Supporting information for Porter *et al.* (September 25, 2001) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.211257298.

Table 5. Expression differences between extraocular and jaw or leg muscles

Accession no.	Gene	Average fold difference EOM vs. leg	EOM vs. jaw	SAM threshold
Transcription factor				
U70132	Paired-like homeodomain transcription factor 2 (Pitx2)	28.5	32.9	0.2
AW120874	*Paternally expressed gene 3 (Peg3)	21.5	14.6	0.4
AF038939	*Paternally expressed gene (Peg3)	9.8	13.6	0.4
D13664	Runt-related transcription factor (Runx2)	4.8	3.9	0.2
AF077861	Inhibitor of DNA binding 2 (Idb2)	4.8	3	--
AB029448	Dlxin-1	2.4	2.5	--
L20450	Zinc finger protein 97 (Zpf97)	2.3	2.1	--
AB012276	ATFx (Atfx)	2.3	ns	--
X56182	Myogenic factor 5 (Myf5)	ns	4.1	--
U20344	Gut-enriched Kruppel-like factor (Klf4)	ns	2.1	--
L03279	*Core binding factor β (Cbfb)	ns	ns	1
X63866	*Cellular nucleic acid binding protein (Cnbp)	ns	ns	0.6
AF041822	T-box 15 (Tbx15)	ns	ns	0.4
U20326	*Cellular nucleic acid binding protein (Cnbp)	ns	-1.7	0.6
U21855	CCR4-NOT transcription complex, subunit 7 (Cnot7)	ns	-2	--
Y07836	Stimulated by retinoic acid 14 (Stra14)	ns	-2	--
M61007	CCAAT/enhancer binding protein (C/EBP), β (Cebpb)	ns	-2.4	0.2
X16995	Nuclear receptor subfamily 4, group A, member 1 (Nr4a1)	ns	-2.4	0.2
X04435	Nuclear receptor subfamily 3, group C, member 1 (Nr3c1)	ns	-2.7	--
AF002283	α-actinin-2 associated LIM protein (Actn2lp)	-2.3	-2.1	0.4
D14572	*Core binding factor beta (Cbfb)	-2.3	-2.3	0.6
X80338	Sine oculis-related homeobox 2 (Six2)	-20.7	-23.3	0.2
Signal transduction/growth factor				
L04678	Integrin β 4 (Itgb4)	13.3	ns	--
U68058	Secreted frizzled-related sequence protein 3 (Sfrp3)	13.1	16.6	--
AW061337	Adenylate kinase 4 (Ak4)	8.9	8.1	--
AF009246	Ras-related protein, DEXRAS1 (Rasd1)	5.9	5.4	--
X81584	Insulin-like growth factor binding protein-6 (Igfbp6)	4.6	ns	0.2
AB020886	Src suppressed C-kinase substrate, SSeCKS	4	5.7	--
AF087687	Calcium-binding protein S100A1 (S100a1)	3.7	4.1	1
U52073	N-myc downstream regulated-like protein (Ndrl)	3	3.2	--
U67187	G protein signaling regulator RGS2 (Rgs2)	3	ns	--
AF056187	Insulin-like growth factor I receptor (Igf1r)	2.7	ns	--
AI848518	Hematopoietic zinc finger (Hzf)	2.6	2.4	--

		Average fold difference		
Accession no.	Gene	EOM vs. leg	EOM vs. jaw	SAM threshold
AW122197	Protein kinase, cAMP-dependent regulatory, type 1, α (Prkar1a)	2.2	2	1
AF042491	Putative membrane-associated progesterone receptor component (Pgrmc)	2.2	ns	--
AF079528	Immediate early response IER5 (Ier5)	2.1	ns	--
D50086	Neuropilin (Nrp)	2	2.1	0.2
X55957	Inhibin α subunit (Inha)	ns	16.9	--
X58289	Protein tyrosine phosphatase, receptor type, B (Ptprb)	ns	10.6	--
U13370	G protein-coupled receptor 26 (Gpcr26)	ns	9	--
AF011360	Regulator of G protein signaling 7 (Rgs7)	ns	8	--
