Outline

Mapping stats

Peak calling

- Stats peaks
- Number of shared peaks
- Number of peaks in 5kb upstream of up and downregulated genes
- Intersection ATACseq peaks and histones

Aggregation Plots

Outline

Mapping stats

Peak calling

Aggregation Plots

id	reads	Uniquely mapped reads	% Uniquely mapped reads	mapped multiple loci	% mapped multiple loci	unmapped too short
eye1	38,164,421	25,859,480	67.76%	1,086,242	2.85%	26.11%
eye2	39,553,256	33,523,739	84.76%	1,422,159	3.60%	7.81%
ctrl-96h-1	31,165,523	23,912,148	76.73%	790,514	2.54%	18.22%
ctrl-96h-2	42,554,815	33,301,213	78.25%	1,940,209	4.56%	13.04%
11h-0h-ctrl-1	42,755,866	33,232,371	77.73%	996,926	2.33%	17.32%
11h-0h-ctrl-2	40,629,916	30,849,827	75.93%	1,318,698	3.25%	17.48%
11h-0h-1	37,206,314	23,521,988	63.22%	2,055,780	5.53%	26.39%
11h-0h-2	39,172,203	28,179,076	71.94%	1,530,227	3.91%	20.77%
16h-0h-ctrl-1	27,229,630	23,345,989	85.74%	924,314	3.39%	7.59%
16h-0h-ctrl-2	31,163,300	24,285,870	77.93%	887,087	2.85%	16.46%
16h-0h-1	33,530,934	25,385,401	75.71%	985,095	2.94%	18.69%
16h-0h-2	39,498,659	26,695,941	67.59%	959,131	2.43%	27.88%
16h-15h-ctrl-1	33,805,236	19,462,562	57.57%	1,109,199	3.28%	35.99%
16h-15h-ctrl-2	35,428,731	25,439,143	71.80%	1,383,546	3.91%	20.37%
16h-15h-1	34,716,712	28,706,599	82.69%	1,433,437	4.13%	9.57%
16h-15h-2	30,936,937	22,732,653	73.48%	952,562	3.08%	20.47%
16h-25h-ctrl-1	36,511,208	29,609,781	81.10%	1,102,594	3.02%	12.67%
16h-25h-ctrl-2	39,248,886	30,389,394	77.43%	929,551	2.37%	17.50%
16h-25h-1	32,414,365	23,552,045	72.66%	1,348,374	4.16%	19.53%
16h-25h-2	36,262,439	26,846,043	74.03%	1,172,847	3.23%	19.68%
wing Marina	97,722,180	83,644,595	85.59%	2,877,021	2.94%	8.20%
Aerts et al 2015	16,077,656	14,138,498	87.94%	537,516	3.34%	4.21%

Outline

Mapping stats

Peak calling

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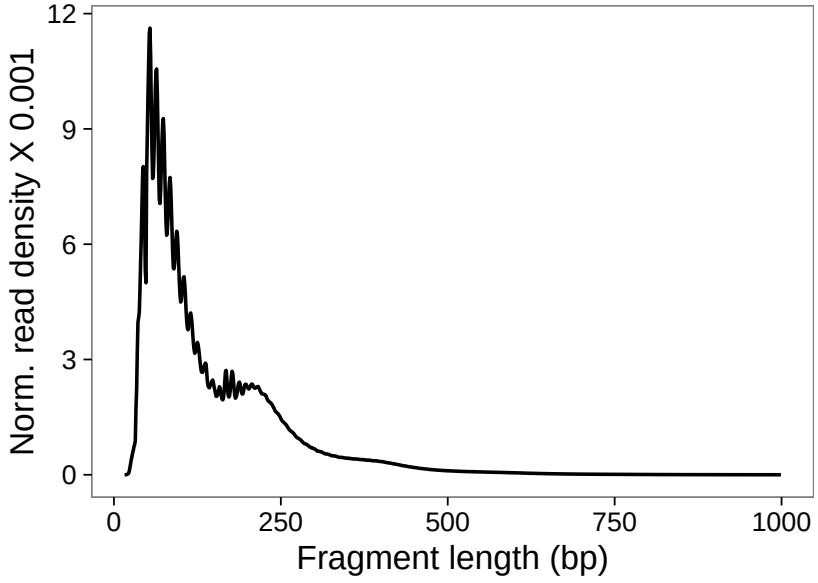
Aggregation Plots

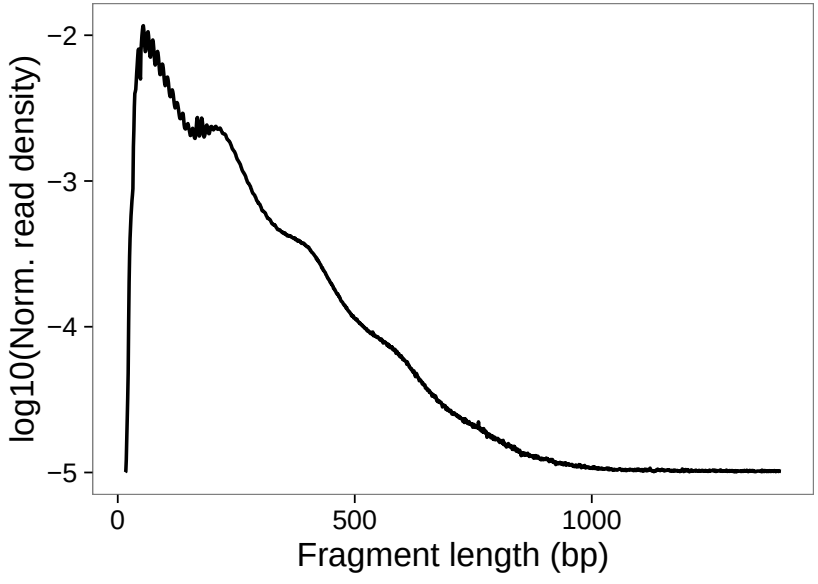
Peak calling

- uniquely mapped reads
- extsize 100
- shift -50
- single-end mode

- macs2 paired-end mode
- fractions: nucleosome-free VS mononucleosome ...

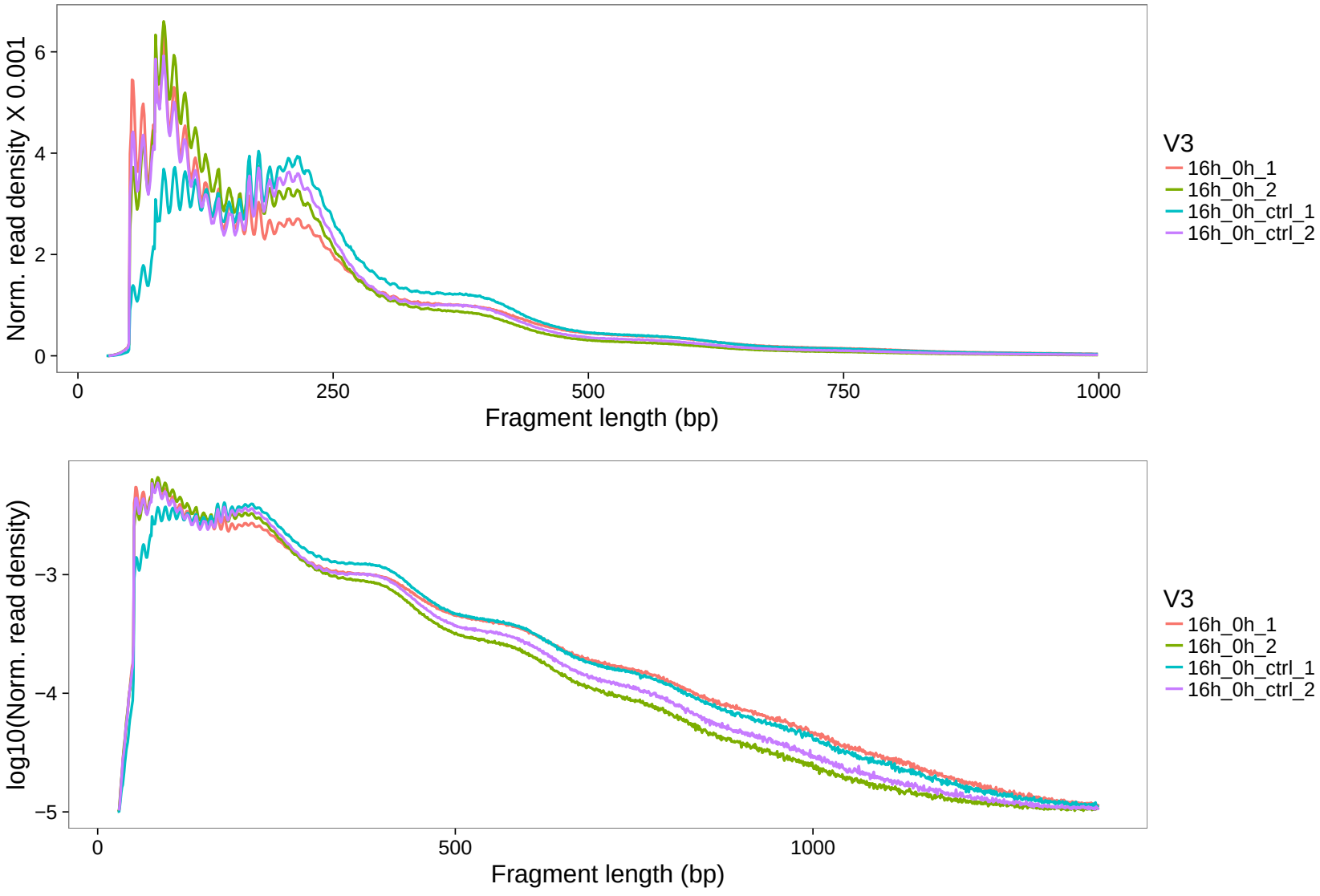
Fractions based on insert sizes - wing disc



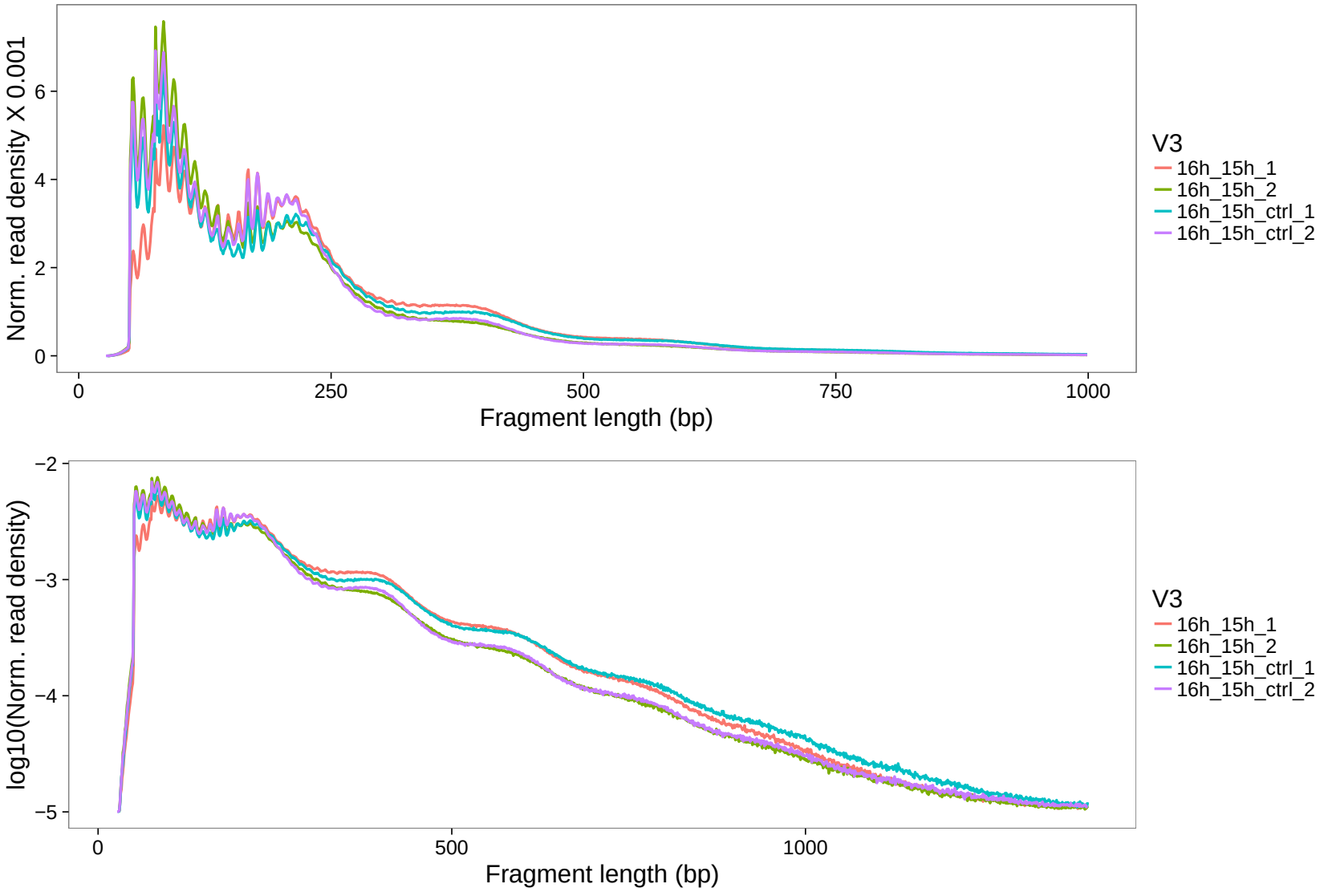


fraction	number of fragment pairs
nucl-free	42,092,211
mono	12004229
di	4584630
tri	278256

