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*Research article*

## **Biomechanical effects on microRNA expression in skeletal muscle differentiation**

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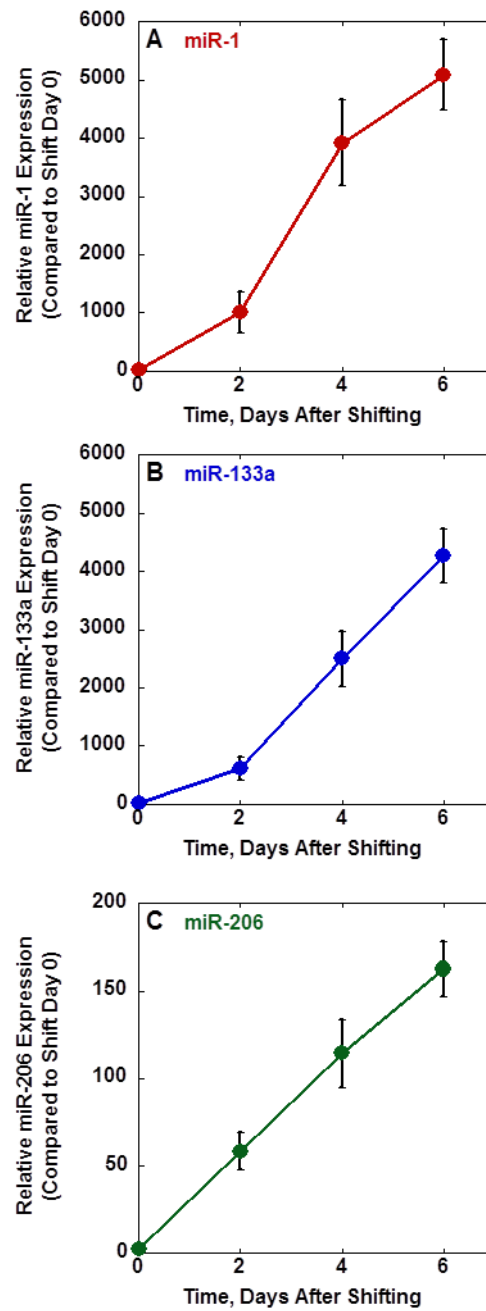
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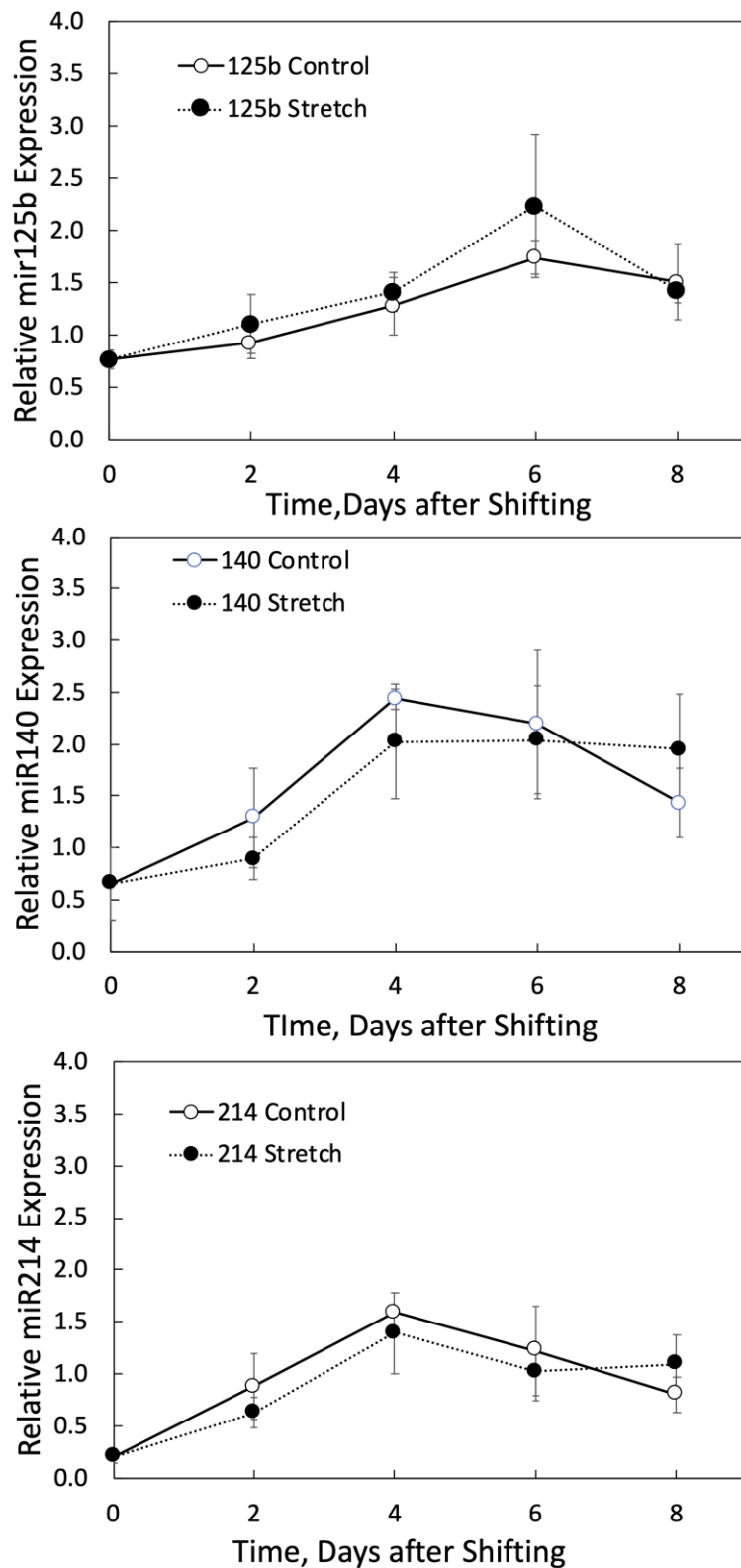
*Appendix*