M70642	Connective tissue growth factor (Ctgf)	ns	7.3	--
Z29532	Follistatin (Fst)	ns	4.2	--
AI848841	Patched homolog (Ptch)	ns	3.5	--
AF031127	Inositol trisphosphate receptor type 2 (Itpr2)	ns	2.7	--
AI845935	Guanine nucleotide binding protein, β 1 (Gnb1)	ns	2.3	--
D45859	Protein phosphatase 1B, magnesium-dependent, β isoform	ns	2	--
L12447	Insulin-like growth factor binding protein 5 (Igfbp5)	ns	ns	1
X95403	RAB2, member RAS oncogene family (Rab2)	ns	ns	0.4
Y10971	Odorant binding protein Ia (Obp1a)	ns	ns	0.4
AW046181	Serum/glucocorticoid-regulated kinase (Sgk)	ns	ns	0.4
AI180687	Phosphodiesterase 4B, cAMP-specific (Pde4b)	ns	-2	--
M81483	Calmodulin-dependent phosphatase catalytic subunit (Cam-Prp) (Ppp3cb)	ns	-2.1	--
U89924	Protein phosphatase 1 binding protein PTG (Ppp1r5)	ns	-2.1	0.2
D78382	Transducer of ErbB-2.1 (Tob1)	ns	-2.2	0.8
AF035646	Small GTPase Rab10 (Rab10)	ns	-2.3	--
M63554	Inhibitor protein of cAMP-dependent protein kinase (Pkia)	ns	-2.3	0.4
AF039840	Mitogen-activated protein (MAP) kinase-activated protein kinase 5 (Mapkapk5)	ns	-2.4	--
M31680	Growth hormone receptor (Ghr)	ns	-2.4	--
D45859	Protein phosphatase 1B, magnesium-dependent, β isoform (Ppm1b)	ns	-2.5	--
X97052	MAP kinase kinase (Map2k6)	ns	-3	--
AF064447	Sex-determination protein homolog (Fem1a)	ns	-3	--
AB025217	Calcium binding protein P22, Sid470p (Chp)	ns	-3.6	--
Y13361	RAB7, member RAS oncogene family, pseudogene 1 (Rab7-ps1)	ns	-6.3	0.2
X66225	Retinoid X receptor-γ (Rxrg)	ns	-8.4	--
U39066	Murine MAP kinase kinase 6c (Map2k6)	ns	-8.4	--
J02935	cAMP-dependent protein kinase type II regulatory subunit mRNA (Prkar2a)	ns	-9	--
AF058799	3-Monooxgenase/tryptophan 5-monooxgenase activation protein, γ-a polypeptide (S12)	ns	-9.8	--
U86405	myc box-dependent interacting protein 1 (Bin1)	-1.7	ns	0.6
D83073	MAP kinase 14, p38b (Mapk14)	-2.2	-2.3	0.2

		Average fold difference		
Accession no.	Gene	EOM vs. leg	EOM vs. jaw	SAM threshold
AB015652	DJ-1	-2.8	-1.9	1
U34973	Protein tyrosine phosphatase-like (Styx)	-4.3	-3.8	--
Cell cycle/apoptosis				
AI154017	LIM only 2 (Lmo2)	12.9	10.8	--
D88792	Double LIM protein-1	7.4	8.6	--
AF041376	Cell death activator (Cidea)	5.8	6.6	--
U47323	Stromal interaction molecule 1 (Stim1)	3.3	4.3	0.8
X65128	Growth arrest -specific 1 (Gas1)	3.1	2.7	0.4
AV138382	Programmed cell death 6 (Pdcd6)	3.1	ns	--
AF022465	High mobility group protein homolog HMG4 (Hmg4)	2.6	ns	--
D88793	Cysteine-rich protein (Csrp)	2.5	ns	--
AW121136	Small protein effector 1 of Cdc42	ns	3.7	--
AW048937	Cyclin-dependent kinase inhibitor 1A, P21 (Cdkn1a)	ns	3.5	--
U49112	Programmed cell death 6 (Pdcd6)	ns	2.2	--
X75316	Seb4 (Seb4)	ns	-2.3	0.6
AB009376	DNA fragmentation factor, α subunit (Dffa)	ns	-2.5	--
U60884	myc box-dependent interacting protein 1, SH3P9 (Bin1)	-2.3	-2.3	1
