More Fancy Figures
(stored on a server)

Wigge's Lab meeting
2018.12.3
Feng Geng

Save the links!

Address:
http://172.26.114.34:81/ (haven't setup a home page yet)

Meta data server:
Username: teamPAW
Password: passwordPAW
http://172.26.114.34:81/admin/metaio/
Template filling:
http://172.26.114.34:81/admin/metaio/tag/softTemplate-Sample-RNASeq-Martin/change/

Figure repository:
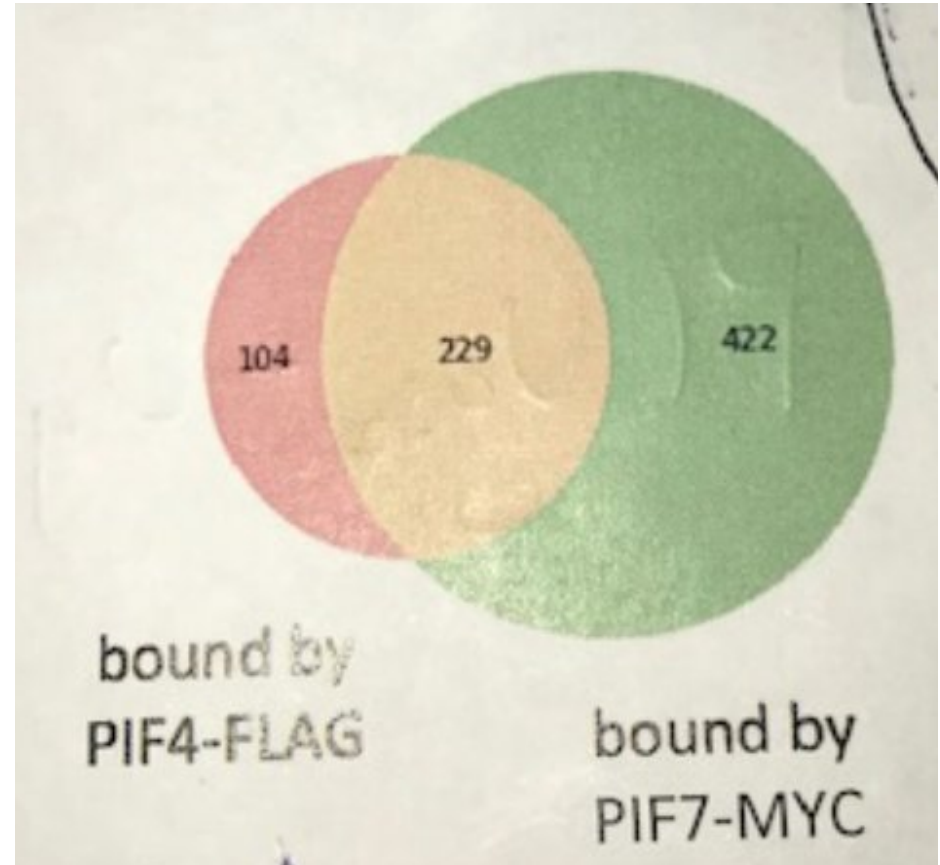http://172.26.114.34:81/static/figures/

Once upon a time….

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Numbers were supposedly produced by me sometime in the history.

Problem: needs to document the cutoff and the ChIP used to derive the numbers.

