

Common Gene Transcript Increases Between EOM and Diaphragm

Accession No.	Gene	Average Fold Difference	
		EOM	Diaphragm
<i>Immune Response</i>			
X73371	Fc receptor, IgG, low affinity IIb (Fcgr2b)	9.45	4.10
BF289368	Lipopolysaccharide binding protein (Lbp)	6.00	2.04
NM_022393	Macrophage galactose N-acetyl-galactosamine specific lectin 1 (Mgl1)	4.59	2.40
NM_031530	Chemokine (C-C motif) ligand 2 (Ccl2)	2.83	5.06
<i>Metabolism</i>			
M33648	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2)	23.83	10.96
<i>Muscle</i>			
M33648	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2)	23.83	10.96
<i>Protein Synthesis/Modification</i>			
None			
<i>Receptor/Ion Channel</i>			
None			
<i>Other</i>			
NM_012532	Ceruloplasmin (Cp)	3.26	2.08
<i>Unclassified</i>			
None			
<i>EST</i>			
None			

Common Gene Transcript Increases between EOM and EDL

Accession No.	Gene	Average Fold Difference	
		EOM	EDL
<i>Immune Response</i>			
AI170394	Macrophage expressed gene 1 (Mpeg1)	13.89	4.06
BF393825	Dendritic cell inhibitory receptor 3 (Dcir3)	8.33	2.80
BI303379	Tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a)	7.69	5.20
NM_053843	Fc receptor, IgG, low affinity III (Fcgr3)	7.14	2.91
NM_053843	Fc receptor, IgG, low affinity III (Fcgr3)	6.79	3.01
L12458	Lysozyme (Lyz)	6.70	3.28
BG380285	Interferon induced transmembrane protein 1 (predicted) (RGD:1307601)	6.08	2.67
NM_017320	Cathepsin S (Ctss)	4.20	2.21
NM_024125	CCAAT/enhancer binding protein (C/EBP), beta (Cebpb)	2.89	2.33
BI285347	Complement component 4a /// complement component 4, gene 2 (C4a /// C4-2)	2.52	2.23
BI292425	Complement component 1, r subcomponent (predicted) (RGD:1309091)	2.36	2.10
AI236590	Myeloid differentiation primary response gene 88 (RGD:735043)	2.29	2.84
<i>Metabolism</i>			
AI233740	Aldo-keto reductase family 1, member B8 (Akr1b8)	9.48	12.15
NM_019230	Solute carrier family 22, member 3 (Slc22a3)	7.02	2.84
L12458	Lysozyme (Lyz)	6.70	3.28
NM_017320	Cathepsin S (Ctss)	4.20	2.21
BM389350	Flavin containing monooxygenase 2 (Fmo2)	3.10	3.71
NM_031972	Aldehyde dehydrogenase family 3, member A1 (Aldh3a1)	2.30	2.46
<i>Transcription Factor</i>			
NM_024125	CCAAT/enhancer binding protein (C/EBP), beta (Cebpb)	2.89	2.33
NM_012912	Activating transcription factor 3 (Atf3)	2.58	2.26
BI284436	Eukaryotic translation initiation factor 4A, isoform 1 (RGD:735141)	2.33	2.03
<i>Muscle</i>			
BF282304	Myosin IG (predicted) (RGD:1306016)	7.49	2.36
AW251450	Musculoskeletal, embryonic nuclear protein 1 (Mustn1)	3.42	2.25
<i>Regeneration</i>			
AW251450	Musculoskeletal, embryonic nuclear protein 1 (Mustn1)	3.42	2.25
<i>Cell Growth/Maintenance</i>			
BF419085	Histone deacetylase 4 (predicted) (RGD:1307563)	3.08	2.82

NM_017259	B-cell translocation gene 2, anti-proliferative (Btg2)	2.28	2.77
<i>Cell-Cell Signaling/Signal Transduction</i>			
U44948	Cysteine and glycine-rich protein 2 (Csrp2)	2.90	3.70
<i>Protein Synthesis/Modification</i>			
AF154349	Legumain (Lgmn)	3.26	2.28
<i>Other</i>			
L01122	Ferritin light chain 1 (Ftl1)	2.01	2.04
<i>EST</i>			
AI044316	Transcribed locus	10.43	7.37
NM_057144	---	6.16	3.26
BG381207	---	4.16	3.82
H31896	Similar to RIKEN cDNA 1700127B04	4.06	5.32
BI294018	Similar to macrophage mannose receptor precursor	4.05	2.25
BF553180	Transcribed locus	3.89	3.66
AA801220	---	3.35	3.05
BE116084	Similar to Extra cellular link domain-containing 1	2.98	2.27
AI179260	Transcribed locus	2.93	2.38
BE109381	Transcribed locus	2.70	3.47
BG379007	Ubiquitin-conjugating enzyme E2G 2 (predicted) (RGD:1304860)	2.65	2.41
AI175045	Transcribed locus	2.63	3.60
AI105243	Transcribed locus	2.62	2.27
BG671196	---	2.49	8.11
BI277836	---	2.44	2.28
BE113397	Transcribed locus	2.30	2.24
BI282191	Similar to ubiquitin-conjugating enzyme E2G 2; ubiquitin-conjugating enzyme 7 homolog	2.19	2.28
BI274101	Transmembrane, prostate androgen induced RNA (predicted) (RGD:1308255)	2.10	2.88
AW435415	Transcribed locus	2.07	2.07

Common Gene Transcript Increases between EDL and Diaphragm

Accession No.	Gene	Average Fold Difference	
		Diaphragm	EDL
<i>Immune Response</i>			
NM_053727	Nuclear factor, interleukin 3 regulated (Nfil3)	3.20	3.88
BF556820	Casitas B-lineage lymphoma b (RGD:620535)	2.39	2.39
BF556820	Casitas B-lineage lymphoma b (RGD:620535)	2.39	2.39
NM_053582	Lipocalin 7 (Lcn7)	2.20	2.42
<i>Metabolism</i>			
BE107890	NTE-related protein (RGD:708466)	3.99	3.57
NM_053623	Acyl-CoA synthetase long-chain family member 4 (Acsl4)	3.36	2.29

AI232474	Cathepsin L (Ctsl)	2.80	4.22
AF202733	Phosphodiesterase 4B (Pde4b)	2.75	3.38
BF565001	Phosphodiesterase 4D (Pde4d)	2.72	2.12
AI144948	Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb)	2.71	2.25
NM_017073	Glutamine synthetase 1 (Glul)	2.50	2.38
AA858930	Phosphodiesterase 4B (Pde4b)	2.31	2.70
AI176595	Cathepsin L (Ctsl)	2.25	2.86
AA893220	Spermidine/spermine N1-acetyl transferase (Sat)	2.23	3.91
<i>Response to Stress/Stimulus</i>			
AI599423	Growth arrest and DNA-damage-inducible 45 gamma (predicted) (RGD:1311796)	3.77	2.54
AI411742	Sestrin 1 (predicted) (RGD:1307517)	3.21	2.48
<i>Transcription Factor</i>			
NM_053727	Nuclear factor, interleukin 3 regulated (Nfil3)	3.20	3.88
NM_019242	Interferon-related developmental regulator 1 (Ifrd1)	2.40	2.76
AI706508	Peroxisome proliferative activated receptor, gamma, coactivator-related 1 (predicted) (RGD:1309688)	2.18	2.42
NM_013172	Myogenic factor 6 (Myf6)	2.15	3.63
NM_013172	Myogenic factor 6 (Myf6)	2.15	3.63
AI070270	Transducer of ERBB2, 2 (Tob2)	2.03	2.09
<i>Muscle</i>			
AI599423	Growth arrest and DNA-damage-inducible 45 gamma (predicted) (RGD:1311796)	3.77	2.54
AI144948	Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb)	2.71	2.25
<i>Regeneration</i>			
BG672052	Microtubule-associated protein 1b (Map1b)	3.38	2.73
BI281702	Microtubule-associated protein 1b (Map1b)	2.48	2.41
NM_019242	Interferon-related developmental regulator 1 (Ifrd1)	2.40	2.76
<i>Cell Growth/Maintenance</i>			
BG672052	Microtubule-associated protein 1b (Map1b)	3.38	2.73
BI281702	Microtubule-associated protein 1b (Map1b)	2.48	2.41
BG375380	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted) (RGD:1307633)	2.47	2.09
AA817668	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted) (RGD:1307633)	2.25	2.11
BM384139	Growth arrest specific 5 (RGD:621549)	2.10	2.19
<i>Cell-Cell Signaling/Signal Transduction</i>			
BI303527	Arrestin domain containing 3 (Arrdc3)	3.18	6.29

