

Table S1. List of mitochondrial related transcripts identified by GO analysis. Genes are listed in order of fold change following NRG + IGF stimulation of Schwann cells as compared to untreated Schwann cells.

NRG.IGF v Control Fold change	P value	Symbol	Description
3.573024018	5.27E-005	Ldlr	low density lipoprotein receptor-related protein 5 (predicted)
2.624189988	0.000196	Brca1	breast cancer 1
2.356672202	3.60E-007	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent)
2.244335644	0.000359	RGD:1303041	NS5A (hepatitis C virus) transactivated protein 9
1.990017823	7.98E-005	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
1.919951041	6.51E-005	LOC361546	similar to RIKEN cDNA 2310005O14
1.917031658	6.02E-006	Ak2	adenylate kinase 2
1.902575622	0.000544	Ung_predicted	uracil-DNA glycosylase
1.861393098	1.49E-005	Bdh	3-hydroxybutyrate dehydrogenase, type 1
1.810721884	4.90E-006	Mrs2l	MRS2-like, magnesium homeostasis factor (S. cerevisiae)
1.777052758	0.000294	Gls	glutaminase
1.768278688	0.00026	RGD:621430	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
1.76202714	0.000282	RGD:1359658	BCS1-like (yeast)
1.756479177	0.000126	Gja1	gap junction membrane channel protein alpha 1
1.737151238	0.000729	Sfxn1_predicted	sideroflexin 1
1.698739739	7.61E-005	Dutp	deoxyuridine triphosphatase
1.695806319	0.000994	LOC499335	frataxin (predicted)
1.652825342	0.000398	Gcsh	glycine cleavage system protein H (aminomethyl carrier)
1.646341115	0.000182	Cycs	cytochrome c, somatic
1.635774633	0.000236	Ckb	creatine kinase, brain
1.626916572	0.000111	Shmt1_predicted	serine hydroxymethyltransferase 1 (soluble)
1.61255442	0.000198	Fh1	fumarate hydratase 1
1.604457078	0.000843	Timm8a	translocase of inner mitochondrial membrane 8 homolog a (yeast)
1.592035784	0.001489	RGD1306651_predicted	similar to mitochondrial carrier protein MGC4399
1.585443702	0.002074	Mrpl14_predicted	mitochondrial ribosomal protein L14 (predicted)
1.579202992	7.06E-006	Pdp2	pyruvate dehydrogenase phosphatase isoenzyme 2
1.57847475	0.000159	Fabp3	fatty acid binding protein 3
1.577600983	9.63E-005	Tmpo	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3
1.576759139	3.89E-005	Slc25a15_predicted	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
1.572970185	0.000102	RGD1305677_predicted	similar to RIKEN cDNA 1810020E01
1.570973923	0.000392	Bckdhh	branched chain keto acid dehydrogenase E1, beta polypeptide
1.570229822	0.000158	Mrpl17	mitochondrial ribosomal protein L17
1.559570939	0.005761	Ogg1	8-oxoguanine DNA-glycosylase 1
1.555353687	0.000277	Dhodh	dihydroorotate dehydrogenase
1.541044079	0.00597	Hk2	hexokinase 2
1.533587454	0.00016	Mtch2_predicted	mitochondrial carrier homolog 2 (C. elegans) (predicted)
1.503375434	0.00138	RGD:1303022	translocase of outer mitochondrial membrane 40 homolog (yeast)
1.47171759	0.004375	Tfb1m	transcription factor B1, mitochondrial
1.470731775	0.001179	Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)
1.468285581	6.91E-005	Hspd1	heat shock protein 1 (chaperonin)
1.465510646	0.002252	RGD1304825_predicted	similar to RIKEN cDNA 2010309E21 (predicted)
1.464126768	0.000822	Nrbf1	mitochondrial trans-2-enoyl-CoA reductase
1.462819058	0.000756	Hspe1	heat shock 10 kDa protein 1 (chaperonin 10)
1.437670109	0.00047	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
1.437243933	0.000210173	Pprc1_predicted	Peroxisome proliferative activated receptor, gamma, coactivator-related 1

