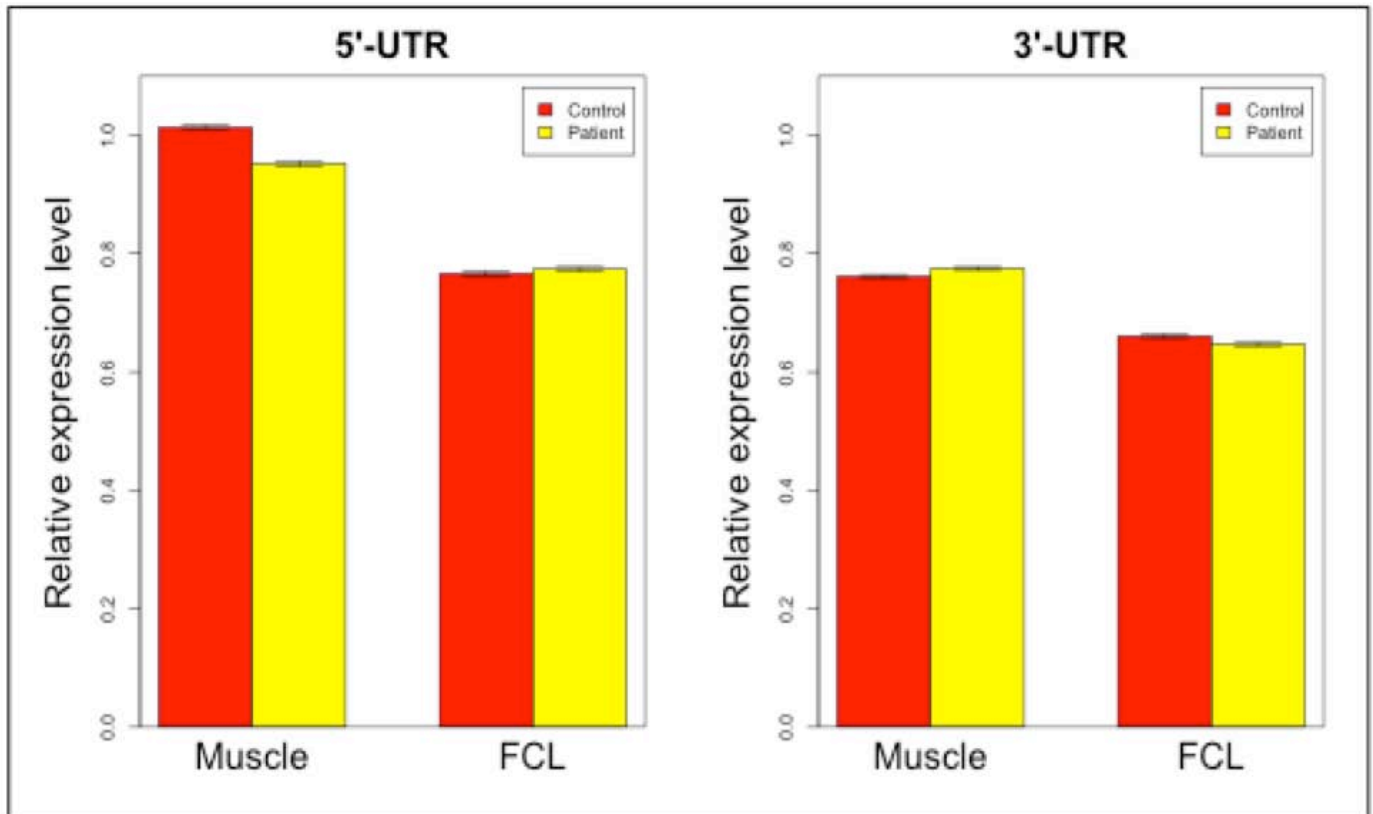


# Figure S11

## Position-specific differential expression within UTRs



**Figure S12**



# Figure S13

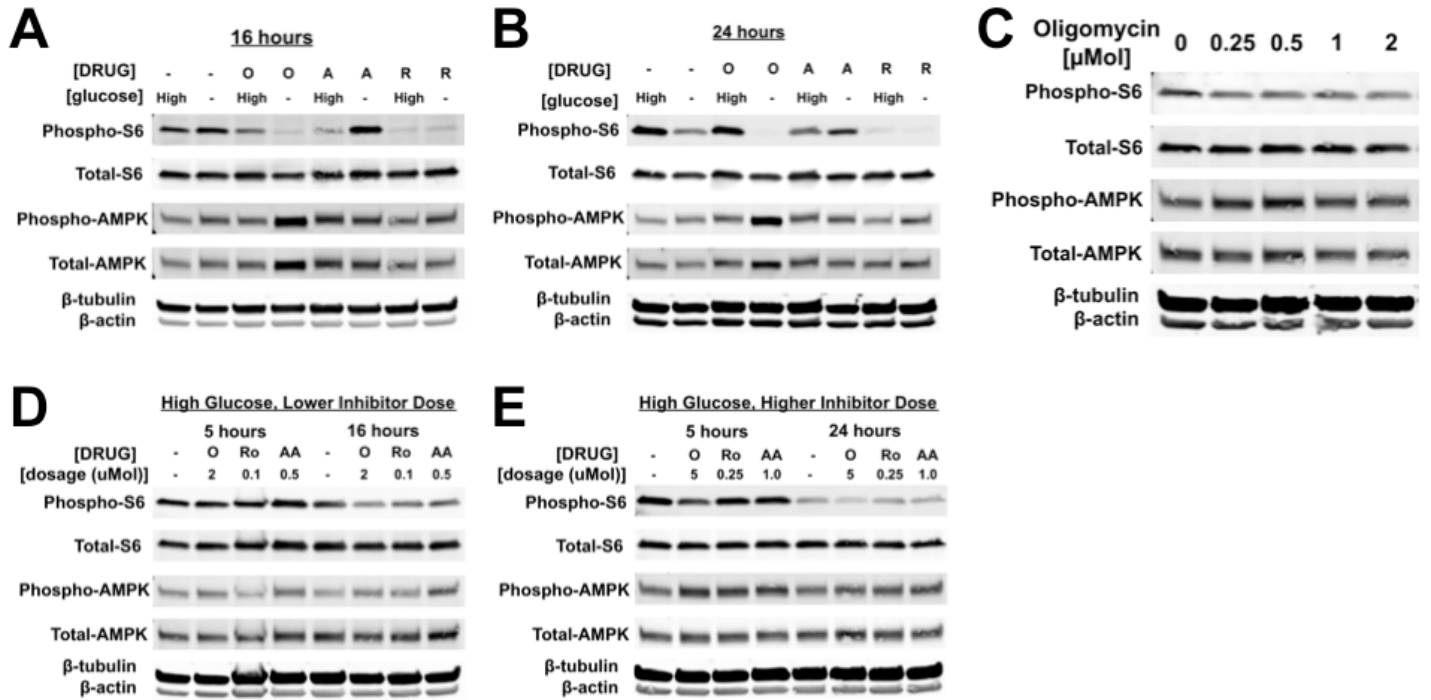


Table S1.

<b>Gene</b>	<b>MELAS</b>	<b>PEO</b>	<b>mtDNA deletion</b>	<b>RC disease</b>	<b>GENE NAME</b>
<i>PGRMC2</i>	28.35	13.82	27.43	13.96	progesterone receptor membrane component 2
<i>UBXN2B</i>	28.86	21.15	22.23	14.89	UBX domain protein 2B
<i>ESYT1</i>	46.67	63.96	37.53	28.61	extended synaptotagmin-like protein 1
<i>DNAJC15</i>	65.72	26.43	42.86	26.89	DnaJ (Hsp40) homolog, subfamily C, member 15
<i>EXOC2</i>	23.64	30.96	20.15	21.43	exocyst complex component 2
<i>SPCS3</i>	10.75	12.11	10.36	32.90	signal peptidase complex subunit 3 homolog ( <i>S. cerevisiae</i> )

