Icahn
School of
Medicine at
**Mount
Sinai**

*The Tisch
Cancer Institute*

NCI
Designated
Cancer Center

*Black Family
Stem Cell Institute*

*Skin Biology
and Diseases
Resource-based
Center*

*Department of Cell,
Developmental and
Regenerative Biology*

BiNGS

Introduction to the Bioinformatics for Next Generation Sequencing (BiNGS) Shared Resource Facility

BFSCI/CDRB/SBDRC

Sep 15, 2022

Dan Hasson

BiNGS.mssm.edu

Acknowledgments

- Ramon Parsons
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- Nicole Jefferson
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- Lili Gai

Mission

- To provide high-end data analysis service at reduced cost to support TCI-, BFSCI-, CDRB-, and SBDRC-affiliated faculty members in the planning, analysis, integration and interpretation of NGS datasets tailored to their research.
- We advise on NGS experimental design and protocols.
- Provide a broad range of bioinformatic analyses (standard and customized) for multiple applications spanning transcriptomics, epigenomics, and genomics.
- Provide extensive training platforms.

Our Team

Ernesto Guccione

Co-Director

Dan Hasson

Co-Director

Deniz Demircioglu

Lead Bioinformatician

Saul Carcamo

Bioinformatician

Xuedi Wang

Bioinformatician

Gargi Damle

Junior Bioinformatician

Gulay Ulukaya

Junior Bioinformatician

Lewis Tomalin

Bioinformatician

Alexander Tsankov

Consultant

Charles Coleman

Junior Bioinformatician

Aman Agarwal

Junior Bioinformatician

Actively recruiting

3x bioinformaticians

The Goal

Create an **informal long-term relationship** between your lab and the core where we;

- Advise on experimental design, perform data analysis and support data generation for publication.
- Our bioinformaticians becomes part of your lab participating in lab meetings and reading literature specific to your studies so their analysis is more informed.
- We meet regularly to discuss results and to set goals for data analysis.
- We are incorporated into your grants.
- We train your lab members and provide tools so they can dig deeper into the data.

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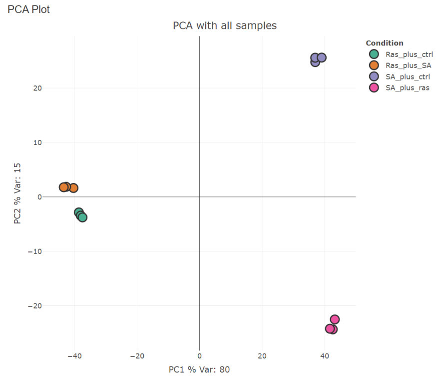
BiNGS

Overview of BiNGS services

Transcriptomics

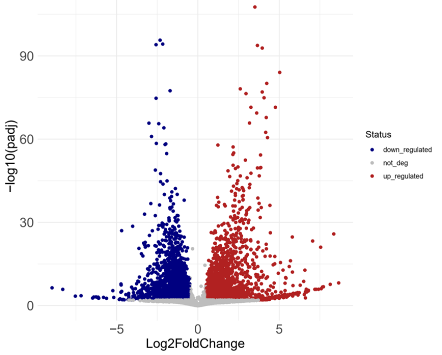
- Bulk RNA-seq
- Alternative Splicing Analysis
- Alternative Promoter Analysis
- Iso-seq
- Transcriptional Analysis of TCGA and other public datasets

Bulk RNA-seq



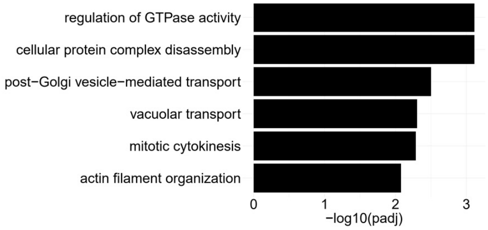
Standard analysis:

- Evaluation of reads quality and alignment statistics
- Samples normalization using internal controls or computational methods
- A link to a UCSC genome browser session for all normalized datasets
- Normalized read counts (TPM)
- Assessment of sample similarity (PCA plot)
- Differential gene expression (tables and interactive heatmaps)
- Gene Set Enrichment Analysis (*GSEA*), Gene-Ontology terms and pathway enrichment analysis



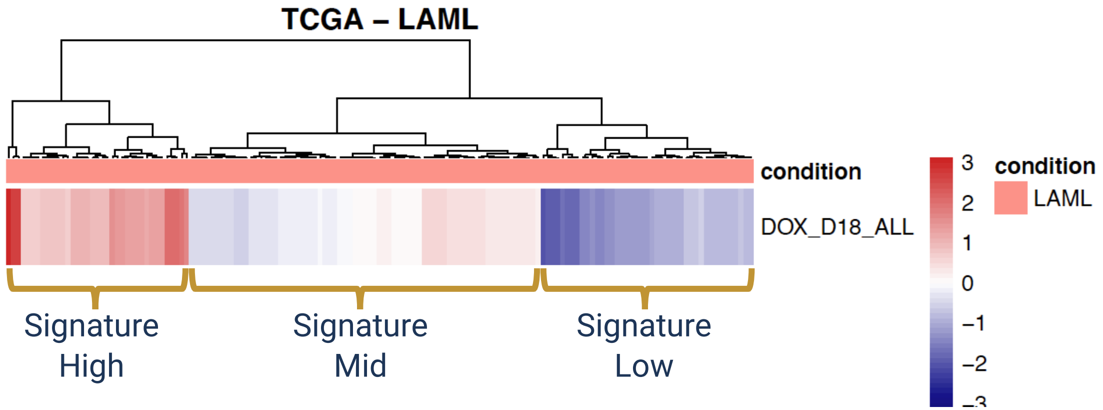
Customized analysis:

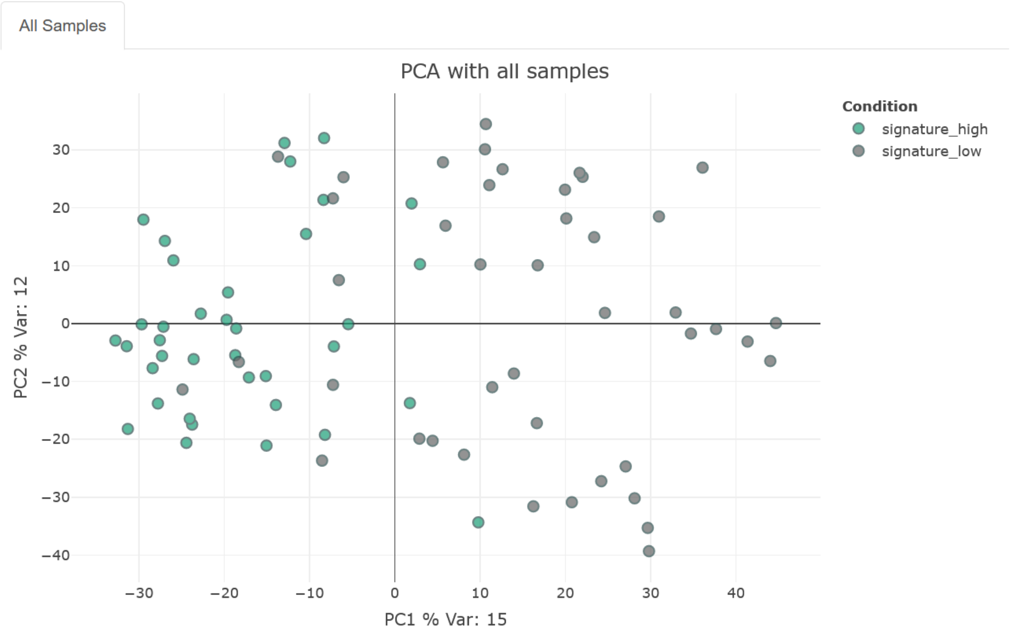
- Motif discovery
- Gene expression modules
- Data integration (e.g. ATAC-seq, ChIP-seq)
- Data integration with publicly available resources (e.g. ENCODE, TCGA)
- Publication quality figures



