

# Comparative Genomics Notes

## • Chromatin Associated Genes

Victoria Suarez Ulloa

Histone

Histone Variants

## Network Analysis

Pipeline run cuffdiff

Correlation Matrix  $\rightarrow$  WGCNA or PLUMA

Graphical  $\rightarrow$  Cytoscape

Vibro 194079

Histone Variants

Automated

placed or removed from Chromatin

Change Access

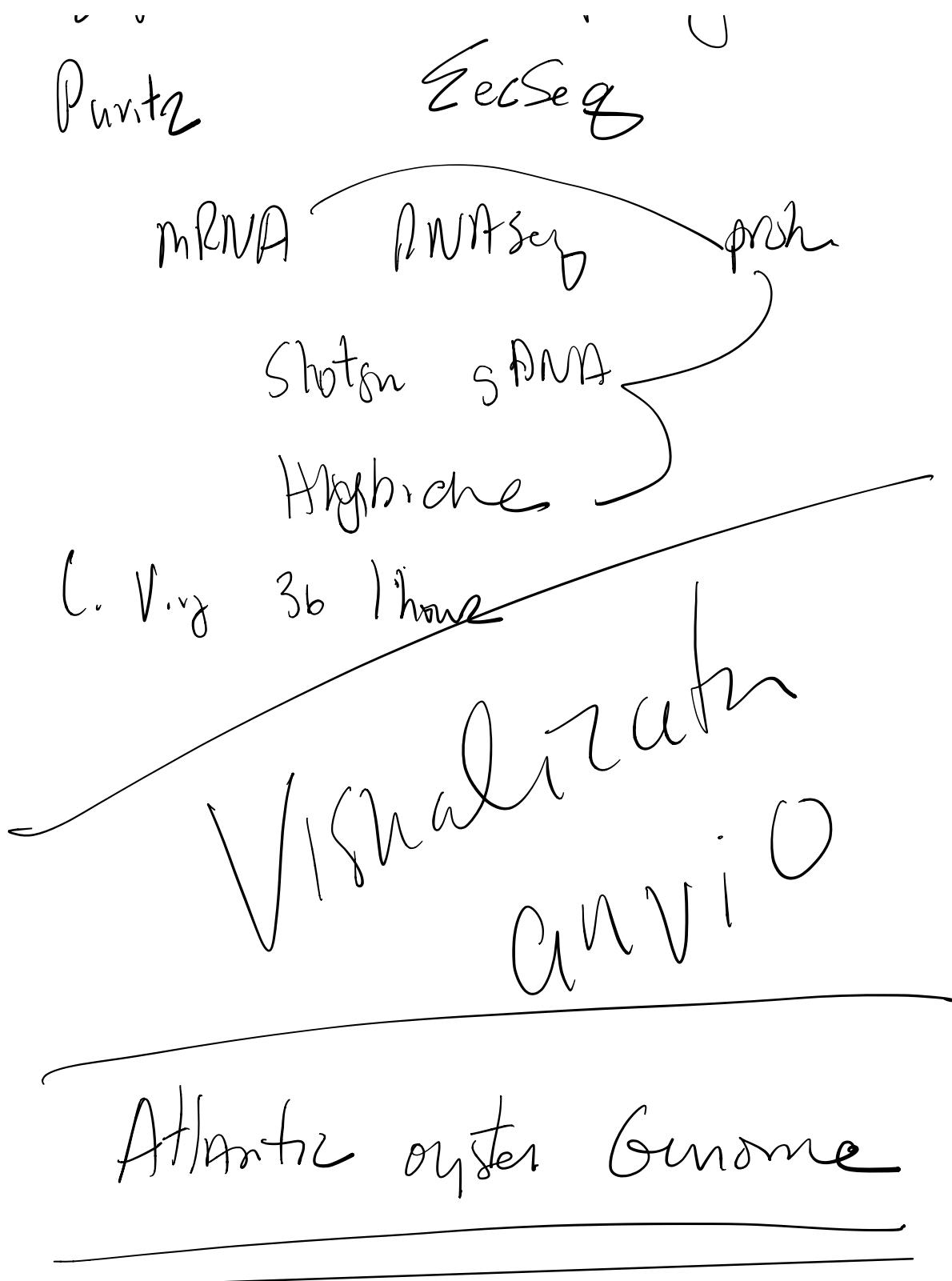
Transcriptional Mach

HAB  $\beta_{HAB}$

Δ Delta

D Uncharacterized proteins

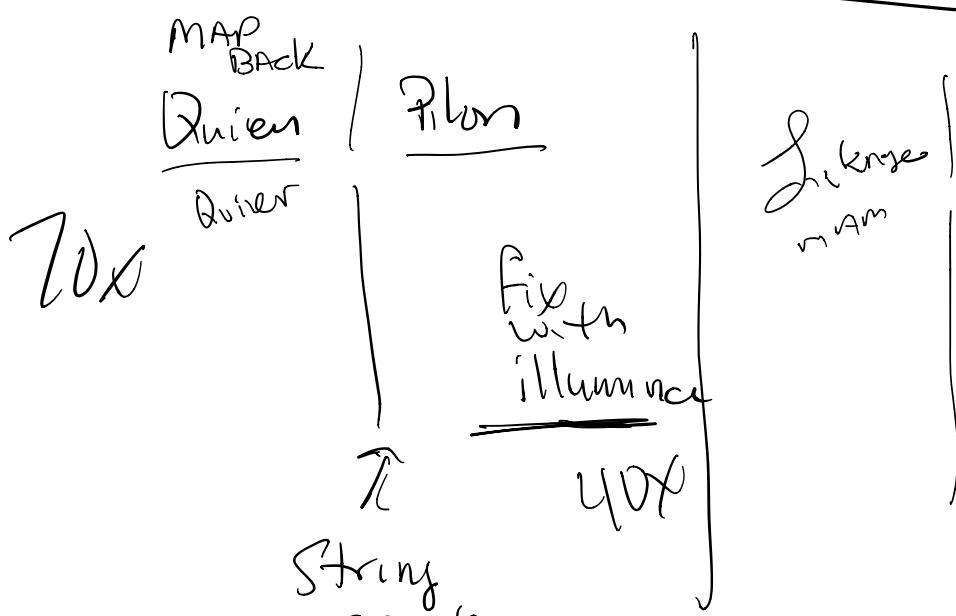
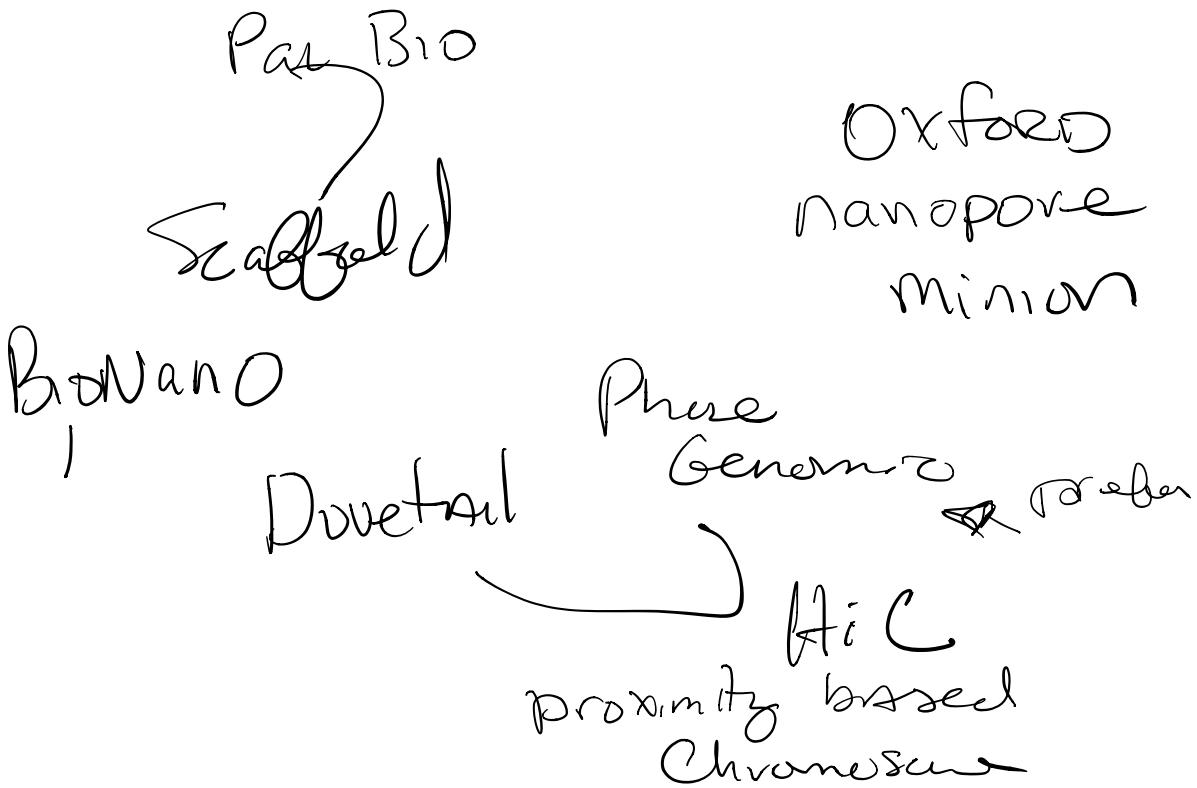
# Exosomal Exome Capture



Codon Number Variation ?

