

S1: Description of microarray experiment and analysis

RNA was extracted from quadriceps muscle from three male *sg/sg* mice and their wild type littermates using TRI-Reagent (Sigma-Aldrich, St. Louis, MO) and RNeasy mini kit (Qiagen, Hilden, Germany) according to the manufacturers' protocol. Total skeletal muscle RNA was assessed for integrity using the Agilent Bioanalyzer 2100 and RNA integrity (RIN) scores above 8.4 were present in all samples. 500ng of RNA was amplified using the Illumina TotalPrep RNA Amplification kit (Ambion, Austin, TX) with an *in vitro* transcription reaction period of 12 hours. Biotinylated, amplified cRNA was assessed for quantity and quality also using the Agilent Bioanalyzer 2100. 1500 ng per array of amplified cRNA was hybridized to Mouse-6.v1 BeadChip arrays (Illumina, San Diego, CA) according to manufacturer directions. Hybridized BeadChip arrays were stained with Amersham fluorolink streptavidin-Cy3 (GE Healthcare, Pittsburgh, PA). BeadChip arrays were scanned with Illumina BeadStation Scanner and data values with detection scores were compiled using BeadStudio v1.5 (Illumina) and imported into GeneSpring GX v10 (Agilent, Santa Clara CA) for data analysis. Mouse Illumina probe set was defined in the GeneSpring Workgroup using the Illumina targetIDs as the unique identifiers and annotated according to array content files supplied by Illumina. All probes values less than 0.01 were set to 0.01. Data was normalized by first applying normalization to the median and per chip normalization to the 50th percentile. Samples were grouped as wild type and Tg-ROR α 1 Δ DE. Statistical analysis was performed using a parametric Welch's t-test (where variances were not assumed equal) with a p-value cutoff of 0.05. Multiple testing corrections were applied to reduce false positives using Benjamini and Hochberg False Discovery Rate.

S2 – Table of all significantly regulated genes in Tg-ROR α 1 Δ DE mice

Symbol	Gene Name	Fold change	Direction	p-value	Accession
Ucp1	Uncoupling protein 1	34.89	Down	0.000	NM_009463.2
Fasn	Fatty acid synthase	8.96	Down	0.001	NM_007988.3
Cidea	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	8.58	Down	0.000	NM_007702.1
A830080H07Rik	RIKEN cdna A830080H07Rik gene	6.31	Up	0.000	
8430408G22Rik	RIKEN cdna 8430408G22 gene	6.03	Down	0.007	NM_145980.1
Scd1	Stearoyl-Coenzyme A desaturase 1	5.47	Down	0.004	NM_009127.3
LOC670615	PREDICTED: similar to alpha-2u globulin PGCL3	5.03	Down	0.003	XM_982323.1
Hp	Haptoglobin	4.22	Down	0.004	NM_017370.1
Prkar2b	Protein kinase, camp dependent regulatory, type II beta	4.06	Down	0.004	NM_011158.3
2210013O21Rik	PREDICTED: RIKEN cdna 2210013O21 gene	3.28	Down	0.000	XM_982708.1
Apoc1	Apolipoprotein C-I	3.11	Down	0.006	NM_007469.2
Igh-6	Immunoglobulin heavy chain 6 (heavy chain of IgM)	2.93	Down	0.014	XM_354710.1
Fah	Fumarylacetoacetate hydrolase	2.72	Down	0.008	NM_010176.1
Zranb3	Zinc finger, RAN-binding domain containing 3	2.64	Up	0.000	NM_172642.1
Tmem45b	Transmembrane protein 45b	2.62	Down	0.000	NM_144936.1
Rom1	Rod outer segment membrane protein 1	2.54	Up	0.000	NM_009073.2
Elovl6	ELOVL family member 6, elongation of long chain fatty acids	2.47	Down	0.000	NM_130450.2
Myo1e	Myosin IE	2.43	Down	0.010	NM_181072.3
Tceal5	Transcription elongation factor A (SII)-like 5	2.43	Up	0.001	NM_177919.1
A130092J06Rik	RIKEN cdna A130092J06 gene	2.28	Up	0.005	NM_175511.2
Col7a1	Procollagen, type VII, alpha 1	2.21	Up	0.010	NM_007738.3
Ces3	Carboxylesterase 3	2.21	Down	0.001	NM_053200.2
A130038J17Rik	RIKEN cdna A130038J17Rik gene	2.11	Down	0.005	
Sfxn1	Sideroflexin 1	2.11	Down	0.013	NM_027324.2
Plekhb1	Pleckstrin homology domain containing, family B (evectins) member 1	2.10	Up	0.001	NM_013746.1
Tnfrsf22	Tumor necrosis factor receptor superfamily, member 22	2.10	Up	0.001	NM_023680.2
BC048679	Cdna sequence BC048679	2.08	Down	0.011	NM_183143.1
Acaca	Acetyl-Coenzyme A carboxylase alpha	2.02	Down	0.002	NM_133360.2
Rab15	RAB15, member RAS oncogene family	2.00	Down	0.008	NM_134050.2
2310040G24Rik	RIKEN cdna 2310040G24Rik gene	2.00	Up	0.002	XM_149767.1
Cox6a1	Cytochrome c oxidase, subunit VI a, polypeptide 1	2.00	Down	0.000	NM_007748.3
Tkt	Transketolase	1.97	Down	0.004	NM_009388.2
1810005K13Rik	RIKEN cdna 1810005K13Rik gene	1.96	Down	0.000	
Tnfrsf22	Tumor necrosis factor receptor superfamily, member 22	1.94	Up	0.001	NM_023680
Fgfbp1	Fibroblast growth factor binding protein 1	1.90	Down	0.006	NM_008009.3
7330410H16Rik	RIKEN cdna 7330410H16Rik gene	1.90	Down	0.011	
Thrsp	Thyroid hormone responsive SPOT14 homolog	1.90	Down	0.006	NM_009381.2
Gfer	Growth factor, erv1 (S. Cerevisiae)-like (augmenter of liver regeneration)	1.90	Up	0.000	NM_023040.3
Sfxn1	Sideroflexin 1	1.90	Down	0.010	NM_027324.2
2810423O19Rik	RIKEN cdna 2810423O19Rik gene	1.88	Down	0.001	NM_026447