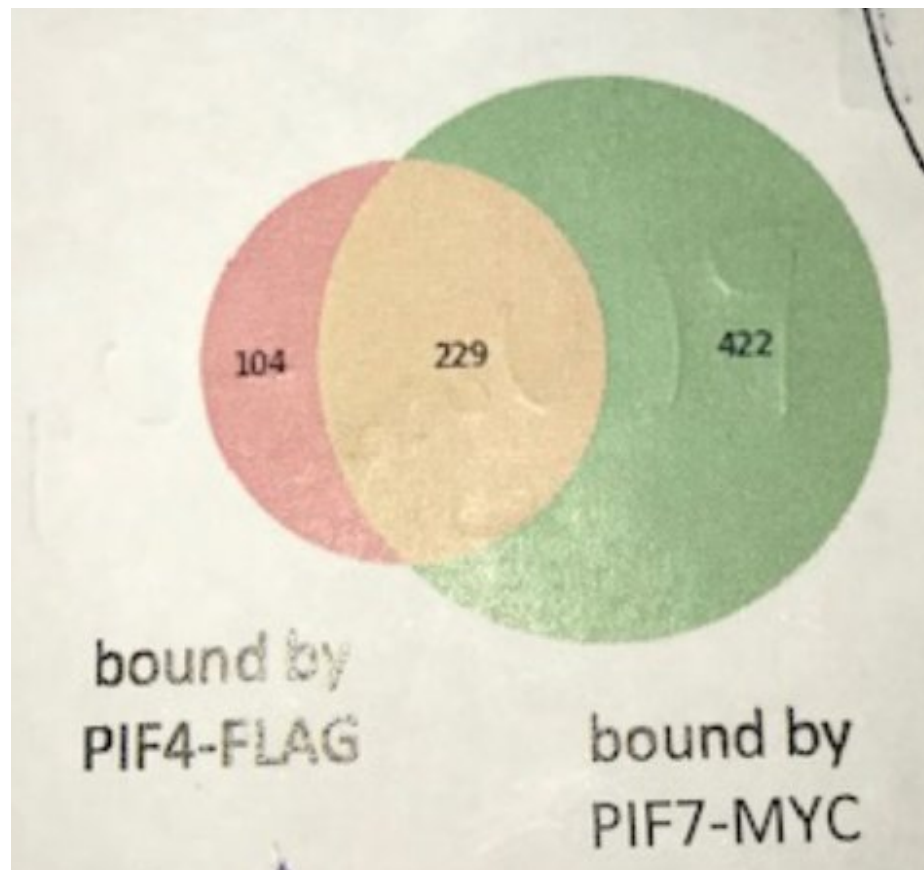*Martin*

Once upon a time...

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Problem: needs to document the cutoff and the ChIP used to derive the numbers.

Just go to the link!
http://172.26.114.34:81/static/figures/1126__PIF7-PIF4__overlap-peaklevel/figure.html

No more need to embed images in the EN as long as you can access SLCU intranet.
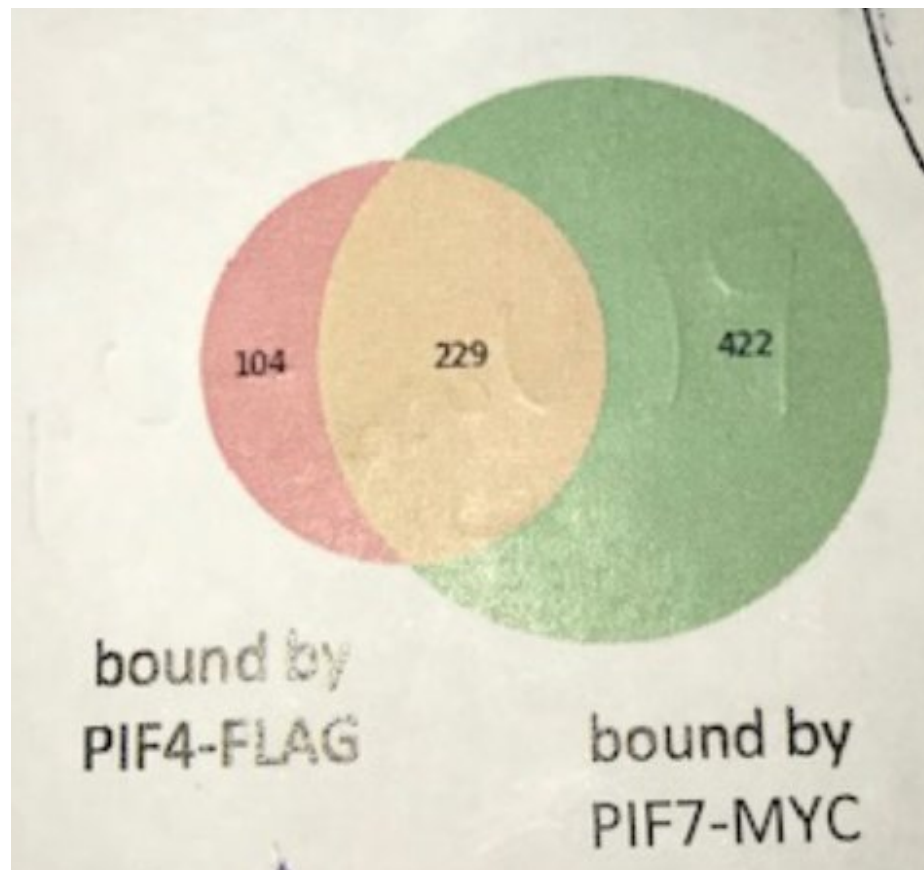

Martin

Once upon a time...

Numbers were supposedly produced by me sometime in the history.

