Supplementary Information

High-resolution genome-wide expression analysis of single myofibers using SMART-Seq

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Inventory of Supplemental Information

Supplemental Tables

Table S1A List of genes expressed in the whole muscle but not in the myofiber

Table S1B GO term analysis of genes expressed in the whole muscle but not in the myofiber

Table S2A List of gene expressed solely in the myofiber

Table S2B GO term analysis of genes expressed solely in the myofiber

Table S3 Alignment statistics of sequenced reads from young and old myofibers

Supplemental Figures

Figure S1: **Isolation of total RNA from a single myofiber.** (A) Isolated myofibers after a properly performed dissection and digestion. (B) Counts of the number of satellite cells per fiber in myofibers treated with and without trypsin. (C) Representative picture of a myofiber stained for PAX7 and counterstained with DAPI after no treatment with trypsin. (D) Representative picture of a myofiber stained for PAX7 and counterstained with DAPI after treatment with trypsin. (E) Representative image of cDNA from 20 fibers (20F), 5 fibers (5F), and single fiber (1F) on an agarose gel after library preparation and size selection. Dashed line indicates the range of library size after tagmentation. (F) Representative picture of cDNA from whole muscle on an agarose gel after library preparation and size selection. Dahsed line indicates the range of library size after tagmentation.

Figure S2: **IGV snapshots of genes associated with slow and fast muscle fiber types.** Young myofiber tracks are labeled in blue and old are in red. (A) Troponin T3 (*Tnnt3*) expressed in fast skeletal muscle. (B) Troponin I2 (Tnni2) expressed in fast skeletal muscle. (C) Troponin T1 (*Tnnt1*) expressed in slow skeletal muscle. (D) Housekeeping gene ribosomal protein S2 (*Rps2*).

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	**Gene Name**
ENSMUSG00000029561	2'-5' oligoadenylate synthetase-like 2(Oasl2)
ENSMUSG00000024899	3'-phosphoadenosine 5'-phosphosulfate synthase 2(Papss2)
ENSMUSG00000046598	3-hydroxybutyrate dehydrogenase, type 1(Bdh1)
ENSMUSG00000038587	A kinase (PRKA) anchor protein (gravin) 12(Akap12)
ENSMUSG00000041828	ATP-binding cassette, sub-family A (ABC1), member 8a(Abca8a)
ENSMUSG00000041797	ATP-binding cassette, sub-family A (ABC1), member 9(Abca9)
ENSMUSG00000026463	ATPase, Ca++ transporting, plasma membrane 4(Atp2b4)
ENSMUSG00000024451	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3(Arap3)
ENSMUSG00000000317	B cell CLL/lymphoma 6, member B(Bcl6b)
ENSMUSG00000026278	BCL2-related ovarian killer(Bok)
ENSMUSG00000031963	BMP-binding endothelial regulator(Bmper)
ENSMUSG00000085208	BRCA1 interacting protein C-terminal helicase 1, opposite strand(Brip1os)
ENSMUSG00000045930	C-type lectin domain family 14, member a(Clec14a)
ENSMUSG00000025784	C-type lectin domain family 3, member b(Clec3b)
ENSMUSG00000017446	C1q and tumor necrosis factor related protein 1(C1qtnf1)
ENSMUSG00000046491	C1q and tumor necrosis factor related protein 2(C1qtnf2)
ENSMUSG00000058914	C1q and tumor necrosis factor related protein 3(C1qtnf3)
ENSMUSG00000071347	C1q and tumor necrosis factor related protein 9(C1qtnf9)
ENSMUSG00000034957	CCAAT/enhancer binding protein (C/EBP), alpha(Cebpa)
ENSMUSG00000028076	CD1d1 antigen(Cd1d1)
ENSMUSG00000056481	CD248 antigen, endosialin(Cd248)
ENSMUSG00000017309	CD300 molecule like family member G(Cd300lg)
ENSMUSG00000016494	CD34 antigen(Cd34)
ENSMUSG00000029084	CD38 antigen(Cd38)
ENSMUSG00000040747	CD53 antigen(Cd53)
ENSMUSG00000024610	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)(Cd74)
ENSMUSG00000027435	CD93 antigen(Cd93)
ENSMUSG00000049521	CDC42 effector protein (Rho GTPase binding) 1(Cdc42ep1)
ENSMUSG00000041598	CDC42 effector protein (Rho GTPase binding) 4(Cdc42ep4)
ENSMUSG00000031875	CKLF-like MARVEL transmembrane domain containing 3(Cmtm3)
ENSMUSG00000033883	DNA segment, Chr 3, ERATO Doi 254, expressed(D3Ertd254e)
ENSMUSG00000020057	DNA-damage regulated autophagy modulator 1(Dram1)
ENSMUSG00000008398	ELK3, member of ETS oncogene family(Elk3)
ENSMUSG00000032349	ELOVL family member 5, elongation of long chain fatty acids (yeast)(Elovl5)
ENSMUSG00000041220	ELOVL family member 6, elongation of long chain fatty acids (yeast)(Elovl6)
ENSMUSG00000038312	ER degradation enhancer, mannosidase alpha-like 2(Edem2)
ENSMUSG00000038235	F11 receptor(F11r)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000001555	FK506 binding protein 10(Fkbp10)
ENSMUSG00000029648	FMS-like tyrosine kinase 1(Flt1)
ENSMUSG00000034037	FYVE, RhoGEF and PH domain containing 5(Fgd5)
ENSMUSG00000058715	Fc receptor, IgE, high affinity I, gamma polypeptide(Fcer1g)
ENSMUSG00000059498	Fc receptor, IgG, low affinity III(Fcgr3)
ENSMUSG00000026656	Fc receptor, IgG, low affinity IIb(Fcgr2b)
ENSMUSG00000015852	Fc receptor-like S, scavenger receptor(Fcrls)
ENSMUSG00000016087	Friend leukemia integration 1(Fli1)
ENSMUSG00000042804	G protein-coupled receptor 153(Gpr153)
ENSMUSG00000022579	GPI-anchored HDL-binding protein 1(Gpihbp1)
ENSMUSG00000004837	GRB2-related adaptor protein(Grap)
ENSMUSG00000054435	GTPase, IMAP family member 4(Gimap4)
ENSMUSG00000056870	GULP, engulfment adaptor PTB domain containing 1(Gulp1)
ENSMUSG00000020928	HIG1 domain family, member 1B(Higd1b)
ENSMUSG00000038366	LIM and SH3 protein 1(Lasp1)
ENSMUSG00000024395	LIM and senescent cell antigen like domains 2(Lims2)
ENSMUSG00000023022	LIM domain and actin binding 1(Lima1)
ENSMUSG00000071656	LRRN4 C-terminal like(Lrrn4cl)
ENSMUSG00000042228	LYN proto-oncogene, Src family tyrosine kinase(Lyn)
ENSMUSG00000036564	N-myc downstream regulated gene 4(Ndrg4)
ENSMUSG00000040280	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2(Ndufa4l2)
ENSMUSG00000068245	PHD finger protein 11D(Phf11d)
ENSMUSG00000004768	RAB23, member RAS oncogene family(Rab23)
ENSMUSG00000019832	RAB32, member RAS oncogene family(Rab32)
ENSMUSG00000024663	RAB3A interacting protein (rabin3)-like 1(Rab3il1)
ENSMUSG00000019066	RAB3D, member RAS oncogene family(Rab3d)
ENSMUSG00000041696	RAS-like, family 12(Rasl12)
ENSMUSG00000021252	RIKEN cDNA 0610007P14 gene(0610007P14Rik)
ENSMUSG00000056313	RIKEN cDNA 1810011O10 gene(1810011O10Rik)
ENSMUSG00000044906	RIKEN cDNA 4930503L19 gene(4930503L19Rik)
ENSMUSG00000090394	RIKEN cDNA 4930523C07 gene(4930523C07Rik)
ENSMUSG00000048489	RIKEN cDNA 8430408G22 gene(8430408G22Rik)
ENSMUSG00000041992	Rap guanine nucleotide exchange factor (GEF) 5(Rapgef5)
ENSMUSG00000044456	Ras and Rab interactor 3(Rin3)
ENSMUSG00000044562	Ras interacting protein 1(Rasip1)
ENSMUSG00000027247	Rho GTPase activating protein 1(Arhgap1)
ENSMUSG00000034255	Rho GTPase activating protein 27(Arhgap27)
ENSMUSG00000052921	Rho guanine nucleotide exchange factor (GEF) 15(Arhgef15)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000021895	Rho guanine nucleotide exchange factor (GEF) 3(Arhgef3)
ENSMUSG00000030220	Rho, GDP dissociation inhibitor (GDI) beta(Arhgdib)
ENSMUSG00000016262	SERTA domain containing 4(Sertad4)
ENSMUSG00000059013	SH2 domain containing 3C(Sh2d3c)
ENSMUSG00000025902	SRY (sex determining region Y)-box 17(Sox17)
ENSMUSG00000046470	SRY (sex determining region Y)-box 18(Sox18)
ENSMUSG00000063060	SRY (sex determining region Y)-box 7(Sox7)
ENSMUSG00000040710	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4(St8sia4)
ENSMUSG00000012428	STEAP family member 4(Steap4)
ENSMUSG00000034412	TBC1 domain family, member 10a(Tbc1d10a)
ENSMUSG00000037410	TBC1 domain family, member 2B(Tbc1d2b)
ENSMUSG00000030579	TYRO protein tyrosine kinase binding protein(Tyrobp)
ENSMUSG00000038296	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 18(Galnt18)
ENSMUSG00000034911	Usher syndrome 1C binding protein 1(Ushbp1)
ENSMUSG00000069792	WAP four-disulfide core domain 17(Wfdc17)
ENSMUSG00000066357	WD repeat domain 6(Wdr6)
ENSMUSG00000028041	a disintegrin and metallopeptidase domain 15 (metargidin)(Adam15)
ENSMUSG00000024299	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10(Adamts10)
ENSMUSG00000001348	acid phosphatase 5, tartrate resistant(Acp5)
ENSMUSG00000032735	actin binding LIM protein family, member 3(Ablim3)
ENSMUSG00000000530	activin A receptor, type II-like 1(Acvrl1)
ENSMUSG00000044017	adhesion G protein-coupled receptor D1(Adgrd1)
ENSMUSG00000004730	adhesion G protein-coupled receptor E1(Adgre1)
ENSMUSG00000056492	adhesion G protein-coupled receptor F5(Adgrf5)
ENSMUSG00000039167	adhesion G protein-coupled receptor L4(Adgrl4)
ENSMUSG00000048040	adipocyte-related X-chromosome expressed sequence 2(Arxes2)
ENSMUSG00000022878	adiponectin, C1Q and collagen domain containing(Adipoq)
ENSMUSG00000074207	alcohol dehydrogenase 1 (class I)(Adh1)
ENSMUSG00000013584	aldehyde dehydrogenase family 1, subfamily A2(Aldh1a2)
ENSMUSG00000001864	allograft inflammatory factor 1-like(Aif1l)
ENSMUSG00000019326	amine oxidase, copper containing 3(Aoc3)
ENSMUSG00000025270	aminolevulinic acid synthase 2, erythroid(Alas2)
ENSMUSG00000033544	angiopoietin-like 1(Angptl1)
ENSMUSG00000002289	angiopoietin-like 4(Angptl4)
ENSMUSG00000024659	annexin A1(Anxa1)
ENSMUSG00000029484	annexin A3(Anxa3)
ENSMUSG00000033420	anthrax toxin receptor 1(Antxr1)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000044338	apelin receptor(Aplnr)
ENSMUSG00000009585	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3(Apobec3)
ENSMUSG00000022548	apolipoprotein D(Apod)
ENSMUSG00000004655	aquaporin 1(Aqp1)
ENSMUSG00000028427	aquaporin 7(Aqp7)
ENSMUSG00000021388	asporin(Aspn)
ENSMUSG00000033059	brain glycogen phosphorylase(Pygb)
ENSMUSG00000040283	butyrophilin-like 9(Btnl9)
ENSMUSG00000032312	c-src tyrosine kinase(Csk)
ENSMUSG00000027230	cAMP responsive element binding protein 3-like 1(Creb3l1)
ENSMUSG00000038543	cDNA sequence BC028528(BC028528)
ENSMUSG00000031871	cadherin 5(Cdh5)
ENSMUSG00000004665	calponin 2(Cnn2)
ENSMUSG00000041261	carbonic anhydrase 8(Car8)
ENSMUSG00000027408	carboxypeptidase X 1 (M14 family)(Cpxm1)
ENSMUSG00000044006	cartilage intermediate layer protein 2(Cilp2)
ENSMUSG00000042254	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase(Cilp)
ENSMUSG00000026029	caspase 8(Casp8)
ENSMUSG00000028111	cathepsin K(Ctsk)
ENSMUSG00000038642	cathepsin S(Ctss)
ENSMUSG00000000058	caveolin 2(Cav2)
ENSMUSG00000030278	cell death-inducing DFFA-like effector c(Cidec)
ENSMUSG00000024526	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A(Cidea)
ENSMUSG00000050910	cerebellar degeneration-related protein 2-like(Cdr2l)
ENSMUSG00000020676	chemokine (C-C motif) ligand 11(Ccl11)
ENSMUSG00000018927	chemokine (C-C motif) ligand 6(Ccl6)
ENSMUSG00000009185	chemokine (C-C motif) ligand 8(Ccl8)
ENSMUSG00000019122	chemokine (C-C motif) ligand 9(Ccl9)
ENSMUSG00000049103	chemokine (C-C motif) receptor 2(Ccr2)
ENSMUSG00000061353	chemokine (C-X-C motif) ligand 12(Cxcl12)
ENSMUSG00000021508	chemokine (C-X-C motif) ligand 14(Cxcl14)
ENSMUSG00000007041	chloride intracellular channel 1(Clic1)
ENSMUSG00000039084	chondroadherin(Chad)
ENSMUSG00000022225	chymase 1, mast cell(Cma1)
ENSMUSG00000022512	claudin 1(Cldn1)
ENSMUSG00000028128	coagulation factor III(F3)
ENSMUSG00000039109	coagulation factor XIII, A1 subunit(F13a1)
ENSMUSG00000032878	coiled-coil domain containing 85A(Ccdc85a)

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Gene ID	**Gene Name**
ENSMUSG00000003208	coiled-coil domain containing 94(Ccdc94)
ENSMUSG00000020241	collagen, type VI, alpha 2(Col6a2)
ENSMUSG00000048126	collagen, type VI, alpha 3(Col6a3)
ENSMUSG00000043719	collagen, type VI, alpha 6(Col6a6)
ENSMUSG00000027966	collagen, type XI, alpha 1(Col11a1)
ENSMUSG00000022371	collagen, type XIV, alpha 1(Col14a1)
ENSMUSG00000028339	collagen, type XV, alpha 1(Col15a1)
ENSMUSG00000040690	collagen, type XVI, alpha 1(Col16a1)
ENSMUSG00000024621	colony stimulating factor 1 receptor(Csf1r)
ENSMUSG00000036896	complement component 1, q subcomponent, C chain(C1qc)
ENSMUSG00000036887	complement component 1, q subcomponent, alpha polypeptide(C1qa)
ENSMUSG00000036905	complement component 1, q subcomponent, beta polypeptide(C1qb)
ENSMUSG00000055172	complement component 1, r subcomponent A(C1ra)
ENSMUSG00000038521	complement component 1, s subcomponent 1(C1s1)
ENSMUSG00000024164	complement component 3(C3)
ENSMUSG00000073418	complement component 4B (Chido blood group)(C4b)
ENSMUSG00000026365	complement component factor h(Cfh)
ENSMUSG00000061780	complement factor D (adipsin)(Cfd)
ENSMUSG00000030707	coronin, actin binding protein 1A(Coro1a)
ENSMUSG00000033022	cysteine dioxygenase 1, cytosolic(Cdo1)
ENSMUSG00000031825	cysteine-rich secretory protein LCCL domain containing 2(Crispld2)
ENSMUSG00000020638	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial(Cmpk2)
ENSMUSG00000061740	cytochrome P450, family 2, subfamily d, polypeptide 22(Cyp2d22)
ENSMUSG00000025479	cytochrome P450, family 2, subfamily e, polypeptide 1(Cyp2e1)
ENSMUSG00000028713	cytochrome P450, family 4, subfamily b, polypeptide 1(Cyp4b1)
ENSMUSG00000015340	cytochrome b-245, beta polypeptide(Cybb)
ENSMUSG00000020810	cytoglobin(Cygb)
ENSMUSG00000044258	cytotoxic T lymphocyte-associated protein 2 alpha(Ctla2a)
ENSMUSG00000027314	delta-like 4 (Drosophila)(Dll4)
ENSMUSG00000038702	dermatan sulfate epimerase-like(Dsel)
ENSMUSG00000028031	dickkopf WNT signaling pathway inhibitor 2(Dkk2)
ENSMUSG00000022048	dihydropyrimidinase-like 2(Dpysl2)
ENSMUSG00000024501	dihydropyrimidinase-like 3(Dpysl3)
ENSMUSG00000019278	dipeptidase 1 (renal)(Dpep1)
ENSMUSG00000035000	dipeptidylpeptidase 4(Dpp4)
ENSMUSG00000040631	docking protein 4(Dok4)
ENSMUSG00000026825	dynamin 1(Dnm1)
ENSMUSG00000057098	early B cell factor 1(Ebf1)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	**Gene Name**
ENSMUSG00000022053	early B cell factor 2(Ebf2)
ENSMUSG00000015085	ectonucleoside triphosphate diphosphohydrolase 2(Entpd2)
ENSMUSG00000029163	elastin microfibril interfacer 1(Emilin1)
ENSMUSG00000024053	elastin microfibril interfacer 2(Emilin2)
ENSMUSG00000029675	elastin(Eln)
ENSMUSG00000054690	endomucin(Emcn)
ENSMUSG00000073599	endothelial cell surface expressed chemotaxis and apoptosis regulator(Ecscr)
ENSMUSG00000001946	endothelial cell-specific adhesion molecule(Esam)
ENSMUSG00000022122	endothelin receptor type B(Ednrb)
ENSMUSG00000031217	ephrin B1(Efnb1)
ENSMUSG00000015766	epidermal growth factor receptor pathway substrate 8(Eps8)
ENSMUSG00000020467	epidermal growth factor-containing fibulin-like extracellular matrix protein 1(Efemp1)
ENSMUSG00000075010	expressed sequence AW112010(AW112010)
ENSMUSG00000043631	extracellular matrix protein 2, female organ and adipocyte specific(Ecm2)
ENSMUSG00000040339	family with sequence similarity 102, member B(Fam102b)
ENSMUSG00000026483	family with sequence similarity 129, member A(Fam129a)
ENSMUSG00000042106	family with sequence similarity 212, member A(Fam212a)
ENSMUSG00000046546	family with sequence similarity 43, member A(Fam43a)
ENSMUSG00000029581	fascin actin-bundling protein 1(Fscn1)
ENSMUSG00000062515	fatty acid binding protein 4, adipocyte(Fabp4)
ENSMUSG00000027533	fatty acid binding protein 5, epidermal(Fabp5)
ENSMUSG00000010663	fatty acid desaturase 1(Fads1)
ENSMUSG00000024664	fatty acid desaturase 3(Fads3)
ENSMUSG00000053158	feline sarcoma oncogene(Fes)
ENSMUSG00000000392	fibroblast activation protein(Fap)
ENSMUSG00000041559	fibromodulin(Fmod)
ENSMUSG00000006369	fibulin 1(Fbln1)
ENSMUSG00000027386	fibulin 7(Fbln7)
ENSMUSG00000025278	filamin, beta(Flnb)
ENSMUSG00000040181	flavin containing monooxygenase 1(Fmo1)
ENSMUSG00000040170	flavin containing monooxygenase 2(Fmo2)
ENSMUSG00000023008	formin-like 3(Fmnl3)
ENSMUSG00000027004	frizzled-related protein(Frzb)
ENSMUSG00000050953	gap junction protein, alpha 1(Gja1)
ENSMUSG00000024084	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)(Qpct)
ENSMUSG00000033318	glutathione S-transferase, theta 2(Gstt2)
ENSMUSG00000035778	glycoprotein galactosyltransferase alpha 1, 3(Ggta1)
ENSMUSG00000031342	glycoprotein m6b(Gpm6b)