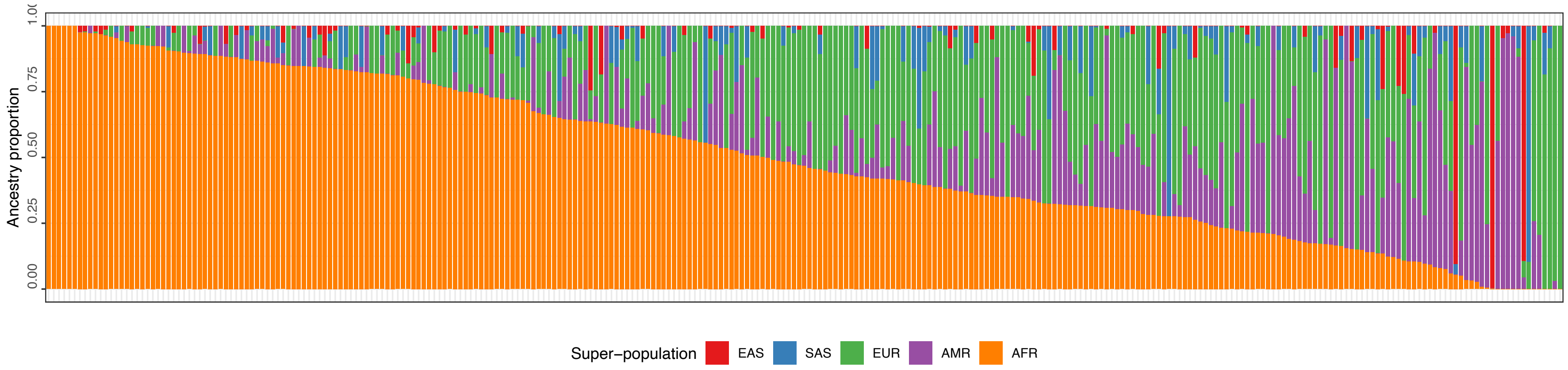
TCGA Signature Analysis (or other publicly available datasets)

CLUSTERING OF TCGA DATA BASED ON DIFFERENTIAL GENE EXPRESSION SIGNATURE (ssGSEA) FROM A CELL LINE UPON PERTURBATION



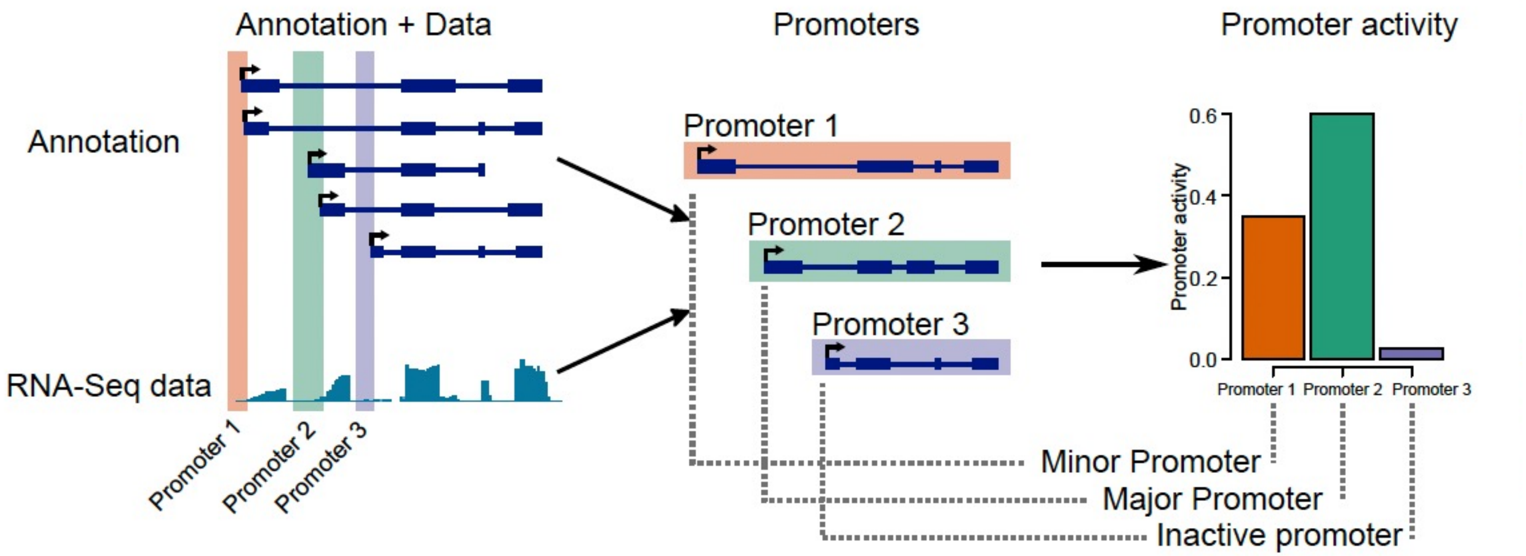


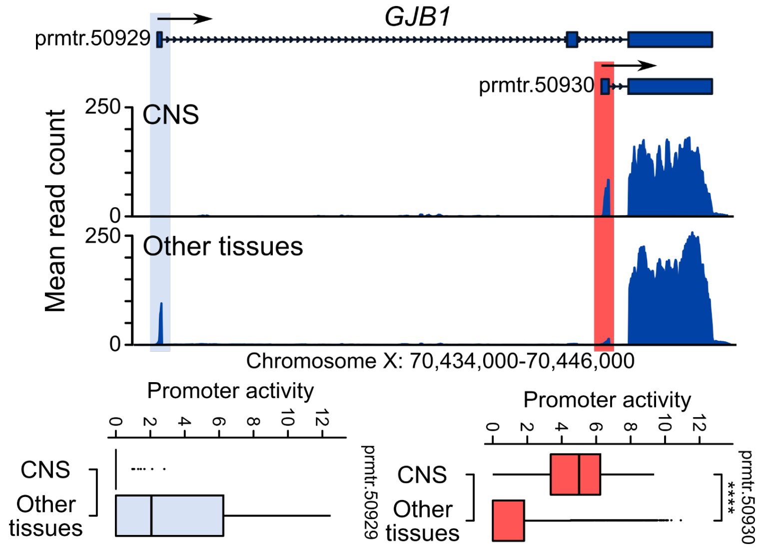
Ancestry analysis (bulk RNA-seq)



Alternative Promoters

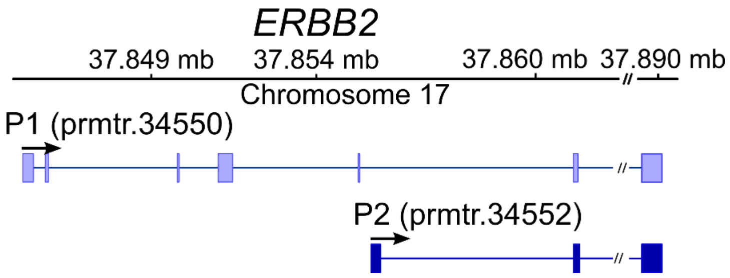
A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through **Alternative Promoters**