Problem: needs to document the cutoff and the ChIP used to derive the numbers.
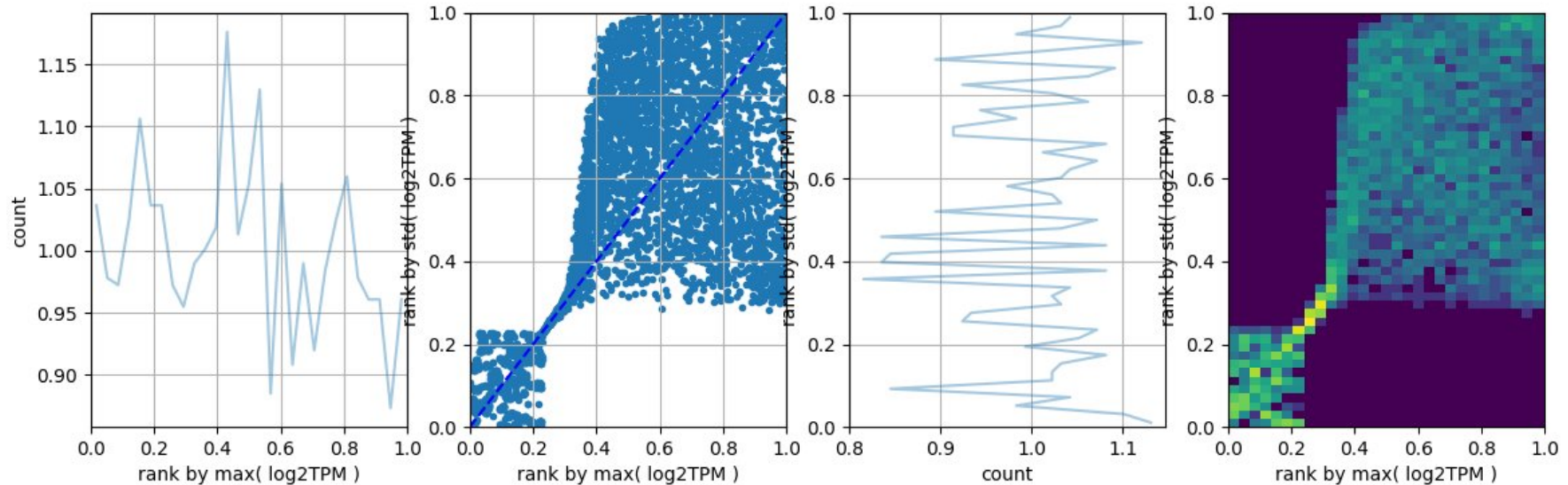
Just go to the link!
http://172.26.114.34:81/static/figures/1126__PIF7-PIF4__overlap-peaklevel/figure.html

No more need to embed images in the EN as long as you can access SLCU intranet.

Martin

Brief update of a quality control measure on RNA-Seq

http://172.26.114.34:81/static/figures/1129__RNAPREP__196R/figure.html

http://172.26.114.34:81/static/figures/1126__PIF7__tempResp-AND-pif7Resp/figure.html

We have done some ChIP-Seqs:
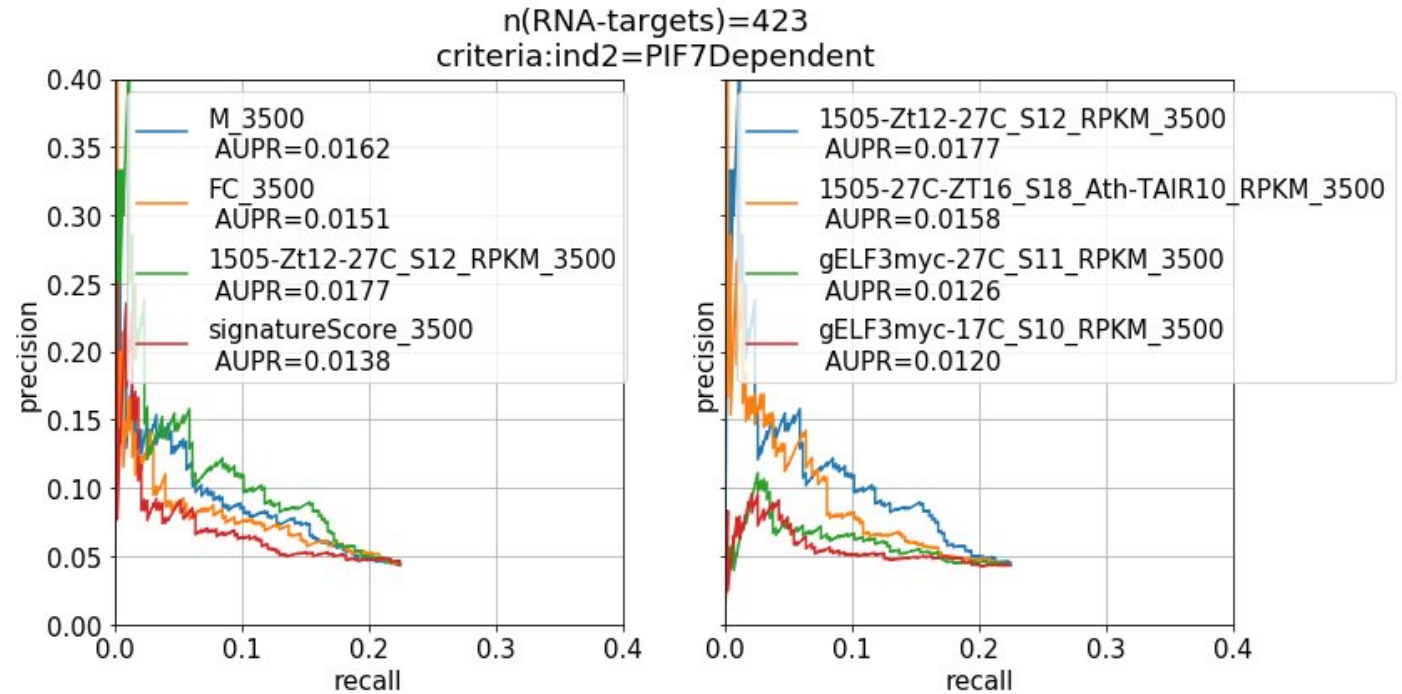
And also some RNA-Seqs