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Gene ID	Gene Name
ENSMUSG00000055653	glypican 3(Gpc3)
ENSMUSG00000021556	golgi membrane protein 1(Golm1)
ENSMUSG00000052957	growth arrest specific 1(Gas1)
ENSMUSG00000034201	growth arrest-specific 2 like 1(Gas2l1)
ENSMUSG00000079363	guanylate binding protein 4(Gbp4)
ENSMUSG00000033910	guanylate cyclase 1, soluble, alpha 3(Gucy1a3)
ENSMUSG00000029298	guanylate-binding protein 9(Gbp9)
ENSMUSG00000032744	hairy/enhancer-of-split related with YRPW motif-like(Heyl)
ENSMUSG00000031722	haptoglobin(Hp)
ENSMUSG00000074793	heat shock protein 12B(Hspa12b)
ENSMUSG00000069919	hemoglobin alpha, adult chain 1(Hba-a1)
ENSMUSG00000069917	hemoglobin alpha, adult chain 2(Hba-a2)
ENSMUSG00000052305	hemoglobin, beta adult s chain(Hbb-bs)
ENSMUSG00000073940	hemoglobin, beta adult t chain(Hbb-bt)
ENSMUSG00000037012	hexokinase 1(Hk1)
ENSMUSG00000067235	histocompatibility 2, Q region locus 10(H2-Q10)
ENSMUSG00000036594	histocompatibility 2, class II antigen A, alpha(H2-Aa)
ENSMUSG00000073421	histocompatibility 2, class II antigen A, beta 1(H2-Ab1)
ENSMUSG00000060586	histocompatibility 2, class II antigen E beta(H2-Eb1)
ENSMUSG00000031613	hydroxyprostaglandin dehydrogenase 15 (NAD)(Hpgd)
ENSMUSG00000043099	hypermethylated in cancer 1(Hic1)
ENSMUSG00000037206	immunoglobulin superfamily containing leucine-rich repeat(Islr)
ENSMUSG00000003477	indolethylamine N-methyltransferase(Inmt)
ENSMUSG00000042745	inhibitor of DNA binding 1(Id1)
ENSMUSG00000038855	inositol 1,4,5-trisphosphate 3-kinase B(Itpkb)
ENSMUSG00000017493	insulin-like growth factor binding protein 4(Igfbp4)
ENSMUSG00000036256	insulin-like growth factor binding protein 7(Igfbp7)
ENSMUSG00000027111	integrin alpha 6(Itga6)
ENSMUSG00000032925	integrin, beta-like 1(Itgbl1)
ENSMUSG00000025780	inter-alpha (globulin) inhibitor H5(Itih5)
ENSMUSG00000001029	intercellular adhesion molecule 2(Icam2)
ENSMUSG00000039997	interferon activated gene 203(Ifi203)
ENSMUSG00000073489	interferon activated gene 204(Ifi204)
ENSMUSG00000054203	interferon activated gene 205(Ifi205)
ENSMUSG00000078920	interferon gamma inducible protein 47(Ifi47)
ENSMUSG00000045932	interferon-induced protein with tetratricopeptide repeats 2(Ifit2)
ENSMUSG00000024810	interleukin 33(Il33)
ENSMUSG00000029469	intraflagellar transport 81(Ift81)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000047485	kelch-like 34(Klhl34)
ENSMUSG00000019932	keratocan(Kera)
ENSMUSG00000062960	kinase insert domain protein receptor(Kdr)
ENSMUSG00000019846	laminin, alpha 4(Lama4)
ENSMUSG00000001123	lectin, galactose binding, soluble 9(Lgals9)
ENSMUSG00000090958	leucine rich repeat containing 32(Lrrc32)
ENSMUSG00000016024	lipopolysaccharide binding protein(Lbp)
ENSMUSG00000021069	liver glycogen phosphorylase(Pygl)
ENSMUSG00000040249	low density lipoprotein receptor-related protein 1(Lrp1)
ENSMUSG00000036446	lumican(Lum)
ENSMUSG00000079018	lymphocyte antigen 6 complex, locus C1(Ly6c1)
ENSMUSG00000022587	lymphocyte antigen 6 complex, locus E(Ly6e)
ENSMUSG00000021998	lymphocyte cytosolic protein 1(Lcp1)
ENSMUSG00000028581	lysosomal-associated protein transmembrane 5(Laptm5)
ENSMUSG00000069515	lysozyme 1(Lyz1)
ENSMUSG00000069516	lysozyme 2(Lyz2)
ENSMUSG00000024529	lysyl oxidase(Lox)
ENSMUSG00000040950	macrophage galactose N-acetyl-galactosamine specific lectin 2(Mgl2)
ENSMUSG00000078680	major urinary protein 10(Mup10)
ENSMUSG00000020695	mannose receptor, C type 2(Mrc2)
ENSMUSG00000037306	mannosidase, alpha, class 1C, member 1(Man1c1)
ENSMUSG00000061068	mast cell protease 4(Mcpt4)
ENSMUSG00000030218	matrix Gla protein(Mgp)
ENSMUSG00000000957	matrix metallopeptidase 14 (membrane-inserted)(Mmp14)
ENSMUSG00000031740	matrix metallopeptidase 2(Mmp2)
ENSMUSG00000029061	matrix metallopeptidase 23(Mmp23)
ENSMUSG00000020814	matrix-remodelling associated 7(Mxra7)
ENSMUSG00000039956	melanocortin 2 receptor accessory protein(Mrap)
ENSMUSG00000027820	membrane metallo endopeptidase(Mme)
ENSMUSG00000024678	membrane-spanning 4-domains, subfamily A, member 4D(Ms4a4d)
ENSMUSG00000001493	mesenchyme homeobox 1(Meox1)
ENSMUSG00000036144	mesenchyme homeobox 2(Meox2)
ENSMUSG00000060572	microfibrillar-associated protein 2(Mfap2)
ENSMUSG00000042436	microfibrillar-associated protein 4(Mfap4)
ENSMUSG00000048450	msh homeobox 1(Msx1)
ENSMUSG00000041445	multimerin 2(Mmrn2)
ENSMUSG00000046916	myc target 1(Myct1)
ENSMUSG00000027375	myelin and lymphocyte protein, T cell differentiation protein(Mal)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000041607	myelin basic protein(Mbp)
ENSMUSG00000056569	myelin protein zero(Mpz)
ENSMUSG00000090272	myeloid nuclear differentiation antigen like(Mndal)
ENSMUSG00000026697	myocilin(Myoc)
ENSMUSG00000018830	myosin, heavy polypeptide 11, smooth muscle(Myh11)
ENSMUSG00000053093	myosin, heavy polypeptide 7, cardiac muscle, beta(Myh7)
ENSMUSG00000013936	myosin, light polypeptide 2, regulatory, cardiac, slow(Myl2)
ENSMUSG00000059741	myosin, light polypeptide 3(Myl3)
ENSMUSG00000022836	myosin, light polypeptide kinase(Mylk)
ENSMUSG00000052384	negative regulator of reactive oxygen species(Nrros)
ENSMUSG00000037362	nephroblastoma overexpressed gene(Nov)
ENSMUSG00000067786	neuronatin(Nnat)
ENSMUSG00000025969	neuropilin 2(Nrp2)
ENSMUSG00000055254	neurotrophic tyrosine kinase, receptor, type 2(Ntrk2)
ENSMUSG00000021806	nidogen 2(Nid2)
ENSMUSG00000026222	nuclear antigen Sp100(Sp100)
ENSMUSG00000072889	nuclear transcription factor, X-box binding-like 1(Nfxl1)
ENSMUSG00000027848	olfactomedin-like 3(Olfml3)
ENSMUSG00000021390	osteoglycin(Ogn)
ENSMUSG00000035863	paralemmin(Palm)
ENSMUSG00000027188	peptidase domain containing associated with muscle regeneration 1(Pamr1)
ENSMUSG00000024011	peptidase inhibitor 16(Pi16)
ENSMUSG00000053198	periaxin(Prx)
ENSMUSG00000030546	perilipin 1(Plin1)
ENSMUSG00000027750	periostin, osteoblast specific factor(Postn)
ENSMUSG00000020674	peroxidasin(Pxdn)
ENSMUSG00000000440	peroxisome proliferator activated receptor gamma(Pparg)
ENSMUSG00000048960	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2(Prex2)
ENSMUSG00000027513	phosphoenolpyruvate carboxykinase 1, cytosolic(Pck1)
ENSMUSG00000002847	phospholipase A1 member A(Pla1a)
ENSMUSG00000052160	phospholipase D family, member 4(Pld4)
ENSMUSG00000017754	phospholipid transfer protein(Pltp)
ENSMUSG00000013698	phosphoprotein enriched in astrocytes 15A(Pea15a)
ENSMUSG00000045658	phosphotyrosine interaction domain containing 1(Pid1)
ENSMUSG00000031538	plasminogen activator, tissue(Plat)
ENSMUSG00000029231	platelet derived growth factor receptor, alpha polypeptide(Pdgfra)
ENSMUSG00000024620	platelet derived growth factor receptor, beta polypeptide(Pdgfrb)
ENSMUSG00000028073	platelet endothelial aggregation receptor 1(Pear1)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	**Gene Name**
ENSMUSG00000029373	platelet factor 4(Pf4)
ENSMUSG00000031595	platelet-derived growth factor receptor-like(Pdgfrl)
ENSMUSG00000032006	platelet-derived growth factor, D polypeptide(Pdgfd)
ENSMUSG00000020717	platelet/endothelial cell adhesion molecule 1(Pecam1)
ENSMUSG00000040624	pleckstrin homology domain containing, family G (with RhoGef domain) member 1(Plekhg1)
ENSMUSG00000031557	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2(Plekha2)
ENSMUSG00000025608	podocalyxin-like(Podxl)
ENSMUSG00000001098	potassium channel tetramerisation domain containing 10(Kctd10)
ENSMUSG00000030247	potassium inwardly-rectifying channel, subfamily J, member 8(Kcnj8)
ENSMUSG00000045573	preproenkephalin(Penk)
ENSMUSG00000015354	procollagen C-endopeptidase enhancer 2(Pcolce2)
ENSMUSG00000029718	procollagen C-endopeptidase enhancer protein(Pcolce)
ENSMUSG00000023191	prolyl 3-hydroxylase 3(P3h3)
ENSMUSG00000061119	prolylcarboxypeptidase (angiotensinase C)(Prcp)
ENSMUSG00000036986	promyelocytic leukemia(Pml)
ENSMUSG00000030513	proprotein convertase subtilisin/kexin type 6(Pcsk6)
ENSMUSG00000021108	protein kinase C, eta(Prkch)
ENSMUSG00000041187	protein kinase D2(Prkd2)
ENSMUSG00000002997	protein kinase, cAMP dependent regulatory, type II beta(Prkar2b)
ENSMUSG00000020154	protein tyrosine phosphatase, receptor type, B(Ptprb)
ENSMUSG00000024440	protocadherin 12(Pcdh12)
ENSMUSG00000020641	radical S-adenosyl methionine domain containing 2(Rsad2)
ENSMUSG00000001240	receptor (calcitonin) activity modifying protein 2(Ramp2)
ENSMUSG00000030844	regulator of G-protein signalling 10(Rgs10)
ENSMUSG00000061100	resistin like alpha(Retnla)
ENSMUSG00000012705	resistin(Retn)
ENSMUSG00000030110	ret proto-oncogene(Ret)
ENSMUSG00000019539	reticulocalbin 3, EF-hand calcium binding domain(Rcn3)
ENSMUSG00000021876	ribonuclease, RNase A family 4(Rnase4)
ENSMUSG00000063171	ribosomal protein S4-like(Rps4l)
ENSMUSG00000033107	ring finger protein 125(Rnf125)
ENSMUSG00000020642	ring finger protein 144A(Rnf144a)
ENSMUSG00000003581	ring finger protein 215(Rnf215)
ENSMUSG00000032125	roundabout guidance receptor 4(Robo4)
ENSMUSG00000034463	scavenger receptor class A, member 3(Scara3)
ENSMUSG00000022032	scavenger receptor class A, member 5(Scara5)
ENSMUSG00000037936	scavenger receptor class B, member 1(Scarb1)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000038188	scavenger receptor class F, member 1(Scarf1)
ENSMUSG00000012017	scavenger receptor class F, member 2(Scarf2)
ENSMUSG00000035279	scavenger receptor cysteine rich family, 5 domains(Ssc5d)
ENSMUSG00000072620	schlafen 2(Slfn2)
ENSMUSG00000054404	schlafen 5(Slfn5)
ENSMUSG00000018822	secreted frizzled-related sequence protein 5(Sfrp5)
ENSMUSG00000029304	secreted phosphoprotein 1(Spp1)
ENSMUSG00000020486	septin 4(Sept4)
ENSMUSG00000018398	septin 8(Sept8)
ENSMUSG00000020077	serglycin(Srgn)
ENSMUSG00000034810	sodium channel, voltage-gated, type VII, alpha(Scn7a)
ENSMUSG00000017756	solute carrier family 12, member 7(Slc12a7)
ENSMUSG00000003528	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1(Slc25a1)
ENSMUSG00000040441	solute carrier family 26, member 10(Slc26a10)
ENSMUSG00000027219	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2(Slc28a2)
ENSMUSG00000020264	solute carrier family 36 (proton/amino acid symporter), member 2(Slc36a2)
ENSMUSG00000034401	spermatogenesis associated 6(Spata6)
ENSMUSG00000045092	sphingosine-1-phosphate receptor 1(S1pr1)
ENSMUSG00000067586	sphingosine-1-phosphate receptor 3(S1pr3)
ENSMUSG00000037379	spondin 2, extracellular matrix protein(Spon2)
ENSMUSG00000042286	stabilin 1(Stab1)
ENSMUSG00000047735	sterile alpha motif domain containing 9-like(Samd9l)
ENSMUSG00000030711	sulfotransferase family 1A, phenol-preferring, member 1(Sult1a1)
ENSMUSG00000072941	superoxide dismutase 3, extracellular(Sod3)
ENSMUSG00000028369	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1(Svep1)
ENSMUSG00000090084	sushi-repeat-containing protein(Srpx)
ENSMUSG00000031253	sushi-repeat-containing protein, X-linked 2(Srpx2)
ENSMUSG00000025743	syndecan 3(Sdc3)
ENSMUSG00000046314	syntaxin binding protein 6 (amisyn)(Stxbp6)
ENSMUSG00000023064	synuclein, gamma(Sncg)
ENSMUSG00000033327	tenascin XB(Tnxb)
ENSMUSG00000031250	tenomodulin(Tnmd)
ENSMUSG00000027217	tetraspanin 18(Tspan18)
ENSMUSG00000027858	tetraspanin 2(Tspan2)
ENSMUSG00000075273	tetratricopeptide repeat domain 30B(Ttc30b)
ENSMUSG00000028047	thrombospondin 3(Thbs3)
ENSMUSG00000030317	tissue inhibitor of metalloproteinase 4(Timp4)
ENSMUSG00000068079	transcription factor 15(Tcf15)

Table S1A: List of genes expressed in the whole muscle but not in the myofiber

Gene ID	Gene Name
ENSMUSG00000068735	transformation related protein 53 inducible protein 11(Trp53i11)
ENSMUSG00000027800	transmembrane 4 superfamily member 1(Tm4sf1)
ENSMUSG00000023367	transmembrane protein 176A(Tmem176a)
ENSMUSG00000024168	transmembrane protein 204(Tmem204)
ENSMUSG00000041737	transmembrane protein 45b(Tmem45b)
ENSMUSG00000026109	transmembrane protein with EGF-like and two follistatin-like domains 2(Tmeff2)
ENSMUSG00000030921	tripartite motif-containing 30A(Trim30a)
ENSMUSG00000032186	tropomodulin 2(Tmod2)
ENSMUSG00000091898	troponin C, cardiac/slow skeletal(Tnnc1)
ENSMUSG00000026418	troponin I, skeletal, slow 1(Tnni1)
ENSMUSG00000033825	tryptase beta 2(Tpsb2)
ENSMUSG00000028776	tubulointerstitial nephritis antigen-like 1(Tinagl1)
ENSMUSG00000062210	tumor necrosis factor, alpha-induced protein 8(Tnfaip8)
ENSMUSG00000032175	tyrosine kinase 2(Tyk2)
ENSMUSG00000033191	tyrosine kinase with immunoglobulin-like and EGF-like domains 1(Tie1)
ENSMUSG00000027078	ubiquitin-conjugating enzyme E2L 6(Ube2l6)
ENSMUSG00000032596	ubiquitin-like modifier activating enzyme 7(Uba7)
ENSMUSG00000036908	unc-93 homolog B1 (C. elegans)(Unc93b1)
ENSMUSG00000031710	uncoupling protein 1 (mitochondrial, proton carrier)(Ucp1)
ENSMUSG00000033685	uncoupling protein 2 (mitochondrial, proton carrier)(Ucp2)
ENSMUSG00000062101	zinc finger protein 119b(Zfp119b)
ENSMUSG00000029587	zinc finger protein 12(Zfp12)
ENSMUSG00000047603	zinc finger protein 235(Zfp235)
ENSMUSG00000002617	zinc finger protein 40(Zfp40)
ENSMUSG00000053600	zinc finger protein 472(Zfp472)
ENSMUSG00000071281	zinc finger protein 65(Zfp65)
ENSMUSG00000030469	zinc finger protein 719(Zfp719)
ENSMUSG00000095432	zinc finger protein 748(Zfp748)
ENSMUSG00000095325	zinc finger protein 870(Zfp870)
ENSMUSG00000066000	zinc finger protein 979(Zfp979)

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* Defined genes as expressed solely in the whole muscle if the reads per million (RPM) of the gene was greater or equal to 10 in the whole muscle and 0 in the single myofiber

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

Annotation Cluster 1 **Enrichment Score: 30.313113382224095**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Glycoprotein	192	43.14606742	2.05E-39	445	3815	22680	2.565013916	5.83E-37	5.83E-37	2.72E-36
UP_KEYWORDS	Disulfide bond	171	38.42696629	8.74E-39	445	3124	22680	2.789768231	2.48E-36	1.24E-36	1.16E-35
UP_SEQ_FEATURE	signal peptide	181	40.6741573	1.32E-38	402	3124	18012	2.595992509	1.85E-35	1.85E-35	2.17E-35
UP_KEYWORDS	Signal	199	44.71910112	1.75E-32	445	4543	22680	2.232509825	4.97E-30	1.66E-30	2.32E-29
UP_KEYWORDS	Secreted	112	25.16853933	5.28E-31	445	1685	22680	3.387670456	1.50E-28	3.75E-29	6.99E-28
UP_SEQ_FEATURE	disulfide bond	146	32.80898876	9.31E-30	402	2510	18012	2.606243682	1.30E-26	6.52E-27	1.53E-26
GOTERM_CC_DIRECT	GO:0005576~extracellular region	118	26.51685393	3.62E-29	431	1753	19662	3.070792794	1.11E-26	1.11E-26	4.86E-26
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	167	37.52808989	6.81E-24	402	3563	18012	2.100083361	9.55E-21	3.18E-21	1.12E-20
GOTERM_CC_DIRECT	GO:0005615~extracellular space	86	19.3258427	3.04E-16	431	1504	19662	2.608561238	1.02E-13	2.03E-14	4.44E-13

Annotation Cluster 2 **Enrichment Score: 18.007103024438535**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	41	9.213483146	2.14E-19	431	316	19662	5.918984405	6.53E-17	2.18E-17	2.87E-16
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	39	8.764044944	8.56E-19	431	294	19662	6.051564942	2.61E-16	6.53E-17	1.15E-15
UP_KEYWORDS	Extracellular matrix	33	7.415730337	5.20E-18	445	235	22680	7.156968683	1.48E-15	2.95E-16	6.89E-15

Annotation Cluster 3 **Enrichment Score: 9.933643540042675**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	20	4.494382022	1.36E-14	431	83	19662	10.99264809	4.17E-12	6.94E-13	1.83E-11
UP_KEYWORDS	Collagen	19	4.269662921	4.59E-14	445	85	22680	11.3924653	1.30E-11	2.17E-12	6.08E-11
INTERPRO	IPR008160:Collagen triple helix repeat	18	4.04494382	2.75E-13	434	76	20594	11.2385399	2.15E-10	2.15E-10	4.21E-10
UP_SEQ_FEATURE	domain:C1q	11	2.471910112	3.67E-10	402	29	18012	16.99536799	5.15E-07	1.29E-07	6.05E-07

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR001073:Complement C1q protein	11	2.471910112	6.50E-10	434	32	20594	16.31149194	5.07E-07	1.69E-07	9.94E-07
SMART	SM00110:C1Q	11	2.471910112	2.20E-09	282	29	10425	14.02237711	4.07E-07	2.03E-07	2.72E-06
UP_KEYWORDS	Hydroxylation	14	3.146067416	1.65E-08	445	88	22680	8.108273749	4.69E-06	3.91E-07	2.19E-05
UP_SEQ_FEATURE	domain:Collagen-like	10	2.247191011	2.95E-08	402	33	18012	13.57756671	4.14E-05	8.28E-06	4.87E-05
INTERPRO	IPR008983:Tumour necrosis factor-like domain	11	2.471910112	9.00E-08	434	51	20594	10.23466161	7.03E-05	1.00E-05	1.38E-04

Annotation Cluster 4				**Enrichment Score: 9.64402947910352**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
UP_KEYWORDS	Immunity	35	7.865168539	8.64E-13	445	401	22680	4.448429488	2.45E-10	3.51E-11	1.15E-09
GOTERM_BP_DIRECT	GO:0002376~immune system process	34	7.640449438	3.88E-11	406	383	18082	3.95367143	8.25E-08	2.75E-08	6.71E-08
UP_KEYWORDS	Innate immunity	23	5.168539326	2.55E-09	445	241	22680	4.864002984	7.25E-07	6.59E-08	3.38E-06
GOTERM_BP_DIRECT	GO:0045087~innate immune response	30	6.741573034	3.10E-08	406	400	18082	3.340270936	6.61E-05	1.65E-05	5.37E-05

Annotation Cluster 5				**Enrichment Score: 5.681420312630552**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
UP_KEYWORDS	EGF-like domain	25	5.617977528	1.70E-11	445	224	22680	5.688202247	4.81E-09	6.02E-10	2.25E-08
INTERPRO	IPR000742:Epidermal growth factor-like domain	26	5.842696629	3.99E-11	434	237	20594	5.205662175	3.12E-08	1.56E-08	6.10E-08
SMART	SM00181:EGF	24	5.393258427	5.45E-10	282	181	10425	4.901845539	1.01E-07	1.01E-07	6.75E-07
INTERPRO	IPR013032:EGF-like, conserved site	22	4.943820225	1.23E-09	434	197	20594	5.299164893	9.57E-07	2.39E-07	1.87E-06
INTERPRO	IPR009030:Insulin-like growth factor binding protein, N-terminal	17	3.820224719	1.50E-08	434	130	20594	6.205210918	1.18E-05	2.35E-06	2.30E-05
INTERPRO	IPR001881:EGF-like calcium-binding	16	3.595505618	6.67E-08	434	126	20594	6.025601639	5.21E-05	8.69E-06	1.02E-04
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	13	2.921348315	9.10E-07	434	97	20594	6.359494513	7.11E-04	8.89E-05	0.00139305

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation site	13	2.921348315	1.02E-06	434	98	20594	6.294601712	7.95E-04	7.95E-05	0.001557667
SMART	SM00179:EGF_CA	16	3.595505618	1.39E-06	282	126	10425	4.694360014	2.57E-04	8.58E-05	0.001721267
UP_SEQ_FEATURE	domain:EGF-like 3; calcium-binding	9	2.02247191	2.32E-06	402	40	18012	10.08134328	0.003246306	3.61E-04	0.003821946
UP_SEQ_FEATURE	domain:EGF-like 1	13	2.921348315	6.81E-06	402	111	18012	5.247546054	0.009508256	7.96E-04	0.01122915
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	35	7.865168539	1.52E-05	387	699	17446	2.257229782	0.009147045	0.002294647	0.022487537
UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	6	1.348314607	5.62E-04	402	31	18012	8.672123255	0.545511121	0.042864302	0.922641577
INTERPRO	IPR026823:Complement Clr-like EGF domain	5	1.123595506	8.68E-04	434	21	20594	11.29800307	0.492635322	0.026776002	1.320587274
UP_SEQ_FEATURE	domain:EGF-like 2; calcium-binding	7	1.573033708	0.00100527	402	52	18012	6.031572905	0.75588045	0.062084414	1.643812796
UP_SEQ_FEATURE	domain:EGF-like 4; calcium-binding	5	1.123595506	0.005315511	402	32	18012	7.000932836	0.999431338	0.214189402	8.408426258
UP_SEQ_FEATURE	domain:EGF-like 6; calcium-binding	4	0.898876404	0.013936214	402	23	18012	7.792342635	0.999999997	0.412443985	20.64811226
UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	3	0.674157303	0.106091194	402	25	18012	5.376716418	1	0.91429286	84.24806799

Annotation Cluster 6 **Enrichment Score: 4.952322000714141**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001134:Netrin domain	7	1.573033708	4.68E-06	434	22	20594	15.09824047	0.003647914	3.32E-04	0.0071599
UP_SEQ_FEATURE	domain:NTR	7	1.573033708	4.79E-06	402	21	18012	14.93532338	0.006698724	6.72E-04	0.007900073
INTERPRO	IPR008993:Tissue inhibitor of metalloproteinases-like, OB-fold	7	1.573033708	8.15E-06	434	24	20594	13.84005376	0.006341399	4.54E-04	0.01246302
INTERPRO	IPR018933:Netrin module, non-TIMP type	6	1.348314607	2.02E-05	434	17	20594	16.74762808	0.015625636	9.26E-04	0.030851102
SMART	SM00643:C345C	6	1.348314607	4.70E-05	282	16	10425	13.86303191	0.008655407	0.001737106	0.058127257

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

Annotation Cluster 7 **Enrichment Score: 3.8982336681686043**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04510:Focal adhesion	19	4.269662921	1.98E-06	185	207	7691	3.815876746	3.88E-04	1.29E-04	0.002471434
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	10	2.247191011	2.37E-04	185	88	7691	4.724201474	0.04538139	0.007710682	0.295579417
KEGG_PATHWAY	mmu04151:PI3K-Akt signaling pathway	18	4.04494382	0.004309013	185	351	7691	2.131947332	0.571039878	0.074058911	5.251731512

Annotation Cluster 8 **Enrichment Score: 3.807503589908664**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu05150:Staphylococcus aureus infection	14	3.146067416	9.02E-11	185	50	7691	11.64043243	1.77E-08	1.77E-08	1.13E-07
GOTERM_CC_DIRECT	GO:0072562~blood microparticle	15	3.370786517	1.33E-06	431	133	19662	5.145055213	4.06E-04	4.06E-05	0.001783744
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	12	2.696629213	1.61E-06	185	76	7691	6.564153627	3.16E-04	1.58E-04	0.002014843
UP_KEYWORDS	Complement pathway	7	1.573033708	1.14E-05	445	27	22680	13.21348315	0.003222093	1.90E-04	0.015057254
BIOCARTA	m_compPathway:Complement Pathway	7	1.573033708	6.37E-05	57	18	1289	8.794346979	0.006284818	0.006284818	0.070525673
BIOCARTA	m_classicPathway:Classical Complement Pathway	6	1.348314607	8.13E-05	57	12	1289	11.30701754	0.008011976	0.004014044	0.089976518
GOTERM_BP_DIRECT	GO:0006958~complement activation, classical pathway	7	1.573033708	0.00139617	406	55	18082	5.668338558	0.948928236	0.083768288	2.390632899
GOTERM_BP_DIRECT	GO:0006956~complement activation	4	0.898876404	0.004153138	406	15	18082	11.87651888	0.999858108	0.1718161	6.954041877
KEGG_PATHWAY	mmu05133:Pertussis	7	1.573033708	0.008330798	185	74	7691	3.932578524	0.805957064	0.127715504	9.923272718
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	10	2.247191011	0.008566306	185	147	7691	2.8280934	0.81478327	0.121649792	10.19014736
KEGG_PATHWAY	mmu05020:Prion diseases	3	0.674157303	0.186311812	185	33	7691	3.779361179	1	0.654735561	92.38977639

