

Ischemic Stroke Vis(ium)alized

Daniel Zucha, Pavel Abaffy, Lukas Valihrach

Laboratory of Gene Expression

Institute of Biotechnology, Czech Academy of Sciences

Laboratory of Gene Expression

- Gene expression analysis
 - Bulk RNA-seq
 - Single-cell RNA-seq
 - Spatial transcriptomics
 - Method development and QC
 - Glial cell biology
 - Acute injury
 - Neurodegeneration



Projects with 10x Genomics technology

- Single-cell/nucleus RNA-seq

- Neurobiology - stroke, amyotrophic lateral sclerosis, Alexander disease (mouse models; human iPSCs and organoids)
- Developmental biology - craniofacial bones formation (mouse embryos)
- Healing/regeneration (Xenopus tadpoles)
- Gynaecology and Obstetrics - Asherman's syndrome (patient's sample)
- Plant biology - embryonic cells in Arabidopsis and Sorghum



Pavel Abaffy

- Spatial transcriptomics

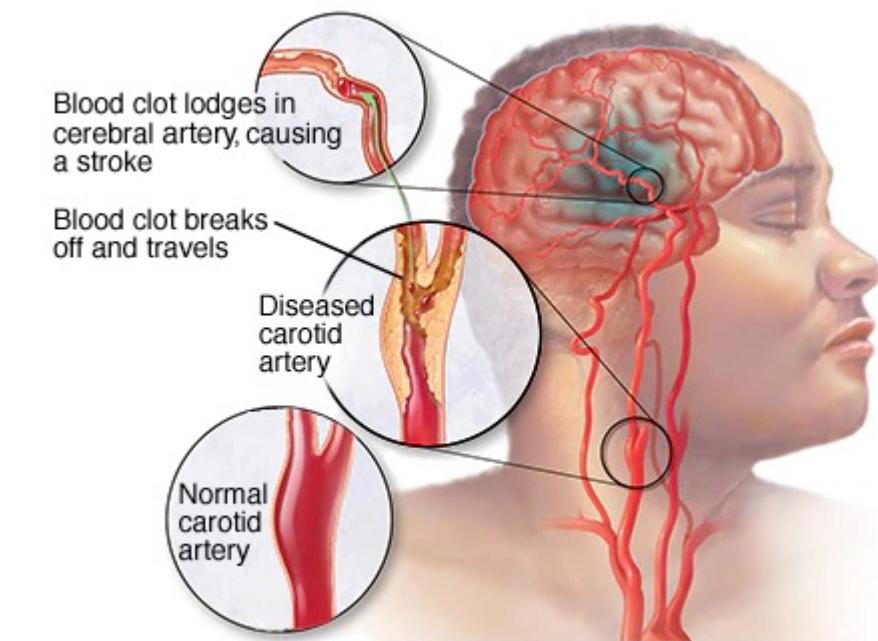
- Neurobiology - stroke (mouse model)
- Developmental biology - craniofacial bones formation (mouse embryos)



Daniel Zucha

Ischemic brain injury (stroke)

- Critical reduction in blood flow caused by either sudden or gradual occlusion of cerebral arteries
- Blockage of blood circulation causes neurologic deficits
- Main pathologic changes includes
 - Energy depletion, calcium overload, reactive oxygen species generation, inflammatory response, and ion imbalance
- Changes detrimental to basic cell functions leading to cell death

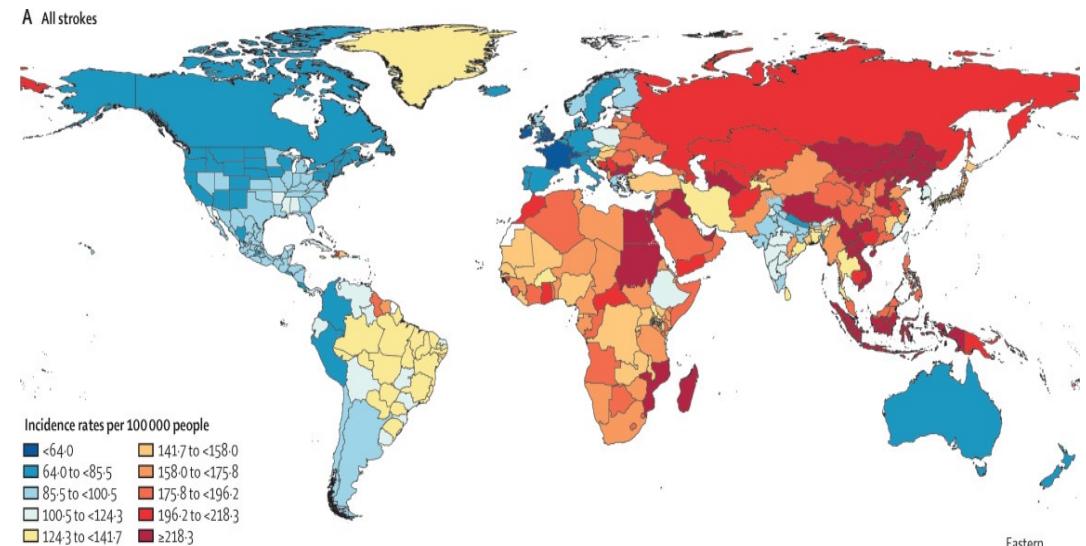


© MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH. ALL RIGHTS RESERVED.

Ischemic brain injury (stroke)

- Affects over 12 millions people per year world-wide
 - Second leading cause of death (6.5 millions)
 - Third leading cause of death and disability combined
- > Major health care and economic burden

- Demand on development of new neuroprotective strategies
 - >1000 drugs investigated
 - >100 tested in clinical trials
- Early clot lysis remains the sole approved therapy



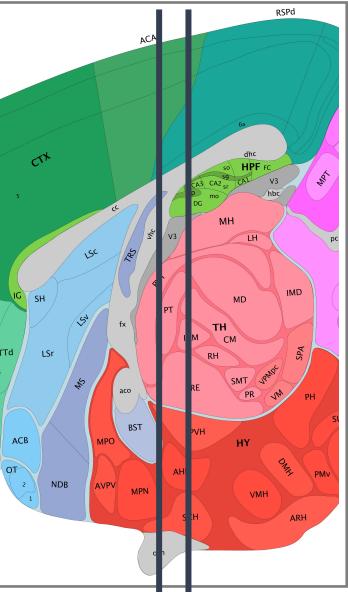
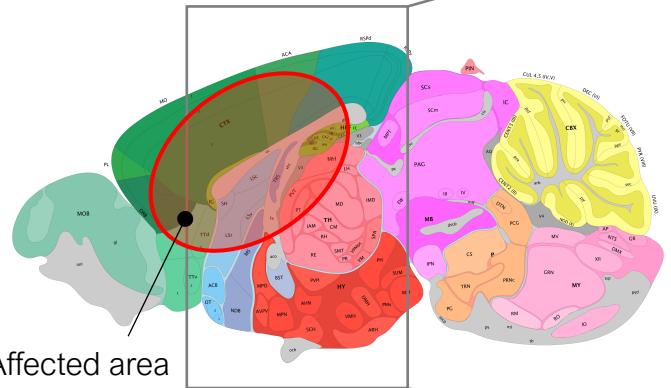
GBD 2019 Stroke Collaborators, 2021