1505-17C-ZT0_S15
1505-17C-ZT16_S16
1505-27C-ZT0_S17
1505-27C-ZT16_S18
1505-ZT12-17C_S11
1505-Zt12-27C_S12
1505-ZT0-17C_S13
PIF7-PIF7-MYC-LD-27C-ZT8_S10
PIF7-PIF7-MYC-LD-17C-ZT12_S11
PIF7-PIF7-MYC-LD-27C-ZT12_S12
PIF7-PIF7-MYC-LD-17C-ZT8_S9

Will:
1. Assess ChIPSeq models after fixing RNA-Seq targets
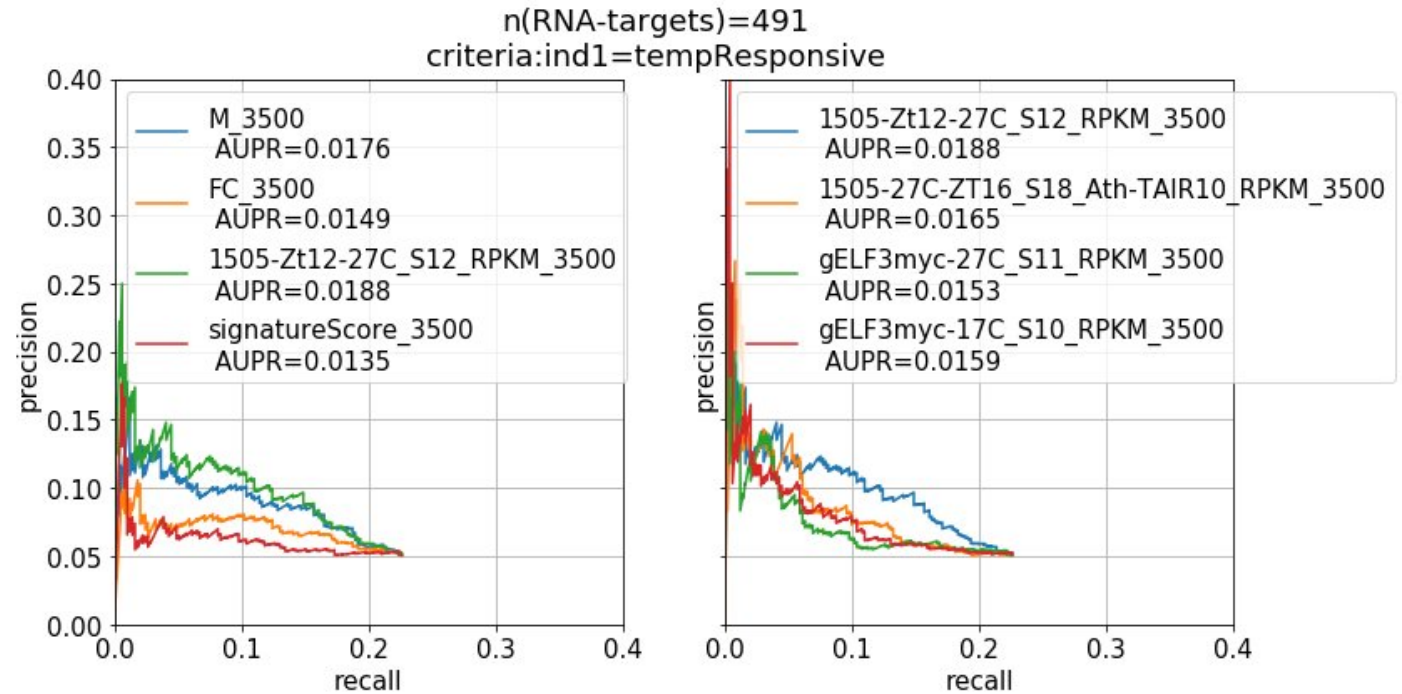2. Assess RNASeq models after fixing ChIP-Seq targets

chipseq2rnaseq: Fixing the RNA-Seq targets according to a criteria

Fold change does not predict RNAseq response as well as average binding.

n(RNA-targets)=423
criteria:ind2=PIF7Dependent

chipseq2rnaseq: Fixing the RNA-Seq targets
according to a criteria

Fold change does
not predict
RNAseq
response as well
as average
binding.

n(RNA-targets)=491
criteria:ind1=tempResponsive

Left panel legend:
M_3500 AUPR=0.0176
FC_3500 AUPR=0.0149
1505-Zt12-27C_S12_RPKM_3500 AUPR=0.0188
signatureScore_3500 AUPR=0.0135

Right panel legend:
1505-Zt12-27C_S12_RPKM_3500 AUPR=0.0188
1505-27C-ZT16_S18_Ath-TAIR10_RPKM_3500 AUPR=0.0165
gELF3myc-27C_S11_RPKM_3500 AUPR=0.0153
gELF3myc-17C_S10_RPKM_3500 AUPR=0.0159

rnaseq2chipseq:
Fixing the ChIP-Seq targets according to a criteria.
Extrapolated from marker targets

