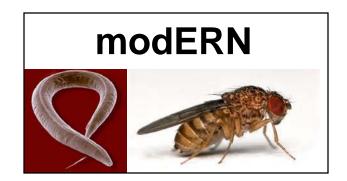
Reinke Lab Update



Michelle Kudron and Mei Han Dec 8th, 2016

Outline

- Summary of ChIP-seq progress
 - Completed and pending datasets
 - Further optimization of chromatin shearing
 - Worm pellets ready for ChIP/growth
 - Specificity of the GoatV GFP Ab
 - N2 GoatV Mock IP subtraction examples
 - ChIP'd factors for RNA-seq
- Summary of RNA-seq progress
 - Backcrossed deletion mutants
 - Backcross in progress
 - RNA isolated for sequencing and backcrossed strains waiting for RNA isolation

Sequencing data for 177 new datasets

33 Bridge	0 Y1Q1	0 Y1Q2	10 Y1Q3	22 Y1Q4	17 Y2Q1	11 Y2Q2	20 Y2Q3	15 Y2Q4	4 Y3Q1	6 Y3Q2	0 Y3Q3	16 Y3Q4	14 Y4Q1	9 Y4Q2
YL482_C06A8.2_YA			CS152_SMA-3_L2	OP418_DMD-4_LE	YL487_SNPC-4_YA	OP399_F22D6.2_YA	OP525_C04F5.9_L1	OP536_IRX-1_L1	OP56_ELT-2_L1	OP566_HLH-15_LE		OP560_POP-1_EE	OP202_CEH-9_LE	N2_FLAG_L4
YL479_EFL-1_YA			AGK154_UNC-130_L4	OP312_LIR-3_L4	YL551_SNPC-4_YA	OP63_HLH-8_LE	OP484_NHR-90_YA	OP537_MXL-1_YA	OP56_ELT-2_L3	OP578_UNC-3_LE		OP659_UNC-120_ME	OP673_CEH-24_LE	OR3349_HIF-1_L4_hypoxia
YL485_F08F3.9_YA			AGK541_UNC-130_YA	OP471_F13H6.1_L2	OP521_SPR-1_L4	OP201_PQM-1_LE	OP533_CEH-18_LE	OP538_HLH-12_YA	OP56_ELT-2_LE	OP562_AHR-1_LE		OP573_HND-1_EE	OP652_FKH-8_L1	XIL99_VAB-15_sL1
YL497_T02C12.2_YA			OP509_ETS-4_L3	OP511_ZTF-11_L1	OP311_TBX-7_LE	OP154_PAG-3_LE	OP534_ZFP-2_L4	OP210_CEH-90_L1	OP443_Y53C12C.1_L	E OP558_ZTF-16_LE		OP606_F52B5.7_YA	OP646_MEL-28_YA	OP553_CEH-79_yAd
YL478_EFL-1_YA			OP510_F37D6.2_L4	OP508_MADF-10_YA	OP485_LIN-40_YA	OP164_FAX-1_LE	OP487_ETS-7_EE	OP493_NPAX-4_LE		OP476_UNC-86_LE		OP636_TBX-9_YA	OP656_HMBX-1_EE	OP658_F10E7.11_yAd
YL507_DPL-1_YA			OP388_LIM-6_LE	OP460_NHR-80_YA	OP517_SOX-4_L1	OP528_SNU-23_L1	OR3350_HIF-1_L4	OP541_COG-1_ME		OP68_TTX-3_LE		OP598_T26A5.8_YA	OP640_TRA-4_EE	OP552_C34B4.2_L1
OP462_RNT-1_L1			OP512_SWSN-7_L1	OP478_T07F8.4_YA	OP523_HLH-4_L1	OP532_Y116A8C.19_L1	OP489_NHR-232_LE	YL581_REC-8_YA				OP615_Y22D7AL.16_LE	OP662_B0261.1_YA	OP696_M03D4.4_ME
OP401_LSY-27_YA			OP159_TBX-2_LE	OP513_C08G9.2_LE	OP524_CEH-34_LE	B0035.1_XTL1186_YA	OP476_UNC-86_L1	YL576_HIM-1_L4/YA				OP609_CHD-7_YA	OP677_CHE-1_LE	OP563_CEBP-1_yAd
OP474_ZK185.1_YA			OP159_TBX-2_L1	OP159 (L3)	OP55_MEC-3_LE	OP315_CEH-14_LE	QP0661_XND-1_YA	YL577_HIM-1_YA				OP622_GMEB-2_LE	N2_GFP_EM	OP550_F57C9.4_yAd
OP248_MES-2_L4			OP506_XBP-1_L1	GOU883_EGL-13_L1	OP518_NHR-48_L4	OP323_CEH-2_LE	OP494_ZTF-16_LE	OP100_FKH-4_L1				OP631_CEH-48_LE	OP605_F13C5.2_EE	OP688_REPO-1_yAd
JK1107_RPC-1_YA				YL529_LET-607_YA	YL557_WAGO-9_YA	OP496_ZTF-18_YA	OP252_DAO-5_L4	OP385_F55B11.4_YA				OP620_CEH-36_EE	N2_GFP_yAd	
LW1254_SMA-9C2_L2				OP480_NHR-71_L1	YL563_REC-8_YA		OP502_ALY-1_EE	OP544_ZIP-5_LE				OP594_FKH-3_YA	N2_FLAG_EM	
OP470_ZC204.2_L4				OP516_CEH-32_L4	OP529_F10B5.3_L4		RW10702_HLH-6_LE	OP539_NHR-85_L1				OP587_MADF-2_LE	OP565_ZTF-26_YA	
OP358_CEY-2_L4				ZM8745_DAF-16_L4	OP522_DSC-1_L1		OP195_RBR-2_L4	OP543_SDZ-38_YA				OP568_LSY-12_L3	OP579_DPFF-1_YA	
OP372_K09A11.1_LE				OP515_NHR-20_L1	OP383_F49E8.2_L4		RW10316_DIE-1_YA	TH184_HMG-11_L3				OP642_B0310.2_EE	OP638_ATF-7_YA	
OP398_DVE-1_LE				OP514_SPR-4_YA	OP520_REF-2_LE		OP78_FKH-6_LE					OP645_MLS-2_ME	OP581_ZIM-3_YA	
OP398_DVE-1_L4				OP471_F13H6.1_LE	OP111_ELT-4_LE		RW10325_MES-4_YA						OP517_SOX-4_LE	
OP429_F23B12.7_YA				OP370_CEH-31_LE			OP488_SYD-9_LE							
OP433_HLH-30_L4				OP463_NHR-102_L4			OP173_UNC-42_LE							
OP433_HLH-30_LE				OP462_RNT-1_LE			OP465_NHR-179_YA							
OP391_MED-1_ME				OP481_NHR-47_L1			OP92_SDC-2_LE							
OP404_NFYA-1_YA				OP483_NHR-90_L1										
OP404_NFYA-1_L3				ZM7247_DAF-16_L4										
OP404_NFYA-1_EMB														