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

KEGG_PATHWAY	mmu05142:Chagas disease (American trypanosomiasis)	5	1.123595506	0.232584394	185	103	7691	2.018105484	1	0.700805535	96.33776667

Annotation Cluster 9				**Enrichment Score: 3.708834845849344**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
UP_KEYWORDS	Sushi	9	2.02247191	3.26E-06	445	47	22680	9.759502749	9.26E-04	5.79E-05	0.004322464
INTERPRO	IPR000436:Sushi/SCR/CCP	9	2.02247191	2.10E-05	434	56	20594	7.626152074	0.016277998	9.11E-04	0.032149537
UP_SEQ_FEATURE	domain:Sushi 2	7	1.573033708	1.10E-04	402	35	18012	8.96119403	0.143126042	0.010244791	0.181397717
UP_SEQ_FEATURE	domain:Sushi 1	7	1.573033708	1.10E-04	402	35	18012	8.96119403	0.143126042	0.010244791	0.181397717
SMART	SM00032:CCP	8	1.797752809	5.74E-04	282	54	10425	5.476753349	0.100804761	0.015064674	0.708173559
INTERPRO	IPR003410:Hyalin	3	0.674157303	0.001304758	434	3	20594	47.4516129	0.639290088	0.035762057	1.977962809
UP_SEQ_FEATURE	domain:Sushi 3	4	0.898876404	0.01751755	402	25	18012	7.168955224	1	0.453556016	25.26635978

Annotation Cluster 10				**Enrichment Score: 3.128258217689208**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	topological domain:Extracellular	90	20.2247191	3.67E-08	402	2256	18012	1.787472213	5.15E-05	8.58E-06	6.05E-05
GOTERM_CC_DIRECT	GO:0016020~membrane	203	45.61797753	6.15E-07	431	6998	19662	1.323343295	1.88E-04	2.35E-05	8.24E-04
UP_SEQ_FEATURE	topological domain:Cytoplasmic	99	22.24719101	6.61E-06	402	2880	18012	1.540205224	0.009223564	8.42E-04	0.010891387
UP_SEQ_FEATURE	transmembrane region	124	27.86516854	0.001102916	402	4312	18012	1.288483372	0.787144602	0.065054512	1.802124363
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	134	30.11235955	0.002083844	431	4874	19662	1.254208371	0.470718944	0.034729038	2.755889537
UP_KEYWORDS	Membrane	193	43.37078652	0.017424551	445	8683	22680	1.132845144	0.993209246	0.109611611	20.77934184

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_KEYWORDS	Transmembrane	149	33.48314607	0.119632998	445	6955	22680	1.091873117	1	0.386762833	81.51908642
UP_KEYWORDS	Transmembrane helix	146	32.80898876	0.18307073	445	6938	22680	1.072510616	1	0.507843158	93.13989355
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	151	33.93258427	0.535495683	431	6878	19662	1.001532847	1	0.919114695	99.9965425

Annotation Cluster 11

Enrichment Score: 2.960381357218414

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0001725~stress fiber	9	2.02247191	1.03E-04	431	67	19662	6.127991135	0.031053841	0.002250765	0.138466474
UP_KEYWORDS	Actin-binding	14	3.146067416	0.001483938	445	252	22680	2.831460674	0.344102845	0.016090348	1.948632883
GOTERM_MF_DIRECT	GO:0003779~actin binding	16	3.595505618	0.00856673	387	338	17446	2.13396939	0.994464625	0.202233202	11.942902

Annotation Cluster 12

Enrichment Score: 2.7599353017136075

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	16	3.595505618	6.13E-08	406	118	18082	6.038907907	1.30E-04	2.61E-05	1.06E-04
UP_KEYWORDS	Chemotaxis	13	2.921348315	3.06E-07	445	94	22680	7.048529763	8.69E-05	6.69E-06	4.06E-04
GOTERM_BP_DIRECT	GO:0006955~immune response	19	4.269662921	4.47E-05	406	272	18082	3.111036656	0.090772891	0.006323944	0.077379726
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	21	4.719101124	1.05E-04	406	344	18082	2.71882518	0.200193849	0.012333637	0.181551713
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	7	1.573033708	2.45E-04	406	40	18082	7.793965517	0.406558953	0.020656369	0.423580813
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	8	1.797752809	5.04E-04	406	63	18082	5.655485183	0.658462422	0.035176329	0.870096575
INTERPRO	IPR001811:Chemokine interleukin-8-like domain	7	1.573033708	6.06E-04	434	50	20594	6.643225806	0.377294849	0.02038425	0.923757458
GOTERM_MF_DIRECT	GO:0008009~chemokine activity	7	1.573033708	6.32E-04	387	48	17446	6.57418174	0.317206202	0.03129666	0.929512687

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	7	1.573033708	0.00139617	406	55	18082	5.668338558	0.948928236	0.083768288	2.390632899
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	8	1.797752809	0.001809273	406	78	18082	4.567891878	0.978835541	0.101559982	3.087590408
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	9	2.02247191	0.003322008	406	110	18082	3.64393193	0.999161863	0.155216167	5.599949126
GOTERM_BP_DIRECT	GO:0071346~cellular response to interferon-gamma	7	1.573033708	0.004134874	406	68	18082	4.584685598	0.999852458	0.174502865	6.924483495
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	7	1.573033708	0.004445132	406	69	18082	4.51824088	0.999924	0.179301643	7.42540543
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	10	2.247191011	0.005677978	406	146	18082	3.050475741	0.999994566	0.207950995	9.390880675
INTERPRO	IPR000827:CC chemokine, conserved site	4	0.898876404	0.005955204	434	18	20594	10.54480287	0.990579986	0.131824307	8.734406329
SMART	SM00199:SCY	6	1.348314607	0.009123653	282	48	10425	4.621010638	0.816515072	0.15596581	10.72178265
UP_KEYWORDS	Cytokine	10	2.247191011	0.017402177	445	200	22680	2.548314607	0.993165188	0.111932717	20.75543363
GOTERM_MF_DIRECT	GO:0048020~CCR chemokine receptor binding	4	0.898876404	0.023379318	387	28	17446	6.440014766	0.999999377	0.360152188	29.51096139
GOTERM_BP_DIRECT	GO:0048247~lymphocyte chemotaxis	4	0.898876404	0.037055414	406	33	18082	5.398417674	1	0.556038783	48.00087033
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	10	2.247191011	0.049057582	387	214	17446	2.106546886	1	0.541150263	52.45980449
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	9	2.02247191	0.097074137	185	196	7691	1.908963045	0.999999998	0.523495458	72.07558268
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	5	1.123595506	0.104763395	406	80	18082	2.783559113	1	0.829923646	85.2895264
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	9	2.02247191	0.222984253	185	242	7691	1.546102301	1	0.700634952	95.72244703

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

Annotation Cluster 13				Enrichment Score: 2.74686435865684							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	GO:0031838~haptoglobin-hemoglobin complex	5	1.123595506	1.11E-06	431	5	19662	45.61948956	3.38E-04	3.76E-05	0.001485213
GOTERM_MF_DIRECT	GO:0031720~haptoglobin binding	4	0.898876404	4.23E-05	387	4	17446	45.08010336	0.025218911	0.005095445	0.062494427
GOTERM_BP_DIRECT	GO:0098869~cellular oxidant detoxification	4	0.898876404	1.08E-04	406	5	18082	35.62955665	0.205191331	0.011417019	0.186641103
UP_KEYWORDS	Oxygen transport	5	1.123595506	2.19E-04	445	16	22680	15.92696629	0.06024962	0.003102228	0.289526626
INTERPRO	IPR000971:Globin	5	1.123595506	2.87E-04	434	16	20594	14.82862903	0.200827683	0.010618398	0.438253659
INTERPRO	IPR009050:Globin-like	5	1.123595506	2.87E-04	434	16	20594	14.82862903	0.200827683	0.010618398	0.438253659
GOTERM_MF_DIRECT	GO:0005344~oxygen transporter activity	5	1.123595506	3.48E-04	387	16	17446	14.0875323	0.18947494	0.025917228	0.512823838
INTERPRO	IPR012292:Globin, structural domain	5	1.123595506	3.69E-04	434	17	20594	13.95635674	0.250479864	0.013020046	0.563295762
GOTERM_MF_DIRECT	GO:0004601~peroxidase activity	6	1.348314607	5.46E-04	387	31	17446	8.725181295	0.28114563	0.029562979	0.804644056
KEGG_PATHWAY	mmu05144:Malaria	7	1.573033708	9.20E-04	185	48	7691	6.062725225	0.165052406	0.022295977	1.143147804
UP_KEYWORDS	Heme	11	2.471910112	0.002055889	445	171	22680	3.278533412	0.442600817	0.021414553	2.690272626
GOTERM_MF_DIRECT	GO:0019825~oxygen binding	5	1.123595506	0.002398713	387	26	17446	8.669250646	0.765561759	0.077425215	3.487918474
GOTERM_CC_DIRECT	GO:0005833~hemoglobin complex	4	0.898876404	0.002523111	431	13	19662	14.03676602	0.537228241	0.039742454	3.327777063
UP_KEYWORDS	Iron	16	3.595505618	0.007398353	445	375	22680	2.174561798	0.878633855	0.060143189	9.371565329
KEGG_PATHWAY	mmu05143:African trypanosomiasis	5	1.123595506	0.009302922	185	35	7691	5.938996139	0.839892049	0.122651071	11.02018423
GOTERM_MF_DIRECT	GO:0020037~heme binding	10	2.247191011	0.016089418	387	175	17446	2.576005906	0.999944384	0.278604579	21.3198102
GOTERM_BP_DIRECT	GO:0015671~oxygen transport	3	0.674157303	0.01999422	406	10	18082	13.36108374	1	0.423782068	29.51583421

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_BP_DIRECT	GO:0048821~erythrocyte development	4	0.898876404	0.021907162	406	27	18082	6.598066046	1	0.441336287	31.86101582
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme distal ligand)	3	0.674157303	0.023808953	402	11	18012	12.21981004	1	0.55263466	32.77381189
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme proximal ligand)	3	0.674157303	0.037704697	402	14	18012	9.601279318	1	0.667022504	46.92019885
GOTERM_MF_DIRECT	GO:0005506~iron ion binding	10	2.247191011	0.046717823	387	212	17446	2.12641997	1	0.542064205	50.70103306
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	5	1.123595506	0.24909948	402	114	18012	1.965174129	1	0.993399427	99.10946028

Annotation Cluster 14 **Enrichment Score: 2.5444970918259306**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR020635:Tyrosine-protein kinase, catalytic domain	12	2.696629213	1.01E-06	434	81	20594	7.029868578	7.89E-04	8.77E-05	0.001546438
UP_KEYWORDS	Immunoglobulin domain	28	6.292134831	1.12E-06	445	481	22680	2.966852765	3.18E-04	2.12E-05	0.001482369
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	15	3.370786517	1.48E-06	402	132	18012	5.091587517	0.002072589	2.96E-04	0.002438686
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	15	3.370786517	1.62E-06	402	133	18012	5.053304904	0.002270009	2.84E-04	0.002671239
INTERPRO	IPR016243:Tyrosine-protein kinase, CSF-1/PDGF receptor	5	1.123595506	6.42E-06	434	7	20594	33.89400922	0.004998374	4.17E-04	0.009817021
INTERPRO	IPR008266:Tyrosine-protein kinase, active site	12	2.696629213	7.49E-06	434	99	20594	5.751710655	0.005831622	4.50E-04	0.011458257
SMART	SM00219:TyrKc	12	2.696629213	1.02E-05	282	81	10425	5.476753349	0.001882769	4.71E-04	0.012604076
INTERPRO	IPR001824:Tyrosine-protein kinase, receptor class III, conserved site	5	1.123595506	1.26E-05	434	8	20594	29.65725806	0.009806732	6.57E-04	0.019306576
UP_KEYWORDS	Tyrosine-protein kinase	12	2.696629213	1.39E-05	445	113	22680	5.412349607	0.00392817	2.19E-04	0.01836304
GOTERM_BP_DIRECT	GO:0007169~transmembrane receptor protein	12	2.696629213	1.47E-05	406	100	18082	5.344433498	0.03089981	0.003133807	0.025529209

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

	tyrosine kinase signaling pathway										
INTERPRO	IPR003598:Immunoglobulin subtype 2	18	4.04494382	1.57E-05	434	242	20594	3.529458811	0.012212507	7.68E-04	0.024071474
PIR_SUPERFAMILY	PIRSF000615:tyrosine-protein kinase, CSF-1/PDGF receptor type	5	1.123595506	2.34E-05	55	7	1807	23.46753247	0.001097919	0.001097919	0.022197505
INTERPRO	IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain	13	2.921348315	3.85E-05	434	139	20594	4.437920631	0.029620914	0.0015813	0.058893597
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	12	2.696629213	7.82E-05	387	121	17446	4.470754052	0.046111833	0.007837267	0.115475142
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	9	2.02247191	9.77E-05	406	65	18082	6.166654036	0.187868718	0.012166167	0.169133509
GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	8	1.797752809	1.78E-04	387	54	17446	6.678533831	0.1018095	0.01522197	0.262446633
UP_SEQ_FEATURE	domain:Ig-like C2-type 4	8	1.797752809	2.33E-04	402	56	18012	6.400852878	0.278732821	0.020214494	0.383330671
INTERPRO	IPR013783:Immunoglobulin-like fold	42	9.438202247	2.79E-04	434	1099	20594	1.813437436	0.195967893	0.010846551	0.426426978
SMART	SM00408:IGc2	18	4.04494382	2.93E-04	282	242	10425	2.749692281	0.052822013	0.009003929	0.362318228
GOTERM_MF_DIRECT	GO:0005021~vascular endothelial growth factor-activated receptor activity	4	0.898876404	3.52E-04	387	7	17446	25.76005906	0.191593954	0.023355256	0.519200275
UP_SEQ_FEATURE	domain:Ig-like C2-type 5	7	1.573033708	6.53E-04	402	48	18012	6.53420398	0.599755145	0.044751668	1.070546511
INTERPRO	IPR003599:Immunoglobulin subtype	24	5.393258427	6.67E-04	434	518	20594	2.198530328	0.406277196	0.021488377	1.016229564
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	8	1.797752809	0.003477765	402	88	18012	4.073270014	0.992435773	0.155005368	5.579494556
INTERPRO	IPR007110:Immunoglobulin-like domain	32	7.191011236	0.006928957	434	920	20594	1.650490884	0.99561844	0.147614329	10.09286288
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	11	2.471910112	0.00837332	406	183	18082	2.677084175	0.999999983	0.257965788	13.5516713

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR013098:Immunoglobulin I-set	9	2.02247191	0.012672488	434	147	20594	2.90520079	0.999952769	0.225390605	17.72870622
SMART	SM00409:IG	24	5.393258427	0.012725625	282	518	10425	1.712807032	0.906458352	0.179175298	14.65558456
GOTERM_BP_DIRECT	GO:0010863~positive regulation of phospholipase C activity	3	0.674157303	0.012814319	406	8	18082	16.70135468	1	0.332218325	20.01741722
GOTERM_BP_DIRECT	GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling	6	1.348314607	0.014231808	406	64	18082	4.17533867	1	0.345477897	21.98326659
UP_KEYWORDS	Proto-oncogene	7	1.573033708	0.015845223	445	103	22680	3.463728592	0.989284634	0.104735445	19.07528585
INTERPRO	IPR017441:Protein kinase, ATP binding site	16	3.595505618	0.020283216	434	394	20594	1.926969052	0.999999888	0.299279107	26.91562803
UP_KEYWORDS	Kinase	23	5.168539326	0.022807965	445	707	22680	1.658026477	0.998573418	0.127602288	26.34181659
UP_SEQ_FEATURE	domain:Ig-like C2-type 6	4	0.898876404	0.031055605	402	31	18012	5.781415503	1	0.609790578	40.54187472
GOTERM_BP_DIRECT	GO:0043552~positive regulation of phosphatidylinositol 3-kinase activity	4	0.898876404	0.031537882	406	31	18082	5.746702686	1	0.523641319	42.59236611
GOTERM_BP_DIRECT	GO:0048015~phosphatidylinositol-mediated signaling	4	0.898876404	0.046190694	406	36	18082	4.948549535	1	0.609750339	55.91394535
UP_SEQ_FEATURE	active site:Proton acceptor	24	5.393258427	0.047898298	402	710	18012	1.514568005	1	0.733761966	55.46402751
UP_SEQ_FEATURE	domain:Ig-like C2-type 7	3	0.674157303	0.048296378	402	16	18012	8.401119403	1	0.730033606	55.76989911
KEGG_PATHWAY	mmu04015:Rap1 signaling pathway	10	2.247191011	0.070072871	185	214	7691	1.942662288	0.999999345	0.447499304	59.64955253
GOTERM_MF_DIRECT	GO:0016301~kinase activity	22	4.943820225	0.074182957	387	674	17446	1.47145738	1	0.661315414	67.99981201
UP_KEYWORDS	Nucleotide-binding	44	9.887640449	0.075402972	445	1754	22680	1.27851588	1	0.297710781	64.61439308
INTERPRO	IPR000719:Protein kinase, catalytic domain	16	3.595505618	0.128718699	434	515	20594	1.474224867	1	0.761850647	87.85688281

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_KEYWORDS	Transferase	40	8.988764045	0.132270956	445	1654	22680	1.232558455	1	0.411493535	84.74155228
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	17	3.820224719	0.134256619	387	531	17446	1.44324248	1	0.765729426	88.13016539
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	19	4.269662921	0.145886945	406	612	18082	1.382682958	1	0.891753981	93.48467041
INTERPRO	IPR011009:Protein kinase-like domain	16	3.595505618	0.195852272	434	556	20594	1.36551404	1	0.871398966	96.43966513
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	17	3.820224719	0.223321264	406	576	18082	1.31445847	1	0.955406504	98.74360523
UP_SEQ_FEATURE	domain:Protein kinase	15	3.370786517	0.235208356	402	502	18012	1.338823809	1	0.991932063	98.79540077
KEGG_PATHWAY	mmu04014:Ras signaling pathway	8	1.797752809	0.308581523	185	229	7691	1.452330934	1	0.778379971	99.00467372
UP_SEQ_FEATURE	binding site:ATP	16	3.595505618	0.320275863	402	583	18012	1.229666419	1	0.99840943	99.82744909
UP_KEYWORDS	ATP-binding	30	6.741573034	0.347358386	445	1363	22680	1.121781925	1	0.698777472	99.64989226
GOTERM_MF_DIRECT	GO:0016740~transferase activity	35	7.865168539	0.418353078	387	1472	17446	1.071877458	1	0.977759579	99.96680771
GOTERM_MF_DIRECT	GO:0005524~ATP binding	34	7.640449438	0.551980818	387	1507	17446	1.017069352	1	0.993601554	99.99929978
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	42	9.438202247	0.642452402	387	1936	17446	0.977977449	1	0.997994898	99.99997505
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	21	4.719101124	0.65870256	402	963	18012	0.977077231	1	0.999998187	99.99999798

Annotation Cluster 15 **Enrichment Score: 2.5365441682276826**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:TSP N-terminal	5	1.123595506	7.19E-04	402	19	18012	11.79104478	0.635435439	0.046913942	1.179065405
SMART	SM00210:TSPN	5	1.123595506	0.002575579	282	22	10425	8.401837524	0.379417537	0.051630186	3.140710007
INTERPRO	IPR013320:Concanavalin A-like lectin/glucanase, subgroup	12	2.696629213	0.005223947	434	211	20594	2.698669928	0.983270744	0.11999803	7.701661072

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR001791:Laminin G domain	6	1.348314607	0.007378033	434	58	20594	4.908787542	0.996922403	0.148414801	10.71296893

Annotation Cluster 16 **Enrichment Score: 2.359676200880176**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000859:CUB domain	7	1.573033708	0.001114517	434	56	20594	5.931451613	0.58143501	0.031741722	1.691860075
SMART	SM00042:CUB	7	1.573033708	0.002364072	282	51	10425	5.074050897	0.354590983	0.053262939	2.886252812
UP_SEQ_FEATURE	domain:CUB 2	5	1.123595506	0.011756389	402	40	18012	5.600746269	0.999999937	0.377316838	17.70731141
UP_SEQ_FEATURE	domain:CUB 1	5	1.123595506	0.011756389	402	40	18012	5.600746269	0.999999937	0.377316838	17.70731141

Annotation Cluster 17 **Enrichment Score: 2.3565711912640457**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:EGF-like 1	13	2.921348315	6.81E-06	402	111	18012	5.247546054	0.009508256	7.96E-04	0.01122915
UP_SEQ_FEATURE	domain:EGF-like 4	7	1.573033708	0.001353639	402	55	18012	5.702578019	0.850294752	0.07607892	2.207517153
UP_SEQ_FEATURE	domain:EGF-like 7	5	1.123595506	0.002113219	402	25	18012	8.96119403	0.94848425	0.107806137	3.426108553
UP_SEQ_FEATURE	domain:EGF-like 8	5	1.123595506	0.002454072	402	26	18012	8.616532721	0.968090052	0.11978279	3.968288395
UP_SEQ_FEATURE	domain:EGF-like 2	8	1.797752809	0.002675735	402	84	18012	4.267235252	0.976632465	0.125547598	4.319341652
INTERPRO	IPR002049:EGF-like, laminin	5	1.123595506	0.007357341	434	37	20594	6.412380122	0.996871888	0.151920358	10.68448419
UP_SEQ_FEATURE	domain:EGF-like 6	5	1.123595506	0.009830372	402	38	18012	5.895522388	0.999999034	0.342761428	15.0240305
UP_SEQ_FEATURE	domain:EGF-like 9	4	0.898876404	0.013936214	402	23	18012	7.792342635	0.999999997	0.412443985	20.64811226
SMART	SM00180:EGF_Lam	5	1.123595506	0.014024904	282	35	10425	5.281155015	0.926683809	0.159869678	16.03500337

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_SEQ_FEATURE	domain:EGF-like 5	5	1.123595506	0.015072945	402	43	18012	5.209996529	0.999999999	0.428988572	22.14223015
UP_SEQ_FEATURE	domain:EGF-like 3	6	1.348314607	0.015715322	402	66	18012	4.073270014	1	0.434153185	22.97484162
UP_KEYWORDS	Laminin EGF-like domain	3	0.674157303	0.122768506	445	31	22680	4.932221819	1	0.391034772	82.37252828

Annotation Cluster 18 **Enrichment Score: 2.12152079505643**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0035924~cellular response to vascular endothelial growth factor stimulus	6	1.348314607	1.06E-04	406	22	18082	12.14643977	0.201565287	0.011777573	0.182945226
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth factor receptor signaling pathway	3	0.674157303	0.038123322	406	14	18082	9.543631246	1	0.562868687	48.99060286
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	0.674157303	0.107168216	406	25	18082	5.344433498	1	0.834870319	85.95909311

Annotation Cluster 19 **Enrichment Score: 2.08042287004266**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Developmental protein	37	8.314606742	2.20E-04	445	976	22680	1.93212378	0.060557518	0.002970279	0.291051178
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	36	8.08988764	0.009401255	406	1029	18082	1.558143877	0.999999998	0.277005771	15.09078087
UP_KEYWORDS	Differentiation	16	3.595505618	0.277491255	445	646	22680	1.262323025	1	0.625436041	98.65262268