Ischemic brain injury (stroke)

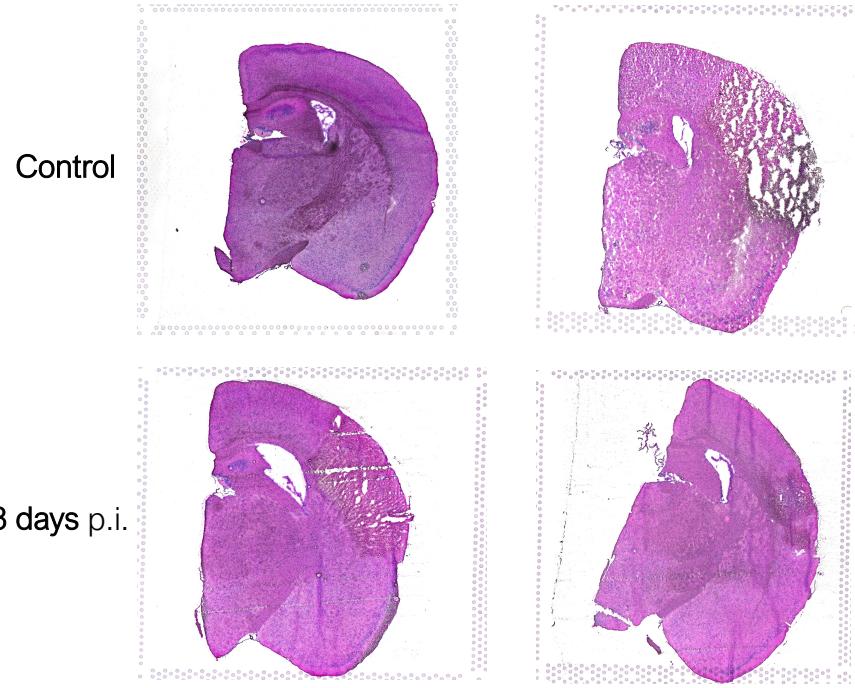
- The major reasons causing the lack of new therapeutics
 - a) Complexity of the disease involving interactions of many cell types
 - b) Existence of heterogeneity exaggerating the complexity of the disease
 - c) Temporal and spatial factors defining the role of cell types in the disease
- Unique opportunity to apply recent technologies for transcriptomic analysis
 - Single-cell RNA-sequencing
 - Spatial transcriptomics
 - Integrative analysis

Experimental model

Allen brain atlas (brain-map.org)



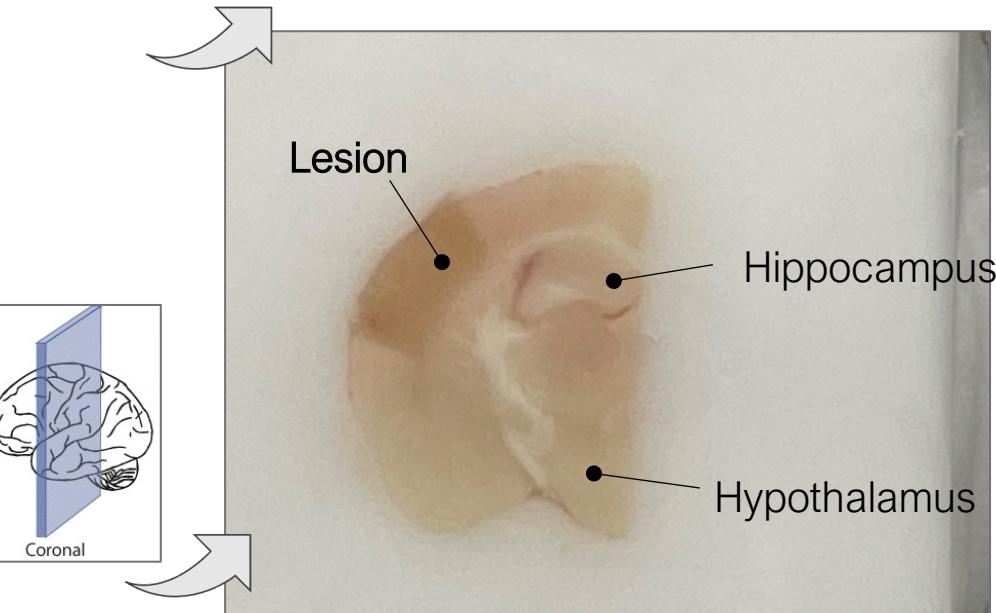
Pre-defined area of interest



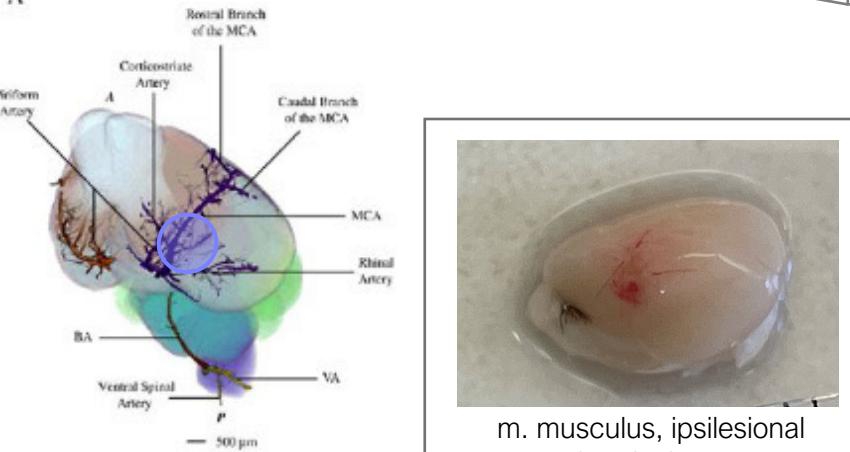
1 day post injury

3 days p.i.

7 days p.i.