AA818910	Arrestin domain containing 3 (Arrdc3)	2.98	5.46
NM_022602	Serine/threonine-protein kinase pim-3 (RGD:620462)	2.93	2.43
<i>Cell Death/Apoptosis</i>			
AI599423	Growth arrest and DNA-damage-inducible 45 gamma (predicted) (RGD:1311796)	3.77	2.54
NM_022602	Serine/threonine-protein kinase pim-3 (RGD:620462)	2.93	2.43
NM_031135	TGFB inducible early growth response (RGD:621652)	2.51	3.20
<i>Protein Synthesis/Modification</i>			
NM_053857	Eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1)	3.66	3.38
NM_053582	Lipocalin 7 (Lcn7)	2.20	2.42
BF400606	Sequestosome 1 (Sqstm1)	2.14	2.18
<i>Receptor/Ion Channel</i>			
NM_053857	Eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1)	3.66	3.38
AI102520	Gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1 (predicted) (RGD:1308051)	2.06	2.25
<i>Other</i>			
BG663284	Fibrinogen-like 2 (RGD:620170)	2.67	3.52
BF561454	Fibrinogen-like 2 (RGD:620170)	2.61	2.75
AF323608	Fibrinogen-like 2 (RGD:620170)	2.41	2.72
<i>EST</i>			
BF406350	---	4.58	4.56
BF402375	Transcribed locus	4.48	6.28
BM390487	CDNA clone MGC:94732 IMAGE:7193534, complete cds	4.28	2.73
AI502258	Similar to hypothetical protein DKFZp566A1524 (predicted) (RGD1305961_predicted)	4.04	4.26
BE111904	Transcribed locus	3.68	5.89
BE103875	Transcribed locus	3.51	2.18
BE349698	---	3.26	2.60
BE108930	Transcribed locus	3.09	2.50
BI278288	Similar to RIKEN cDNA 0610039C21 (predicted) (RGD1309044_predicted)	3.05	2.69
AI407797	Transcribed locus	2.79	4.72
BG381414	LOC361797 (LOC361797)	2.67	2.24
AI071166	Similar to 1110007F12Rik protein	2.61	4.07
BF396108	Transcribed locus	2.61	2.71
BF287008	Growth arrest specific 5 (RGD:621549)	2.56	2.61
AI111775	Transcribed locus	2.48	2.10
BF283610	Transcribed locus	2.43	3.17

AI175790	Alpha-mannosidase-like protein mRNA, 3' UTR	2.42	2.22
BI290895	Similar to prostate cancer overexpressed gene 1	2.35	2.11
BI303073	---	2.30	2.05
AI031032	Similar to erythroid differentiation-related factor	2.26	2.48
AI717218	Transcribed locus	2.24	2.22
NM_022392	---	2.24	2.35
AI175594	Transcribed locus	2.19	2.03
AI176041	---	2.19	2.21
BI301532	Transcribed locus	2.17	3.61
BE113491	---	2.06	2.39
AA818353	Transcribed locus	2.02	3.24

Gene Transcripts Increased Only in EOM

Accession No.	Gene	Average Fold Difference	
		EOM	
<i>Immune Response</i>			
BF282961	Similar to gp49B2 (LOC292594)	32.04	
AF053312	Chemokine (C-C motif) ligand 20 (Ccl20)	24.46	
NM_021866	Chemokine (C-C motif) receptor 2 (RGD:620876)	22.20	
NM_053372	Secretory leukocyte peptidase inhibitor /// similar to secretory leukocyte protease inhibitor (RGD:621768 /// LOC296356)	15.98	
AI009823	Secreted and transmembrane 1 (Sectm1)	13.46	
AI177292	CD18 leukocyte adhesion molecule (Cd18)	7.96	
NM_133542	Immunoglobulin superfamily, member 6 (Igsf6)	7.45	
BI301490	Major histocompatibility complex, class II, DM alpha (RGD:735053)	7.40	
BF387360	Immunoglobulin superfamily, member 7 (Igsf7)	6.64	
NM_012523	CD53 antigen (Cd53)	6.51	
AI102519	Tyro protein tyrosine kinase binding protein (Tyrobp)	6.26	
NM_053619	Complement component 5, receptor 1 (C5r1)	6.15	
AI639117	B-factor, properdin (Bf)	5.98	
BE098739	Endothelial type gp91-phox gene (Cybb)	5.83	
AI177761	CD68 antigen (predicted) (RGD:1305970)	5.71	
BM391631	Fc receptor, IgG, high affinity I (predicted) (RGD:1309912)	5.41	
AI715202	RT1 class II, locus Bb (RT1-Bb)	5.26	
Y00480	MHC Class II alpha chain, alpha-1 domain /// Immunoglobulin-like	5.24	
NM_017196	Allograft inflammatory factor 1 (Aif1)	5.24	
AA849399	Cathepsin Y (RGD:708479)	5.03	
AF071495	Scavenger receptor class B, member 1 (Scarb1)	5.00	
AI176057	Endothelial type gp91-phox gene (Cybb)	4.92	
BI295964	SLAM family member 9 (predicted) (RGD:1305945)	4.80	

BF395317	Membrane-spanning 4-domains, subfamily A, member 11 (predicted) (RGD:1305800)	4.77
AF307302	RT1 class II, locus Ba (RT1-Ba)	4.54
AJ222813	Interleukin 18 (Il18)	4.48
AI171966	Major histocompatibility complex, class II, DM beta (RGD:735096)	4.41
AI177403	Killer cell lectin-like receptor, subfamily A, member 17 (predicted) (RGD:1310720)	4.18
BE109711	Lymphocyte cytosolic protein 1 (predicted) (RGD:1308288)	3.95
BI278559	Dendritic cell inhibitory receptor 4 (Dcir4)	3.84
NM_013185	Hemopoietic cell kinase (Hck)	3.79
NM_013069	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74)	3.76
NM_021744	CD14 antigen (Cd14)	3.64
NM_020542	Macrophage inflammatory protein-1 alpha receptor gene (Ccr1)	3.61
BF394142	Complement component 2 (C2)	3.45
NM_012618	S100 calcium-binding protein A4 (S100a4)	3.40
AI137605	Chemokine-like factor super family 7 (predicted) (RGD:1305682)	3.32
AF065147	CD44 antigen (Cd44)	3.04
AJ243338	RT1 class I, CE5 (RT1-CE5)	2.99
NM_031797	Kangai 1 (Kai1)	2.96
AI102495	Nucleoside phosphorylase (Np)	2.91
NM_031541	Scavenger receptor class B, member 1 (Scarb1)	2.86
AF169636	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (predicted) (RGD:1307219)	2.72
BE095824	Chemokine (C-C motif) ligand 6 (RGD:1303200)	2.59
AF065438	Lectin, galactoside-binding, soluble, 3 binding protein (Lgals3bp)	2.48
AW434057	Complement component 1, q subcomponent, beta polypeptide (C1qb)	2.44
BI285793	Similar to Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (LOC307403)	2.39
AI012109	Lymphocyte specific 1 (predicted) (RGD:1306133)	2.33
AI716125	B-factor, properdin (Bf)	2.33
NM_080767	Proteosome (prosome, macropain) subunit, beta type 8 (Psm8)	2.24
AI170362	Similar to nuclear factor kappa B subunit p100 (predicted) (RGD1307189_predicted)	2.16
AI044222	Chemokine (C-X-C motif) ligand 9 (Cxcl9)	2.16
BF407234	Platelet-activating factor receptor (Ptafr)	2.12
AI012221	Chloride intracellular channel 1 (RGD:1303043)	2.11
NM_134390	TORID (RGD:708403)	2.09