AB016080	Cyclin-dependent kinase inhibitor C (P57), Calcium binding protein Kip2 (Cdkn1c)	-10	-10.9	0.4
Metabolism--glucose				
X51905	Lactate dehydrogenase 2, B chain (Ldh2)	2.3	3.6	0.6
M32599	Glyceraldehyde-3-phosphate dehydrogenase (Gapd)	ns	2.7	0.4
M17516	Lactate dehydrogenase 1, A chain (Ldh1)	ns	ns	0.6
L31777	Triosephosphate isomerase (Tpi)	ns	ns	0.6
AF029843	Phosphoglycerate mutase	ns	ns	0.4
L09104	Glucose phosphate isomerase 1 complex (Gpi1)	ns	ns	0.4
AJ001418	Pyruvate dehydrogenase kinase 4 (Pdk4)	ns	ns	0.4
J03293	Phosphorylase kinase γ (Phkg)	ns	-2	0.6
M19381	Calmodulin (Calm)	-2.3	ns	0.6
X13586	2,3-Bisphosphoglycerate mutase (Bpgm)	-2.3	-2.4	--
X74616	Phosphorylase kinase α 1 (Phak1)	-3.8	-4	0.4
AF080469	Glucose-6-phosphatase transport protein 1, putative glycogen storage disease type 1b protein	-19.4	-25.1	0.4
X98848	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase (Pfkfb1)	-19.5	-19.1	--
D42083	Fructose 1,6-bisphosphatase (Fdb2)	-19.5	-26.5	0.2
Metabolism--lipid				
U48403	Glycerol kinase (Gyk)	11.8	14.1	--
M26270	Stearoyl-coenzyme A desaturase 2 (Scd2)	2.9	2.1	0.2
M28729	Peroxisomal acyl-CoA oxidase, muspaox (Acox)	2.2	2.2	0.8
X57638	Peroxisome proliferator-activated receptor (Ppara)	2.1	ns	--
M21285	Stearoyl-coenzyme A desaturase 1 (Scd1)	ns	3.1	0.4
AF049330	Peroxisome proliferative-activated receptor, γ, coactivator 1 (Ppargc1)	ns	2.6	--

		Average fold difference		
Accession no.	**Gene**	**EOM vs. leg**	**EOM vs. jaw**	**SAM threshold**
AF030343	Peroxisomal/mitochondrial dienoyl-CoA isomerase ECH1p (Ech1)	ns	2.1	1
U89352	Lysophospholipase I (Lypla1)	ns	-6	--
D50430	Glycerol-3-phosphate dehydrogenase (Gdm1)	-2.7	-2.1	--
M25558	Glycerolphosphate dehydrogenase 1, cytoplasmic adult (Gdc1)	-3	-3.1	0.6
Metabolism--other				
AB001607	Prostacyclin synthase (Ptgis)	7	ns	--
J04758	Tryptophan hydroxylase (Tph)	5	ns	--
AI851255	Cathepsin B (Ctsb)	4.3	4.3	--
J02980	Alkaline phosphatase 2 (Akp2)	4.2	3.6	--
AF068199	D-dopachrome tautomerase (Ddt)	4.1	3.8	0.2
Z49204	Nicotinamide nucleotide transhydrogenase (Nnt)	2.3	3.3	0.6
AF061017	UDP-glucose dehydrogenase (Ugdh)	2.3	ns	--
AI551087	Xanthine dehydrogenase (Xdh)	2.1	ns	--
U20892	Phosphoribosylglycinamide formyltransferase (Gart)	ns	2.2	0.2
M88694	Thioether *S*-methyltransferase (Temt)	ns	2	--
AF023463	Lupus nephritis-associated peptide 1 (Lnap1)	ns	1.7	0.4
AF055983	Proteasome (prosome, macropain) subunit, α type 3 (Psma3)	ns	ns	0.4
Z50159	Suppressor of initiator codon mutations, related sequence 1 (Sui1-rs1)	ns	ns	0.4
AB021122	Translocase of inner mitochondrial membrane 23 homolog (Timm23)	ns	ns	0.4
U08440	Cytochrome c oxidase, subunit VI a, polypeptide 1 (Cox6a1)	ns	ns	0.4
AI153959	Sialyltransferase 10 (α-2,3-sialyltransferase VI) (Siat10)	ns	-2.8	0.4
AF017639	Carboxypeptidase X2	ns	-4.5	--
Y15003	β-galactoside α-2,3-sialyltransferase (Siat9)	-4.3	-4.8	0.4