• 33 completed datasets for Bridge year (24 factors that missed the data

freeze were sequenced at Stanford)

- 32 completed datasets for year 1
- 64 completed factors for year 2
- 25 completed factors for year 3
- 23 so far for year 4, quarters 1 and 2
- In total, data for 163 new TFs

OP109_BLMP-1_L2 OP354_ELT-1_EMB

OP383_F49E8.2_YA OP33_NHR-25_L4

OP405_ODD-2_LE OP154_PAG-3_L1 OP312_LIR-3_L1

OP477_NHR-43_L3 N2_RPC-1_YA

Completed factors for year 4, quarters 1 and 2 (23)

	Factor	Strain name	Stage
*	CEH-9	OP202	LE
*	CEH-24	OP673	LE
	FKH-8	OP652	L1
	MEL-28	OP646	yAd
	HMBX-1	OP656	EE
	TRA-4	OP640	EE
	B0261.1	OP662	yAd
	CHE-1	OP677	LE
	F13C5.2	OP605	EE
	ZTF-26	OP565	yAd
	DPFF-1	OP579	yAd
	ATF-7	OP638	yAd
	ZIM-3	OP581	yAd
*	SOX-4	OP517	LE
	HIF-1	OR3349	L4
	VAB-15	XIL99	sL1
	CEH-79	OP553	yAd
	F10E7.11	OP658	yAd
	C34B4.2	OP552	L1
*	M03D4.4	OP696	ME
	CEBP-1	OP563	yAd
	F57C9.4	OP550	yAd
	REPO-1	OP688	yAd

Asterisk indicates factors for the RNA-seq project

Pending factors (16)

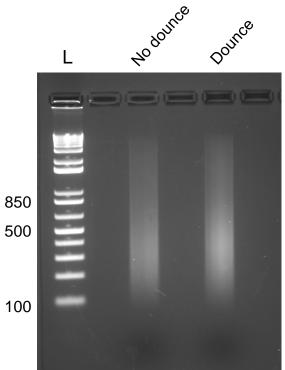
	Factor	Strain name	Stage	Status
	ZTF-3	OP614	yAd	Awaiting sequencing
:	LIN-11	OP62	ĹE	Awaiting sequencing
	ZTF-27	OP705	yAd	Awaiting sequencing
	ATHP-1	OP685	yAd	Awaiting sequencing
	SPTF-1	OP707	EM	Awaiting sequencing
	CEH-1	OP571	L1	Failed again, given up on this one for now
	N2_FLAG	N2	yAd	Repeated, failed again, process new pellets
	HAM-2	OP639	EM	Repeated, failed again, needs regrowth
	ATTF-2	OP657	EE	Repeated, failed again, needs regrowth
	BED-3	OP651	EM	Repeated, failed again, needs regrowth
	HND-1	OP573	yAd	No enrichment, regrow
	CEH-89	OP556	yAd	Failed, needs to be repeated
	C33H5.17	OP570	L4	Failed again, despite regrowth and douncing
	CCCH-3	OP627	yAd	Failed again, despite regrowth and douncing
	GEI-17	OP572	yAd	One rep concentration too low despite
				douncing
	SAEG-1	OP580	yAd	One rep failed despite douncing

Asterisk indicates factors for the RNA-seq project

Addition of douncing step to ChIP protocol improves DNA yield and library success rate

- Resuspend frozen pellet in .75 mLs of FA buffer and transfer to 2 mL dounce tube
- Dounce with small pestle 2 times, 15 plunges each, turning pestle a quarter turn each time, icing for one minute between each of the 15 plunges
- Dounce with large pestle 4 times, 15 plunges each, turning pestle a quarter turn each time, icing for one minute between each of the 15 plunges
- Transfer to conical, spin down, and bring volume to 1.5 mLs and then continue with sonication

```
Lane 1: Kb plus ladder
Lane 3: OP638_ATF-7_yAd
No dounce
Lane 5: OP638_ATF-7_yAd
Dounce
```



OP638_ATF-7_yAd No dounce IP

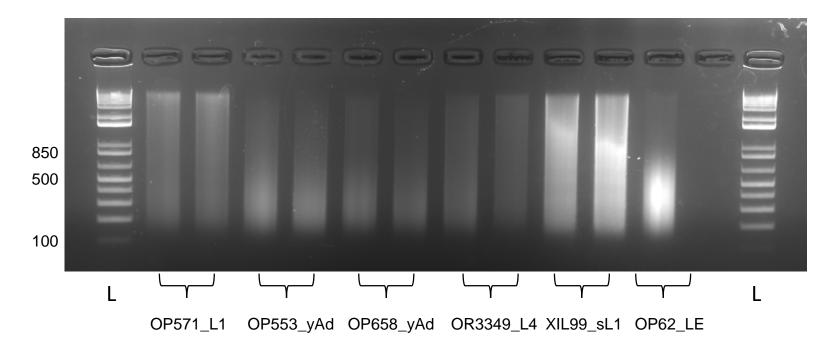
sample failed library/sequencing. Repeated with another pellet that was dounced and the library and sequencing passed

IP library success rates:

Failure rate of IP libraries before increasing amplitude = 62% (36/58) Failure after increasing amplitude and adding douncing = 20.4% (11/54). Last call it was 12.5% (2/16).