Cox6a1	Cytochrome c oxidase, subunit VI a, polypeptide 1	1.86	Down	0.000	NM_007748.3
BC054059	Cdna sequence BC054059	1.85	Down	0.000	NM_145635.2
D12Ert647e	DNA segment, Chr 12, ERATO Doi 647, expressed, transcript variant 4	1.85	Down	0.006	NM_194068.1
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	1.84	Down	0.000	NM_026212.1
Pygl	Liver glycogen phosphorylase	1.84	Down	0.000	NM_133198.1
2510002J07Rik	RIKEN cdna 2510002J07Rik gene	1.84	Down	0.005	AK002422
Ehhadh	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	1.83	Down	0.007	NM_023737.2
scl0015365.1_6	Cdna sequence scl0015365.1_6	1.83	Up	0.000	BC064076.1
Aoc3	Amine oxidase, copper containing 3	1.81	Down	0.012	NM_009675.1
M6prbp1	Mannose-6-phosphate receptor binding protein 1	1.81	Down	0.003	NM_025836.1
Tob1	Transducer of erbb-2.1	1.79	Up	0.011	NM_009427.2
ldh1	Isocitrate dehydrogenase 1 (NADP+), soluble	1.79	Down	0.007	NM_010497.2
Stab2	Stabilin 2	1.79	Up	0.001	NM_138673.1
Atp1b4	Atpase, (Na+)/K+ transporting, beta 4 polypeptide	1.78	Down	0.000	NM_133690.2
Exod1	Exonuclease domain containing 1	1.77	Down	0.012	NM_027698.3
Camk2n2	PREDICTED: calcium/calmodulin-dependent protein kinase II inhibitor 2	1.77	Up	0.003	XM_993468.1
2810416G20Rik	RIKEN cdna 2810416G20Rik gene	1.77	Down	0.001	XM_487719
Hsd17b12	Hydroxysteroid (17-beta) dehydrogenase 12	1.76	Down	0.002	NM_019657.2
Wnt4	Wingless-related MMTV integration site 4	1.76	Down	0.004	NM_009523.1
Cebpa	CCAAT/enhancer binding protein	1.75	Down	0.005	NM_007678.2
Slc27a2	Solute carrier family 27 (fatty acid transporter), member 2	1.73	Down	0.009	NM_011978.2
7330410H16Rik	RIKEN cdna 7330410H16Rik gene	1.72	Down	0.007	
Apoc1	Apolipoprotein C-I	1.72	Down	0.013	NM_007469.2
Il17re	Interleukin 17 receptor E, transcript variant 2	1.71	Up	0.001	NM_001034029.1
Tmcc3	Transmembrane and coiled coil domains 3	1.71	Down	0.004	NM_172051.2
Zfp691	Zinc finger protein 691	1.71	Down	0.000	NM_183140.1
Olfm1	Olfactomedin 1, transcript variant 2	1.68	Down	0.010	NM_001038612.1
Gnao1	Guanine nucleotide binding protein, alpha o	1.68	Down	0.007	NM_010308.3
Gcat	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	1.67	Down	0.012	NM_013847
BC013481	Cdna sequence BC013481	1.66	Down	0.012	NM_139065.1
3110023G01Rik	RIKEN cdna 3110023G01Rik gene	1.65	Up	0.006	AK014074
Abhd8	Abhydrolase domain containing 8	1.64	Down	0.005	NM_022419.1
Pparg	Peroxisome proliferator activated receptor gamma	1.64	Down	0.001	NM_011146.1
A730009E18Rik	RIKEN cdna A730009E18Rik gene	1.64	Up	0.004	
Cox8a	Cytochrome c oxidase, subunit viiia	1.63	Down	0.001	NM_007750.2
Tspo	Translocator protein	1.62	Down	0.001	NM_009775.2
Lrtm1	Leucine-rich repeats and transmembrane domains 1	1.62	Down	0.001	NM_176920.2
Igh-1a	Immunoglobulin heavy chain 1a	1.62	Down	0.002	XM_354704.1
Slc16a10	Solute carrier family 16 (monocarboxylic acid transporters), member 10	1.62	Down	0.001	NM_028247.1
Lgals1	Lectin, galactose binding, soluble 1	1.61	Up	0.000	NM_008495.2
Slc22a4	Solute carrier family 22 (organic cation transporter), member 4	1.61	Up	0.007	NM_019687.3
Tspo	Translocator protein	1.60	Down	0.003	NM_009775.2

SUPPLEMENTARY FIGURES FROM "Identification and validation of the pathways and functions regulated by the orphan nuclear receptor, ROR alpha, in skeletal muscle." S Raichur *et al*

Hsd11b1	Hydroxysteroid 11-beta dehydrogenase 1, transcript variant 2	1.60	Down	0.001	NM_001044751.1
Slc25a30	Solute carrier family 25, member 30	1.60	Down	0.001	NM_026232
Htra4	PREDICTED: htra serine peptidase 4	1.60	Down	0.008	XM_911236.2
Ush1c	Usher syndrome 1C homolog, transcript variant a1	1.59	Up	0.008	NM_023649.1
Hp	Haptoglobin	1.59	Down	0.007	NM_017370.1
Cd1d1	CD1d1 antigen	1.59	Down	0.000	NM_007639.1
B930041F14Rik	RIKEN cdna B930041F14 gene	1.59	Up	0.002	NM_178699.3
EG433923	Predicted gene, EG433923	1.57	Down	0.003	NM_001081233.1
Ppp1r1a	Protein phosphatase 1, regulatory (inhibitor) subunit 1A	1.57	Down	0.008	NM_021391.3
Exoc7	Exocyst complex component 7	1.57	Down	0.014	NM_016857
Arhgap26	Rho gtpase activating protein 26	1.56	Down	0.001	NM_175164.4
Maged2	Melanoma antigen, family D, 2	1.55	Up	0.003	NM_030700.1
Atf5	Activating transcription factor 5	1.55	Down	0.009	NM_030693.1
Vldlr	Very low density lipoprotein receptor	1.55	Down	0.012	NM_013703.1
Mrap	Melanocortin 2 receptor accessory protein	1.54	Down	0.001	NM_029844.1
Mif	Macrophage migration inhibitory factor	1.54	Down	0.009	NM_010798.1
C030044C12Rik	RIKEN cdna C030044C12Rik gene	1.53	Up	0.014	
Idh3b	Isocitrate dehydrogenase 3 (NAD+) beta	1.53	Down	0.007	NM_130884.1
Cdk5rap1	CDK5 regulatory subunit associated protein 1	1.53	Down	0.010	NM_025876.2
LOC673040	PREDICTED: similar to La-related protein 4 (La ribonucleoprotein domain family member 4)	1.53	Down	0.004	XM_001003792.1
4931406C07Rik	RIKEN cdna 4931406C07 gene	1.53	Down	0.004	NM_133732.2
Ibrdc2	IBR domain containing 2	1.52	Down	0.015	NM_146042
0610007N19Rik	RIKEN cdna 0610007N19Rik gene	1.52	Down	0.000	AK007719
1700037H04Rik	RIKEN cdna 1700037H04 gene	1.52	Down	0.013	NM_026091.1
Ociad2	OClA domain containing 2	1.52	Down	0.009	NM_026950.3
Gdf11	Growth differentiation factor 11	1.52	Up	0.007	NM_010272.1
1110059G02Rik	RIKEN cdna 1110059G02Rik gene	1.51	Up	0.011	
5430432N15Rik	RIKEN cdna 5430432N15Rik gene	1.51	Up	0.000	NM_172418.1
Ras11b	RAS-like, family 11, member B	1.50	Down	0.009	NM_026878.1
Sfxn3	Sideroflexin 3	1.50	Up	0.010	NM_053197.2
Rab11fip5	RAB11 family interacting protein 5 (class I), transcript variant 2	1.50	Up	0.009	NM_177466.4
Synpo2l	Synaptopodin 2-like	1.50	Up	0.008	NM_175132.3
5730472N09Rik	RIKEN cdna 5730472N09 gene	1.50	Down	0.012	NM_175392.3
Hes1	Hairy and enhancer of split 1	1.49	Up	0.001	NM_008235.2
9630055N22Rik	PREDICTED: RIKEN cdna 9630055N22 gene, transcript variant 3	1.49	Down	0.010	XM_900121.2
Adfp	Adipose differentiation related protein	1.48	Down	0.001	NM_007408.3
LOC669042	PREDICTED: similar to zinc finger protein EZ1, transcript variant 3	1.48	Down	0.001	XM_972708.1
Csnk1e	Casein kinase 1, epsilon	1.48	Down	0.010	NM_013767.3
Uros	Uroporphyrinogen III synthase	1.48	Down	0.013	NM_009479.2
1200004M23Rik	RIKEN cdna 1200004M23 gene	1.47	Down	0.002	NM_026169.3
Actr1b	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	1.47	Up	0.001	NM_146107
2810008M24Rik	RIKEN cdna 2810008M24 gene	1.47	Down	0.007	NM_001048250.1
Actr1b	ARP1 actin-related protein 1 homolog B	1.47	Up	0.007	NM_146107.2
Rala	V-ral simian leukemia viral oncogene homolog A (ras related)	1.47	Up	0.004	NM_019491.5
BC034902	cDNA sequence BC034902	1.46	Down	0.002	NM_177654.2
Sms	Spermine synthase	1.46	Up	0.000	NM_009214.3
Got2	Glutamate oxaloacetate transaminase 2, mitochondrial	1.46	Down	0.001	NM_010325.1