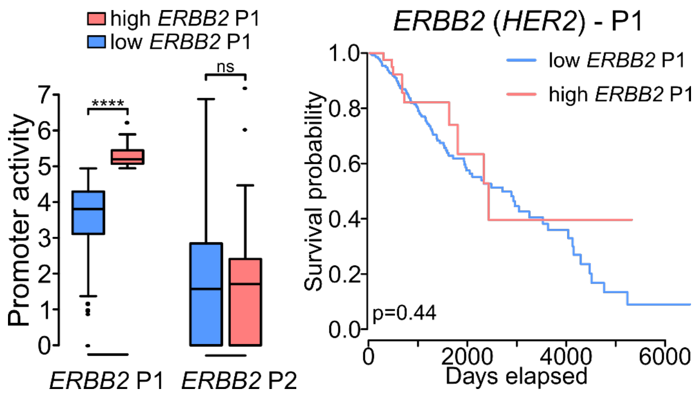


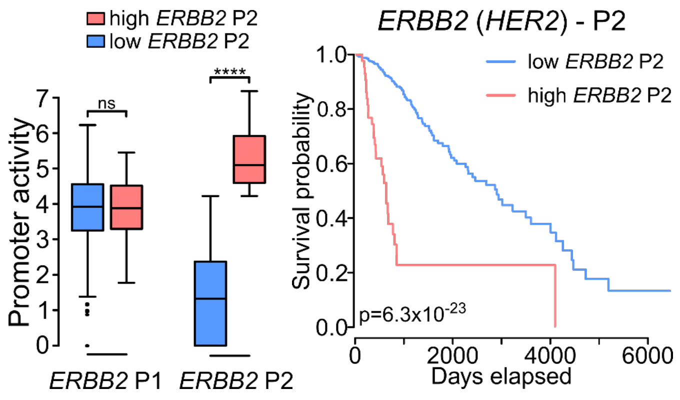


Alternative Promoters (TCGA)

A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through **Alternative Promoters**



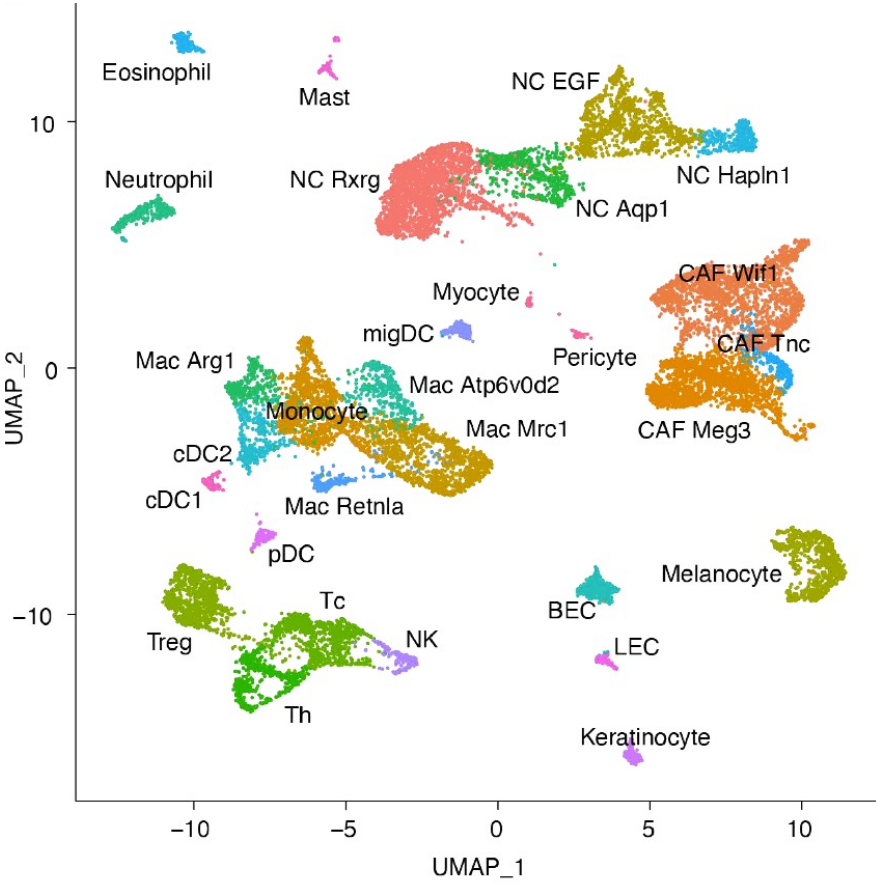


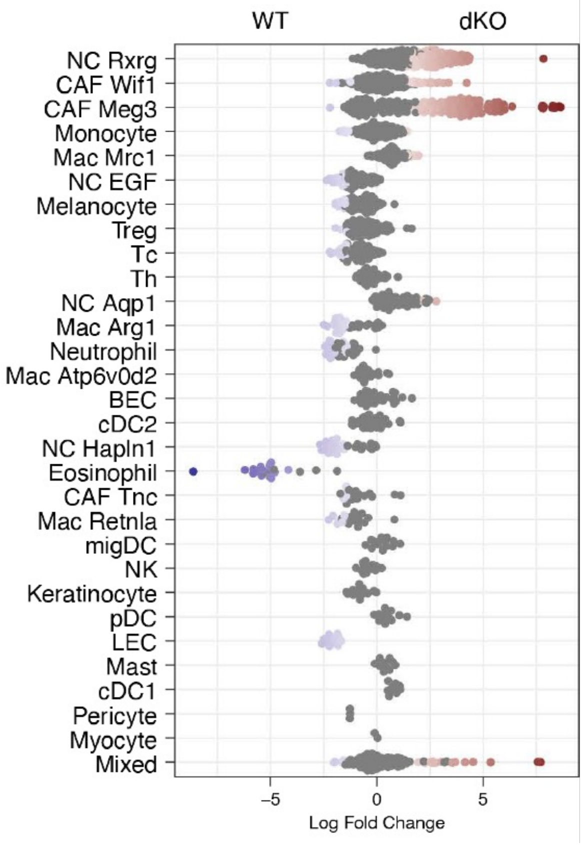


Single Cell Platforms

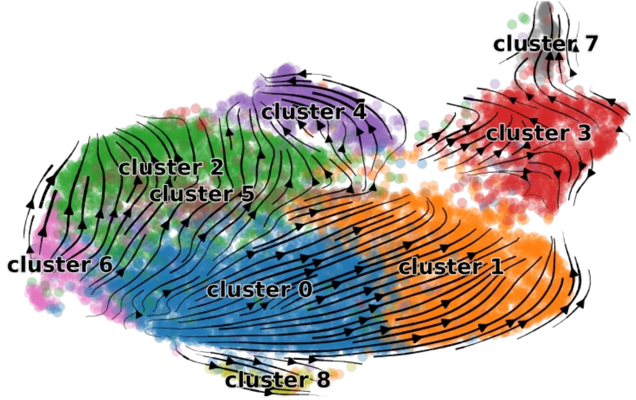
- scRNA-seq
- scATAC-seq
- Single Nucleus Multiome ATAC + RNA
- Spatial Transcriptomics