**Table S1.** Comparison of microarray and RT-PCR results.

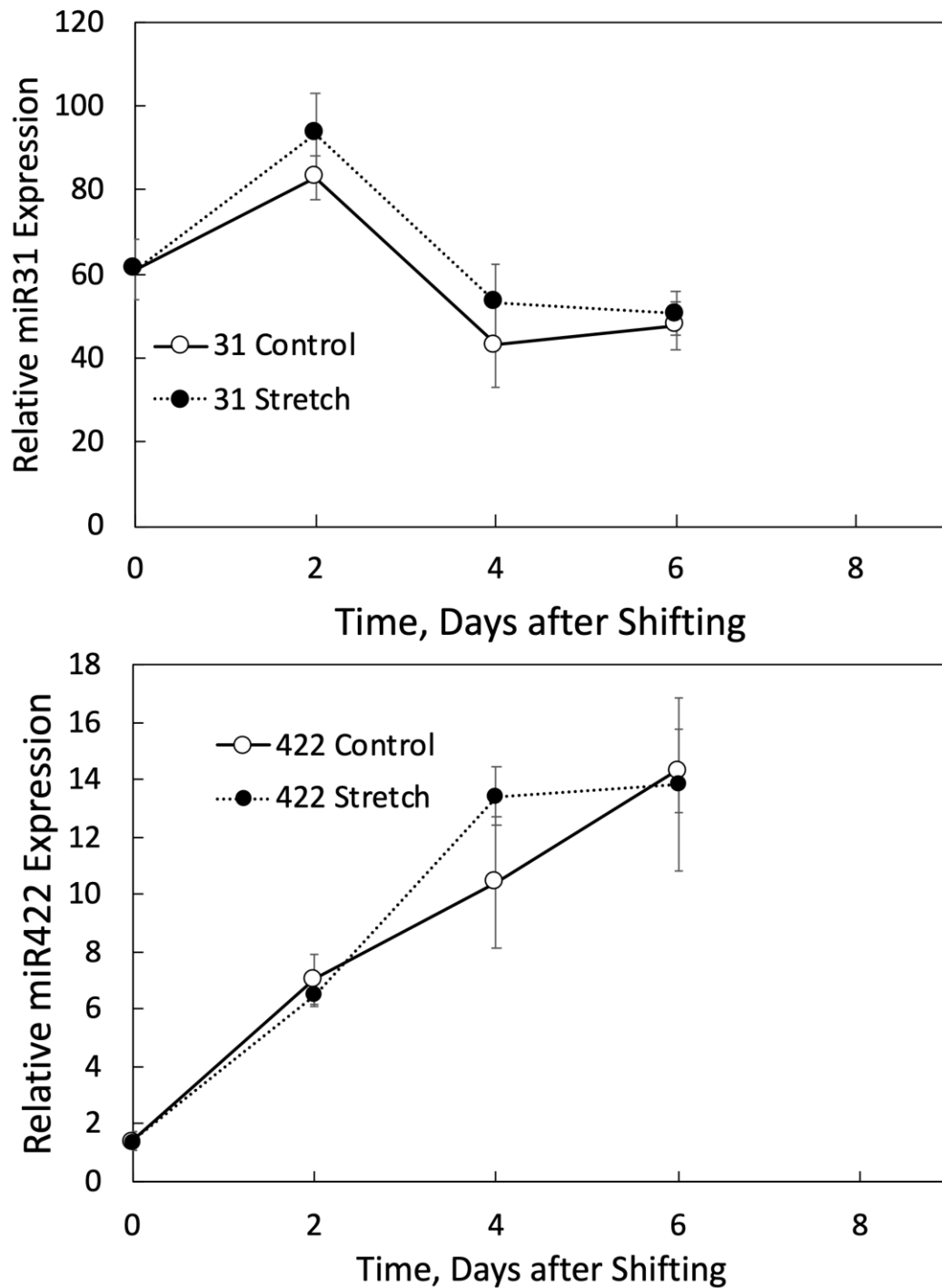
MicroRNA	MicroArray Mean $\pm$ SEM (n)	RT PCR Mean $\pm$ SEM (n)
miR-31	1.5 $\pm$ 0.1 (n = 3)	1.7 $\pm$ 0.4 (n = 5)
miR-133a	1.62 $\pm$ 0.19 (n = 3)	1.9 $\pm$ 0.3 (n = 5)
miR-125b	2 (n = 1)	1.2 $\pm$ 0.3 (n = 4)
miR-206	1.65 $\pm$ 0.23 (n = 3)	1.55 $\pm$ 0.4 (n = 4)
miR-214	1.17 $\pm$ 0.34 (n = 3)	1.2 $\pm$ 0.4 (n = 4)
miR-422b	1.45 $\pm$ 0.05 (n = 2)	1.9 $\pm$ 0.8 (n = 4)