A



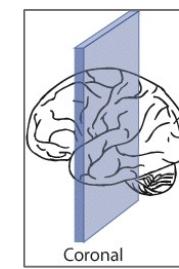
Middle cerebral artery occlusion (MCAO)



m. musculus, ipsilesional hemisphere



Freeze on dry ice



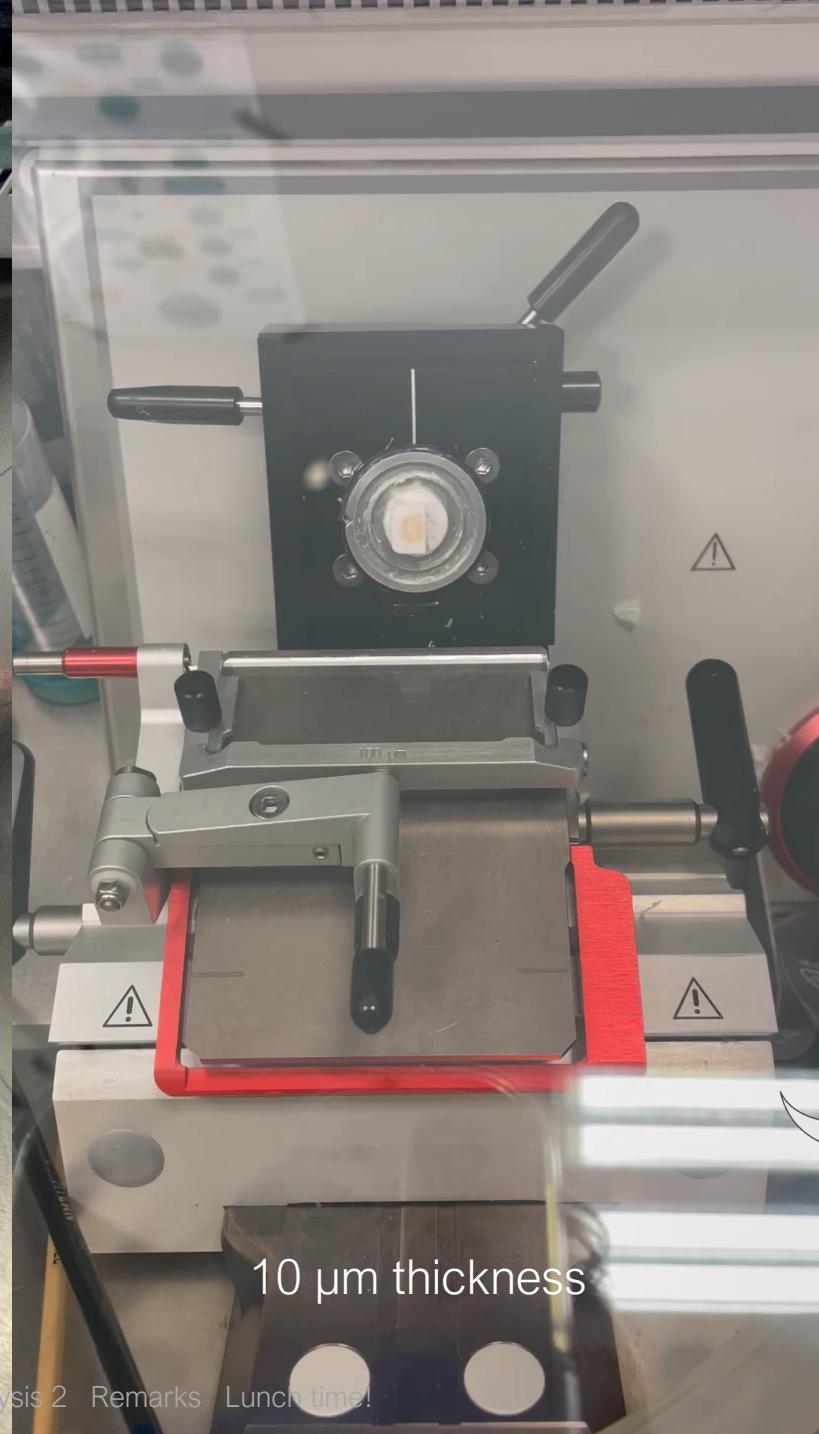
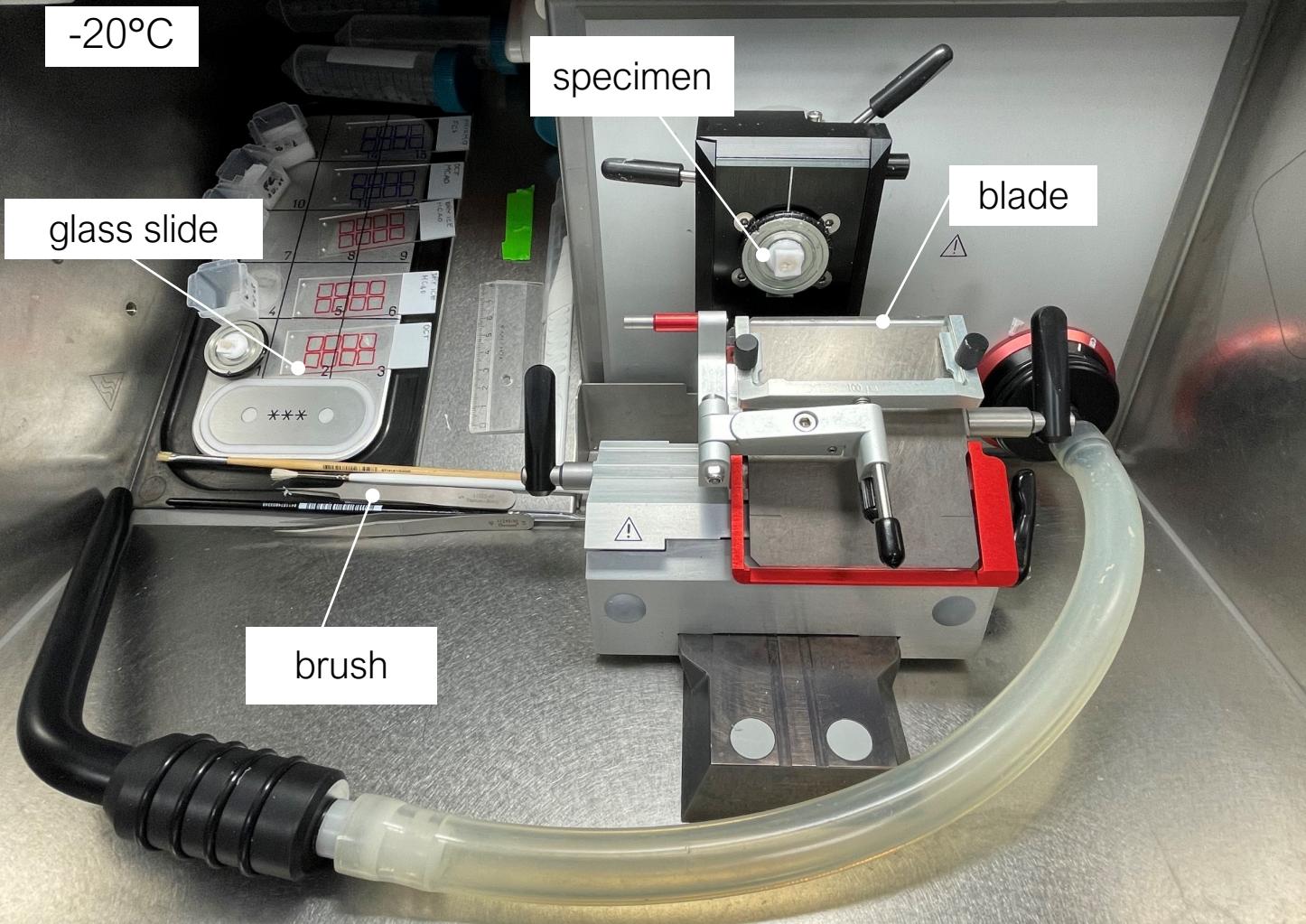
Coronal