Metabolism

BI294974	Squalene epoxidase (Sqle)	5.45
AF071495	Scavenger receptor class B, member 1 (Scarb1)	5.00
BI274054	Folate receptor 2 (fetal) (predicted) (RGD:1308515)	3.55
AA859827	Uridine monophosphate kinase (predicted) (RGD:1304844)	3.55
NM_031559	Carnitine palmitoyltransferase 1, liver (Cpt1a)	3.32
NM_017260	Arachidonate 5-lipoxygenase activating protein (Alox5ap)	3.24
U88294	Carnitine palmitoyltransferase 1, liver (Cpt1a)	3.23
AI232788	Cytochrome b-245, alpha polypeptide (Cyba)	3.11
AI102495	Nucleoside phosphorylase (Np)	2.91
NM_031541	Scavenger receptor class B, member 1 (Scarb1)	2.86
AI548897	Acyl-coenzyme A:cholesterol acyltransferase (Soat1)	2.63
AW251315	Sphingomyelin phosphodiesterase, acid-like 3B (predicted) (RGD:1307458)	2.35
AI717483	GM2 ganglioside activator protein (RGD:628651)	2.30
BI293600	Solute carrier family 35, member B2 (Slc35b2)	2.25
NM_053896	Aldehyde dehydrogenase family 1, subfamily A2 (Aldh1a2)	2.23
BI275763	Phytanoyl-CoA dioxygenase domain containing 1 (predicted) (RGD:1310377)	2.11
NM_012562	Fucosidase, alpha-L- 1, tissue (Fuca)	2.06
D17310	3-alpha-hydroxysteroid dehydrogenase (RGD:708361)	2.03
M61937	3-alpha-hydroxysteroid dehydrogenase (RGD:708361)	2.01

Response to Stress/Stimulus

NM_012523	CD53 antigen (Cd53)	6.51
BE098739	Endothelial type gp91-phox gene (Cybb)	5.83
AI176057	Endothelial type gp91-phox gene (Cybb)	4.92
AA800587	Glutathione peroxidase 2 (Gpx2)	2.61
NM_012715	Adrenomedullin (Adm)	2.46

Transcription Factor

BG378630	Placenta-specific 8 (predicted) (RGD:1308102)	2.72
BE126420	AE binding protein 1 (predicted) (RGD:1306922)	2.71
NM_017334	cAMP responsive element modulator (Crem)	2.45
BF282365	NIMA (never in mitosis gene a)-related expressed kinase 6 (Nek6)	2.35

Cell Adhesion/Migration

M88469	Spondin 1 (Spon1)	5.81
AI228417	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (predicted) (RGD:1304636)	3.24

U72660	Ninjurin 1 (Ninj1)	2.72
NM_053719	Embigin (Emb)	2.48
NM_031145	Calcium and integrin binding 1 (calmyrin) (Cib1)	2.36
AA893484	Fibronectin 1 (Fn1)	2.23
<i>Muscle</i>		
AI764088	Myosin IF (predicted) (RGD:1309750)	7.17
BI296317	Similar to RIKEN cDNA C730007L20 gene	6.49
AI411057	Coactosin-like 1 (Dictyostelium) (predicted) (RGD:1305498)	3.43
AW918670	Filamin C, gamma (actin binding protein 280) (predicted) (RGD:1308807)	2.24
AF053361	Tropomyosin 3, gamma /// tropomyosin isoform 6 (RGD:621546 /// RGD:708368)	2.11
NM_031813	Myosin binding protein H (Mybph)	2.00
<i>Regeneration</i>		
AA955902	Myogenic differentiation 1 (Myod1)	2.04
<i>Cell Growth/Maintenance</i>		
NM_019296	Cell division cycle 2 homolog A (S. pombe) (Cdc2a)	3.85
BM385031	Proteolipid protein 2 (Plp2)	2.48
D38468	Protein tyrosine phosphatase, non-receptor type substrate 1 (Ptpns1)	2.37
NM_013016	Protein tyrosine phosphatase, non-receptor type substrate 1 (Ptpns1)	2.27
NM_030847	Epithelial membrane protein 3 (Emp3)	2.27
BF419366	MAD2 mitotic arrest deficient-like 2 (yeast) (predicted) (RGD:1307499)	2.11
M15481	Insulin-like growth factor 1 (Igf1)	2.02
<i>Cell-Cell Signaling/Signal Transduction</i>		
BE116750	Rho GTPase activating protein 9 (predicted) (RGD:1305342)	4.67
NM_057124	Pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2ry6)	4.58
AI010476	RAS-related C3 botulinum substrate 2 (predicted) (RGD:1307568)	3.48
NM_020101	Centaurin-alpha2 protein (Centa2)	2.98
NM_031797	Kangai 1 (Kai1)	2.96
AI070875	Matrix Gla protein (Mgp)	2.74
BG375902	Ras homolog gene family, member G (predicted) (RGD:1307062)	2.33
AW916153	Protein tyrosine phosphatase, non-receptor type 18 (predicted) (RGD:1311586)	2.27
NM_031514	Janus kinase 2 (Jak2)	2.19
AW253722	RAB13, member RAS oncogene family (Rab13)	2.12
NM_019370	Ectonucleotide pyrophosphatase/phosphodiesterase 3 (Enpp3)	2.04

Cell Death/Apoptosis

NM_133416	B-cell leukemia/lymphoma 2 related protein A1 (RGD:620621)	16.06
NM_017196	Allograft inflammatory factor 1 (Aif1)	5.24
AI136555	Castration induced prostatic apoptosis-related protein 1 (RGD:708342)	3.64
BM389261	Interferon gamma inducible protein 30 (predicted) (RGD:1310758)	3.52
BG666928	BH3 interacting domain death agonist (Bid)	3.42
AF140346	Secreted frizzled-related protein 4 (RGD:621075)	2.29

Protein Synthesis/Modification

NM_031531	Serine protease inhibitor (Spin2c)	14.33
NM_053538	Lysosomal-associated protein transmembrane 5 (Laptm5)	11.14
NM_012488	Alpha-2-macroglobulin (A2m)	6.22
AA849399	Cathepsin Y (RGD:708479)	5.03
BF406601	Lysosomal-associated protein transmembrane 5 (Laptm5)	4.78
NM_133523	Matrix metalloproteinase 3 (RGD:621317)	4.18
AI409867	Cystatin B (Cstb)	2.08

