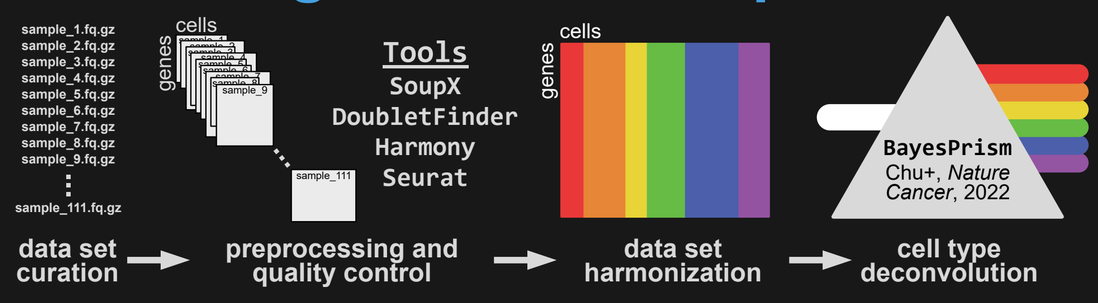
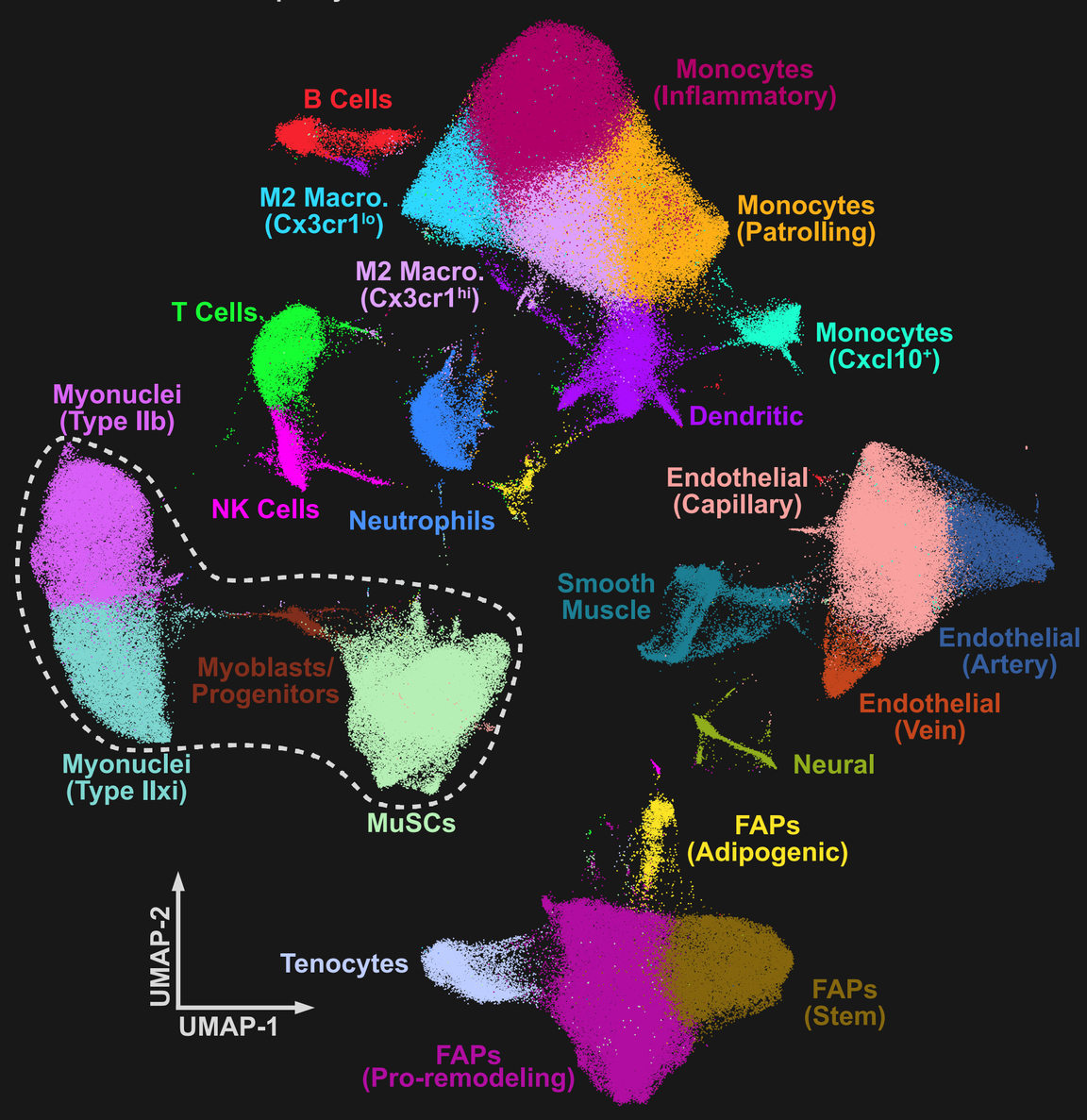
Strength in numbers: Exploring muscle regeneration through single-cell and spatial transcriptomics