D12780	*S*-adenosylmethionine decarboxylase (Amd1)	-8.6	-6.4	1
Z23077	*S-adenosylmethionine decarboxylase 3 (Amd2)	-17.4	-16	1
Z23077	*S-adenosylmethionine decarboxylase 3 (Amd2)	-29.5	-27.6	0.6
Sarcomeric protein/excitation-contraction coupling				
X56518	Acetylcholinesterase (Ache)	13.9	ns	--
M17640	Acetylcholine receptor α-subunit (Chrna1)	9.9	6.5	0.4
D85923	Myosin heavy chain 11, smooth muscle (Myh11)	6.6	3.9	0.2
L47600	Cardiac troponin T isoform A3b (Tnt2)	3	3.7	--
M14537	Acetylcholine receptor β (Chrnb1)	2.1	ns	--
M15501	Actin, α, cardiac (Actc1)	2	2.1	1
AJ242874	Troponin I, skeletal, slow 1 (Tnni1)	ns	85.3	1
M76599	Myosin heavy chain, cardiac muscle, adult (Myhca)	ns	5	--
AJ131711	Troponin T1, skeletal, slow (Tnnt1)	ns	2.5	0.4
X12973	Myosin light chain, alkali, fast skeletal muscle (Mylf)	ns	ns	0.8
M29793	Troponin C, cardiac/slow skeletal (Tncc)	ns	ns	0.8
L48989	Troponin T3, skeletal, fast (Tnnt3)	ns	ns	0.6

Accession no.	Gene	Average fold difference		SAM threshold
		EOM vs. leg	EOM vs. jaw	
M91602	Myosin light chain, phosphorylatable, cardiac ventricles (Mylpc)	ns	ns	0.6
X12972	Myosin light chain, alkali, cardiac ventricles (Mylc)	ns	ns	0.6
AJ223361	Myosin, heavy polypeptide 4, skeletal muscle (Myh4)	ns	ns	0.6
AJ223362	Slow myosin heavy chain-beta	ns	ns	0.4
M12347	Actin, α 1, skeletal muscle (Acta1)	ns	ns	0.4
AW124250	Myosin heavy chain, cardiac muscle, α, adult (Myhca)	ns	ns	0.4
U04541	Tropomyosin 5 (Tpm5)	ns	ns	0.6
AB010144	Mitsugumin29 (Mg29)	ns	-2.4	0.4
U36579	Caveolin 3 (Cav3)	ns	-2.4	0.4
AF091998	*Calpain 3 (Capn3)	-1.9	-1.9	0.4
X92523	*Calpain 3 (Capn3)	-2.4	-2.6	0.2
AJ001038	M-protein (Myom2)	-68.7	-66	0.4
Channel/transporter				
Y00305	Potassium voltage-gated channel, shaker-related subfamily, member 1 (Kcna1)	12.5	13.9	--
AI849533	*Mitochondrial chloride intracellular channel 4 (Clic4)	11.3	ns	--
D00466	Apolipoprotein E (Apoe)	10.6	4.4	0.4
M28383	Solute carrier family 4 (anion exchanger), member 3 (Slc4a3)	10.5	13	1
X82648	Apolipoprotein D (Apod)	4.8	5.2	0.6
U09383	Calcium-activated potassium channel (Kcnma1)	4.1	4.7	0.4
X60367	Retinol binding protein 1 (Rpb1)	4	5	--
M63801	Connexin 43, α-1 gap junction (Gja1)	2.6	2.6	0.2
AI845237	*Mitochondrial chloride intracellular channel 4 (Clic4)	2.2	ns	--
X59382	*Parvalbumin (Pva)	ns	20.2	1
AF000149	ATP-binding cassette, subfamily A (ABC1), member 4 (Abca4)	ns	6.4	--
U93291	Calsequestrin (Casq1)	ns	4.7	1
U49430	Ceruloplasmin (Cp)	ns	3.3	--
AF068244	Cardiac calsequestrin (Casq)	ns	2.7	0.2
AI839697	ATPase, Na+/K+ transporting, α 2 polypeptide (Atp1a2)	ns	2.2	0.6
AB017112	Solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20 (Slc25a20)	ns	ns	0.4
L48687	Sodium channel, voltage-gated, type I, β polypeptide (Scn1b)	ns	-1.6	0.4
U16959	FK506 binding protein 5 (Fkbp5)	ns	-2.1	--