Receptor/Ion Channel

NM_013125	Sodium channel, voltage-gated, type V, alpha polypeptide (Scn5a)	34.09
NM_057124	Pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2ry6)	4.58
AI008680	Benzodiazepin receptor (Bzrp)	2.49
NM_021909	FXFD domain-containing ion transport regulator 5 (Fxyd5)	2.41

Other

BF411331	Serine (or cysteine) proteinase inhibitor, clade B, member 1a (predicted) (RGD:1306203)	6.10
AI176034	Tenascin C (Tnc)	5.06
BE100150	Serine (or cysteine) proteinase inhibitor, clade B, member 1a (predicted) (RGD:1306203)	4.75
NM_130411	Coronin, actin binding protein 1A (RGD:620009)	4.60
NM_012907	Apolipoprotein B editing complex 1 (Apobec1)	4.37
NM_022278	Glutaredoxin 1 (thioltransferase) (Glrx1)	3.12
NM_130413	Src family associated phosphoprotein 2 (Scap2)	3.09
AF319950	Glutaredoxin 1 (thioltransferase) (Glrx1)	2.92
BI290559	Microsomal glutathione S-transferase 2 (predicted) (RGD:1311218)	2.72
BF395171	EH-domain containing 4 (Ehd4)	2.35
AA801107	EH-domain containing 4 (Ehd4)	2.35

Unclassified

AW523847	Similar to intermediate filament-like protein MGC:2625 isoform 2; HOM-TES-103 tumor	3.95
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	antigen-like (predicted) (RGD1308257_predicted)	
AI234533	Unc-93 homolog B (<i>C. elegans</i>) (predicted) (RGD:1311984)	3.74
NM_019358	Glycoprotein 38 (Gp38)	3.20
BM384693	Capping protein (actin filament), gelsolin-like (predicted) (RGD:1311724)	3.16
NM_019289	Actin related protein 2/3 complex, subunit 1B (Arpc1b)	2.77
BG378832	Similar to intermediate filament-like protein MGC:2625 isoform 2; HOM-TES-103 tumor antigen-like	2.49
AI229933	Membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (Dusp3)	2.28
U23407	Cellular retinoic acid binding protein 2 (Crabp2)	2.15
NM_021584	Activity and neurotransmitter-induced early gene protein 4 (ania-4) (RGD:621187)	2.12
<i>EST</i>		
AI714002	Antigen identified by monoclonal antibody Ki-67 (predicted) /// similar to Antigen KI-67 (RGD:1305476 /// LOC310382)	25.03
AI045955	Transcribed locus	15.12
BF396369	Transcribed locus	13.83
AI454285	Similar to RIKEN cDNA 1810019A08	10.17
AI044869	Similar to group IID secreted phospholipase A2	9.09
BF398196	Transcribed locus	8.88
AI044644	Transcribed locus	8.39
BM386570	---	7.50
AI237698	Transcribed locus	7.17
AA926318	Transcribed locus	6.49
BG379338	Transcribed locus	6.07
NM_013122	---	5.68
BE111722	---	5.29
BI279526	---	4.83
AA944180	---	4.68
AA817708	Transcribed locus	4.09
AI555295	---	4.04
BF287967	Similar to GLI pathogenesis-related 1 (glioma); related to testes-specific, vespid, and pathogenesis proteins	3.97
AA924459	Similar to RIKEN cDNA 1200013B08	3.64
BI279526	---	3.51
AI639103	Transcribed locus	3.50
BG666787	---	3.29
BI279325	---	3.18
AI406660	Similar to KIAA1410 protein	3.11
AI177645	Similar to cDNA sequence BC032204 (predicted) (RGD1310168_predicted)	3.06
BF288130	---	3.05
BE119164	---	3.05

BF288115	---	3.04
BF558056	Similar to KIAA1410 protein	3.02
BI279744	Similar to interleukin 17 receptor	3.00
BF392605	Transcribed locus	2.95
AI232440	Similar to hypothetical protein MGC28931	2.92
BF416753	Transcribed locus	2.90
BG380058	---	2.89
BF283802	Transcribed locus	2.84
AI102790	---	2.83
BI294855	---	2.77
AI012031	---	2.76
BI289400	Feline sarcoma oncogene (predicted) (RGD:1309351)	2.61
BF283798	---	2.59
BM384374	Transcribed locus, strongly similar to NP_083008.1 RIKEN cDNA 4632428N05 gene [Mus musculus]	2.55
AW528719	---	2.54
AA848420	Similar to uracil-DNA glycosylase	2.52
BI281946	---	2.48
J04943	---	2.43
BE099838	---	2.42
BI292558	Uridine phosphorylase 1 (predicted) (RGD:1305566)	2.41
BG380430	Clone UI-R-FJ0-cpx-m-14-0-UI unknown mRNA	2.40
BI275261	---	2.36
AA963228	---	2.35
AA800199	---	2.34
BF282632	Transmembrane 4 superfamily member 7 (predicted) /// similar to transmembrane 4 superfamily member 7; tetraspanin 4; novel antigen 2; tetraspan TM4SF (RGD:1305810 /// LOC368016)	2.31
BF287282	Similar to schwannoma-associated protein	2.31
BE098803	Transcribed locus	2.27
AI411618	---	2.25
AI408294	---	2.22
BG673602	---	2.18
BF561368	Similar to C11orf17 protein (predicted) (RGD1306959_predicted)	2.17
AA799992	Similar to C11orf17 protein (predicted) (RGD1306959_predicted)	2.16
BE105131	---	2.16
BM384466	Similar to Ab2-389	2.11
BM388911	Hypothetical LOC297077 (predicted) (RGD1310725_predicted)	2.10
BM384071	---	2.07
BI284307	---	2.06
NM_022597	---	2.04
BF288303	Transcribed locus, strongly similar to	2.02

	NP_032531.1 LIM domain only 2 [Mus musculus]	
BM391920	Transcribed locus	2.02
BE095854	---	2.01
BG666075	SH3 domain binding glutamic acid-rich protein-like 3 (predicted) (RGD:1308118)	2.01

Gene Transcripts Increased Only in Diaphragm

Accession No.	Gene	Average Fold Difference Diaphragm
<i>Immune Response</i>		
NM_019205	Small inducible cytokine subfamily A11 (Scya11)	35.95
NM_016994	Complement component 3 (C3)	2.50
<i>Metabolism</i>		
NM_031543	Cytochrome P450, family 2, subfamily e, polypeptide 1 (Cyp2e1)	7.29
NM_133606	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (Ehhadh)	4.13
AF245172	Guanine deaminase (Gda)	2.15
<i>Transcription Factor</i>		
NM_053611	Nuclear protein 1 (Nupr1)	2.15
<i>Muscle</i>		
NM_012620	Serine (or cysteine) proteinase inhibitor, clade E, member 1 (Serpine1)	42.23
AW530361	Protein phosphatase 1, regulatory (inhibitor) subunit 3C (predicted) (RGD:1309132)	2.05
<i>Regeneration</i>		
NM_012620	Serine (or cysteine) proteinase inhibitor, clade E, member 1 (Serpine1)	42.23
AI500951	Serine (or cysteine) proteinase inhibitor, clade E, member 1 (Serpine1)	11.10
BI285141	CD24 antigen (Cd24)	2.74
<i>Cell-Cell Signaling/Signal Transduction</i>		
NM_053923	Phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide (Pik3c2g)	3.17
AA819268	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (Pik3r1)	2.22
AW530361	Protein phosphatase 1, regulatory (inhibitor) subunit 3C (predicted) (RGD:1309132)	2.05
<i>Protein Synthesis/Modification</i>		
NM_012620	Serine (or cysteine) proteinase inhibitor, clade E,	42.23