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

Annotation Cluster 20				Enrichment Score: 1.9740279921456423							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
UP_KEYWORDS	Zymogen	14	3.146067416	3.11E-04	445	213	22680	3.349897136	0.084563895	0.004008069	0.411409762
UP_SEQ_FEATURE	propeptide:Activation peptide	9	2.02247191	4.38E-04	402	81	18012	4.978441128	0.459287636	0.035522423	0.720129819
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	14	3.146067416	9.12E-04	387	212	17446	2.976987958	0.423558456	0.041490196	1.33921312
UP_KEYWORDS	Protease	23	5.168539326	0.001120908	445	542	22680	2.162776235	0.272772897	0.013183841	1.475191735
GOTERM_BP_DIRECT	GO:0006508~proteolysis	25	5.617977528	0.003151504	406	582	18082	1.913099047	0.998793639	0.151178207	5.319874458
UP_SEQ_FEATURE	domain:Peptidase S1	9	2.02247191	0.003984918	402	114	18012	3.537313433	0.996294794	0.170224875	6.368270865
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	22	4.943820225	0.005557842	387	516	17446	1.922019911	0.965482886	0.148111817	7.908628405
UP_KEYWORDS	Serine protease	10	2.247191011	0.007212997	445	173	22680	2.946028447	0.872024271	0.060399453	9.14704673
GOTERM_MF_DIRECT	GO:0008236~serine-type peptidase activity	10	2.247191011	0.01049597	387	163	17446	2.765650513	0.99829309	0.225023697	14.442243
INTERPRO	IPR001314:Peptidase S1A, chymotrypsin-type	9	2.02247191	0.014702022	434	151	20594	2.828241829	0.999990531	0.245827902	20.27874507
UP_SEQ_FEATURE	active site:Charge relay system	11	2.471910112	0.016900817	402	205	18012	2.404222788	1	0.449779724	24.48949609
INTERPRO	IPR001254:Peptidase S1	9	2.02247191	0.020115993	434	160	20594	2.669153226	0.999999872	0.302811226	26.72451612
INTERPRO	IPR009003:Trypsin-like cysteine/serine peptidase domain	9	2.02247191	0.026004796	434	168	20594	2.542050691	0.999999999	0.337390736	33.18076597
SMART	SM00020:Tryp_SPc	9	2.02247191	0.063913773	282	158	10425	2.105777	0.999995063	0.457160224	55.83610355
UP_KEYWORDS	Hydrolase	37	8.314606742	0.266390182	445	1646	22680	1.145657843	1	0.611704508	98.35092797
INTERPRO	IPR018114:Peptidase S1, trypsin family, active site	5	1.123595506	0.32561564	434	137	20594	1.73181069	1	0.963424451	99.75899946

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	35	7.865168539	0.520797943	387	1533	17446	1.029226104	1	0.991584324	99.99810673

Annotation Cluster 21 **Enrichment Score: 1.6415986377900782**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Proteoglycan	8	1.797752809	2.51E-05	445	45	22680	9.060674157	0.007098367	3.75E-04	0.033233192
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...) (keratan sulfate)	3	0.674157303	0.001461382	402	3	18012	44.80597015	0.871310881	0.078741149	2.38124371
INTERPRO	IPR003591:Leucine-rich repeat, typical subtype	11	2.471910112	0.004021462	434	175	20594	2.982672811	0.957023155	0.099588256	5.97962689
INTERPRO	IPR000372:Leucine-rich repeat-containing N-terminal	6	1.348314607	0.005031279	434	53	20594	5.371880706	0.980539092	0.11933302	7.427747298
UP_SEQ_FEATURE	compositionally biased region:Cys-rich	9	2.02247191	0.010758438	402	135	18012	2.987064677	0.999999741	0.35983607	16.32708747
SMART	SM00013:LRRNT	6	1.348314607	0.01372013	282	53	10425	4.185066238	0.922369685	0.178480652	15.71328262
UP_SEQ_FEATURE	repeat:LRR 11	7	1.573033708	0.013752094	402	88	18012	3.564111262	0.999999996	0.416834553	20.40358542
SMART	SM00369:LRR_TYP	11	2.471910112	0.020071741	282	175	10425	2.323708207	0.976506803	0.208986524	22.18925499
INTERPRO	IPR001611:Leucine-rich repeat	12	2.696629213	0.021668609	434	259	20594	2.198530328	0.999999963	0.305126942	28.48110345
BIOCARTA	m_slrpPathway:Small Leucine-rich Proteoglycan (SLRP) molecules	3	0.674157303	0.024855146	57	6	1289	11.30701754	0.917235484	0.564205853	24.33340871
UP_SEQ_FEATURE	repeat:LRR 7	9	2.02247191	0.025318971	402	158	18012	2.552238806	1	0.566622731	34.4671335
UP_SEQ_FEATURE	repeat:LRR 10	7	1.573033708	0.027591144	402	103	18012	3.045065932	1	0.58996405	36.9397983
UP_SEQ_FEATURE	repeat:LRR 6	10	2.247191011	0.027688383	402	191	18012	2.345862311	1	0.583060749	37.04363633
UP_SEQ_FEATURE	repeat:LRR 12	6	1.348314607	0.031446561	402	79	18012	3.402985075	1	0.606727923	40.93599636

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_KEYWORDS	Leucine-rich repeat	11	2.471910112	0.045241484	445	275	22680	2.038651685	0.999998051	0.219703377	45.85435929
UP_SEQ_FEATURE	repeat:LRR 5	10	2.247191011	0.04617009	402	210	18012	2.133617626	1	0.727320792	54.11294824
UP_SEQ_FEATURE	repeat:LRR 9	7	1.573033708	0.057114635	402	123	18012	2.549933261	1	0.764615189	62.06029632
UP_SEQ_FEATURE	repeat:LRR 4	10	2.247191011	0.07003629	402	228	18012	1.965174129	1	0.816702911	69.77726862
UP_SEQ_FEATURE	repeat:LRR 8	7	1.573033708	0.079218376	402	134	18012	2.340610381	1	0.849965755	74.33641009
UP_SEQ_FEATURE	repeat:LRR 2	11	2.471910112	0.08754616	402	274	18012	1.798779824	1	0.869822867	77.90503297
UP_SEQ_FEATURE	repeat:LRR 1	11	2.471910112	0.08754616	402	274	18012	1.798779824	1	0.869822867	77.90503297
UP_SEQ_FEATURE	repeat:LRR 3	10	2.247191011	0.112530597	402	253	18012	1.770986962	1	0.923843235	86.01730508
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	4	0.898876404	0.2147843	434	76	20594	2.497453311	1	0.885892336	97.52732126
SMART	SM00082:LRRCT	4	0.898876404	0.329222415	282	75	10425	1.971631206	1	0.856876377	99.28531769

Annotation Cluster 22 **Enrichment Score: 1.6270706201910659**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	13	2.921348315	0.021922478	387	279	17446	2.100506608	0.999998467	0.350716757	27.94048874
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	14	3.146067416	0.022302559	431	316	19662	2.021116626	0.998971117	0.199014404	26.07823371
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	10	2.247191011	0.02688709	406	189	18082	2.356452159	1	0.486737684	37.62610913

Annotation Cluster 23 **Enrichment Score: 1.597922731370309**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_BP_DIRECT	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	7	1.573033708	3.14E-07	406	14	18082	22.26847291	6.68E-04	1.11E-04	5.44E-04
GOTERM_BP_DIRECT	GO:0019882~antigen processing and presentation	8	1.797752809	1.92E-04	406	54	18082	6.598066046	0.335380502	0.017605808	0.331782058
KEGG_PATHWAY	mmu04145:Phagosome	13	2.921348315	7.87E-04	185	171	7691	3.160518413	0.142946427	0.021795379	0.97835991
KEGG_PATHWAY	mmu05152:Tuberculosis	13	2.921348315	0.001015256	185	176	7691	3.070730958	0.180524944	0.021878377	1.260935163
GOTERM_CC_DIRECT	GO:0042613~MHC class II protein complex	4	0.898876404	0.001972677	431	12	19662	15.20649652	0.452427749	0.034806915	2.610664101
KEGG_PATHWAY	mmu05310:Asthma	5	1.123595506	0.002315575	185	24	7691	8.661036036	0.365157846	0.044421047	2.854549424
GOTERM_BP_DIRECT	GO:0048002~antigen processing and presentation of peptide antigen	3	0.674157303	0.00291425	406	4	18082	33.40270936	0.997997776	0.143873743	4.9288524
KEGG_PATHWAY	mmu05323:Rheumatoid arthritis	7	1.573033708	0.013471917	185	82	7691	3.548912327	0.929942809	0.153083108	15.58640744
GOTERM_BP_DIRECT	GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	3	0.674157303	0.016233459	406	9	18082	14.8456486	1	0.375543366	24.68185083
UP_KEYWORDS	MHC II	3	0.674157303	0.018710983	445	11	22680	13.89989785	0.995319089	0.114776441	22.14278667
INTERPRO	IPR014745:MHC class II, alpha/beta chain, N-terminal	3	0.674157303	0.021396169	434	11	20594	12.94134897	0.999999954	0.307337474	28.17574822
KEGG_PATHWAY	mmu05145:Toxoplasmosis	7	1.573033708	0.03967166	185	105	7691	2.771531532	0.999641681	0.341363498	39.69146077
KEGG_PATHWAY	mmu05416:Viral myocarditis	6	1.348314607	0.040369481	185	79	7691	3.157440985	0.999689262	0.332241074	40.23664073
UP_SEQ_FEATURE	domain:Ig-like C1-type	4	0.898876404	0.045506146	402	36	18012	4.978441128	1	0.729081452	53.58372668

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

KEGG_PATHWAY	mmu04612:Antigen processing and presentation	6	1.348314607	0.046197489	185	82	7691	3.041924852	0.999905842	0.356899311	44.6159139
UP_SEQ_FEATURE	region of interest:Connecting peptide	4	0.898876404	0.052066133	402	38	18012	4.71641791	1	0.750489342	58.57024099
INTERPRO	IPR011162:MHC classes I/II-like antigen recognition protein	5	1.123595506	0.057337563	434	69	20594	3.438522674	1	0.53045707	59.48555123
KEGG_PATHWAY	mmu05168:Herpes simplex infection	10	2.247191011	0.061578498	185	208	7691	1.998700624	0.99999611	0.432336686	54.79550635
KEGG_PATHWAY	mmu05140:Leishmaniasis	5	1.123595506	0.066505078	185	64	7691	3.247888514	0.999998613	0.443709145	57.67237543
KEGG_PATHWAY	mmu04672:Intestinal immune network for IgA production	4	0.898876404	0.078428545	185	42	7691	3.959330759	0.999999888	0.45973935	63.95218145
KEGG_PATHWAY	mmu05332:Graft-versus-host disease	4	0.898876404	0.12754388	185	52	7691	3.197920998	1	0.577966824	81.8138901
KEGG_PATHWAY	mmu05330:Allograft rejection	4	0.898876404	0.1496399	185	56	7691	2.969498069	1	0.60719114	86.80028782
INTERPRO	IPR003597:Immunoglobulin C1-set	5	1.123595506	0.163618228	434	101	20594	2.349089748	1	0.825226931	93.50365824
KEGG_PATHWAY	mmu04940:Type I diabetes mellitus	4	0.898876404	0.184832232	185	62	7691	2.682127289	1	0.66127366	92.21508564
KEGG_PATHWAY	mmu05164:Influenza A	7	1.573033708	0.226261131	185	171	7691	1.701817607	1	0.697930228	95.94242458
KEGG_PATHWAY	mmu05320:Autoimmune thyroid disease	4	0.898876404	0.241020573	185	71	7691	2.342139322	1	0.699160312	96.81012054
GOTERM_MF_DIRECT	GO:0042605~peptide antigen binding	3	0.674157303	0.26259216	387	45	17446	3.005340224	1	0.93050341	98.89244109
INTERPRO	IPR003006:Immunoglobulin/major histocompatibility complex, conserved site	4	0.898876404	0.265195805	434	85	20594	2.233017078	1	0.933070369	99.10418696
SMART	SM00407:IGc1	5	1.123595506	0.27156263	282	98	10425	1.886126791	1	0.821658764	98.01726246
KEGG_PATHWAY	mmu05321:Inflammatory bowel disease (IBD)	3	0.674157303	0.414368966	185	59	7691	2.113879982	1	0.836043114	99.87496094

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

KEGG_PATHWAY	mmu05166:HTLV-I infection	7	1.573033708	0.65266016	185	276	7691	1.054386996	1	0.936927697	99.99981682

Annotation Cluster 24 **Enrichment Score: 1.58788806428931**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0001725~stress fiber	9	2.02247191	1.03E-04	431	67	19662	6.127991135	0.031053841	0.002250765	0.138466474
UP_KEYWORDS	Calmodulin-binding	5	1.123595506	0.289753617	445	139	22680	1.833319861	1	0.636572002	98.92606469
GOTERM_MF_DIRECT	GO:0005516~calmodulin binding	5	1.123595506	0.575018408	387	182	17446	1.238464378	1	0.995147858	99.99967914

Annotation Cluster 25 **Enrichment Score: 1.5048163336056697**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR014715:Fibrinogen, alpha/beta/gamma chain, C-terminal globular, subdomain 2	4	0.898876404	0.010562919	434	22	20594	8.627565982	0.999749867	0.196075974	14.99744055
SMART	SM00186:FBG	4	0.898876404	0.020423836	282	22	10425	6.721470019	0.978017928	0.201132736	22.53449542
INTERPRO	IPR014716:Fibrinogen, alpha/beta/gamma chain, C-terminal globular, subdomain 1	4	0.898876404	0.022499494	434	29	20594	6.545050056	0.999999981	0.309449875	29.40489888
INTERPRO	IPR002181:Fibrinogen, alpha/beta/gamma chain, C-terminal globular domain	4	0.898876404	0.029168827	434	32	20594	5.931451613	1	0.35892557	36.42611169
INTERPRO	IPR020837:Fibrinogen, conserved site	3	0.674157303	0.048712747	434	17	20594	8.373814042	1	0.507931209	53.42692908
UP_SEQ_FEATURE	domain:Fibrinogen C-terminal	3	0.674157303	0.135658305	402	29	18012	4.63510036	1	0.952671832	90.95091729

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

Annotation Cluster 26 **Enrichment Score: 1.4502255705010767**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0005044~scavenger receptor activity	7	1.573033708	6.32E-04	387	48	17446	6.57418174	0.317206202	0.03129666	0.929512687
INTERPRO	IPR001190:Speract/scavenger receptor	3	0.674157303	0.116647321	434	28	20594	5.084101382	1	0.749382845	85.01115156
INTERPRO	IPR017448:Speract/scavenger receptor-related	3	0.674157303	0.123621235	434	29	20594	4.908787542	1	0.756285562	86.72312223
SMART	SM00202:SR	3	0.674157303	0.173675453	282	28	10425	3.960866261	1	0.703872792	90.56294245

Annotation Cluster 27 **Enrichment Score: 1.4088413156006931**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0019864~IgG binding	3	0.674157303	0.009526094	387	7	17446	19.3200443	0.996915425	0.214071319	13.19414971
GOTERM_BP_DIRECT	GO:0045576~mast cell activation	3	0.674157303	0.033159727	406	13	18082	10.27775673	1	0.530331059	44.23479744
GOTERM_BP_DIRECT	GO:0006911~phagocytosis, engulfment	4	0.898876404	0.079426937	406	45	18082	3.958839628	1	0.766867054	76.14735563
GOTERM_BP_DIRECT	GO:0050766~positive regulation of phagocytosis	4	0.898876404	0.092287125	406	48	18082	3.711412151	1	0.80273145	81.30508808

Annotation Cluster 28 **Enrichment Score: 1.3427894755428242**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SMART	SM00327:VWA	7	1.573033708	0.012036208	282	71	10425	3.644740785	0.893563591	0.184256436	13.91521537
INTERPRO	IPR002035:von Willebrand factor, type A	7	1.573033708	0.01817046	434	99	20594	3.355164549	0.999999397	0.288935039	24.46646056
UP_SEQ_FEATURE	domain:VWFA 1	3	0.674157303	0.048296378	402	16	18012	8.401119403	1	0.730033606	55.76989911
UP_SEQ_FEATURE	domain:VWFA 2	3	0.674157303	0.053948633	402	17	18012	7.906935909	1	0.756754814	59.90545923

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_SEQ_FEATURE	domain:VWFA	3	0.674157303	0.339079856	402	54	18012	2.489220564	1	0.998736104	99.8913236

Annotation Cluster 29 **Enrichment Score: 1.233977855072754**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:VWFC	3	0.674157303	0.053948633	402	17	18012	7.906935909	1	0.756754814	59.90545923
INTERPRO	IPR001007:von Willebrand factor, type C	4	0.898876404	0.0546662	434	41	20594	4.629425649	1	0.524868229	57.6927004
SMART	SM00214:VWC	4	0.898876404	0.067354575	282	35	10425	4.224924012	0.999997502	0.458974978	57.80334436

Annotation Cluster 30 **Enrichment Score: 1.2251359177671484**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	6	1.348314607	1.64E-04	406	24	18082	11.13423645	0.295434656	0.015791003	0.284449308
UP_KEYWORDS	Collagen degradation	3	0.674157303	0.042838913	445	17	22680	8.994051553	0.999996021	0.212684082	44.0207352
INTERPRO	IPR024079:Metallopeptidase, catalytic domain	6	1.348314607	0.053900809	434	97	20594	2.935151314	1	0.525785501	57.16551253
UP_KEYWORDS	Metalloprotease	7	1.573033708	0.062564566	445	143	22680	2.494853461	0.999999989	0.263472224	57.51976363
GOTERM_MF_DIRECT	GO:0008237~metallopeptidase activity	8	1.797752809	0.065347445	387	160	17446	2.254005168	1	0.630489058	63.17595878
INTERPRO	IPR021190:Peptidase M10A	3	0.674157303	0.083512869	434	23	20594	6.189340813	1	0.638158937	73.66856832
INTERPRO	IPR001818:Peptidase M10, metallopeptidase	3	0.674157303	0.083512869	434	23	20594	6.189340813	1	0.638158937	73.66856832
INTERPRO	IPR006026:Peptidase, metallopeptidase	3	0.674157303	0.123621235	434	29	20594	4.908787542	1	0.756285562	86.72312223
GOTERM_MF_DIRECT	GO:0004222~metalloendopeptidase activity	6	1.348314607	0.137438234	387	123	17446	2.199029432	1	0.768677564	88.75893314
SMART	SM00235:ZnMc	3	0.674157303	0.18341087	282	29	10425	3.824284666	1	0.713347654	91.85018438

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_SEQ_FEATURE	short sequence motif:Cysteine switch	3	0.674157303	0.215301564	402	39	18012	3.446613088	1	0.988583223	98.16029284
UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	5	1.123595506	0.27360608	402	119	18012	1.882603788	1	0.995769582	99.48455832

Annotation Cluster 31 **Enrichment Score: 1.221102979152116**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:TSP type-1	3	0.674157303	0.048296378	402	16	18012	8.401119403	1	0.730033606	55.76989911
INTERPRO	IPR000884:Thrombospondin, type 1 repeat	5	1.123595506	0.050152532	434	66	20594	3.594819159	1	0.512077009	54.49392456
SMART	SM00209:TSP1	5	1.123595506	0.08963624	282	63	10425	2.933975008	0.999999972	0.530163857	68.71522647

Annotation Cluster 32 **Enrichment Score: 1.2000886019689037**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Metal-binding	89	20	0.003112431	445	3395	22680	1.336082474	0.587413217	0.031123541	4.046648442
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	82	18.42696629	0.205245361	387	3355	17446	1.101808786	1	0.881713549	96.64897211
UP_KEYWORDS	Zinc	44	9.887640449	0.392971612	445	2099	22680	1.068373918	1	0.737479188	99.86595833

Annotation Cluster 33 **Enrichment Score: 1.1928792488817384**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0030246~carbohydrate binding	14	3.146067416	0.001824712	387	229	17446	2.755988852	0.668170019	0.070903035	2.663754752
INTERPRO	IPR016186:C-type lectin-like	8	1.797752809	0.025928719	434	137	20594	2.770897104	0.999999999	0.342114446	33.10086066
INTERPRO	IPR016187:C-type lectin fold	8	1.797752809	0.033837993	434	145	20594	2.618020022	1	0.392175698	40.9471277

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_KEYWORDS	Lectin	8	1.797752809	0.054381697	445	173	22680	2.356822758	0.999999873	0.243157718	52.33451983
INTERPRO	IPR001304:C-type lectin	6	1.348314607	0.120872992	434	124	20594	2.296045786	1	0.757580336	86.07155443
SMART	SM00034:CLECT	6	1.348314607	0.242721431	282	124	10425	1.788778312	1	0.79957734	96.79424289
INTERPRO	IPR018378:C-type lectin, conserved site	3	0.674157303	0.291111341	434	51	20594	2.791271347	1	0.947808684	99.48285655
UP_SEQ_FEATURE	domain:C-type lectin	4	0.898876404	0.385156161	402	100	18012	1.792238806	1	0.999396108	99.96696775
Annotation Cluster 34				**Enrichment Score: 1.1849416718469874**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	GO:0035023~regulation of Rho protein signal transduction	6	1.348314607	0.02921372	406	77	18082	3.470411362	1	0.504090628	40.15908008
UP_KEYWORDS	Guanine-nucleotide releasing factor	7	1.573033708	0.047052642	445	133	22680	2.682436428	0.999998863	0.220314489	47.19973767
INTERPRO	IPR000219:Dbl homology (DH) domain	5	1.123595506	0.054884301	434	68	20594	3.489089184	1	0.520381285	57.84180998
GOTERM_MF_DIRECT	GO:0005085~guanyl-nucleotide exchange factor activity	8	1.797752809	0.058655897	387	156	17446	2.311800172	1	0.598578214	59.08041151
GOTERM_MF_DIRECT	GO:0005089~Rho guanyl-nucleotide exchange factor activity	5	1.123595506	0.081439092	387	74	17446	3.04595293	1	0.672213201	71.51363795
SMART	SM00325:RhoGEF	5	1.123595506	0.097838488	282	65	10425	2.843698854	0.999999995	0.519348212	72.02979531
UP_SEQ_FEATURE	domain:DH	4	0.898876404	0.143924575	402	59	18012	3.037692891	1	0.959397118	92.27624954
Annotation Cluster 35				**Enrichment Score: 1.1241069565118231**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR011993:Pleckstrin homology-like domain	17	3.820224719	0.01330597	434	409	20594	1.972316429	0.999971389	0.23013722	18.53272406
INTERPRO	IPR001849:Pleckstrin homology domain	11	2.471910112	0.051172552	434	262	20594	1.99224329	1	0.513116381	55.23596507
SMART	SM00233:PH	11	2.471910112	0.146080939	282	253	10425	1.607308048	1	0.647742383	85.83024726
UP_SEQ_FEATURE	domain:PH	7	1.573033708	0.320549435	402	208	18012	1.507893226	1	0.998295519	99.82859

Annotation Cluster 36				Enrichment Score: 1.104322357699511							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
INTERPRO	IPR004021:HIN-200/IF120x	4	0.898876404	9.92E-04	434	10	20594	18.98064516	0.539456256	0.029380795	1.507601316
UP_SEQ_FEATURE	domain:HIN-200	3	0.674157303	0.009641235	402	7	18012	19.20255864	0.999998738	0.345874495	14.75614384
INTERPRO	IPR004020:DAPIN domain	4	0.898876404	0.018572915	434	27	20594	7.029868578	0.999999562	0.288591142	24.93883292
SMART	SM01289:SM01289	4	0.898876404	0.035165574	282	27	10425	5.476753349	0.998670261	0.307835632	35.78721047
GOTERM_BP_DIRECT	GO:0035458~cellular response to interferon-beta	4	0.898876404	0.063619933	406	41	18082	4.345067884	1	0.700739984	67.96762983
UP_SEQ_FEATURE	domain:DAPIN	3	0.674157303	0.120648182	402	27	18012	4.978441128	1	0.934855215	87.98218453
GOTERM_MF_DIRECT	GO:0001047~core promoter binding	4	0.898876404	0.230877426	387	75	17446	2.404272179	1	0.906187985	97.93600079
GOTERM_MF_DIRECT	GO:0001078~transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	5	1.123595506	0.319619653	387	129	17446	1.747290828	1	0.958676923	99.66300471
GOTERM_MF_DIRECT	GO:0008134~transcription factor binding	10	2.247191011	0.346115218	387	342	17446	1.318131677	1	0.964292216	99.81266675
GOTERM_MF_DIRECT	GO:0003690~double-stranded DNA binding	4	0.898876404	0.582231336	387	136	17446	1.325885393	1	0.995389722	99.99975087

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_CC_DIRECT	GO:0005730~nucleolus	9	2.02247191	0.998271409	431	842	19662	0.487619247	1	0.999999905	100