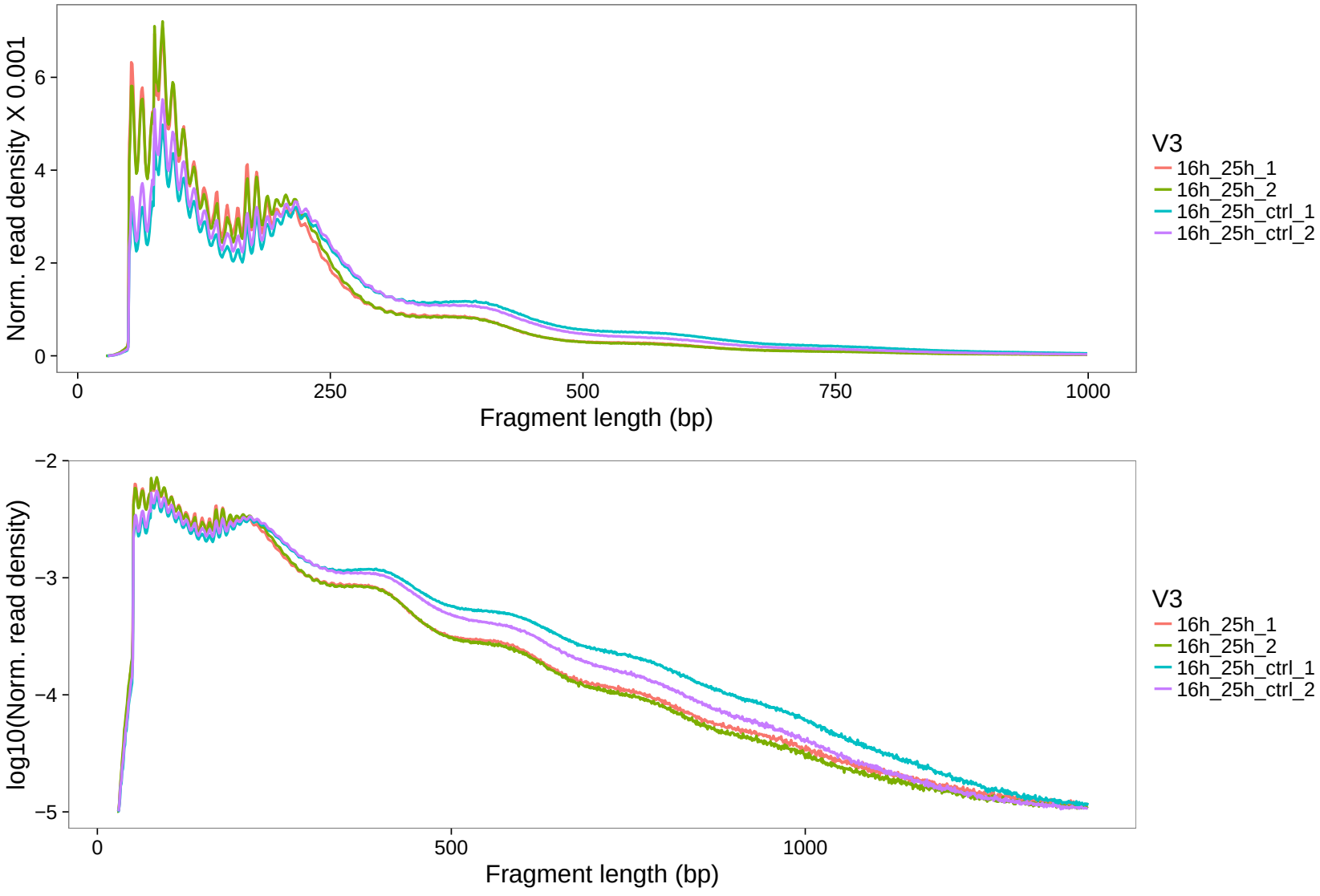
Fractions based on insert sizes - 0h



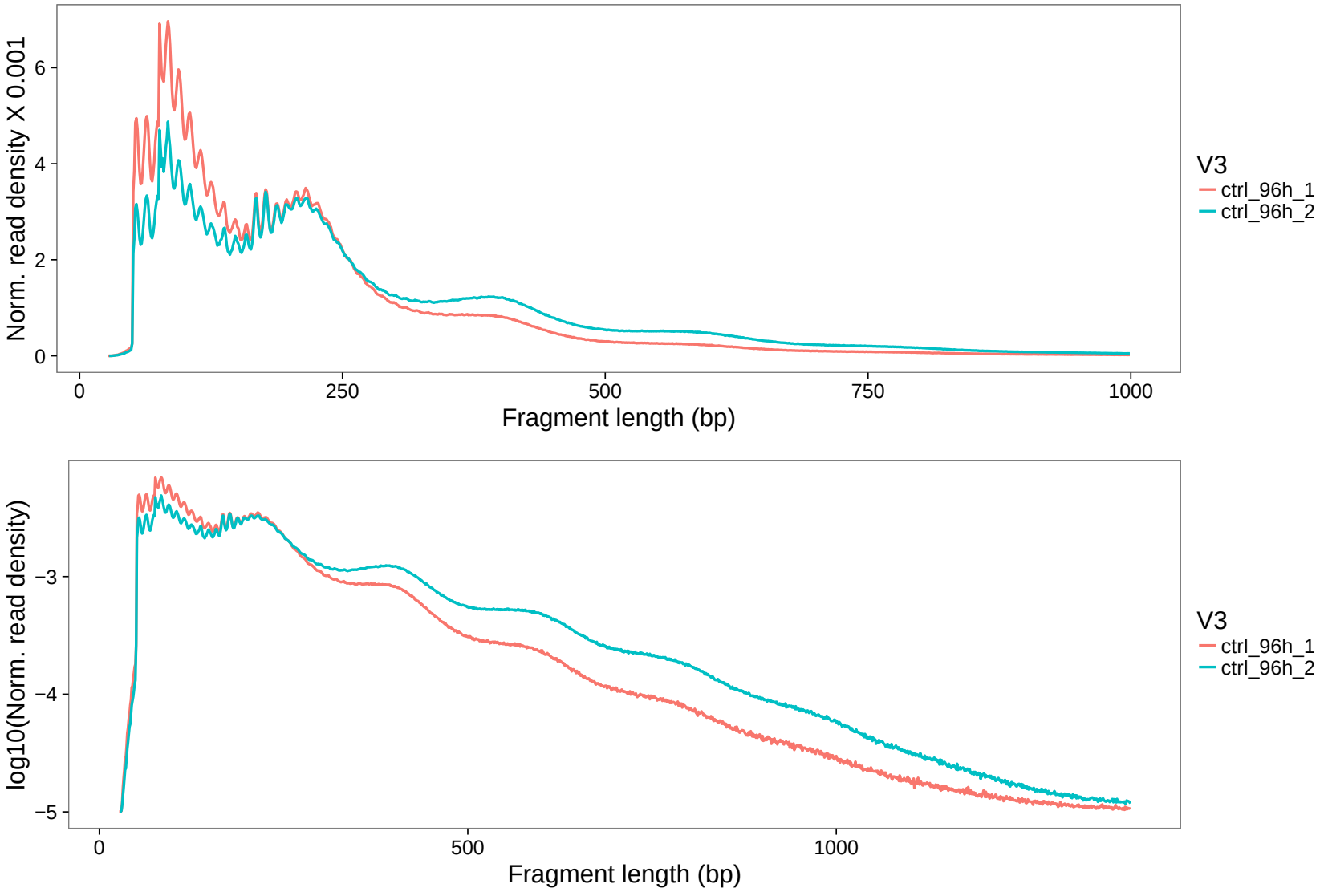
Fractions based on insert sizes - 15h



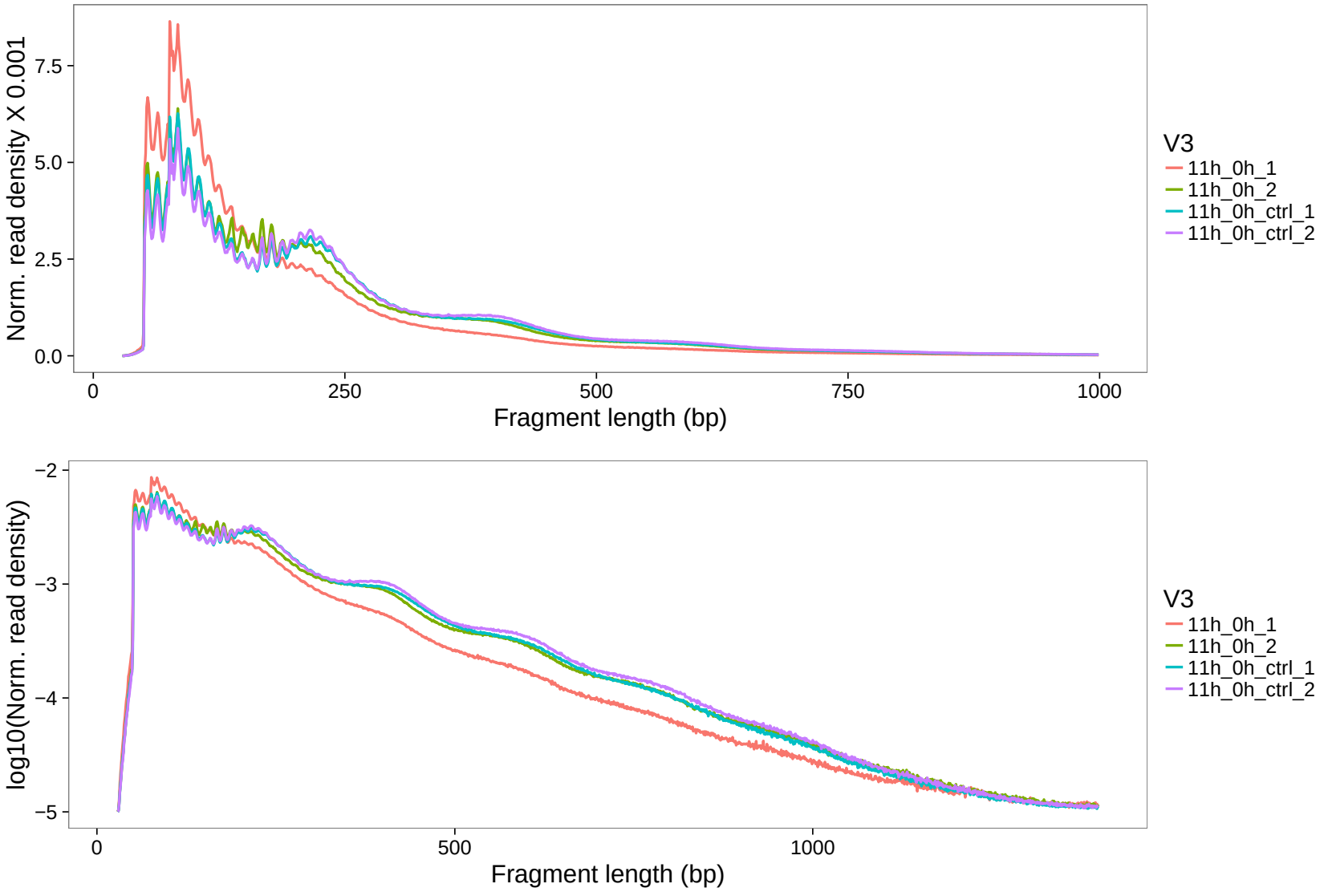
Fractions based on insert sizes - 25h



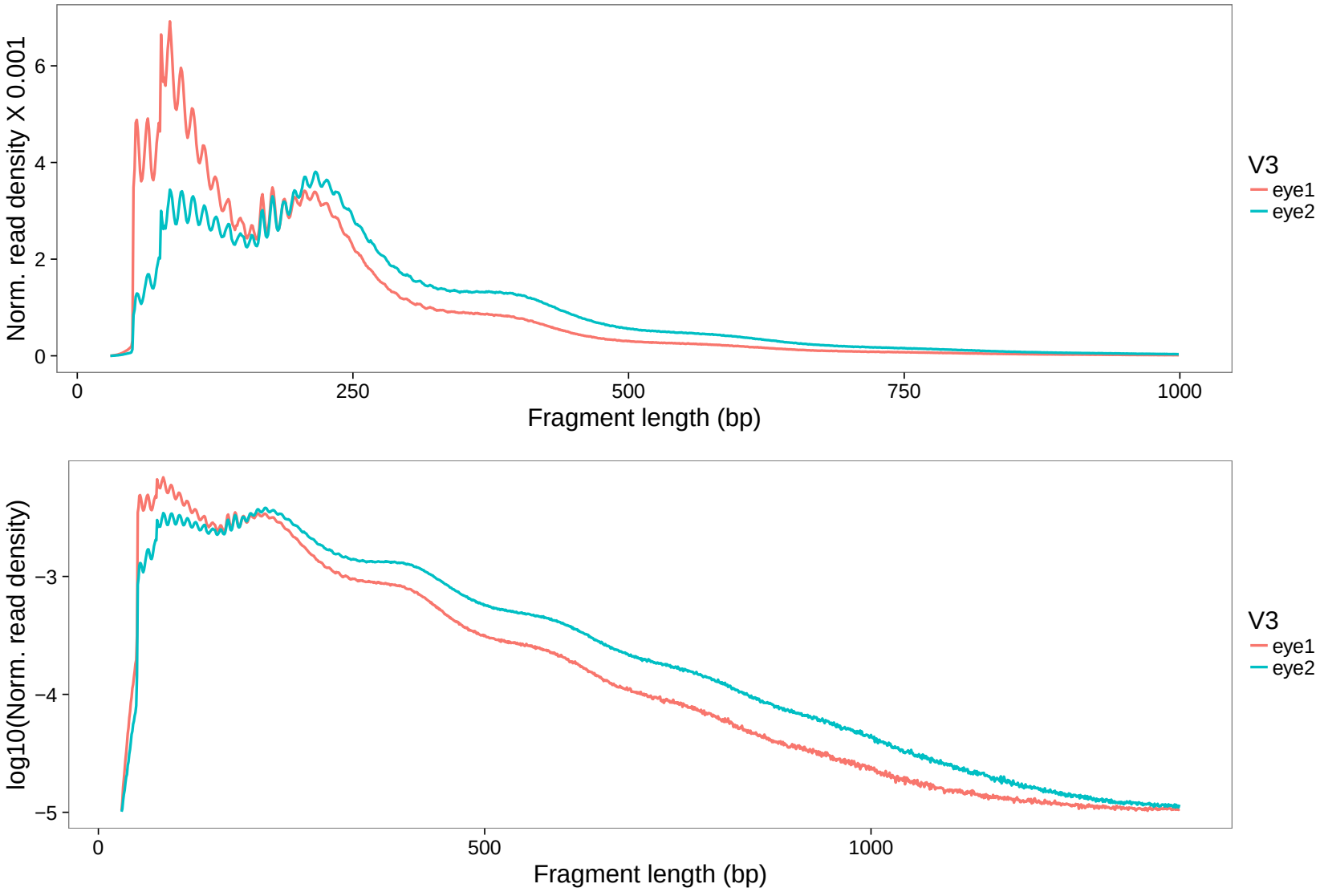
Fractions based on insert sizes - ctrl 96h



Fractions based on insert sizes - 11h 0h



Fractions based on insert sizes - Eye



Fractions based on insert sizes - all samples

id	nucl-free	mono	di	tri
0h-1	6,129,882	4,333,130	3,659,895	510,191
0h-2	6,269,128	5,412,114	3,248,375	347,018
0h-ctrl-1	2,770,309	5,615,358	3,983,128	482,007
0h-ctrl-2	5,405,129	5,340,743	3,349,028	387,543
15h-1	4,980,535	6,382,416	4,577,044	566,713
15h-2	6,507,398	4,296,627	2,543,032	290,468
15h-ctrl-1	4,711,736	3,860,261	2,804,415	376,195
15h-ctrl-2	6,804,296	5,593,703	2,958,907	349,555
25h-1	6,482,540	4,628,686	2,804,122	346,291
25h-2	7,290,341	5,582,622	3,100,546	366,222
25h-ctrl-1	5,217,748	5,755,094	5,041,894	802,015
25h-ctrl-2	5,927,054	6,134,869	4,754,099	634,246
ctrl-96h-1	6,155,717	4,932,449	2,855,064	322,025
ctrl-96h-2	5,907,824	6,816,521	5,854,948	958,598
11h-0h-1	8,176,040	3,635,359	2,186,136	246,082
11h-0h-2	6,805,457	5,216,570	3,863,008	499,805
11h-0h-ctrl-1	7,724,505	6,237,958	4,676,809	597,584
11h-0h-ctrl-2	6,613,723	6,126,914	4,706,771	635,411
eye1	6,624,768	5,389,430	3,106,366	324,902
eye2	3,807,276	7,699,708	6,415,797	816,916