AI500951	member 1 (Serpine1) Serine (or cysteine) proteinase inhibitor, clade E, member 1 (Serpine1)	11.10
BE112261	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (predicted) (RGD:1304841)	3.55
<i>Other</i>		
AI511405	TCDD-inducible poly(ADP-ribose) polymerase (predicted) (RGD:1306171)	2.81
BM386695	Similar to microtubule-associated protein 7 (---)	2.74
BI285616	Adipose differentiation-related protein (ADRP)	2.13
<i>Unclassified</i>		
BI297236	Transformation related protein 53 inducible nuclear protein 1 (Trp53inp1)	2.75
BE108198	Zinc finger, CCHC domain containing 11 (predicted) (RGD:1310138)	2.71
AI101356	DDHD domain containing 1 (predicted) (RGD:1308576)	2.28
NM_031345	Delta sleep inducing peptide, immunoreactor (Dsipi)	2.20
<i>EST</i>		
BF419899	---	16.97
AI137160	Transcribed locus	3.73
BG670036	---	2.95
BF416979	---	2.85
BI300566	---	2.81
NM_012559	---	2.58
AI178069	Parathyroid hormone regulated sequence (205bp)	2.47
AI029492	---	2.39
BE329364	---	2.21
AI171987	---	2.21
AW522471	---	2.11
BF283990	Transcribed locus	2.05
AA894188	Transcribed locus, moderately similar to XP_346694.1 hypothetical gene supported by NM_022857 [Rattus norvegicus]	2.02
AA945854	Transcribed locus	2.01

Gene Transcripts Increased Only in EDL

Accession No.	Gene	Average Fold Difference EDL
<i>Immune Response</i>		
BI284349	Myeloid differentiation primary response gene	2.94

	116 (RGD:621526)	
D88250	Complement component 1, s subcomponent (C1s)	2.34
BI285863	Signal transducer and activator of transcription 3 (Stat3)	2.15
BE113920	Signal transducer and activator of transcription 3 (Stat3)	2.07
<i>Metabolism</i>		
BI277879	Solute carrier family 30 (zinc transporter), member 2 (Slc30a2)	9.97
BI295776	Similar to sorbin and SH3 domain containing 1	2.11
BF417391	Similar to solute carrier family 31, member 2	2.10
AB000280	Peptide/histidine transporter (Slc15a4)	2.09
<i>Response to Stress/Stimulus</i>		
NM_012551	Early growth response 1 (Egr1)	2.73
BE111342	Heat shock factor 2 (Hsf2)	2.08
BG671521	Heat shock protein 1, alpha (Hspca)	2.08
NM_031694	Heat shock factor 2 (Hsf2)	2.04
<i>Transcription Factor</i>		
BI288825*	Ankyrin repeat domain 1 (cardiac muscle) (Ankrd1)	7.34
BE109520	Zinc finger protein 622	3.27
NM_012551	Early growth response 1 (Egr1)	2.73
BF285187	Immediate early response 5 (Ier5)	2.70
BI288619	V-jun sarcoma virus 17 oncogene homolog (avian) (Jun)	2.20
BE109520	Zinc finger protein 622	2.11
AB012600	Aryl hydrocarbon receptor nuclear translocator-like (Arntl)	2.08
AI171219	Hepatoma-derived growth factor, related protein 2 (Hdgfrp2)	2.02
NM_021835	V-jun sarcoma virus 17 oncogene homolog (avian) (Jun)	2.01
NM_024360	Hairy and enhancer of split 1 (Drosophila) (Hes1)	2.00
<i>Cell Adhesion/Migration</i>		
NM_012649	Syndecan 4 (Sdc4)	4.26
AW525176	Filamin A interacting protein 1 (Filip1)	2.32
BF405144	Sertolin (LOC64038)	2.26
<i>Muscle</i>		
BI288825*	Ankyrin repeat domain 1 (cardiac muscle) (Ankrd1)	7.34
NM_019298	Cholinergic receptor, nicotinic, delta polypeptide (Chrnd)	4.00

Regeneration

BI288825* Ankyrin repeat domain 1 (cardiac muscle)
(Ankrd1) 7.34

Cell Growth/Maintenance

NM_019151 Growth differentiation factor 8 (Gdf8) 3.69

NM_012945 Diphtheria toxin receptor (Dtr) 3.15

AI603439 Unc-51 like kinase 1 (C. elegans) (Ulk1) 2.10

NM_031515 Kirsten rat sarcoma viral oncogene homologue 2
(active) (Kras2) 2.08

BE109242 Kirsten rat sarcoma viral oncogene homologue 2
(active) (Kras2) 2.06

AI230479 Unc-51 like kinase 1 (C. elegans) (Ulk1) 2.03

Cell-Cell Signaling/Signal Transduction

BE111515 Forkhead box O1A (Foxo1a) 8.12

NM_019232 Serum/glucocorticoid regulated kinase (Sgk) 3.19

BI294230 Connector enhancer of kinase suppressor of
Ras 1 (predicted) (RGD:1311879) 2.54

NM_019186 ADP-ribosylation-like 4 (Arl4) 2.09

AI407134 Similar to Rho GTPase activating protein 12 2.04

NM_022542 RhoB gene (Rhob) 2.04

Protein Synthesis/Modification

NM_017277 Adaptor protein complex AP-1, beta 1 subunit
(Ap1b1) 2.19

NM_024400 A disintegrin-like and metalloprotease
(reprolysin type) with thrombospondin type 1
motif, 1 (Adamts1) 2.12

BE111342 Heat shock factor 2 (Hsf2) 2.08

BG671521 Heat shock protein 1, alpha (Hspca) 2.08

NM_080905 Seven in absentia 1A (RGD:620449) 2.07

M69056 Farnesyltransferase, CAAX box, beta (Fntb) 2.05

NM_031694 Heat shock factor 2 (Hsf2) 2.04

Receptor/Ion Channel

NM_019298 Cholinergic receptor, nicotinic, delta polypeptide
(Chrnd) 4.00

BF542912 Sodium channel, voltage-gated, type III, beta
(Scn3b) 2.41

BE099085 Similar to copine family member 2.07

Other

AI170193 Down syndrome critical region homolog 1
(human) (Dscr1) 2.55

BI284261 Similar to carbon catabolite repression 4 protein
homolog 2.11

BF554283 Opioid growth factor receptor-like 1 (predicted)
(RGD:1308498) 2.03

AI231999	Tumor protein D52-like 1 (predicted) (RGD:1310098)	2.03
<i>Unclassified</i>		
AW520812	Pleckstrin homology-like domain, family A, member 3 (predicted) (RGD:1310502)	2.54
BI304056	Similar to hypothetical protein FLJ12085	2.21
BF392191	Similar to hypothetical protein FLJ12085	2.09
AB050011	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian) (RGD:619953)	2.07
BI275908	Similar to KIAA1401 protein (Srr)	2.03
BI284461	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) (RGD:628633)	2.02
<i>EST</i>		
AI145231	Transcribed locus	11.79
AW530004	Transcribed locus	9.43
BF415939	---	9.27
BI281823	Death associated protein kinase 1 (predicted) (RGD:1311629)	6.87
AI178746	Transcribed locus	5.37
BI276015	Similar to hypothetical protein E130310N06 (LOC301709)	4.58
BE111121	Transcribed locus	3.54
BF392065	---	3.24
BG671786	Transcribed locus	3.13
AI105018	Similar to Xin	3.09
BI295739	Transcribed locus	3.09
BI296929	Similar to hypothetical protein E130310N06	2.99
AI717553	Transcribed locus, strongly similar to XP_521426.1 similar to hypothetical protein DKFZp761A052 [Pan troglodytes]	2.77
BE329273	---	2.65
AA894192	Similar to tensin	2.60
AI406494	Similar to 5730438N18Rik protein (predicted) (RGD1308342_predicted)	2.51
AI600020	Transcribed locus	2.48
BI285035	Transcribed locus, weakly similar to NP_062289.1 DNA binding protein with his-thr domain [Mus musculus]	2.44
AI599232	Transcribed locus	2.43
BE112898	---	2.41
BM385463	Similar to RIKEN cDNA 1200015A22 (MGC94413)	2.32
AI172126	Transcribed locus	2.26
AW534519	---	2.25
NM_031970	---	2.23
AI235476	---	2.23
BI278826	---	2.20