Annotation Cluster 37 **Enrichment Score: 1.1034380306263285**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0038083~peptidyl-tyrosine autophosphorylation	5	1.123595506	0.013067194	406	41	18082	5.431334855	1	0.333587669	20.37150445
INTERPRO	IPR000980:SH2 domain	7	1.573033708	0.032201913	434	113	20594	2.939480445	1	0.382657238	39.3983189
UP_KEYWORDS	SH2 domain	6	1.348314607	0.05554679	445	105	22680	2.912359551	0.999999911	0.24409055	53.10690161
UP_SEQ_FEATURE	domain:SH2	6	1.348314607	0.056655555	402	93	18012	2.890707752	1	0.767805047	61.75472968
GOTERM_CC_DIRECT	GO:0031234~extrinsic component of cytoplasmic side of plasma membrane	5	1.123595506	0.06163417	431	68	19662	3.354374232	0.999999996	0.338220799	57.35398564
GOTERM_MF_DIRECT	GO:0004715~non-membrane spanning protein tyrosine kinase activity	4	0.898876404	0.077185077	387	45	17446	4.007120299	1	0.6680148	69.49994345
SMART	SM00252:SH2	5	1.123595506	0.301815192	282	103	10425	1.794567238	1	0.850282665	98.82694926
SMART	SM00326:SH3	5	1.123595506	0.782409784	282	197	10425	0.938276272	1	0.998586457	99.99999936

Annotation Cluster 38 **Enrichment Score: 1.0767404003528633**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR013128:Peptidase C1A, papain	4	0.898876404	0.018572915	434	27	20594	7.029868578	0.999999562	0.288591142	24.93883292
INTERPRO	IPR013201:Proteinase inhibitor I29, cathepsin propeptide	3	0.674157303	0.059597986	434	19	20594	7.492359932	1	0.538855727	60.94687946

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

INTERPRO	IPR025660:Cysteine peptidase, histidine active site	3	0.674157303	0.071224775	434	21	20594	6.778801843	1	0.594109103	67.716358
INTERPRO	IPR000668:Peptidase C1A, papain C-terminal	3	0.674157303	0.083512869	434	23	20594	6.189340813	1	0.638158937	73.66856832
SMART	SM00848:SM00848	3	0.674157303	0.09166763	282	19	10425	5.837066069	0.999999981	0.52341877	69.5681531
SMART	SM00645:Pept_C1	3	0.674157303	0.126586655	282	23	10425	4.821924144	1	0.604408514	81.26454206
GOTERM_MF_DIRECT	GO:0008234~cysteine-type peptidase activity	5	1.123595506	0.379941835	387	141	17446	1.598585226	1	0.972906516	99.91457277

Annotation Cluster 39 **Enrichment Score: 1.067087143462728**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	4	0.898876404	0.026841998	434	31	20594	6.122788762	0.999999999	0.34076055	34.05422649
INTERPRO	IPR000203:GPS domain	4	0.898876404	0.029168827	434	32	20594	5.931451613	1	0.35892557	36.42611169
SMART	SM00303:GPS	4	0.898876404	0.046035766	282	30	10425	4.929078014	0.99983653	0.368014354	44.1872181
INTERPRO	IPR000832:GPCR, family 2, secretin-like	4	0.898876404	0.072189209	434	46	20594	4.126227209	1	0.593545061	68.22552281
INTERPRO	IPR017981:GPCR, family 2-like	4	0.898876404	0.122674724	434	58	20594	3.272525028	1	0.758203033	86.50200512
UP_SEQ_FEATURE	domain:GPS	3	0.674157303	0.151053693	402	31	18012	4.336061627	1	0.964113707	93.27057945
GOTERM_MF_DIRECT	GO:0004888~transmembrane signaling receptor activity	7	1.573033708	0.703399546	387	316	17446	0.998609885	1	0.99908012	99.99999842

Annotation Cluster 40 **Enrichment Score: 1.003615687057064**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

GOTERM_BP_DIRECT	GO:0050830~defense response to Gram-positive bacterium	7	1.573033708	0.018128651	406	93	18082	3.352243233	1	0.401004024	27.15563902
GOTERM_BP_DIRECT	GO:0050829~defense response to Gram-negative bacterium	4	0.898876404	0.130306537	406	56	18082	3.181210415	1	0.871255516	91.08948768
UP_KEYWORDS	Antimicrobial	4	0.898876404	0.412877527	445	119	22680	1.713152677	1	0.750298255	99.91382978

Annotation Cluster 41 **Enrichment Score: 1.001968264227595**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	6	1.348314607	0.010956572	406	60	18082	4.453694581	1	0.302916689	17.37026254
GOTERM_BP_DIRECT	GO:0006897~endocytosis	7	1.573033708	0.220875841	406	181	18082	1.722423319	1	0.954467923	98.67330666
UP_KEYWORDS	Endocytosis	4	0.898876404	0.407635774	445	118	22680	1.72767092	1	0.747656088	99.90305872

Annotation Cluster 42 **Enrichment Score: 1.0018184126016334**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0017144~drug metabolic process	5	1.123595506	5.91E-04	406	18	18082	12.37137384	0.716207448	0.039815103	1.01933854
KEGG_PATHWAY	mmu00982:Drug metabolism - cytochrome P450	5	1.123595506	0.072772809	185	66	7691	3.149467649	0.99999963	0.446981721	61.08891424
GOTERM_MF_DIRECT	GO:0004497~monooxygenase activity	5	1.123595506	0.217239229	387	108	17446	2.087041822	1	0.893697211	97.32358794
UP_KEYWORDS	Microsome	5	1.123595506	0.259365294	445	132	22680	1.930541369	1	0.608212991	98.12894866
UP_KEYWORDS	Monooxygenase	5	1.123595506	0.263669814	445	133	22680	1.91602602	1	0.611260286	98.26802878
GOTERM_CC_DIRECT	GO:0031090~organelle membrane	4	0.898876404	0.338586084	431	94	19662	1.941254875	1	0.777080939	99.60650878

Table S1B: Go term analysis of genes expressed in the whole muscle but not in the myofiber

UP_KEYWORDS	NADP	5	1.123595506	0.448563813	445	175	22680	1.456179775	1	0.781927707	99.96246132

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* GO term analysis of genes not expressed in the myofiber but found in the whole muscle, defined as having a reads per million (RPM) value equal to or greater than 10 in the whole muscle and 0 in the single myofiber. We Used DAVID 6.8 online functional annotation tool with the ENSEMBL_GENE_ID identifier and with a classification stringency of medium (1).

