				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 *
rpl-4	B0041.4	GTCTGCCTTCAAGAAGCTTGATAC	CTTTGGAGCTCTGATAGCCTTAAC	0.99	0.89	**1.45**	**0.030**
rpl-6	R151.3	ACGACGAGTACTTCAAGAGAAAGTC	GTGAGAATCTCGTTCCAAGGTATC	1.01	0.78	**1.41**	**0.029**
rpl-7	F53G12.10	AACAAGGAGAAGAAGACCCAATACT	CTTTGGATGAAGCTGGTTGATA	0.97	0.78	**1.51**	**0.020**
rpl-9	R13A5.8	AAACAGAACTGTTGAGATCCGTAAC	GGACATCATTTCCCTCGACTAC	0.97	0.99	1.29	0.060
rpl-19	C09D4.5	GAAACTCCAAATACTGGGTAGCA	CAGAAATCTCGCTGACCTCATT	0.94	0.21	**1.58**	**0.018**
rpl-21	C14B9.7	CTCCACCTACTACACCCAGTACAAG	GATGTTGATTCTCTTTGGAAGAATG	0.96	0.70	1.18	0.177
rpl-23	B0336.10	GCCAAGAACTTGTTCGTCATCT	TTCTTTCTGAGCTCTGGCTTTC	1.04	0.41	**1.43**	**0.024**
rpl-27	C53H9.1	CCTTCGATAAGACCAACATCAAC	CAATTTGGTGAAGAACCACTTGT	0.93	0.55	**1.41**	**0.047**
rpl-30	Y106G6H.3	AGAAAAATGCTGAGAACATCAACTC	CGTAGTACTCAATCTCGGACTTTCT	1.04	0.73	1.15	0.333
rpl-31	W09C5.6	GACACCAAGCTCAACAAGTTCAT	AACGTAGGTGCAGAGGGTGTAG	0.97	0.86	1.23	0.158
rpl-35	ZK652.4	AGTTCTACGCTGACCACAAGTACA	GGATAACAATGAATACAAGCCACTT	1.01	0.79	**1.44**	**0.020**
rpl-36	F37C12.4	GTCAAAACAGACACAAGGGAGTC	GGAGTTCCTCTCTCTTTCCCTTAG	0.96	0.45	**1.39**	**0.040**
rpl-43	Y48B6A.2	AGAACTAAGAAGGTCGGAATCGT	CAGTCTTCTGATGGTGGATCTG	1.05	0.92	1.35	0.051
rps-0	B0393.1	ACCAAATATCATCAACGTCAAGAAG	GTTGGTAAGACATCCTGGAGAGAA	1.09	0.24	**1.56**	**0.033**
rps-1	F56F3.5	GAACAATAACAAGATGGGAAAGAAG	TAGTTCCTTGGGTTCTGTTGATAAG	1.09	0.31	**1.47**	**0.022**
rps-2	C49H3.11	GAAGACTCGTCAAGGAGAAGAAGAT	GAGATCTTGAGGACCTCGTCTTTA	1.06	0.55	1.24	0.116
rps-3	C23G10.3	AAGGTCAAGATCATGCTTCCATAC	AACATCCTTCTTCTCCTCCTTGT	1.04	0.45	**1.27**	**0.036**
rps-8	F42C5.8	CACCACACCATGAAAAAGTACAC	AGTTCCTTTCCTTCGAGGATGTAT	1.01	0.76	**1.45**	**0.031**
rps-9	F40F8.10	CTGAAGACTGTGCAATCTAAAGTGA	CTTTGGATCCTTGTCTTCAAGAGT	1.06	0.48	**1.34**	**0.047**
rps-10	D1007.6	ACACCAAGCTCATCTATGAGTACCT	GTACTCACGGAGGTACAAGATTCC	1.04	0.60	**1.42**	**0.027**
rps-11	F40F11.1	GGATCTAAGAAGACTCCACGTTACA	CGGTACTTCTTGATGTAGTGAAGGT	0.95	0.54	1.22	0.089
rps-13	C16A3.9	AGGATTTGTACCATCTCGTCAAG	AGCTGACGCTTGGTCTTGTAGTAT	0.98	1.00	**1.55**	**0.043**
rps-15	F36A2.6	AATCTACAACGGAAAGGTTTTCAAC	GGAAGAGTGGGTAGCTCCAATAC	1.01	0.86	1.21	0.062
rps-18	Y57G11C.16	CCTTAACAGACAAAAGGACATCAAG	ACAATCAGACTTATCCTCCCTTCTT	0.97	0.31	**1.27**	**0.040**
rps-19	T05F1.3	CAGTCTTGCTCGTCACTTGTATTT	CTTCTCAACCCACTTGATCTTCTC	0.92	0.43	1.30	0.060
rps-24	T07A9.11	AAGCTTTATAAGACCACTCCAGACA	GGACCTTCTTTTGTCTGTTCTTTC	0.93	0.33	1.14	0.144
rps-27	F56E10.4	GTTCAACACCCAAACTCCTACTTC	CAATTACGGGAAACTTATTGCTTCT	1.02	0.50	**1.37**	**0.028**

Supplemental table 2. qRT-PCR of selected ribosomal protein subunits. 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).