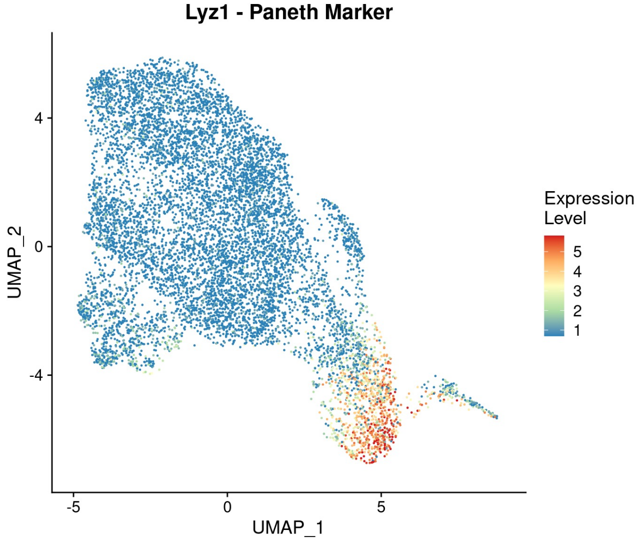
Single Cell RNA-Seq



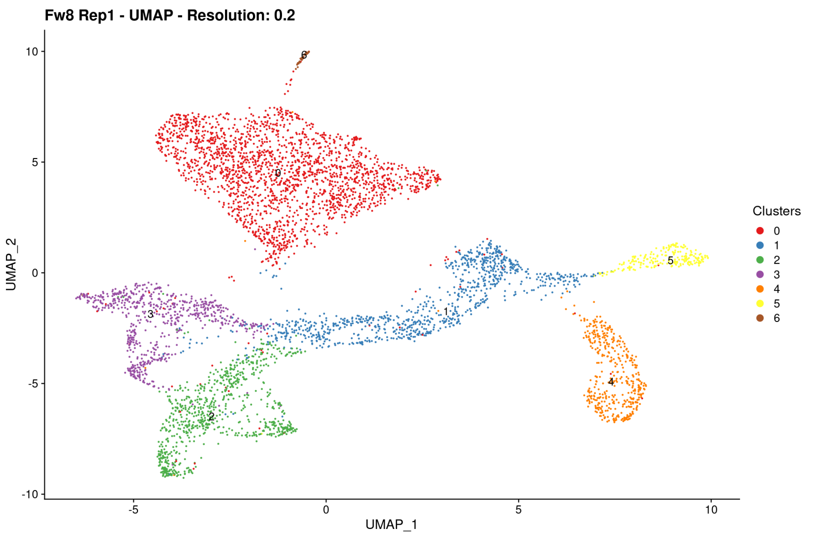


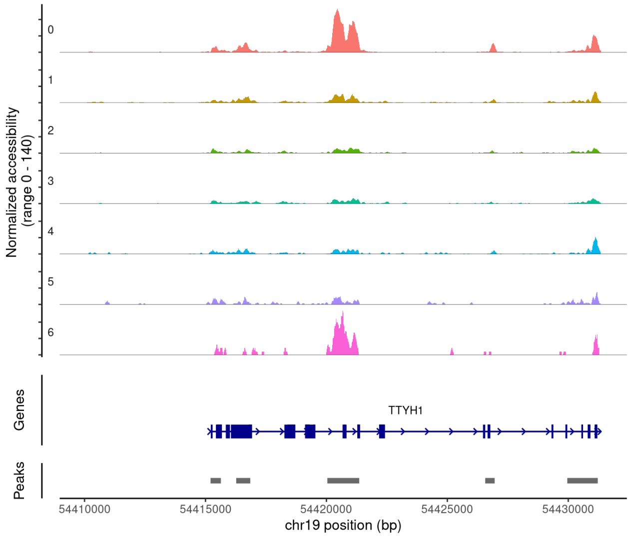
Velocity

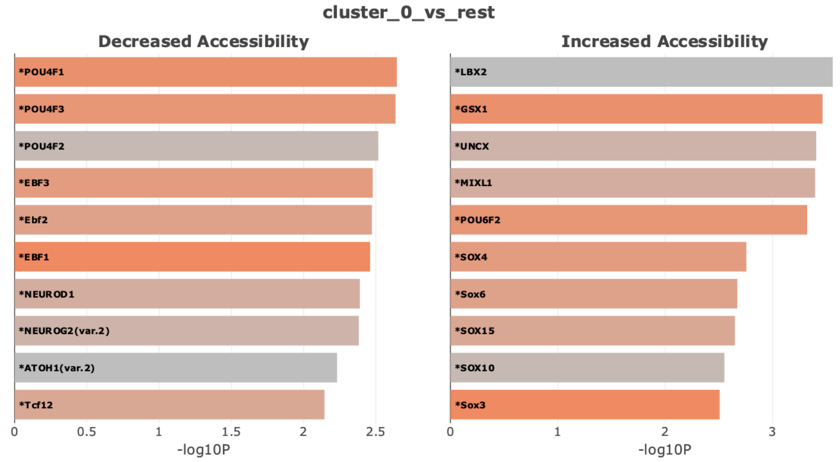


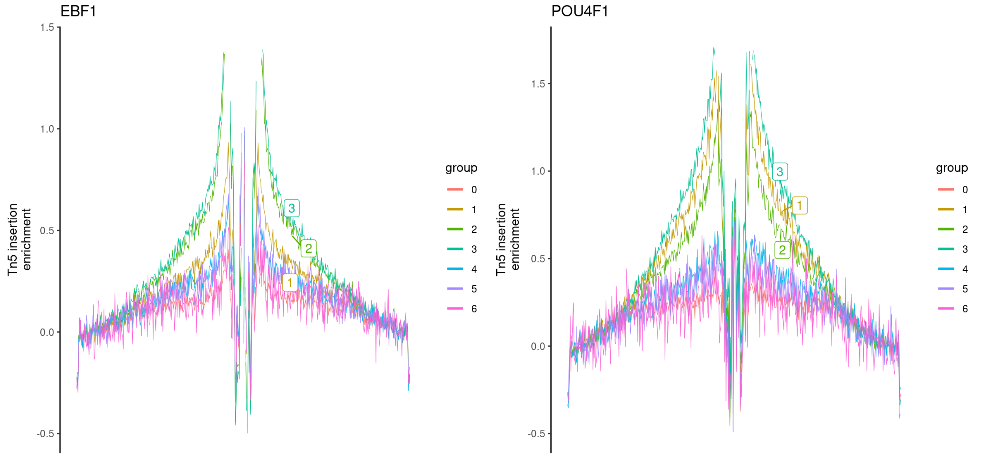


Single Cell ATAC-Seq

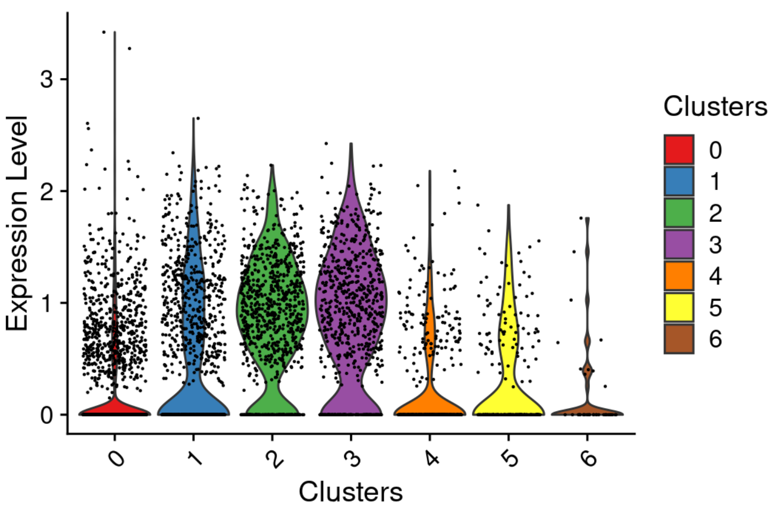








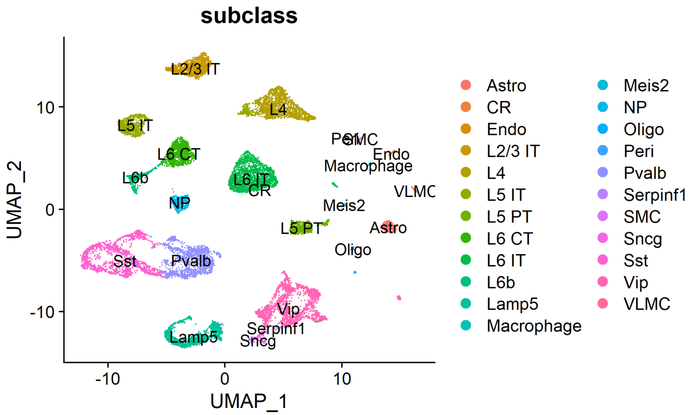