David W. McKellar[1], Madhav Mantri[3], Lauren D. Walter[2], John S.L. Parker[4], Praveen Sethupathy[5], Benjamin D. Cosgrove[1,*], and Iwijn De Vlaminck[1,*]

[1]Meinig School of Biomedical Engineering, Cornell University, Ithaca, NY, USA
[2]Department of Molecular Biology & Genetics, Cornell University, Ithaca, NY, USA
[3]Department of Computational Biology, Cornell University, Ithaca, NY, USA
[4]Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University, Ithaca, NY, USA.
[5]Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY, USA

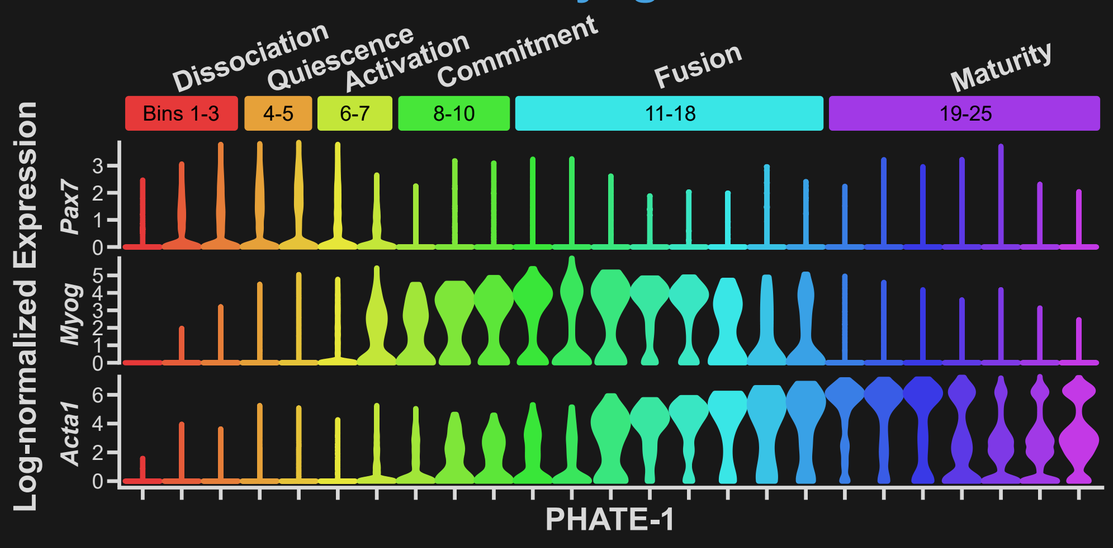
scMuscle: integrative analysis of skeletal muscle single-cell transcriptomics data