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Cdk5rap1	CDK5 regulatory subunit associated protein 1	1.46	Down	0.002	NM_025876.2
Hsd11b1	Hydroxysteroid 11-beta dehydrogenase 1, transcript variant 2	1.46	Down	0.008	NM_001044751.1
AW548124	PREDICTED: expressed sequence AW548124	1.46	Up	0.002	XM_916849.2
Ephx2	Epoxide hydrolase 2, cytoplasmic	1.46	Down	0.002	NM_007940.3
Gca	Grancalcin	1.46	Down	0.004	NM_145523.2
8430403J19Rik	RIKEN cdna 8430403J19Rik gene	1.46	Down	0.005	AK033358
5730409N16Rik	RIKEN cdna 5730409N16Rik gene	1.46	Down	0.006	
Pfkl	Phosphofructokinase, liver, B-type	1.45	Down	0.002	NM_008826.2
EG432436	Predicted gene, EG432436	1.45	Down	0.008	NM_001004162.1
Gstm2	Glutathione S-transferase, mu 2	1.45	Down	0.010	NM_008183.2
LOC208080	cDNA sequence LOC208080	1.45	Up	0.001	XM_146931.2
Trio	PREDICTED: triple functional domain (PTPRF interacting), transcript variant 1	1.45	Down	0.005	XM_888341.2
Cdh13	Cadherin 13	1.44	Down	0.007	NM_019707.2
Ptplb	Protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	1.44	Down	0.004	NM_023587
4930430F08Rik	RIKEN cdna 4930430F08 gene	1.44	Down	0.010	NM_175128.1
C1qtnf4	C1q and tumor necrosis factor related protein 4	1.44	Up	0.006	NM_026161.1
Car14	Carbonic anhydrase 14	1.43	Down	0.010	AK009805
LOC385505	cDNA sequence LOC385505	1.43	Down	0.011	XM_358255.1
C920006O11Rik	RIKEN cdna C920006O11Rik gene	1.43	Down	0.007	XM_489286
Tbc1d1	TBC1 domain family, member 1	1.43	Down	0.000	NM_019636.2
Nudt8	Nudix (nucleoside diphosphate linked moiety X)-type motif 8	1.43	Down	0.011	NM_025529.2
Akt2	Thymoma viral proto-oncogene 2	1.43	Down	0.005	NM_007434.2
Csnk1e	Casein kinase 1, epsilon	1.42	Down	0.004	NM_013767.3
Sorl1	Sortilin-related receptor containing LDLR class A repeats	1.42	Up	0.009	NM_011436
Des	Desmin	1.42	Up	0.004	NM_010043.1
Pter	Phosphotriesterase related	1.41	Down	0.003	NM_008961.2
Acsf5	Acyl-coa synthetase long-chain family member 5	1.41	Down	0.007	NM_027976.2
1700052O22Rik	RIKEN cdna 1700052O22Rik gene	1.41	Down	0.000	
Slc25a5	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	1.40	Down	0.005	NM_007451.2
LOC383153	cDNA sequence LOC383153	1.40	Down	0.011	XM_356899.1
LOC625421	PREDICTED: similar to zinc finger protein 570	1.40	Down	0.001	XM_889991.2
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	1.40	Up	0.002	NM_053179.2
Zc3h13	Zinc finger CCCH type containing 13	1.40	Down	0.004	NM_026083.2
Ccl25	Chemokine (C-C motif) ligand 25	1.40	Up	0.002	NM_009138.1
LOC669267	PREDICTED: similar to calcium/calmodulin-dependent protein kinase I	1.39	Up	0.000	XM_974106.1
LOC666756	PREDICTED: similar to Polyadenylate-binding protein 1	1.39	Down	0.002	XR_001916.1
Csad	Cysteine sulfinic acid decarboxylase	1.39	Down	0.009	NM_144942
Pdhb	Pyruvate dehydrogenase (lipoamide) beta	1.39	Down	0.009	AK084507
Chst1	Carbohydrate keratan sulfate Gal-6) sulfotransferase 1	1.39	Down	0.010	NM_023850.1
Rrm1	Ribonucleotide reductase M1	1.39	Up	0.002	NM_009103
Eif1ay	Eukaryotic translation initiation factor 1A, Y-linked	1.39	Up	0.012	NM_025437
Wipi1	WD repeat domain, phosphoinositide interacting 1	1.39	Down	0.002	NM_145940.2
scl0001483.1_25	cDNA sequence scl0001483.1_25	1.39	Down	0.007	

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BC039632	PREDICTED: cDNA sequence BC039632	1.39	Up	0.004	XM_986159.1
Pcp2	Purkinje cell protein 2	1.38	Down	0.006	AK013674
Cebpg	CCAAT/enhancer binding protein	1.38	Down	0.005	NM_009884.2
2310004I03Rik	RIKEN cDNA 2310004I03Rik gene	1.38	Down	0.003	
E030030I06Rik	PREDICTED: RIKEN cDNA E030030I06 gene, transcript variant 4	1.38	Down	0.001	XM_912802.2
Txnip	Thioredoxin interacting protein, transcript variant 1	1.38	Down	0.006	NM_001009935.2
Igh-1a	Immunoglobulin heavy chain 1a	1.38	Down	0.013	XM_354704.1
A530082L16Rik	RIKEN cDNA A530082L16Rik gene	1.38	Down	0.012	AK080217
Setd8	SET domain containing (lysine methyltransferase) 8	1.38	Up	0.007	NM_030241.2
5031439G07Rik	RIKEN cDNA 5031439G07Rik gene	1.37	Down	0.013	XM_128281
MGC5739	PREDICTED: similar to hypothetical protein FLJ20010	1.37	Down	0.003	XM_917134.2
Igfbp5	Insulin-like growth factor binding protein 5	1.37	Up	0.000	NM_010518
E130309L16Rik	RIKEN cDNA E130309L16Rik gene	1.37	Down	0.006	AK053808
D430041D05Rik	RIKEN cDNA D430041D05 gene	1.37	Up	0.004	NM_001033347.2
LOC381490	cDNA sequence LOC381490	1.37	Down	0.007	XM_355443.1
2310007H09Rik	RIKEN cDNA 2310007H09 gene	1.37	Down	0.007	NM_029609.1
LOC673040	PREDICTED: similar to La-related protein 4 (La ribonucleoprotein domain family member 4)	1.37	Down	0.009	XM_001003792.1
Rpl10a	Ribosomal protein L10A	1.37	Down	0.005	NM_011287.1
2610200G18Rik	RIKEN cDNA 2610200G18 gene	1.37	Up	0.007	NM_025998.1
2610042G18Rik	RIKEN cDNA 2610042G18Rik gene	1.37	Down	0.004	
Irak1	Interleukin-1 receptor-associated kinase 1	1.36	Down	0.004	NM_008363.2
Mllt3	Myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila), transcript variant 2	1.36	Up	0.008	NM_029931.2
Uck1	Uridine-cytidine kinase 1	1.36	Down	0.004	NM_011675.1
Rcl1	RNA terminal phosphate cyclase-like 1	1.36	Down	0.002	NM_021525.2
E330018D03Rik	RIKEN cDNA E330018D03 gene	1.36	Down	0.009	NM_177133.1
C530036F05Rik	RIKEN cDNA C530036F05Rik gene	1.36	Down	0.015	
Rod1	Regulator of differentiation 1	1.36	Down	0.010	NM_144904
D030011M22Rik	RIKEN cDNA D030011M22Rik gene	1.36	Down	0.004	AK050726
Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	1.36	Down	0.003	NM_133978.1
Zbtb12	Zinc finger and BTB domain containing 12	1.35	Up	0.012	NM_198886.2
Spr	Sepiapterin reductase	1.35	Down	0.006	NM_011467.1
Kcnj11	Potassium inwardly-rectifying channel, subfamily J, member 11	1.35	Down	0.001	NM_010602
2310040C09Rik	RIKEN cDNA 2310040C09 gene	1.35	Down	0.010	NM_178618.3
Tug1	Taurine upregulated gene 1	1.35	Down	0.007	NR_002322.1
2310007A19Rik	RIKEN cDNA 2310007A19 gene	1.35	Up	0.001	NM_025506.2
Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	1.35	Up	0.006	NM_025891.3
Hdac4	Histone deacetylase 4	1.35	Up	0.000	NM_207225.1
Eif3s2	Eukaryotic translation initiation factor 3, subunit 2 (beta)	1.35	Up	0.002	NM_018799.1
Mical3	Microtubule associated monooxygenase, calponin and LIM domain containing 3	1.34	Down	0.011	NM_153396.1
Hectd2	HECT domain containing 2	1.34	Down	0.001	NM_172637.1
St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2, transcript variant 2	1.34	Up	0.006	NM_178048.2
Ccdc25	Coiled-coil domain containing 25	1.34	Down	0.003	NM_145944.4
Slc25a15	Solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.34	Up	0.000	NM_181325.2