BF523068	Chromodomain helicase DNA binding protein 7 (predicted) (RGD:1311921)	2.19
AI058889	Similar to RRS1 ribosome biogenesis regulator homolog; regulator for ribosome resistance homolog (<i>S. cerevisiae</i>); DNA segment, Chr 1, ERATO Doi 701, expressed	2.19
BF411859	---	2.19
AI178019	Similar to Suppressor of SWI4 1 homolog (Ssf- 1) (Peter Pan homolog)	2.18
NM_053477	---	2.18
BE117514	Transcribed locus	2.16
BF283340	Transcribed locus	2.13
AW917731	Transcribed locus	2.11
BM384656	---	2.08
AI579023	CDNA clone MGC:94141 IMAGE:7127379, complete cds	2.06
BG374464	---	2.04
AI008371	Transcribed locus	2.02

*A different probe for Ankrd1 showed increased expression in all three muscles

Gene Transcripts Decreased in Both EOM and Diaphragm

Accession No.	Gene	Average Fold Difference	
		EOM	Diaphragm
<i>Receptor/Ion Channel</i>			
AI235942	Aquaporin 4 (Aqp4)	-2.65	-2.35
<i>EST</i>			
AW251334	---	-2.68	-2.04
BI295947	---	-2.49	-2.08
AI104922	Transcribed locus	-2.12	-2.56

Gene Transcripts Decreased in Both EOM and EDL

Accession No.	Gene	Average Fold Difference	
		EOM	EDL
<i>Immune Response</i>			
BG665525	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (LOC366256)	-2.38	-2.27
<i>Metabolism</i>			
NM_080688	Phospholipase C, delta 4 (Plcd4)	-2.25	-3.16
<i>Response to Stress/Stimulus</i>			
None			
<i>Transcription Factor</i>			
BG665525	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (LOC366256)	-2.38	-2.27
BF557192	Doublesex and mab-3 related transcription factor 2 (predicted) (RGD:1309047)	-2.01	-2.15
<i>Cell-Cell Signaling/Signal Transduction</i>			
BE113289	Peroxisome proliferator-activated receptor gamma coactivator 1 beta (Perc)	-3.64	-2.85
<i>Protein Synthesis/Modification</i>			
AI045958	tRNA splicing 2' phosphotransferase 1 homolog (S. cerevisiae) (predicted) (RGD:1310831)	-2.04	-2.68
<i>Receptor/Ion Channel</i>			
AI578145	Calcium channel, voltage-dependent, alpha 2/delta 3 subunit (Cacna2d3)	-2.99	-3.14
<i>Unclassified</i>			
AI410818	Similar to RIKEN cDNA 5730509K17 gene (predicted) (RGD1310307_predicted)	-2.67	-2.86
BG374986	Similar to RIKEN cDNA C330023F11	-2.13	-2.01

BG664142	Similar to RIKEN cDNA C330023F11	-2.12	-2.06
<i>EST</i>			
BI295858	Transcribed locus	-4.49	-3.03
BI290853	Transcribed locus	-2.88	-2.49
AA926180	---	-2.19	-2.18
AA923873	---	-2.16	-2.04
AA964188	---	-2.16	-2.04
AA819332	---	-2.10	-2.08
AA901290	Transcribed locus	-2.01	-2.65

Gene Transcripts Decreased in Both EDL and Diaphragm

Accession No.	Gene	Average Fold Difference	
		Diaphragm	EDL
<i>Metabolism</i>			
AI176540	Similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted) (RGD1307844_predicted)	-2.27	-2.22
<i>Transcription Factor</i>			
NM_133303	Basic helix-loop-helix domain containing, class B3 (Bhlhb3)	-2.14	-3.70
<i>Muscle</i>			
NM_053381	ATPase, (Na+)/K+ transporting, beta 4 polypeptide (Atp1b4)	-3.64	-3.09
AW435036	Smoothelin (predicted) (RGD:1310216)	-2.96	-3.05
<i>Cell-Cell Signaling/Signal Transduction</i>			
AI407487	Guanine nucleotide binding protein (G protein), gamma 10 (Gng10)	-2.76	-2.69
<i>Cell Death/Apoptosis</i>			
AF230520	SH3-domain kinase binding protein 1 (Sh3kbp1)	-2.43	-2.57
AF255888	SH3-domain kinase binding protein 1 (Sh3kbp1)	-2.27	-2.76
<i>Receptor/Ion Channel</i>			
BF417032	Transferrin receptor (Tfrc)	-6.78	-4.14
M58040	Transferrin receptor (Tfrc)	-6.42	-4.12
NM_053381	ATPase, (Na+)/K+ transporting, beta 4 polypeptide (Atp1b4)	-3.64	-3.09
<i>Other</i>			
AW434918	Similar to CGI-112 protein (predicted) (RGD1308113_predicted)	-2.10	-2.03

<i>Unclassified</i>			
AI639162	Similar to open reading frame 5	-2.63	-2.25
BF388757	Similar to RIKEN cDNA 1700025G04 gene (predicted) (RGD1309104_predicted)	-2.29	-2.06
AW252076	Similar to putative protein family member (XC177) (LOC361179)	-2.15	-2.05
<i>EST</i>			
BF389910	Transcribed locus, strongly similar to XP_214293.2 similar to FKSG24 [Rattus norvegicus]	-5.23	-3.80
AI059738	Transcribed locus	-3.56	-6.25
BE101285	Transcribed locus	-3.38	-4.28
AI044539	Transcribed locus	-3.33	-4.14
AI639060	---	-2.90	-7.66
AW918413	Transcribed locus	-2.54	-2.48
AW916472	Transcribed locus	-2.50	-2.07
AA858705	Transcribed locus, moderately similar to XP_488797.1 hypothetical gene supported by AJ131021; BC038251; BC043064; BC051079; BC055331; BC056946; BC066063; NM_011299 [Mus musculus]	-2.49	-2.18
AA996810	Transcribed locus	-2.26	-2.29
AI171656	Transcribed locus, strongly similar to XP_347062.1 LOC362536 [Rattus norvegicus]	-2.18	-2.60
BI279384	Transcribed locus	-2.03	-2.41