D86037	ATP-binding cassette, subfamily C (CFTR/MRP), member 9 (Abcc9)	ns	-2.1	--
X57349	Transferrin receptor	ns	-2.1	0.2
U48398	Aquaporin 4 (Aqp4)	ns	-2.7	--
AF020772	*Karyopherin (importin) α 3 (Kpna3)	ns	-5.4	--
AF020771	Karyopherin (importin) α 4 (Kpna4)	ns	-6	--

		Average fold difference		
Accession no.	**Gene**	**EOM vs. leg**	**EOM vs. jaw**	**SAM threshold**
X16645	ATPase, Na+/K+ transporting, β 2 polypeptide (Atp1b2)	ns	-10.4	--
AW047023	*Karyopherin (importin) α 3 (Kpna3)	-1.9	-1.8	0.4
X59382	*Parvalbumin (Pva)	-2.1	ns	1
U20619	Karyopherin (importin) α 2 (Kpna1)	-2.1	-2.4	0.2
AJ006306	Skeletal muscle calcium channel, γ-subunit (Cacng1)	-32.8	-29.4	1
Extracellular matrix/cytoskeleton				
X13986	Secreted phosphoprotein 1 (Spp1)	12.2	14.3	--
X70854	*BM-90/fibulin extracellular matrix glycoprotein (Fbln1)	11.4	13	--
D78274	Dermatan sulphate proteoglycan 3 (Dspg3)	9.5	11.7	--
X13297	Vascular smooth muscle α-actin (Actvs)	8.3	ns	0.2
X70853	*BM-90/fibulin extracellular matrix glyroprotein (Fbln1)	6.7	2.5	--
M11533	Myelin basic protein (Mbp)	6	5.7	0.2
D00613	Matrix γ-carboxyglutamate (gla) protein (Mglap)	4.2	3.8	0.2
M37335	Myelin proteolipid protein (Plp)	4	ns	--
AF013262	Lumican (Lum)	3.7	2.7	0.4
Z38110	Peripheral myelin protein (Pmp22)	3.6	2.8	0.4
AB010266	Creb-rp, Tnx and Cyp21 genes for cAMP response element binding protein-related protein, tenascin-X and steroid 21-hydroxylase	2.8	2.5	0.2
X53928	Biglycan (Bgn)	2.7	2.5	0.6
X52046	Procollagen, type III, α 1 (Col3a1)	2.6	1.8	0.6
AW121179	Microfibrillar-associated protein 5 (Mfap5)	2.4	2.8	0.2
M28729	Tubulin α-1 (Tuba1)	2.3	2.3	0.8
L23769	Microfibril-associated glycoprotein (Mfap2)	ns	3.5	--
U69262	Matrilin-2 precursor (Matn2)	ns	3	--
AI845652	Proteolipid M6B isoform TMD-omega (M6b)	ns	2.6	--
AI843799	Actin-crosslinking protein 7 (Aclp7)	ns	2.5	0.2
U43541	Laminin, β 2 (Lamb2)	ns	2.1	--
M28727	Tubulin α 2 (Tuba2)	ns	1.6	0.4
L29468	Cofilin 2, muscle (Cfl2)	ns	ns	0.4
X69064	Ankyrin 1 (Ank1)	ns	-2	0.4
AB014464	MGC-24v	ns	-2	0.4
D17577	Kinesin heavy chain member 1B (Kif1b)	ns	-2.9	0.2
AF057301	Keratocan (Ktcn)	ns	-3.1	--
L18880	Vinculin (Vcl)	ns	-5.1	--
U16741	Capping protein α 2 (Cappa2)	-2	ns	0.4
Immunology/cell defense				
M29009	*Complement factor H-related protein	12.3	5.8	0.2
X78445	Cytochrome P450 (Cyp1-b-1)	8.8	9.1	--
X07967	pM1 protein, member of XLR family expressed in lymphoid cells (Xlr)	3.7	ns	--
AB024538	Immunoglobulin superfamily containing leucine-rich repeat (Islr)	3.4	2.3	0.2
AB012693	CD47 antigen (Itgp)	3.2	2.7	0.2
M29008	*Complement factor H-related protein	ns	5.4	--
M12660	Complement component factor h (Cfh)	ns	4.3	0.2

		Average fold difference		
Accession no.	**Gene**	**EOM vs. leg**	**EOM vs. jaw**	**SAM threshold**
V00835	Metallothionein 1 (Mt1)	ns	3	0.2
U38261	Extracellular superoxide dismutase (Sod3)	ns	2.7	0.2