Outline

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Aggregation Plots

Number of peaks called

nb of peaks
single-end mode

sample	nb of peaks
11h-0h-1	19,417
11h-0h-2	21,033
11h-0h-ctrl-1	25,150
11h-0h-ctrl-2	24,026
16h-0h-1	23,532
16h-0h-2	26,079
16h-0h-ctrl-1	24,022
16h-0h-ctrl-2	23,053
16h-15h-1	25,156
16h-15h-2	24,234
16h-15h-ctrl-1	23,522
16h-15h-ctrl-2	24,701
16h-25h-1	24,337
16h-25h-2	24,156
16h-25h-ctrl-1	23,795
16h-25h-ctrl-2	23,234
ctrl-96h-1	25,866
ctrl-96h-2	25,850
eye1	23,095
eye2	24,956

nb of peaks
paired-end mode

sample	nb peaks
11h-0h-1	10,284
11h-0h-2	11,812
11h-0h-ctrl-1	12,809
11h-0h-ctrl-2	12,207
16h-0h-1	12,354
16h-0h-2	14,026
16h-0h-ctrl-1	13,404
16h-0h-ctrl-2	13,031
16h-15h-1	14,228
16h-15h-2	14,123
16h-15h-ctrl-1	12,174
16h-15h-ctrl-2	13,639
16h-25h-1	13,470
16h-25h-2	14,252
16h-25h-ctrl-1	12,739
16h-25h-ctrl-2	12,728
ctrl-96h-1	14,379
ctrl-96h-2	11,940
eye1	15,685
eye2	16,025

nb of peaks
paired-end mode nucl-free

sample	nb peaks
11h-0h-1	21,740
11h-0h-2	20,249
11h-0h-ctrl-1	23,738
11h-0h-ctrl-2	21,787
16h-0h-1	22,196
16h-0h-2	23,543
16h-0h-ctrl-1	18,173
16h-0h-ctrl-2	21,880
16h-15h-1	21,957
16h-15h-2	24,099
16h-15h-ctrl-1	21,747
16h-15h-ctrl-2	24,043
16h-25h-1	22,777
16h-25h-2	23,455
16h-25h-ctrl-1	20,819
16h-25h-ctrl-2	20,906
ctrl-96h-1	24,110
ctrl-96h-2	22,454
eye1	21,782
eye2	19,447

Number of peaks called shared by replicates

Peaks should have 50% overlap between replicates

nb of peaks for each replicate

sample	nb of peaks
11h-0h-1	19,417
11h-0h-2	21,033
11h-0h-ctrl-1	25,150
11h-0h-ctrl-2	24,026
16h-0h-1	23,532
16h-0h-2	26,079
16h-0h-ctrl-1	24,022
16h-0h-ctrl-2	23,053
16h-15h-1	25,156
16h-15h-2	24,234
16h-15h-ctrl-1	23,522
16h-15h-ctrl-2	24,701
16h-25h-1	24,337
16h-25h-2	24,156
16h-25h-ctrl-1	23,795
16h-25h-ctrl-2	23,234
ctrl-96h-1	25,866
ctrl-96h-2	25,850
eye1	23,095
eye2	24,956

nb of peaks shared by replicates

sample	shared peaks
11h-0h-ctrl	19318
11h-0h	12671
16h-0h-ctrl	17180
16h-0h	19080
16h-15h-ctrl	17950
16h-15h	18711
16h-25h-ctrl	18291
16h-25h	17989
ctrl-96h	19037

Number of peaks - comparison between samples

Peaks should have 40% overlap between samples

Used only the peaks shared by both replicates

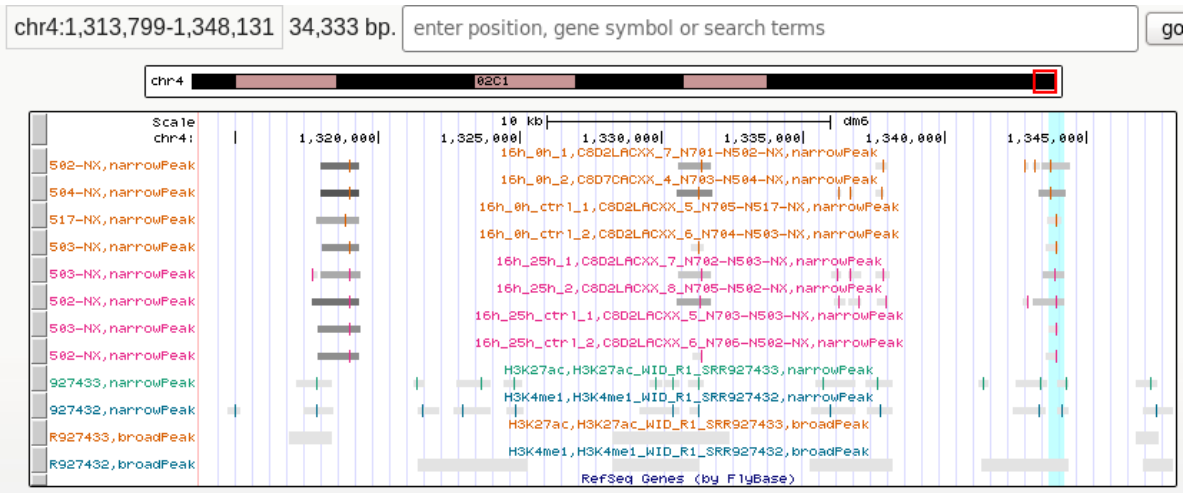
nb of peaks shared in each comparison

sample	shared peaks
16h-0h-treat VS 16h-25h-treat	15041
16h-0h-ctrl VS 16h-0h-treat	14775
16h-0h-ctrl VS 16h-25h-ctrl	14298
16h-25h-ctrl VS 16h-25h-treat	14668

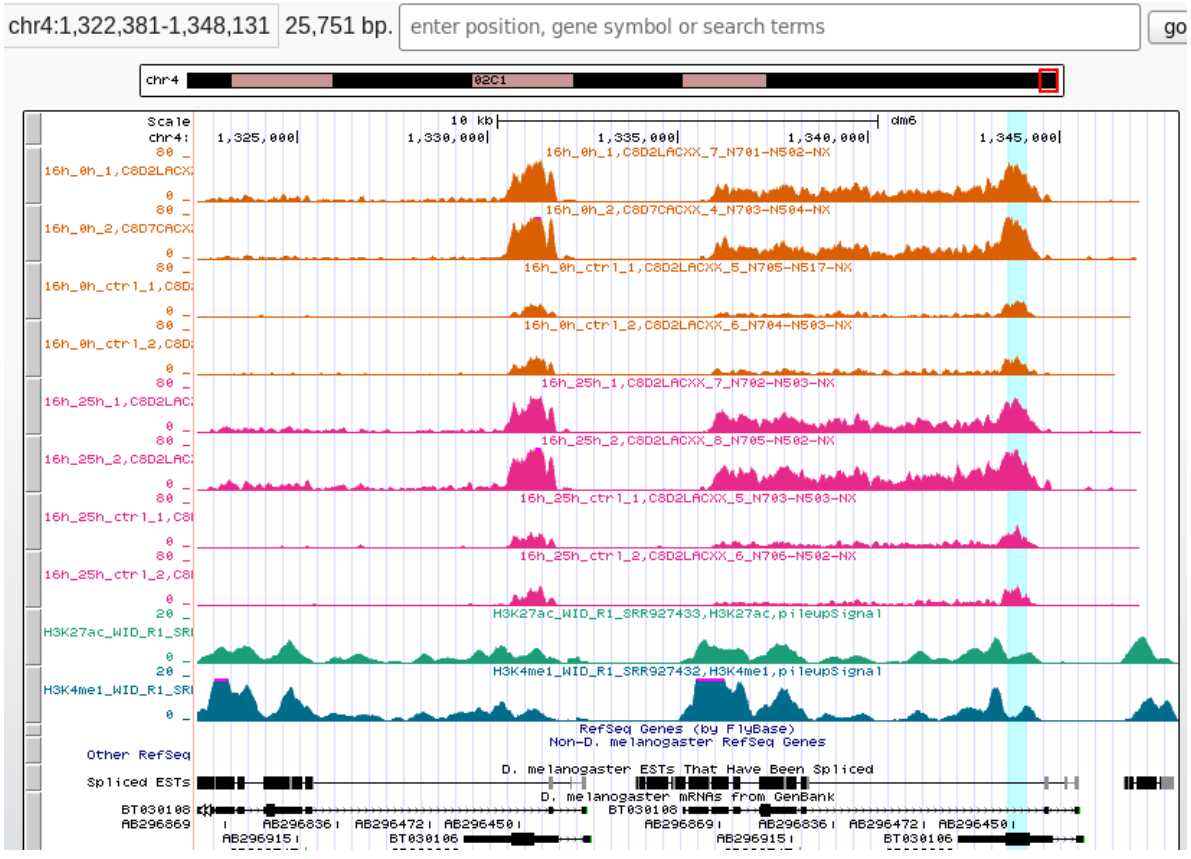
nb of peaks different in each comparison

sample	different peaks
16h-0h-treat VS 16h-25h-treat	4048
16h-25h-treat VS 16h-0h-treat	2692
16h-0h-ctrl VS 16h-0h-treat	2412
16h-0h-treat VS 16h-0h-ctrl	4262
16h-0h-ctrl VS 16h-25h-ctrl	2890
16h-25h-ctrl VS 16h-0h-ctrl	3755
16h-25h-ctrl VS 16h-25h-treat	3631
16h-25h-treat VS 16h-25h-ctrl	3189

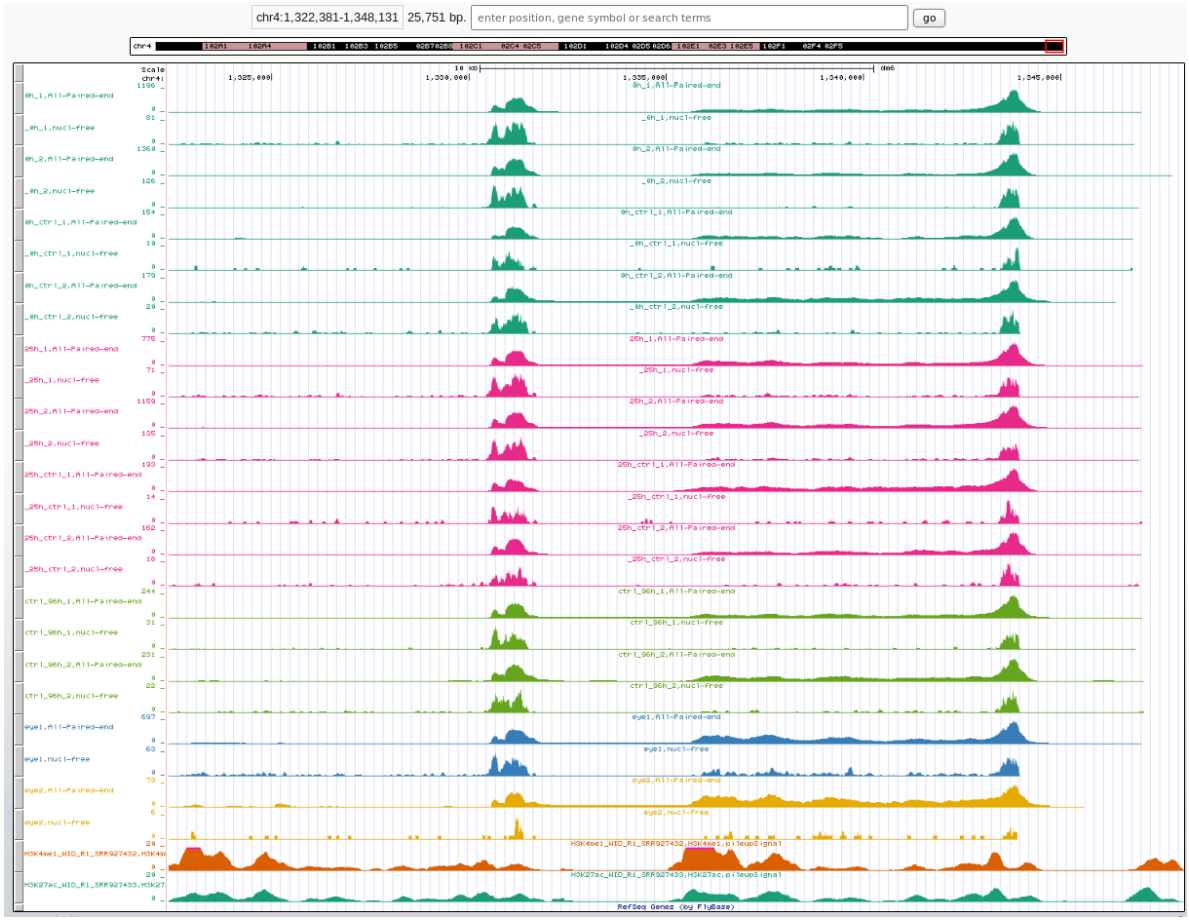
Compare peaks heights between 0h control and 0h treatment



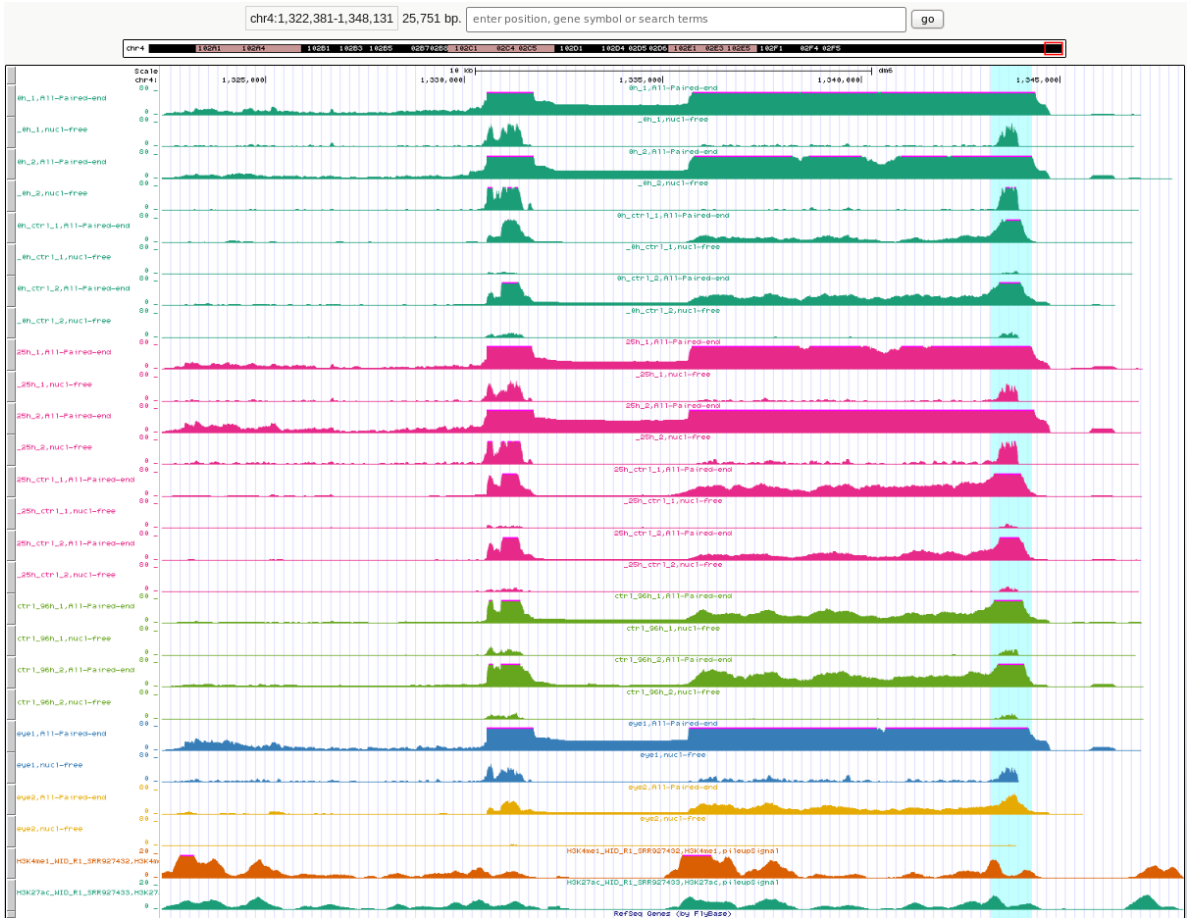
Compare peaks heights between 0h control and 0h treatment