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Klc2	Kinesin light chain 2	1.34	Up	0.007	NM_008451
Ldb3	LIM domain binding 3, transcript variant 2	1.34	Down	0.003	NM_001039071.2
Epdr1	Ependymin related protein 1	1.34	Up	0.012	NM_134065.2
Slc11a2	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	1.34	Up	0.010	AK049856
Tmem129	Transmembrane protein 129	1.34	Down	0.001	NM_026698.2
1110001N06Rik	RIKEN cdna 1110001N06Rik gene	1.34	Down	0.006	AK003256
D630035D13Rik	RIKEN cdna D630035D13Rik gene	1.34	Down	0.000	AK085493
Fusip1	FUS interacting protein (serine-arginine rich) 1, transcript variant 2	1.34	Down	0.009	NM_001080387.1
Ing1	Inhibitor of growth family, member 1	1.34	Down	0.014	NM_011919.4
Abca15	ATP-binding cassette, sub-family A (ABC1), member 15	1.34	Up	0.006	NM_177213.3
LOC671348	PREDICTED: similar to Peroxisome assembly protein 10	1.34	Down	0.010	XM_992743.1
E130309F12Rik	RIKEN cdna E130309F12 gene	1.34	Up	0.000	NM_178756.2
Mon1b	MON1 homolog b (yeast), transcript variant 2	1.34	Down	0.007	NM_001048143.1
Luc7l2	LUC7-like 2 (S. cerevisiae)	1.33	Down	0.004	NM_138680
Dnmt3l	DNA (cytosine-5-)-methyltransferase 3-like, transcript variant 2	1.33	Down	0.001	NM_001081695.1
LOC672178	PREDICTED: similar to ribosomal protein SA	1.33	Down	0.008	XR_003738.1
2310039L15Rik	RIKEN cdna 2310039L15Rik gene	1.33	Up	0.009	XM_290098.1
H2-D1	Histocompatibility 2, D region locus 1	1.33	Down	0.004	NM_010380.2
Itga5	Integrin alpha 5 (fibronectin receptor alpha)	1.33	Down	0.010	NM_010577.2
Pip5k2b	PREDICTED: phosphatidylinositol-4-phosphate 5-kinase, type II, beta, transcript variant 4	1.33	Up	0.003	XM_991639.1
5830417C01Rik	RIKEN cdna 5830417C01 gene	1.33	Up	0.004	NM_024282.3
C230043G09Rik	RIKEN cdna C230043G09Rik gene	1.33	Up	0.000	AK048752
Sdownt6h	Suppressor of Ty 6 homolog	1.33	Down	0.002	NM_009297
Ptp4a2	Protein tyrosine phosphatase 4a2	1.33	Up	0.003	NM_008974.3
Zfp288	Zinc finger protein 288	1.33	Down	0.003	AK034574
Col11a2	Procollagen, type XI, alpha 2	1.33	Up	0.006	NM_009926.1
D930024H10Rik	RIKEN cdna D930024H10Rik gene	1.33	Down	0.010	AK086373
Prkcq	Protein kinase C, theta	1.32	Up	0.014	NM_008859.2
1500032D16Rik	RIKEN cdna 1500032D16 gene	1.32	Down	0.005	NM_030087.1
Stxbp2	Syntaxin binding protein 2	1.32	Down	0.011	NM_011503.3
Uqcrb	Ubiquinol-cytochrome c reductase binding protein	1.32	Down	0.008	AK017907
D15Mit260	DNA Segment, Chr 15 Massachusetts Institute of Technology 260	1.32	Down	0.010	
Rnf26	Ring finger protein 26	1.32	Down	0.012	NM_153762.3
Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog	1.32	Down	0.011	NM_008144.3
Stk24	Serine/threonine kinase 24 (STE20 homolog, yeast)	1.32	Down	0.014	NM_145465.2
Mgst1	Microsomal glutathione S-transferase 1	1.32	Down	0.011	NM_019946.3
Mia1	Melanoma inhibitory activity 1	1.32	Down	0.012	NM_019394
Cyp51	Cytochrome P450, family 51	1.32	Down	0.000	NM_020010.2
Cyb5	Cytochrome b5	1.32	Down	0.006	NM_025797
LOC385506	cDNA sequence LOC385506	1.32	Down	0.007	XM_358256.1
Ssbp2	Single-stranded DNA binding protein 2	1.32	Up	0.012	NM_024186.1
Nr1h3	Nuclear receptor subfamily 1, group H, member 3	1.32	Down	0.001	NM_013839.2
Sat1	Spermidine/spermine N1-acetyl transferase 1	1.31	Down	0.007	NM_009121.3
Mg29	Mitsugumin 29	1.31	Down	0.009	AK052749
Otub2	OTU domain, ubiquitin aldehyde binding 2	1.31	Down	0.000	NM_026580.1

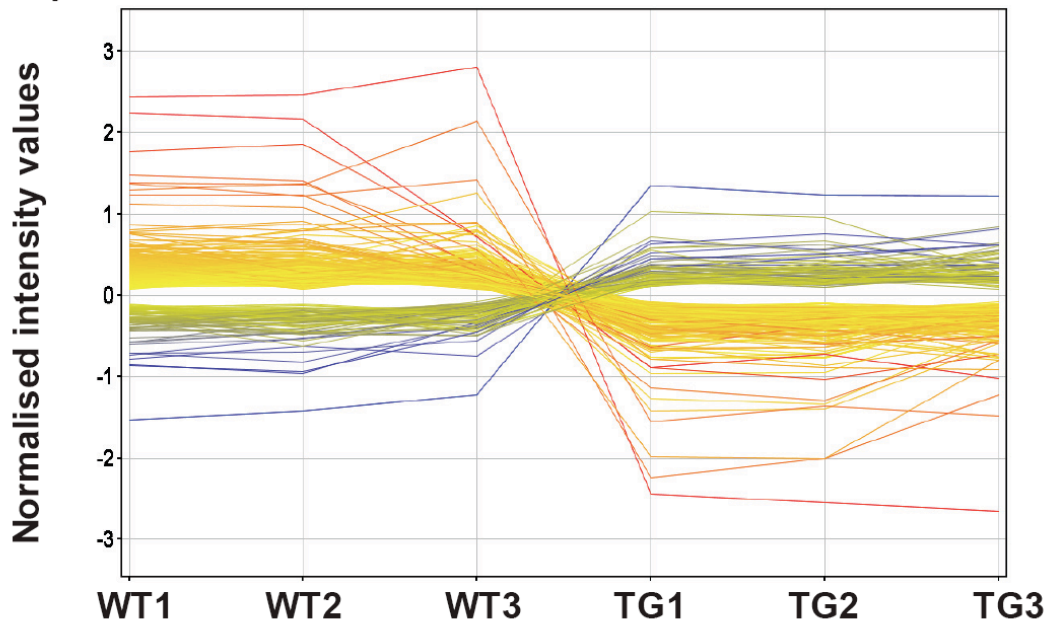
SUPPLEMENTARY FIGURES FROM "Identification and validation of the pathways and functions regulated by the orphan nuclear receptor, ROR alpha, in skeletal muscle." S Raichur *et al*