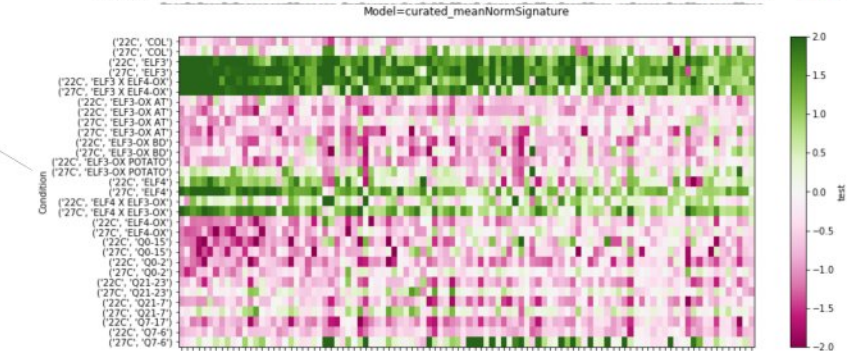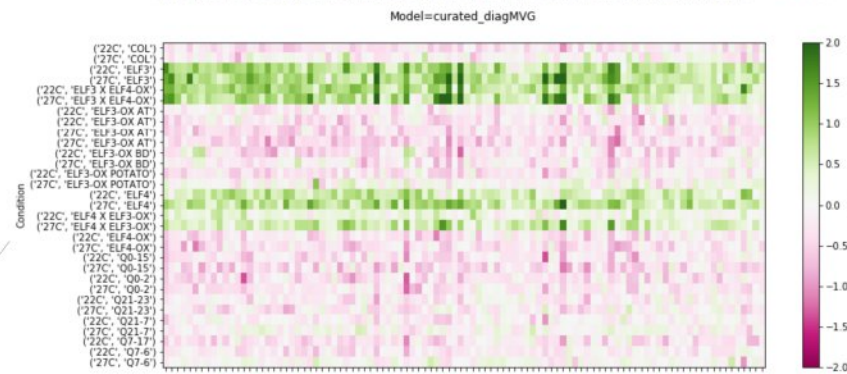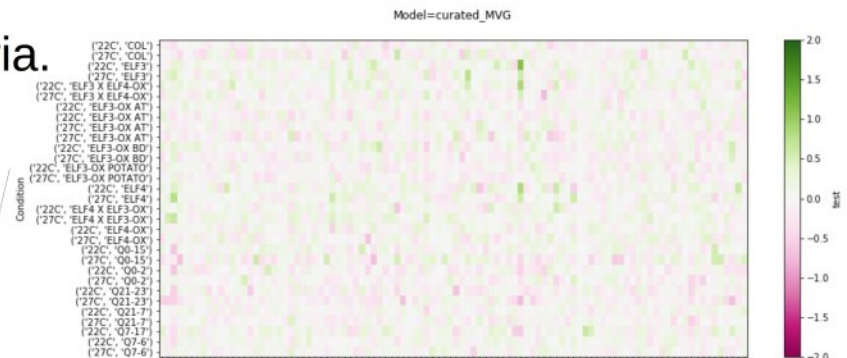Marker targets
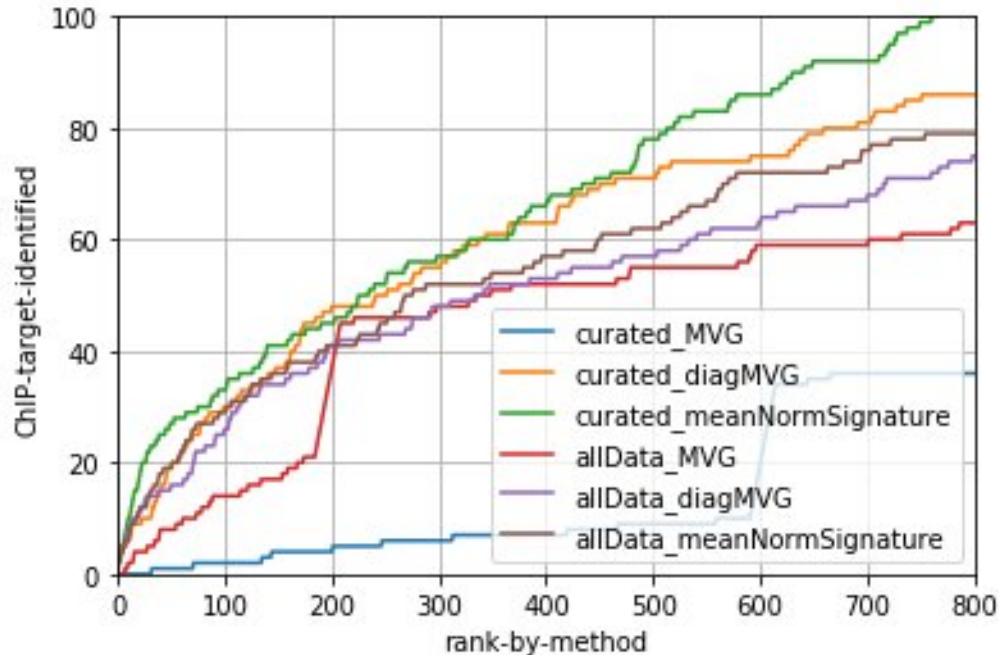
allData: ZT8 ZT12
