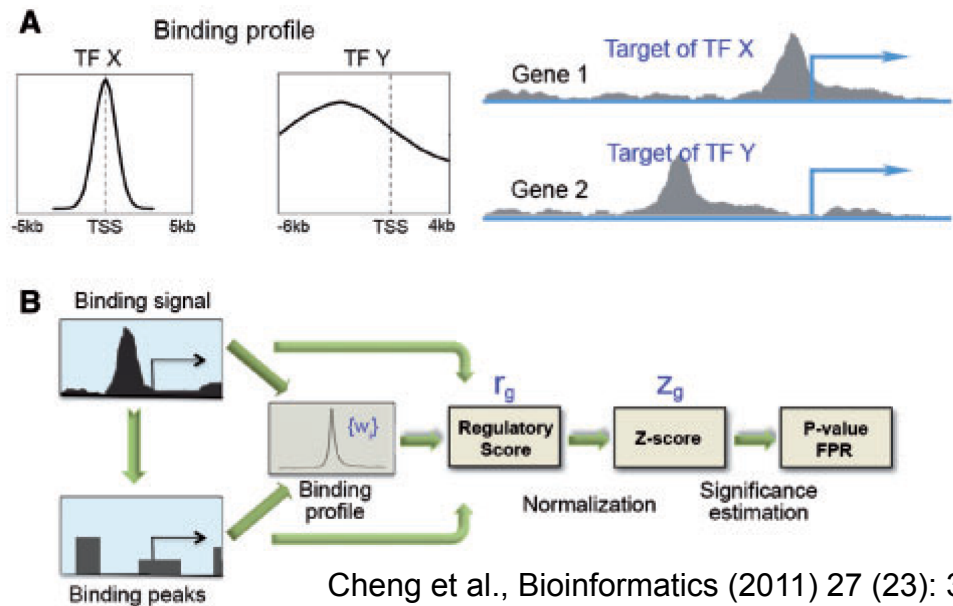Application of TIP to worm-fly ChIP-Seq data: input control and signal profiles

TECH, 11 August 2015
TG, KKY
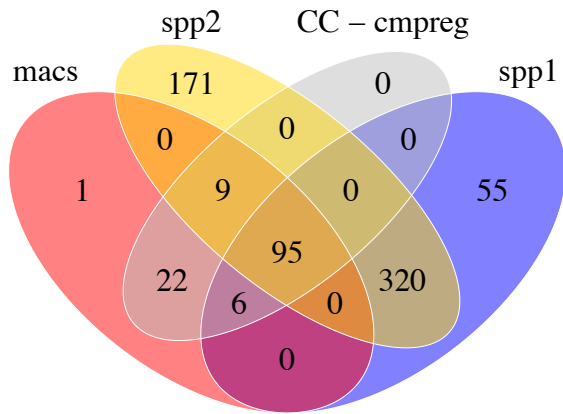
Target Identification from Profiles (TIP)

