

Supplementary Table 2. All secondary candidate genes

The profile ns-down-up

Accession number	Gene name	6 wk	Frog	Tail NF62
BC046371	propionyl Coenzyme A carboxylase, beta polypeptide	0.70	1.87	0.52
U08408	arginase, type II	0.62	1.70	0.59
BC045005	holocytochrome c synthase (cytochrome c heme-lyase)	0.68	2.45	0.43
BC057214	mitochondrial ribosomal protein L55	0.69	1.97	NS
BX846125	RP42 homolog	0.43	1.91	NS
BU910126	SVAP1 protein	0.65	1.58	NS
CD101250	oncomodulin	0.37	4.00	0.15
CD301095	esterase D/formylglutathione hydrolase	0.64	1.34	0.37
CB941244	Unk. EST	0.60	3.19	1.69
AB072007	transmembrane protein 52	0.68	1.81	NS
BU916064	benzodiazapine receptor (peripheral) associated protein 1	0.64	2.56	0.61
BX853095	chromosome 9 open reading frame 61	0.64	3.87	0.22
BC042287	carbonic anhydrase II	0.59	4.63	3.44
CD253778	HNF1 alpha	0.50	3.45	0.25
BC045100	phosphofructokinase, muscle	0.61	23.59	0.16
CD253447	nipsnap homolog 3A (C. elegans)	0.65	1.81	NS
BC041492	hypothetical protein FLJ10006	0.69	2.10	NS
AW766955	Unk. EST	0.57	1.63	NS

The profile ns-ns-up

BC054279	eukaryotic translation elongation factor 1 alpha 2	338.77	4.95	
BG162895	NADH dehydrogenase (ubiquinone) Fe-S protein 4	70.84	4.35	
BC059335	proteasome (prosome, macropain) subunit, beta type	34.17	NS	
AY114144	troponin T3, skeletal, fast	32.34	0.12	
CD302014	XFG 5-1 and XFG 5-2 genes for zinc finger proteins	31.83	0.31	

BC054240	enigma (LIM domain protein)	30.78	0.45
BC044330	solute carrier family 16 (monocarboxylic acid transporters), member 3	24.61	0.27
BJ637800	Unk. EST	23.15	NS
BG264196	hemoglobin, alpha 2	22.17	4.04
BX846343	Septin4	21.59	0.26
BC046673	aldolase A, fructose-bisphosphate	16.21	0.19
BX846707	TPA-induced transmembrane protein	16.07	0.28
BC043836	skinny hedgehog like	16.02	0.07
BQ731714	myosin, heavy polypeptide 2, skeletal muscle, adult	15.42	0.59
BC044007	pyruvate kinase, muscle	15.08	0.1
BC060011	glucokinase (hexokinase 4) regulatory protein	14.82	0.21
BX848512	cytochrome c oxidase subunit VIIa polypeptide 2 like	14.40	0.38
BU899397	tetraspan 1	13.51	NS
AJ009306	aldolase A, fructose-bisphosphate	12.79	0.23
BC060028	sodium channel, voltage-gated, type IV, beta	12.71	0.17
BF612261	microtubule/chromatin interaction	12.42	NS
BC043876	phosphoglucomutase 1	12.31	0.05
BG163021	Unk. EST	11.74	1.71
CA983427	hypothetical protein LOC134145	11.59	0.29
BC045015	lactate dehydrogenase A	10.66	0.2
BC045269	glutamic-oxaloacetic transaminase 1	10.44	0.15
CD327121	RAS guanyl releasing protein 1	9.77	NS
BG264233	Clathrin coat assembly protein	9.25	NS
BC043781	phosphoglycerate kinase 1	9.21	0.11
AF421880	calcium channel, voltage-dependent, L type, alpha 1S subunit	8.72	0.28
BC045243	serologically defined colon cancer antigen 1	8.69	NS
BG264811	Unk. EST	8.66	NS
BC041738	amyloid P component, serum	8.34	NS
AW767623	ubiquinol-cytochrome c reductase (6.4kD) subunit	8.05	0.51
CB209556	Unk. EST	8.03	0.12
CF283499	leukocyte cell derived chemotaxin 1	7.94	0.27