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000029314	1-acylglycerol-3-phosphate O-acyltransferase 9(Agpat9)
ENSMUSG00000054027	5'-nucleotidase domain containing 3(Nt5dc3)
ENSMUSG00000025648	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4(Pfkfb4)
ENSMUSG00000040407	A kinase (PRKA) anchor protein (yotiao) 9(Akap9)
ENSMUSG00000031448	ADP-ribosylhydrolase like 1(Adprhl1)
ENSMUSG00000030996	ADP-ribosyltransferase 1(Art1)
ENSMUSG00000029313	AF4/FMR2 family, member 1(Aff1)
ENSMUSG00000019947	AT rich interactive domain 5B (MRF1-like)(Arid5b)
ENSMUSG00000064357	ATP synthase F0 subunit 6(ATP6)
ENSMUSG00000022956	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit(Atp5o)
ENSMUSG00000050856	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E(Atp5k)
ENSMUSG00000030249	ATP-binding cassette, sub-family C (CFTR/MRP), member 9(Abcc9)
ENSMUSG00000019943	ATPase, Ca++ transporting, plasma membrane 1(Atp2b1)
ENSMUSG00000007097	ATPase, Na+/K+ transporting, alpha 2 polypeptide(Atp1a2)
ENSMUSG00000037685	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1(Atp8a1)
ENSMUSG00000061132	B cell linker(Blnk)
ENSMUSG00000020423	B cell translocation gene 2, anti-proliferative(Btg2)
ENSMUSG00000049658	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB(Bdp1)
ENSMUSG00000025612	BTB and CNC homology 1, basic leucine zipper transcription factor 1(Bach1)
ENSMUSG00000040794	C1q and tumor necrosis factor related protein 4(C1qtnf4)
ENSMUSG00000024059	CAP-GLY domain containing linker protein family, member 4(Clip4)
ENSMUSG00000071637	CCAAT/enhancer binding protein (C/EBP), delta(Cebpd)
ENSMUSG00000046186	CD109 antigen(Cd109)
ENSMUSG00000047139	CD24a antigen(Cd24a)
ENSMUSG00000004096	CWC15 spliceosome-associated protein(Cwc15)
ENSMUSG00000027313	ChaC, cation transport regulator 1(Chac1)
ENSMUSG00000020075	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21(Ddx21)
ENSMUSG00000020719	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5(Ddx5)
ENSMUSG00000032097	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6(Ddx6)
ENSMUSG00000000787	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked(Ddx3x)
ENSMUSG00000019362	DNA segment, Chr 8, ERATO Doi 738, expressed(D8Ertd738e)
ENSMUSG00000025408	DNA-damage inducible transcript 3(Ddit3)
ENSMUSG00000061589	DOT1-like, histone H3 methyltransferase (S. cerevisiae)(Dot1l)
ENSMUSG00000014905	DnaJ heat shock protein family (Hsp40) member B9(Dnajb9)
ENSMUSG00000032560	DnaJ heat shock protein family (Hsp40) member C13(Dnajc13)
ENSMUSG00000028967	ERBB receptor feedback inhibitor 1(Errfi1)
ENSMUSG00000025932	EYA transcriptional coactivator and phosphatase 1(Eya1)
ENSMUSG00000047648	F-box protein 30(Fbxo30)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000022358	F-box protein 32(Fbxo32)
ENSMUSG00000003545	FBJ osteosarcoma oncogene B(Fosb)
ENSMUSG00000021250	FBJ osteosarcoma oncogene(Fos)
ENSMUSG00000038274	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)(Fau)
ENSMUSG00000028214	GTP binding protein (gene overexpressed in skeletal muscle)(Gem)
ENSMUSG00000037580	GTP cyclohydrolase 1(Gch1)
ENSMUSG00000016559	H3 histone, family 3B(H3f3b)
ENSMUSG00000025261	HECT, UBA and WWE domain containing 1(Huwe1)
ENSMUSG00000040167	IKAROS family zinc finger 5(Ikzf5)
ENSMUSG00000034154	INO80 complex subunit(Ino80)
ENSMUSG00000028530	Janus kinase 1(Jak1)
ENSMUSG00000101609	KCNQ1 overlapping transcript 1(Kcnq1ot1)
ENSMUSG00000018476	KDM1 lysine (K)-specific demethylase 6B(Kdm6b)
ENSMUSG00000003032	Kruppel-like factor 4 (gut)(Klf4)
ENSMUSG00000005148	Kruppel-like factor 5(Klf5)
ENSMUSG00000000078	Kruppel-like factor 6(Klf6)
ENSMUSG00000055553	KxDL motif containing 1(Kxd1)
ENSMUSG00000037736	LIM and calponin homology domains 1(Limch1)
ENSMUSG00000016239	LON peptidase N-terminal domain and ring finger 3
ENSMUSG00000039108	LSM family member 14B(Lsm14b)
ENSMUSG00000029823	LUC7-like 2 (S. cerevisiae)(Luc7l2)
ENSMUSG00000033499	La ribonucleoprotein domain family, member 4B(Larp4b)
ENSMUSG00000032688	MALT1 paracaspase(Malt1)
ENSMUSG00000006024	N-ethylmaleimide sensitive fusion protein attachment protein alpha(Napa)
ENSMUSG00000027438	N-ethylmaleimide sensitive fusion protein attachment protein beta(Napb)
ENSMUSG00000020936	N-myristoyltransferase 1(Nmt1)
ENSMUSG00000078572	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 8(Ndufaf8)
ENSMUSG00000036199	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13(Ndufa13)
ENSMUSG00000014294	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2(Ndufa2)
ENSMUSG00000035674	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3(Ndufa3)
ENSMUSG00000022450	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)(Ndufa6)
ENSMUSG00000041881	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)(Ndufa7)
ENSMUSG00000037152	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1(Ndufc1)
ENSMUSG00000024038	NADH dehydrogenase (ubiquinone) flavoprotein 3(Ndufv3)
ENSMUSG00000064341	NADH dehydrogenase subunit 1(ND1)
ENSMUSG00000064345	NADH dehydrogenase subunit 2(ND2)
ENSMUSG00000064363	NADH dehydrogenase subunit 4(ND4)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000064368	NADH dehydrogenase subunit 6(ND6)
ENSMUSG00000001056	NHP2 ribonucleoprotein(Nhp2)
ENSMUSG00000026020	NOP58 ribonucleoprotein(Nop58)
ENSMUSG00000024413	Niemann-Pick type C1(Npc1)
ENSMUSG00000022141	Nipped-B homolog (Drosophila)(Nipbl)
ENSMUSG00000043415	OTU domain containing 1(Otud1)
ENSMUSG00000027108	Obg-like ATPase 1(Ola1)
ENSMUSG00000021493	PDZ and LIM domain 7(Pdlim7)
ENSMUSG00000025340	RAB guanine nucleotide exchange factor (GEF) 1(Rabgef1)
ENSMUSG00000031504	RAB20, member RAS oncogene family(Rab20)
ENSMUSG00000020132	RAB21, member RAS oncogene family(Rab21)
ENSMUSG00000039318	RAB3 GTPase activating protein subunit 2(Rab3gap2)
ENSMUSG00000030643	RAB30, member RAS oncogene family(Rab30)
ENSMUSG00000064147	RAB44, member RAS oncogene family(Rab44)
ENSMUSG00000003226	RAN binding protein 2(Ranbp2)
ENSMUSG00000032238	RAR-related orphan receptor alpha(Rora)
ENSMUSG00000043644	RIKEN cDNA 0610009L18 gene(0610009L18Rik)
ENSMUSG00000039195	RIKEN cDNA 1110008P14 gene(1110008P14Rik)
ENSMUSG00000022507	RIKEN cDNA 1810013L24 gene(1810013L24Rik)
ENSMUSG00000021458	RIKEN cDNA 2010111I01 gene(2010111I01Rik)
ENSMUSG00000028396	RIKEN cDNA 2310002L09 gene(2310002L09Rik)
ENSMUSG00000079283	RIKEN cDNA 2310009B15 gene(2310009B15Rik)
ENSMUSG00000062619	RIKEN cDNA 2310039H08 gene(2310039H08Rik)
ENSMUSG00000058833	RIKEN cDNA 2810428I15 gene(2810428I15Rik)
ENSMUSG00000036046	RIKEN cDNA 5031439G07 gene(5031439G07Rik)
ENSMUSG00000048109	RNA binding motif protein 15(Rbm15)
ENSMUSG00000008658	RNA binding protein, fox-1 homolog (C. elegans) 1(Rbfox1)
ENSMUSG00000019782	RWD domain containing 1(Rwdd1)
ENSMUSG00000038975	Rab geranylgeranyl transferase, b subunit(Rabggtb)
ENSMUSG00000019854	RalBP1 associated Eps domain containing protein(Reps1)
ENSMUSG00000039844	Rap guanine nucleotide exchange factor (GEF) 1(Rapgef1)
ENSMUSG00000037533	Rap guanine nucleotide exchange factor (GEF) 6(Rapgef6)
ENSMUSG00000031880	Ras-related associated with diabetes(Rrad)
ENSMUSG00000020580	Rho-associated coiled-coil containing protein kinase 2(Rock2)
ENSMUSG00000078974	SEC61, gamma subunit(Sec61g)
ENSMUSG00000008384	SERTA domain containing 1(Sertad1)
ENSMUSG00000037111	SET domain containing (lysine methyltransferase) 7(Setd7)
ENSMUSG00000054766	SET nuclear oncogene(Set)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000027660	SKI-like(Skil)
ENSMUSG00000024515	SMAD family member 4(Smad4)
ENSMUSG00000030655	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)(Smg1)
ENSMUSG00000026207	SPEG complex locus(Speg)
ENSMUSG00000051910	SRY (sex determining region Y)-box 6(Sox6)
ENSMUSG00000000567	SRY (sex determining region Y)-box 9(Sox9)
ENSMUSG00000036391	Sec24 related gene family, member A (S. cerevisiae)(Sec24a)
ENSMUSG00000049323	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)(Smcr8)
ENSMUSG00000022961	Son DNA binding protein(Son)
ENSMUSG00000054321	TATA-box binding protein associated factor 4b(Taf4b)
ENSMUSG00000031939	TATA-box binding protein associated factor, RNA polymerase I, D(Taf1d)
ENSMUSG00000029174	TBC1 domain family, member 1(Tbc1d1)
ENSMUSG00000034640	TCDD-inducible poly(ADP-ribose) polymerase(Tiparp)
ENSMUSG00000055320	TEA domain family member 1(Tead1)
ENSMUSG00000015755	TGF-beta activated kinase 1/MAP3K7 binding protein 2(Tab2)
ENSMUSG00000047407	TGFB-induced factor homeobox 1(Tgif1)
ENSMUSG00000027692	TRAF2 and NCK interacting kinase(Tnik)
ENSMUSG00000028381	UDP-glucose ceramide glucosyltransferase(Ugcg)
ENSMUSG00000037470	UDP-glucose glycoprotein glucosyltransferase 1(Uggt1)
ENSMUSG00000034216	VPS18 CORVET/HOPS core subunit(Vps18)
ENSMUSG00000020128	VPS54 GARP complex subunit(Vps54)
ENSMUSG00000073643	WD repeat and FYVE domain containing 1(Wdfy1)
ENSMUSG00000038733	WD repeat domain 26(Wdr26)
ENSMUSG00000030189	Y box protein 3(Ybx3)
ENSMUSG00000022893	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1(Adamts1)
ENSMUSG00000031972	actin, alpha 1, skeletal muscle(Acta1)
ENSMUSG00000038774	activating signal cointegrator 1 complex subunit 3(Ascc3)
ENSMUSG00000026628	activating transcription factor 3(Atf3)
ENSMUSG00000042406	activating transcription factor 4(Atf4)
ENSMUSG00000026663	activating transcription factor 6(Atf6)
ENSMUSG00000022602	activity regulated cytoskeletal-associated protein(Arc)
ENSMUSG00000005686	adenosine monophosphate deaminase 3(Ampd3)
ENSMUSG00000021536	adenylate cyclase 2(Adcy2)
ENSMUSG00000030168	adiponectin receptor 2(Adipor2)
ENSMUSG00000030695	aldolase A, fructose-bisphosphate(Aldoa)
ENSMUSG00000032845	alpha-kinase 2(Alpk2)
ENSMUSG00000028029	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1(Aimp1)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000035048	anaphase promoting complex subunit 13(Anapc13)
ENSMUSG00000041688	angiomotin(Amot)
ENSMUSG00000013076	angiomotin-like 1(Amotl1)
ENSMUSG00000031980	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)(Agt)
ENSMUSG00000069601	ankyrin 3, epithelial(Ank3)
ENSMUSG00000034768	ankyrin repeat and SOCS box-containing 16(Asb16)
ENSMUSG00000024803	ankyrin repeat domain 1 (cardiac muscle)(Ankrd1)
ENSMUSG00000035569	ankyrin repeat domain 11(Ankrd11)
ENSMUSG00000014496	ankyrin repeat domain 28(Ankrd28)
ENSMUSG00000022237	ankyrin repeat domain 33B(Ankrd33b)
ENSMUSG00000055489	anoctamin 5(Ano5)
ENSMUSG00000020610	archaelysin family metallopeptidase 2(Amz2)
ENSMUSG00000040459	arginine and glutamate rich 1(Arglu1)
ENSMUSG00000036698	argonaute RISC catalytic subunit 2(Ago2)
ENSMUSG00000074794	arrestin domain containing 3(Arrdc3)
ENSMUSG00000024587	asparaginyl-tRNA synthetase(Nars)
ENSMUSG00000055435	avian musculoaponeurotic fibrosarcoma oncogene homolog(Maf)
ENSMUSG00000030103	basic helix-loop-helix family, member e40(Bhlhe40)
ENSMUSG00000047721	bolA-like 2 (E. coli)(Bola2)
ENSMUSG00000067336	bone morphogenetic protein receptor, type II (serine/threonine kinase)(Bmpr2)
ENSMUSG00000050071	brain expressed X-linked 1(Bex1)
ENSMUSG00000025372	brain-specific angiogenesis inhibitor 1-associated protein 2(Baiap2)
ENSMUSG00000040481	bromodomain PHD finger transcription factor(Bptf)
ENSMUSG00000024335	bromodomain containing 2(Brd2)
ENSMUSG00000019132	cDNA sequence BC005537(BC005537)
ENSMUSG00000022235	carboxymethylenebutenolidase-like (Pseudomonas)(Cmbl)
ENSMUSG00000068267	centromere protein B(Cenpb)
ENSMUSG00000034024	chaperonin containing Tcp1, subunit 2 (beta)(Cct2)
ENSMUSG00000038467	charged multivesicular body protein 4B(Chmp4b)
ENSMUSG00000023959	chloride intracellular channel 5(Clic5)
ENSMUSG00000024843	choline kinase alpha(Chka)
ENSMUSG00000027107	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)(Chrna1)
ENSMUSG00000047126	clathrin, heavy polypeptide (Hc)(Cltc)
ENSMUSG00000022037	clusterin(Clu)
ENSMUSG00000025981	coenzyme Q10B(Coq10b)
ENSMUSG00000007721	coiled-coil domain containing 124(Ccdc124)
ENSMUSG00000048701	coiled-coil domain containing 6(Ccdc6)
ENSMUSG00000024732	coiled-coil domain containing 86(Ccdc86)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000049422	coiled-coil-helix-coiled-coil-helix domain containing 10(Chchd10)
ENSMUSG00000028841	connector enhancer of kinase suppressor of Ras 1(Cnksr1)
ENSMUSG00000030399	creatine kinase, muscle(Ckm)
ENSMUSG00000032060	crystallin, alpha B(Cryab)
ENSMUSG00000004364	cullin 3(Cul3)
ENSMUSG00000021258	cyclin K(Ccnk)
ENSMUSG00000027829	cyclin L1(Ccnl1)
ENSMUSG00000048895	cyclin-dependent kinase 5, regulatory subunit 1 (p35)(Cdk5r1)
ENSMUSG00000023067	cyclin-dependent kinase inhibitor 1A (P21)(Cdkn1a)
ENSMUSG00000005054	cystatin B(Cstb)
ENSMUSG00000024846	cystatin E/M(Cst6)
ENSMUSG00000032515	cysteine-serine-rich nuclear protein 1(Csrnp1)
ENSMUSG00000064370	cytochrome b(CYTB)
ENSMUSG00000064354	cytochrome c oxidase subunit II(COX2)
ENSMUSG00000064358	cytochrome c oxidase subunit III(COX3)
ENSMUSG00000025488	cytochrome c oxidase subunit VIIIb(Cox8b)
ENSMUSG00000074218	cytochrome c oxidase subunit VIIa 1(Cox7a1)
ENSMUSG00000030785	cytochrome c oxidase subunit VIa polypeptide 2(Cox6a2)
ENSMUSG00000020300	cytoplasmic polyadenylation element binding protein 4(Cpeb4)
ENSMUSG00000054499	death effector domain-containing DNA binding protein 2(Dedd2)
ENSMUSG00000023106	density-regulated protein(Denr)
ENSMUSG00000021905	diphthamine biosynthesis 3(Dph3)
ENSMUSG00000034574	dishevelled associated activator of morphogenesis 1(Daam1)
ENSMUSG00000044716	docking protein 7(Dok7)
ENSMUSG00000022946	dopey family member 2(Dopey2)
ENSMUSG00000021768	dual specificity phosphatase 13(Dusp13)
ENSMUSG00000027368	dual specificity phosphatase 2(Dusp2)
ENSMUSG00000039661	dual specificity phosphatase 26 (putative)(Dusp26)
ENSMUSG00000034765	dual specificity phosphatase 5(Dusp5)
ENSMUSG00000022897	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a(Dyrk1a)
ENSMUSG00000026131	dystonin(Dst)
ENSMUSG00000045103	dystrophin, muscular dystrophy(Dmd)
ENSMUSG00000038418	early growth response 1(Egr1)
ENSMUSG00000039840	ectopic P-granules autophagy protein 5 homolog (C. elegans)(Epg5)
ENSMUSG00000001542	elongation factor RNA polymerase II 2(Ell2)
ENSMUSG00000022995	enabled homolog (Drosophila)(Enah)
ENSMUSG00000015092	endothelial differentiation-related factor 1(Edf1)
ENSMUSG00000096768	erythroid differentiation regulator 1(Erdr1)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000025967	eukaryotic translation elongation factor 1 beta 2(Eef1b2)
ENSMUSG00000071644	eukaryotic translation elongation factor 1 gamma(Eef1g)
ENSMUSG00000035530	eukaryotic translation initiation factor 1(Eif1)
ENSMUSG00000057561	eukaryotic translation initiation factor 1A(Eif1a)
ENSMUSG00000006941	eukaryotic translation initiation factor 1B(Eif1b)
ENSMUSG00000074656	eukaryotic translation initiation factor 2, subunit 2 (beta)(Eif2s2)
ENSMUSG00000024991	eukaryotic translation initiation factor 3, subunit A(Eif3a)
ENSMUSG00000030738	eukaryotic translation initiation factor 3, subunit C(Eif3c)
ENSMUSG00000031029	eukaryotic translation initiation factor 3, subunit F(Eif3f)
ENSMUSG00000070319	eukaryotic translation initiation factor 3, subunit G(Eif3g)
ENSMUSG00000022312	eukaryotic translation initiation factor 3, subunit H(Eif3h)
ENSMUSG00000027236	eukaryotic translation initiation factor 3, subunit J1(Eif3j1)
ENSMUSG00000053565	eukaryotic translation initiation factor 3, subunit K(Eif3k)
ENSMUSG00000031490	eukaryotic translation initiation factor 4E binding protein 1(Eif4ebp1)
ENSMUSG00000021282	eukaryotic translation initiation factor 5(Eif5)
ENSMUSG00000026083	eukaryotic translation initiation factor 5B(Eif5b)
ENSMUSG00000050812	expressed sequence AI314180(AI314180)
ENSMUSG00000038112	expressed sequence AW551984(AW551984)
ENSMUSG00000038014	family with sequence similarity 120, member A(Fam120a)
ENSMUSG00000022270	family with sequence similarity 134, member B(Fam134b)
ENSMUSG00000029461	family with sequence similarity 168, member A(Fam168a)
ENSMUSG00000045761	family with sequence similarity 179, member A(Fam179a)
ENSMUSG00000071604	family with sequence similarity 189, member A2(Fam189a2)
ENSMUSG00000032244	feminization 1 homolog b (C. elegans)(Fem1b)
ENSMUSG00000037712	fermitin family member 2(Fermt2)
ENSMUSG00000024661	ferritin heavy polypeptide 1(Fth1)
ENSMUSG00000050708	ferritin light polypeptide 1(Ftl1)
ENSMUSG00000031137	fibroblast growth factor 13(Fgf13)
ENSMUSG00000068699	filamin C, gamma(Flnc)
ENSMUSG00000035992	folliculin interacting protein 1(Fnip1)
ENSMUSG00000033713	forkhead box N3(Foxn3)
ENSMUSG00000044167	forkhead box O1(Foxo1)
ENSMUSG00000034295	formin homology 2 domain containing 3(Fhod3)
ENSMUSG00000032643	four and a half LIM domains 3(Fhl3)
ENSMUSG00000027680	fragile X mental retardation gene 1, autosomal homolog(Fxr1)
ENSMUSG00000031266	galactosidase, alpha(Gla)
ENSMUSG00000030161	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1(Gabarapl1)
ENSMUSG00000031950	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2(Gabarapl2)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000026473	glutamate-ammonia ligase (glutamine synthetase)(Glul)
ENSMUSG00000074994	glutamine and serine rich 1(Qser1)
ENSMUSG00000026615	glutamyl-prolyl-tRNA synthetase(Eprs)
ENSMUSG00000021591	glutaredoxin(Glrx)
ENSMUSG00000004032	glutathione S-transferase, mu 5(Gstm5)
ENSMUSG00000057666	glyceraldehyde-3-phosphate dehydrogenase(Gapdh)
ENSMUSG00000019528	glycogenin(Gyg)
ENSMUSG00000024026	glyoxalase 1(Glo1)
ENSMUSG00000038708	golgi autoantigen, golgin subfamily a, 4(Golga4)
ENSMUSG00000029708	golgi coiled coil 1(Gcc1)
ENSMUSG00000036390	growth arrest and DNA-damage-inducible 45 alpha(Gadd45a)
ENSMUSG00000015312	growth arrest and DNA-damage-inducible 45 beta(Gadd45b)
ENSMUSG00000021453	growth arrest and DNA-damage-inducible 45 gamma(Gadd45g)
ENSMUSG00000020611	guanine nucleotide binding protein, alpha 13(Gna13)
ENSMUSG00000042354	guanine nucleotide binding protein-like 3 (nucleolar)(Gnl3)
ENSMUSG00000004951	heat shock protein 1(Hspb1)
ENSMUSG00000041548	heat shock protein 8(Hspb8)
ENSMUSG00000023944	heat shock protein 90 alpha (cytosolic), class B member 1(Hsp90ab1)
ENSMUSG00000005413	heme oxygenase 1(Hmox1)
ENSMUSG00000024486	heparin-binding EGF-like growth factor(Hbegf)
ENSMUSG00000007836	heterogeneous nuclear ribonucleoprotein A0(Hnrnpa0)
ENSMUSG00000029328	heterogeneous nuclear ribonucleoprotein D-like(Hnrnpdl)
ENSMUSG00000000628	hexokinase 2(Hk2)
ENSMUSG00000034088	high density lipoprotein (HDL) binding protein(Hdlbp)
ENSMUSG00000038239	histidine rich calcium binding protein(Hrc)
ENSMUSG00000019791	histidine triad nucleotide binding protein 3(Hint3)
ENSMUSG00000060639	histone cluster 1, H4i(Hist1h4i)
ENSMUSG00000026313	histone deacetylase 4(Hdac4)
ENSMUSG00000027177	homeodomain interacting protein kinase 3(Hipk3)
ENSMUSG00000043421	hypoxia inducible lipid droplet associated(Hilpda)
ENSMUSG00000053560	immediate early response 2(Ier2)
ENSMUSG00000056708	immediate early response 5(Ier5)
ENSMUSG00000046879	immunity-related GTPase family M member 1(Irgm1)
ENSMUSG00000034275	immunoglobulin superfamily, member 9B(Igsf9b)
ENSMUSG00000024423	impact, RWD domain protein(Impact)
ENSMUSG00000030662	importin 5(Ipo5)
ENSMUSG00000020644	inhibitor of DNA binding 2(Id2)
ENSMUSG00000021385	inositol 1,3,4,5,6-pentakisphosphate 2-kinase(Ippk)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000038894	insulin receptor substrate 2(Irs2)
ENSMUSG00000005534	insulin receptor(Insr)
ENSMUSG00000033581	insulin-like growth factor 2 mRNA binding protein 2(Igf2bp2)
ENSMUSG00000005533	insulin-like growth factor I receptor(Igf1r)
ENSMUSG00000027009	integrin alpha 4(Itga4)
ENSMUSG00000078853	interferon gamma induced GTPase(Igtp)
ENSMUSG00000051495	interferon regulatory factor 2 binding protein 2(Irf2bp2)
ENSMUSG00000041515	interferon regulatory factor 8(Irf8)
ENSMUSG00000001627	interferon-related developmental regulator 1(Ifrd1)
ENSMUSG00000023206	interleukin 15 receptor, alpha chain(Il15ra)
ENSMUSG00000037851	isoleucine-tRNA synthetase(Iars)
ENSMUSG00000037876	jumonji domain containing 1C(Jmjd1c)
ENSMUSG00000038518	jumonji, AT rich interactive domain 2(Jarid2)
ENSMUSG00000052837	jun B proto-oncogene(Junb)
ENSMUSG00000073700	kelch-like 21(Klhl21)
ENSMUSG00000026308	kelch-like 30(Klhl30)
ENSMUSG00000074001	kelch-like 40(Klhl40)
ENSMUSG00000075307	kelch-like 41(Klhl41)
ENSMUSG00000042747	keratinocyte associated protein 2(Krtcap2)
ENSMUSG00000018334	kinase suppressor of ras 1(Ksr1)
ENSMUSG00000021843	kinectin 1(Ktn1)
ENSMUSG00000020821	kinesin family member 1C(Kif1c)
ENSMUSG00000022629	kinesin family member 21A(Kif21a)
ENSMUSG00000032497	leucine rich repeat (in FLII) interacting protein 2(Lrrfip2)
ENSMUSG00000045776	leucine-rich repeats and transmembrane domains 1(Lrtm1)
ENSMUSG00000044471	long non-protein coding RNA, Trp53 induced transcript(Lncpint)
ENSMUSG00000030201	low density lipoprotein receptor-related protein 6(Lrp6)
ENSMUSG00000031948	lysyl-tRNA synthetase(Kars)
ENSMUSG00000033307	macrophage migration inhibitory factor(Mif)
ENSMUSG00000024085	mannosidase 2, alpha 1(Man2a1)
ENSMUSG00000038886	mannosidase 2, alpha 2(Man2a2)
ENSMUSG00000034297	mediator complex subunit 13(Med13)
ENSMUSG00000021112	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)(Mpp5)
ENSMUSG00000039100	membrane-associated ring finger (C3HC4) 6(March6)
ENSMUSG00000070576	meningioma 1(Mn1)
ENSMUSG00000009376	met proto-oncogene(Met)
ENSMUSG00000031765	metallothionein 1(Mt1)
ENSMUSG00000031762	metallothionein 2(Mt2)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000031760	metallothionein 3(Mt3)
ENSMUSG00000092341	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)(Malat1)
ENSMUSG00000033039	microtubule associated monooxygenase, calponin and LIM domain containing -like 1(Micall1)
ENSMUSG00000051586	microtubule associated monooxygenase, calponin and LIM domain containing 3(Mical3)
ENSMUSG00000003810	microtubule associated serine/threonine kinase 2(Mast2)
ENSMUSG00000034751	microtubule associated serine/threonine kinase family member 4(Mast4)
ENSMUSG00000035621	midnolin(Midn)
ENSMUSG00000037772	mitochondrial ribosomal protein L23(Mrpl23)
ENSMUSG00000026087	mitochondrial ribosomal protein L30(Mrpl30)
ENSMUSG00000010406	mitochondrial ribosomal protein L52(Mrpl52)
ENSMUSG00000034932	mitochondrial ribosomal protein L54(Mrpl54)
ENSMUSG00000021967	mitochondrial ribosomal protein L57(Mrpl57)
ENSMUSG00000023967	mitochondrial ribosomal protein S18A(Mrps18a)
ENSMUSG00000054312	mitochondrial ribosomal protein S21(Mrps21)
ENSMUSG00000021936	mitogen-activated protein kinase 8(Mapk8)
ENSMUSG00000024383	mitogen-activated protein kinase kinase kinase 2(Map3k2)
ENSMUSG00000024235	mitogen-activated protein kinase kinase kinase 8(Map3k8)
ENSMUSG00000022671	mitotic spindle organizing protein 2(Mzt2)
ENSMUSG00000069769	musashi RNA-binding protein 2(Msi2)
ENSMUSG00000028348	muscle-related coiled-coil protein(Murc)
ENSMUSG00000032355	muscular LMNA-interacting protein(Mlip)
ENSMUSG00000042485	musculoskeletal, embryonic nuclear protein 1(Mustn1)
ENSMUSG00000022346	myelocytomatosis oncogene(Myc)
ENSMUSG00000038612	myeloid cell leukemia sequence 1(Mcl1)
ENSMUSG00000028496	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 3(Mllt3)
ENSMUSG00000005583	myocyte enhancer factor 2C(Mef2c)
ENSMUSG00000009471	myogenic differentiation 1(Myod1)
ENSMUSG00000024049	myomesin 1(Myom1)
ENSMUSG00000020067	myopalladin(Mypn)
ENSMUSG00000072720	myosin XVIIIb(Myo18b)
ENSMUSG00000020061	myosin binding protein C, slow-type(Mybpc1)
ENSMUSG00000044951	myosin light chain kinase family, member 4(Mylk4)
ENSMUSG00000061816	myosin, light polypeptide 1(Myl1)
ENSMUSG00000049173	myozenin 3(Myoz3)
ENSMUSG00000061315	nascent polypeptide-associated complex alpha polypeptide(Naca)
ENSMUSG00000032525	natural killer tumor recognition sequence(Nktr)
ENSMUSG00000026950	nebulin(Neb)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000049134	nebulin-related anchoring protein(Nrap)
ENSMUSG00000024589	neural precursor cell expressed, developmentally down-regulated gene 4-like(Nedd4l)
ENSMUSG00000029361	nitric oxide synthase 1, neuronal(Nos1)
ENSMUSG00000023087	nocturnin(Noct)
ENSMUSG00000014907	nuclear assembly factor 1 ribonucleoprotein(Naf1)
ENSMUSG00000003847	nuclear factor of activated T cells 5(Nfat5)
ENSMUSG00000035356	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta(Nfkbiz)
ENSMUSG00000092274	nuclear paraspeckle assembly transcript 1 (non-protein coding)(Neat1)
ENSMUSG00000048490	nuclear receptor interacting protein 1(Nrip1)
ENSMUSG00000023034	nuclear receptor subfamily 4, group A, member 1(Nr4a1)
ENSMUSG00000028341	nuclear receptor subfamily 4, group A, member 3(Nr4a3)
ENSMUSG00000015176	nucleolar and coiled-body phosphoprotein 1(Nolc1)
ENSMUSG00000057113	nucleophosmin 1(Npm1)
ENSMUSG00000045211	nudix (nucleoside diphosphate linked moiety X)-type motif 18(Nudt18)
ENSMUSG00000061462	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF(Obscn)
ENSMUSG00000026672	optineurin(Optn)
ENSMUSG00000074063	oxidative stress induced growth inhibitor 1(Osgin1)
ENSMUSG00000002265	paternally expressed 3(Peg3)
ENSMUSG00000020893	period circadian clock 1(Per1)
ENSMUSG00000055866	period circadian clock 2(Per2)
ENSMUSG00000029167	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha(Ppargc1a)
ENSMUSG00000040430	phosphatidylinositol transfer protein, cytoplasmic 1(Pitpnc1)
ENSMUSG00000028525	phosphodiesterase 4B, cAMP specific(Pde4b)
ENSMUSG00000038170	phosphodiesterase 4D interacting protein (myomegalin)(Pde4dip)
ENSMUSG00000021699	phosphodiesterase 4D, cAMP specific(Pde4d)
ENSMUSG00000020475	phosphoglycerate mutase 2(Pgam2)
ENSMUSG00000028917	pleckstrin homology domain containing, family M (with RUN domain) member 2(Plekhm2)
ENSMUSG00000019817	pleiomorphic adenoma gene-like 1(Plagl1)
ENSMUSG00000028583	podoplanin(Pdpn)
ENSMUSG00000040511	poliovirus receptor(Pvr)
ENSMUSG00000022283	poly(A) binding protein, cytoplasmic 1(Pabpc1)
ENSMUSG00000011257	poly(A) binding protein, cytoplasmic 4(Pabpc4)
ENSMUSG00000056851	poly(rC) binding protein 2(Pcbp2)
ENSMUSG00000029642	polymerase (RNA) I polypeptide D(Polr1d)
ENSMUSG00000033020	polymerase (RNA) II (DNA directed) polypeptide F(Polr2f)
ENSMUSG00000019738	polymerase (RNA) II (DNA directed) polypeptide I(Polr2i)
ENSMUSG00000031226	polysaccharide biosynthesis domain containing 1(Pbdc1)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000027895	potassium voltage gated channel, Shaw-related subfamily, member 4(Kcnc4)
ENSMUSG00000087006	predicted gene 13889(Gm13889)
ENSMUSG00000041716	predicted gene 20604(Gm20604)
ENSMUSG00000068606	predicted gene 4841(Gm4841)
ENSMUSG00000024346	prefoldin 1(Pfdn1)
ENSMUSG00000001289	prefoldin 5(Pfdn5)
ENSMUSG00000030417	programmed cell death 5(Pdcd5)
ENSMUSG00000031485	proline synthetase co-transcribed(Prosc)
ENSMUSG00000039262	proline-rich coiled-coil 2B(Prrc2b)
ENSMUSG00000040225	proline-rich coiled-coil 2C(Prrc2c)
ENSMUSG00000028932	proteasome (prosome, macropain) 26S subunit, ATPase 2(Psmc2)
ENSMUSG00000040850	proteasome (prosome, macropain) activator subunit 4(Psme4)
ENSMUSG00000028518	protein kinase, AMP-activated, alpha 2 catalytic subunit(Prkaa2)
ENSMUSG00000038205	protein kinase, AMP-activated, beta 2 non-catalytic subunit(Prkab2)
ENSMUSG00000040435	protein phosphatase 1, regulatory (inhibitor) subunit 15A(Ppp1r15a)
ENSMUSG00000067279	protein phosphatase 1, regulatory (inhibitor) subunit 3C(Ppp1r3c)
ENSMUSG00000028161	protein phosphatase 3, catalytic subunit, alpha isoform(Ppp3ca)
ENSMUSG00000021816	protein phosphatase 3, catalytic subunit, beta isoform(Ppp3cb)
ENSMUSG00000028788	protein tyrosine phosphatase 4a2(Ptp4a2)
ENSMUSG00000036057	protein tyrosine phosphatase, non-receptor type 23(Ptpn23)
ENSMUSG00000024014	proviral integration site 1(Pim1)
ENSMUSG00000020594	pumilio RNA-binding family member 2(Pum2)
ENSMUSG00000062078	quaking(Qk)
ENSMUSG00000052852	receptor accessory protein 1(Reep1)
ENSMUSG00000020372	receptor for activated C kinase 1(Rack1)
ENSMUSG00000022951	regulator of calcineurin 1(Rcan1)
ENSMUSG00000020275	reticuloendotheliosis oncogene(Rel)
ENSMUSG00000030401	reticulon 2 (Z-band associated protein)(Rtn2)
ENSMUSG00000001305	ribosomal RNA processing 15 homolog (S. cerevisiae)(Rrp15)
ENSMUSG00000008682	ribosomal protein L10(Rpl10)
ENSMUSG00000037805	ribosomal protein L10A(Rpl10a)
ENSMUSG00000059291	ribosomal protein L11(Rpl11)
ENSMUSG00000038900	ribosomal protein L12(Rpl12)
ENSMUSG00000000740	ribosomal protein L13(Rpl13)
ENSMUSG00000025794	ribosomal protein L14(Rpl14)
ENSMUSG00000012405	ribosomal protein L15(Rpl15)
ENSMUSG00000062328	ribosomal protein L17(Rpl17)
ENSMUSG00000059070	ribosomal protein L18(Rpl18)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000045128	ribosomal protein L18A(Rpl18a)
ENSMUSG00000017404	ribosomal protein L19(Rpl19)
ENSMUSG00000041453	ribosomal protein L21(Rpl21)
ENSMUSG00000039221	ribosomal protein L22 like 1(Rpl22l1)
ENSMUSG00000028936	ribosomal protein L22(Rpl22)
ENSMUSG00000071415	ribosomal protein L23(Rpl23)
ENSMUSG00000060938	ribosomal protein L26(Rpl26)
ENSMUSG00000063316	ribosomal protein L27(Rpl27)
ENSMUSG00000046364	ribosomal protein L27A(Rpl27a)
ENSMUSG00000030432	ribosomal protein L28(Rpl28)
ENSMUSG00000048758	ribosomal protein L29(Rpl29)
ENSMUSG00000058600	ribosomal protein L30(Rpl30)
ENSMUSG00000073702	ribosomal protein L31(Rpl31)
ENSMUSG00000057841	ribosomal protein L32(Rpl32)
ENSMUSG00000062006	ribosomal protein L34(Rpl34)
ENSMUSG00000062997	ribosomal protein L35(Rpl35)
ENSMUSG00000060636	ribosomal protein L35A(Rpl35a)
ENSMUSG00000057863	ribosomal protein L36(Rpl36)
ENSMUSG00000079435	ribosomal protein L36A(Rpl36a)
ENSMUSG00000041841	ribosomal protein L37(Rpl37)
ENSMUSG00000046330	ribosomal protein L37a(Rpl37a)
ENSMUSG00000057322	ribosomal protein L38(Rpl38)
ENSMUSG00000079641	ribosomal protein L39(Rpl39)
ENSMUSG00000032399	ribosomal protein L4(Rpl4)
ENSMUSG00000093674	ribosomal protein L41(Rpl41)
ENSMUSG00000058558	ribosomal protein L5(Rpl5)
ENSMUSG00000029614	ribosomal protein L6(Rpl6)
ENSMUSG00000043716	ribosomal protein L7(Rpl7)
ENSMUSG00000062647	ribosomal protein L7A(Rpl7a)
ENSMUSG00000003970	ribosomal protein L8(Rpl8)
ENSMUSG00000047215	ribosomal protein L9(Rpl9)
ENSMUSG00000003429	ribosomal protein S11(Rps11)
ENSMUSG00000061983	ribosomal protein S12(Rps12)
ENSMUSG00000090862	ribosomal protein S13(Rps13)
ENSMUSG00000024608	ribosomal protein S14(Rps14)
ENSMUSG00000063457	ribosomal protein S15(Rps15)
ENSMUSG00000008683	ribosomal protein S15A(Rps15a)
ENSMUSG00000037563	ribosomal protein S16(Rps16)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000061787	ribosomal protein S17(Rps17)
ENSMUSG00000008668	ribosomal protein S18(Rps18)
ENSMUSG00000040952	ribosomal protein S19(Rps19)
ENSMUSG00000044533	ribosomal protein S2(Rps2)
ENSMUSG00000028234	ribosomal protein S20(Rps20)
ENSMUSG00000039001	ribosomal protein S21(Rps21)
ENSMUSG00000049517	ribosomal protein S23(Rps23)
ENSMUSG00000025290	ribosomal protein S24(Rps24)
ENSMUSG00000009927	ribosomal protein S25(Rps25)
ENSMUSG00000025362	ribosomal protein S26(Rps26)
ENSMUSG00000090733	ribosomal protein S27(Rps27)
ENSMUSG00000020460	ribosomal protein S27A(Rps27a)
ENSMUSG00000067288	ribosomal protein S28(Rps28)
ENSMUSG00000034892	ribosomal protein S29(Rps29)
ENSMUSG00000028081	ribosomal protein S3A1(Rps3a1)
ENSMUSG00000031320	ribosomal protein S4, X-linked(Rps4x)
ENSMUSG00000012848	ribosomal protein S5(Rps5)
ENSMUSG00000089872	ribosomal protein S6 kinase polypeptide 1(Rps6kc1)
ENSMUSG00000031309	ribosomal protein S6 kinase polypeptide 3(Rps6ka3)
ENSMUSG00000047675	ribosomal protein S8(Rps8)
ENSMUSG00000006333	ribosomal protein S9(Rps9)
ENSMUSG00000032518	ribosomal protein SA(Rpsa)
ENSMUSG00000025508	ribosomal protein, large P2(Rplp2)
ENSMUSG00000067274	ribosomal protein, large, P0(Rplp0)
ENSMUSG00000007892	ribosomal protein, large, P1(Rplp1)
ENSMUSG00000075376	ring finger and CCCH-type zinc finger domains 2(Rc3h2)
ENSMUSG00000040782	ring finger and WD repeat domain 2(Rfwd2)
ENSMUSG00000063760	ring finger protein 217(Rnf217)
ENSMUSG00000022952	runt related transcription factor 1(Runx1)
ENSMUSG00000030592	ryanodine receptor 1, skeletal muscle(Ryr1)
ENSMUSG00000001508	sarcoglycan, alpha (dystrophin-associated glycoprotein)(Sgca)
ENSMUSG00000029189	sel-1 suppressor of lin-12-like 3 (C. elegans)(Sel1l3)
ENSMUSG00000042682	selenoprotein K(Selk)
ENSMUSG00000075700	selenoprotein T(Selt)
ENSMUSG00000058013	septin 11(Sept11)
ENSMUSG00000062604	serine/arginine-rich protein specific kinase 2(Srpk2)
ENSMUSG00000036371	serpine1 mRNA binding protein 1(Serbp1)
ENSMUSG00000068739	seryl-aminoacyl-tRNA synthetase(Sars)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000036432	seven in absentia 2(Siah2)
ENSMUSG00000004040	signal transducer and activator of transcription 3(Stat3)
ENSMUSG00000031609	sin3 associated polypeptide(Sap30)
ENSMUSG00000022452	single-pass membrane protein with aspartate rich tail 1(Smdt1)
ENSMUSG00000020063	sirtuin 1(Sirt1)
ENSMUSG00000040824	small nuclear ribonucleoprotein D2(Snrpd2)
ENSMUSG00000006587	snail family zinc finger 3(Snai3)
ENSMUSG00000028645	solute carrier family 2 (facilitated glucose transporter), member 1(Slc2a1)
ENSMUSG00000027397	solute carrier family 20, member 1(Slc20a1)
ENSMUSG00000020334	solute carrier family 22 (organic cation transporter), member 4(Slc22a4)
ENSMUSG00000022462	solute carrier family 38, member 2(Slc38a2)
ENSMUSG00000052310	solute carrier family 39 (zinc transporter), member 1(Slc39a1)
ENSMUSG00000019558	solute carrier family 6 (neurotransmitter transporter, creatine), member 8(Slc6a8)
ENSMUSG00000034801	son of sevenless homolog 2 (Drosophila)(Sos2)
ENSMUSG00000071669	sorting nexin 29(Snx29)
ENSMUSG00000023927	special AT-rich sequence binding protein 1(Satb1)
ENSMUSG00000096054	spectrin repeat containing, nuclear envelope 1(Syne1)
ENSMUSG00000025283	spermidine/spermine N1-acetyl transferase 1(Sat1)
ENSMUSG00000050931	sphingomyelin synthase 2(Sgms2)
ENSMUSG00000022114	sprouty homolog 2 (Drosophila)(Spry2)
ENSMUSG00000004085	sterile alpha motif and leucine zipper containing kinase AZK(Zak)
ENSMUSG00000021838	sterile alpha motif domain containing 4(Samd4)
ENSMUSG00000021770	sterile alpha motif domain containing 8(Samd8)
ENSMUSG00000020961	stonin 2(Ston2)
ENSMUSG00000035673	strawberry notch homolog 2 (Drosophila)(Sbno2)
ENSMUSG00000032802	sulfiredoxin 1 homolog (S. cerevisiae)(Srxn1)
ENSMUSG00000022982	superoxide dismutase 1, soluble(Sod1)
ENSMUSG00000020027	suppressor of cytokine signaling 2(Socs2)
ENSMUSG00000014873	surfeit gene 2(Surf2)
ENSMUSG00000023805	synaptojanin 2(Synj2)
ENSMUSG00000050315	synaptopodin 2(Synpo2)
ENSMUSG00000017009	syndecan 4(Sdc4)
ENSMUSG00000020903	syntaxin 8(Stx8)
ENSMUSG00000052698	talin 2(Tln2)
ENSMUSG00000074743	thrombomodulin(Thbd)
ENSMUSG00000051747	titin(Ttn)
ENSMUSG00000070544	topoisomerase (DNA) I(Top1)
ENSMUSG00000001604	transcription elongation factor A (SII), 3(Tcea3)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000055839	transcription elongation factor B (SIII), polypeptide 2(Tceb2)
ENSMUSG00000024498	transcription elongation regulator 1 (CA150)(Tcerg1)
ENSMUSG00000022858	transformer 2 beta homolog (Drosophila)(Tra2b)
ENSMUSG00000039239	transforming growth factor, beta 2(Tgfb2)
ENSMUSG00000030852	transforming, acidic coiled-coil containing protein 2(Tacc2)
ENSMUSG00000091537	translational machinery associated 7(Tma7)
ENSMUSG00000027076	translocase of inner mitochondrial membrane 10(Timm10)
ENSMUSG00000039016	translocase of inner mitochondrial membrane 8B(Timm8b)
ENSMUSG00000057137	transmembrane protein 140(Tmem140)
ENSMUSG00000046675	transmembrane protein 251(Tmem251)
ENSMUSG00000036372	transmembrane protein 258(Tmem258)
ENSMUSG00000074634	transmembrane protein 267(Tmem267)
ENSMUSG00000047554	transmembrane protein 41B(Tmem41b)
ENSMUSG00000023153	transmembrane protein 52(Tmem52)
ENSMUSG00000032501	tribbles pseudokinase 1(Trib1)
ENSMUSG00000028834	tripartite motif-containing 63(Trim63)
ENSMUSG00000022263	triple functional domain (PTPRF interacting)(Trio)
ENSMUSG00000061723	troponin T3, skeletal, fast(Tnnt3)
ENSMUSG00000043091	tubulin, alpha 1C(Tuba1c)
ENSMUSG00000023905	tumor necrosis factor receptor superfamily, member 12a(Tnfrsf12a)
ENSMUSG00000000296	tumor protein D52-like 1(Tpd52l1)
ENSMUSG00000060126	tumor protein, translationally-controlled 1(Tpt1)
ENSMUSG00000038538	ubinuclein 2(Ubn2)
ENSMUSG00000024208	ubiquinol-cytochrome c reductase complex assembly factor 2(Uqcc2)
ENSMUSG00000066036	ubiquitin protein ligase E3 component n-recognin 4(Ubr4)
ENSMUSG00000037487	ubiquitin protein ligase E3 component n-recognin 5(Ubr5)
ENSMUSG00000025616	ubiquitin specific peptidase 16(Usp16)
ENSMUSG00000032267	ubiquitin specific peptidase 28(Usp28)
ENSMUSG00000056342	ubiquitin specific peptidase 34(Usp34)
ENSMUSG00000022710	ubiquitin specific peptidase 7(Usp7)
ENSMUSG00000038965	ubiquitin-conjugating enzyme E2L 3(Ube2l3)
ENSMUSG00000026558	uridine-cytidine kinase 2(Uck2)
ENSMUSG00000042622	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)(Maff)
ENSMUSG00000018143	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)(Mafk)
ENSMUSG00000046230	vacuolar protein sorting 13A(Vps13a)
ENSMUSG00000023951	vascular endothelial growth factor A(Vegfa)
ENSMUSG00000024924	very low density lipoprotein receptor(Vldlr)
ENSMUSG00000049641	vestigial like family member 2(Vgll2)