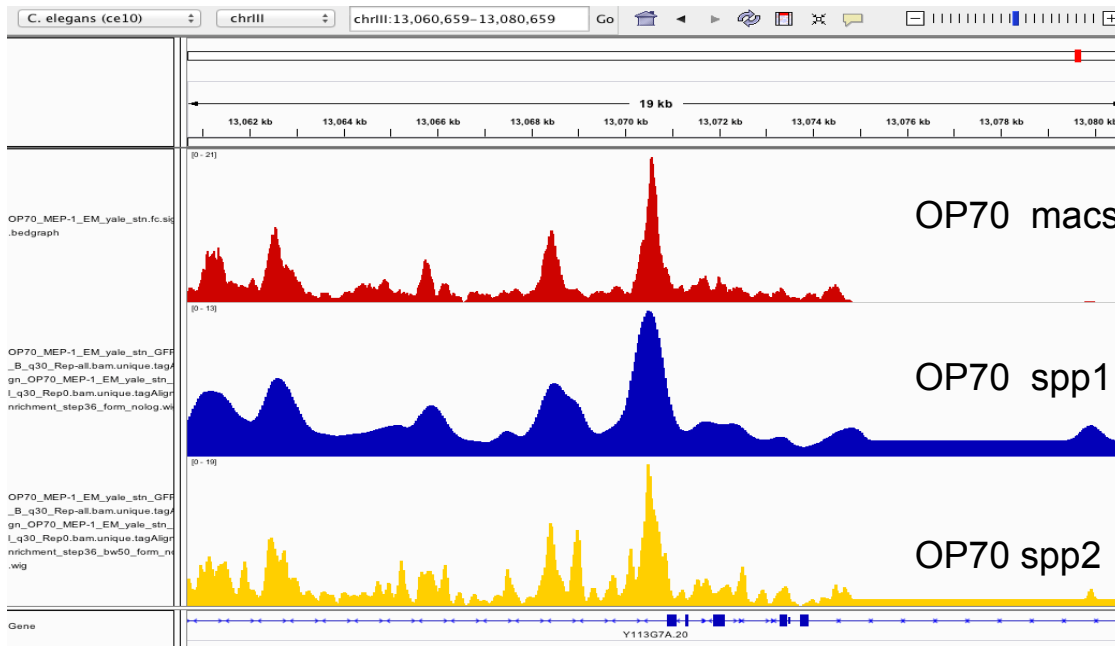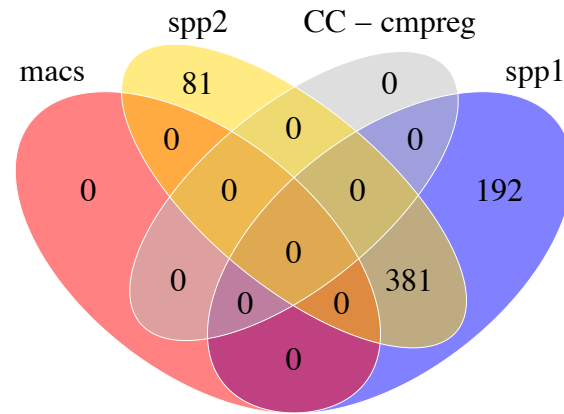Cheng et al., Bioinformatics (2011) 27 (23): 3221

- TIP method (tip, CC et. al. 2011)
    - uses signal track files, no input control

- worm-fly target predictions (cmpreg, Boyle et. al. 2014)
    - (peaks were called using SPP by modENCODE)
    - TIP targets were predicted based on MACS2 fold change signal files