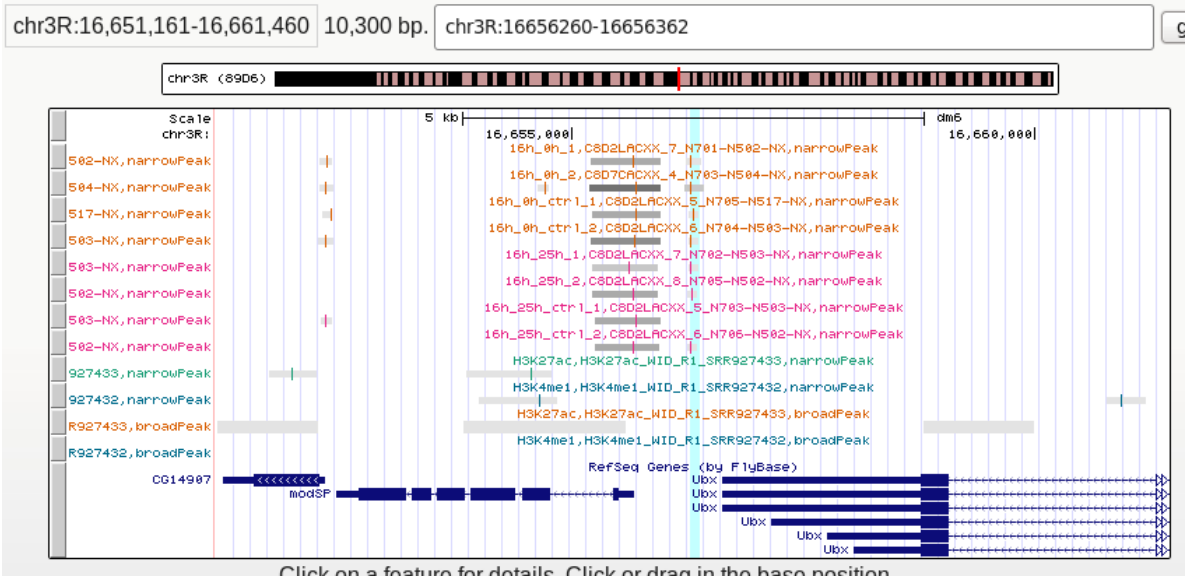
Compare peaks heights between 0h control and 0h treatment



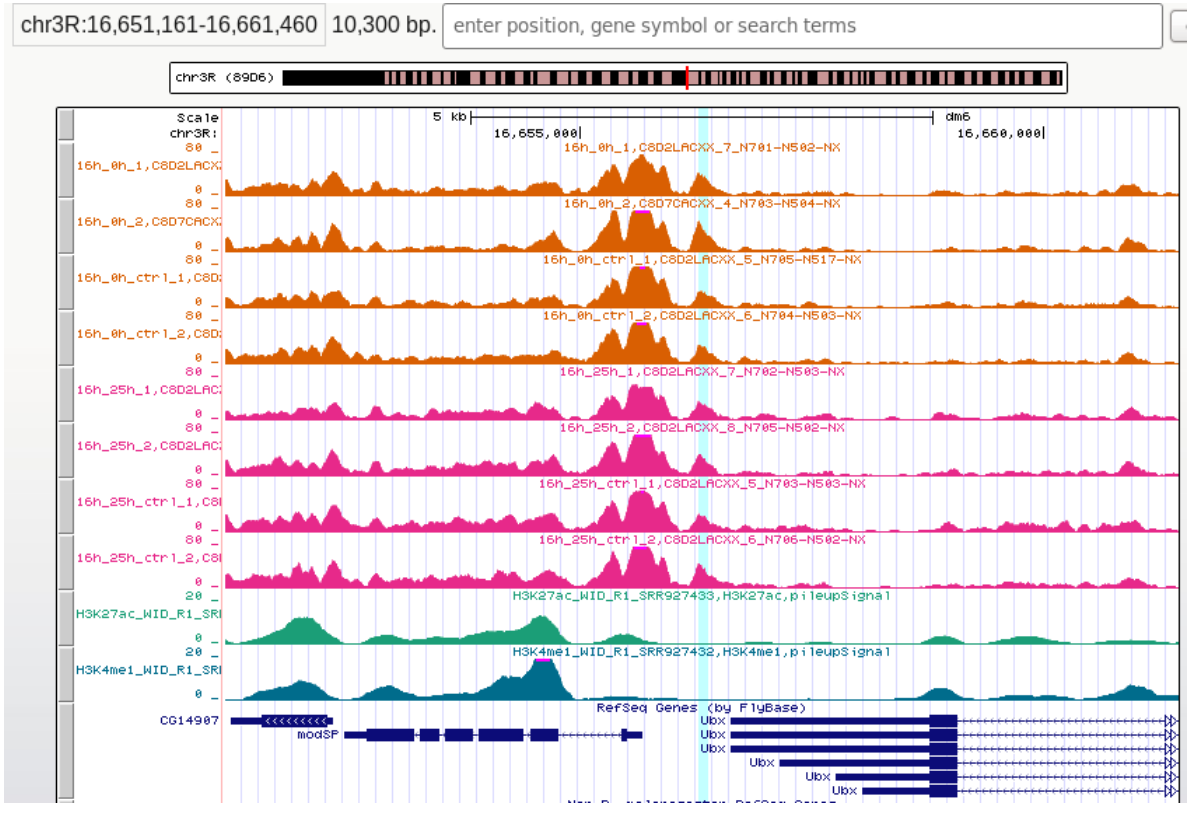
Compare peaks heights between 0h control and 0h treatment



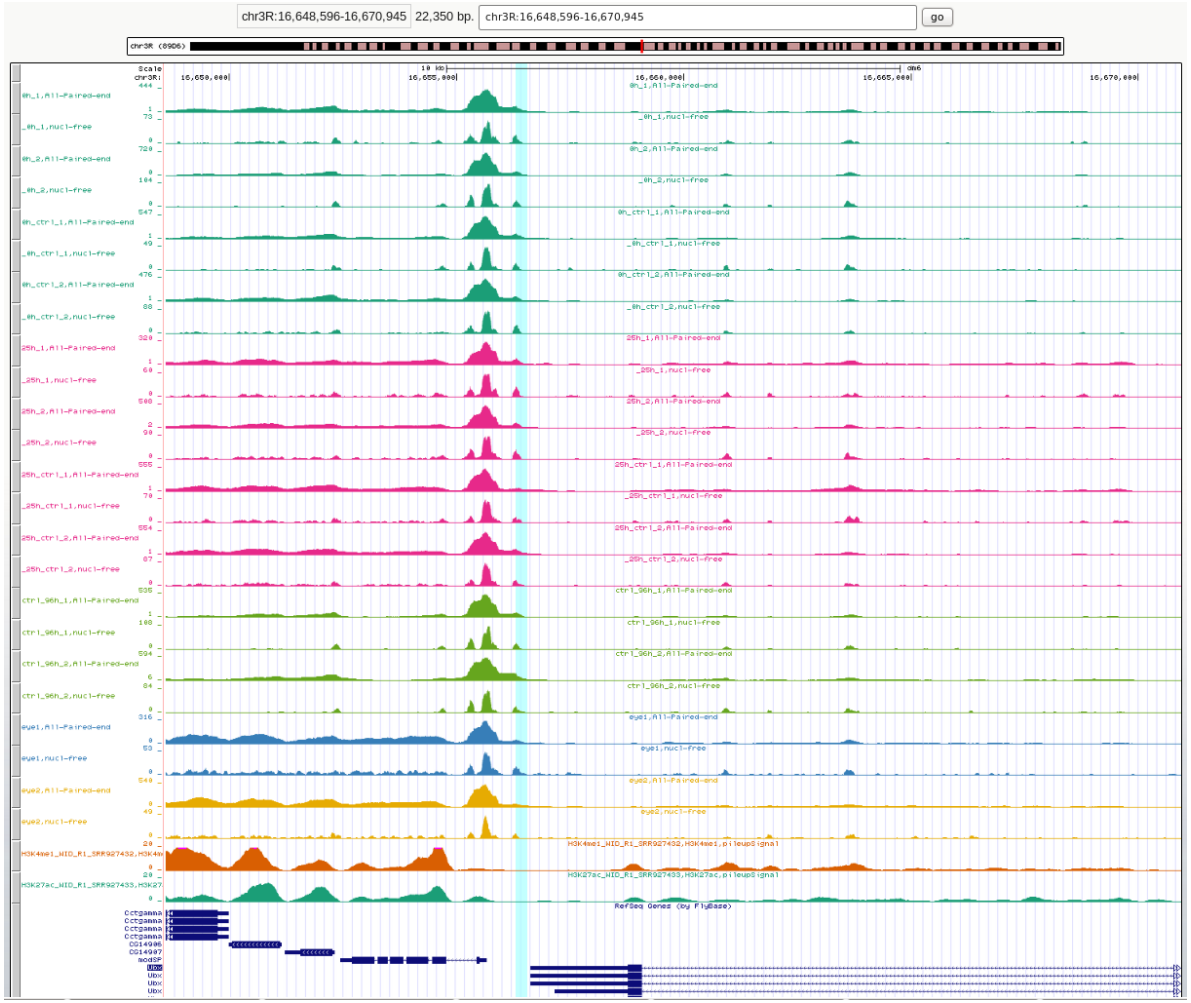
Compare peaks heights between 0h control and 0h treatment



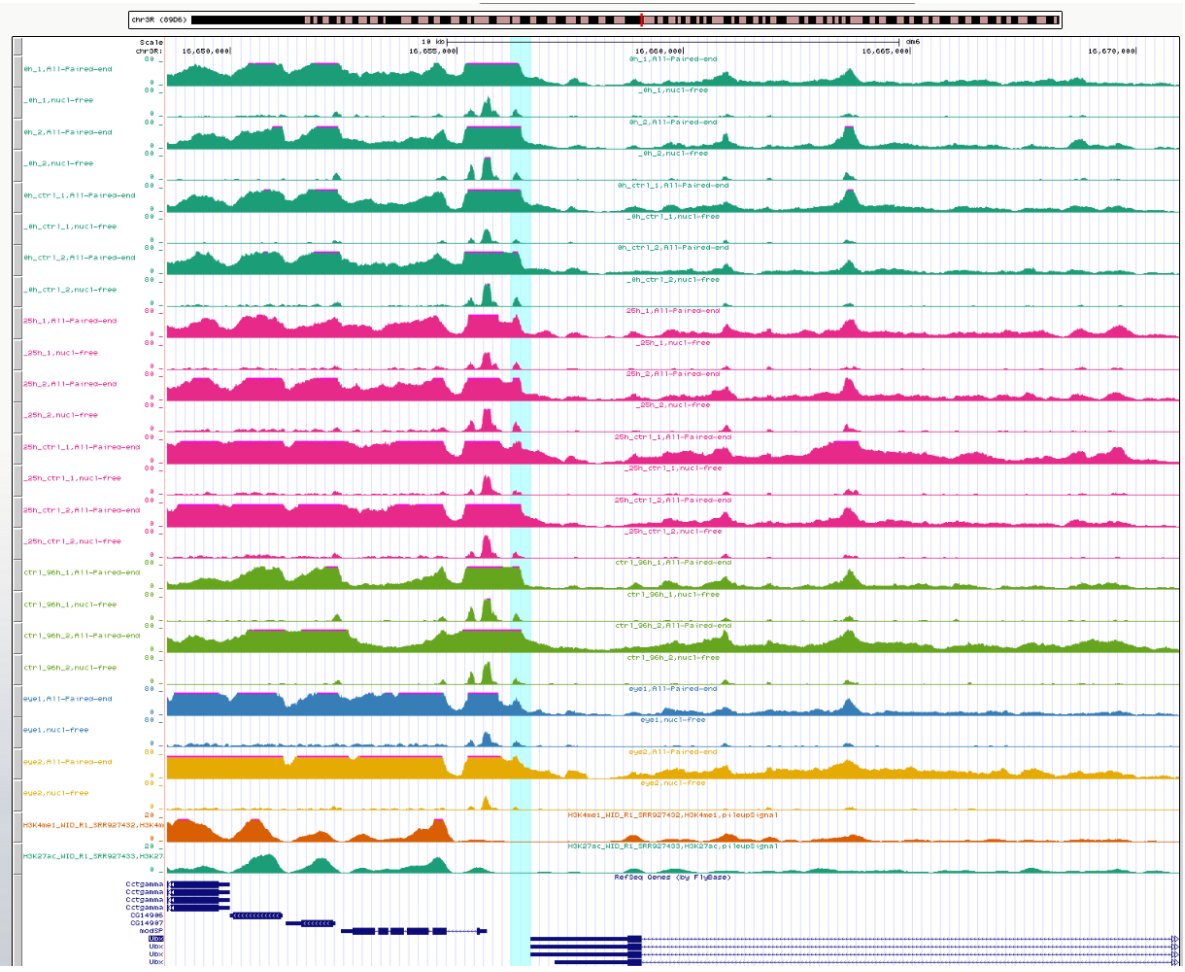
Compare peaks heights between 0h control and 0h treatment



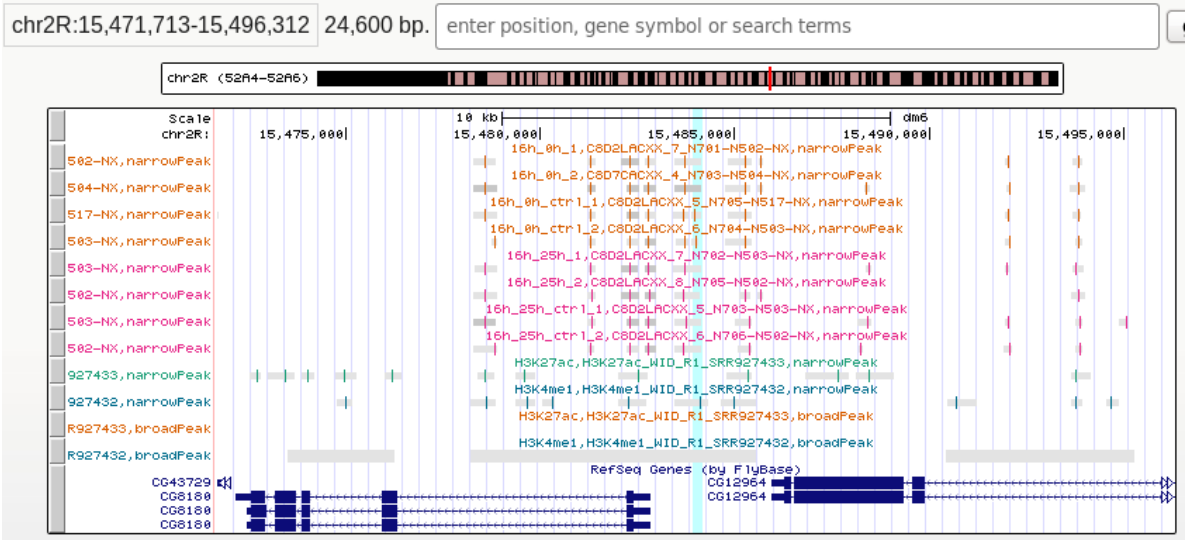
Compare peaks heights between 0h control and 0h treatment