Pter	Phosphotriesterase related	1.31	Down	0.004	NM_008961.2
1190008K20Rik	RIKEN cdna 1190008K20Rik gene	1.31	Down	0.012	AK028012
2310016C16Rik	RIKEN cdna 2310016C16 gene	1.31	Down	0.005	NM_027127.1
Kif18a	Kinesin family member 18A	1.31	Up	0.001	NM_139303.1
LOC433141	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kda laminin receptor)	1.31	Down	0.007	XM_484667.3
Ccdc134	Coiled-coil domain containing 134	1.31	Down	0.001	NM_172428.2
9430025M13Rik	PREDICTED: RIKEN cdna 9430025M13 gene	1.31	Down	0.012	XM_001001939.1
1700041B20Rik	RIKEN cdna 1700041B20Rik gene	1.31	Down	0.013	XM_485065
Ntf3	Neurotrophin 3	1.31	Down	0.014	NM_008742.2
Gstk1	Glutathione S-transferase kappa 1	1.31	Down	0.009	NM_029555.2
BC013481	Cdna sequence BC013481	1.31	Down	0.006	NM_139065.1
B3galnt2	UDP-galnac:betaglcnac beta 1,3-galactosaminyltransferase, polypeptide 2	1.31	Down	0.002	NM_178640.2
Nfix	Nuclear factor I/X, transcript variant 1,	1.31	Down	0.006	NM_001081982.1
Nqo2	NAD(P)H dehydrogenase, quinone 2	1.31	Up	0.006	NM_020282.2
A530021P12Rik	RIKEN cdna A530021P12Rik gene	1.31	Down	0.012	AK040738
E130006N16Rik	RIKEN cdna E130006N16Rik gene	1.31	Down	0.001	
2210015D19Rik	PREDICTED: RIKEN cdna 2210015D19 gene, transcript variant 5	1.31	Down	0.007	XM_900750.2
Reep6	Receptor accessory protein 6	1.31	Down	0.005	NM_139292.1
Ihpk3	Inositol hexaphosphate kinase 3	1.31	Down	0.013	NM_173027.1
C230066K19Rik	RIKEN cdna C230066K19Rik gene	1.31	Down	0.005	
Rai14	Retinoic acid induced 14	1.31	Up	0.004	NM_030690.2
Parp6	Poly (ADP-ribose) polymerase family, member 6	1.31	Up	0.001	NM_029922.2
Pleckhg3	Pleckstrin homology domain containing, family G (with rhogef domain) member 3	1.31	Down	0.013	NM_153804.3
Tex2	Testis expressed gene 2	1.31	Up	0.009	NM_198292.3
4833416J08Rik	RIKEN cdna 4833416J08Rik gene	1.30	Down	0.001	
Mfge8	Milk fat globule-EGF factor 8 protein	1.30	Down	0.009	NM_008594.2
Slc25a1	Solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	1.30	Down	0.003	NM_153150.1
Saal1	PREDICTED: serum amyloid A-like 1, transcript variant 2	1.30	Down	0.006	XM_001003894.1
Eef1a1	Eukaryotic translation elongation factor 1 alpha 1	1.30	Down	0.009	NM_010106.2
H28	Histocompatibility 28	1.30	Down	0.004	NM_031367.1
BC044804	cDNA sequence BC044804	1.30	Down	0.001	NM_178035
Tex2	Testis expressed gene 2	1.30	Up	0.000	NM_198292.3
2810021O14Rik	RIKEN cdna 2810021O14Rik gene	1.30	Down	0.010	AK076679
Tspan12	Tetraspanin 12	1.30	Down	0.005	NM_173007.1
Ptpn4	Protein tyrosine phosphatase, non-receptor type 4	1.30	Down	0.001	NM_019933.2
Mrpl15	Mitochondrial ribosomal protein L15	1.30	Down	0.006	AK003026

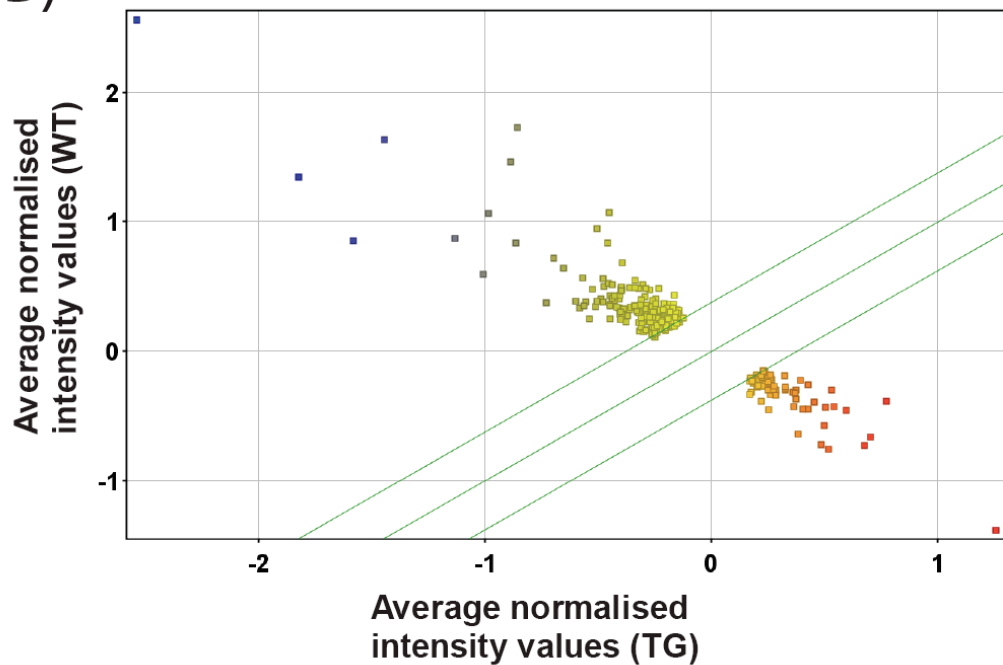
SUPPLEMENTARY FIGURES FROM “Identification and validation of the pathways and functions regulated by the orphan nuclear receptor, ROR alpha, in skeletal muscle.” S Raichur *et al*

S3: Differentially expressed genes from the Illumina BeadArray analysis comparing Tg-ROR Δ DE to wildtype mice were analysed. P-values represent Fisher's Exact Test with the threshold at 0.05.

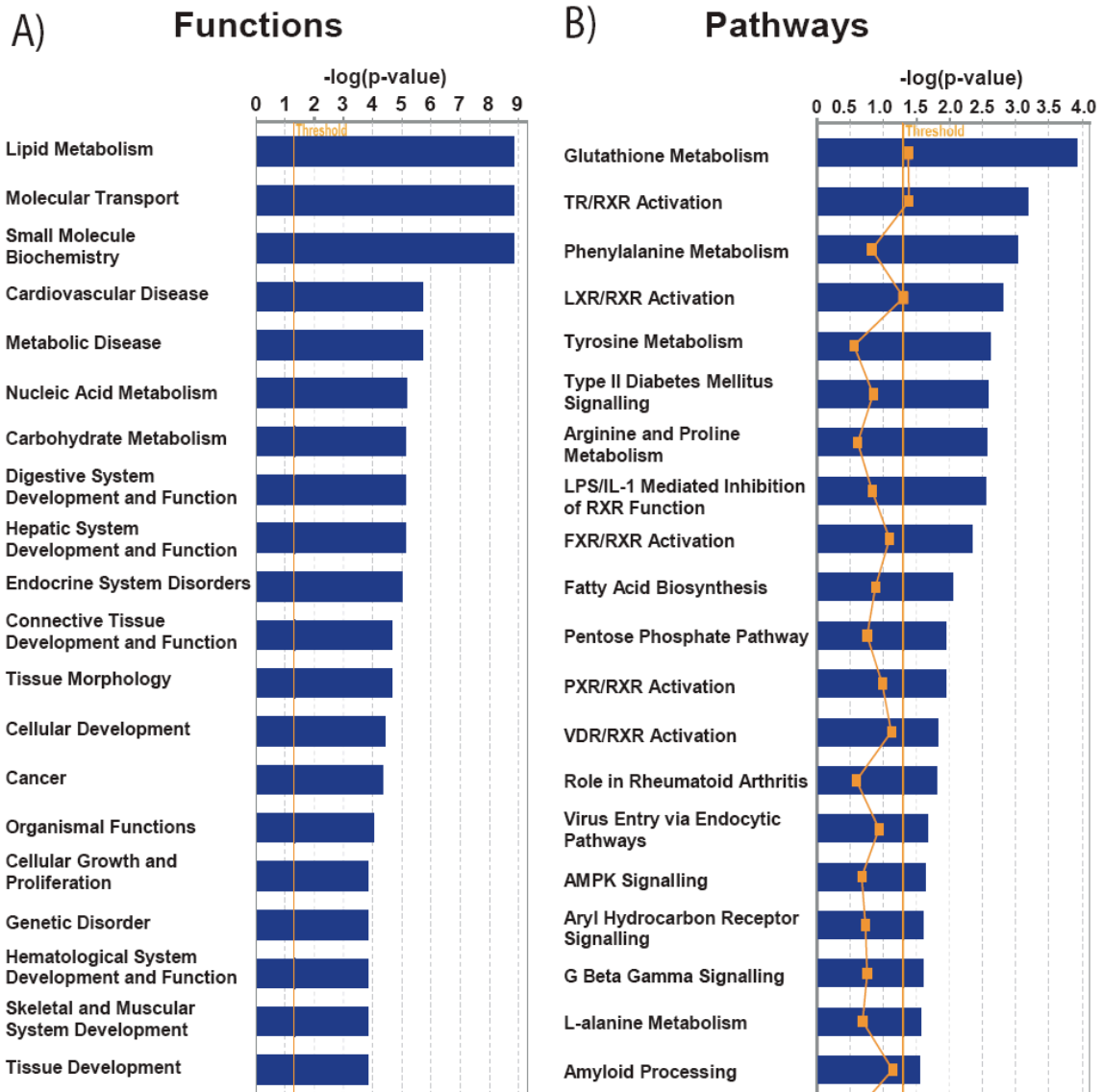
A)



B)



S4: Ingenuity pathway analysis of differentially expressed genes from the Illumina BeadArray analysis comparing Tg-ROR α DE to wild type mice to identify A, the top 20 functions and B, the top 20 pathways.