--- 11 --- here

10x genomics → phase genome



graph

# Falcon Assembler

a)

C Falcon Unzip

— i  
future )

Separate  
Haplotype

# Bw500

1.0 Assembly 695 Mb  
size

3.0 Assembly 810 Mb

↗  
Duplicated  
Sequences

30,474

NCBI Gene Count

Repeat Annotation

total masking 40

7.7M 20 Tandem

22% unclassified

Next Steps

- Submit second assembly
- Generate whole genome



Copy number variation

8 fm

H. ci ~~IGV~~ ~~Seq~~ MAP MASK LIST windows

maybe 22% redundancy

ORTHO BD

Busco

CeGMA

Diploid Assembly → Pick Haplak

Where do we go next

Brainstorming →

CRISPR

- - - - -

- Disease

## Brainstorming

Crispr → Yes an option

Disease is a major issue

Look at variation across range

Disease Resistance →

Look at Selective Sweep  
Selected lines

Effect of glycome immune mechanism

Horizontal gene transfer

Histone Variants: Look + ID those

High Quality }

Acidification Environmental Adaptations

- Environmental Adaptation

- Stressors ]

-

Repeats ]

Comparat

DARK Genome ]

- miCRO RNA

- lnc RNA

- Repeats

- Stuff in human  
↳ Wes

→ Tissue differences ]

Gene family  
expansion

immune

UK Keyshavery

→ Structural Variant

→ Repetition

→ Determining Allels

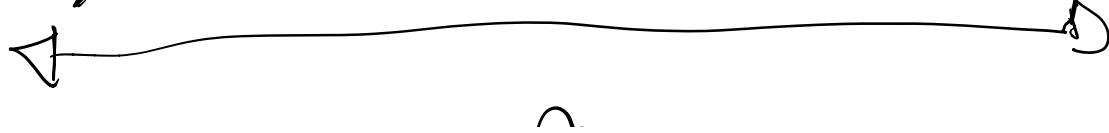
$\rightarrow$  Rare Defects  $\rightarrow$  gene exprs  
alleles

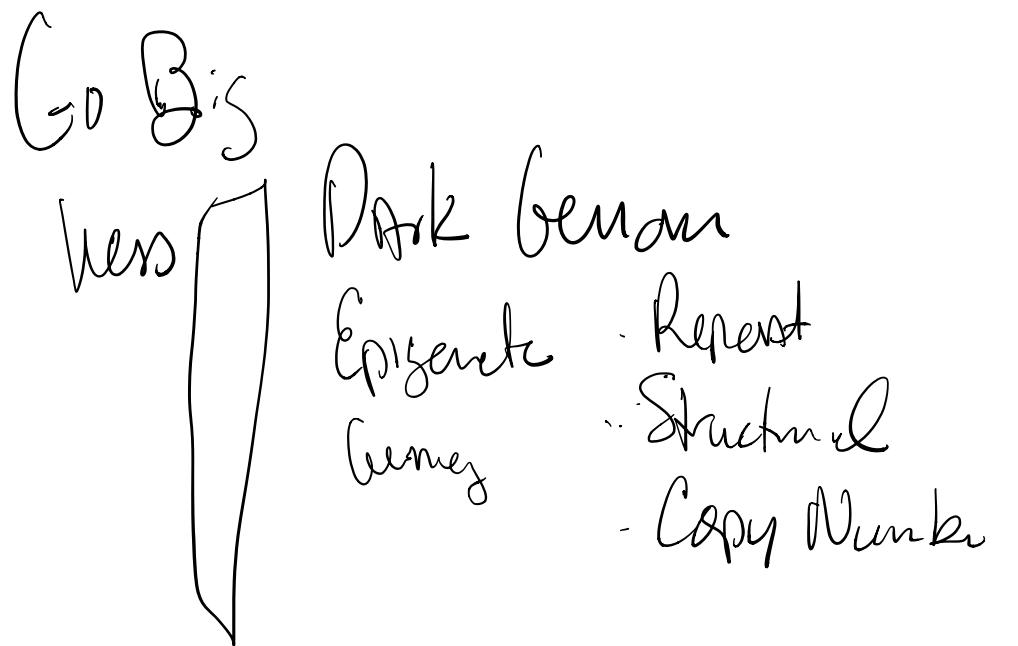
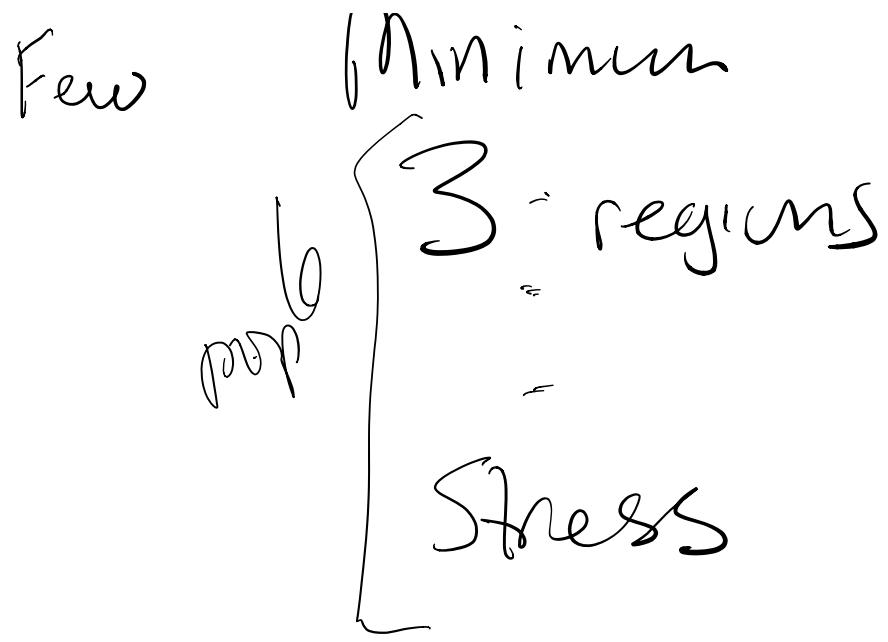
→ Integrative Biological Organization