Compare peaks heights between 0h control and 0h treatment



Compare peaks heights between 0h control and 0h treatment



Compare peaks heights between 0h control and 0h treatment

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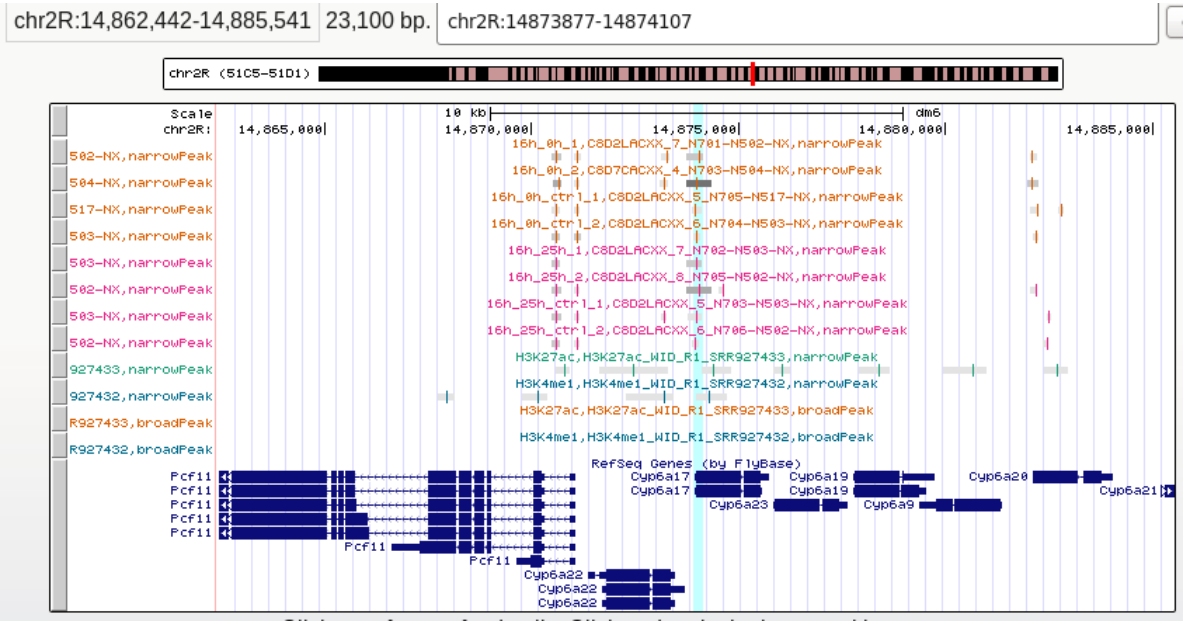
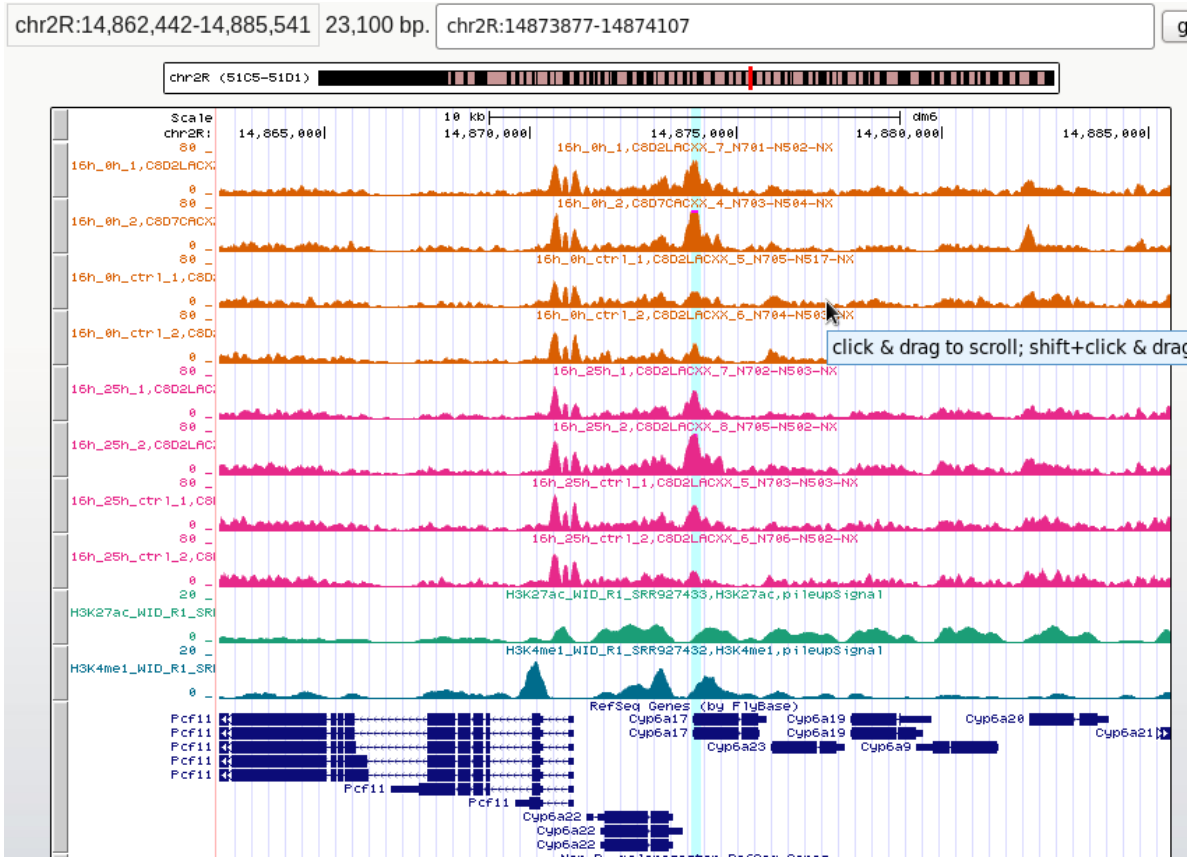
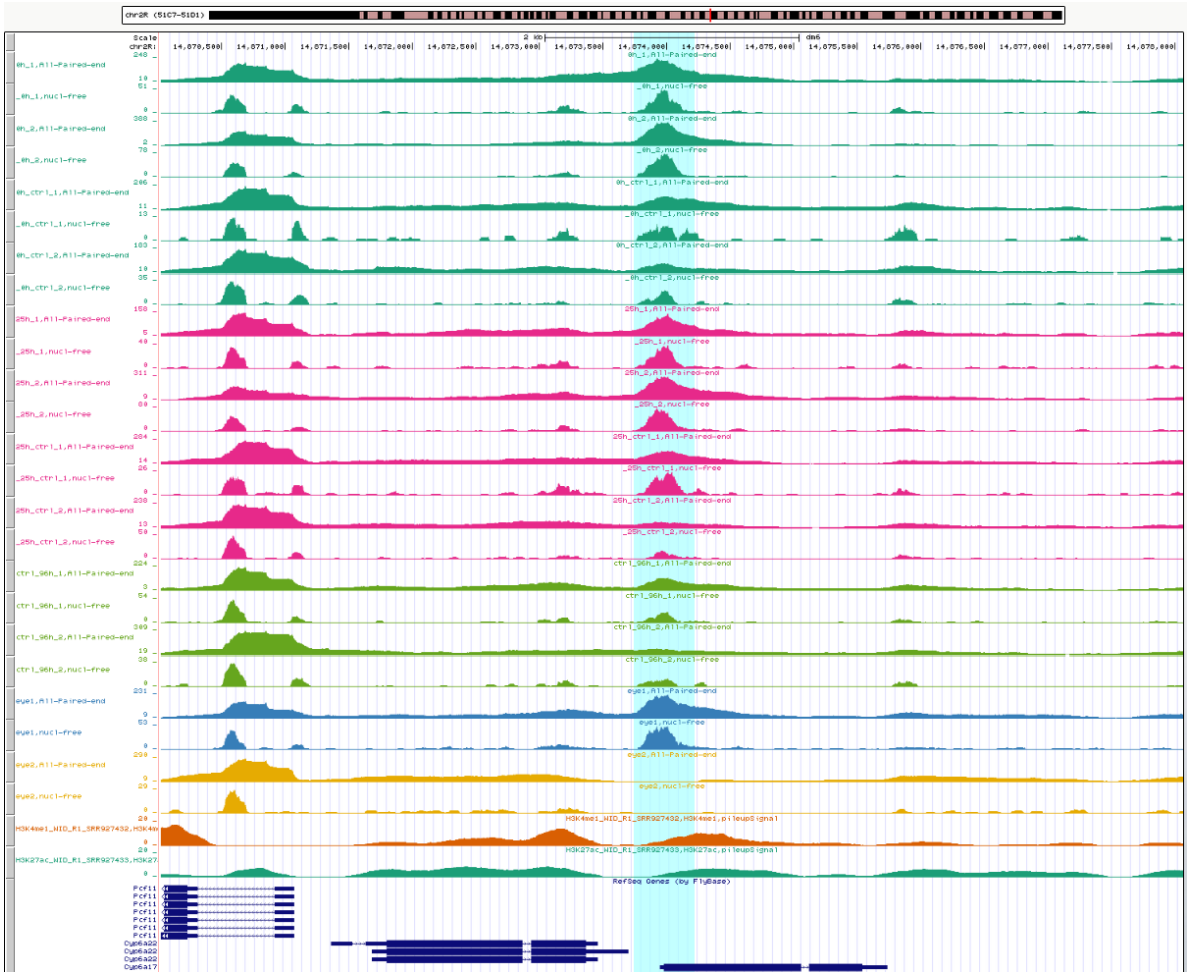


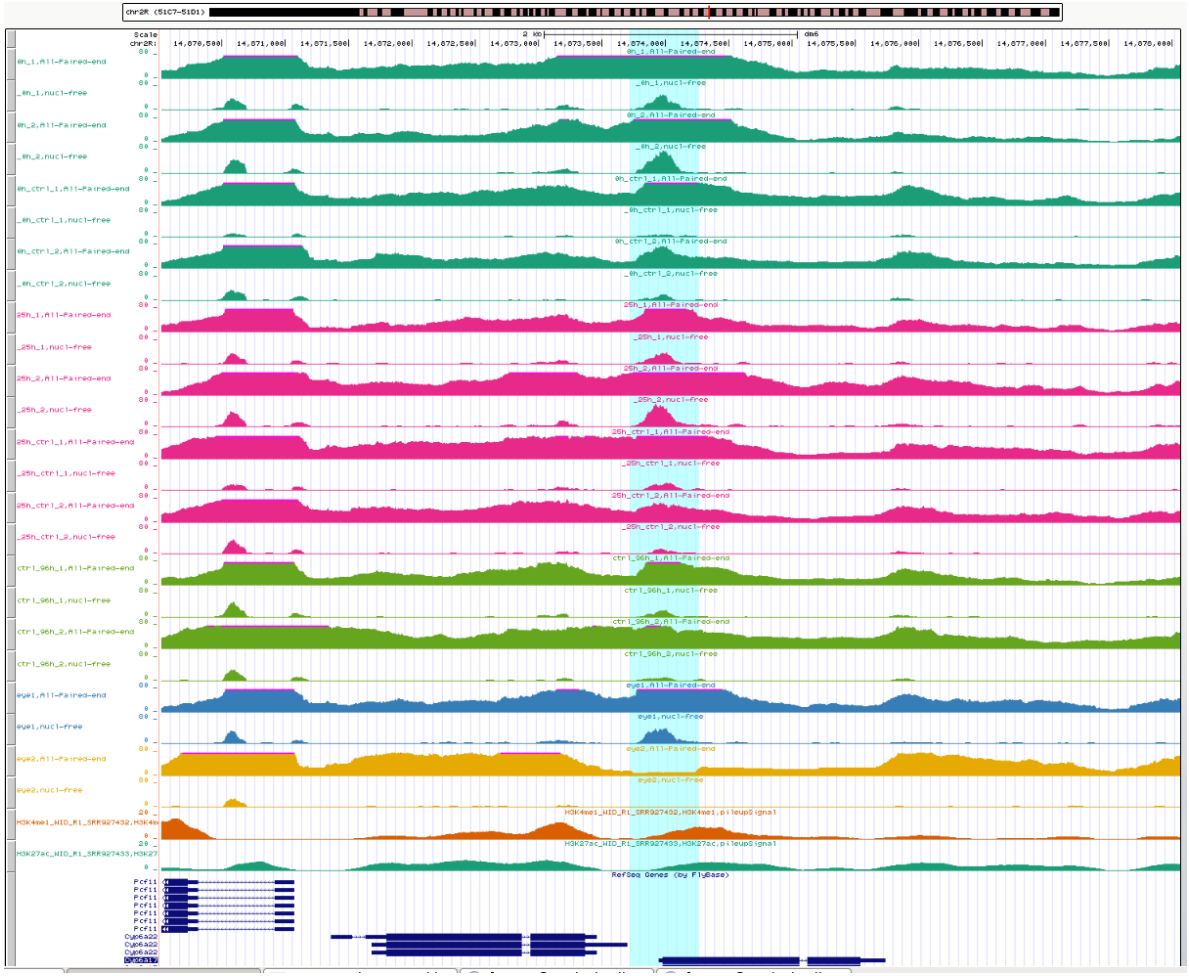
Compare peaks heights between 0h control and 0h treatment



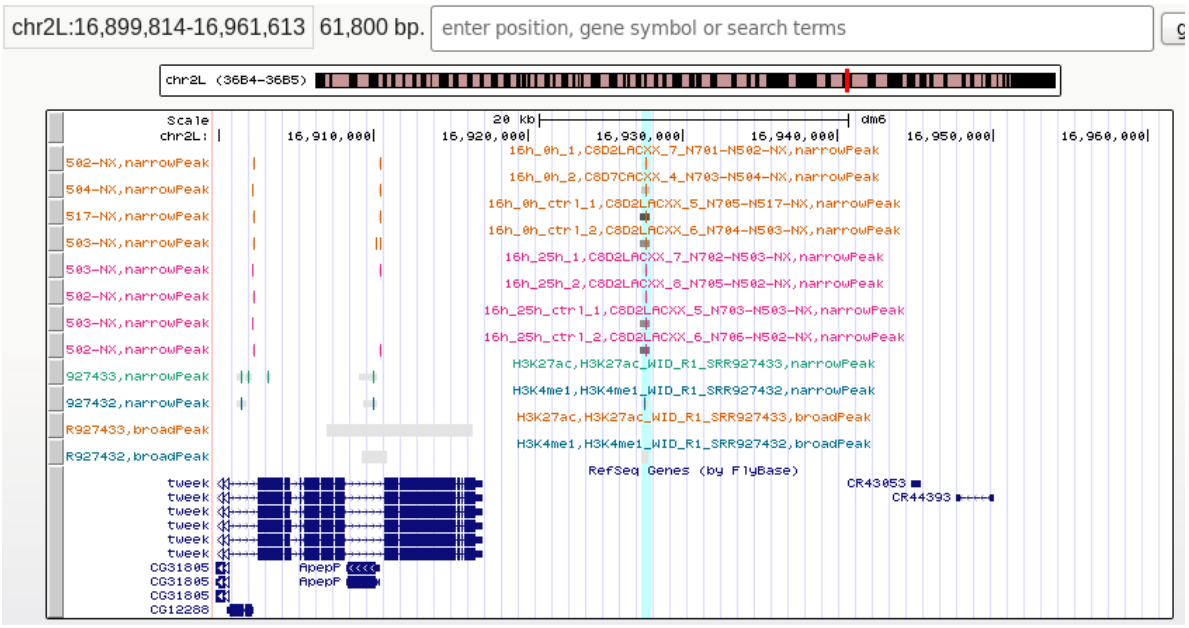
Compare peaks heights between 0h control and 0h treatment