BU916269	Unk. EST	7.90	0.58
BX848751	amylase-1, 6-glucosidase, 4-alpha-glucanotransferase	7.56	0.37
CA980988	peroxiredoxin 3	7.23	NS
BM190826	SH3 multiple domains 2	7.10	0.16
BX854153	PTD008 protein	6.91	1.45
BF614639	ATPase inhibitory factor 1	6.91	NS
BE490891	Unk. EST	6.64	NS
CF519937	Unk. EST	6.35	NS
BC060486	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	6.33	0.41
BC059972	pyruvate dehydrogenase kinase, isoenzyme 2	5.95	0.42
AY362041	superoxide dismutase 2, mitochondrial	5.91	0.51
BG347956	Xenopus laevis myosin light chain 1v	5.89	0.41
CB592100	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	5.87	0.27
BF047364	ATP synthase, mitochondrial F0 complex, subunit f, isoform 2	5.85	0.50
CB199961	ATP synthase, mitochondrial F0 complex, subunit e	5.82	NS
BG486716	ring finger protein (C3HC4 type)	5.75	NS
M16259	ATP synthase, mitochondrial F1 complex, alpha subunit, isoform 1	5.73	0.22
BU908919	dentin sialophosphoprotein preproprotein	5.73	0.56
BF611222	cytochrome c oxidase subunit VIIa polypeptide 2 like	5.65	0.33
CB198532	ubiquinol-cytochrome c reductase binding protein	5.62	0.35
BC041213	carbonic anhydrase II	5.49	1.82
U03878	pyruvate kinase, muscle	5.46	0.17
CD099091	Unk. EST	5.45	NS
CD360625	PCTAIRE protein kinase 1	5.45	0.70
BF231948	Low log int. Unk. EST	5.35	NS
U39669	pyruvate dehydrogenase (lipoamide) beta	5.35	0.38
BU904087	cytochrome c oxidase subunit IV isoform 2	5.34	NS
AW634424	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	5.31	0.56
BG161583	Unk. EST	5.31	0.20
BC042271	hypothetical protein MGC15416	5.27	0.29
BG017618	mitochondrial inner membrane	5.26	0.35

BC042931	ubiquinol-cytochrome c reductase core protein II	5.09	0.32
BG159998	alpha fast tropomyosin	5.05	NS
CD325457	complexin 4	5.00	0.61
CA985882	ataxin 2 related protein	4.97	0.38
BC044313	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	4.91	NS
CA972639	genethonin 1 muscle	4.90	NS
BC049394	NADH dehydrogenase (ubiquinone) Fe-S protein 1	4.90	0.39
BQ728067	sex comb on midleg-like 2	4.87	NS
BX850233	Unk. EST	4.86	3.39
BE025729	acetyl-Coenzyme A acetyltransferase 1	4.82	0.14
BC054959	ATP synthase, mitochondrial F1 complex, alpha subunit, isoform 1	4.82	0.24
BG233847	molecule interacting with Rab13	4.80	NS
CB560135	Unk. EST	4.79	NS
BC047980	hypothetical protein MGC15416	4.78	0.22
CB563732	senescence downregulated leo1-like	4.76	0.37
AW200073	ATP synthase, mitochondrial F1 complex, delta subunit	4.76	0.39
AB030904	thimet oligopeptidase 1	4.75	NS
BC049288	ubiquinol-cytochrome c reductase core protein I	4.75	0.35
CB592159	eukaryotic translation initiation factor 4E-like 3	4.74	NS
BX855415	Unk. EST	4.71	NS
BC046577	voltage-dependent anion channel 1	4.70	0.17
CD302686	carbonic anhydrase	4.70	0.63
BC060436	nipsnap homolog 3A (<i>C. elegans</i>)	4.69	0.32
AW200445	NADH dehydrogenase 1, subcomplex unknown, 2, 14.5kDa	4.64	0.47
BU906294	acetyl-Coenzyme A acetyltransferase 1	4.63	0.20
BE506967	NADH dehydrogenase 1 alpha subcomplex, 6, 14kDa	4.62	0.40
CA974094	cytochrome c, somatic	4.60	NS
BQ734654	transcription factor NSCL-1	4.58	1.62
AW634109	low molecular mass ubiquinone-binding protein (9.5kD)	4.55	0.21
AW199851	ATP synthase, mitochondrial F0 complex, subunit F6	4.54	NS
BC046379	isocitrate dehydrogenase 2 (NADP+), mitochondrial	4.49	0.32