M68898	Mast cell protease 5 (Mcpt5)	ns	2.2	--
U60473	CD59 antigen (Cd59a)	ns	2	0.2
U47737	Lymphocyte antigen 6 complex, locus E (Ly6e)	ns	ns	0.4
L41365	Decay accelerating factor 2 (Daf2)	ns	-10.7	0.2
J03398	P glycoprotein 2 (Pgy2)	-2.3	ns	--
V00821	Immunoglobulin mu encoding the C terminus of the membrane-bound form	-4	-3.5	--
D63679	Decay accelerating factor 1 (Daf1)	-5	-7	--
Other/uncharacterized				
AI838080	Leukemia-associated gene (Lag)	9.6	9.6	--
X83569	Neuronatin (Nnat)	7.7	8.2	--
U24703	Reelin (Reln)	7.3	5.8	--
AW046850	Odorant-binding protein Ib (Obp1b)	6.2	ns	--
AF084482	Transmembrane protein (Wfs1)	5.5	6.9	1
AI835274	RAD21 homolog, *Schizosaccharomyces pombe* (Rad21)	5.2	ns	--
AJ000990	Legumain (Prsc1)	4	ns	0.2
X66402	Matrix metalloproteinase 3 (Mmp3)	3.9	ns	--
M91380	Follistatin-like (Fstl)	3	2.3	--
AF042139	60-kDa ribonucleoprotein Ro (Ssa2)	2.6	ns	--
AB025406	Sid23p	2.5	2.5	0.2
X86000	N-glycan α 2,8-sialyltransferase (Siat8d)	2.2	ns	--
AA717826	Early quiescence protein-1 (Eq1)	2.2	ns	--
AF096875	Type 2 deiodinase (Dio2)	2.1	ns	--
AI853172	Ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21	ns	5.9	--
AB025412	odd Oz/ten-m homolog 3 (Odz3)	ns	4.5	--
Y07812	Myelin and lymphocyte protein; T cell differentiation protein (Mal)	ns	2.6	--
AF002718	ATPase inhibitor (Atpi)	ns	2.1	0.2
M74495	Adenylosuccinate synthetase 1, muscle (Adss1)	ns	ns	0.8
AF008595	Major allergen 1-like (Mja1l)	ns	ns	0.6
X58196	H19 fetal liver	ns	ns	0.6
U78770	Trefoil factor 2 (spasmolytic protein 1) (Tff2)	ns	ns	0.4
AJ002307	Synaptogyrin 2 (Syngr2)	ns	ns	0.4
D14485	DbpA murine homologue	ns	ns	0.4
AB017918	Gross cystic disease fluid protein 15	ns	ns	0.4
X06407	Translationally regulated transcript (21 kDa) (Trt)	ns	ns	0.4
AW121235	Vesicle-associated membrane protein, associated protein A (33 kDa) (Vapa)	ns	ns	0.4
AI847314	Anaphase-promoting complex subunit 5 (Anpc5)	ns	ns	0.4
AI854802	Muscleblind-like (*Drosophila*)	ns	ns	0.4
AW122882	Vesicle-associated membrane protein 2 (Vamp2)	ns	ns	0.4
U00677	Syntrophin, acidic 1 (Snta1)	ns	-1.8	0.4
AW227647	LAG protein (Lag)	ns	-2.2	0.2
AW046579	F-box protein (Fba)	ns	-2.7	--
AW120711	DNA j protein b9 (Dnajb9)	ns	-3	--

		Average fold difference		
Accession no.	Gene	EOM vs. leg	EOM vs. jaw	SAM threshold
AJ011118	Skeletal muscle and cardiac protein	ns	-3.3	0.2
X76652	Retinoic acid induced, 23f8 (Rai2)	ns	-4.1	--
AW227650	Casein κ (Csnk)	ns	-4.7	0.2
AI837005	Testis abundant mRNA sequence	ns	-5.4	--
AF088983	Heat shock protein hsp40-3	ns	-23.1	--
AW048272	Src homology 3-binding domain glutamic acid-rich protein (Sh3bgr)	-1.6	ns	0.4
AI843476	Pantophysin (Pphn)	-1.8	ns	0.4
AI845732	T-complex protein 1, related sequence 1 (Tcp1-rs1)	-2.1	-2	0.4
AI846152	Down’s syndrome critical region homolog 1 (human) (Dscr1)	-2.9	-3.1	0.4