Table S2A: List of genes expressed solely in the myofiber

Gene ID	Gene Name
ENSMUSG00000026469	xenotropic and polytropic retrovirus receptor 1(Xpr1)
ENSMUSG00000079243	xin actin-binding repeat containing 1(Xirp1)
ENSMUSG00000027022	xin actin-binding repeat containing 2(Xirp2)
ENSMUSG00000044068	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1(Zrsr1)
ENSMUSG00000031370	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2(Zrsr2)
ENSMUSG00000027091	zinc finger CCCH-type containing 15(Zc3h15)
ENSMUSG00000022635	zinc finger CCHC-type and RNA binding motif 1(Zcrb1)
ENSMUSG00000069114	zinc finger and BTB domain containing 10(Zbtb10)
ENSMUSG00000022708	zinc finger and BTB domain containing 20(Zbtb20)
ENSMUSG00000027288	zinc finger protein 106(Zfp106)
ENSMUSG00000094870	zinc finger protein 131(Zfp131)
ENSMUSG00000060206	zinc finger protein 462(Zfp462)
ENSMUSG00000007812	zinc finger protein 655(Zfp655)
ENSMUSG00000085795	zinc finger protein 703(Zfp703)
ENSMUSG00000027520	zinc finger, DBF-type containing 2(Zdbf2)
ENSMUSG00000037553	zinc finger, DHHC domain containing 18(Zdhhc18)
ENSMUSG00000074578	zinc finger, NFX1-type containing 1, antisense RNA 1(Zfas1)
ENSMUSG00000030967	zinc finger, RAN-binding domain containing 1(Zranb1)

* List of genes exclusively expressed in the single myofiber, defined as genes with a q value lower than 0.01 between single fiber and whole muscle, that are more highly expressed in the single fiber with a Log_2 fold change of less than -1, more highly expressed than 10 RPM and with a difference in expression between single fiber and whole muscle of at least 10 RPM

Table S2B: GO term analysis of genes expressed solely in myofibers

Annotation Cluster 1 **Enrichment Score: 41.59143623593712**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Ribosomal protein	61	17.13483146	2.25E-60	349	203	22680	19.52771465	5.33E-58	5.33E-58	2.90E-57
KEGG_PATHWAY	mmu03010:Ribosome	61	17.13483146	2.67E-57	214	145	7691	15.11927167	4.80E-55	4.80E-55	3.29E-54
GOTERM_CC_DIRECT	GO:0005840~ribosome	58	16.29213483	2.20E-55	339	188	19662	17.89361702	7.43E-53	7.43E-53	2.99E-52
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	61	17.13483146	9.74E-49	319	264	17446	12.63662487	4.74E-46	4.74E-46	1.40E-45
UP_KEYWORDS	Ribonucleoprotein	61	17.13483146	1.49E-48	349	308	22680	12.8705392	3.54E-46	1.77E-46	1.92E-45
GOTERM_BP_DIRECT	GO:0006412~translation	64	17.97752809	1.24E-40	332	401	18082	8.692485653	2.20E-37	2.20E-37	2.11E-37
GOTERM_CC_DIRECT	GO:0030529~intracellular ribonucleoprotein complex	57	16.01123596	4.52E-40	339	320	19662	10.33125	1.53E-37	7.63E-38	6.15E-37
GOTERM_CC_DIRECT	GO:0022627~cytosolic small ribosomal subunit	28	7.865168539	5.07E-34	339	53	19662	30.64150943	1.71E-31	5.71E-32	6.90E-31
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	31	8.707865169	1.19E-30	339	91	19662	19.75824176	4.01E-28	1.00E-28	1.62E-27
GOTERM_MF_DIRECT	GO:0044822~poly(A) RNA binding	81	22.75280899	2.67E-27	319	1113	17446	3.980109676	1.30E-24	6.50E-25	3.83E-24
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	44	12.35955056	1.80E-22	339	391	19662	6.52685422	6.09E-20	8.70E-21	2.45E-19

Annotation Cluster 2 **Enrichment Score: 12.979686554524369**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Respiratory chain	23	6.460674157	1.21E-24	349	62	22680	24.1075885	2.88E-22	5.75E-23	1.56E-21
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	35	9.831460674	1.81E-23	214	139	7691	9.049452027	3.25E-21	1.63E-21	2.23E-20
UP_KEYWORDS	Mitochondrion inner membrane	36	10.11235955	3.23E-23	349	254	22680	9.210567877	7.65E-21	1.27E-21	4.16E-20
GOTERM_CC_DIRECT	GO:0070469~respiratory chain	22	6.179775281	8.56E-23	339	58	19662	22	2.89E-20	4.82E-21	1.17E-19

Table S2B: GO term analysis of genes expressed solely in myofibers

KEGG_PATHWAY	mmu05012:Parkinson's disease	35	9.831460674	2.08E-22	214	149	7691	8.442106254	3.75E-20	1.25E-20	2.56E-19
UP_KEYWORDS	Electron transport	23	6.460674157	7.12E-19	349	107	22680	13.96888306	1.69E-16	2.41E-17	9.18E-16
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	39	10.95505618	2.89E-18	339	387	19662	5.84496124	9.76E-16	1.22E-16	3.93E-15
GOTERM_CC_DIRECT	GO:0005747~mitochondrial respiratory chain complex I	17	4.775280899	3.67E-17	339	47	19662	20.9787234	1.24E-14	1.24E-15	5.00E-14
KEGG_PATHWAY	mmu05010:Alzheimer's disease	32	8.988764045	5.80E-17	214	177	7691	6.497491948	2.00E-14	5.00E-15	1.33E-13
KEGG_PATHWAY	mmu05016:Huntington's disease	32	8.988764045	1.75E-15	214	198	7691	5.808364014	3.20E-13	6.39E-14	2.19E-12
KEGG_PATHWAY	mmu04932:Non-alcoholic fatty liver disease (NAFLD)	28	7.865168539	1.24E-14	214	157	7691	6.409548187	2.24E-12	3.73E-13	1.53E-11
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	70	19.66292135	2.00E-11	339	1721	19662	2.35909355	6.77E-09	4.51E-10	2.73E-08
UP_KEYWORDS	Mitochondrion	48	13.48314607	5.88E-11	349	1058	22680	2.948310322	1.39E-08	1.39E-09	7.58E-08
UP_KEYWORDS	Ubiquinone	9	2.528089888	2.44E-09	349	25	22680	23.39484241	5.79E-07	5.26E-08	3.15E-06
GOTERM_MF_DIRECT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	10	2.808988764	9.24E-09	319	35	17446	15.62561576	4.50E-06	1.50E-06	1.32E-05
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	31	8.707865169	7.59E-06	332	676	18082	2.497602837	0.013363031	0.001920029	0.01286143
UP_KEYWORDS	Transport	46	12.92134831	0.002449138	349	1901	22680	1.572509718	0.440749474	0.021294365	3.109423935
KEGG_PATHWAY	mmu01100:Metabolic pathways	48	13.48314607	0.019405427	214	1269	7691	1.359404344	0.97061624	0.25468085	21.44535353
GOTERM_BP_DIRECT	GO:0006810~transport	45	12.64044944	0.034846545	332	1822	18082	1.345155595	1	0.55345664	45.18637711
UP_KEYWORDS	NAD	7	1.966292135	0.063495213	349	183	22680	2.485790784	0.999999823	0.315593835	57.04650709
Annotation Cluster 3				**Enrichment Score: 3.344968202809536**							

Table S2B: GO term analysis of genes expressed solely in myofibers

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR002068:Alpha crystallin/Hsp20 domain	5	1.404494382	2.10E-05	337	11	20594	27.77717831	0.016005692	0.005363951	0.032035079
INTERPRO	IPR001436:Alpha crystallin/Heat shock protein	4	1.123595506	2.27E-04	337	8	20594	30.55489614	0.16008353	0.028656848	0.345818269
UP_KEYWORDS	Stress response	7	1.966292135	0.001033852	349	75	22680	6.065329513	0.217412509	0.009384517	1.323634198
INTERPRO	IPR008978:HSP20-like chaperone	4	1.123595506	0.008474695	337	26	20594	9.401506505	0.998562446	0.42039069	12.18719162

Annotation Cluster 4 **Enrichment Score: 3.087280652744633**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Translation regulation	9	2.528089888	1.66E-04	349	101	22680	5.790802576	0.038565766	0.002067813	0.213538978
GOTERM_BP_DIRECT	GO:0006417~regulation of translation	9	2.528089888	0.001739215	332	121	18082	4.051030569	0.954329995	0.100957171	2.907652286
GOTERM_BP_DIRECT	GO:0017148~negative regulation of translation	7	1.966292135	0.00189616	332	71	18082	5.369675887	0.965440825	0.102866895	3.166083221

Annotation Cluster 5 **Enrichment Score: 2.863609521148051**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0005753~mitochondrial proton-transporting ATP synthase complex	7	1.966292135	3.85E-07	339	18	19662	22.55555556	1.30E-04	6.20E-06	5.24E-04
GOTERM_BP_DIRECT	GO:0006754~ATP biosynthetic process	6	1.685393258	5.12E-05	332	23	18082	14.20796228	0.086723862	0.008213086	0.086695087
GOTERM_BP_DIRECT	GO:0015986~ATP synthesis coupled proton transport	6	1.685393258	5.12E-05	332	23	18082	14.20796228	0.086723862	0.008213086	0.086695087
UP_KEYWORDS	Hydrogen ion transport	6	1.685393258	6.10E-04	349	45	22680	8.664756447	0.134669731	0.006553162	0.783107771

Table S2B: GO term analysis of genes expressed solely in myofibers

GOTERM_BP_DIRECT	GO:0015992~proton transport	7	1.966292135	6.53E-04	332	58	18082	6.57322393	0.686146426	0.04713737	1.101817829
UP_KEYWORDS	CF(0)	4	1.123595506	7.11E-04	349	12	22680	21.66189112	0.155107101	0.007301276	0.91191894
GOTERM_BP_DIRECT	GO:0046034~ATP metabolic process	6	1.685393258	7.76E-04	332	40	18082	8.169578313	0.747320364	0.053538811	1.3066037
UP_KEYWORDS	ATP synthesis	4	1.123595506	9.14E-04	349	13	22680	19.9955918	0.194786351	0.008628465	1.170648524
GOTERM_CC_DIRECT	GO:0045263~proton-transporting ATP synthase complex, coupling factor F(o)	4	1.123595506	9.87E-04	339	12	19662	19.33333333	0.28381851	0.009770242	1.334776129
GOTERM_CC_DIRECT	GO:0000276~mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	4	1.123595506	9.87E-04	339	12	19662	19.33333333	0.28381851	0.009770242	1.334776129
GOTERM_MF_DIRECT	GO:0046933~proton-transporting ATP synthase activity, rotational mechanism	4	1.123595506	0.001881068	319	14	17446	15.62561576	0.600260677	0.063397116	2.665162693
GOTERM_MF_DIRECT	GO:0015078~hydrogen ion transmembrane transporter activity	4	1.123595506	0.020140248	319	32	17446	6.836206897	0.999950246	0.281277974	25.31590099
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	7	1.966292135	0.158742929	319	200	17446	1.914137931	1	0.765760475	91.62572264
UP_KEYWORDS	Ion transport	13	3.651685393	0.243139277	349	619	22680	1.364804125	1	0.673402168	97.23616625
GOTERM_BP_DIRECT	GO:0006811~ion transport	13	3.651685393	0.38532889	332	584	18082	1.212380343	1	0.994297438	99.97386505

Annotation Cluster 6				**Enrichment Score: 2.7891107355696447**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	GO:0004129~cytochrome-c oxidase activity	7	1.966292135	9.40E-06	319	28	17446	13.67241379	0.004565935	6.54E-04	0.013481183

Table S2B: GO term analysis of genes expressed solely in myofibers

KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	11	3.08988764	4.66E-05	214	77	7691	5.134178905	0.008353438	0.001197643	0.057386581
GOTERM_CC_DIRECT	GO:0005751~mitochondrial respiratory chain complex IV	4	1.123595506	0.001964962	339	15	19662	15.46666667	0.485629012	0.017807392	2.640634492
UP_SEQ_FEATURE	topological domain:Mitochondrial matrix	4	1.123595506	0.013656687	326	28	18012	7.893076249	0.999999998	0.981458265	20.35074823
GOTERM_BP_DIRECT	GO:0006123~mitochondrial electron transport, cytochrome c to oxygen	3	0.842696629	0.019533065	332	12	18082	13.61596386	1	0.431133872	28.42234892
UP_SEQ_FEATURE	topological domain:Mitochondrial intermembrane	4	1.123595506	0.080254748	326	56	18012	3.946538124	1	0.998312434	74.95051382

Annotation Cluster 7				**Enrichment Score: 2.7596899671556194**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
SMART	SM00338:BRLZ	8	2.247191011	1.02E-05	158	51	10425	10.34996277	0.001508918	0.001508918	0.012155145
INTERPRO	IPR004827:Basic-leucine zipper domain	8	2.247191011	2.65E-05	337	54	20594	9.053302561	0.020178033	0.005083134	0.040469865
UP_SEQ_FEATURE	domain:Leucine-zipper	9	2.528089888	7.60E-04	326	108	18012	4.604294479	0.667906044	0.667906044	1.250094721
INTERPRO	IPR008917:Eukaryotic transcription factor, Skn-1-like, DNA-binding	4	1.123595506	0.002469826	337	17	20594	14.37877466	0.850677321	0.173176946	3.705761661
UP_SEQ_FEATURE	DNA-binding region:Basic motif	9	2.528089888	0.007469565	326	156	18012	3.187588485	0.999981009	0.933985492	11.66771477
GOTERM_BP_DIRECT	GO:1990440~positive regulation of transcription from RNA polymerase II promoter in response to	3	0.842696629	0.016474697	332	11	18082	14.85377875	1	0.387913744	24.54196195

Table S2B: GO term analysis of genes expressed solely in myofibers

	endoplasmic reticulum stress										
INTERPRO	IPR004826:Basic leucine zipper domain, Maf-type	3	0.842696629	0.018383546	337	13	20594	14.10225976	0.999999364	0.613735804	24.67326914
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	18	5.056179775	0.072844249	319	633	17446	1.555156071	1	0.58396708	66.21394373

Annotation Cluster 8 Enrichment Score: 2.5829907559851213

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	16	4.494382022	4.02E-04	339	316	19662	2.936708861	0.127134595	0.004522208	0.545853582
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	14	3.93258427	0.001897561	319	279	17446	2.744283772	0.603464611	0.059803139	2.688235687
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	9	2.528089888	0.023355034	332	189	18082	2.593516925	1	0.464935758	33.00783177

Annotation Cluster 9 Enrichment Score: 2.5296778101308597

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	31	8.707865169	7.59E-06	332	676	18082	2.497602837	0.013363031	0.001920029	0.01286143
UP_KEYWORDS	Oxidoreductase	17	4.775280899	0.038826877	349	639	22680	1.728883329	0.999916057	0.218846452	39.95809558
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	17	4.775280899	0.08744228	319	604	17446	1.539278374	1	0.620442146	73.09379559

Annotation Cluster 10 Enrichment Score: 2.2944128109355715

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0000122~negative regulation of	30	8.426966292	7.93E-05	332	729	18082	2.241310923	0.131121112	0.010753421	0.134288242

Table S2B: GO term analysis of genes expressed solely in myofibers

	transcription from RNA polymerase II promoter										
UP_KEYWORDS	Nucleus	100	28.08988764	8.76E-05	349	4534	22680	1.433296721	0.020543473	0.001152526	0.11276014
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	35	9.831460674	3.54E-04	332	995	18082	1.91581401	0.466123416	0.034265323	0.598230148
UP_KEYWORDS	Transcription regulation	47	13.20224719	4.45E-04	349	1799	22680	1.697791355	0.100080739	0.005008853	0.571518923
UP_KEYWORDS	Transcription	47	13.20224719	8.89E-04	349	1859	22680	1.642994431	0.190063958	0.008744872	1.139231673
UP_KEYWORDS	Activator	19	5.337078652	0.008200109	349	624	22680	1.978730439	0.857930361	0.06297745	10.06359504
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	49	13.76404494	0.011600696	332	1885	18082	1.415771308	0.999999999	0.328238072	17.94630583
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	19	5.337078652	0.019768799	332	576	18082	1.796550786	1	0.429888453	28.71351291
UP_KEYWORDS	DNA-binding	35	9.831460674	0.035216739	349	1604	22680	1.418016563	0.999795895	0.205184549	36.98734199
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	24	6.741573034	0.055027421	319	883	17446	1.486468544	1	0.506763487	55.60462999
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	18	5.056179775	0.072844249	319	633	17446	1.555156071	1	0.58396708	66.21394373
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	52	14.60674157	0.073886954	332	2279	18082	1.242703151	1	0.743579491	72.77852594
GOTERM_MF_DIRECT	GO:0003677~DNA binding	43	12.07865169	0.078076418	319	1847	17446	1.273229655	1	0.593334812	68.84873656
Annotation Cluster 11				**Enrichment Score: 2.1327195935472854**							

Table S2B: GO term analysis of genes expressed solely in myofibers

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Biological rhythms	8	2.247191011	0.003352474	349	126	22680	4.126074499	0.548811953	0.028023806	4.23360407
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	8	2.247191011	0.003722216	332	108	18082	4.034359661	0.998655593	0.163641019	6.125754047
GOTERM_BP_DIRECT	GO:0048511~rhythmic process	8	2.247191011	0.009279345	332	128	18082	3.403990964	0.999999934	0.281494374	14.61769197
GOTERM_BP_DIRECT	GO:0032922~circadian regulation of gene expression	5	1.404494382	0.025435328	332	61	18082	4.464250444	1	0.474489022	35.3860553