Further optimization of chromatin shearing

• Currently optimizing conditions on new sonicator



• Test fixation step

- Starved L1s and embryos have a lot more chromatin. The formaldehyde may not be penetrating the worm effectively.

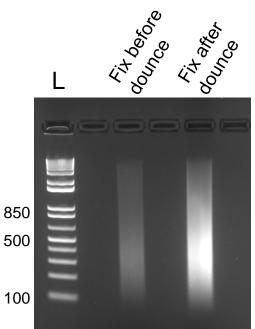
- Fix after douncing worms

Are we able to get more chromatin from worms if we fix after douncing?

Fix before douncing (current protocol)

Modified from Ercan et al., 2007

- Collect worms
- 2% formaldehyde 28 min, RT
- Flash freeze and store at -80 degrees
- Thaw and dounce (30 strokes "A", 60 "B")
 - Sonicate

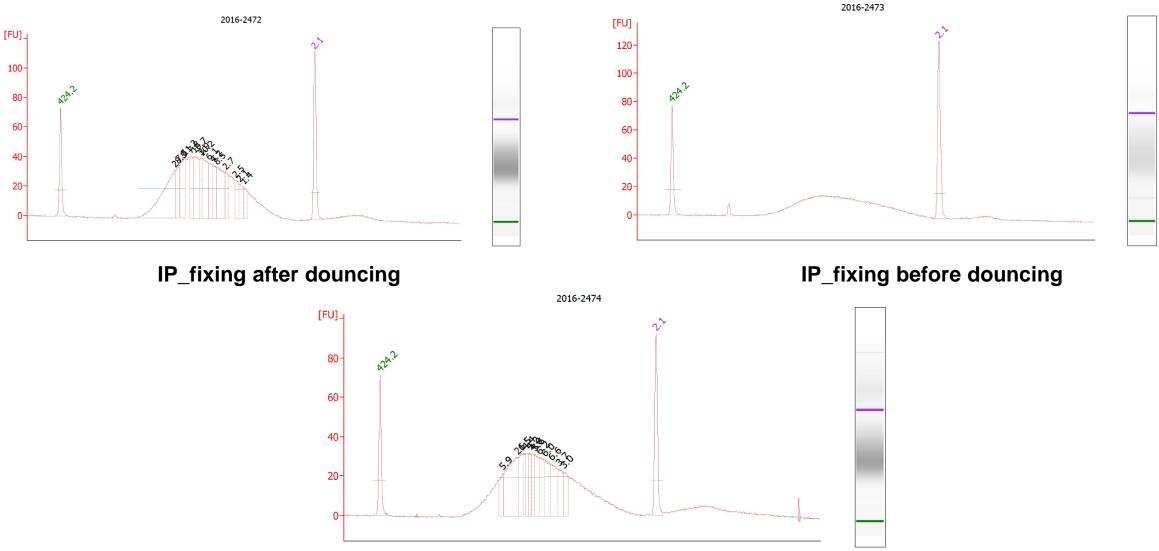


Fix after douncing

Modified from Ni et al., 2014

- Collect worms, flash freeze in liquid nitrogen
- Thaw and dounce (30 strokes "A", 60 "B")
 - 2% formaldehyde 10 min, 4 degrees
 - Sonicate

Library enrichment is vastly improved when the sample is fixed after douncing



Input_fixing after douncing

Factors ready for ChIP (25)

Factor	Strain name	Stage
CEH-93	OP554	L1
NHR-111	OP569	L4
GEI-8	OP589	L4
ZIP-4	OP590	L1
CEH-88	OP593	L4
LPD-2	OP649	L1
Y55F3AM.14	OP608	L2
SUP-37	OP611	L1
C28G1.4	OP630	yAd
HMG-4	OP660	EE
MBL-1	OP664	L1
CEH-74	OP680	EE
Y5F2A.4	OP682	L4
PHA-2	OP687	LE
DMD-10	OP689	LE
T26A8.4	OP692	L4
HLH-17	OP643	L1
MLS-1	OP694	L1
SPR-3	OP703	L4
B0336.7	OP714	yAd
R151.8	OP672	L1
SDZ-12	OP670	L4
CEH-49	OP699	ME
DRAP-1	OP700	ME
ALR-1	OP362	L1

Asterisk indicates factors for the RNA-seq project

Factors awaiting growth and collection (18)