Cryosectioning



Critical step

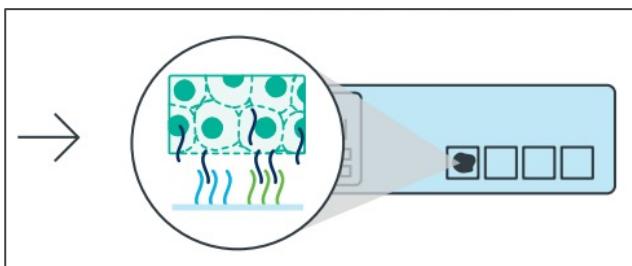
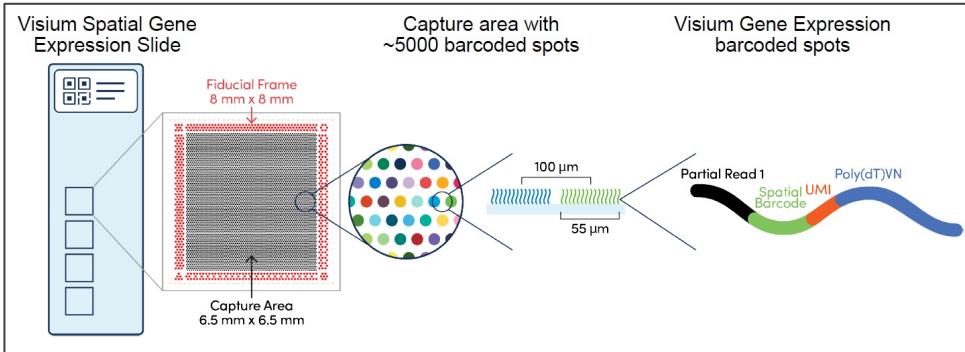


Visium Spatial
Gene Expression
Slide
PN: 2000233
SN: V10M09-040
Exp: 2021-03-09
Store at Ambient

Visium Spatial
Gene Expression
Slide
PN: 2000233
SN: V10M09-040
Exp: 2021-03-09
Store at Ambient