LIMA1 - Cluster 3 Marker

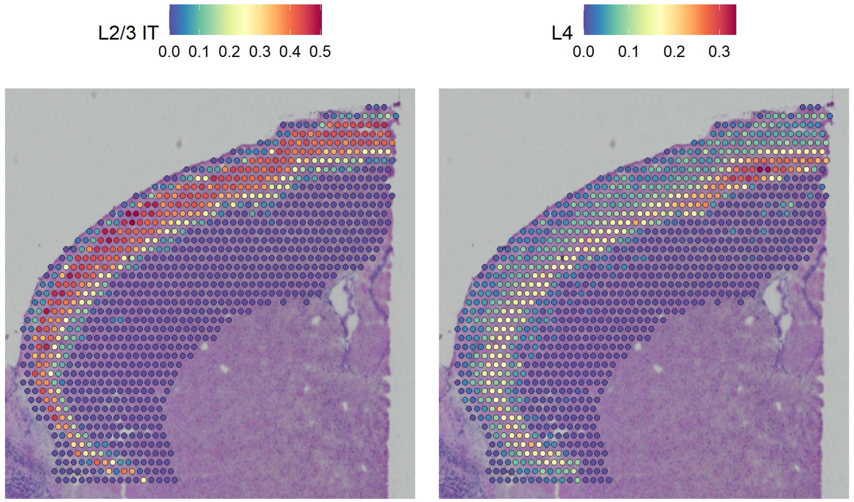


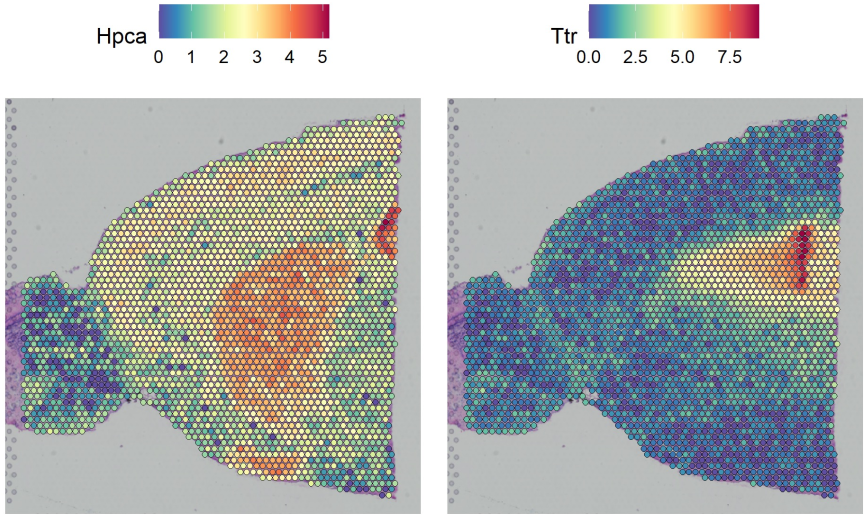
Spatial Transcriptomics

Single-cell data from mouse cortical cells, generated with the SMART-seq2 protocol.

Cell types identified based on single-cell data, can be used to ‘deconvolute’ the underlying composition of cell-types in the spatial omic spots.