- Currently (U Chicago):
    - (peaks are being called using SPP)
    - we have been trying to apply TIP, starting with spp-generated fold change signal
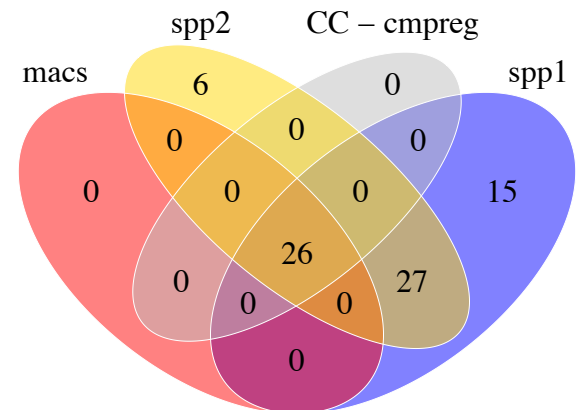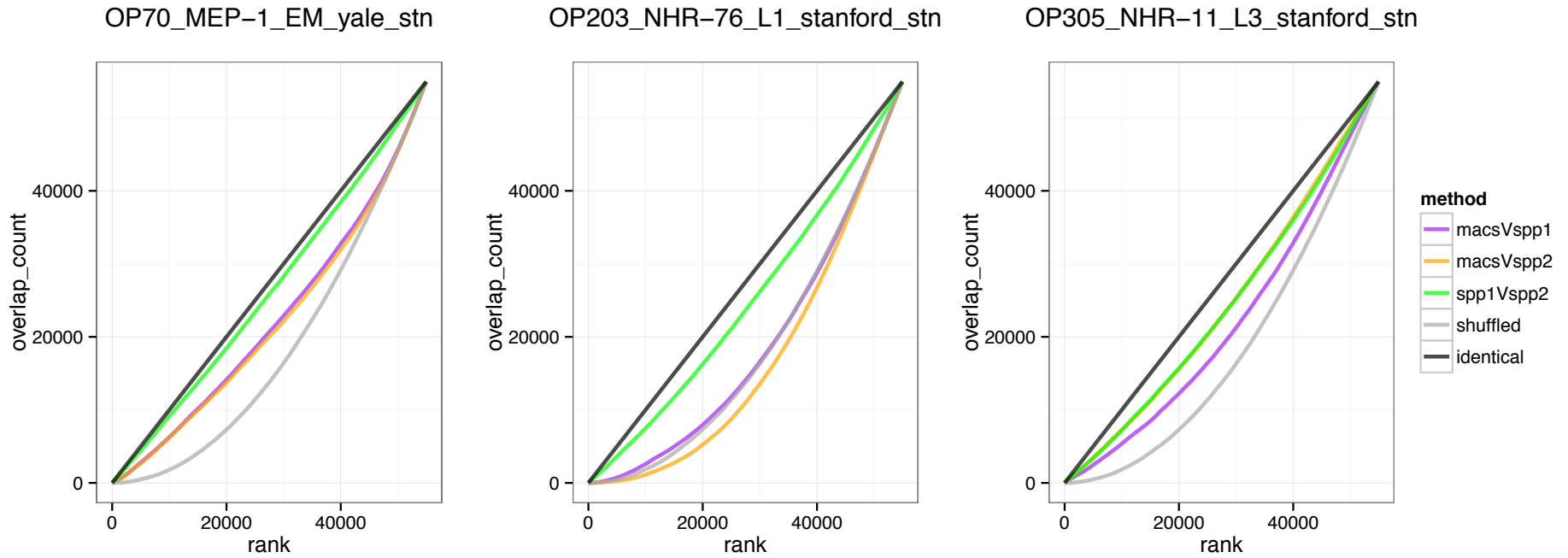
Q<0.05 target predictions:

OP70_MEP−1_EM_yale_stn

OP203_NHR−76_L1_stanford_stn
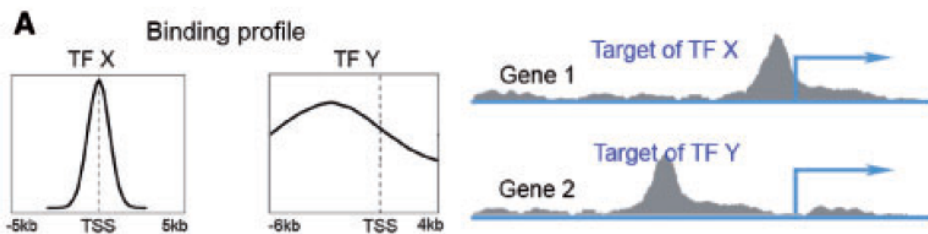

OP305_NHR−11_L3_stanford_stn

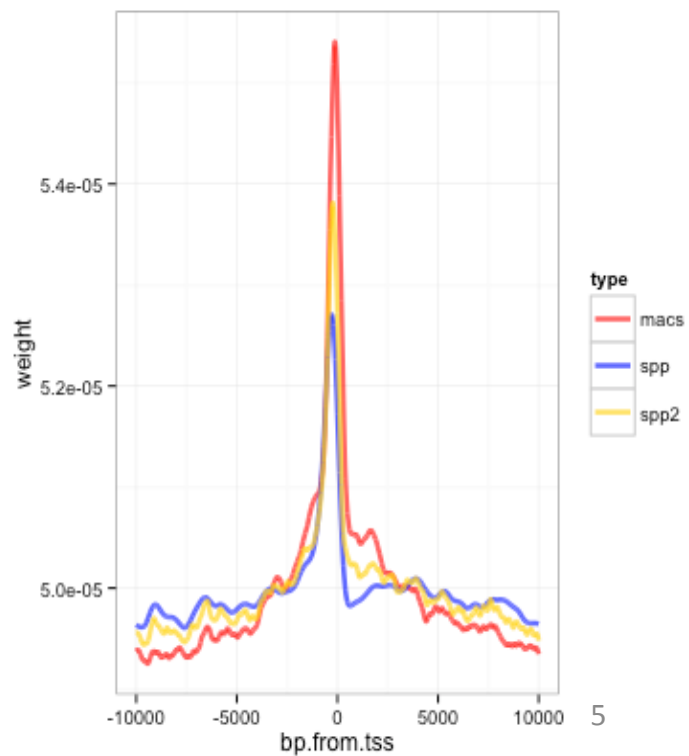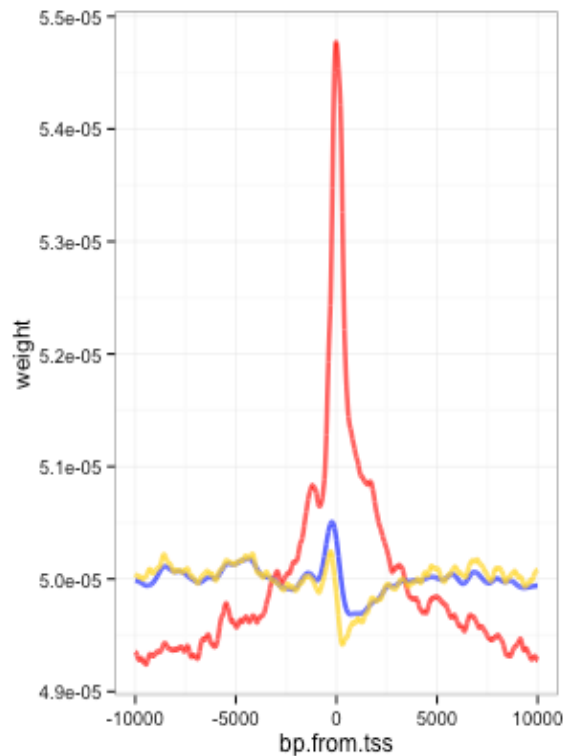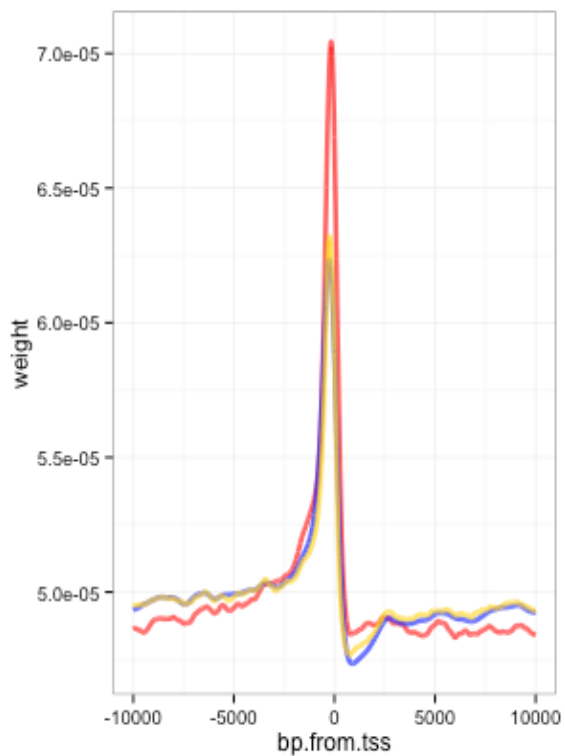**Overlap vs rank (IDR type):**

Profiles:

A — Binding profile

Cheng et al., Bioinformatics (2011) 27 (23): 3221
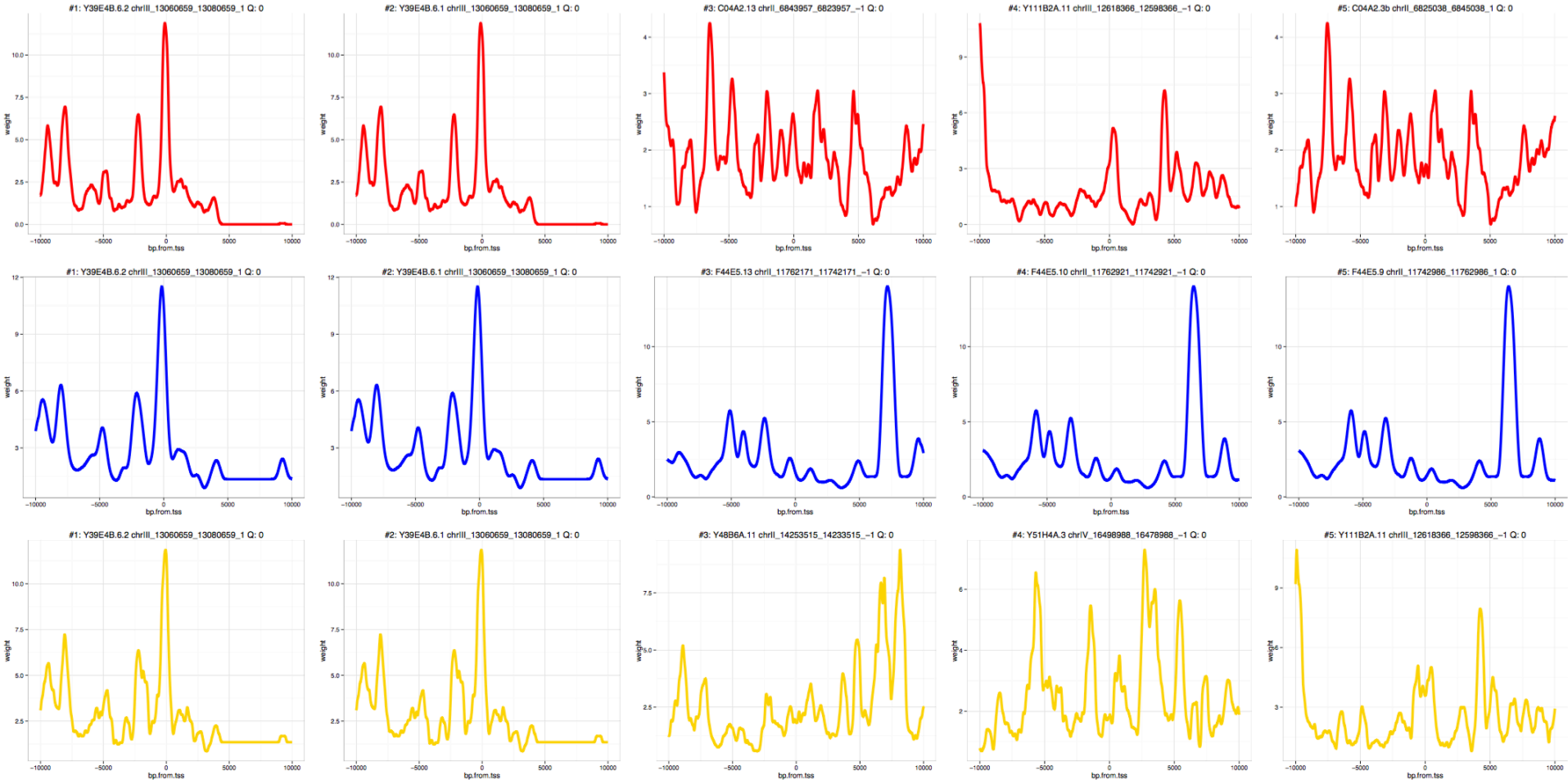

