## The CARM1 transcriptome and arginine methylproteome mediate skeletal muscle integrative biology



**Tiffany L. vanLieshout**<sup>1</sup>, Derek W. Stouth<sup>1</sup>, Nicolas G. Hartel<sup>2</sup>, Goutham Vasam<sup>3</sup>, Sean Y. Ng<sup>1</sup>, Erin K. Webb<sup>1</sup>, Irena A. Rebalka<sup>1</sup>, Andrew I. Mikhail<sup>1</sup>, Nicholas A. Graham<sup>2</sup>, Keir J. Menzies<sup>3</sup>, Thomas J. Hawke<sup>1</sup>, Vladimir Ljubicic<sup>1</sup>

<sup>1</sup>McMaster University <sup>2</sup>University of Southern California <sup>3</sup>University of Ottawa

Mitochondrial respiration

Muscle contraction

Functional tests

Acute exercise

Immunofluorescence

Transmission

electron microscopy

## METHODS RESULTS WT CARM1 mKO Arginine methylation occurence is comparable to phosphorylation and ubiquitination. CARM1 mK0 mice displayed remodeled transcriptomic and proteomic signatures, including muscle contraction and atrophy. RT-qPCR RNA seq Altered skeletal muscle contractile and NMJ characteristics, and decreased ability to exercise. Attenuated exercise-induced gene expression of Western blot Proteomics PGC-1a despite a preservation of upstream p-AMPK.

In **conclusion**, our findings assert an elevated prominence of arginine methylation in skeletal muscle, particularly that regulated by CARM1, as well as reveal the necessity for the methyltransferase to maintain and remodel muscle homeostasis.