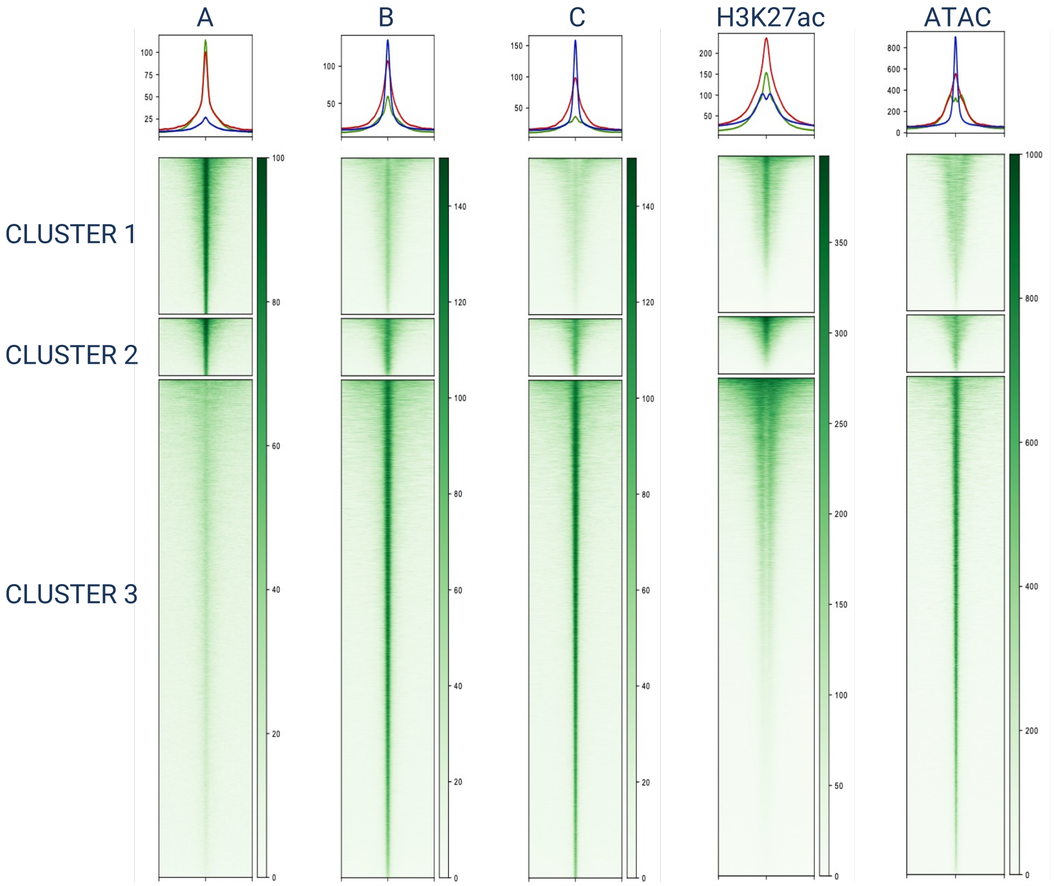


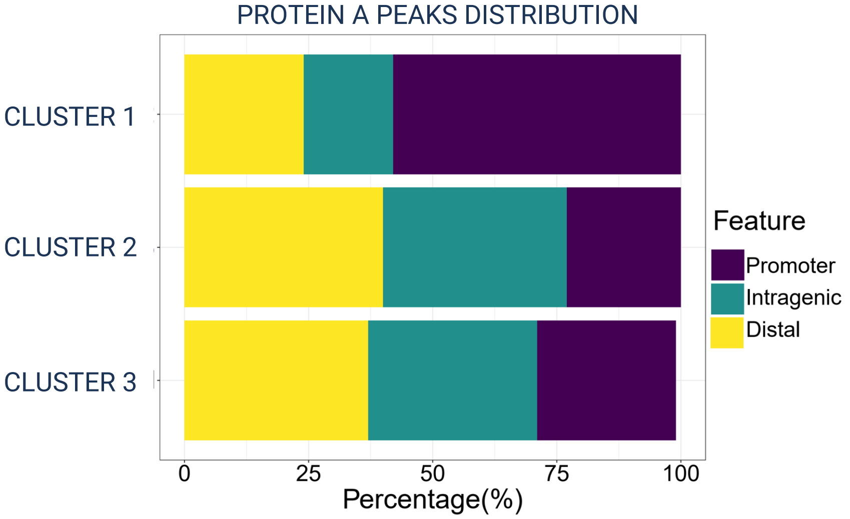


Epigenetics

- ChIP-seq
- Bulk ATAC-Seq
- CUT&RUN and CUT&Tag
- HiC/HiChIP
- Methy Seq

ChIP-Seq

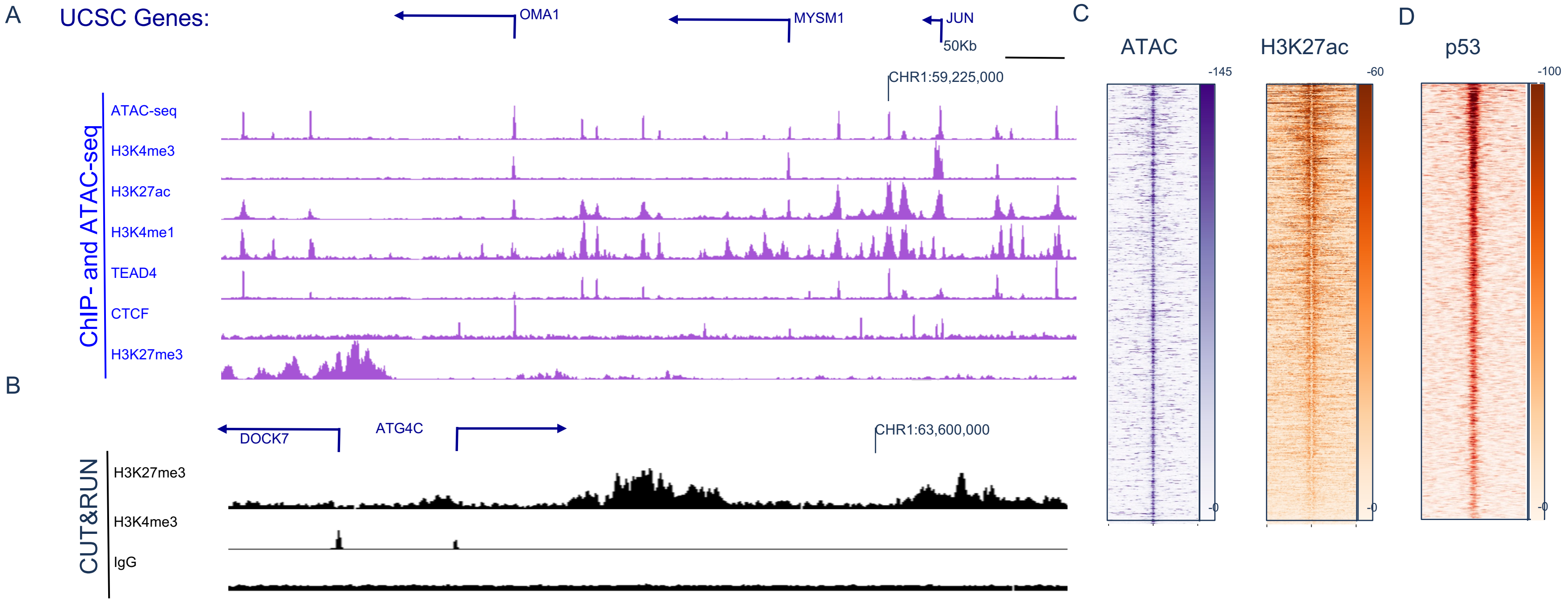


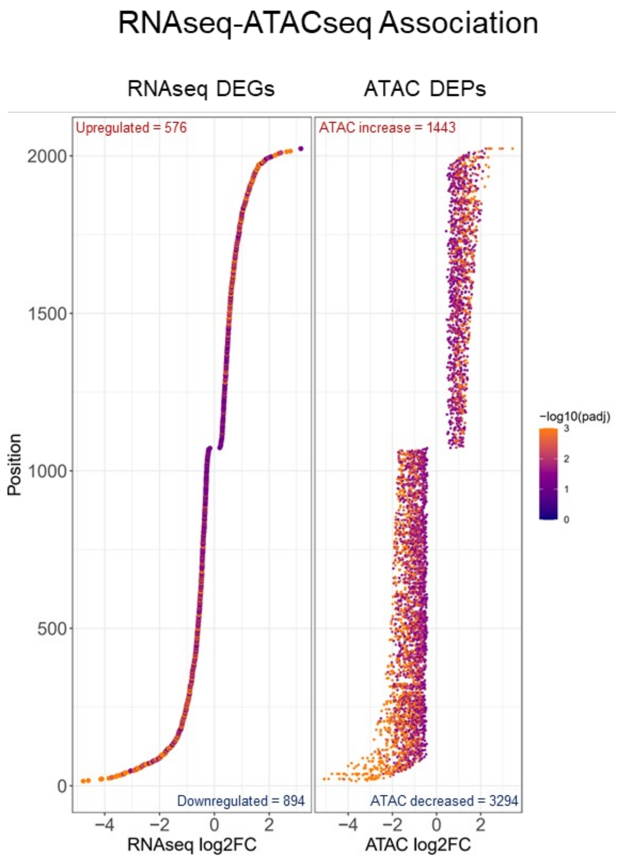

PROTEIN A PEAKS DISTRIBUTION

CLUSTER 1 MOTIF ANALYSIS

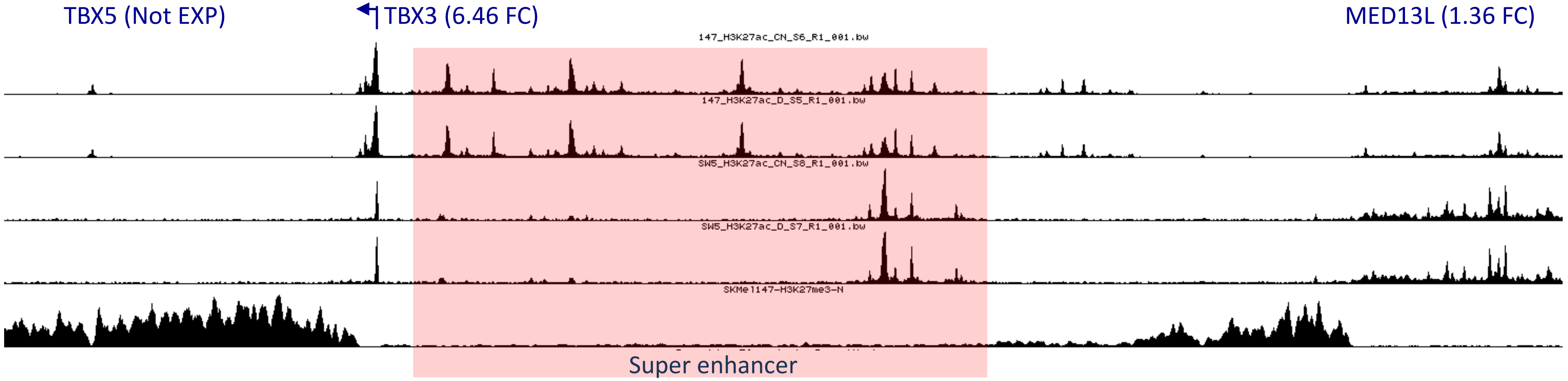
Motif	Name	P-val	Rank
	AP-1(FOSL2)	1e-18728	1(3)
	RUNX2	1e-2008	2
	SOX15(SOX10)	1e-1132	3(4)
	CTCFL(CTCF)	1e-1109	4(2)
	ETV2(FLI1)	1e-904	5(2)