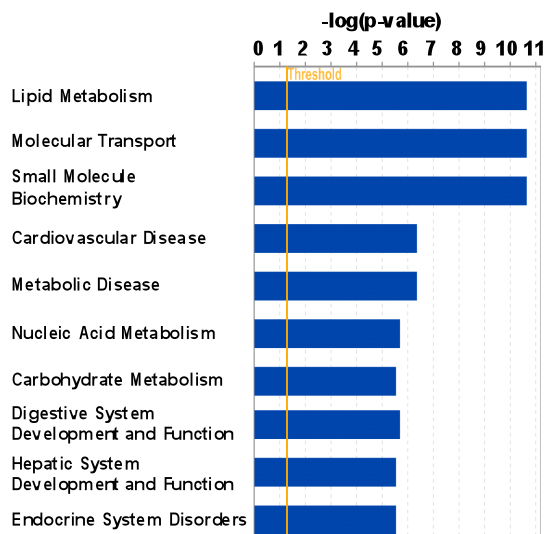


S5: Ingenuity pathway analysis of up and down regulated genes from the Illumina BeadArray analysis, comparing Tg-ROR Δ DE to wild type mice. A, functional annotation of genes regulated in ROR α 1 Δ DE that are associated with metabolism. B and C, the top 10 functional categories and pathways that were identified from down-regulated genes.

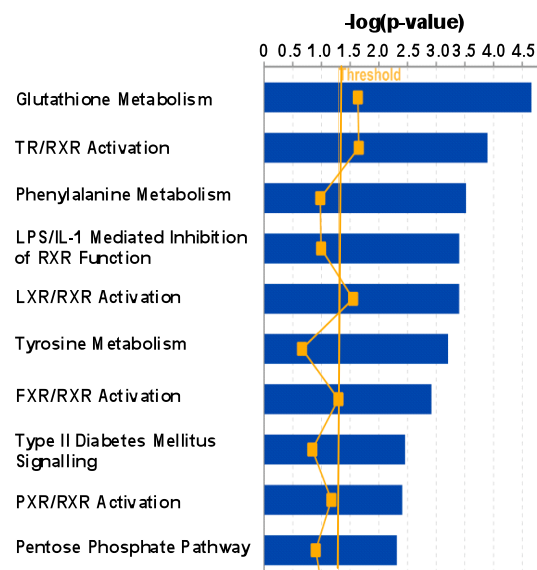
A

Function Annotation	Number of Reg. Genes	Regulated Genes
Lipid Metabolism	36	↓ Acaca, ↓ Acs15, ↓ Adrp, ↓ Agpat2, ↓ Akt2, ↓ Apoc1, ↓ Atp5a1, ↓ Cebpa, ↓ Ces1, ↓ Cidea, ↓ Eef1a1, ↓ Ehhadh, ↓ Elovl6, ↓ Ephx2, ↓ Etfdh, ↓ Fasn, ↓ Gnao1, ↓ Got2, ↓ Hp, ↓ Hsd11b1, ↓ Idh1, ↓ Ihpk3, ↓ Lgals1, ↓ Mif, ↓ Nr1h3, ↓ Pdhb, ↓ Pparg, ↓ Prkar2b, ↓ Sat1, ↓ Scd, ↑ Slc22a4, ↓ Slc27a2, ↓ Thrsp, ↓ Tspo, ↓ Ucp1, ↓ Vldlr
Carbohydrate Metabolism	23	↓ Agpat2, ↓ Akt2, ↓ Apoc1, ↓ B3galnt2, ↓ Cebpa, ↓ Chst1, ↓ Idh1, ↓ Idh3b, ↓ Ihpk3, ↓ Kcnj11, ↑ Lgals1, ↓ Mif, ↑ Nans, ↓ Pfkf, ↓ Pparg, ↓ Ppp1r1a, ↓ Prkar2b, ↓ Pygl, ↓ Scd, ↑ St3gal2, ↑ Stab2, ↓ Tkt, ↓ Ucp1

B Functional categories of down-regulated genes



C Pathways associated with down-regulated genes



S6: Relative quantification of lipogenic gene expression in skeletal muscle of transgenic compared to wt littermate controls, normalized to 18S mRNA.

Entrez gene symbol-TaqMan assay ID	$\Delta\Delta Ct$	P. Value	B. Value	t. Value	RQ. Log10	RQ. Linear	Significance	adj. P.Val	Significance FDR
Abca1-Mm00442646_m1	0.628	0.038	-4.081	2.283	-0.189	0.647	Significant	0.080	Non Significant
Abcg1-Mm00437390_m1	0.099	0.760	-6.337	0.311	-0.030	0.933	Non Significant	0.802	Non Significant
Acadm-Mm00431611_m1	0.269	0.506	-6.149	0.682	-0.081	0.830	Non Significant	0.565	Non Significant
Acsl4-Mm00490331_m1	1.396	0.001	-0.313	4.273	-0.420	0.380	Significant	0.012	Significant
Apoe-Mm00437573_m1	0.483	0.103	-4.963	1.739	-0.146	0.715	Non Significant	0.140	Non Significant
Cav1-Mm00483057_m1	0.718	0.073	-4.666	1.932	-0.216	0.608	Non Significant	0.115	Non Significant
Cav3-Mm01182632_m1	0.452	0.043	-4.190	2.220	-0.136	0.731	Significant	0.081	Non Significant
Cd36-Mm00432403_m1	1.115	0.013	-3.121	2.814	-0.335	0.462	Significant	0.042	Significant
Cebpa-Mm00514283_s1	0.055	0.878	-6.374	0.156	-0.016	0.963	Non Significant	0.878	Non Significant
Cebpb-Mm00843434_s1	0.908	0.023	-3.614	2.546	-0.273	0.533	Significant	0.061	Non Significant
Cebpd-Mm00786711_s1	1.086	0.029	-3.827	2.428	-0.327	0.471	Significant	0.068	Non Significant
Fabp4-Mm00445880_m1	0.721	0.089	-4.842	1.819	-0.217	0.606	Non Significant	0.130	Non Significant
Fasn-Mm00662319_m1	1.844	0.005	-2.163	3.316	-0.555	0.279	Significant	0.023	Significant
Hif1a-Mm00468875_m1	0.797	0.013	-3.082	2.834	-0.240	0.575	Significant	0.042	Significant
Scd1-Mm00772290_m1	2.099	0.001	-0.881	3.978	-0.632	0.233	Significant	0.012	Significant
Scd2-Mm00485951_g1	0.413	0.208	-5.538	1.317	-0.124	0.751	Non Significant	0.264	Non Significant
Ski-Mm00448744_m1	0.249	0.256	-5.695	1.182	-0.075	0.841	Non Significant	0.304	Non Significant
Skil-Mm00456917_m1	0.543	0.065	-4.572	1.991	-0.164	0.686	Non Significant	0.113	Non Significant
Srebf1-Mm00550338_m1	0.764	0.004	-2.034	3.383	-0.230	0.589	Significant	0.023	Significant
Npy-Mm00445771_m1	1.707	0.683	-6.225	0.419	-0.514	0.306	Non Significant	0.777	Non Significant
Npy2r-Mm01956783_s1	-7.241	0.244	-5.569	-1.230	2.180	151.272	Non Significant	0.366	Non Significant

Significance was assigned by the application of the Empirical Bayes statistic. RQ – Relative quantification, FDR – False detection rate.

S7: Relative quantification of NR gene expression in skeletal muscle of transgenic compared to wt littermate controls, normalized to *gusB*, *hprt1*, and *gapdh*.

