				DR *glp-4 daf-16; daf-2*		*glp-4; daf-2*	
Gene	Coding sequence	Forward primer	Reverse primer	Fold change	*P* value*	Fold change	*P* value*
act-1	T04C12.6	ATCGTCACCACCAGCTTTCTAT	GCAAATGAGTGAAAGGACAATAAG	0.93	9.79E-01	**1.79**	**2.66E-04**
anc-1	ZK973.6	GAAATTATTGAGGAACGACGTAGAA	CGATTTTTATCGTTGTCTTGGTAAG	**0.59**	**4.27E-02**	1.10	8.84E-01
csq-1	F40E10.3	AACTGAGGTTCTGACCGAGAAG	TACTGGTCAAGCTCTGAGTCGTC	**0.62**	**1.37E-03**	**6.15**	**5.47E-07**
myo-1	R06C7.10	TACACTGACTCTGTTGCTCGTATGT	ATTCTCATGGTCTTGAAGCATGTA	**1.65**	**1.44E-02**	**2.55**	**2.17E-04**
lev-11	Y105E8B.1	CAAGTCGACGAGGCTAAGGTTAT	CCTCAAGTGACTTCAAGTTGTTTC	1.41	2.16E-01	**2.20**	**1.29E-03**
mlc-1	C36E6.3	CCCTTAGTTTTATAGCCGAGATCAT	AAAACCATTTGGAGTGATAGAAGTG	0.53	1.70E-01	**3.51**	**1.68E-04**
mlc-2	C36E6.5	GAGCTTTTGCTATGTTCGATAAGAA	CTTTCCCTTGTACATAGCCTTGAC	0.82	9.52E-02	**3.43**	**3.14E-06**
mlc-3	F09F7.2	CAAGGAACCTACGCTGACTTCTAC	ACCTTCTTGATGAAATCCTCGTACT	1.01	4.38E-01	**3.46**	**1.72E-05**
myo-2	T18D3.4	ACTAAAACCGCTGGAGATAATGTAA	CATCGTTAAGGAAAGTCAGGTTAGA	**1.71**	**1.33E-02**	**3.10**	**1.10E-04**
myo-3	K12F2.1	TAACTGTGAAGGGAAACCAGATTAC	TCAAAAAGGTCAAGTTAGCCATATC	**1.84**	**1.36E-02**	**9.19**	**2.90E-05**
pfn-3	K03E6.6	AACTATCCAAGCCGTTATTATTTCC	ATTGTGATCAGTACTTGATGGACCT	0.56	1.67E-01	**2.04**	**1.56E-03**
tni-3	T20B3.2	TCTTGACTCCAGAAAGAAAGAAGAA	TAGATCTTCAAGAGTTGTCCCTGAT	0.90	1.19E-01	**1.36**	**5.90E-03**
unc-15	F07A5.7	AGTATGAAGAGCAAATCGAGATCAT	CCTTCTCAAGATCAACGATAAGAAC	0.90	2.34E-01	**3.89**	**7.06E-07**
unc-27	ZK721.2	TCACTCAAGAAGGTGTCGAAGTA	GGCTTGTCGTCCTTCTTCTTAAC	0.40	1.30E-01	**3.20**	**1.02E-03**
unc-54	F11C3.3	GCAGTTGTGGATTAACTTCGTAAAC	ACTCTTCATCAAGCATGGAGATAAT	0.80	1.63E-01	**3.86**	**3.23E-05**
unc-60	C38C3.5	GTCTTCTTCACATTTTCACCTCTTAAC	TACCCGGCACATTGTATTAAATTAG	0.92	4.43E-01	1.18	9.19E-02

Supplemental table 3. qRT-PCR of selected muscle-related proteins. Average mRNA expression level of muscle expressed genes compared to the fully fed *glp-4 daf-16,daf-2* strain (FF, fully fed; DR, dietary restricted by bacterial dilution) with corresponding *P* values and the 95% Confidence interval (CI) levels (-95% CI, lower interval; +95% CI, upper interval).