Cell Systems, Volume 10

Supplemental Information

Molecular and Functional Networks Linked

to Sarcopenia Prevention by Caloric

Restriction in Rhesus Monkeys

Timothy W. Rhoads, Josef P. Clark, Grace E. Gustafson, Karl N. Miller, Matthew W. Conklin, Tyler M. DeMuth, Mark E. Berres, Kevin W. Eliceiri, Laura K. Vaughan, Christine W. Lary, T. Mark Beasley, Ricki J. Colman, and Rozalyn M. Anderson

Supplemental Figure Legends.

Fig. S1, related to Table 1. Longitudinal upper leg lean mass for study animals. The upper leg lean mass as a fraction of body weight (*left*) or total upper leg lean mass in grams (*right*), from DEXA measurements is presented as a function of either time on study (*top*) or animal age (*bottom*). A polynomial regression is fit to each diet group, with 95% confidence intervals denoted by the shaded regions. N = 5 for control and 8 for CR.

Figure S2, related to Figure 1. Chr7 miRNAs and putative gene targets statistically different between control and CR. Network diagram depicting miR members of the Chr7 locus and putative targets identified by TargetScan that were also statistically significant between control and CR.

Fig. S3, related to Fig. 2. Relative expression of lipid metabolism genes. Box plots of delta Ct values for lipid metabolism genes involved in: Fatty acid biosynthesis (*ACACA, FASN, SCD*), beta-oxidation (*CPT1A, ACADL*), lipid droplet metabolism (*PLIN2, PLIN3, PLIN4, PLIN5*), and lipid biosynthesis (*DGAT2, GPAT4*). 18S rRNA is used as the reference gene. N = 5 for control and 8 for CR.

Figure S4, related to Figure 4. Activity counts. Accelerometer counts for morning (*left*), afternoon (*middle*), and night (*right*) time periods. N = 5 for control and 8 for CR (box – Interquartile range, whiskers – minimum and maximum values, bar – median, small box – mean).

Figure S5, related to Figure 4. Regression analysis of skeletal muscle mass. Linear regressions of skeletal muscle mass measures with age and activity counts; ESM % of peak vs. age (*top*), ESM % of peak vs. 24 hour accelerometer counts (*middle*), and UL Lean % of peak vs. night accelerometer counts (*bottom*).





Fig. S3, related to Fig.2



Fig. S4, related to Fig. 4





Table S1, related to Figure 1; Microarray analysisFormatted as excel sheet with 3 tabs:-BAM genes-PAGE pathways-IPA details

Table S2, related to Figure 1; MicroRNA analysisFormatted as excel sheet with 2 tabs:

- All miRs
 Families/
- Families/loci of interest

Lifetime component	Control mean	CR mean	F-stat	p-value			
τ _M (ps)	1024.603 ± 86.650	924.025 ± 41.280	305.210	< 0.0001*			
τ ₁ (ps)	406.735 ± 32.389	383.676 ± 30.844	36.26	< 0.0001*			
τ_2 (ps)	2328.184 ± 67.003	2220.502 ± 93.971	40.31	< 0.0001*			
a₁(%)	67.856 ± 2.934	70.681 ± 0.622	187.62	< 0.0001*			
All data is presented as sample mean ± standard deviation							
*n < 0.0E	-						

Table S3, related to Figure 2; 2-photon microscopy lifetime components

*p < 0.05

Measure	Control	CR	Fstat	p-value
Fiber size				
Type I (pixel ²)	48369.551 ± 24057.213	46543.754 ± 16048.230	.02	0.882
Type II (pixel ²)	45612.918 ± 23128.762	68979.970 ± 34874.971	1.77	0.186
MMF (pixel ²)	58394.446 ± 20459.225	95402.143 ± 46398.013	3.41	0.067
Cyt c Ox intensity				
Туре І	42.757 ± 13.602	70.353 ± 17.075*	5.39	0.022
Type II	48.697 ± 19.863	45.000 ± 15.864	0.08	0.780
MMF	18.778 ± 9.593	15.927 ± 7.529	0.84	0.361
Intensity localization				
Mid	118.149 ± 17.010	138.272 ± 18.216		0.173
Perimeter	152.509 ± 24.023	187.790 ± 27.730*		0.021
	p-value < 0.0001*	p-value < 0.0001*		
	Control mid vs peri	CR mid vs peri		
0/ / /''	10,000, 10,000	40.044 0.500	10.00	0.005
% non-contractile	19.806 ± 12.292	12.214 ± 3.592	13.26	0.005
aica				

Table S4, related to Figure 3; Fiber histology parameters

Biometric	p-value	
Body weight (g)	4.39 x 10 ⁻³	
Total lean mass (g)	0.75	
% fat	0.05	
ESM as % of peak	0.34	
UL lean as % of peak	0.01	
Basal glucose (mg/dL)	0.12	
Basal insulin (µU/mL)	0.09	
Insulin sensitivity index; Si (x10 ⁻⁴)	0.23	
Metabolic cost of movement (x10 ^{-₄})	0.03	

 Table S5, related to Figure 4. P values for differences in variance between diet groups across biometric measures