1.43188639	0.000602	Noc4_predicted	COX4 neighbor
1.421084307	0.001475	Acat1	acetyl-coenzyme A acetyltransferase 1
1.416512711	0.002369	Timm17a	translocator of inner mitochondrial membrane 17a
1.41450971	0.005451	Phb	prohibitin
1.413290603	0.00353	LOC362322	similar to citrin (predicted)
1.405131265	0.00294		hairy/enhancer-of-split related with YRPW motif 2
1.400641847	0.000977	Mrpl45_predicted	mitochondrial ribosomal protein L45 (predicted)
1.396029655	0.004937	Mrpl49_predicted	mitochondrial ribosomal protein L49
1.395301851	0.00354	RGD1309529_predicted	similar to DNA segment, Chr 10, ERATO Doi 214, expressed (predicted)
1.390965364	0.000165	Mor1	malate dehydrogenase 2, NAD (mitochondrial)
1.390657293	0.00063	RGD1311696_predicted	tyrosyl-tRNA synthetase 2 (mitochondrial)
1.382955594	0.000318	Cyc1_predicted	cytochrome c-1 (predicted)
1.38121754	0.001414	Mrps26_predicted	mitochondrial ribosomal protein S26 (predicted)
1.378509205	0.004046	Cyb5m	cytochrome b5 type B
1.377406499	0.005125	Gosr2	golgi SNAP receptor complex member 2
1.365918229	0.001124	Slc25a5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1.360045929	0.001909	Gapd	glyceraldehyde-3-phosphate dehydrogenase
1.359016377	0.001257	RGD:1359688	nipsnap homolog 3A (C. elegans)
1.35236727	0.00041	RGD:1359733	TNF receptor-associated protein 1
1.350929535	0.005333	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25
1.349667007	0.004712	Mrps2_predicted	mitochondrial ribosomal protein S2 (predicted)
1.344860767	0.000527	Atad3a_predicted	ATPase family, AAA domain containing 3A
1.339208796	0.001961	Aldh7a1_predicted	aldehyde dehydrogenase family 7, member A1
1.333965076	0.001705	Bcap37	prohibitin 2
1.3269251	0.001647	Acs15	acyl-CoA synthetase long-chain family member 5
1.322791266	0.000382	Tbfg4_predicted	transforming growth factor beta regulated gene 4
1.310095015	0.0021	LOC361596	similar to NADP+-specific isocitrate dehydrogenase
1.295618365	0.005419	Ndufb8_predicted	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (predicted)
1.294485835	0.003069	RGD1311696_predicted	dynamin 1-like
1.29341834	0.003037	RGD1311462_predicted	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)
1.270623334	0.00185	Dbi	diazepam binding inhibitor
1.265237133	0.002281	Nme2	expressed in non-metastatic cells 2
1.261804167	0.004679		solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
1.252537292	0.005302	Prss15	protease, serine, 15
1.251565413	0.003469	Smfn_predicted	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
1.24095222	0.002123	Afg311_predicted	AFG3(ATPase family gene 3)-like 1 (yeast) (predicted)
1.237459986	0.002789	RGD1308697_predicted	similar to hypothetical protein FLJ10579
-1.234634239	0.004196	Ttc11_predicted	fission 1 (mitochondrial outer membrane) homolog (yeast)
-1.236030438	0.004188	RGD:1303003	homolog of zebrafish ES1
-1.247581063	0.003685	Itm2b	integral membrane protein 2B
-1.250190352	0.003671	Mlycd	malonyl-CoA decarboxylase
-1.269202814	0.00442	Slc25a12_predicted	solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)
-1.272272995	0.005896		PET112-like (yeast) (predicted)
-1.288210514	0.002582	Slc25a17_predicted	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 (predicted)
-1.289285904	0.002192	Sod1	superoxide dismutase 1
-1.300554592	0.002813	Acadv1	acyl-Coenzyme A dehydrogenase, very long chain
-1.316009636	0.000633	Cat	catalase
-1.334617178	0.00236	RGD:1359171	mitochondrial ribosomal protein L9
-1.35421263	0.00182	Psap	prosaposin

-1.365581295	0.000338	Amacr	alpha-methylacyl-CoA racemase
-1.40232708	5.40E-005	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4
-1.416084706	0.000126	Ech1	enoyl coenzyme A hydratase 1, peroxisomal
-1.418760691	0.00152	Dguok_predicted	deoxyguanosine kinase (predicted)
-1.450501516	0.001332	Cpt1a	carnitine palmitoyltransferase 1a, liver
-1.474072678	0.000694	Otc	ornithine transcarbamylase
-1.489190604	0.001014	Ppqb_predicted	protective protein for beta-galactosidase
-1.505932636	0.001121	Aldoc	aldolase C
-1.545669774	0.000113	Sfxn3	sideroflexin 3
-1.566623979	0.001428	Pts	6-pyruvoyl-tetrahydropterin synthase
-1.573789732	0.000364	Auh_predicted	AU RNA binding protein/enoyl-coenzyme A hydratase (predicted)
-1.588417844	0.000288	Bnip3l	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like
-1.595884312	6.18E-005	Hspa1a	heat shock 70kD protein 1A
-1.59638791	0.000459	Cdc42bpa	chaperone, ABC1 activity of bc1 complex like (S. pombe)
-1.64897021	0.000181	Glul	glutamate-ammonia ligase (glutamine synthase)
-1.670068879	0.000694	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2
-1.814866991	5.16E-005	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4
-2.069340949	3.71E-006	Ghr	growth hormone receptor