Curated:ZT12-only
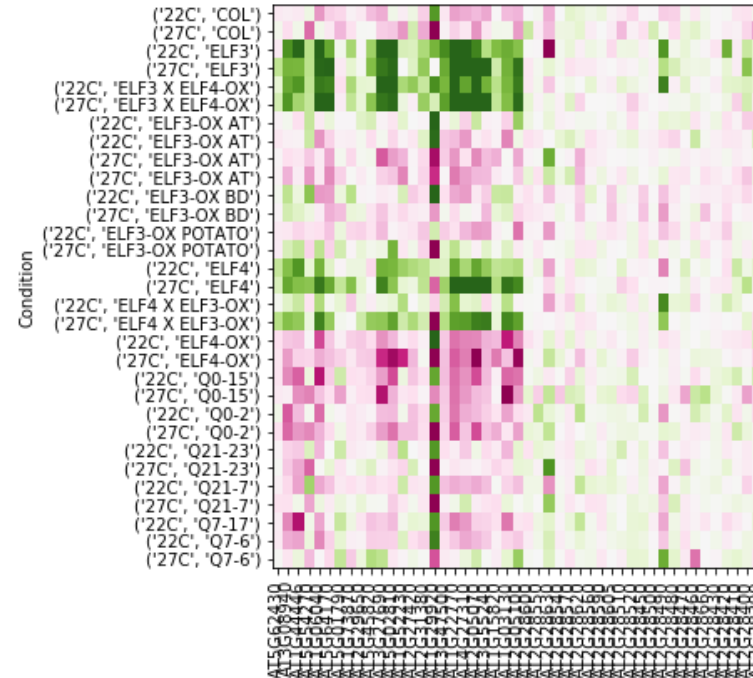
Fixing the ChIP-Seq targets according to a criteria.
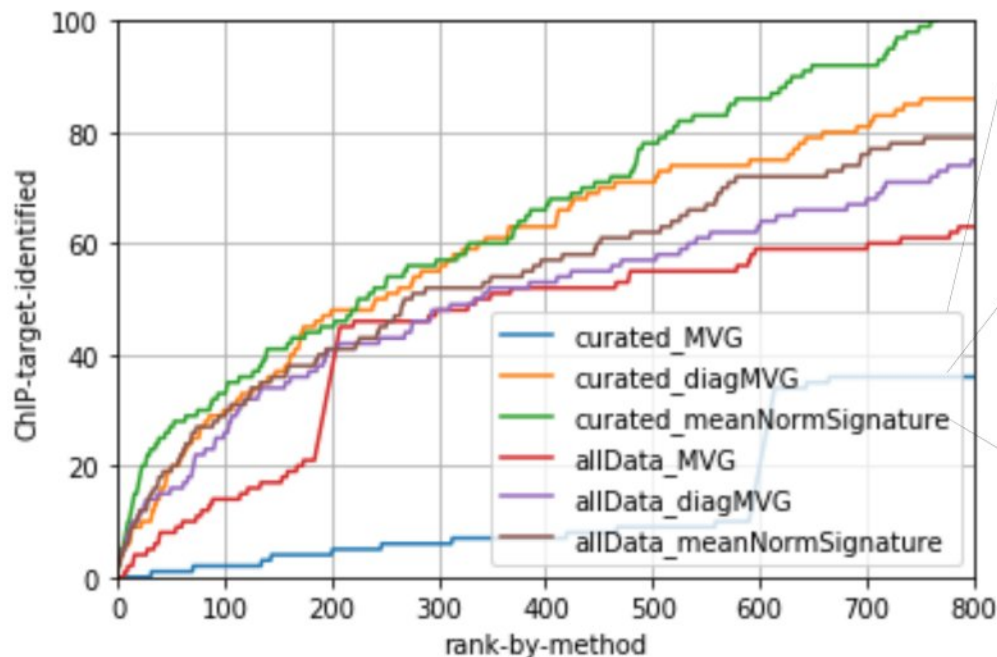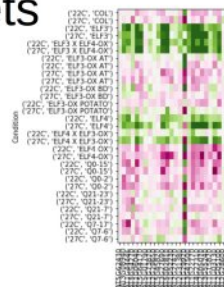