AI846214	Pleckstrin homology-like domain, family A, member 3 (Phlda3)	-3.1	-2.4	0.6
AF100171	Myelodysplasia/myeloid leukemia factor 1 (Mlf1)	-4.6	-4.5	1
Expressed sequence tags (EST)				
AI853444	EST	25.4	20.5	0.8
AI854793	EST, moderately similar to human guanine nucleotide-binding protein G(T) γ-1 subunit	19.6	19.2	0.2
AW120882	EST, weakly similar to *Escherichia coli* 3-oxoacyl-[acyl-carrier protein] reductase	19	24.9	0.2
AI853444	EST	17.3	16.1	0.8
AI606967	EST	12.1	9.1	--
AW046708	EST, highly similar to rat spectrin α chain, nonerythyroid	12.1	ns	--
AW046857	EST, highly similar to human myosin light chain 1, slow-twitch muscle A isoform	11.1	5.6	0.2
AW215551	EST, highly similar to *Caenorhabditis elegans* hypothetical 94.2-kDa protein C38D4.5 in chromosome III	9.8	12.7	--
AW122372	DNA segment, chromosome 10, Brigham & Women's Genetics 0791 expressed	6	7	--
AI839718	EST	6	6.4	--
AI006228	EST, highly similar to ERBB3 rat ERBB-3 receptor protein-tyrosine kinase precursor	5.8	6.4	--
AI837116	EST	4.3	4	0.8
AW123061	EST	4.1	2.8	--
AI747444	EST, highly similar to human KIAA0512 protein	3.5	ns	--
AA919594	EST	3.4	4.3	0.6
AI504338	EST	3.4	2.7	--
C85523	EST	3	ns	0.4
AI843802	EST	2.9	ns	--
AI836446	EST, moderately similar to human KIAA1398 protein	2.8	2.6	--
AI852098	EST	2.8	2.5	--
AA822174	EST	2.6	2.8	--
AI642389	EST, highly similar to ER23 human ER lumen protein retaining receptor 3	2.6	ns	--
AI844626	EST, highly similar to Gatm rat glycine amidinotransferase precursor	2.5	2.5	--

Accession no.	Gene	Average fold difference EOM vs. leg	 EOM vs. jaw	SAM threshold
AA839379	EST	2.4	2.5	--
AI848584	EST	2.4	2.5	0.2
AI836916	EST	2.3	ns	--
AW046661	EST, moderately similar to human KIAA1029 protein	2.1	2	--
AW210370	DNA segment, chromosome 16, ERATO Doi 536, expressed D16Ertd536e	2.1	ns	--
AI854771	EST	2	2	0.6
AW122271	EST	ns	7.2	--
AI840925	EST, highly similar to hypothetical *Saccharomyces cerevisiae* 66.5-kDa protein in ADE12-RAP1 intergenic region	ns	4.9	--
AW046158	DNA segment, chromosome 13, ERATO Doi 275, expressed D13Ertd275e	ns	4.2	--
AA407132	EST	ns	4	--
AI853019	EST	ns	3.9	--
AI841606	EST	ns	3.8	--
AF037312	EST, highly similar to *Mus muscularis* sulfonylurea receptor-1	ns	3.2	--
AI844839	EST, Weakly similar to *M. musculus* Form mouse formin	ns	3.1	--
AI643731	EST	ns	2.5	--
AI854020	DNA segment, chromosome 18, UCLA 3 D18Ucla3	ns	2.3	--
AI195392	EST, highly similar to human α-actin 1, cytoskeletal isoform	ns	2	--
AI835359	EST	ns	ns	0.6
AA870917	EST	ns	ns	0.4
AI853444	EST	ns	ns	0.4
AI848056	EST, highly similar to IF31_human eukaryotic tranlation initiation factor 3, subunit 1	ns	ns	0.4
AI842808	EST	ns	ns	0.4
AI837403	EST	ns	ns	0.4
AI842432	EST	ns	ns	0.4
AI837905	EST	ns	ns	0.4
AW045632	EST	ns	ns	0.6
AW124226	EST	ns	ns	0.4
AI849271	EST	ns	ns	0.4
AI836718	EST	ns	ns	0.4
AI847584	EST	ns	ns	0.4
