

Table S2. List of hits identified from the RNAi screen as potential regulators of muscle assembly

Comments	Gene name	FBgn#	Human homolog	Protein domains	Molecular function	Expression in myoblasts and/or muscles		
						BDGP in situ	Furlong lab.	Michelson lab.
Class I. Muscles are rounded up								
Severe	CG2165	FBgn0025704	ATP2B3	Calcium-translocating P-type ATPase, PMCA-type	Calcium-transporting ATPase activity	N/A	Yes	No
Medium	Fit1	FBgn0035498	PLEKHC1	FERM, Pleckstrin-like, Band 4.1, PH	Cell adhesion molecule binding	N/A	Yes	N/A
Medium	ldh	FBgn0001248	IDH1	Isocitrate dehydrogenase NADP-dependent	Isocitrate dehydrogenase (NADP ⁺) activity	N/A	No	No
Medium	Fit2	FBgn0036688	PLEKHC1	FERM, Pleckstrin homology-type, Band 4.1	Cell adhesion molecule binding	N/A	Yes	No
Class II. Muscles are spread, myosin filaments still show a striated pattern, but actin filaments show no discernible striations								
Severe	CG6640	FBgn0036068		Sugar transporter superfamily	Transporter activity	N/A	No	No
Severe	eIF-4E	FBgn0015218	EIF4E	Eukaryotic translation initiation factor 4E (eIF-4E)	Translation	N/A	No	N/A
Severe	Pros26	FBgn0002284	PSMB1	20S proteasome, A and B subunits	Endopeptidase activity	Yes	Yes	N/A
Severe	CG8789	FBgn0036896	MAP3K12	Protein kinase	Protein kinase activity	N/A	No	N/A
Severe	Prosbeta2	FBgn0023174	PSMB7	20S proteasome, A and B subunits,	Mitosis and meiosis	N/A	Yes	Yes
Severe	abs	FBgn0015331	DDX41	DEAD/DEAH box helicase	ATP-dependent RNA helicase activity	N/A	Yes	No
Severe	CG9779	FBgn0037231	VPS24	Snf7	Vacuolar protein sorting 24	N/A	No	N/A
Severe	CG9776	FBgn0027866		Zn-finger, C2H2 type	Nucleic acid binding, zinc ion binding	N/A	N/A	N/A
Severe	Taf4	FBgn0010280	TAF4B	Transcription initiation factor TFIID component TAF	Transcription initiation factor activity	Yes	No	No
Severe	CG14648	FBgn0037245		5-formyltetrahydrofolate cyclo-ligase	Catalytic activity	N/A	N/A	No
Severe	CG5027	FBgn0036579		Thioredoxin domain 2, Thioredoxin-related, Calsequestrin	Electron transporter activity	No	N/A	N/A
Severe	CG31523	FBgn0051523		Multicopper oxidase, copper-binding site	Acyltransferase activity; copper ion binding	Yes	Yes	No
Severe	pygo	FBgn0043900	PYGO2	Zn-finger-like, PHD finger, Aminoacyl-tRNA synthetase	DNA binding; ATP binding; tRNA ligase activity; protein binding	N/A	Yes	No
Severe	deltaCOP	FBgn0028969	ARCN1	Longin-like, Mu2 adaptin subunit (AP50) of AP2		N/A	No	No
Severe	CG1890	FBgn0039869	TBCA	Tubulin binding cofactor A	Unfolded protein binding	N/A	Yes	No
Severe	CG3457	FBgn0024984		N/A	N/A	N/A	N/A	N/A
Severe	PH4alphaNE1	FBgn0039780		Tetratricopeptide-like helical, Hpt, Prolyl 4-hydroxylase,	Procollagen-proline 4-dioxygenase activity	N/A	N/A	N/A
Severe	lva	FBgn0029688		Microfilament/microtubule-associated proteins (MMAPs)	Actin binding; microtubule binding; protein binding; spectrin binding	N/A	N/A	N/A