OP70_MEP-1_EM_yale_stn
norm ave profile

OP203_NHR-76_L1_stanford_stn
norm ave profile

OP305_NHR-11_L3_stanford_stn
norm ave profile

type
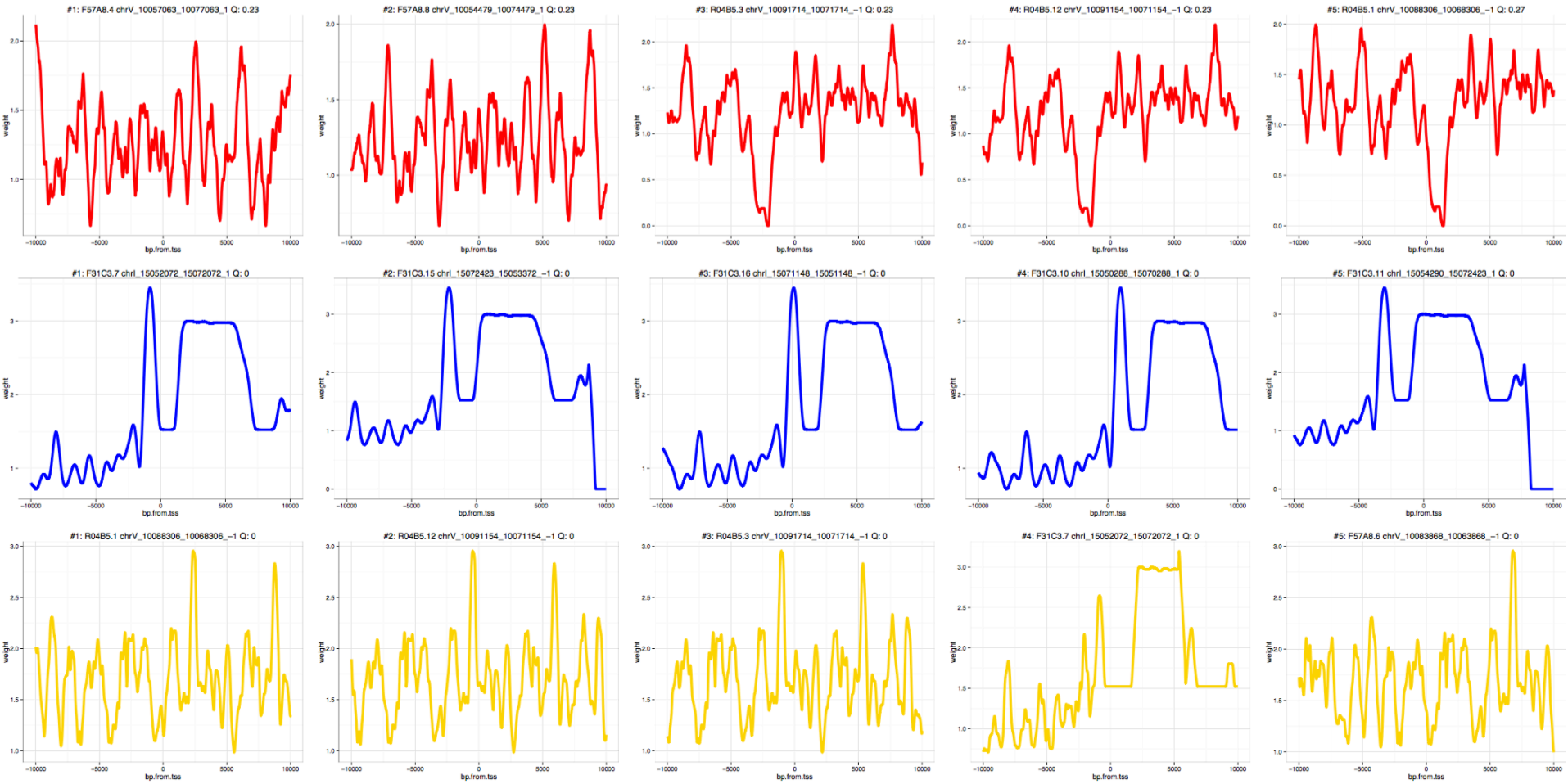macs
spp
spp2

Top target profiles
OP70_MEP-1_EM_yale_stn

Top target profiles
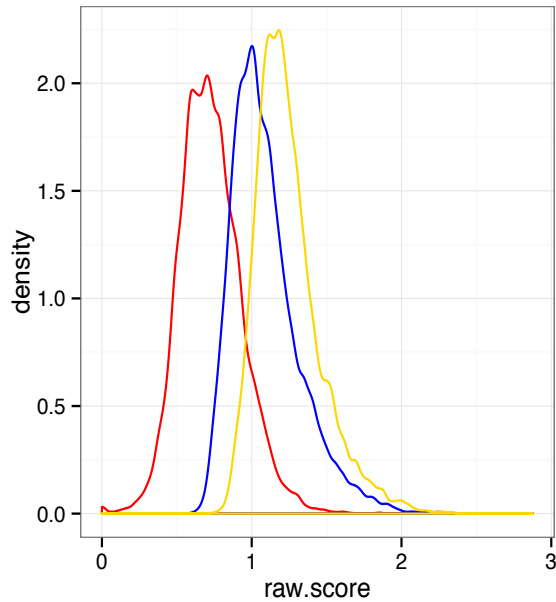OP203_NHR-76_L1_stanford_stn

Top target profiles
OP305_NHR-11_L3_stanford_stn