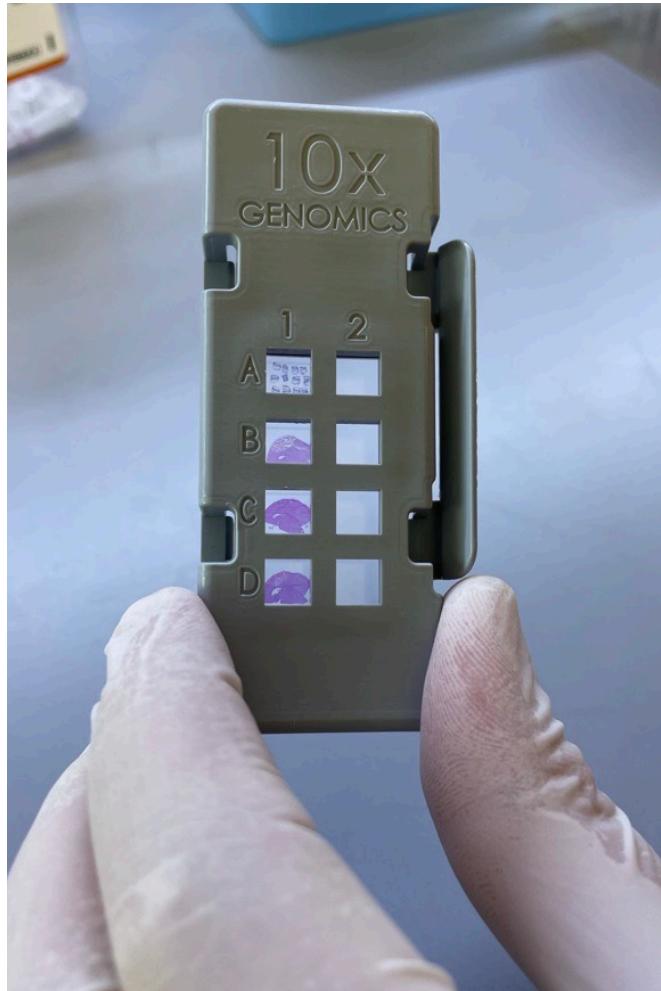
VACUUM
SUSPENSION
SYSTEM

Visium

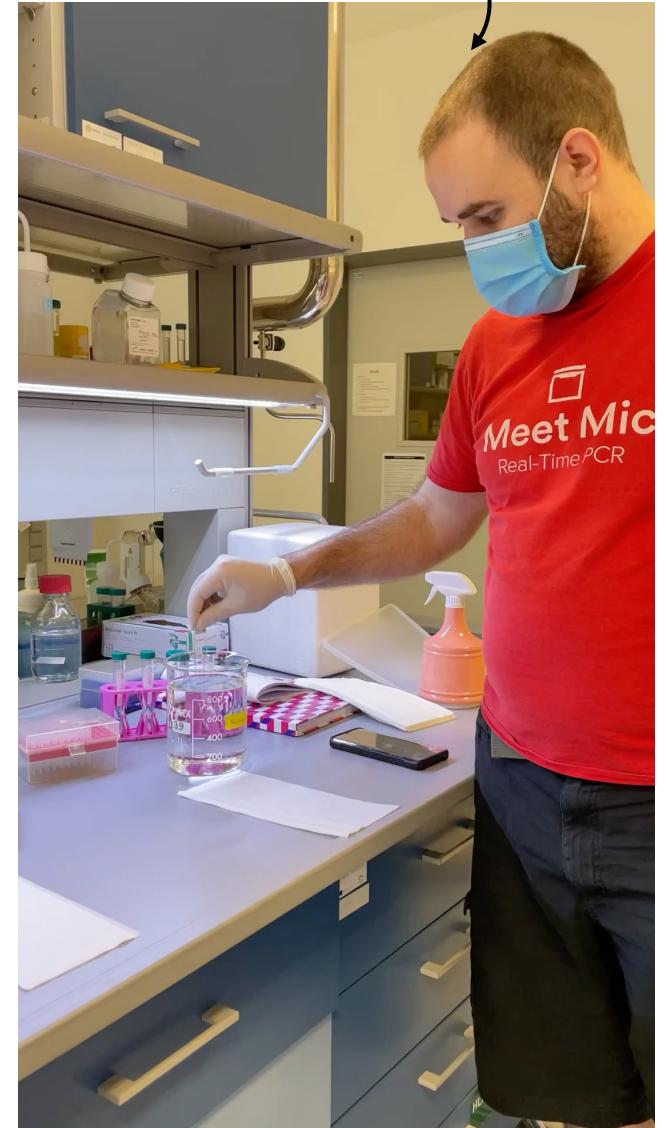


Transcriptome-wide with
spatial localization

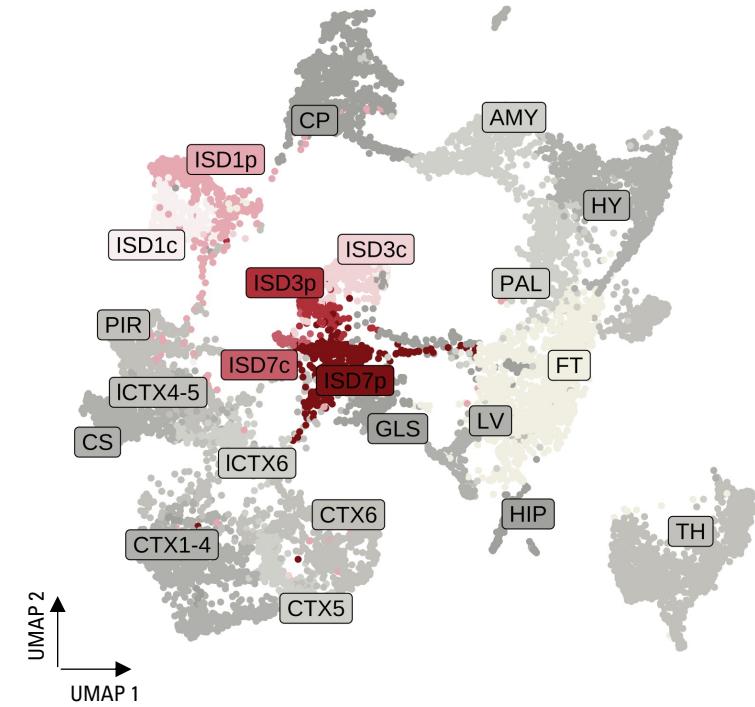
Not single-cell resolution



100 % concentrated and enjoying!:-)

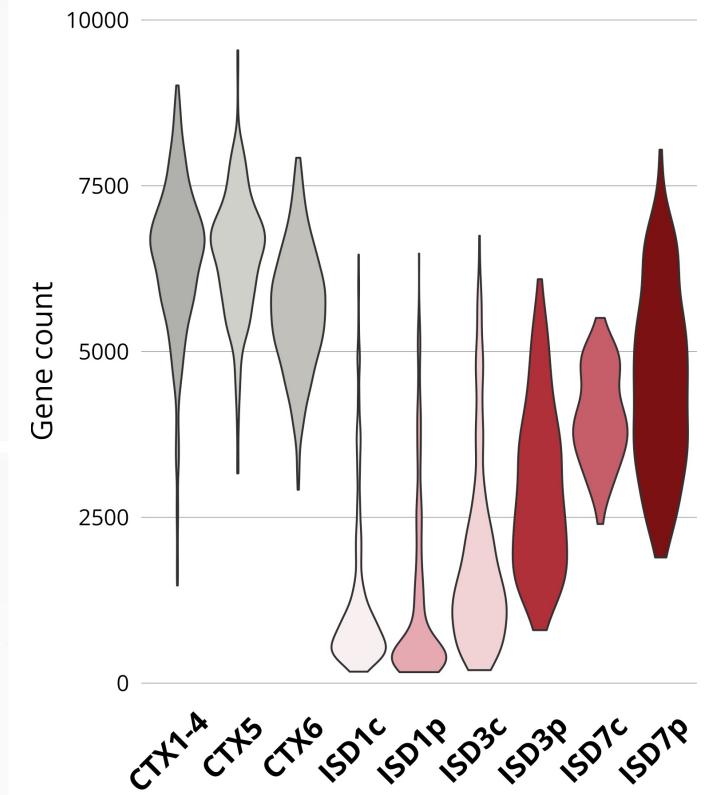
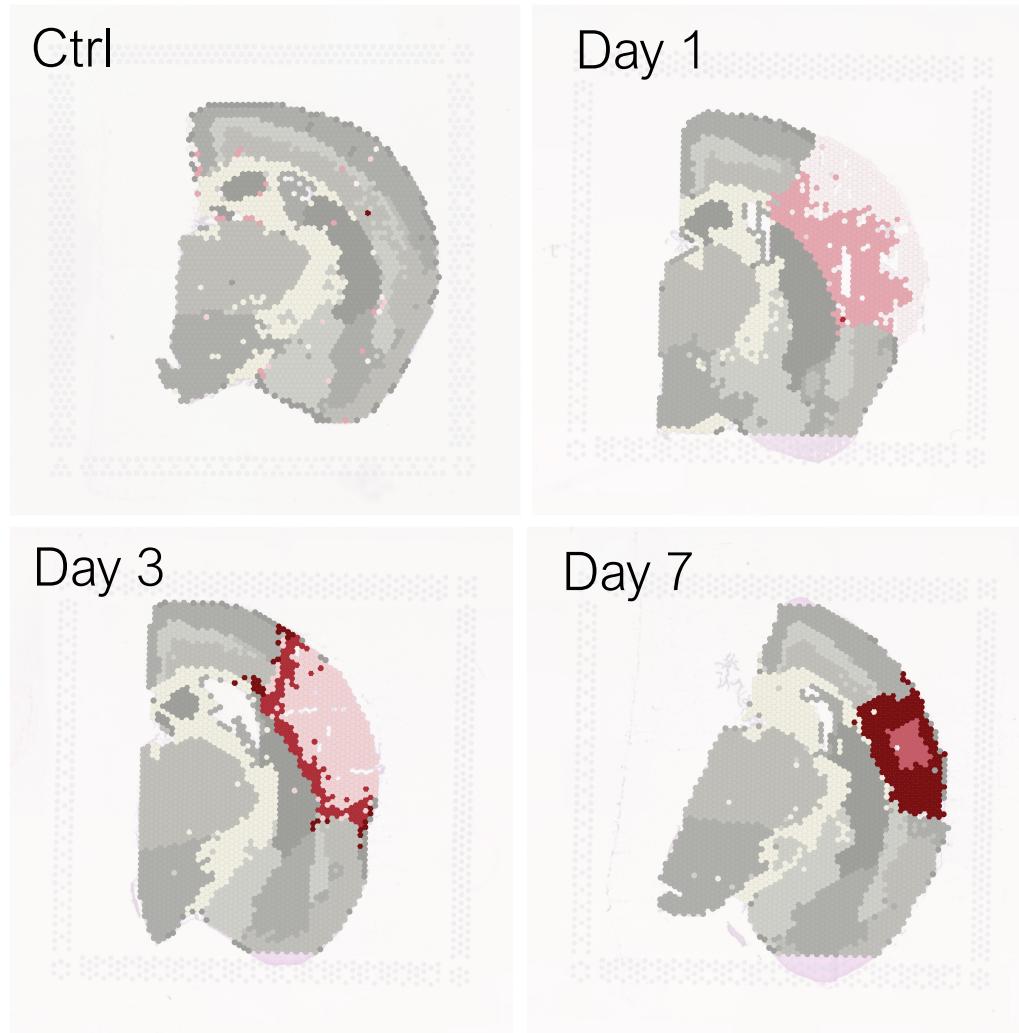