Medium	CG6020	FBgn0037001	NDUFA9	N/A	NADH dehydrogenase (ubiquinone) activity	Yes	N/A	N/A
Medium	CG6014	FBgn0027542		N/A	N/A	N/A	N/A	N/A
Medium	atms	FBgn0010750	PD2	RNA polymerase II associated, Paf1	Kinesin activity	N/A	N/A	N/A
Medium	CG1544	FBgn0039827	DHTKD1	Transketolase, central region, 2-oxoglutarate dehydrogenase E1 component		N/A	Yes	No
Medium	Nf1	FBgn0015269	NF1	Rho GTPase activation protein, Ras GTPase-activating protein, Cellular retinaldehyde-binding/triple function, C-, HEAT	Ras GTPase activator activity; receptor binding	N/A	Yes	N/A
Medium	Mgat2	FBgn0039738	MGAT2	N-acetylglucosaminyltransferase II		No	Yes	No
Severe	RhoGAP100F	FBgn0039883		PDZ/DHR/GLGF, RhoGAP, C2	GTPase activator activity; receptor binding	N/A	Yes	No
Severe	Actn	FBgn0000667	ACTN1	EF-Hand type, Actin-binding, actinin-type	Actin filament binding	N/A	Yes	No
Severe	Rpn1	FBgn0028695	PSMD2	Proteasome/cyclosome, regulatory subunit	Endopeptidase activity, enzyme regulatory activity	N/A	No	N/A
Severe	Rpn2	FBgn0028692	PSMD1	Proteasome/cyclosome, regulatory subunit	Endopeptidase activity, enzyme regulatory activity	N/A	Yes	No

Class III. Muscles are spread, and both actin and myosin filaments lack striation

Severe	Prm	FBgn0003149		Myosin tail	Striated muscle thick filament	N/A	Yes	No
Severe	bt	FBgn0005666		Protein kinase-like, Fibronectin, type III-like fold	Myosin-light-Chain kinase activity	N/A	Yes	No
Severe	Mlc2	FBgn0002773	MYL2	EF-Hand type, Calcium-binding EF-hand	Microfilament motor activity	N/A	Yes	No
Severe	Tmod	FBgn0082582	TMOD1	Tropomodulin	Tropomyosin binding; actin binding;	N/A	Yes	No
Medium	polo	FBgn0003124	PLK1	POLO box duplicated region, Protein kinase	Receptor signaling protein serine/threonine kinase activity	N/A	Yes	Yes

Class IV. Muscles with short and/or thin myofibrils

Severe	Ac76E	FBgn0004852		Guanylate cyclase	Guanylate cyclase activity, G protein coupled receptor pathway	N/A	Yes	No
Severe	CG5931	FBgn0036548	ASCC3L1	DEAD/DEAH box helicase, Sec63	ATP-dependent RNA helicase activity	N/A	Yes	No
Severe	CG31374	FBgn0051374		Actin binding WH2 domains	Actin binding, actin assembly	N/A	No	No
Severe	CG8636	FBgn0029629	EIF354	Zn-finger, CCHC type, RNA-binding region RNP-1	Translation initiation factor activity;	Yes	No	No
Severe	CG8743	FBgn0036904	MCOLN3	Cation (not K+) channel, Ca ²⁺ /Na ⁺ channel	Calcium channel activity	N/A	No	No
Severe	crn	FBgn0000377	CRNKL1	Phosphatidylinositol transfer protein-like, N-termi	Pre-mRNA splicing factor activity; transporter activity	N/A	No	No
Severe	Taf2	FBgn0011836	TAF2	N-6 Adenine-specific DNA methylase	General RNA polymerase transcription factor activity	Yes	No	No
Severe	Trn	FBgn0024921	TNPO1	Armadillo-like helical, Importin-beta, N-terminal,	Protein carrier activity	N/A	N/A	No

Severe	Vinc	FBgn0004397	VCL	Vinculin/alpha-catenin, Vinculin	Actin binding; structural constituent of cytoskeleton	N/A	N/A	No
Severe	RpL4	FBgn0003279	RPL4	Ribosomal protein L4/L1e	Nucleic acid binding; structural constituent of ribosome	N/A	No	No
Severe	RpS12	FBgn0014027	RPS12	Ribosomal protein L7Ae/L30e/S12e/Gadd45	Nucleic acid binding; structural constituent of ribosome	Yes	No	No
Severe	RpS9	FBgn0010408	RPS9	RNA-binding S4, Ribosomal protein S4/9,	Nucleic acid binding; structural constituent of ribosome	N/A	Yes	No

RNAi phenotypes could be observed with an independent second set of amplicons. The hits are grouped into four distinct phenotypic classes (see Results) and are listed by the severity of their RNAi muscle phenotypes in primary culture. Human orthologs were determined by reciprocal BLASTP. The putative expression of *Drosophila* genes in the mesoderm (either myoblasts and/or muscles) were based on the Berkeley *Drosophila* Genome Project (BDGP) in situ expression database (<http://www.fruitfly.org/cgi-bin/ex/in situ.pl>), Dmef2 loss-of-function microarray database [the fold enrichment log₂ (mutant/wild type) is at least 0.5 or lower] (Sandmann et al., 2006) and Dmef2 chip-on-chip database (Sandmann et al., 2006) (<http://furlonglab.embl.de/data>), and myoblast gene expression database [the fold enrichment log₂ (mutant/wild type) is at least 0.7 or lower] (Estrada et al., 2006).