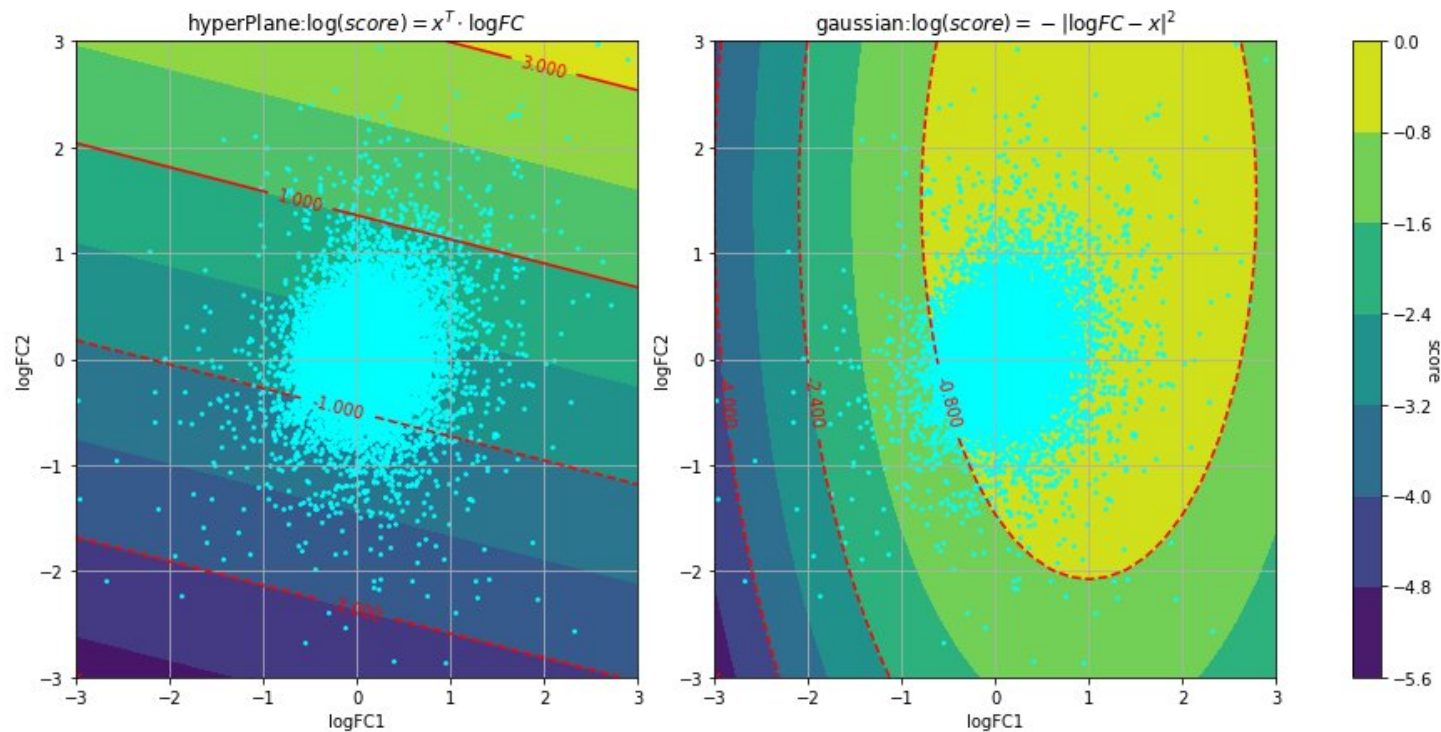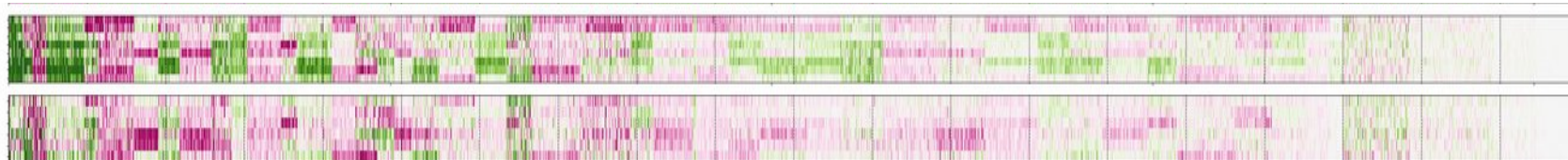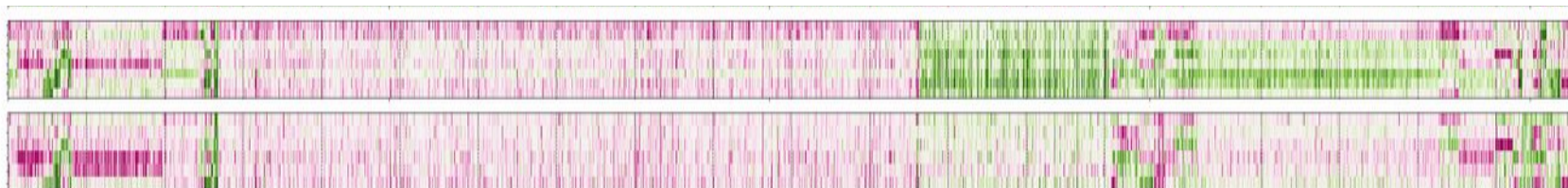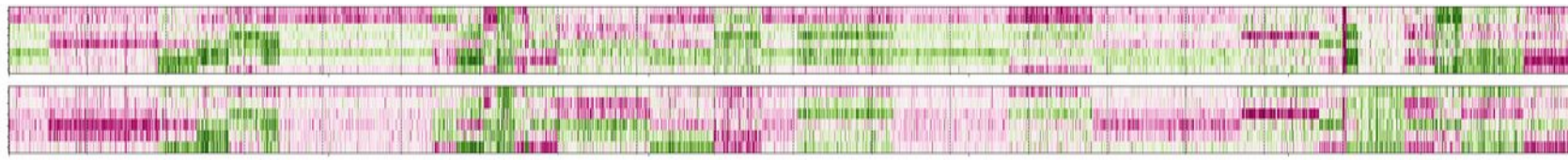Extrapolated from marker targets