UMAP clustering



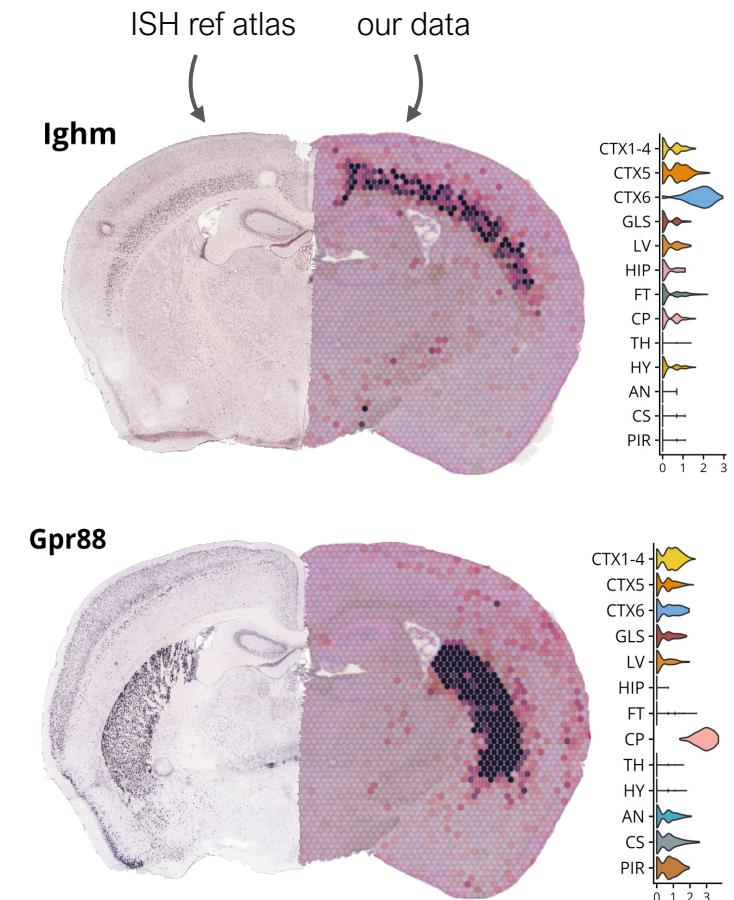
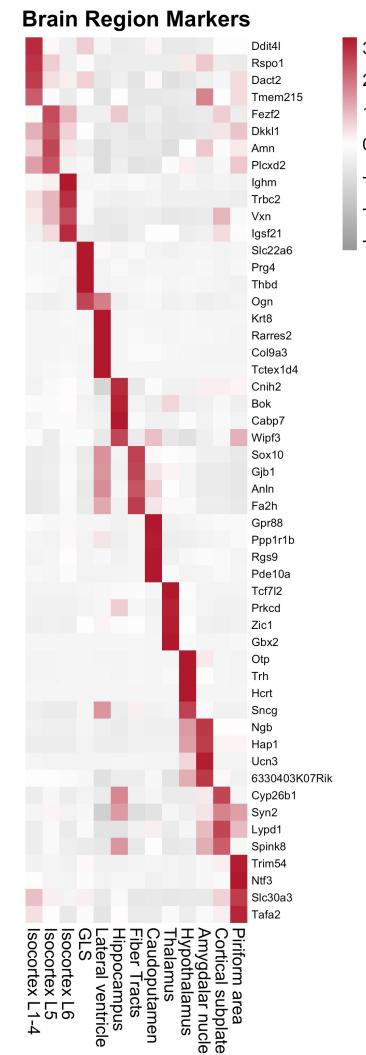
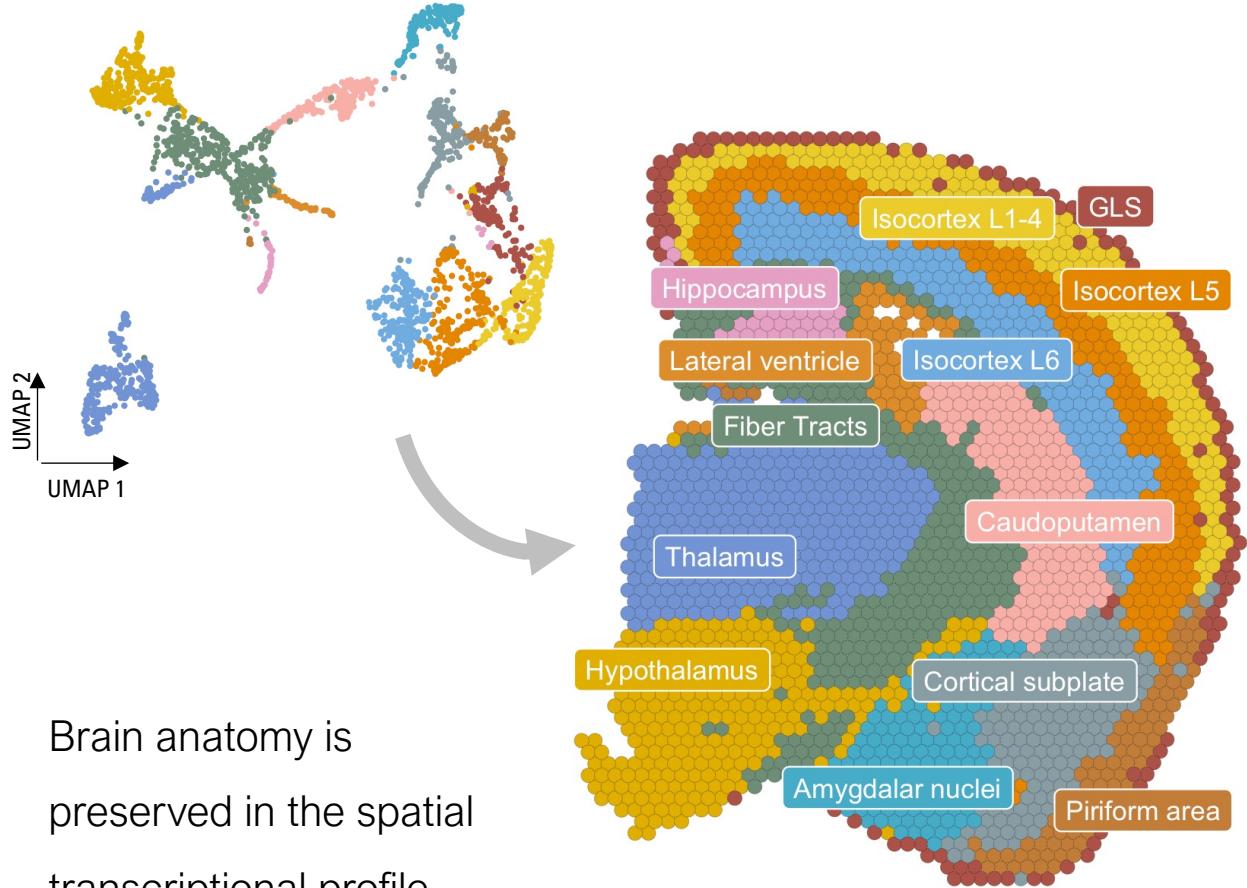
Basic Analysis – 10X Loupe Browser

Advanced – R (Seurat), Python (scipy)