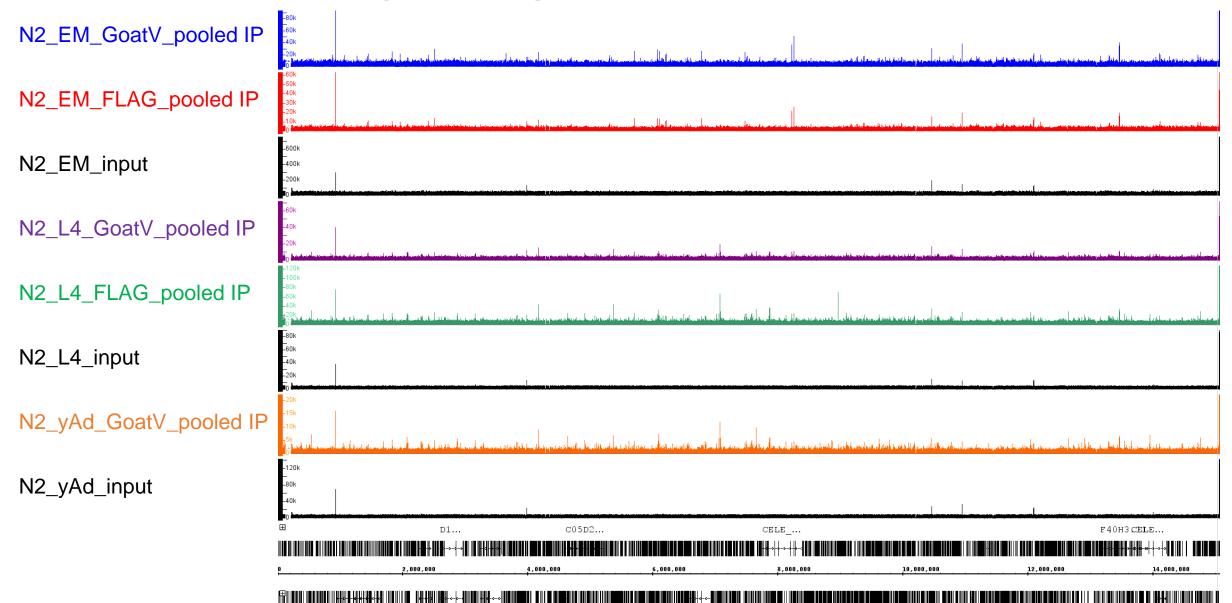
Factor	Strain name	Stage
SEM-2	OP701	EE
FLH-1	OP702	EE
TBX-8	RW10470	EE
C38D4.7	OP708	LE
T23F11.4	OP709	LE
NHR-190	OP448	yAd
PAX-3	OP190	L2
CEH-40	OP232	yAd
LIR-2	OP175	yAd
ZTF-1	OP207	L2
NHR-270	OP208	L1
K12H6.12	OP214	yAd
F26F4.8	OP716	yAd
TAG-97	OP719	yAd
LSL-1	OP720	yAd
ATTF-5	OP724	L4
SKNR-1	OP726	L4
CEH-83	OP727	EE

Testing the specificity of the GoatV GFP Antibody

- Perform ChIP using GoatV and FLAG Abs on N2 worms in 3 different stages:
 - Embryo (EM)
 - Late larval (L4)
 - Young adult (yAd)
- Perform ChIP with FLAG Ab on a factor that has previously passed using GoatV to test the overlap of GoatV and FLAG peaks
 - OP609_CHD-7_yAd

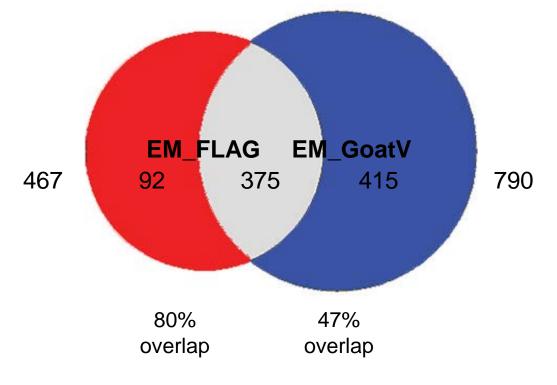
Factor	Stage	GoatV GFP Antibody	FLAG Antibody
	EM	Sequencing complete	Sequencing complete
	L4	Sequencing complete	Sequencing complete
N2	yAd	Sequencing complete	Failed
CHD-7	yAd	2 replicates completed for comparison	Sequencing complete

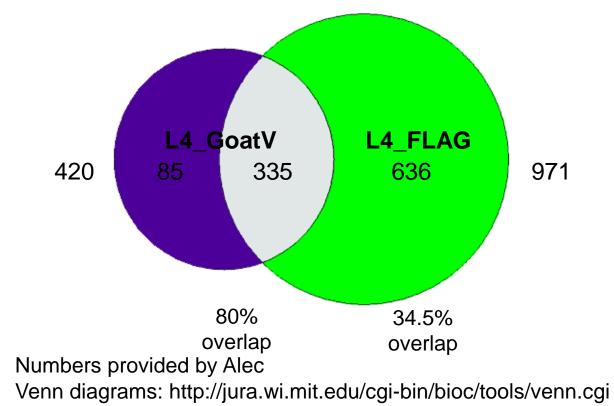
Non-specific binding of Flag and GoatV GFP antibodies in N2



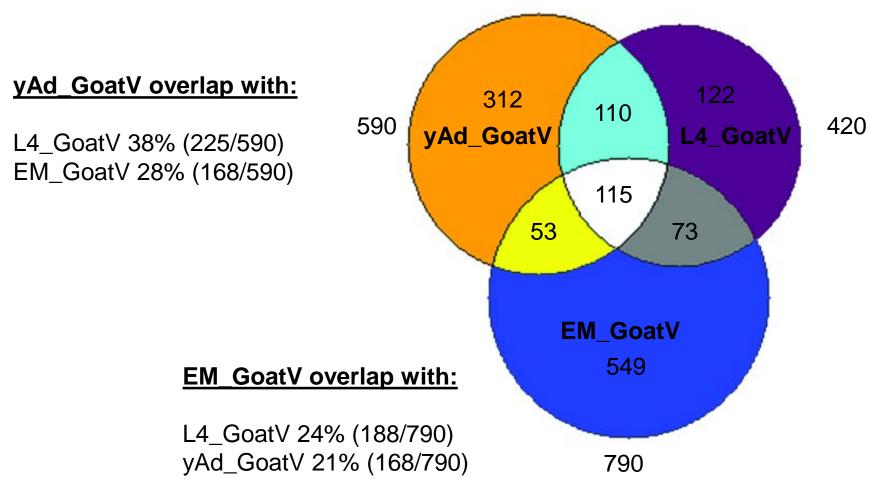
Comparison of embryo, L4 and young adult N2 ChIP-seq with GoatV GFP and Flag antibodies