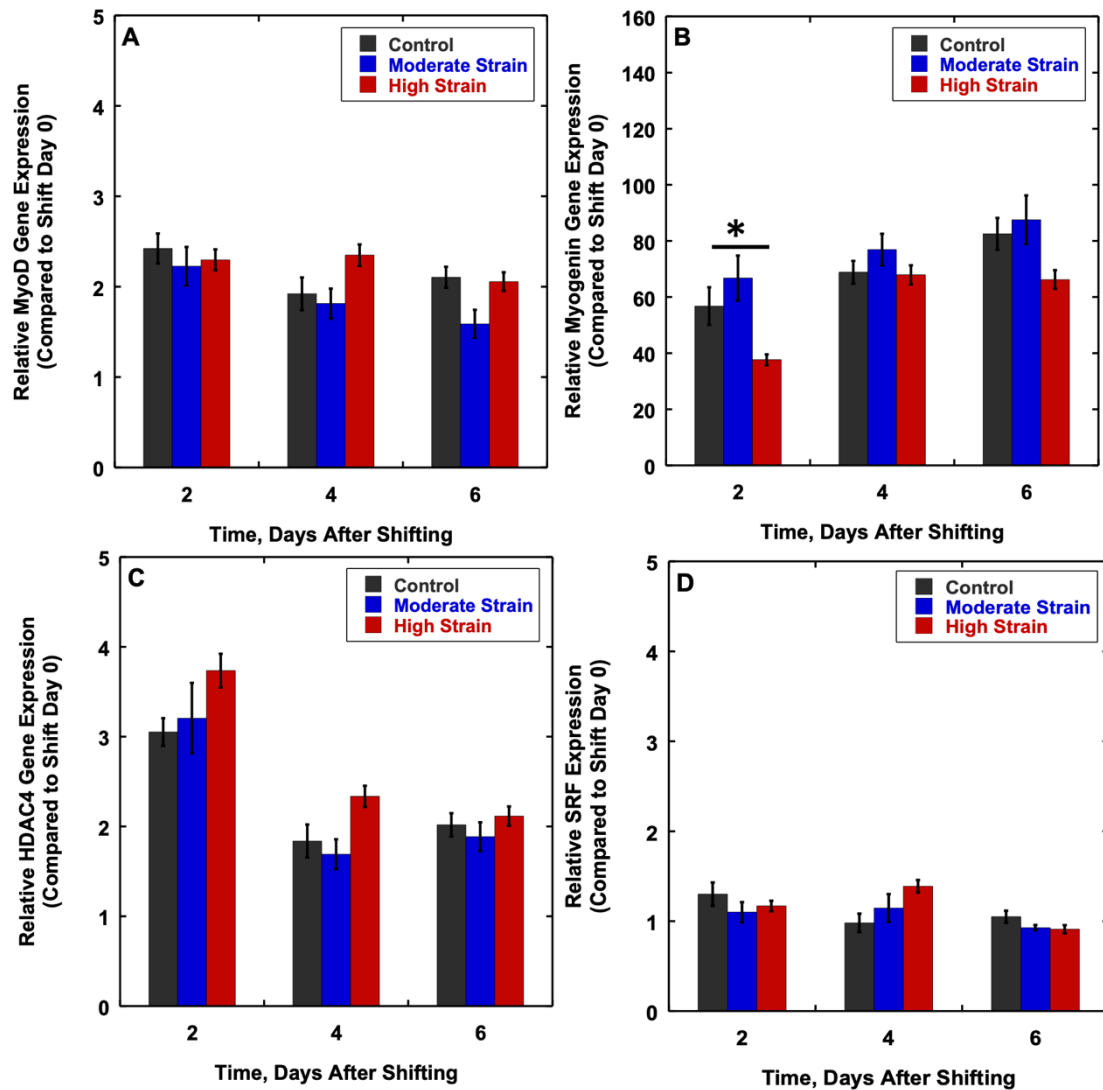
**Figure S1.** Temporal regulation of muscle specific miRNAs. (A) miR-1, (B) 133a, and (C) 206, all three exhibit this significant up-regulation with shifting media from GM to DM *in vitro*. Mean  $\pm$  SEM, n = 8.



**Figure S2.** Relative expression of miR-125b, miR-140 and miR-214 in myoblasts subjected unstretched control conditions or to the moderate strain regimen for 8 days, post differentiation. Micro RNA levels were assessed via qRT-PCR. Mean  $\pm$  SEM,  $n = 4$



**Figure S3.** Relative expression of miR-31 and miR-422b in myoblasts subjected unstretched control conditions or to the moderate strain regimen for 6 days, post differentiation. Micro RNA levels were assessed via qRT-PCR. Mean  $\pm$  SEM  $n = 5$  (for miR-422b) and  $n = 7$  (for miR-31).



**Figure S4.** Gene expression analysis in myoblasts subjected to moderate and high strain regimens via quantitative RT-PCR for (A) MyoD, (B) Myogenin, (C) HDAC4, and (D) SRF. There was no major effect of time or stretch regimen on MyoD, Myogenin, HDAC4, or SRF. Data are presented as mean  $\pm$  SEM, and  $n = 12\text{--}13$  for control samples,  $n = 6\text{--}7$  for the moderate strain regimen, and  $n = 4\text{--}5$  for the high strain regimen (\* $p < 0.05$  between moderate and high stretch).



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