Entrez gene symbol-TaqMan assay ID	$\Delta\Delta Ct$	P. Value	B. Value	t. Value	RQ. Log10	RQ. Linear	Significance	adj. P.Val	Significance FDR
Ar-Mm00442688_m1	0.304	0.469	-5.520	0.766	-0.091	0.810	N.S.	0.776	N.S.
Esr1-Mm00433149_m1	0.490	0.147	-4.657	1.630	-0.148	0.712	N.S.	0.705	N.S.
Esr2-Mm00599819_m1	-0.908	0.299	-5.214	-1.122	0.273	1.877	N.S.	0.776	N.S.
Esrra-Mm00433143_m1	0.031	0.936	-5.809	0.083	-0.009	0.979	N.S.	0.956	N.S.
Esrrb-Mm00442411_m1	0.452	0.247	-5.070	1.264	-0.136	0.731	N.S.	0.776	N.S.
Esrrg-Mm00516267_m1	0.516	0.110	-4.414	1.829	-0.155	0.699	N.S.	0.659	N.S.
Hnf4a-Mm00433964_m1	-6.271	0.169	-4.770	-1.534	1.888	77.243	N.S.	0.736	N.S.
Hnf4g-Mm00443563_m1	-3.485	0.575	-5.638	-0.587	1.049	11.194	N.S.	0.789	N.S.
Nr0b1-Mm00431729_m1	-2.294	0.677	-5.716	-0.434	0.691	4.905	N.S.	0.831	N.S.
Nr0b2-Mm00442278_m1	-0.389	0.752	-5.757	-0.328	0.117	1.310	N.S.	0.831	N.S.
Nr1d1-Mm00520708_m1	0.392	0.461	-5.510	0.780	-0.118	0.762	N.S.	0.776	N.S.
Nr1d2-Mm00441730_m1	0.166	0.547	-5.611	0.632	-0.050	0.891	N.S.	0.789	N.S.
Nr1h2-Mm00437262_m1	-0.275	0.349	-5.325	-1.004	0.083	1.210	N.S.	0.776	N.S.
Nr1h3-Mm00443454_m1	0.814	0.039	-3.531	2.522	-0.245	0.569	Significant	0.393	N.S.
Nr1h4-Mm00436419_m1	0.494	0.411	-5.436	0.875	-0.149	0.710	N.S.	0.776	N.S.
Nr1h5-Mm01308716_m1	-1.083	0.834	-5.789	-0.217	0.326	2.118	N.S.	0.883	N.S.
Nr1i2-Mm00803092_m1	-7.720	0.108	-4.399	-1.841	2.324	210.800	N.S.	0.659	N.S.
Nr1i3-Mm00437986_m1	-2.887	0.356	-5.340	-0.987	0.869	7.397	N.S.	0.776	N.S.
Nr2c1-Mm00449123_m1	0.601	0.032	-3.353	2.661	-0.181	0.659	Significant	0.393	N.S.
Nr2e1-Mm00455855_m1	1.112	0.846	-5.792	0.201	-0.335	0.463	N.S.	0.883	N.S.
Nr2e3-Mm00443299_m1	-0.963	0.415	-5.443	-0.866	0.290	1.949	N.S.	0.776	N.S.
Nr2f1-Mm00657937_m1	-0.262	0.564	-5.627	-0.605	0.079	1.199	N.S.	0.789	N.S.
Nr2f2-Mm00772789_m1	0.146	0.609	-5.667	0.534	-0.044	0.904	N.S.	0.813	N.S.
Nr2f6-Mm00438762_m1	-0.081	0.762	-5.762	-0.315	0.024	1.058	N.S.	0.831	N.S.
Nr3c1-Mm00433832_m1	0.912	0.005	-1.734	4.037	-0.275	0.531	Significant	0.234	N.S.
Nr3c2-Mm01241595_m1	0.188	0.640	-5.691	0.488	-0.057	0.878	N.S.	0.821	N.S.
Nr4a1-Mm00439358_m1	-0.443	0.557	-5.621	-0.616	0.133	1.359	N.S.	0.789	N.S.
Nr4a2-Mm00443056_m1	-0.037	0.962	-5.812	-0.049	0.011	1.026	N.S.	0.962	N.S.
Nr4a3-Mm00450074_m1	-2.220	0.335	-5.296	-1.035	0.668	4.657	N.S.	0.776	N.S.
Nr5a1-Mm00446826_m1	0.211	0.423	-5.456	0.850	-0.064	0.864	N.S.	0.776	N.S.
Nr5a2-Mm00446088_m1	0.642	0.732	-5.748	0.356	-0.193	0.641	N.S.	0.831	N.S.
Nr6a1-Mm00599848_m1	0.341	0.274	-5.150	1.186	-0.103	0.790	N.S.	0.776	N.S.
Pgr-Mm00435625_m1	-3.825	0.437	-5.476	-0.824	1.152	14.176	N.S.	0.776	N.S.
Ppara-Mm00440939_m1	0.273	0.572	-5.635	0.592	-0.082	0.828	N.S.	0.789	N.S.
Ppard-Mm00803186_g1	0.926	0.041	-3.564	2.496	-0.279	0.526	Significant	0.393	N.S.
Pparg-Mm00440945_m1	-0.322	0.501	-5.561	-0.708	0.097	1.250	N.S.	0.789	N.S.
Rara-Mm00436264_m1	0.319	0.356	-5.340	0.987	-0.096	0.801	N.S.	0.776	N.S.
Rarb-Mm01319676_m1	-0.189	0.726	-5.744	-0.365	0.057	1.140	N.S.	0.831	N.S.
Rarg-Mm00441083_m1	0.590	0.208	-4.938	1.386	-0.177	0.665	N.S.	0.776	N.S.
Rora-Mm00443103_m1	0.260	0.445	-5.489	0.809	-0.078	0.835	N.S.	0.776	N.S.
Rorb-Mm00524993_m1	3.784	0.141	-4.626	1.655	-1.139	0.073	N.S.	0.705	N.S.
Rorc-Mm00441139_m1	0.860	0.019	-2.911	3.013	-0.259	0.551	Significant	0.393	N.S.
Rxra-Mm00441182_m1	0.559	0.068	-4.001	2.156	-0.168	0.679	N.S.	0.542	N.S.
Rxrb-Mm00441193_m1	0.130	0.650	-5.698	0.474	-0.039	0.914	N.S.	0.821	N.S.
Rxrg-Mm00436410_m1	0.118	0.731	-5.747	0.358	-0.035	0.922	N.S.	0.831	N.S.
Thra-Mm00617505_m1	0.962	0.322	-5.269	1.065	-0.290	0.513	N.S.	0.776	N.S.
Thrb-Mm00437044_m1	-0.326	0.441	-5.483	-0.816	0.098	1.254	N.S.	0.776	N.S.
Vdr-Mm00437297_m1	0.595	0.400	-5.419	0.896	-0.179	0.662	N.S.	0.776	N.S.

RQ – Relative quantification, FDR – False detection rate. Significance was assigned by the application of the Empirical Bayes statistic.

SUPPLEMENTARY FIGURES FROM “Identification and validation of the pathways and functions regulated by the orphan nuclear receptor, ROR alpha, in skeletal muscle.” S Raichur *et al*

S8: Relative quantification of glucose homeostatic gene expression in skeletal muscle of transgenic compared to wt littermate controls, normalized to 18S mRNA.