- N2_EM_GoatV = 811 peaks, IDR = 1.57
- N2_EM_Flag = 482 peaks, IDR = .95
- N2_L4_GoatV = 448, IDR = .84
- N2_L4_Flag= 987, IDR = .80
- N2_yAd_GoatV = 598, IDR = .97





GoatV GFP Ab binds mainly to different sites in the embryo, L4 and young adult stages



L4_GoatV overlap with:

EM_GoatV 45% (188/420) yAd_GoatV 54% (225/420)

Need to perform IPs in the other stages: L1, L2, L3 and other embryonic stages

Numbers provided by Alec 15 Venn diagrams: http://jura.wi.mit.edu/cgi-bin/bioc/tools/venn.cgi

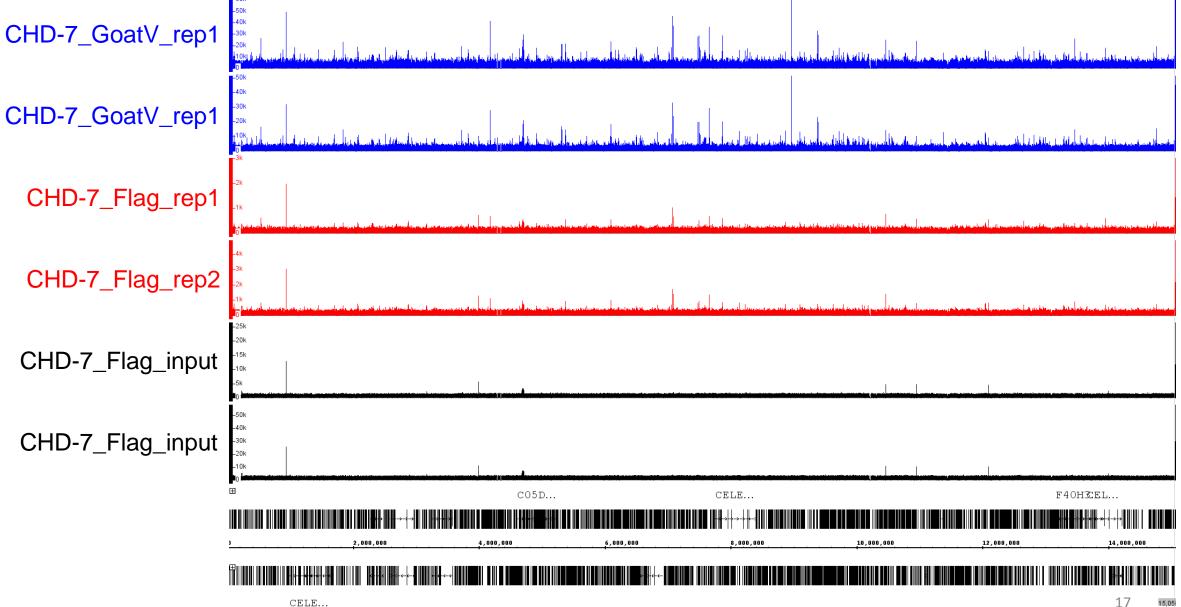
How many of these non-specific sites are HOT?

- N2_EM_GoatV = 73% are HOT (576/790)
- N2_EM_Flag = 91% are HOT (424/467)
- N2_L4_GoatV = 84% are HOT (351/420)
- N2_L4_Flag = 73% are HOT (711/971)
- N2_yAd_GoatV = 75% are HOT (441/590)

GoatV GFP and Flag antibodies are mainly binding to HOT sites

16

CHD-7_yAd binding using GoatV GFP and Flag antibodies



CHD-7 binding using GoatV GFP and Flag antibodies

• Stats of Flag and GoatV datasets

- OP609_CHD-7_yAd_Flag = 148 peaks, IDR .98
- OP609_CHD-7_yAd_GoatV = 1843 peaks, IDR 1.26

Comparison of Flag and GoatV datasets

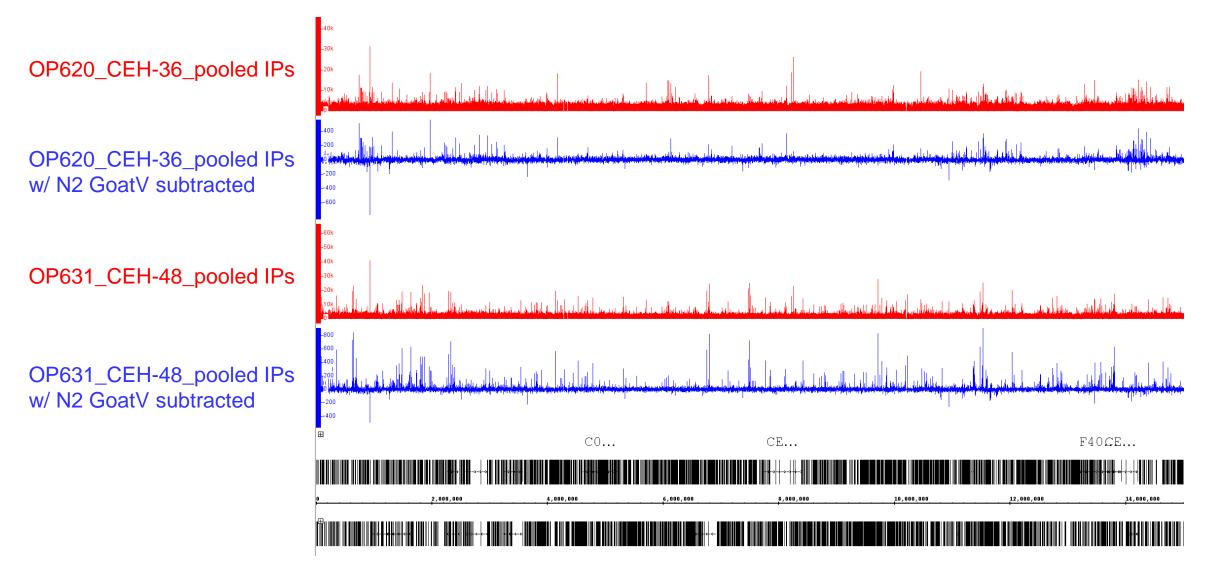
- 23 unique to the FLAG dataset.
- 1678 are unique to the GoatV dataset
- 121 peaks are common between the two datasets.