CB941908	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	4.48	NS
CA987906	Unk. EST	4.46	1.41
CA986227	lin-9 homolog	4.44	NS
CB207420	phosphoglycerate kinase 1	4.42	0.29
BJ613977	Alstrom syndrome 1	4.40	NS
BG233756	beta-1-adrenergic receptor	4.40	NS
AW200171	ATP synthase, mitochondrial F0 complex, subunit g	4.37	NS
BM180516	Unk. EST	4.36	1.83
BG019694	alpha(E)-catenin core and promoter element binding protein	4.31	1.57
BC044122	IMP (inosine monophosphate) dehydrogenase 2	4.27	0.24
BJ092399	FK506 binding protein 9	4.27	NS
M58019	major histocompatibility complex, class I-related	4.26	NS
BJ642521	Unk. EST	4.23	1.97
BC044112	pyruvate dehydrogenase kinase, isoenzyme 2	4.22	NS
BQ731027	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	4.19	0.34
BC056098	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa	4.16	NS
BI313290	eukaryotic translation elongation factor 1 alpha 2	4.14	NS
BM191554	hypothetical protein BC011916	4.13	0.65
BC054183	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	4.11	0.49
CB201255	four and a half LIM domains 1	4.09	NS
BE575890	Proto-oncogene serine/threonine-protein kinase pim-1	4.05	NS
CD303590	delta-notch-like EGF repeat-containing transmembrane	4.01	NS
CB196956	Unk. EST	3.99	NS
BX848879	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 7	3.96	NS
CD255428	hypothetical protein FLJ31842	3.95	NS
AW767983	testis development protein NYD-SP29	3.95	2.71
BU900090	transcription termination factor, RNA polymerase II	3.92	0.16
CF286827	Unk. EST	3.90	NS
AF072455	matrix metalloproteinase 9	3.89	NS
BJ056778	Unk. EST	3.89	NS
AF430140	dihydrolipoamide S-acetyltransferase	3.88	0.28

AW200087	zinc finger protein 183 (RING finger, C3HC4 type)	3.87	0.62
AB037700	zona pellucida glycoprotein 4	3.86	NS
BJ635842	ribosomal protein L36a	3.86	0.34
BC044274	estrogen-related receptor alpha	3.86	NS
BI444049	zinc finger protein 225	3.83	2.33
CD254416	protein kinase, AMP-activated, beta 1 non-catalytic subunit	3.83	0.41
AF087650	mesoderm posterior 1	3.83	0.55
BG019985	Unk. EST	3.80	NS
BU913405	proline-rich nuclear receptor coactivator 2	3.80	2.61
BC045001	guanidinoacetate N-methyltransferase	3.78	0.09
BC048770	glyceraldehyde-3-phosphate dehydrogenase	3.78	NS
CD326222	Unk. EST	3.76	NS
BC044021	adenylosuccinate lyase	3.75	0.18
BE189549	Unk. EST	3.74	NS
BX848741	AD-003 protein	3.74	0.28
BG021145	Unk. EST	3.73	NS
CA987423	Unk. EST	3.73	NS
AW147428	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa	3.73	0.40
CD327911	Unk. EST	3.72	2.53
U19618	fibrinogen, B beta polypeptide	3.71	NS
BI315522	Unk. EST	3.71	NS
BC058770	RNA binding motif protein 5	3.69	NS
BC046571	citrate synthase	3.66	0.55
BC053793	aldo-keto reductase family 1, member C3	3.66	4.18
U68724	myeloperoxidase	3.64	NS
BG884818	epoxide hydrolase 2, cytoplasmic	3.64	NS
BU909526	membrane component, chromosome 17, surface marker 2	3.62	NS
BC045127	cytochrome c-1	3.58	0.28
BF072220	Unk. EST	3.57	NS
BG407150	Unk. EST	3.57	NS
CB205976	Unk. EST	3.56	NS