allData: ZT8 ZT12
Curated:ZT12-only

MeanNormSignature leads to a statistical model based on hyperplane instead of ellipses (on which Normal distributions are based).
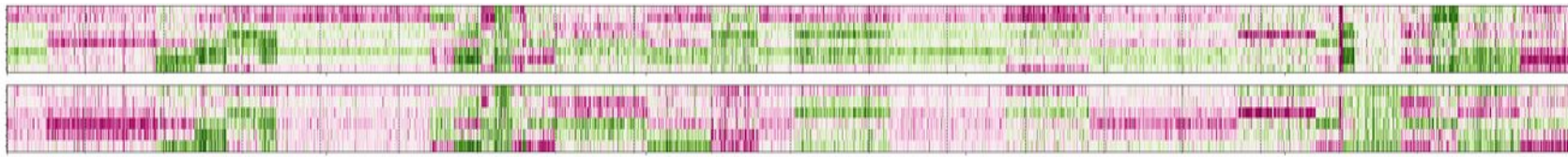
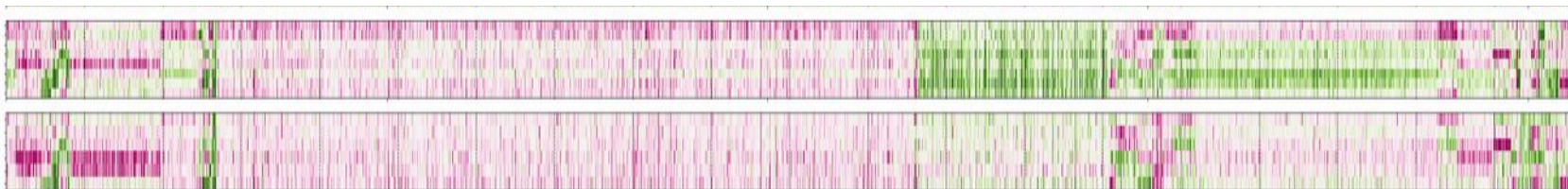# Use hyper-plane scoring in the latent-variable-model for unsupervised clustering

Use hyper-plane scoring in the latent-variable-model for unsupervised clustering
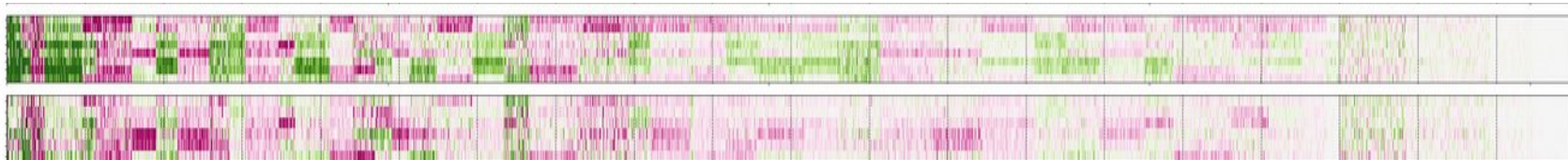

HyperPlane Mixture

HyperPlane Mixture

Gaussian Mixture

Use hyper-plane scoring in the latent-variable-model for unsupervised clustering

Effect of elf3-1 at Wk2,SD

Effect of elf3-1 at Wk3,SD

Effect of phyC-KO at Wk2,SD

Effect of ppd1-1 at Wk3,SD

Effect of LD at Wk2

Effect of LD at Wk3

Summary:

- Hyperplane outperforms multivariate Gaussian in identifying co-regulated groups.

- It's possibly to automatically define group of genes that share RNASeq signature and ChIP-Seq signature through an iterative/alternative scheme (similar to expectation maximisation).

- Each side of the algorithm itself can also be used alone to

- Leverage the server capacity for better organisation of reproducible plots and easier documentation of experiment info.

- Special thanks to **Martin** for trying out all these new techs!

- update on CAMTA:
http://172.26.114.34:81/static/figures/1119__peakBW__CAMTA__194C-4Cel__sigTarg/figure.html
http://172.26.114.34:81/static/figures/1122__rnaSeq__149R__chipTarg/figure.html
http://172.26.114.34:81/static/figures/1121__CAMTA__190R-191R__PCA/ISOMAP.html