• Overlap with HOT sites

- 122/144 FLAG peaks are HOT sites, 85%.
- 113/121 common peaks are HOT sites, 94%.
- 1497/1800 GFP peaks are HOT sites, 83%.

Flag IP did not work very well, used same lysate as used for GoatV IP

Goat V mock IP subtractions on "good" TFs in embryos



Most of the peaks are retained

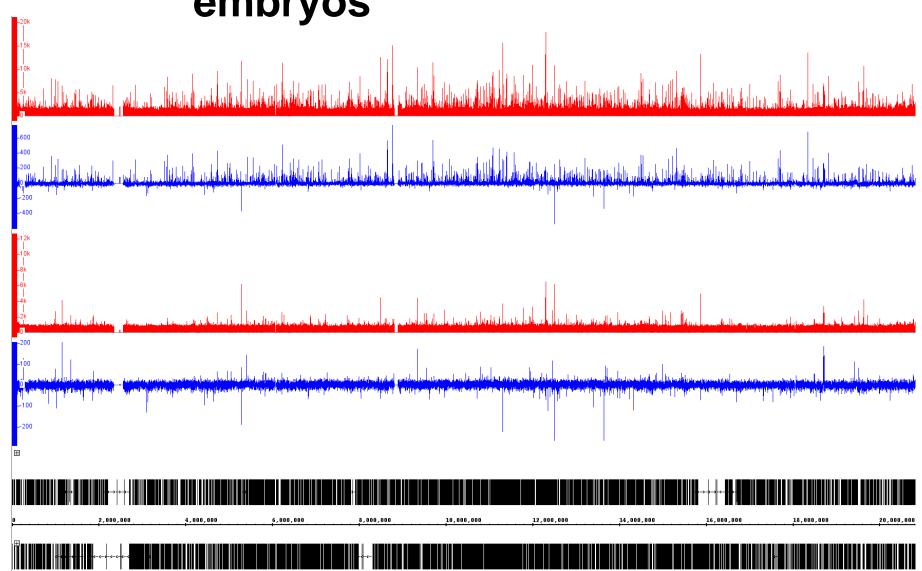
Goat V mock IP subtractions on "good" TFs in embryos

OP56_ELT-2_pooled IPs

OP56_ELT-2_pooled IPs w/ N2 GoatV subtracted

OP578_UNC-3_pooled IPs

OP578_UNC-3_pooled IPs w/ N2 GoatV subtracted



Most of the peaks are retained in OP56_ELT-2, OP578_UNC-3 is more of a moderate TF, where more peaks are lost ²⁰ ChrIV

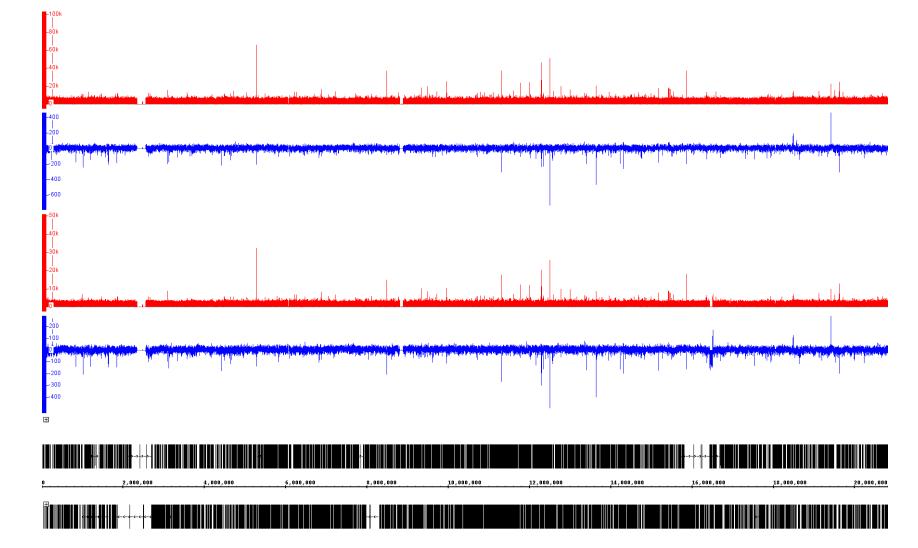
Goat V mock IP subtractions on "bad" TFs in embryos