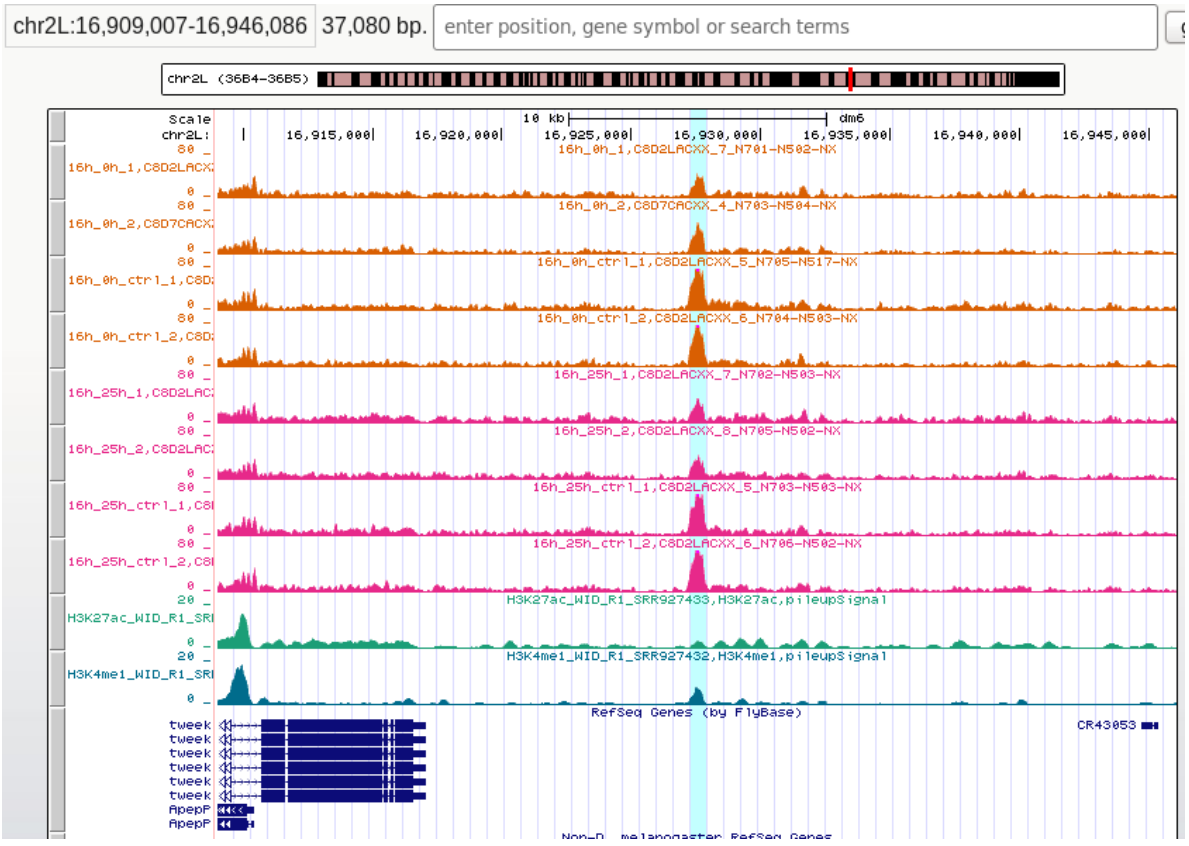
Compare peaks heights between 0h control and 0h treatment



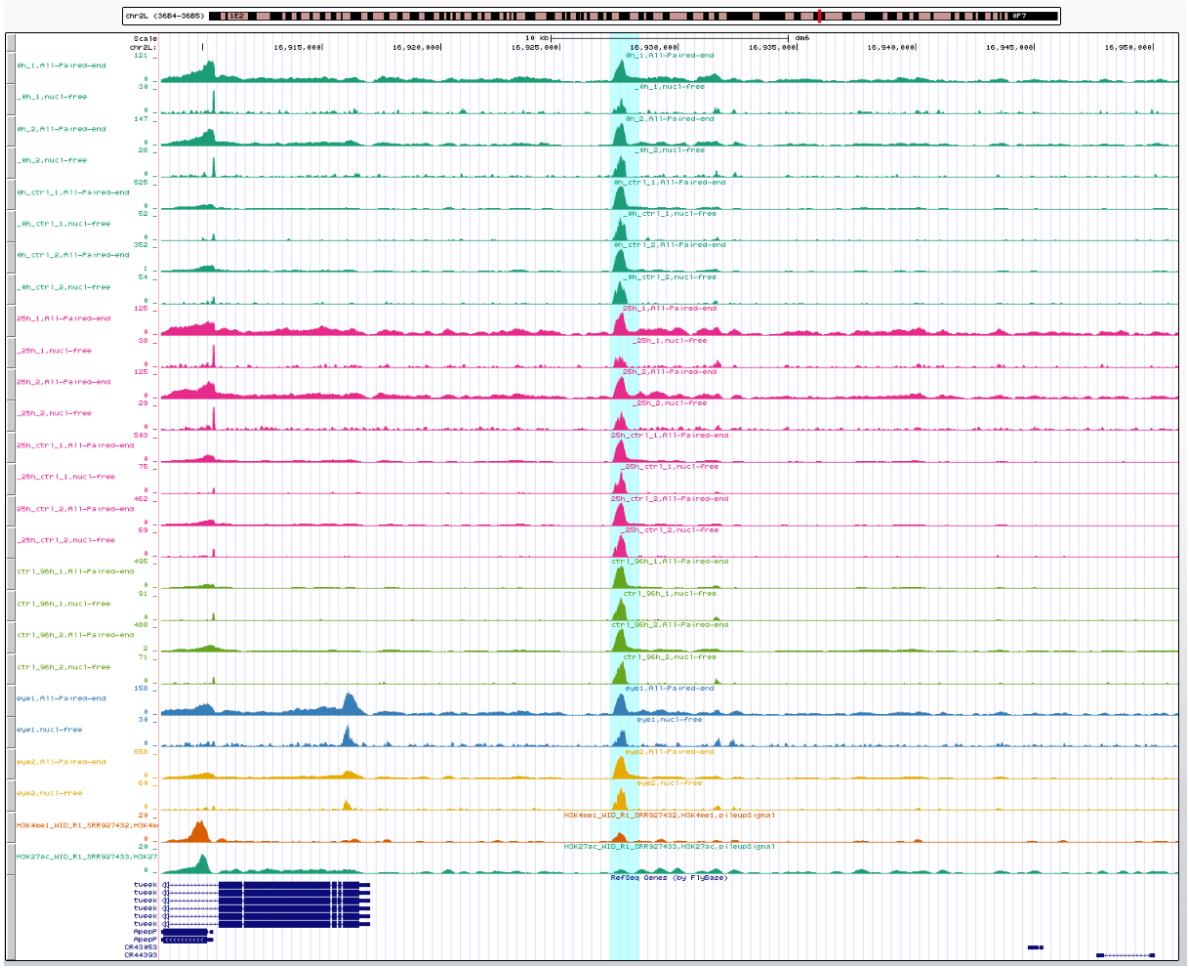
Compare peaks heights between 0h control and 0h treatment



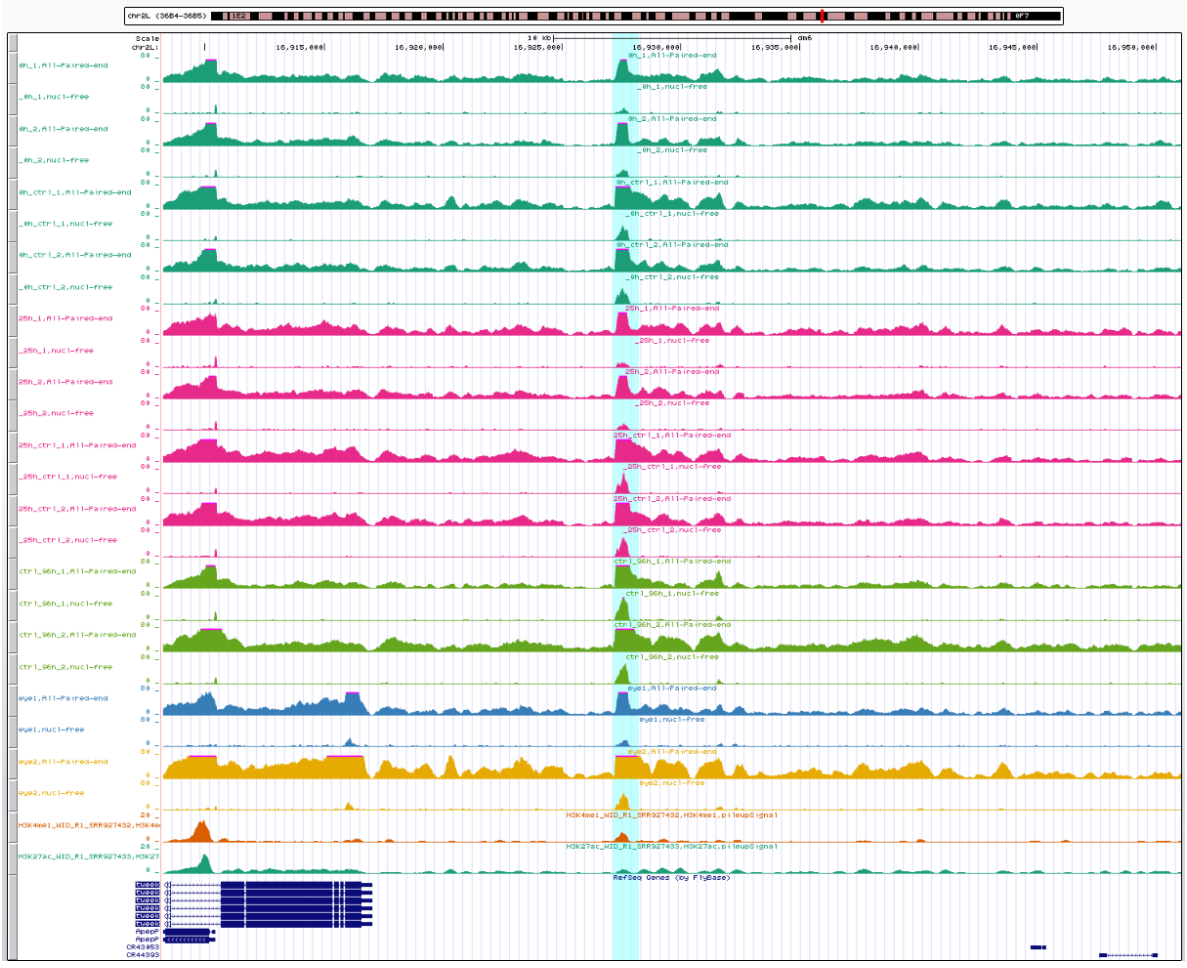
Compare peaks heights between 0h control and 0h treatment



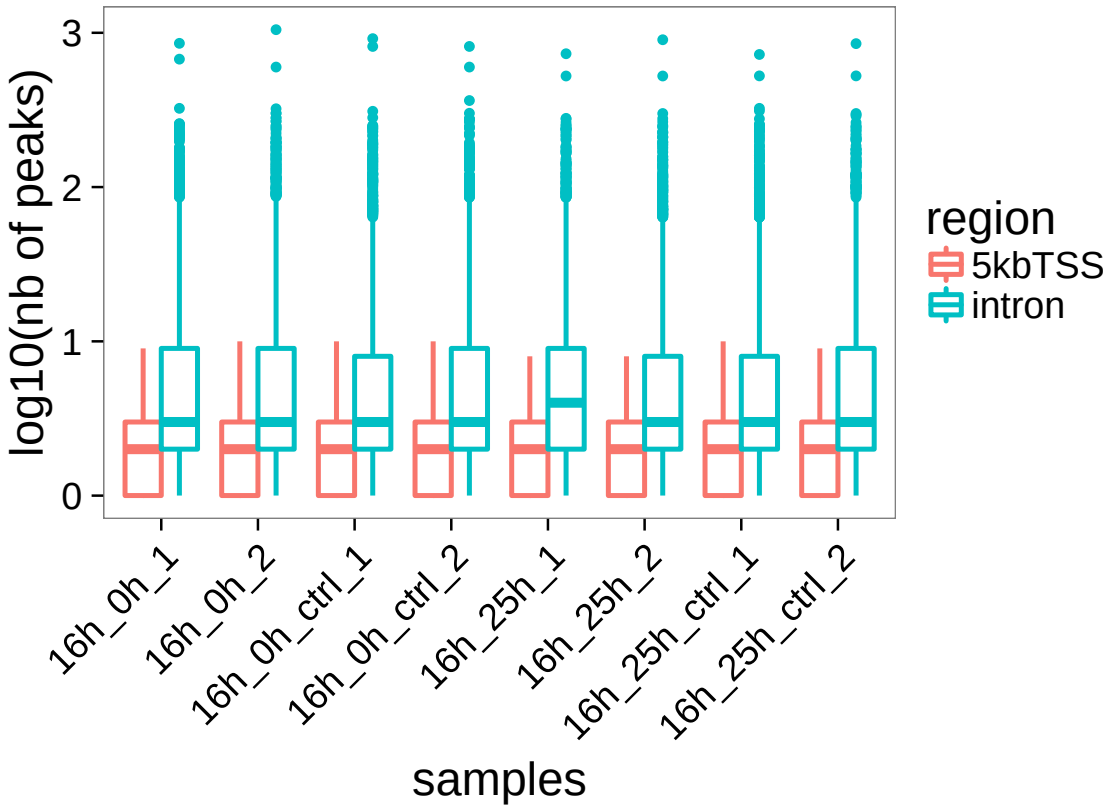
Compare peaks heights between 0h control and 0h treatment



Compare peaks heights between 0h control and 0h treatment



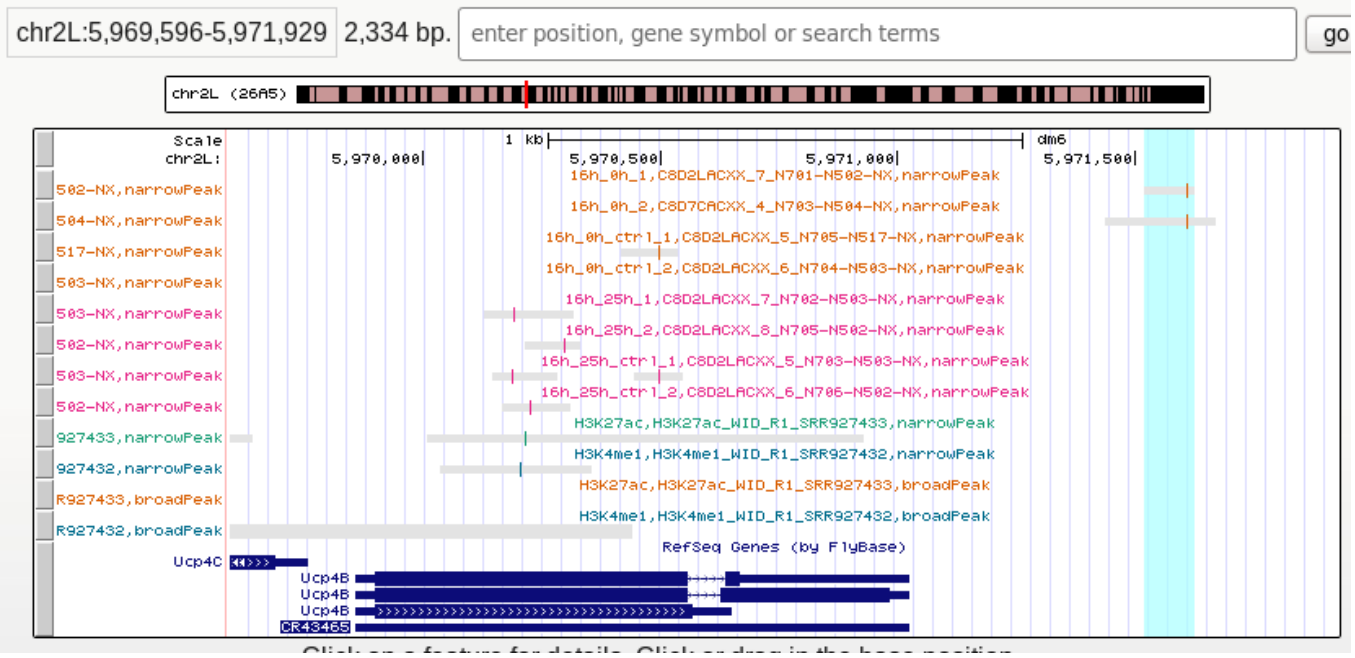
Number of peaks in the 5kb upstream of genes