Table S2

ID	Symbol	Muscle					FCL					Full name		
		Mean_Ctrl	Mean_Mto	Mto_Ctrl	Fold_change	P_SAM	FDR_SAM	Mean_Ctrl	Mean_Mto	Mto_Ctrl	Fold_change		P_SAM	FDR_SAM
6648	SOD2	9.92	10.44	0.52	1.43	0.01	0.04	10.75	11.56	0.80	1.75	0.00	0.08	superoxide dismutase 2, mitochondrial
30001	ERO1L	6.75	7.17	0.42	1.34	0.01	0.04	10.34	10.56	0.22	1.16	0.04	0.16	ERO1-like (S. cerevisiae)
29103	DNAJC15	7.33	7.68	0.34	1.27	0.02	0.06	9.77	10.10	0.33	1.26	0.02	0.10	Dnaj (Hsp40) homolog, subfamily C, member 15
81671	VMP1	7.87	8.19	0.32	1.25	0.01	0.04	10.69	10.83	0.14	1.10	0.03	0.14	vacuole membrane protein 1
3454	IFNAR1	7.39	7.65	0.27	1.20	0.04	0.11	9.66	9.90	0.25	1.19	0.04	0.14	interferon (alpha, beta and omega) receptor 1
25853	DCAF12	7.42	7.67	0.25	1.19	0.03	0.09	9.09	9.27	0.18	1.13	0.02	0.12	DDB1 and CUL4 associated factor 12
1317	SLC31A1	6.61	6.85	0.24	1.18	0.02	0.05	10.61	10.84	0.23	1.17	0.02	0.10	solute carrier family 31 (copper transporters), member 1
79607	FAM118B	7.30	7.53	0.23	1.18	0.03	0.06	9.23	9.37	0.15	1.11	0.01	0.10	family with sequence similarity 118, member B
54994	C20orf11	7.39	7.62	0.23	1.17	0.01	0.04	8.92	9.02	0.10	1.07	0.03	0.12	chromosome 20 open reading frame 11
5663	PSEN1	7.11	7.34	0.22	1.17	0.03	0.09	9.76	9.97	0.21	1.15	0.01	0.08	presenilin 1
3920	LAMP2	8.49	8.71	0.22	1.17	0.04	0.11	11.09	11.26	0.16	1.12	0.03	0.12	lysosomal-associated membrane protein 2
54877	ZCCHC2	6.85	7.06	0.21	1.16	0.05	0.12	8.29	8.53	0.23	1.17	0.03	0.14	zinc finger, CCHC domain containing 2
2120	ETV6	7.01	7.22	0.21	1.16	0.04	0.11	9.33	9.50	0.18	1.13	0.03	0.12	ets variant 6
55731	C17orf63	7.43	7.63	0.20	1.15	0.01	0.04	8.33	8.43	0.10	1.07	0.03	0.12	chromosome 17 open reading frame 63
55084	SOBP	7.15	7.34	0.19	1.14	0.01	0.04	7.00	7.21	0.21	1.16	0.05	0.16	sine oculis binding protein homolog (Drosophila)
4087	SMAD2	7.81	8.00	0.19	1.14	0.01	0.03	9.57	9.70	0.14	1.10	0.02	0.12	SMAD family member 2
84945	ABHD13	7.34	7.52	0.18	1.13	0.03	0.06	8.96	9.13	0.17	1.13	0.03	0.12	abhydrolase domain containing 13
284058	KIAA1267	7.23	7.40	0.17	1.12	0.03	0.09	8.43	8.62	0.18	1.13	0.04	0.16	KIAA1267
56160	NDNL2	6.88	7.02	0.14	1.10	0.02	0.05	8.17	8.29	0.12	1.09	0.03	0.14	necdin-like 2
55851	PSENEN	7.77	7.90	0.13	1.09	0.04	0.11	10.71	10.84	0.13	1.10	0.02	0.12	presenilin enhancer 2 homolog (C. elegans)
199223	TTC21A	6.50	6.43	-0.07	0.95	0.04	0.09	7.18	7.04	-0.15	0.90	0.00	0.03	tetratricopeptide repeat domain 21A
57732	ZFYVE28	6.86	6.79	-0.07	0.95	0.03	0.09	7.48	7.40	-0.08	0.95	0.04	0.12	zinc finger, FYVE domain containing 28
81029	WNT5B	6.72	6.64	-0.08	0.95	0.04	0.09	7.93	7.73	-0.20	0.87	0.02	0.07	wingless-type MMTV integration site family, member 5B
63898	SH2D4A	7.06	6.98	-0.08	0.95	0.05	0.09	9.17	8.79	-0.38	0.77	0.04	0.12	SH2 domain containing 4A