OP622_GMEB-2_pooled IPs

OP622_GMEB-2_pooled IPs w/ N2 GoatV subtracted

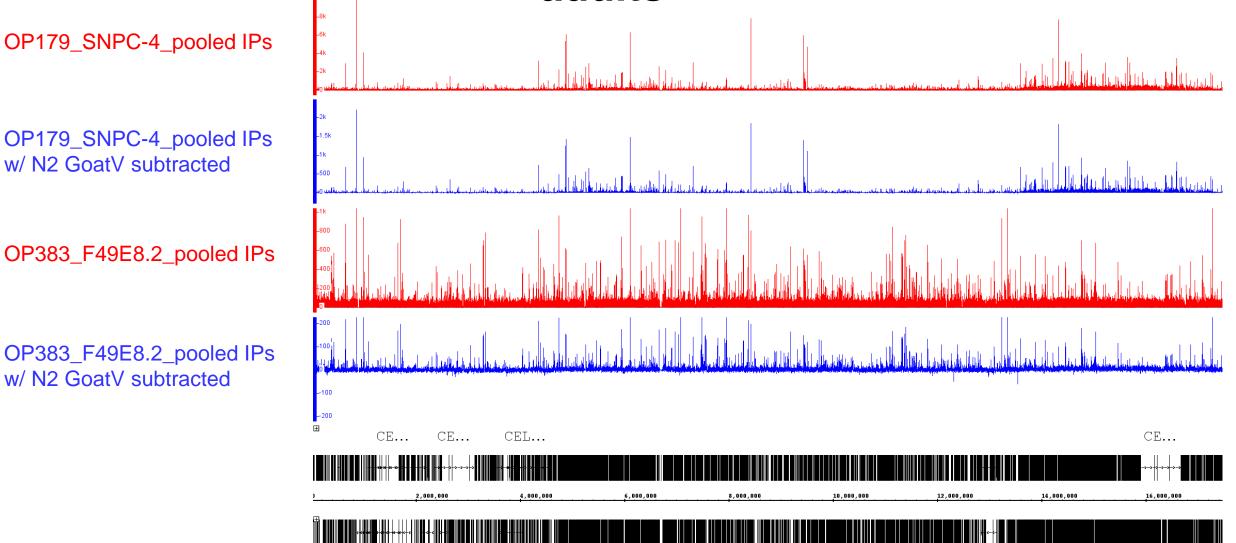
OP615_Y22D7AL.16_pooled IPs

OP615_Y22D7AL.16_pooled IPs w/ N2 GoatV subtracted

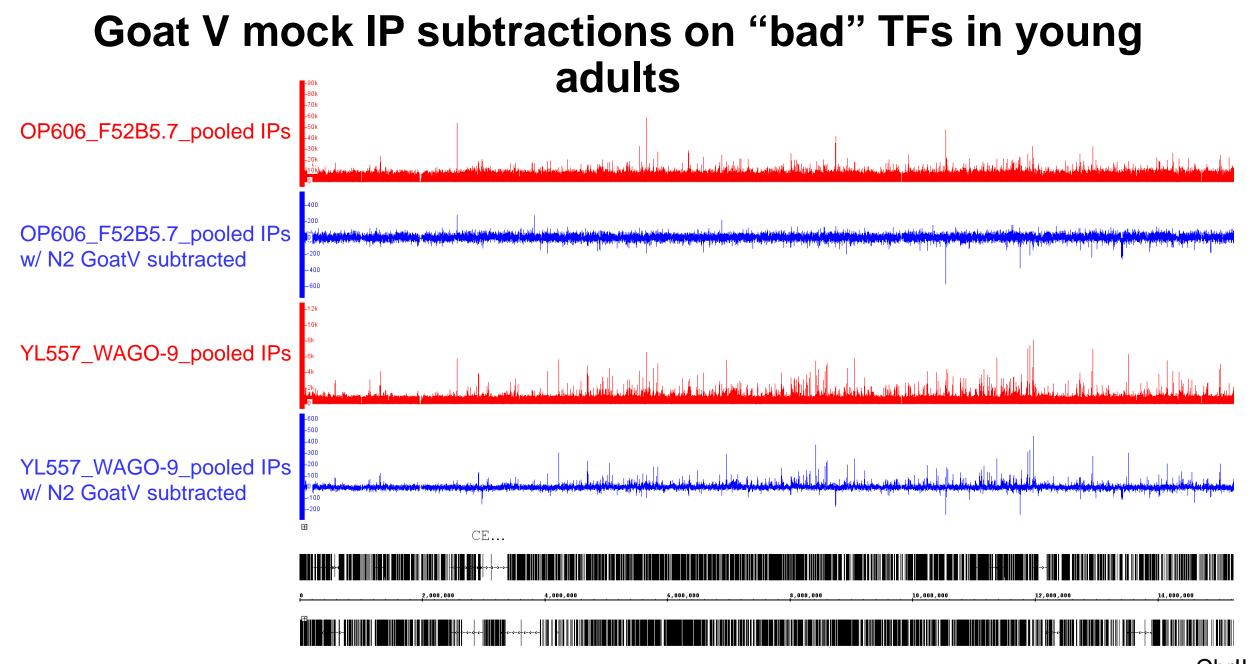


Most of the peaks are lost for these factors

Goat V mock IP subtractions on "good" TFs in young adults



Looks like all of the peaks are retained in OP179_SNPC-4, only a small number were lost in OP383_F49E8.2 ²² ChrIV



Looks like most of the peaks are lost in OP606_F52B5.7, only a small number were lost in YL557_WAGO-9 Chrll

Summary of embryo, L4 and young adult N2 ChIPseq results with GoatV GFP and Flag antibodies

- Looks like GoatV GFP Ab binds to different sites in the embryo, L4 and young adult stages
 - need to perform the IPs in other stages: L1, L2, L3 and other embryonic stages
- GoatV GFP and Flag binding sites largely overlap with HOT sites
- Is the antibody binding to regions of open chromatin?
- Are these peaks background peaks that we would see in actual data?
- Should these non-specific peaks or HOT sites be subtracted from the data?
 - For the "bad" TFs examined, most peaks disappear
 - For the "good" TFs examined, the data looks cleaner, many of the peaks are retained

Summary of ChIP'd TFs for TF(RNAi/del)/RNA-seq

TFs with completed ChIP-seq data (44) Deletion strain available (37) RNAi clone available (7)

CEH-22 CEH-26 DMD-4 HLH-8 SDC-2 COG-1 SYD-9

ion strain avail	able (37)	RNAi clo
CEH-30	UNC-86	
FKH-10	TTX-3	
MAB-5	BLMP-1	
PAX-1	CES-1	
LIM-6	DVE-1	
RNT-1	CEH-31	
MEC-3	C08G9.2	
ELT-4	CEH-24	
TBX-7	GMEB-2	
CEH-34	CEH-48	
CEH-14	CEH-9	
CEH-2	Y22D7AL.16	
FAX-1	CEH-24	
PQM-1	SOX-4	
PAG-3	M03D4.4	
UNC-42		
HLH-6		
CEH-18		
FKH-6		
ZIP-5		
HLH-15		
UNC-3		