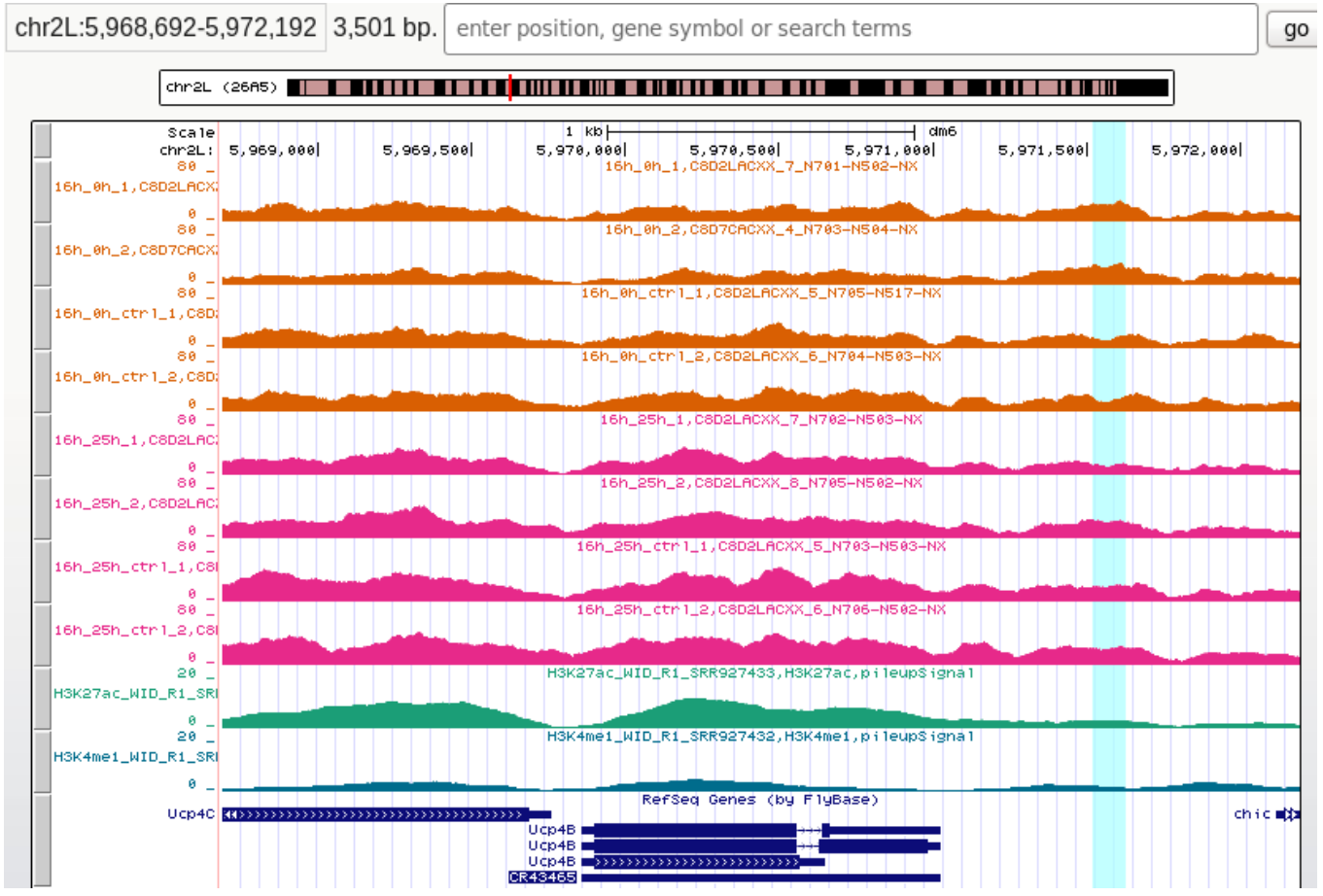
Number of peaks in the TSS of 41 upregulated genes

meta-gene	0h-ctrl-1	0h-ctrl-2	0h-treat-1	0h-treat-2	25h-treat-1	25h-treat-2
CG31955-mRNA-FBgn0051955	3	2	1	2	2	2
CR43465-ncRNA-FBgn0263442	0	0	1	1	0	0
CG12560-mRNA-FBgn0031974	3	4	3	4	2	3
Aldh-mRNA-FBgn0012036	1	0	0	1	1	0
CR44845-ncRNA-FBgn0266139	3	3	3	4	1	3
CG7294-mRNA-FBgn0032284	1	1	1	2	2	1
Adh-mRNA-FBgn0000055	0	0	1	2	0	0
CG10621-mRNA-FBgn0032726	0	0	0	1	0	1
fon-mRNA-FBgn0032773	2	3	3	2	3	3
CG33509-mRNA-FBgn0053509	0	0	0	1	0	0
ppk13-mRNA-FBgn0053508	1	1	1	2	1	1
scaf-mRNA-FBgn0033033	3	2	3	2	3	3
Cpr49Ah-mRNA-FBgn0033731	2	3	3	2	2	2
CG6701-mRNA-FBgn0033889	2	2	3	3	2	3
Arc1-mRNA-FBgn0033926	5	5	5	4	4	3
LamC-mRNA-FBgn0010397	2	3	1	2	1	3
CG10527-mRNA-FBgn0034583	4	3	3	3	3	4
lama-mRNA-FBgn0016031	4	5	5	5	5	4
rpr-mRNA-FBgn0011706	5	5	5	4	4	4