Entrez gene symbol-TaqMan assay ID	$\Delta\Delta Ct$	P. Value	B. Value	t. Value	RQ. Log10	RQ. Linear	Significance	adj. P.Val	Significance FDR
Akt2-Mm00545827_m1	1.684	0.001	-0.621	4.337	-0.507	0.311	Significant	0.037	Significant
Cs- Mm00466043_m1	0.515	0.011	-2.781	3.061	-0.155	0.700	Significant	0.087	Non Significant
Foxo1-Mm00490672_m1	1.229	0.042	-4.074	2.295	-0.370	0.427	Significant	0.173	Non Significant
Gys1-Mm00472712_m1	0.320	0.161	-5.260	1.500	-0.096	0.801	Non Significant	0.372	Non Significant
Hk2-Mm00443385_m1	0.574	0.082	-4.678	1.911	-0.173	0.672	Non Significant	0.225	Non Significant
lfng-Mm00801778_m1	0.534	0.913	-6.333	0.112	-0.161	0.691	Non Significant	0.961	Non Significant
Il15-Mm00434210_m1	1.076	0.026	-3.634	2.561	-0.324	0.474	Significant	0.132	Non Significant
Il6- Mm00446190_m1	0.150	0.788	-6.300	0.275	-0.045	0.902	Non Significant	0.929	Non Significant
Insr- Mm00439693_m1	0.110	0.581	-6.172	0.568	-0.033	0.927	Non Significant	0.710	Non Significant
Irs1- Mm00439720_s1	-0.185	0.403	-5.955	-0.868	0.056	1.137	Non Significant	0.559	Non Significant
Lep- Mm00434759_m1	-0.193	0.955	-6.338	-0.058	0.058	1.143	Non Significant	0.961	Non Significant
Lepr-Mm00440181_m1	1.173	0.009	-2.664	3.129	-0.353	0.443	Significant	0.087	Non Significant
Lipe-Mm00495359_m1	0.438	0.180	-5.353	1.429	-0.132	0.738	Non Significant	0.372	Non Significant
Pck1-Mm00440636_m1	0.905	0.271	-5.674	1.157	-0.272	0.534	Non Significant	0.497	Non Significant
Pdk1-Mm00554306_m1	0.284	0.356	-5.872	0.962	-0.085	0.822	Non Significant	0.556	Non Significant
Pdk2-Mm00446681_m1	0.034	0.883	-6.328	0.150	-0.010	0.977	Non Significant	0.961	Non Significant
Pdk3-Mm00455220_m1	1.071	0.028	-3.703	2.520	-0.323	0.476	Significant	0.132	Non Significant
Pdk4-Mm00443325_m1	0.887	0.018	-3.293	2.763	-0.267	0.541	Significant	0.119	Non Significant
Pfkm-Mm00445461_m1	0.167	0.264	-5.653	1.176	-0.050	0.890	Non Significant	0.497	Non Significant
Pnpla2-Mm00503040_m1	0.730	0.072	-4.571	1.981	-0.220	0.603	Non Significant	0.220	Non Significant
Ptgs2-Mm00478374_m1	0.346	0.500	-6.090	0.696	-0.104	0.787	Non Significant	0.644	Non Significant
Pygm-Mm00478582_m1	0.286	0.174	-5.324	1.451	-0.086	0.820	Non Significant	0.372	Non Significant
Rab18-Mm00441057_m1	0.299	0.115	-4.977	1.708	-0.090	0.813	Non Significant	0.292	Non Significant
Rock1-Mm00485745_m1	0.202	0.406	-5.960	0.862	-0.061	0.869	Non Significant	0.559	Non Significant
Rock2-Mm00485761_m1	0.319	0.349	-5.856	0.978	-0.096	0.801	Non Significant	0.556	Non Significant
Slc2a2-Mm00446224_m1	1.283	0.825	-6.313	0.227	-0.386	0.411	Non Significant	0.939	Non Significant
Slc2a4-Mm00436615_m1	0.347	0.061	-4.414	2.083	-0.105	0.786	Non Significant	0.220	Non Significant
Slc2a8-Mm00444634_m1	0.231	0.318	-5.790	1.046	-0.070	0.852	Non Significant	0.551	Non Significant
Socs3-Mm00545913_s1	-0.027	0.961	-6.339	-0.050	0.008	1.019	Non Significant	0.961	Non Significant
Stat3-Mm00456961_m1	0.172	0.507	-6.098	0.685	-0.052	0.887	Non Significant	0.644	Non Significant
Stat5b-Mm00839889_m1	0.892	0.003	-1.646	3.723	-0.269	0.539	Significant	0.053	Non Significant
Tcf7l2-Mm00501505_m1	0.185	0.370	-5.898	0.933	-0.056	0.880	Non Significant	0.556	Non Significant
Tsc22d3-Mm00726417_s1	1.085	0.073	-4.580	1.976	-0.326	0.472	Non Significant	0.220	Non Significant

Significance was assigned by the application of the Empirical Bayes statistic. RQ – Relative quantification, FDR – False detection rate.

Note: Glut1 mRNA expression performed independently by qPCR. RQ= 0.6219, Non Significant

SUPPLEMENTARY FIGURES FROM “Identification and validation of the pathways and functions regulated by the orphan nuclear receptor, ROR alpha, in skeletal muscle.” S Raichur *et al*

S9: Table of Relative quantification of myogenic gene expression in skeletal muscle of transgenic compared to wt littermate controls, normalized to 18S mRNA.

Entrez gene symbol- TaQMan assay ID	$\Delta\Delta Ct$	P. Value	B. Value	t. Value	RQ. Log10	RQ. Linear	Significance	adj. P.Val	Significance FDR
Acvr1-Mm00431645_m1	0.288	0.304	-5.735	1.078	-0.087	0.819	Non Significant	0.418	Non Significant
Acvr2a-Mm00431657_m1	0.616	0.029	-3.719	2.502	-0.185	0.653	Significant	0.123	Non Significant
Acvr2b-Mm00431664_m1	-0.009	0.968	-6.316	-0.040	0.003	1.006	Non Significant	0.968	Non Significant
Bhlhb2-Mm00478593_m1	-0.115	0.819	-6.288	-0.235	0.035	1.083	Non Significant	0.872	Non Significant
Gdf10-Mm00521349_m1	0.650	0.148	-5.170	1.552	-0.196	0.637	Non Significant	0.288	Non Significant
Gdf8-Mm00440328_m1	0.888	0.047	-4.155	2.234	-0.267	0.540	Significant	0.141	Non Significant
Hdac4-Mm01304741_m1	7.002	0.402	-5.930	0.871	-2.108	0.008	Non Significant	0.498	Non Significant
Hdac5-Mm00515917_m1	0.599	0.001	-0.721	4.283	-0.180	0.660	Significant	0.026	Significant
Hdac7a-Mm00469520_m1	0.281	0.172	-5.291	1.460	-0.085	0.823	Non Significant	0.308	Non Significant
Mef2a-Mm00488969_m1	0.397	0.042	-4.061	2.293	-0.119	0.760	Significant	0.140	Non Significant
Mef2c-Mm00600423_m1	-0.078	0.734	-6.253	-0.349	0.023	1.055	Non Significant	0.807	Non Significant
Mef2d-Mm00504929_m1	0.499	0.021	-3.398	2.693	-0.150	0.708	Significant	0.114	Non Significant
Myod1-Mm00440387_m1	0.094	0.876	-6.303	0.160	-0.028	0.937	Non Significant	0.903	Non Significant
Myog-Mm00446194_m1	-0.279	0.548	-6.118	-0.619	0.084	1.214	Non Significant	0.646	Non Significant
Ski- Mm00448744_m1	0.249	0.141	-5.125	1.585	-0.075	0.841	Non Significant	0.288	Non Significant
Skil- Mm00456917_m1	0.536	0.060	-4.379	2.094	-0.161	0.690	Non Significant	0.165	Non Significant
Smad1-Mm00484721_m1	0.503	0.034	-3.847	2.424	-0.151	0.706	Significant	0.123	Non Significant
Smad2-Mm00487530_m1	0.701	0.011	-2.793	3.050	-0.211	0.615	Significant	0.087	Non Significant
Smad3-Mm00489637_m1	0.311	0.407	-5.938	0.861	-0.094	0.806	Non Significant	0.498	Non Significant
Smad4-Mm00484724_m1	0.249	0.294	-5.710	1.102	-0.075	0.841	Non Significant	0.418	Non Significant
Smad6-Mm00484738_m1	0.446	0.087	-4.714	1.874	-0.134	0.734	Non Significant	0.192	Non Significant
Smad7-Mm00484741_m1	-0.371	0.237	-5.548	-1.250	0.112	1.294	Non Significant	0.366	Non Significant
Smurf1-Mm00547102_m1	0.455	0.178	-5.318	1.439	-0.137	0.730	Non Significant	0.308	Non Significant
Tcf7l2-Mm00501505_m1	0.185	0.362	-5.859	0.951	-0.056	0.880	Non Significant	0.478	Non Significant
Tgfr1-Mm00436971_m1	1.296	0.002	-0.925	4.157	-0.390	0.407	Significant	0.026	Significant
Tgfr2-Mm00436978_m1	0.675	0.013	-2.977	2.941	-0.203	0.626	Significant	0.087	Non Significant
Tnni1-Mm00502426_m1	1.886	0.232	-5.531	1.264	-0.568	0.271	Non Significant	0.366	Non Significant
Tnni2-Mm00437157_g1	0.510	0.009	-2.561	3.185	-0.154	0.702	Significant	0.087	Non Significant

Significance was assigned by the application of the Empirical Bayes statistic. RQ – Relative quantification, FDR – False detection rate.