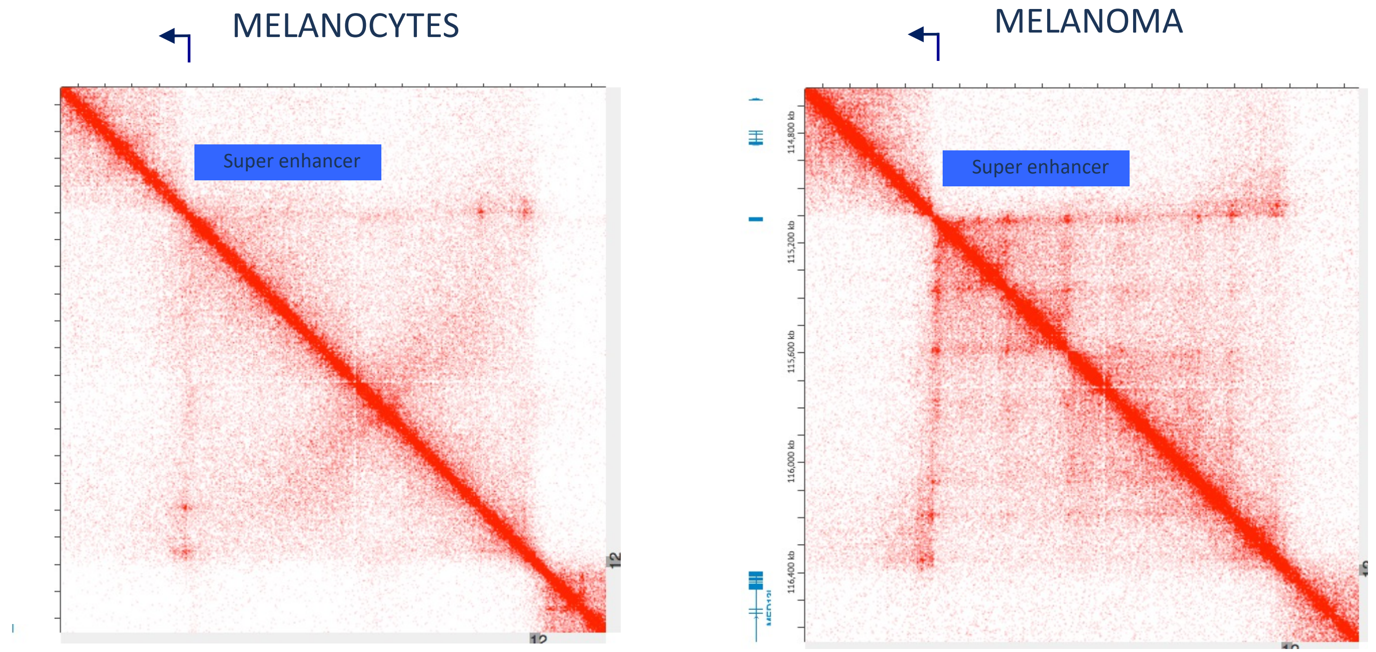
ChIP-Seq/Cut&Run





HiC/HiCHIP





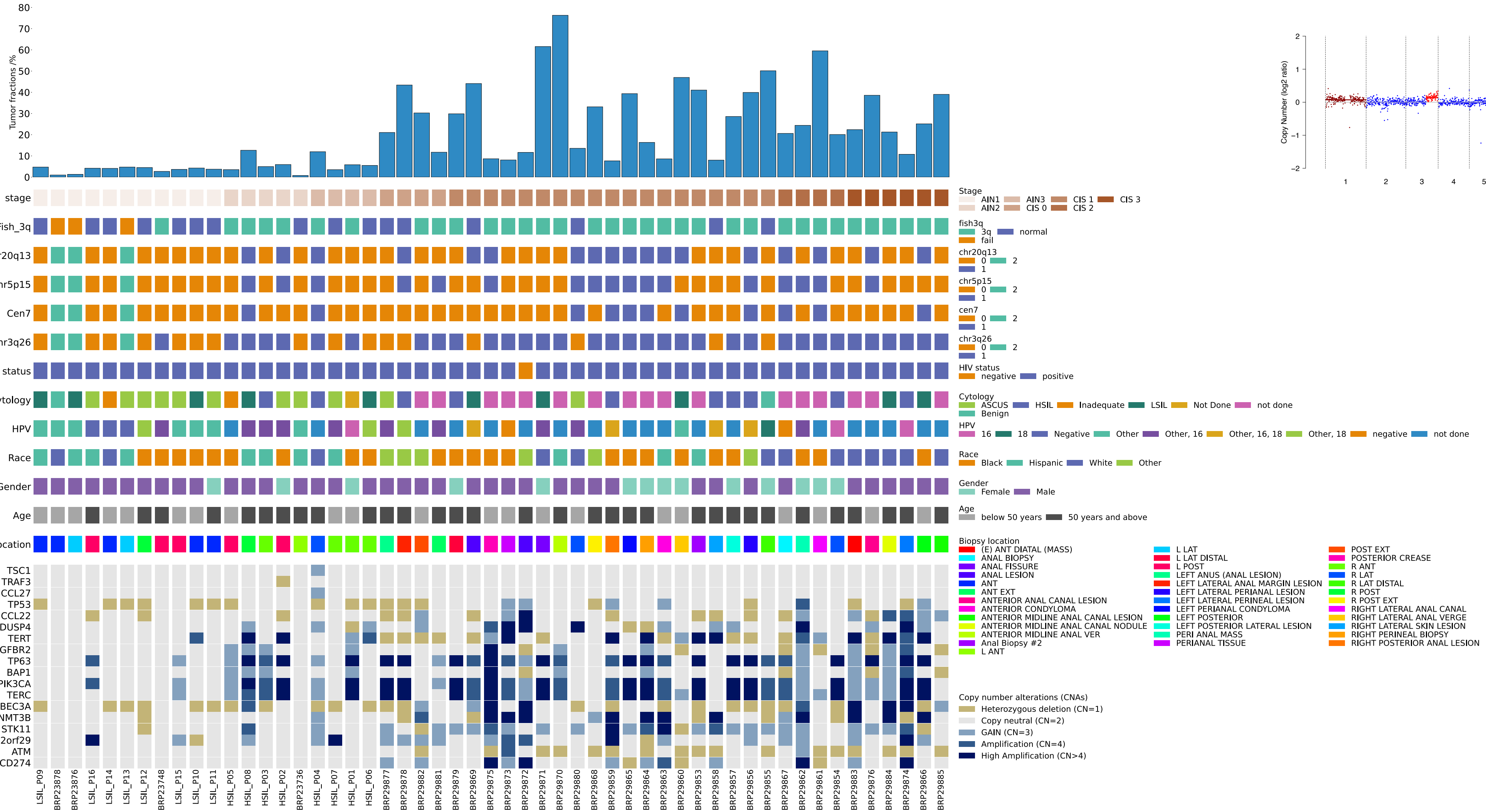
LONG RANGE CHROAMTIN INTERACTION BETWEEN GENE PROMOTER AND A SUPER ENHANCER OBSERVED DIFFERENTIALY IN MELANOMA CELLS