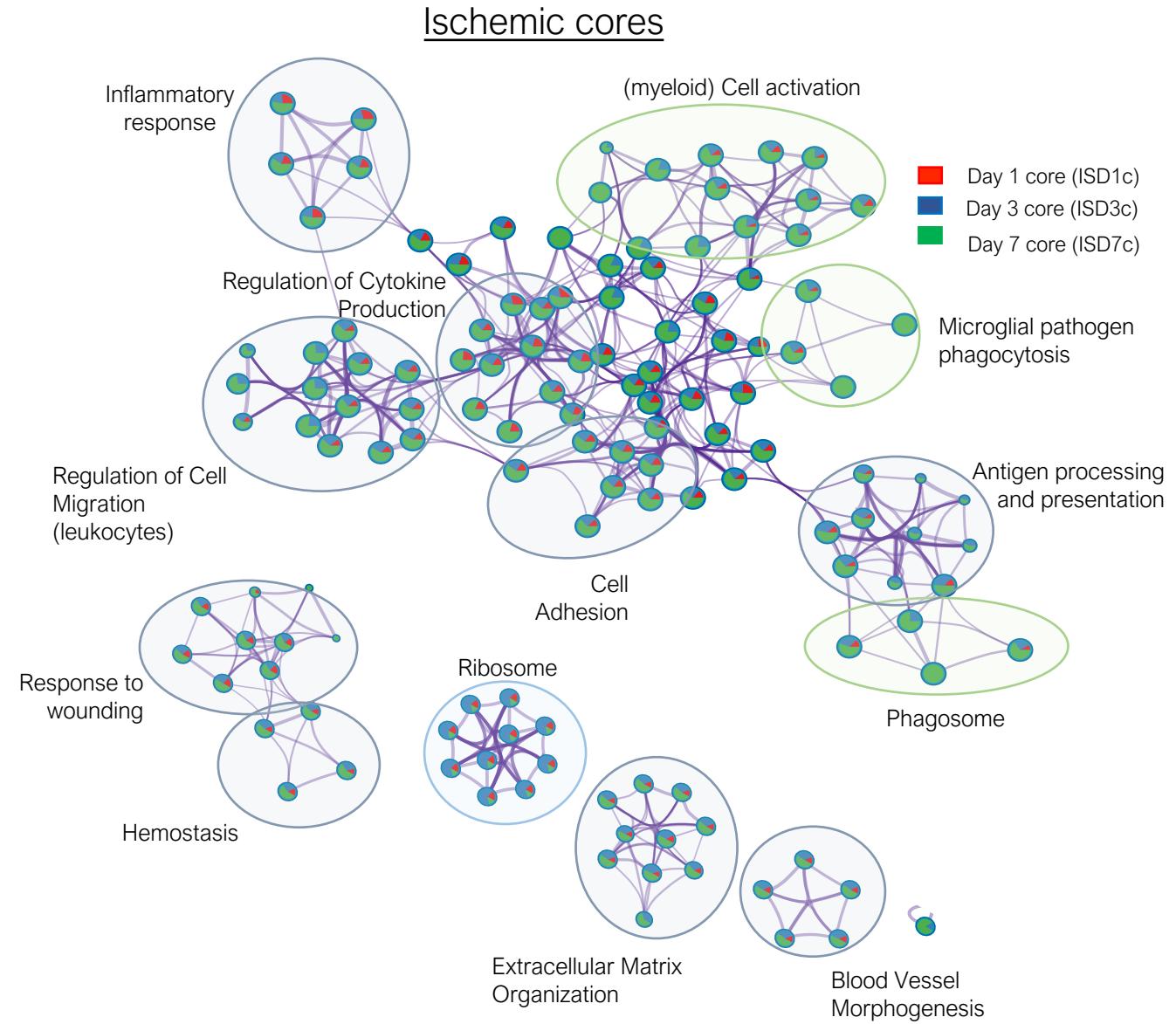
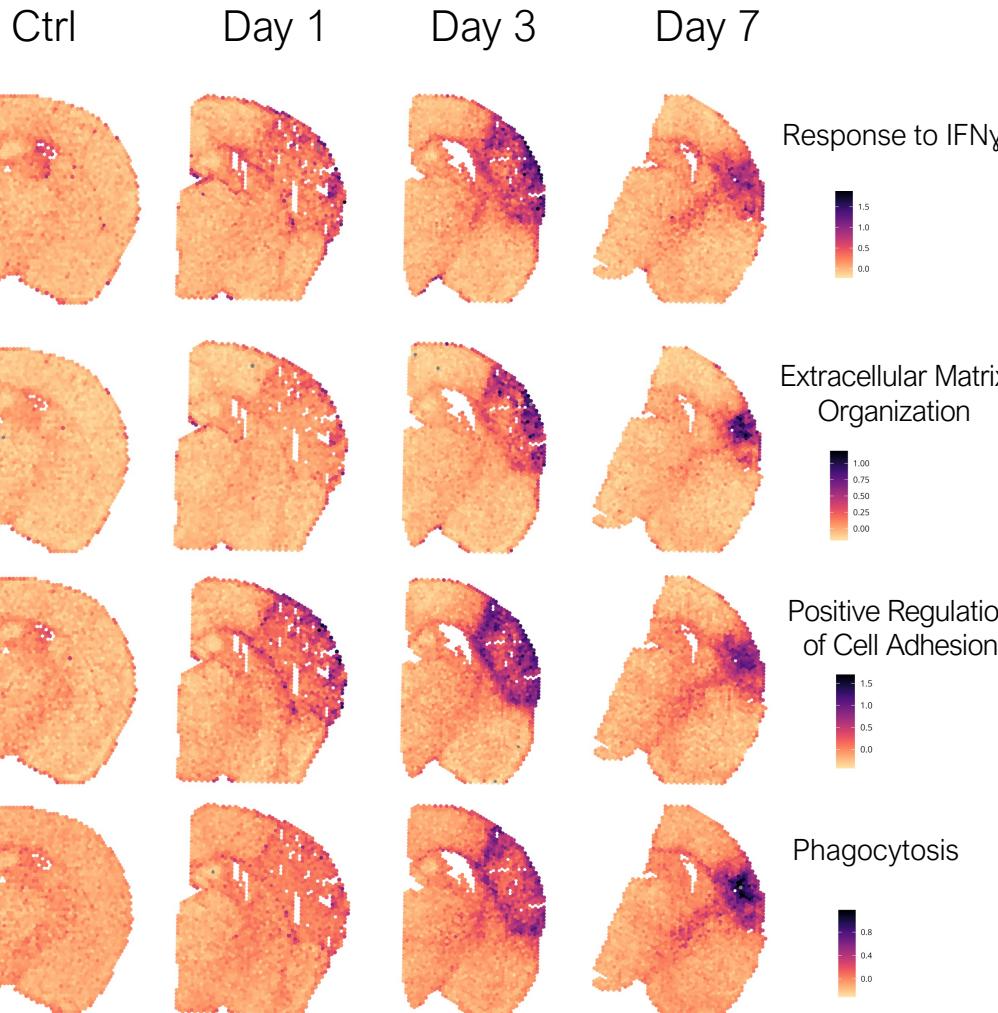
Gene abundance across the cortical landscape
(IS = ischemic area; c = center, p = periphery)