Gene Transcripts Decreased only in EOM

Accession No.	Gene	Average Fold Difference	
		EOM	
<i>Immune Response</i>			
AI576094	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (LOC366256)	-2.51	
AB032395	Decay accelerating factor 1 (Daf)	-2.16	
BI297612	Pre-B-cell colony enhancing factor 1 (Pbef1)	-2.06	
<i>Metabolism</i>			
BF522030	Sialyltransferase 10 (alpha-2,3-sialyltransferase VI) (RGD:1303279)	-3.92	
AA891949	Adenylate kinase 3-like 2 (Ak3l2)	-2.43	
AA850195	Similar to pantothenate kinase 1 beta	-2.39	
BE109334	Kinesin family member 1B (Kif1b)	-2.33	
NM_012621	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 (Pfkfb1)	-2.28	
BI296064	Similar to amylo-1,6-glucosidase, 4-alpha-glucanotransferase isoform 1; glycogen debranching enzyme; amylo-1,6-glucosidase, 4-	-2.16	

BE111083	alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III); Amylo-1,6-glucosidase, 4-alpha-... Mannose-binding protein associated serine protease-1 (Masp1)	-2.15
AI638990	Aconitase 2, mitochondrial (Aco2)	-2.06
BE109171	Kinesin family member 1B (Kif1b)	-2.04
AI412898	Dihydrolipoamide branched chain transacylase E2 (Dbt)	-2.02
BM392117	Similar to pantothenate kinase 2; PANK2	-2.01
NM_031154	Glutathione S-transferase, mu type 3 (RGD:621287)	-2.01

Response to Stress/Stimulus

NM_031971	Heat shock 70kD protein 1A /// heat shock 70kD protein 1B (Hspa1a /// Hspa1b)	-2.23
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Transcription Factor

BF408593	Ankyrin repeat and SOCS box-containing 18 (predicted) (RGD:1310850)	-2.77
BI302005	Myeloid leukemia factor 1 (predicted) (RGD:1306854)	-2.54
AI576094	Similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (LOC366256)	-2.51
AI101323	Similar to ets variant gene 5 /// ets variant gene 5 (ets-related molecule) (predicted) (LOC294776 /// RGD:1309590)	-2.33
BM390497	Similar to Protein C8orf1 (hT41)	-2.22
AW252817	Transcription elongation factor A (SII), 3 (predicted) (RGD:1311369)	-2.21
U20796	Nuclear receptor subfamily 1, group D, member 2 (Nr1d2)	-2.21
BF284190	Nuclear receptor subfamily 1, group D, member 2 (Nr1d2)	-2.19
AA963348	Doublesex and mab-3 related transcription factor 2 (predicted) (RGD:1309047)	-2.09
NM_012842	Epidermal growth factor (Egf)	-2.09
BF418812	Transcription elongation factor A (SII)-like 1 (Tceal1)	-2.06

Muscle

AW252385	Similar to Myosin-binding protein H (MyBP-H) (H-protein)	-3.42
BI290684	Similar to muscle-derived protein MDP77 variant 1	-2.81
NM_019274	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (Colq)	-2.55
AI101323	Similar to ets variant gene 5 /// ets variant gene 5 (ets-related molecule) (predicted) (LOC294776 /// RGD:1309590)	-2.33

NM_017239	Myosin heavy chain, polypeptide 6 (Myh6)	-2.31
<i>Cell Growth/Maintenance</i>		
NM_053480	Polymerase (DNA directed), alpha 2 (RGD:621817)	-2.21
AI233135	Sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (predicted) (RGD:1308374)	-2.14
BI281607	Similar to DNA polymerase zeta catalytic subunit	-2.06
BF404786	Down syndrome critical region gene 1-like 1 (Dscr111)	-2.05
<i>Cell-Cell Signaling/Signal Transduction</i>		
AA924620	Rab40b, member RAS oncogene family (predicted) (RGD:1305663)	-3.65
BI288833	Dapper homolog 2, antagonist of beta-catenin (xenopus) (predicted) (RGD:1310742)	-3.04
AI717707	Protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha (predicted) (RGD:1306958)	-2.86
NM_031623	Growth factor receptor bound protein 14 (Grb14)	-2.75
U93307	Kinase insert domain protein receptor (Kdr)	-2.32
NM_057103	A kinase (PRKA) anchor protein (gravin) 12 (Akap12)	-2.19
BF284017	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (predicted) (RGD:1308387)	-2.15
AI233135	Sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (predicted) (RGD:1308374)	-2.14
NM_053772	Protein kinase inhibitor, alpha (RGD:621021)	-2.13
BM389005	Similar to G protein-coupled receptor 68	-2.02
<i>Protein Synthesis/Modification</i>		
BF390554	Similar to WD repeat domain 17 (LOC361188)	-2.98
NM_013018	RAB3A, member RAS oncogene family (Rab3a)	-2.41
U68544	Peptidylprolyl isomerase F (cyclophilin F) (Ppif)	-2.02
<i>Receptor/Ion Channel</i>		
NM_012721	Purinergic receptor P2X-like 1, orphan receptor (P2rx11)	-2.12
NM_017094	Growth hormone receptor (Ghr)	-2.07
<i>Other</i>		
BE109334	Kinesin family member 1B (Kif1b)	-2.33
AI411941	Fibronectin type III domain containing 1 (predicted) (RGD:1310640)	-2.29
AF080594	Vascular endothelial growth factor A (RGD:619991)	-2.17
NM_053955	Crystallin, mu (RGD:620943)	-2.08
BE109171	Kinesin family member 1B (Kif1b)	-2.04

Unclassified

AI501165	Similar to 3632451O06Rik protein (predicted) (RGD1310110_predicted)	-3.69
AI454794	Similar to RIKEN cDNA 2310005P05	-3.11
AI171466	Similar to RIKEN cDNA 2700055K07	-3.00
AI411848	Tubulointerstitial nephritis antigen (Tinag)	-2.68
BE103940	Limb and neural patterns (predicted) (RGD:1312042)	-2.52
BM392225	Similar to D11Ertd498e protein	-2.50
BG380274	Similar to KIAA1290 protein	-2.38
AA891228	Similar to RIKEN cDNA 2310003M01	-2.35
AI535506	Similar to RIKEN cDNA 1110030K22 (predicted) (RGD1311701_predicted)	-2.31
AI172305	Similar to RIKEN cDNA 2310003M01 (LOC298139)	-2.27
AI029410	Similar to KIAA0970 protein (LOC317224)	-2.25
BE095833	Similar to RIKEN cDNA 1110067D22 (predicted) (RGD1307414_predicted)	-2.24
AI716973	Similar to RIKEN cDNA 2310003M01 (LOC298139)	-2.23
AI102758	Similar to RIKEN cDNA 9530058B02 (predicted) (RGD1311273_predicted)	-2.18
AI171799	Upregulated in colorectal cancer gene 1 protein (MGC94579)	-2.13
AI717543	Similar to hypothetical protein MGC14816 (LOC295396)	-2.12
BI279030	Nephroblastoma overexpressed gene (Nov)	-2.09
BI275737	Similar to RIKEN cDNA 1110067D22	-2.06
AI639268	Similar to DKFZP566O084 protein (predicted) (RGD1306989_predicted)	-2.05
BF284058	Similar to expressed sequence AI597479 (predicted) (RGD1310553_predicted)	-2.04
AA946382	Similar to hypothetical protein FLJ10204 (predicted) (RGD1311362_predicted)	-2.04
AI102249	Similar to RIKEN cDNA 1810048J11 (predicted) (RGD1305147_predicted)	-2.03
AA851385	Similar to KIAA0669 gene product	-2.02
BE104114	Similar to RIKEN cDNA 4930429H24	-2.01
AW142481	Similar to RIKEN cDNA 4930429H24	-2.00
AI008697	Unknown (protein for MGC:72959) (Commd3)	-2.00