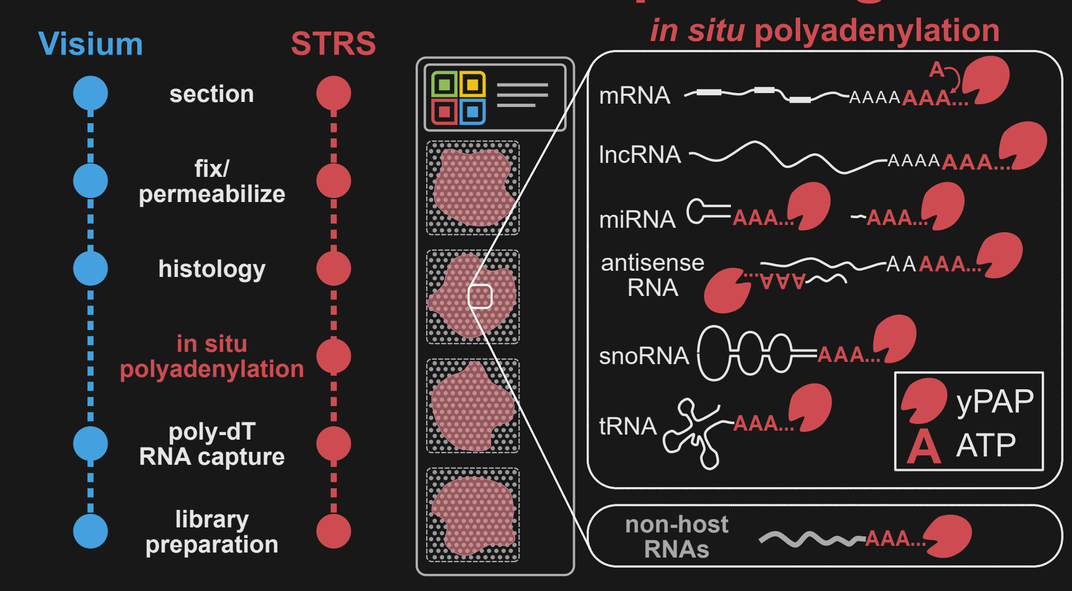
The scMuscle atlas consists of 111 murine skeletal muscle single-cell/nucleus RNA-sequencing datasets (88 public + 23 new), comprising >365k cells/nuclei. Raw sequencing data was downloaded, processed, and annotated. We used scMuscle to model myogenesis and to annotate spatial transcriptomics data.