<u>eletion strain available</u> LIN-11



Outline

- Summary of RNA-seq progress
 - Backcrossed deletion mutants
 - Backcross in progress
 - RNA isolated for sequencing and backcrossed strains waiting for RNA isolation

4X Backcrossed mutant strains with VC2010

	Deletion	Strain	GFP	Embryo	Backcross
Name	Strain	Available	Strain	Chip	
ceh-30	ceh-30(n4289) X.	MT13544	OP120	Yes	4X
mab-5	mab-5(gk670) III.	VC1477	OP19/26/27	Yes	4X
ceh-2	ceh-2(ch4) I.	TB200	OP323	Yes	4X
mec-3	mec-3(gk1126) IV.	VC2396	OP55	Yes	4X
tbx-7	tbx-7(gk1033) III.	VC1976	OP311	Yes	4X
fkh-10	fkh-10(ok733) I.	R8884	OP337/DCC4025	Yes	4X
pqm-1	pqm-1(ok485) II.	RB711	OP201	Yes	4X
rnt-1	rnt-1(ok351) I.	VC200	OP462	Yes	4X
pag-3	pag-3(ok488) X.	VC369	OP154	Yes	4X
ceh-31	ceh-31 X.	tm239	OP370	Yes	4X
ceh-18	ceh-18 X.	tm6181	OP533	Yes	4X
ceh-14	ceh-14(ch3) X.	TB528	OP315	Yes	4X
lim-6	lim-6(nr2073) X.	OH110	OP388	Yes	4X
elt-4	elt-4(ca16) X.	JM124	OP111	Yes	4X
fax-1	fax-1(ok624) X.	RB812	OP164	Yes	4X
C08G9.2	C08G9.2 IV.	tm4339	OP513	Yes	4X
blmp-1	blmp-1 I.	tm548	OP109	Yes	4X
dve-1	dve-1 X.	tm4803	OP398	Yes	4X
ces-1	ces-1 l.	tm1036	OP174	Yes	4X
fkh-6	fkh-6 II.	tm439	OP78	Yes	4X
zip-5	zip-5(gk646)_V.	VC1392	OP544	Yes	4X
unc-42	unc-42 V.	tm5335	OP173	Yes	4X
lin-11	lin-11 l.	tm5323	OP62	Yes	4X
hlh-15	hlh-15 X.	tm1824	OP566	Yes	4X
ttx-3	ttx-3 X.	tm268	OP68	Yes	4X
unc-86	unc-86 III.	tm6459	OP476	Yes	4X
unc-3	unc-3 X.	tm4776	OP578	Yes	4X
ceh-9	ceh-9 I.	tm2747	OP202	Yes	4X
sox-4	sox-4(gk700) X.	VC1544	OP517	Yes	4X
eyg-1	eyg-1 (gk851) II.	VC1800	OP443	Yes	4X
ceh-24	ceh-24(cc539) V.	PD4588	OP673	Yes	4X
ham-2	ham-2 X.	tm5501	OP639	Yes	4X
Y22D7AL.16	Y22D7AL.16 III.	tm4265	OP615	Yes	4X
gmeb-2	gmeb-2 X.	tm6823	OP622	Yes	4X
M03D4.4	M03D4.4 IV	tm559	OP696	Yes	2X
C5289.2	C52B9.2 X.	tm413	No	No	2X
hlh-19	hlh-19 X.	tm3105	No	No	2X
F55B11.4	F55B11.4 IV.	tm4294	OP385	No expression	4X
npax-1	npax-1 II.	tm1367	OP626	Dauer express	2X
dac-1	dac-1(gk211) III.	VC392	OP188/189	Not available	4X
ZK337.2	ZK337.2 X.	tm706	OP355	No expression	4X
unc-55	unc-55 I.	tm3355	DCC4035	Not available	4X
ceh-33	ceh-33 V.	tm244	OP575	Cytoplasmic	4X
gei-3	gei-3 X.	tm4380	OP180	No expression	4X
unc-98	unc-98 X.	tm601	OP85	Cytoplasmic	4X
C34D1.1	dmd-10(gk1131) V.	VC2341	OP689	Dauer express	2X

41 Deletion strainswith 4X backcrossed,34 of them have been chipped.

5 Deletion strainswith 2X backcrossed,1 of them has been chipped.

Backcross in progress

Gene	Deletion	Strains	GFP	Embryos	Backcross
Name	Strains	Available	Strains	Chip	
M03D4.4	M03D4.4 IV.	tm559	OP696	Yes	2X

31 RNA for 6-timepoints shipped to UW for sequencing

Y2Q3	Y2Q4	Y3Q1	Y3Q2	Y3Q3	Y3Q4	Y4Q1
VC1477_mab-5	TB200_ceh-2	RB812_fax-1	tm4339_C08G9.2	tm1824_hlh-15	tm268_ttx-3	VC1544_sox-4
MT13544_ceh-30	VC2396_mec-3	tm548_blmp-1	tm6181_ceh-18	tm4776_unc-3	tm6459_unc-86	VC1800_eyg-1
	RB884_fkh-10	tm1036_ces-1	VC369_pag-3	tm439_fkh-6(Repeat)		tm2747_ceh-9
	VC1976_tbx-7	tm439_fkh-6	tm239_ceh-31			PD4588_ceh-24
	RB711_pqm-1		TB528_ceh-14			
	VC200_rnt-1		JM124_elt-4			
			tm4803_elt-4			
			OH110_lim-6			
			tm5323_lin-11			
			VC1392_zip-5			
			tm5335_unc-42			

Backcrossed strains waiting for RNA isolation

Gene	Strains	GFP	Embryo	Backcross	RNA Isolation
Name	Available	Strains	Chip		
gmeb-2	gmeb-2 X.	tm6823	OP622	4X	Ready to send
ham-2	ham-2 X.	tm5501	OP639	4X	Need to repeat
Y22D7AL.16	Y22D7AL.16 III.	tm4265	OP615	4X	Waiting