modERN Call

White Lab

09-24-2015

ChIP-seq Status

	FY1 8/2013-7/2014	FY2 7/2014-7/2015	FY3 7/2015-7/2016	FY4	FY5
BACs Tagged and sent	60/60	70/70	80/80	17/90^	100
Transgenic Fly lines	80/80	32*/80	80	60	20
Fly ChIP-seq	60/60	70/70	47[!]/80	90	100
Worm ChIP-seq	60/60	70/70	9[!]/80	90	100

*: As of 9/11/15. Doesn't include 13 new lines from 8/20. 9 new lines from 9/11.

^: As of 6/22/16. Doesn't include 54 large BACs sent.

!: As of 09/23/15

modERN ChIP-seq datasets

177 lines complete data sets

- ab, **Abd-B**, acj6[!], Antp-mimic, Atf-2, Atf3, Bab2, br, brk, Bteb2, btn, **cad**, Camta-mimic, CG10565, CG10631, CG11398, CG12236, CG12744, CG13624, CG14965, CG1620, CG1647, CG16863, CG1792, CG18476, CG2120, CG32264, CG31627, CG3163, CG33213, CG3838, CG4282, CG4854, CG5204, CG7786, CG8089, CG8944, CG9305, CG9609, CG9876, CHES-1-like, chif*, chn, **cic**, cnc, corto, crebA-mimic, crc-mimic, **crp**, cyc, da, **dac**, Dad, **Dfd**, Dif, Dip3, disco, dl*, dm, dpn-mimic, dsf, dsx, **EcR, ;***, Eip75B-MiMIC, Eip78C, Eip93F, emc, ems, en, ERR, esn, Ets21C, Ets65A(ets3), Ets97D, **eve**, **exd**, ey, eyg, foxo, ftz-f1, fru-mimic, fu2, GATAd, gcm2, gfzf, grh, **grn**, gro, **h**, her, HLH54F, HLHm7, HmgD, Hmx-MiMIC, Hnf4, Hr38, Hr39, **Hr4**[!], Hr46, Hr51, **Hr78**, Hr83, Hr96, hsf, insv, jim, **jing**, Jra*, jumu-mimic, kn, lbe, lilli , **lola***, Lpt, luna-mimic, lz, Mad, maf-s, mam-mimic, Max, med, Mes4, Met, Mio, Mnt, mod(mdg4), myb, **N**, NC2alpha, NC2beta, Neu2, NK7.1, **nmo**, OdsH[!], ovo, p53-mimic, pb, pdm3, **pdp1**(&mimic), pho, Pif1A, Pif1B, pnt-MiMIC, psq[!], pum-mimic, Rel, repo, sage, sens, shn, side-mimic, sima, slou, slp2, Smox, Sox102F, Sox14, Sry-delta, **Stat92E**, Su(H), Su(var)3-7, sv, svp, tai, **tio**, **tll**, toe, topi, trh, trl-mimic, tup, tx, **usp**, vfl, vri, Vsx2, woc, Zfh2.

- **15 already submitted under last grant**
- 151 un-submitted
* multiple isoforms run
! Multiple time-points collected
XX: verifying data with rerun.

Fly ChIP-seq

MiMIC being expanded for ChIP-seq (ADD1, CG16779, CG9727, dsx, foxo, Snoo)

52 tagged lines being expanded for ChIP-seq
Target Stages:

    Embryo: achi, bcd, cato, CG10462, CG10543, CG11723, CG13775, CG12104, CG15073, CG15479, CG1602, CG1832, CG31388, CG3065, CG4617, CG4820, CG5245, CG8388, CG9727, CG9883$^{\shortparallel}$, Chrac-16, E(bx), E(spl)m3, E(var)3-9, fkh, kay$^{\shortparallel}$, Kr$^{\shortparallel}$, Sp1, TFAM, tin, unpg, Xbp1, YL-1.

    W3L: CG7839^{phenotype}

    WPP: bsh, caup$^{\shortparallel}$, CG11902, CG12155$^{\shortparallel}$, CG18619, CG32006, CG30431, CG33017, CG4318, CG34402(AKA CG34406), CG6792, CG8632, CG9139, E(z), Sox15.

    AM: CG3919, CG7045.

    Adult: Crg-1.

Repeat: Abd-B(for sue), cic, crp, dac, grn, insv, jing, nmo-small, tio

Comparison with modENCODE data:

    TF Ab: CG8478 @ WPP, usp @ W3L, Stat92E @ WPP

    GFP: Dfd @ W3L, Abd-B @ W3L, EcR @WPP

NLS-GFP Controls 5629/30: WPP, E0-24, W3L(done), AF, AM

W1118 Ab controls: GoatV, h, Mad, Hr39.

$^{\shortparallel}$: failed once

03: Chromatin extracted
01: IPed
08: Libraried
    08: @ HGAC
    00: Processing
    00: awaiting reps or PCR

Worm ChIP-seq

- Received:
  - Additional reps for: YL561, OP56 , OP443

- Received:
  - OP566, OP578, OP562, OP550, OP553, OP556

Current Work

- Breakdown of # peaks vs expression level in fly
  - Also needed for Gal4 UAS::nlsGFP dosage test
- Rerunning old Fly data with current pipeline
- Searching for old worm data and downloading for rerun
- Further comparison between nls-GFP and datasets
  - In W3L datasets, overlap of nls-GFP peaks correlates with total # of peaks ($R^2=0.79$)
- Upload all wigs and bed files after DCC approval
  - These are the only remaining files
  - Potential public release when finished.
- Test new version of IDR