## → Environmental

→ Temp

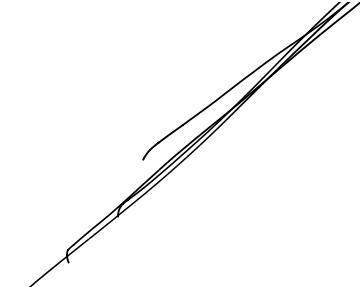
→ All mix





36 bands

Methyl



## NAMES

Steven Roberts Lindsay Green

Paul Ratson Victoria Scirce

Katie Lotterhos Hollie Putnam

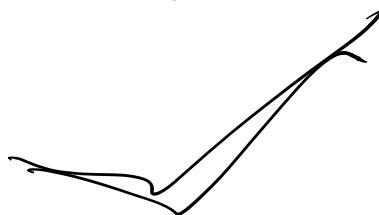
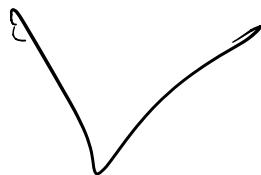
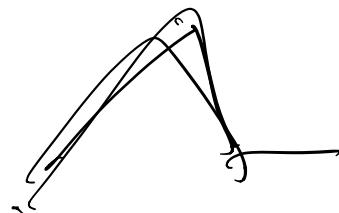
Laura Spencer

Yaamini Venkataraman

Bonnie Blalock

# Network Analysis

Plasma  $\leftrightarrow$  WCGWA  
 $\xrightarrow{\text{Hierarchical}}$   
 $\overbrace{\quad}$   
 $\nabla_c$



String  $\rightarrow$  P P interaction

Cytoscape

Help forum

Flow  
DEG

↓ Network

String Blast Cytoscape

Refer to Biological

Bingo Handouts  
Demo! STRING

?

Cytoscape

Affinibank

Bingo

Subnetwork

↳ Using

→ Layouts → from

R&D

over clustering

NCBI

↓ Docent

Bash pipeline

Already in place

# Genetics Tuesday

## Genetic Load

←

Maine Animal

- High polymorphic
- Large Census - small eff pop size
- High gene flow

m

Mutation rate -

Genetic Load = genotype dep mortality.

Segregation distortion

Load = totality of expression  
v QTL

17-18 No laterism alleles

100% - in each inbred family.

99% → Selection occurs during development

↳ Metamorphosis

Explains mechanism of ~~but~~ ~~del~~ alleles

Where do these alleles come from?

Review for Current Zoology  
Pop Genomics Seminar



WS Heterozygous ??

Linkage - Statistical  
Lod scores -  
Genome Scan

Haig Boddy 2002 look  
at single cross vs Pool

Sperm competition wild vs mass

Evan Durland

C. gigas OA

1:30

1L  
10:50

Dopamine ?

U U

Apoll Seg  
Fisher's exact

Slow growers do better  
by good pop success

G → Olympia  
do slow

growers do better

Tetraploids - revert  
more in mantle.