Continuous model of myogenic differentiation



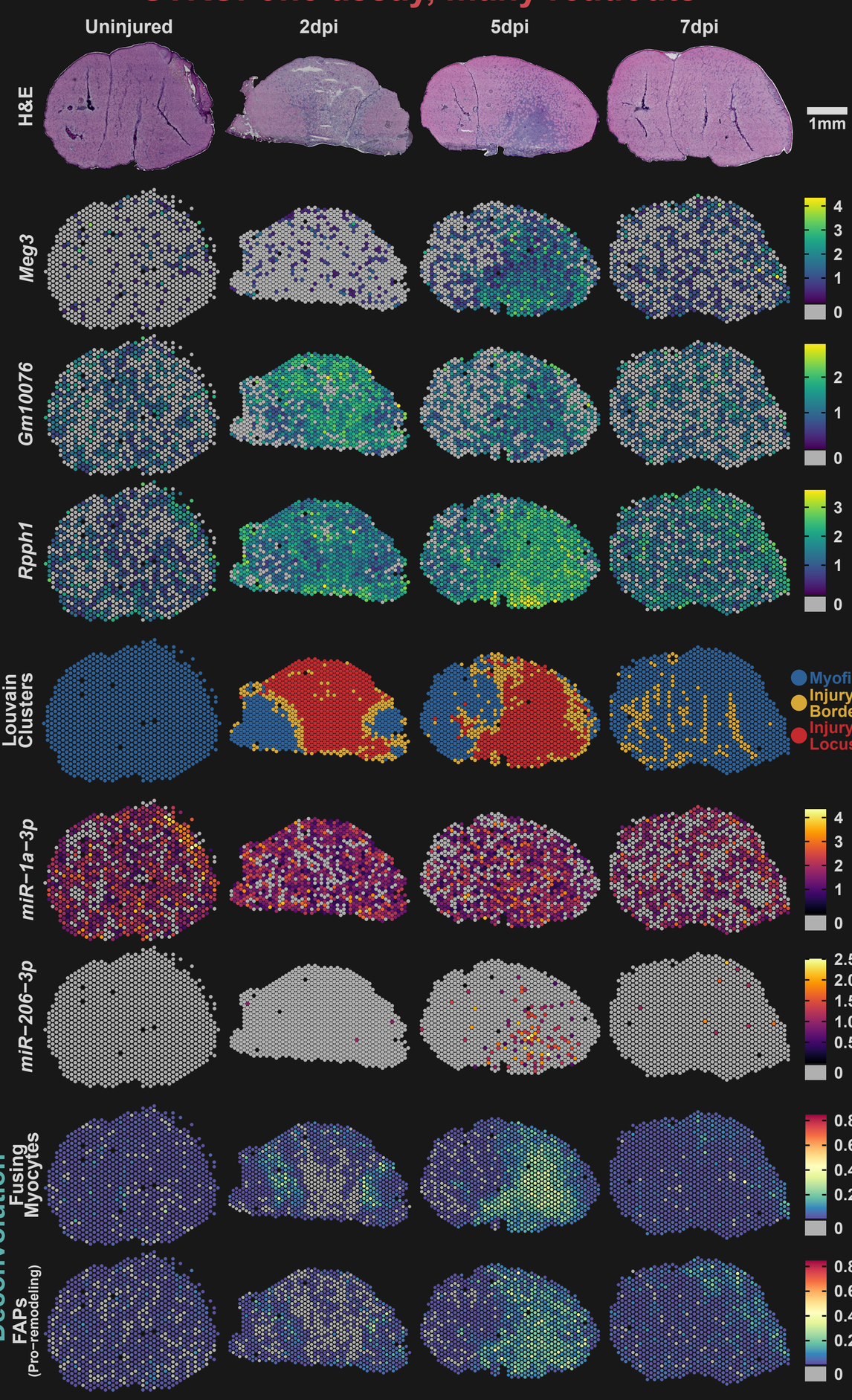
scMuscle2: single-cell transcriptomics across species

Mapping noncoding RNAs with Spatial Total RNA-Sequencing



Spatial Total RNA-Sequencing (STRS) uses *in situ* polyadenylation to capture non-A-tailed RNAs with existing spatial transcriptomics platforms. STRS enables spatial mapping of both coding and noncoding RNAs, including mature miRNAs. Spatial maps of cell types can also be achieved via spot cell type deconvolution.

STRS: one assay, many readouts



Links

scMuscle
McKellar et al, *Comms Bio*, 2021

STRS
McKellar et al, *Nat Biotech*, 2022

Contact

dwm269@cornell.edu
mckellardw.github.io
@dwmckellar
@IwijnDeVlaminck
@bdcosgrove

Acknowledgements

Thanks to Peter Schweitzer and the Cornell Biotechnology Resource Center for help with sequencing, to the Cornell Center for Animal Resources and Education for animal housing and care, to Michael Shanahan and Zhao Lai for their help generating the small RNAseq data. Thanks also to Benjamin Grodner, Hao Shi, and other members of the Cosgrove and De Vlaminck labs for helpful discussions and feedback.

This work was supported by the NIH grants 1DP2AI138242 to IDV, R21AI144557 to IDV and JSP, R01AG058630 to BDC and IDV, and T32EB023860 to DWM; American Diabetes Association Pathway to Stop Diabetes Award 1-16-ACE-47 to PS; Seed Funding Award from the Cornell Genomics Innovation Hub.