91544	UBXN11	6.85	6.76	-0.08	0.94	0.04	0.09	7.63	7.55	-0.08	0.95	0.04	0.12	UBX domain protein 11
147	ADRA1B	7.11	7.03	-0.08	0.94	0.03	0.09	7.78	7.52	-0.26	0.84	0.03	0.10	adrenergic, alpha-1B-, receptor
9942	XYLB	7.01	6.93	-0.09	0.94	0.03	0.09	8.77	8.54	-0.23	0.86	0.00	0.03	xylulokinase homolog (H. influenzae)
5865	RAB3B	6.68	6.59	-0.09	0.94	0.02	0.06	9.36	8.66	-0.70	0.62	0.01	0.07	RAB3B, member RAS oncogene family
56120	PCDHGB8P	6.80	6.71	-0.09	0.94	0.04	0.09	7.48	7.29	-0.18	0.88	0.01	0.06	protocadherin gamma subfamily B, 8 pseudogene
58538	MPP4	6.49	6.39	-0.10	0.93	0.02	0.06	6.95	6.78	-0.18	0.89	0.03	0.10	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
114784	CSMD2	6.77	6.67	-0.10	0.93	0.01	0.06	7.70	7.43	-0.27	0.83	0.04	0.12	CUB and Sushi multiple domains 2
79413	ZBED2	6.71	6.61	-0.10	0.93	0.05	0.09	6.95	6.85	-0.10	0.93	0.01	0.05	zinc finger, BED-type containing 2
199221	DZIP1L	6.77	6.67	-0.10	0.93	0.01	0.06	7.26	7.18	-0.08	0.94	0.02	0.07	DAZ interacting protein 1-like
26266	SLC13A4	6.91	6.81	-0.11	0.93	0.03	0.09	7.42	7.30	-0.12	0.92	0.02	0.08	solute carrier family 13 (sodium/sulfate symporters), member 4
100303749	LOC100303749	6.23	6.12	-0.11	0.93	0.04	0.09	6.52	6.37	-0.15	0.90	0.01	0.06	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) pseudogene
435	ASL	7.21	7.10	-0.12	0.92	0.00	0.06	8.93	8.67	-0.27	0.83	0.03	0.10	argininosuccinate lyase
388948	LOC388948	6.53	6.41	-0.12	0.92	0.04	0.09	7.06	6.89	-0.18	0.88	0.01	0.05	hypothetical LOC388948
10505	SEMA4F	6.89	6.77	-0.12	0.92	0.01	0.06	8.18	7.98	-0.20	0.87	0.02	0.07	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
28956	LAMTOR2	7.40	7.27	-0.13	0.92	0.02	0.06	8.58	8.44	-0.14	0.91	0.03	0.10	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2
284344	LOC284344	6.41	6.27	-0.13	0.91	0.00	0.06	6.69	6.47	-0.22	0.86	0.01	0.04	hypothetical LOC284344
2817	GPC1	8.18	8.03	-0.14	0.90	0.03	0.06	9.91	9.60	-0.31	0.81	0.04	0.12	glypican 1
388610	TRNP1	7.29	7.12	-0.17	0.89	0.00	0.06	8.57	8.34	-0.24	0.85	0.05	0.14	TMF1-regulated nuclear protein 1
5675	PSG6	6.83	6.62	-0.21	0.86	0.02	0.06	8.18	7.65	-0.52	0.70	0.01	0.06	pregnancy specific beta-1-glycoprotein 6
51334	PRR16	7.40	7.16	-0.24	0.85	0.02	0.06	8.98	8.70	-0.28	0.83	0.03	0.10	proline rich 16
5339	PLEC	8.59	8.33	-0.26	0.84	0.04	0.09	9.90	9.71	-0.19	0.88	0.04	0.12	plectin
10370	CITED2	8.29	8.01	-0.28	0.83	0.01	0.06	10.21	9.89	-0.32	0.80	0.02	0.07	Ctbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
7170	TPM3	10.13	9.80	-0.32	0.80	0.04	0.09	8.46	8.31	-0.16	0.90	0.01	0.07	tropomyosin 3
4633	MYL2	13.39	12.79	-0.61	0.66	0.01	0.06	6.65	6.56	-0.09	0.94	0.03	0.12	myosin, light chain 2, regulatory, cardiac, slow