Annotation Cluster 12 **Enrichment Score: 1.941512977302931**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR004038:Ribosomal protein L7Ae/L30e/S12e/Gadd45	6	1.685393258	5.91E-06	337	17	20594	21.56816198	0.004534782	0.004534782	0.009024961
GOTERM_BP_DIRECT	GO:0006950~response to stress	6	1.685393258	4.12E-04	332	35	18082	9.336660929	0.518662983	0.037752474	0.696635893
INTERPRO	IPR024824:Growth arrest and DNA damage-inducible protein GADD45	3	0.842696629	7.88E-04	337	3	20594	61.10979228	0.454431869	0.082920472	1.196003713
GOTERM_BP_DIRECT	GO:0051726~regulation of cell cycle	8	2.247191011	0.004547127	332	112	18082	3.890275387	0.999690466	0.182914105	7.434666259
GOTERM_BP_DIRECT	GO:0000185~activation of MAPKKK activity	3	0.842696629	0.008696538	332	8	18082	20.42394578	0.999999812	0.275760632	13.7622652
GOTERM_BP_DIRECT	GO:1900745~positive regulation of p38MAPK cascade	3	0.842696629	0.03790937	332	17	18082	9.611268604	1	0.566392443	48.06152502
GOTERM_BP_DIRECT	GO:0006469~negative regulation of protein kinase activity	5	1.404494382	0.096792556	332	95	18082	2.866518706	1	0.823696052	82.19504122

Table S2B: GO term analysis of genes expressed solely in myofibers

GOTERM_BP_DIRECT	GO:0046330~positive regulation of JNK cascade	3	0.842696629	0.367671606	332	70	18082	2.334165232	1	0.992953131	99.95776033
KEGG_PATHWAY	mmu04115:p53 signaling pathway	3	0.842696629	0.558038581	214	67	7691	1.609220254	1	0.979095408	99.99571424
KEGG_PATHWAY	mmu04110:Cell cycle	4	1.123595506	0.672828883	214	124	7691	1.159330721	1	0.986142295	99.9998945

Annotation Cluster 13 **Enrichment Score: 1.5614457063684288**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	repeat:2-1	4	1.123595506	0.015032772	326	29	18012	7.620901206	1	0.974280432	22.16969713
UP_SEQ_FEATURE	repeat:2-2	4	1.123595506	0.015032772	326	29	18012	7.620901206	1	0.974280432	22.16969713
UP_SEQ_FEATURE	repeat:1-2	4	1.123595506	0.016484325	326	30	18012	7.366871166	1	0.968033509	24.04605947
UP_SEQ_FEATURE	repeat:1-4	3	0.842696629	0.029188826	326	15	18012	11.05030675	1	0.963269095	38.74859251
UP_SEQ_FEATURE	repeat:1-3	3	0.842696629	0.041056074	326	18	18012	9.208588957	1	0.977612279	50.02783355
UP_SEQ_FEATURE	repeat:1-1	3	0.842696629	0.095847854	326	29	18012	5.715675904	1	0.999048123	81.12362887

Annotation Cluster 14 **Enrichment Score: 1.5116632183915852**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	domain:Actin-binding	4	1.123595506	0.001827702	326	14	18012	15.7861525	0.929531757	0.734541447	2.981749335
INTERPRO	IPR001589:Actinin-type, actin-binding, conserved site	4	1.123595506	0.005984098	337	23	20594	10.62778996	0.990103711	0.342690038	8.757886912
UP_SEQ_FEATURE	domain:CH 1	4	1.123595506	0.006083067	326	21	18012	10.52410167	0.999856243	0.947614632	9.603558396
UP_SEQ_FEATURE	domain:CH 2	4	1.123595506	0.006083067	326	21	18012	10.52410167	0.999856243	0.947614632	9.603558396

Table S2B: GO term analysis of genes expressed solely in myofibers

UP_KEYWORDS	Actin-binding	10	2.808988764	0.016247827	349	252	22680	2.578796562	0.979397876	0.110990454	19.02418909
UP_SEQ_FEATURE	repeat:Spectrin 4	3	0.842696629	0.025597554	326	14	18012	11.83961437	1	0.956426831	34.88947628
UP_SEQ_FEATURE	repeat:Spectrin 3	3	0.842696629	0.036925865	326	17	18012	9.75027066	1	0.973670686	46.34456909
UP_SEQ_FEATURE	repeat:Spectrin 2	3	0.842696629	0.045350737	326	19	18012	8.72392638	1	0.980910337	53.60496596
UP_SEQ_FEATURE	repeat:Spectrin 1	3	0.842696629	0.045350737	326	19	18012	8.72392638	1	0.980910337	53.60496596
INTERPRO	IPR002017:Spectrin repeat	3	0.842696629	0.062239968	337	25	20594	7.333175074	1	0.935776169	62.51724631
SMART	SM00150:SPEC	3	0.842696629	0.07021763	158	29	10425	6.825621999	0.999979086	0.785468783	57.9953602
SMART	SM00033:CH	4	1.123595506	0.077199462	158	66	10425	3.998849252	0.999993146	0.733180358	61.60298977
INTERPRO	IPR018159:Spectrin/alpha-actinin	3	0.842696629	0.080764954	337	29	20594	6.32170265	1	0.954215766	72.36166309
GOTERM_MF_DIRECT	GO:0003779~actin binding	11	3.08988764	0.091629762	319	338	17446	1.779840849	1	0.615244979	74.81192784
INTERPRO	IPR001715:Calponin homology domain	4	1.123595506	0.127572012	337	76	20594	3.216304857	1	0.969751641	87.55710044
INTERPRO	IPR011992:EF-hand-like domain	8	2.247191011	0.159809028	337	273	20594	1.790763144	1	0.978198978	92.99791022

Annotation Cluster 15				**Enrichment Score: 1.5095728180165189**							
Category	**Term**	**Count**	**%**	**PValue**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
BIOCARTA	m_pgc1aPathway:Regulation of PGC-1a	4	1.123595506	0.013205511	38	18	1289	7.538011696	0.72089688	0.72089688	13.61999353
BIOCARTA	m_hdacPathway:Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	4	1.123595506	0.043534713	38	28	1289	4.845864662	0.986060589	0.759333965	38.75208137

Table S2B: GO term analysis of genes expressed solely in myofibers

BIOCARTA	m_nfatPathway:NFAT and Hypertrophy of the heart (Transcription in the broken heart)	5	1.404494382	0.051486178	38	50	1289	3.392105263	0.993745512	0.637558143	44.13244584

Annotation Cluster 16 **Enrichment Score: 1.5036720844528069**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Glycolysis	6	1.685393258	1.84E-04	349	35	22680	11.14040115	0.042621136	0.002175434	0.236462286
GOTERM_BP_DIRECT	GO:0006096~glycolytic process	6	1.685393258	4.72E-04	332	36	18082	9.077309237	0.566794041	0.040964417	0.796611063
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	6	1.685393258	0.035503164	214	66	7691	3.267204758	0.998506706	0.393785161	35.93431751
KEGG_PATHWAY	mmu01230:Biosynthesis of amino acids	5	1.404494382	0.158979778	214	76	7691	2.364424496	1	0.806072257	88.14764729
KEGG_PATHWAY	mmu01200:Carbon metabolism	6	1.685393258	0.21850726	214	116	7691	1.858926845	1	0.891276223	95.2015073
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics	8	2.247191011	0.381541002	214	214	7691	1.343523452	1	0.954456407	99.73117128
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	4	1.123595506	0.730705352	332	206	18082	1.057550591	1	0.999985328	99.99999998

Annotation Cluster 17 **Enrichment Score: 1.4409867721490395**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006914~autophagy	8	2.247191011	0.01575401	332	142	18082	3.068386221	1	0.37947546	23.59918337
UP_KEYWORDS	Autophagy	6	1.685393258	0.041296986	349	123	22680	3.170032846	0.999954383	0.226080765	41.91570081
GOTERM_CC_DIRECT	GO:0000421~autophagosome membrane	3	0.842696629	0.073068504	339	26	19662	6.692307692	1	0.395202698	64.38314855

Annotation Cluster 18 **Enrichment Score: 1.3782022776750231**

Table S2B: GO term analysis of genes expressed solely in myofibers

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0005667~transcription factor complex	12	3.370786517	0.006741959	339	267	19662	2.606741573	0.898378353	0.055559384	8.793190221
GOTERM_MF_DIRECT	GO:0044212~transcription regulatory region DNA binding	10	2.808988764	0.02737552	319	233	17446	2.347195501	0.999998653	0.344547913	32.8495535
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	24	6.741573034	0.055027421	319	883	17446	1.486468544	1	0.506763487	55.60462999
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	10	2.808988764	0.059636119	319	270	17446	2.025542784	1	0.526981564	58.61194383
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	18	5.056179775	0.072844249	319	633	17446	1.555156071	1	0.58396708	66.21394373
GOTERM_MF_DIRECT	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	11	3.08988764	0.121942199	319	359	17446	1.675727596	1	0.697272458	84.52173953

Annotation Cluster 19 **Enrichment Score: 1.2397110249897572**

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Chaperone	9	2.528089888	0.009536021	349	191	22680	3.062152147	0.896778879	0.068505558	11.61167118
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	5	1.404494382	0.048071455	319	75	17446	3.645977011	1	0.46813936	50.67862797
GOTERM_BP_DIRECT	GO:0006457~protein folding	4	1.123595506	0.416497567	332	128	18082	1.701995482	1	0.996248267	99.98918267

Annotation Cluster 20 **Enrichment Score: 1.1494022205001033**

Table S2B: GO term analysis of genes expressed solely in myofibers

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0031463~Cul3-RING ubiquitin ligase complex	6	1.685393258	0.005893967	339	67	19662	5.194029851	0.864401233	0.049941939	7.728015962
UP_SEQ_FEATURE	repeat:Kelch 5	5	1.404494382	0.018321039	326	56	18012	4.933172656	1	0.964967684	26.35941541
UP_SEQ_FEATURE	repeat:Kelch 4	5	1.404494382	0.02177554	326	59	18012	4.682333368	1	0.958924288	30.53212773
UP_KEYWORDS	Kelch repeat	5	1.404494382	0.023688439	349	71	22680	4.57645587	0.996592323	0.149843634	26.56880272
UP_SEQ_FEATURE	repeat:Kelch 2	5	1.404494382	0.02428505	326	61	18012	4.528814241	1	0.960864409	33.42294268
UP_SEQ_FEATURE	repeat:Kelch 3	5	1.404494382	0.02428505	326	61	18012	4.528814241	1	0.960864409	33.42294268
UP_SEQ_FEATURE	repeat:Kelch 1	5	1.404494382	0.02428505	326	61	18012	4.528814241	1	0.960864409	33.42294268
INTERPRO	IPR017096:Kelch-like protein, gigaxonin	4	1.123595506	0.029064741	337	41	20594	5.961930955	1	0.757711684	36.26304619
SMART	SM00612:Kelch	4	1.123595506	0.052032429	158	56	10425	4.712929476	0.99963235	0.928361736	47.09225283
UP_SEQ_FEATURE	repeat:Kelch 6	4	1.123595506	0.055513251	326	48	18012	4.604294479	1	0.989956398	61.13484088
SMART	SM00875:SM00875	4	1.123595506	0.059093305	158	59	10425	4.473288994	0.999878412	0.894991929	51.60107832
INTERPRO	IPR011705:BTB/Kelch-associated	4	1.123595506	0.071769655	337	59	20594	4.143036765	1	0.950919439	67.9304412
INTERPRO	IPR006652:Kelch repeat type 1	4	1.123595506	0.08063637	337	62	20594	3.942567244	1	0.960546328	72.30256739
UP_SEQ_FEATURE	domain:BACK	3	0.842696629	0.084801706	326	27	18012	6.139059305	1	0.998378742	76.9227873
PIR_SUPERFAMILY	PIRSF037037:kelch-like protein, gigaxonin type	4	1.123595506	0.101947635	51	41	1807	3.456719273	0.993614748	0.993614748	63.98780715
INTERPRO	IPR015915:Kelch-type beta propeller	3	0.842696629	0.22015168	337	54	20594	3.39498846	1	0.994304103	97.75632575
SMART	SM00225:BTB	6	1.685393258	0.231908247	158	218	10425	1.815991174	1	0.950401078	95.68659454

Table S2B: GO term analysis of genes expressed solely in myofibers

UP_SEQ_FEATURE	domain:BTB	5	1.404494382	0.282431088	326	149	18012	1.854078314	1	0.999999938	99.58795685
INTERPRO	IPR000210:BTB/POZ-like	6	1.685393258	0.295966846	337	222	20594	1.651616008	1	0.999011791	99.52935078
INTERPRO	IPR011333:BTB/POZ fold	6	1.685393258	0.327747619	337	232	20594	1.580425663	1	0.999516597	99.7675321
GOTERM_MF_DIRECT	GO:0004842~ubiquitin-protein transferase activity	8	2.247191011	0.380992634	319	326	17446	1.342077428	1	0.944075354	99.8973295
GOTERM_BP_DIRECT	GO:0016567~protein ubiquitination	8	2.247191011	0.489544262	332	362	18082	1.203621114	1	0.998410965	99.99887924

Annotation Cluster 21

Enrichment Score: 1.081681977243882

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_DIRECT	GO:0033017~sarcoplasmic reticulum membrane	4	1.123595506	0.018768443	339	33	19662	7.03030303	0.998345109	0.135449804	22.72403092
UP_KEYWORDS	Sarcoplasmic reticulum	3	0.842696629	0.115176052	349	38	22680	5.130447896	1	0.44011149	79.32609256
GOTERM_CC_DIRECT	GO:0016529~sarcoplasmic reticulum	3	0.842696629	0.263125926	339	58	19662	3	1	0.785696745	98.43045265

Annotation Cluster 22

Enrichment Score: 1.0392648112335818

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006413~translational initiation	5	1.404494382	0.017012304	332	54	18082	5.042949576	1	0.392696593	25.23810038
UP_KEYWORDS	Initiation factor	4	1.123595506	0.075330372	349	64	22680	4.061604585	0.999999991	0.344169786	63.53743468
UP_KEYWORDS	Protein biosynthesis	6	1.685393258	0.076471245	349	147	22680	2.652476463	0.999999994	0.342283269	64.11273235
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	4	1.123595506	0.127275737	319	68	17446	3.21703854	1	0.707046574	85.81729702
KEGG_PATHWAY	mmu03013:RNA transport	6	1.685393258	0.51015119	214	170	7691	1.2684442	1	0.979609428	99.98478246

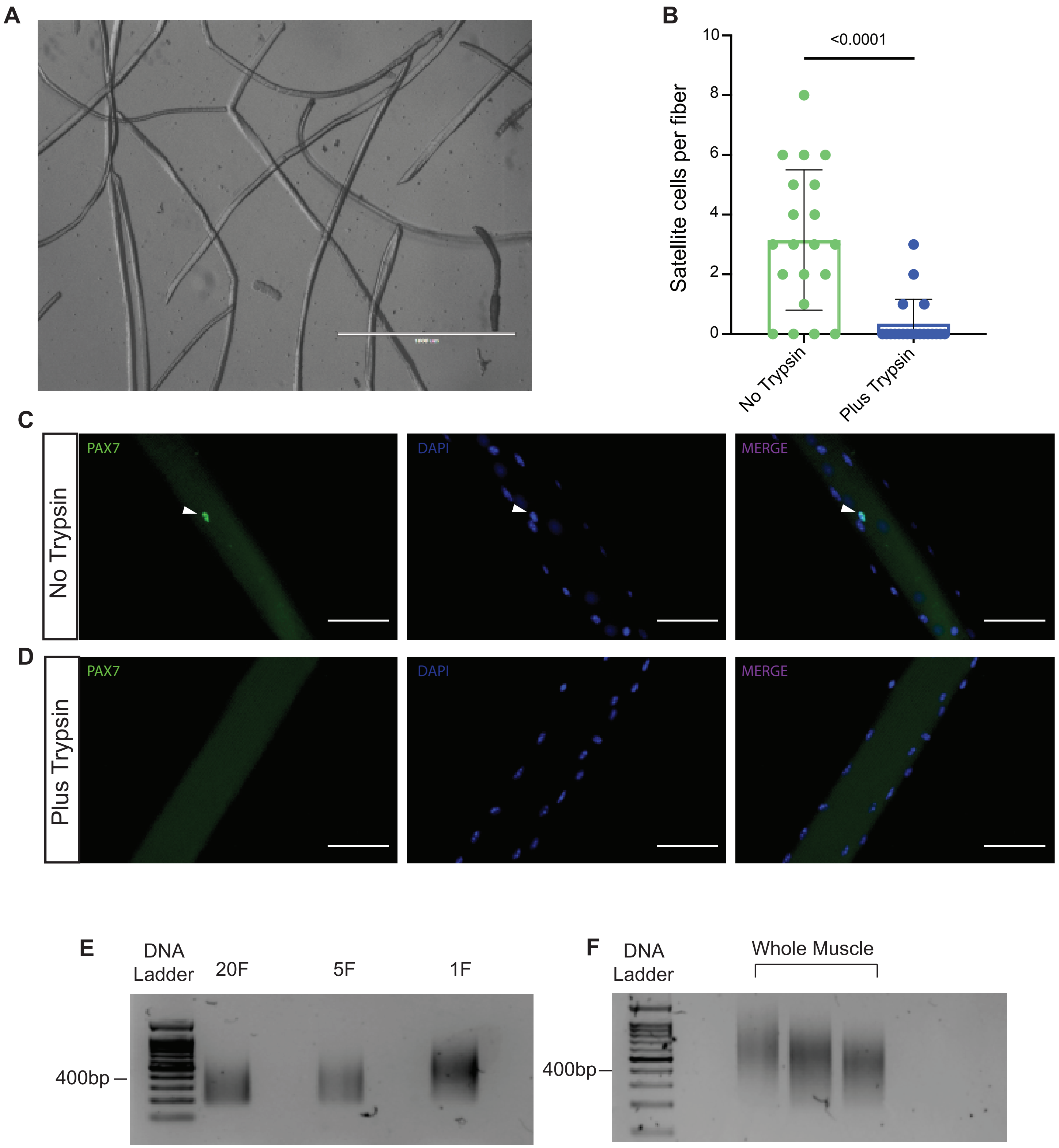
* Go term analysis of genes exclusively expressed in the single myofiber, defined as genes with a q value lower than 0.01 between single fiber and whole muscle, more highly expressed in the single fiber with a Log2 fold change of less than -1, more highly expressed than 10 RPM and with a difference in expression between single fiber and whole muscle of at least 10 RPM. Used DAVID 6.8 online functional annotation tool with the ENSEMBL_GENE_ID identifier and with a classification stringency of medium.

Table S3: Alignment statistics of sequenced reads from young and old myofibers

Sample	No Feature	Ambiguous	Unique	% overall alignment rate	% unique alignment
1M SF1	6783051	6805642	31809772	85.06	70.07
1M SF2	7516309	8878533	35451356	85.50	68.38
3M SF1	9839266	5780069	24273800	75.34	60.85
3M SF2	8509055	13154637	31692716	84.05	59.40
3M SF3	6307020	3744695	16002158	75.79	61.42
19M SF1	14806391	15264491	48244515	81.09	61.60
19M SF2	5255899	5987465	31378173	87.67	73.62
19M SF3	7121590	11497612	28455416	84.87	60.45
WM 1	2188178	1917476	9300343	83.68	69.37
WM 2	6680813	4020883	22788368	80.05	68.05
WM 3	7793097	4584231	24389338	78.80	66.34

* Alignment statistics of reads sequenced from 1 month-old single myofibers (1M SF), 3 month-old single myofibers (3M SF), 19 month-old single myofibers (19M SF) and 3 month-old whole muscle (WM). No feature is defined as reads that did not map to the genome, ambiguous as reads that mapped to more than one region and unique reads are those that mapped to a single region of the genome.

Figure S1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B
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8
6
4
2
0
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No Trypsin
Plus Trypsin
C
No Trypsin
PAX7
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MERGE
D
Plus Trypsin
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1F
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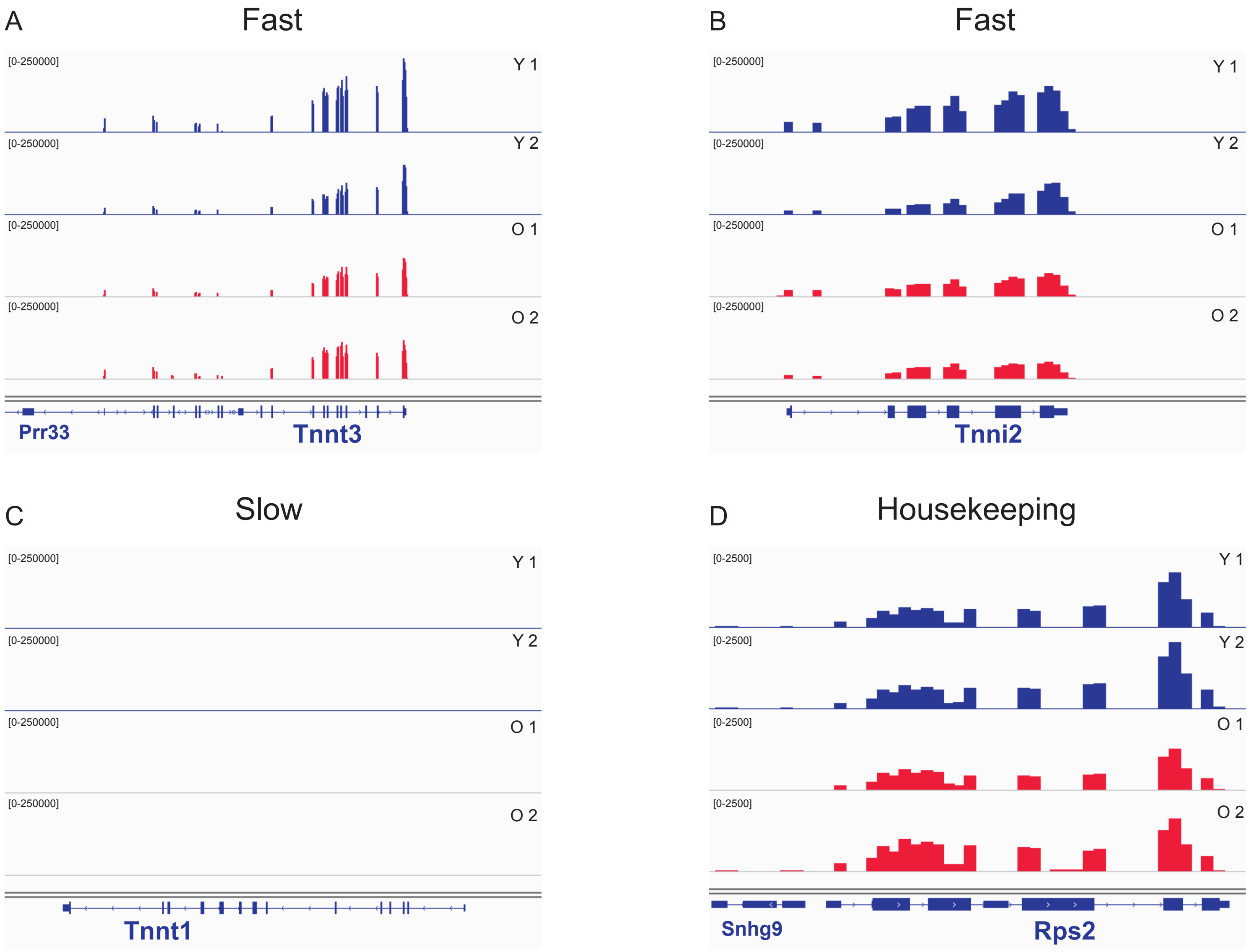
F
DNA Ladder
Whole Muscle
400bp

Figure S2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[0-250000]
Y 2
[0-250000]
O 1
[0-250000]
O 2
Prr33
Tnnt3
B
Fast
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Y 2
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O 1
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O 2
Tnni2
C
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D
Housekeeping
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Y 1
[0-2500]
Y 2
[0-2500]
O 1
[0-2500]
O 2
Snhg9
Rps2

References

1. Huang, D. W., Sherman, B. T., Tan, Q., Collins, J. R., Alvord, W. G., Roayaei, J., Stephens, R., Baseler, M. W., Lane, H. C., and Lempicki, R. A. (2007) The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists. *Genome Biol* **8**, R183