Raw scores distribution:
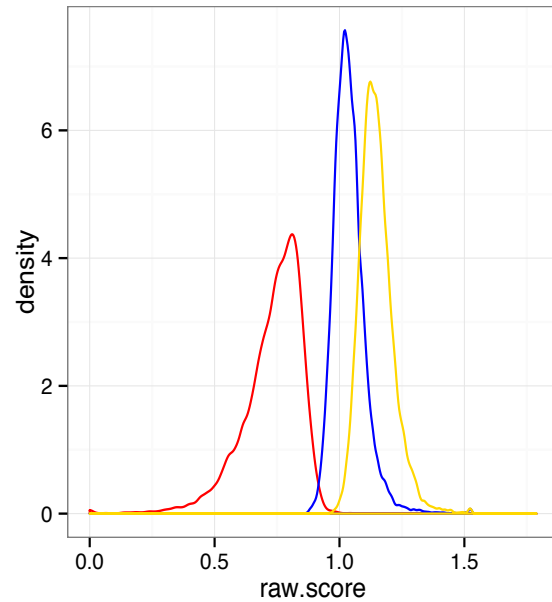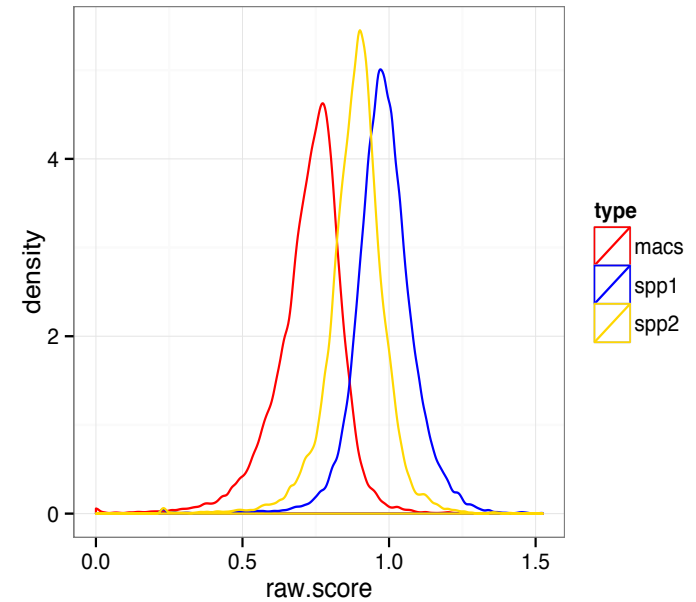

What should we do?

- try something else, some modifications to the approach/method
- or ... just use macs2 (consistent w cmpreg paper) identify targets, build networks ... see if further results make sense
- or build networks based on peaks overlapping TSS or something else
- or anything else?