BQ734743	arginine-rich, mutated in early stage tumors	3.56	NS
BG019287	ubiquinol-cytochrome c reductase hinge protein	3.53	0.51
CB198477	adenylate kinase 1	3.53	0.28
CD255923	Unk. EST	3.52	NS
BU914114	likely ortholog of mouse Sds3	3.51	NS
AF062387	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	3.51	0.57
CA974238	ATP synthase, mitochondrial F0 complex, subunit c isoform 3	3.50	0.41
BM179029	Unk. EST	3.49	NS
U25285	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)	3.49	NS
BQ109740	Unk. EST	3.48	NS
BC060417	ATPase, H+ transporting, lysosomal V0 subunit a isoform 4	3.47	0.51
BX844184	hypothetical protein LOC114971	3.47	0.33
AB048259	sestrin 1	3.44	NS
BC054322	complement component 3	3.44	NS
BU915007	Unk. EST	3.43	NS
BI446653	Unk. EST	3.43	NS
AW199639	Unk. EST	3.41	0.37
L20730	major histocompatibility complex, class I-related	3.41	NS
BE680023	Unk. EST	3.40	0.44
BC043859	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	3.40	0.55
CB208454	Unk. EST	3.39	NS
CA987607	Unk. EST	3.38	0.19
CA982161	granulin	3.37	NS
BX849222	Unk. EST	3.34	0.26
CA982303	hypothetical protein LOC114971	3.34	0.41
BF048570	Unk. EST	3.34	2.23
BJ045539	hypothetical protein FLJ10884	3.34	1.73
BG023549	myosin IXA	3.33	3.78
BG360019	hypothetical protein MGC34290	3.33	NS
CA790822	Unk. EST	3.32	NS
BQ387496	Unk. EST	3.27	NS

BU899537	Unk. EST	3.25	0.69
CB755961	Unk. EST	3.25	NS
BQ385192	Unk. EST	3.23	NS
AY277253	SH3 protein interacting with Nck, 90 kDa	3.19	0.33
BU915756	apolipoprotein L, 3	3.19	NS
BG021169	Unk. EST	3.19	NS
BU901481	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	3.19	NS
BG731777	Unk. EST	3.18	0.60
BX848343	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	3.18	0.47
CD363295	Unk. EST	3.17	0.58
BJ068590	Unk. EST	3.16	NS
AW199788	Unk. EST	3.16	NS
BC054185	fibrinogen, gamma polypeptide	3.15	0.70
BU907566	hypothetical protein MGC8721	3.14	NS
BC045222	hydroxyacyl-Coenzyme A dehydrogenase	3.14	0.40
BG439738	Unk. EST	3.13	NS
BQ733484	trinucleotide repeat containing 6	3.13	1.42
BG161528	Unk. EST	3.13	NS
BC047261	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	3.12	0.36
BC041195	tubulin, alpha 3	3.10	NS
BI478075	Unk. EST	3.09	2.88
CF521207	Unk. EST	3.08	2.36
AW200323	hypothetical protein HSPC132	3.08	0.54
CF287016	NADH dehydrogenase (ubiquinone) Fe-S protein 1	3.07	0.46
BC046580	small inducible cytokine subfamily E, member 1	3.07	0.25
BJ616370	Unk. EST	3.07	NS
BI315361	Unk. EST	3.06	NS
CA971655	small nuclear ribonucleoprotein D3 polypeptide 18kDa	3.05	NS
BC060456	transforming growth factor beta regulator 4	3.03	0.41
CD252735	synuclein, beta	3.02	0.75
AY069942	myeloperoxidase	3.02	1.48

AW198984	Unk. EST	3.02	1.39
BC043807	BCL2-associated athanogene 3	3.02	NS
BG345920	Unk. EST	3.01	NS
CA789403	acetyl-Coenzyme A acetyltransferase 1	3.01	0.20
BG019821	Unk. EST	3.00	1.95

The numbers are ratio of the log intensity of three experimental hybridization values (6 wk transgenic limbs and control frog limbs) relative to the control NF55 tadpole limb or NF62 tail compared to NF54 tail.

NS or no entry mean the expression ratio is not significant. Note that none of these have an entry for 2 wk.