AI844737	EST	ns	-1.8	0.4
AW049373	EST	ns	-1.9	0.4
AA681807	EST, Highly similar to *Oryctolagus cuniculus* glycogen debranching enzyme	ns	-2.1	0.2
AI853642	EST, highly similar to human eukaryotic initiation factor 4 γ	ns	-2.2	0.4
AW060212	EST, weakly similar to *M. musculus* ubiquitin-protein ligase E3-α	ns	-2.3	--
AI854008	EST, Weakly similar to *D.melanogaster* CG7611 gene product	ns	-2.5	--

Accession no.	**Gene**	**Average fold difference** **EOM vs. leg**	 **EOM vs. jaw**	**SAM threshold**
AA822412	EST, weakly similar to *S. cerevisiae* ADP-ribosylation factor	ns	-2.5	--
AW125421	DNA segment, chromosome 16, Wayne State Univ. 65, expressed D16Wsu65e	ns	-2.5	0.2
AW230891	EST, highly similar to human leucine-rich α-2-glycoprotein	ns	-2.9	--
AI851119	DNA segment, chromosome 17, ERATO Doi 315, expressed D17Ertd315e	ns	-3	--
AA288979	EST	ns	-3	--
AI853240	EST, moderately similar to human β-tubulin cofactor E	ns	-3.1	--
AI842192	EST	ns	-3.1	0.2
AW122957	EST	ns	-3.2	--
AI846896	EST	ns	-3.2	0.2
AA717740	EST, Weakly similar to *D.melanogaster* CG5181 gene product	ns	-4.1	--
AW227650	EST	ns	-4.7	0.4
AW124346	EST	ns	-5.2	--
AW122517	EST, highly similar to *M. musculus* probable ubiquitin carboxyl-terminal hydrolase	ns	-7.2	--
AI020029	EST	ns	-7.6	--
AI852376	*M. musculus* adult male kidney cDNA, RIKEN full-length enriched library, clone:0610017I22, full insert sequence	ns	-10.1	--
AI848325	EST	-1.7	ns	0.4
AW122625	EST, moderately similar to PTD015	-1.8	ns	0.4
AI787713	DNA segment, chromosome 19, ERATO Doi 721, expressed D19Ertd721e	-2.2	ns	--
AW121304	DNA segment, chromosome 6, ERATO Doi 253, expressed D6Ertd253e	-2.2	-2.3	0.2
AW120683	EST, highly similar to human ubiquitin-conjugating enzyme E2-CDC34 complementing	-2.4	-2.3	0.4
AI853930	EST	-2.4	-2.4	0.2
AW045965	EST, weakly similar to *C. elegans* predicted by using Genefinder	-2.4	-2.6	--
AA867340	EST, highly similar to human; the ha0919 gene product is novel	-2.6	-2.3	0.4
AW124623	EST, highly similar to *A. thaliana* ubiquitin-conjugating enzyme E2-19 KD	-2.7	-2.5	0.6
AI836034	EST, weakly similar to *M. musculus* AF114379_1 cypher2	-2.8	-2.7	0.4
AA690483	EST	-3	-2.6	--
C80836	EST	-3.5	-3.4	0.2
AA795541	EST, weakly similar to *M. muscularis* AF159856_1 N system amino acids transporter NAT-1	-4.3	-4.3	0.4
AA873956	EST	-20.4	-17.6	--

For Affymetrix analysis, positive values indicate higher gene expression in EOM, negative values indicate lower expression in EOM, and ns indicates comparison was not significant, either because the replicates did not all agree on the direction of change or the average fold difference was < 2-fold. SAM thresholds also are indicated for each gene. -- indicates did not meet SAM analysis threshold between 0.4 and 1. * denotes results obtained with two different probes in the Affymetrix microarray.