EST

BG378310	Transcribed locus, strongly similar to NP_075024.1 sciellin [Mus musculus]	-4.32
AI715999	---	-4.14
AI044340	---	-3.75
BF281697	Transcribed locus	-3.45
BG378317	---	-3.24
AI029414	---	-3.23
AW918480	Transcribed locus	-3.22
BF284519	Transcribed locus	-3.17

BM390716	Transcribed locus	-3.08
BF556107	---	-2.90
BG372437	---	-2.90
AW530670	Transcribed locus	-2.81
AA849871	---	-2.75
BE112523	---	-2.58
BM387773	Transcribed locus	-2.56
AI175732	---	-2.53
BI294990	Transcribed locus	-2.52
AI070450	Transcribed locus	-2.45
BG372771	---	-2.44
AW534967	Transcribed locus	-2.34
BG664461	Transcribed locus	-2.34
BE109107	---	-2.29
AA818643	Transcribed locus	-2.27
AI172334	---	-2.25
BI296177	---	-2.20
AI171288	---	-2.20
BG664080	Transcribed locus, strongly similar to NP_620090.1 transmembrane 4 superfamily member 10 [Mus musculus]	-2.19
AI058292	Transcribed locus	-2.19
BI287330	Transcribed locus	-2.18
BF284719	Transcribed locus, strongly similar to NP_919267.1 hypothetical protein BC017881 [Homo sapiens]	-2.17
BF284363	Transcribed locus	-2.16
BM387062	Transcribed locus	-2.15
H31802	---	-2.14
BE110785	---	-2.13
AW524414	Transcribed locus	-2.11
AI171676	Transcribed locus, strongly similar to XP_233499.1 similar to four and half LIM domain protein 3 [Rattus norvegicus]	-2.07
AW527690	---	-2.07
AI105382	Transcribed locus	-2.07
BF284876	Transcribed locus, strongly similar to XP_214806.1 similar to RIKEN cDNA 6720465F12 [Rattus norvegicus]	-2.06
BF413366	Transcribed locus	-2.05
BI290522	---	-2.04
AI137418	Transcribed locus	-2.04
AI548256	---	-2.02
BI295878	---	-2.02
BF551356	---	-2.02
BI280298	---	-2.00

Gene Transcripts Decreased only in Diaphragm

Accession No.	Gene	Average Fold Difference Diaphragm
<i>Metabolism</i>		
J02585	Stearoyl-Coenzyme A desaturase 1 (RGD:621176)	-4.09
NM_024484	Aminolevulinic acid synthase 1 (Alas1)	-2.46
NM_031796	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (Galnt5)	-2.22
NM_031589	Solute carrier family 37 (glycerol-6-phosphate transporter), member 4 (Slc37a4)	-2.01
<i>Transcription Factor</i>		
BF403703	DNA-damage inducible transcript 3 (Ddit3)	-2.66
AI236615	Zinc finger, MYND domain containing 17 (predicted) (RGD:1309408)	-2.61
<i>Cell Adhesion/Migration</i>		
NM_021760	Collagen, type V, alpha 3 (Col5a3)	-2.71
AF020045	Integrin, alpha E, epithelial-associated (RGD:621644)	-2.41
<i>Muscle</i>		
AI172075	Similar to mitsugumin 23 (MGC93811)	-2.12
<i>Cell-Cell Signaling/Signal Transduction</i>		
AI177057	Apelin, AGTRL1 ligand (Apln)	-2.93
<i>Protein Synthesis/Modification</i>		
NM_016998	Carboxypeptidase A1 (Cpa1)	-4.99
<i>Receptor/Ion Channel</i>		
NM_030834	Monocarboxylate transporter (Slc16a3)	-2.58
<i>Other</i>		
U25281	SH3 domain binding protein CR16 (RGD:708559)	-2.77
<i>EST</i>		
AI408151	---	-3.57
BE116867	Transcribed locus	-3.53
BE110205	Transcribed locus	-3.00
AI171372	Transcribed locus	-2.68
AI102148	Transcribed locus, moderately similar to XP_531128.1 LOC464141 [Pan troglodytes]	-2.62
BM387260	Transcribed locus	-2.56
AW528719	---	-2.55

BF418132	Transcribed locus	-2.47
BI285456	---	-2.31
AI502132	Transcribed locus	-2.30
BG373049	Transcribed locus	-2.29
AI547837	---	-2.27
AA963184	Transcribed locus	-2.24
AW525428	---	-2.21
BI281183	---	-2.08
BI296250	---	-2.06
H31802	---	-2.05

Gene Transcripts Decreased only in EDL

Accession No.	Gene	Average Fold Difference EDL
<i>Metabolism</i>		
BE102814	Sideroflexin 5 (Sfxn5)	-2.34
AF182714	Putative phosphate-phosphoenolpyruvate translocator (RGD:708484)	-2.23
<i>Response to Stress/Stimulus</i>		
NM_012880	Superoxide dismutase 3, extracellular (Sod3)	-2.02
<i>Transcription Factor</i>		
AI556378	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 (Cited4)	-3.51
AI105444	CXXC finger 5 (Cxxc5)	-2.36
BI281838	CXXC finger 5 (Cxxc5)	-2.29
BI294747	Tripartite motif-containing 45 (predicted) (RGD:1309168)	-2.20
BF398848	Sterol regulatory element binding factor 1 (Srebf1)	-2.06
<i>Cell Adhesion/Migration</i>		
BI274110	Similar to Tetraspan NET-5	-2.61
<i>Cell Growth/Maintenance</i>		
BG663107	A kinase (PRKA) anchor protein (gravin) 12 (Akap12)	-2.08
<i>Cell-Cell Signaling/Signal Transduction</i>		
BE107291	Calcium/calmodulin-dependent protein kinase II alpha subunit (Camk2a)	-2.39
NM_031143	Diacylglycerol kinase zeta (Dgkz)	-2.33
AA957410	Similar to SH2/SH3 adaptor protein	-2.21
BG663107	A kinase (PRKA) anchor protein (gravin) 12 (Akap12)	-2.08

Protein Synthesis/Modification

AI138048 Down syndrome critical region gene 1-like 1 (Dscr111) -2.52

Unclassified

AI010430 Similar to AW319517 protein (LOC313974) -2.78
BE114077 Similar to AW319517 protein (LOC313974) -2.46
AI409904 Similar to RIKEN cDNA 1200015N20 -2.35

EST

AI170431 Transcribed locus -3.28
BM389813 --- -3.00
AI045150 Transcribed locus -2.92
BI295140 Transcribed locus -2.81
AW435010 Transcribed locus -2.81
AW535897 Transcribed locus -2.64
BI286025 --- -2.39
BF420311 Transcribed locus -2.35
AB020504 --- -2.31
BF414338 --- -2.29
AI101500 Transcribed locus -2.28
AI578611 --- -2.28
BG380633 Transcribed locus, weakly similar to NP_808495.1 hypothetical protein 9530053H22 [Mus musculus] -2.25
BE118653 Transcribed locus -2.25
AA944552 Transcribed locus -2.22
BE117616 Transcribed locus -2.22
BG371591 --- -2.20
BF415056 Transcribed locus -2.19
BF396723 Transcribed locus -2.17
AI410438 --- -2.12
AI556426 --- -2.10
BG377635 Transcribed locus -2.09
BF561525 Transcribed locus -2.09
AI043697 --- -2.04
BI296334 Transcribed locus, strongly similar to XP_219860.2 similar to KIAA1010 protein [Rattus norvegicus] -2.06