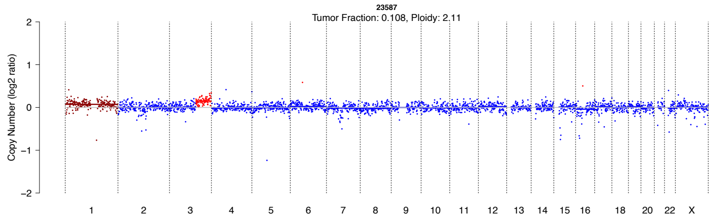
Genomics

- Whole Exome Seq
- Whole Genome Seq

Ultra Low Pass WGS for CNA discovery

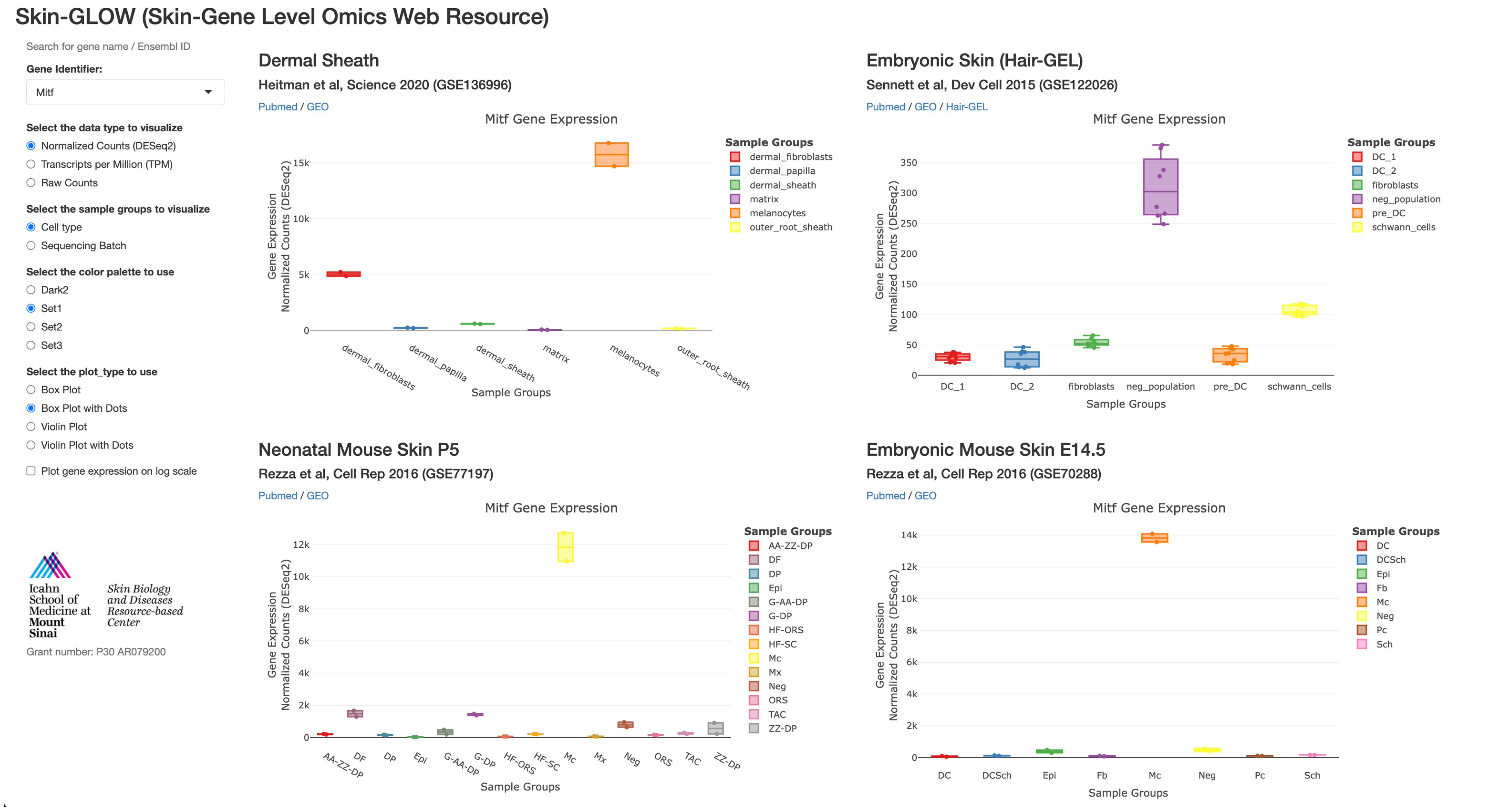
BiNGS





With Keith Sigel

Skin GLOW (Skin-Gene Level Omic Web Tool)



Skin-GLOW (Skin-Gene Level Omics Web Resource)

Search for gene name / Ensembl ID

Gene Identifier:

Mitf

Select the data type to visualize

- ● Normalized Counts (DESeq2)
- ○ Transcripts per Million (TPM)
- ○ Raw Counts

Select the sample groups to visualize

- ● Cell type
- ○ Sequencing Batch

Select the color palette to use

- ○ Dark2
- ● Set1
- ○ Set2
- ○ Set3

Select the plot_type to use

- ○ Box Plot
- ● Box Plot with Dots
- ○ Violin Plot
- ○ Violin Plot with Dots

☐ Plot gene expression on log scale

Icahn School of Medicine at Mount Sinai

Skin Biology and Diseases Resource-based Center

Grant number: P30 AR079200

Dermal Sheath

Heitman et al, Science 2020 (GSE136996)

Pubmed / GEO

Embryonic Skin (Hair-GEL)

Sennett et al, Dev Cell 2015 (GSE122026)

Pubmed / GEO / Hair-GEL

Neonatal Mouse Skin P5

Rezza et al, Cell Rep 2016 (GSE77197)

Pubmed / GEO

Embryonic Mouse Skin E14.5

Rezza et al, Cell Rep 2016 (GSE70288)

Pubmed / GEO

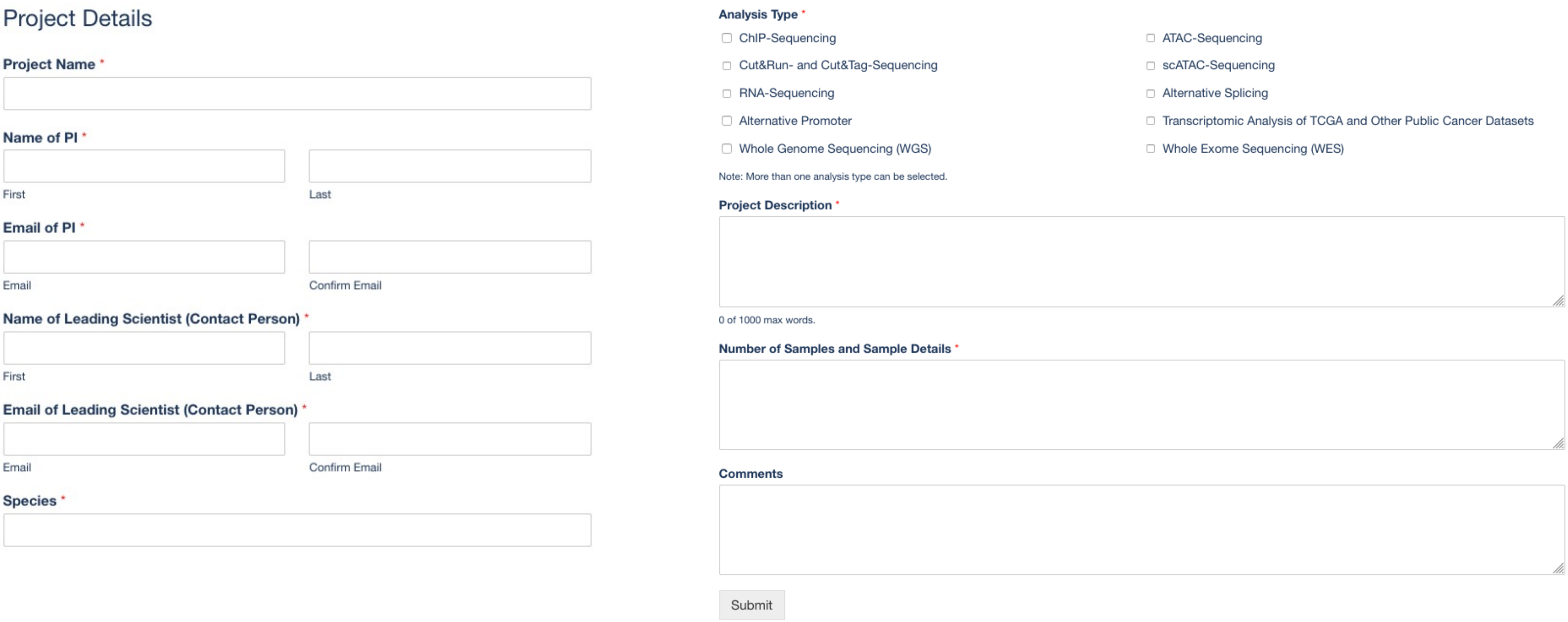
Pricing

We offer two optional payment structures:

1. Hourly (short term): $95 an hour for TCI and BFSCI/CDRB/SBDRC members.
2. % effort (long term): Investigator pays % effort of one of our bioinformaticians (grants)

Priorities: Long term projects; First-come, first-served; and based on bioinformaticians expertise and availability.

Submit a Project (BiNGS.mssm.edu/submit-a-project/)



Project Details

Project Name *

Name of PI *

First

Last

Email of PI *

Email

Confirm Email

Name of Leading Scientist (Contact Person) *

First

Last

Email of Leading Scientist (Contact Person) *

Email

Confirm Email

Species *

Analysis Type *

☐ ChIP-Sequencing

☐ Cut&Run- and Cut&Tag-Sequencing

☐ RNA-Sequencing

☐ Alternative Promoter

☐ Whole Genome Sequencing (WGS)

☐ ATAC-Sequencing

☐ scATAC-Sequencing

☐ Alternative Splicing

☐ Transcriptomic Analysis of TCGA and Other Public Cancer Datasets

☐ Whole Exome Sequencing (WES)

Note: More than one analysis type can be selected.

Project Description *

0 of 1000 max words.

Number of Samples and Sample Details *

Comments

TRAINING

Open office hours:

Mondays 4-6pm

Please contact us to schedule!

Zoom ID: 409 848 3549

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LOOKING FORWARD TO WORKING TOGETHER. THANK YOU!

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