Data robustness



Marker validation with Allen Brain
Atlas *in-situ* hybridization atlas

Functional Annotation



Clustering of the Gene Ontology terms

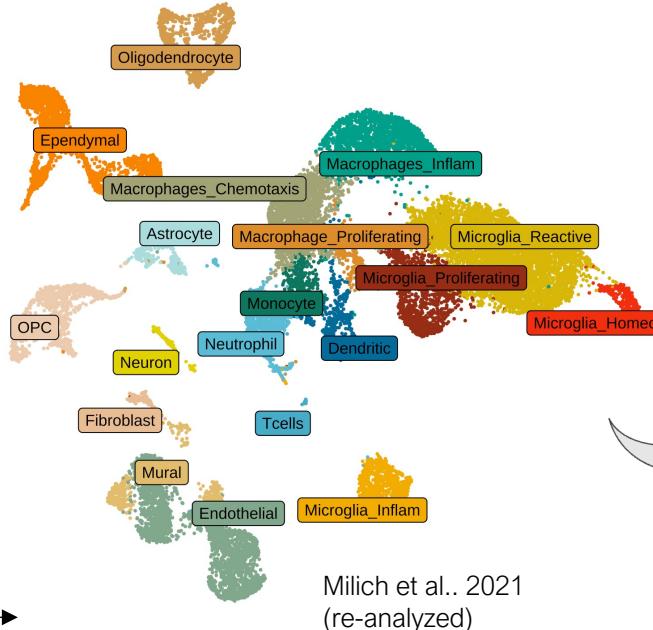
I demand... single-cells! (deconvolution)



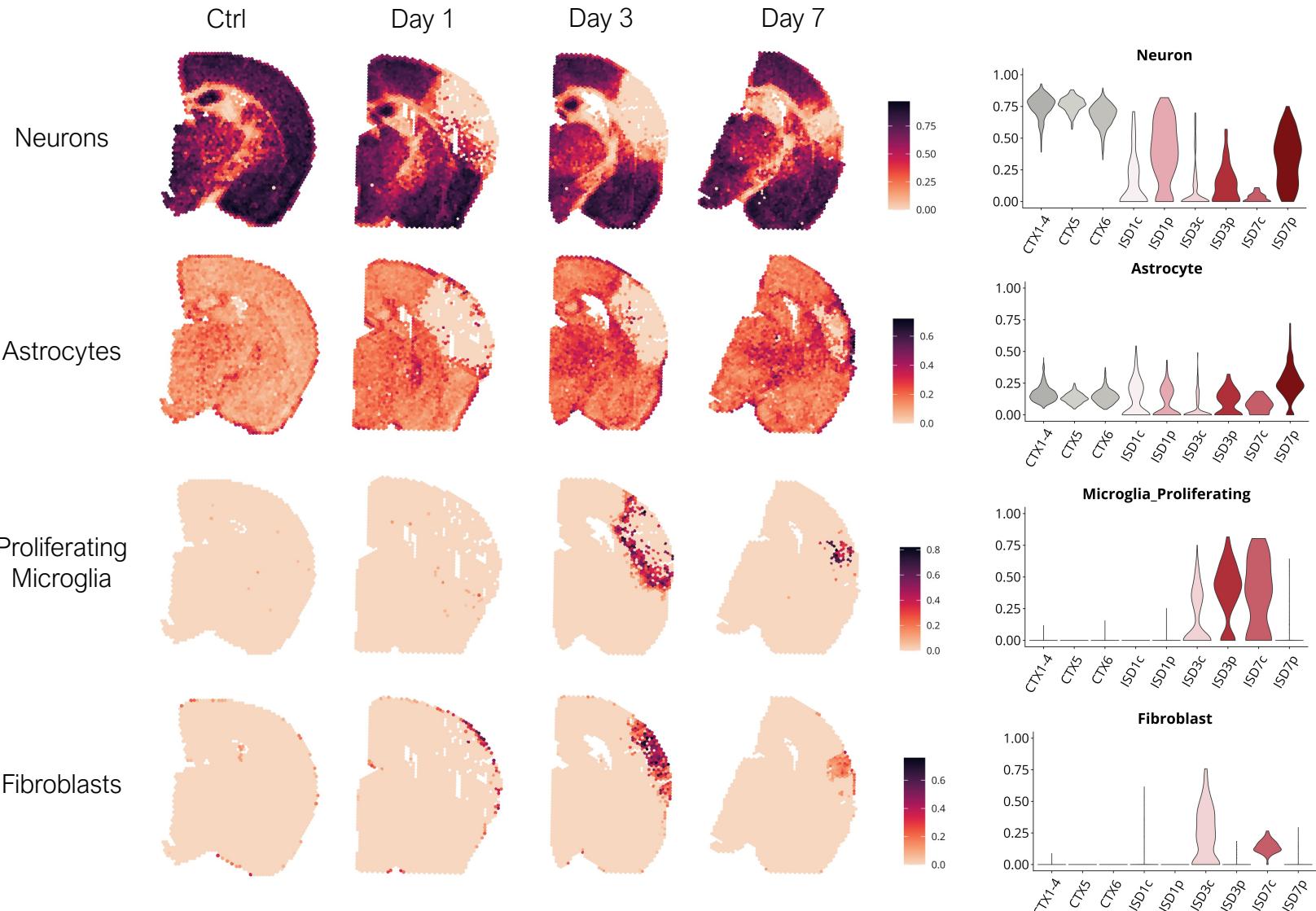
TECHNICAL ADVANCES AND RESOURCES

Single-cell analysis of the cellular heterogeneity and interactions in the injured mouse spinal cord

Lindsay M. Milich^{1,2*}, James S. Choi^{1*}, Christine Ryan^{1,2}, Susana R. Cerqueira¹, Sofia Benavides¹, Stephanie L. Yahn^{1,2}, Pantelis Tsoulfas¹, and Jae K. Lee¹



- Ctrl – Day 1 – Day 3 – Day 7
- “full” cell type diversity coverage
- Good quality data



“None ever wished it longer than it was.”

~ Samuel Johnson on Milton’s ‘Paradise Lost’ (1779)

Concluding remarks

-  Insightful and context-preserving view – allows for exploration
-  Efficient results sharing is key – interactive web tool
-  Hidden treasures – looking beyond the ischemic lesion

Acknowledgements

Laboratory of Gene Expression, Institute of Biotechnology CAS

Mikael Kubista
Pavel Abaffy
Sarka Benesova
Zuzana Benesova
Ruslan Klassen
Eva Rohlova

 @labgenex
@LukasValihrach
@DanielZucha



Department of Cellular Neurophysiology, Institute of Experimental Medicine CAS

Miroslava Anderova
Denisa Kirdajova
Tereza Filipi
Jana Tureckova

Institute for Clinical and Experimental Medicine
Daniel Jirak

Grant support

Grant Agency of the Czech Republic (20-05770S, GA22-10660S), MEYS (EJPRD19-256), Czech Health Research Council (NU21-08-00286) and institutional support (RVO 86652036).

Thank you for your attention!