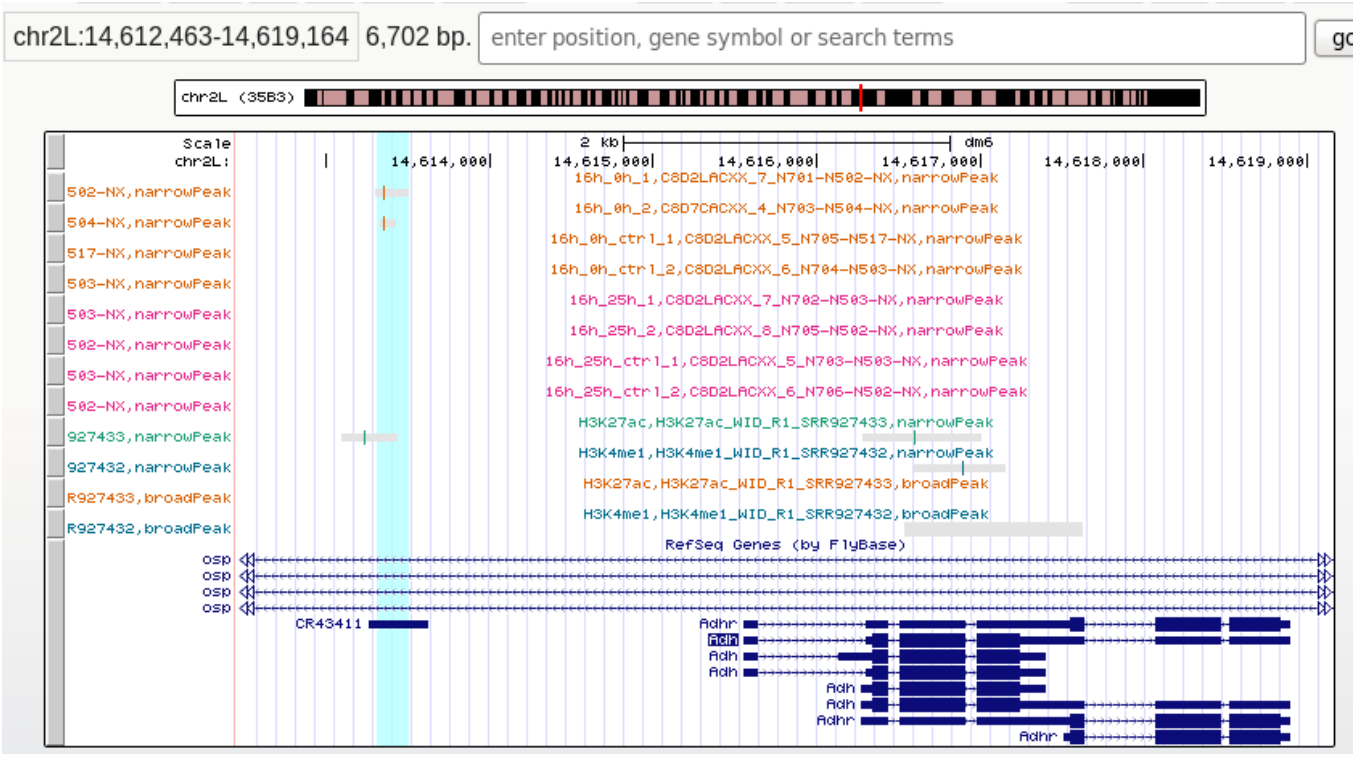
CR43465-ncRNA-FBgn0263442



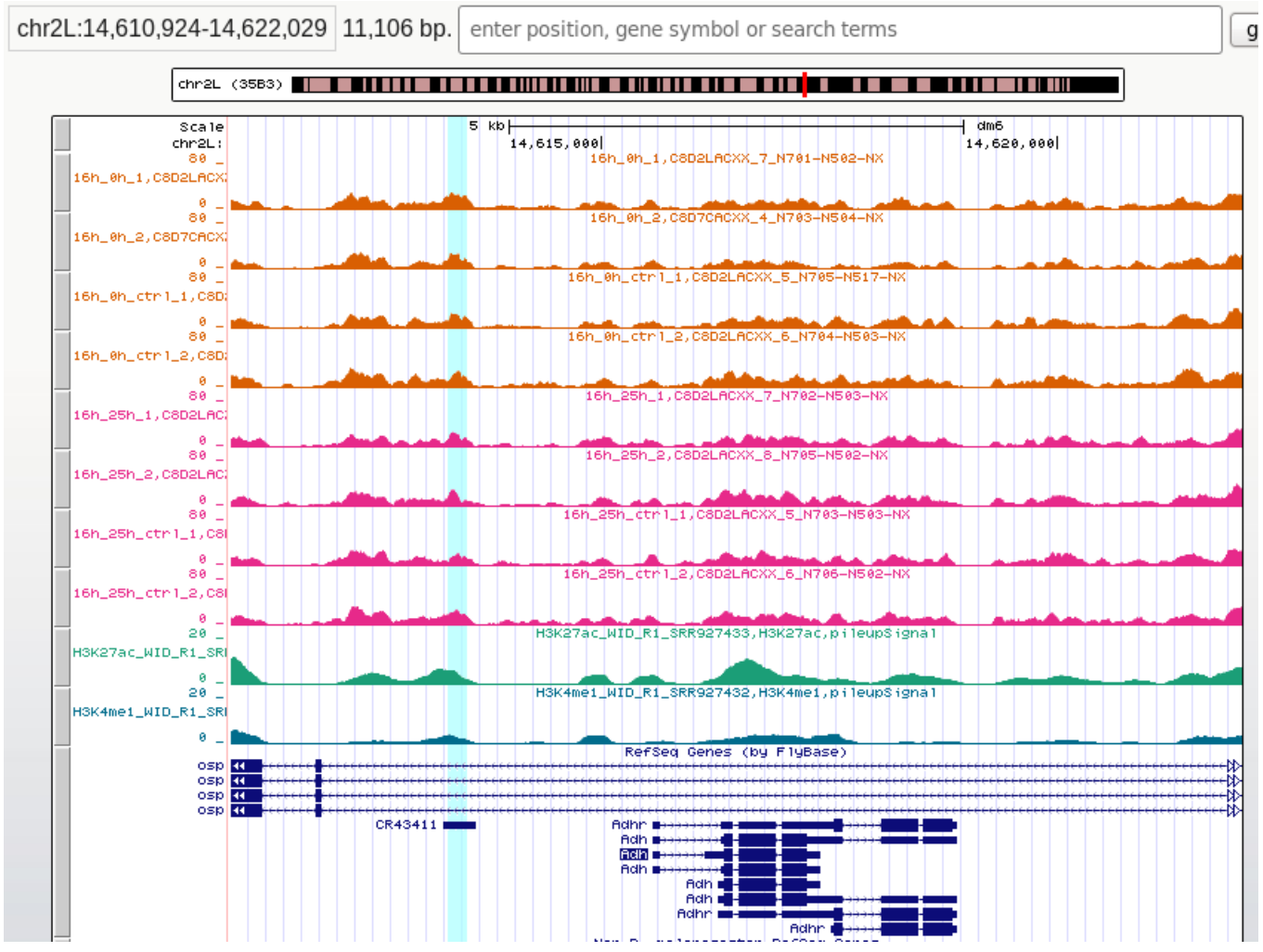
CR43465-ncRNA-FBgn0263442



Adh-mRNA-FBgn0000055



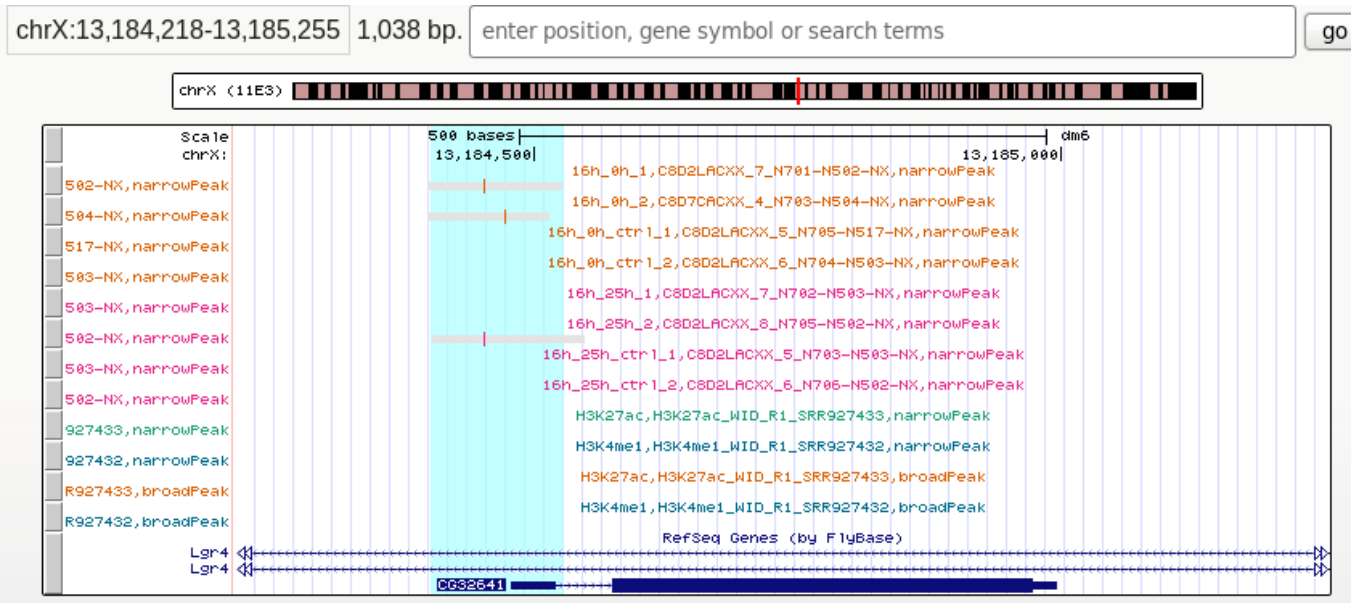
Adh-mRNA-FBgn0000055



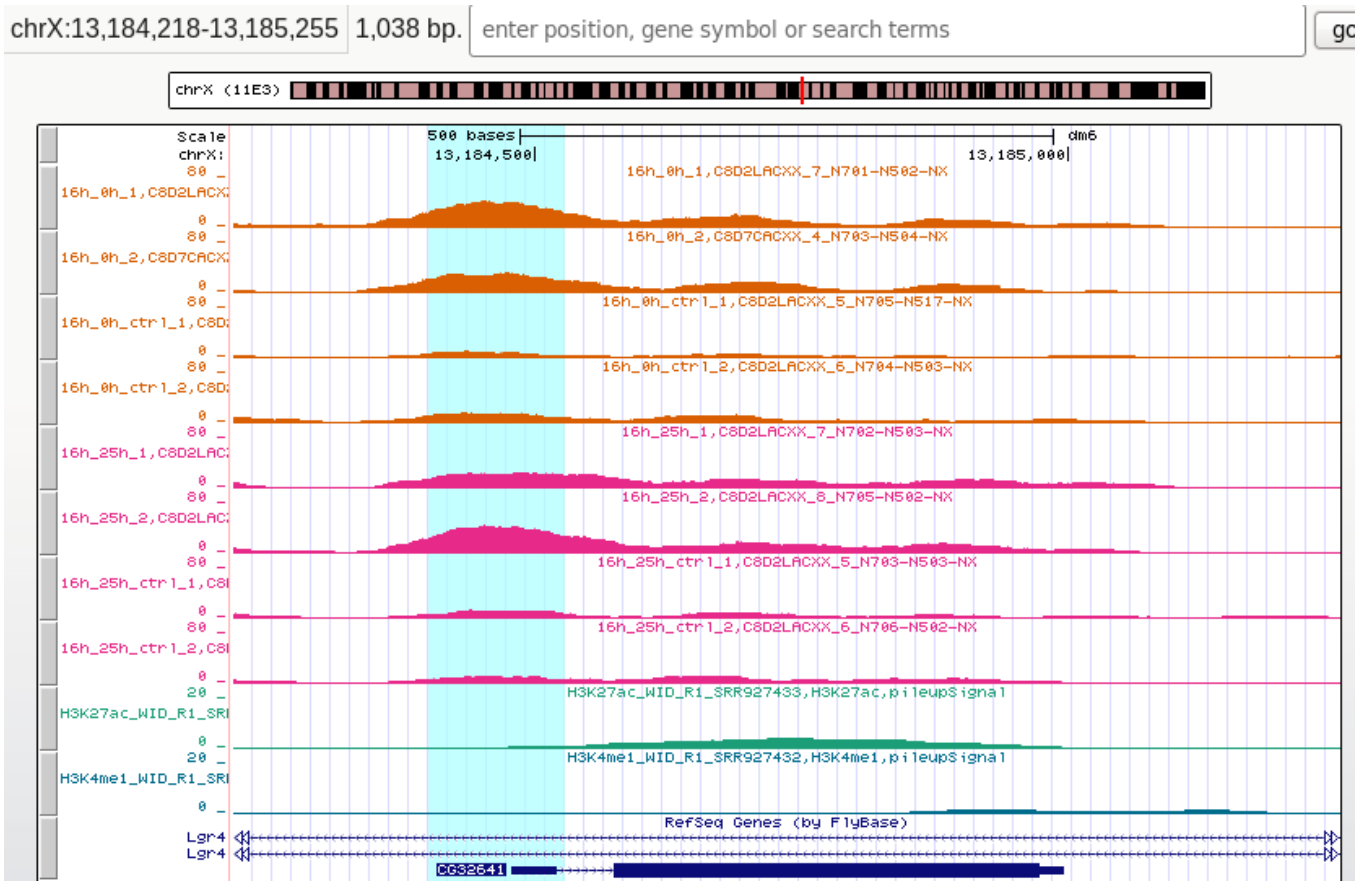
Number of peaks in the TSS of 41 upregulated genes

meta-gene	0h-ctrl-1	0h-ctrl-2	0h-treat-1	0h-treat-2	25h-treat-1	25h-treat-2
TfAP-2-mRNA-FBgn0261953	1	1	2	2	2	2
CR46123-ncRNA-FBgn0267798	0	0	0	1	0	0
alpha-Est2-mRNA-FBgn0015570	2	1	1	1	2	0
Hsp70Ab-mRNA-FBgn0013276	4	4	4	3	2	4
CG5167-mRNA-FBgn0038038	1	1	2	1	4	1
Hsp70Bb-mRNA-FBgn0013278	1	2	2	3	3	3
CG31313-mRNA-FBgn0051313	1	0	0	0	0	0
ea-mRNA-FBgn0000533	2	3	3	3	3	3
CG33099-mRNA-FBgn0053099	1	2	1	2	2	1
CG5326-mRNA-FBgn0038983	2	2	1	2	1	2
Hsp68-mRNA-FBgn0001230	3	2	2	1	1	1
Ude-mRNA-FBgn0039226	2	1	1	2	1	1
CG34291-mRNA-FBgn0085320	4	3	3	5	4	5
CR44030-ncRNA-FBgn0264822	1	2	1	2	1	2
CR40469-ncRNA-FBgn0058469	2	1	3	4	2	3
CG13360-mRNA-FBgn0025620	2	1	1	1	1	1
w-mRNA-FBgn0003996	0	0	1	1	0	1
ssp7-mRNA-FBgn0052667	0	0	0	1	0	0
CG32641-mRNA-FBgn0052641	0	0	1	1	0	1
CR44383-pseudogene-FBgn0265533	1	4	3	4	3	3
CG32581-mRNA-FBgn0052581	2	4	5	7	4	5
CG32857-mRNA-FBgn0052857	0	0	0	1	0	0

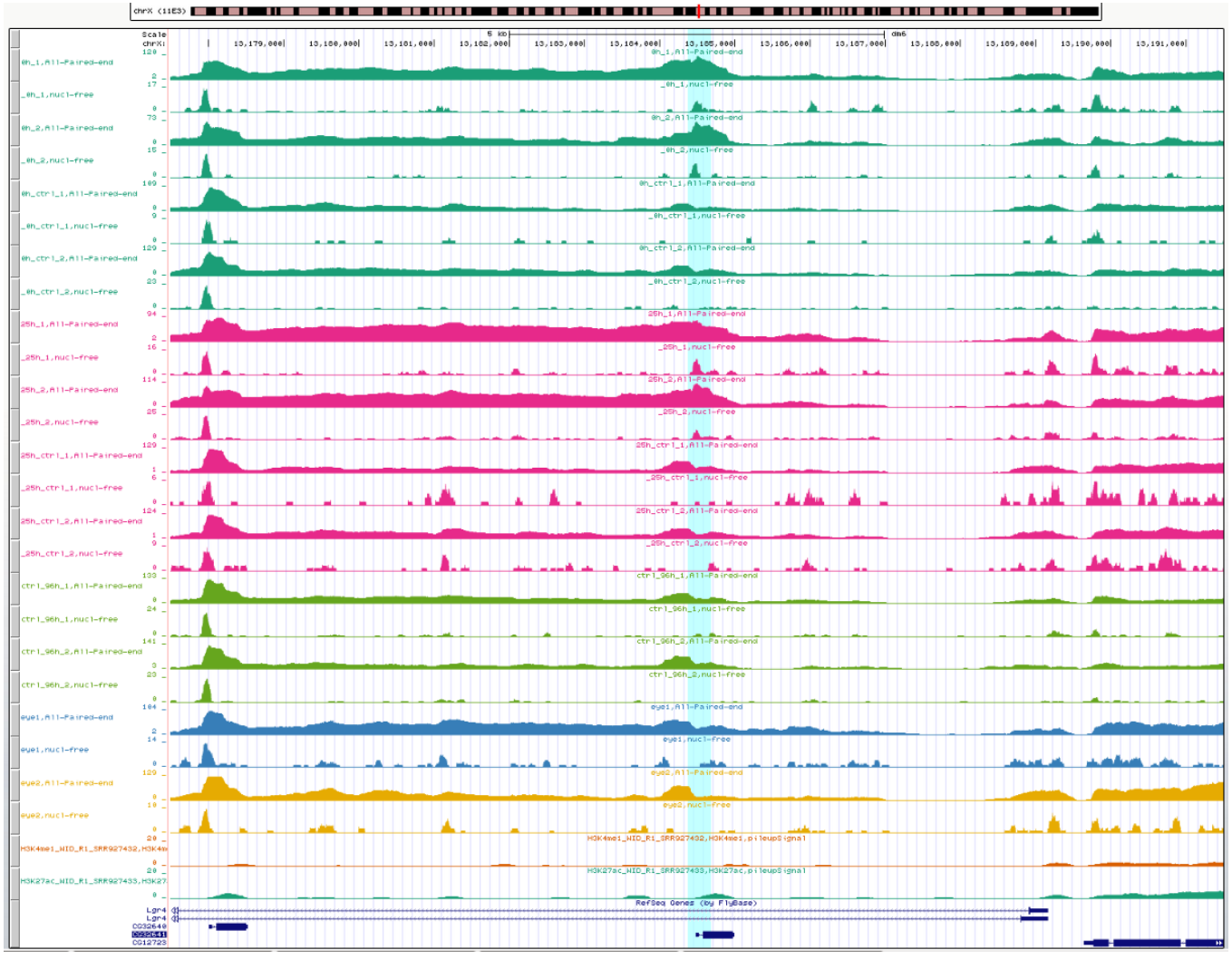
CG32641-mRNA-FBgn0052641



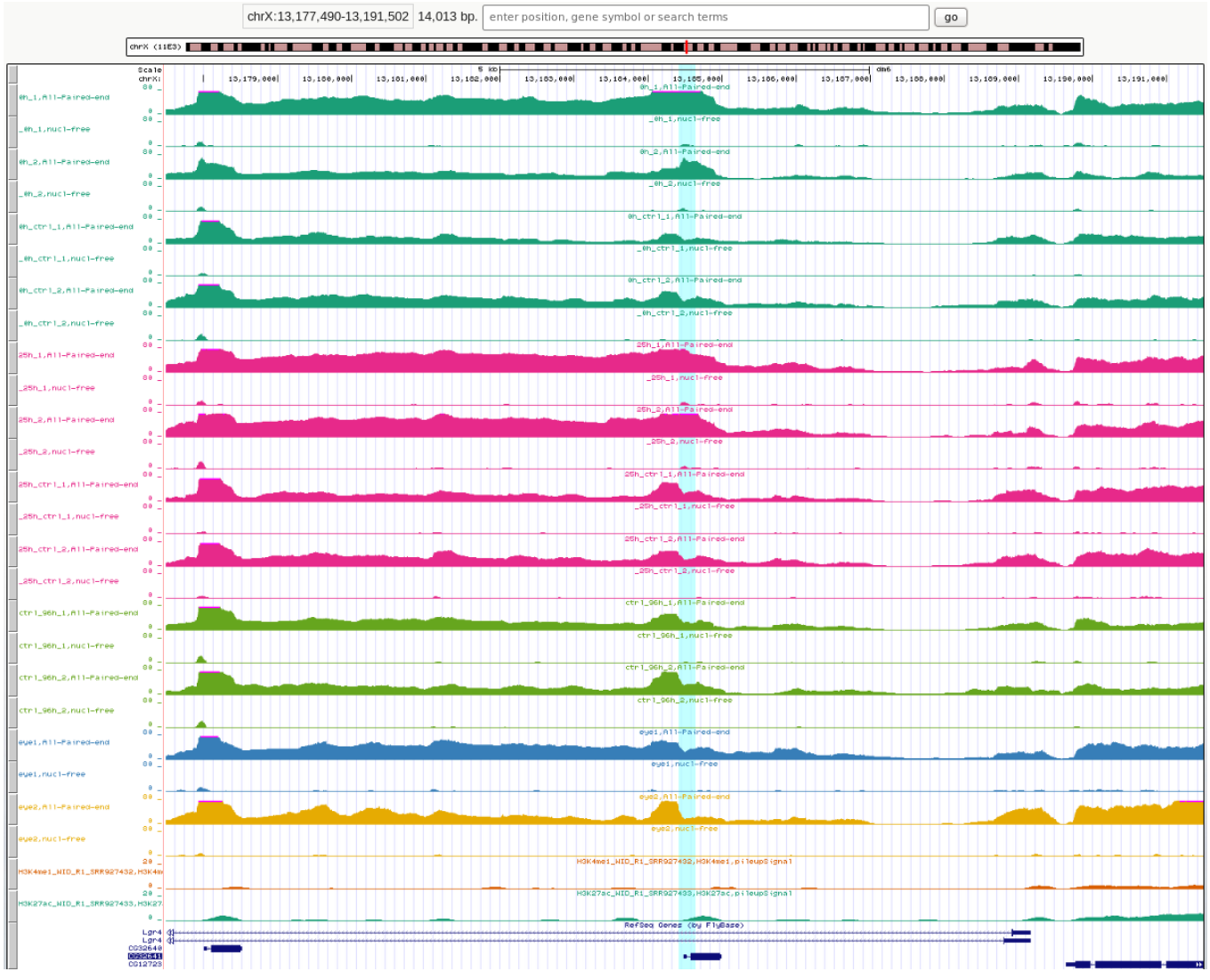
CG32641-mRNA-FBgn0052641



CG32641-mRNA-FBgn0052641



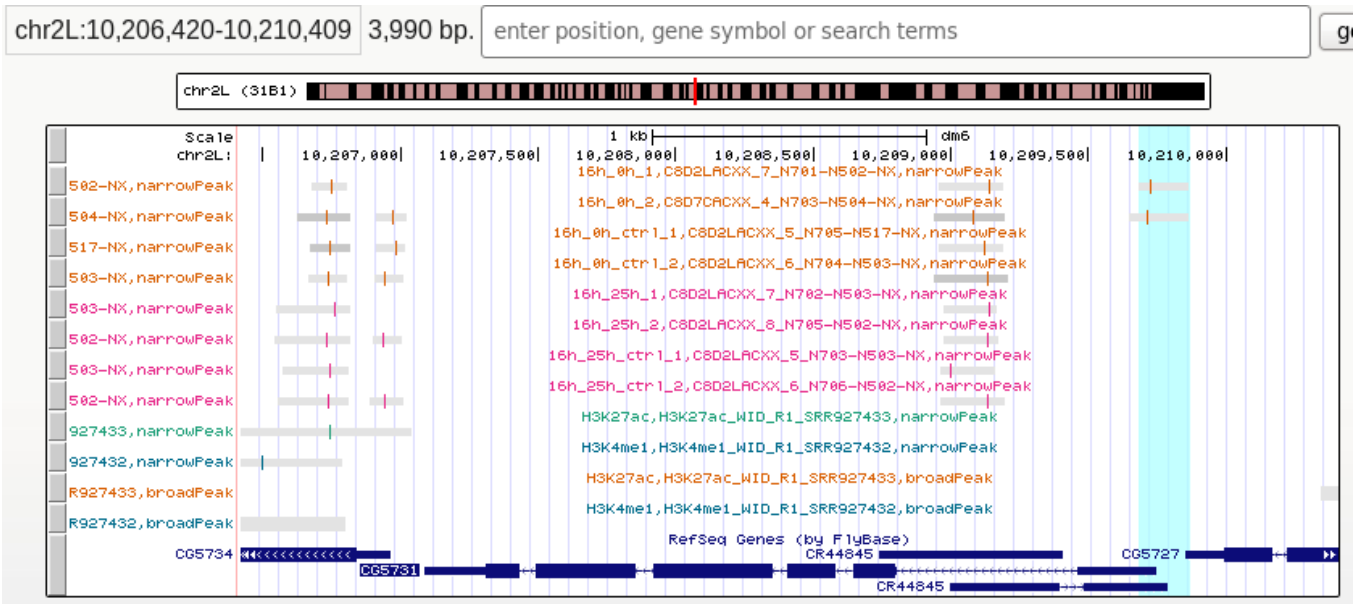
CG32641-mRNA-FBgn0052641



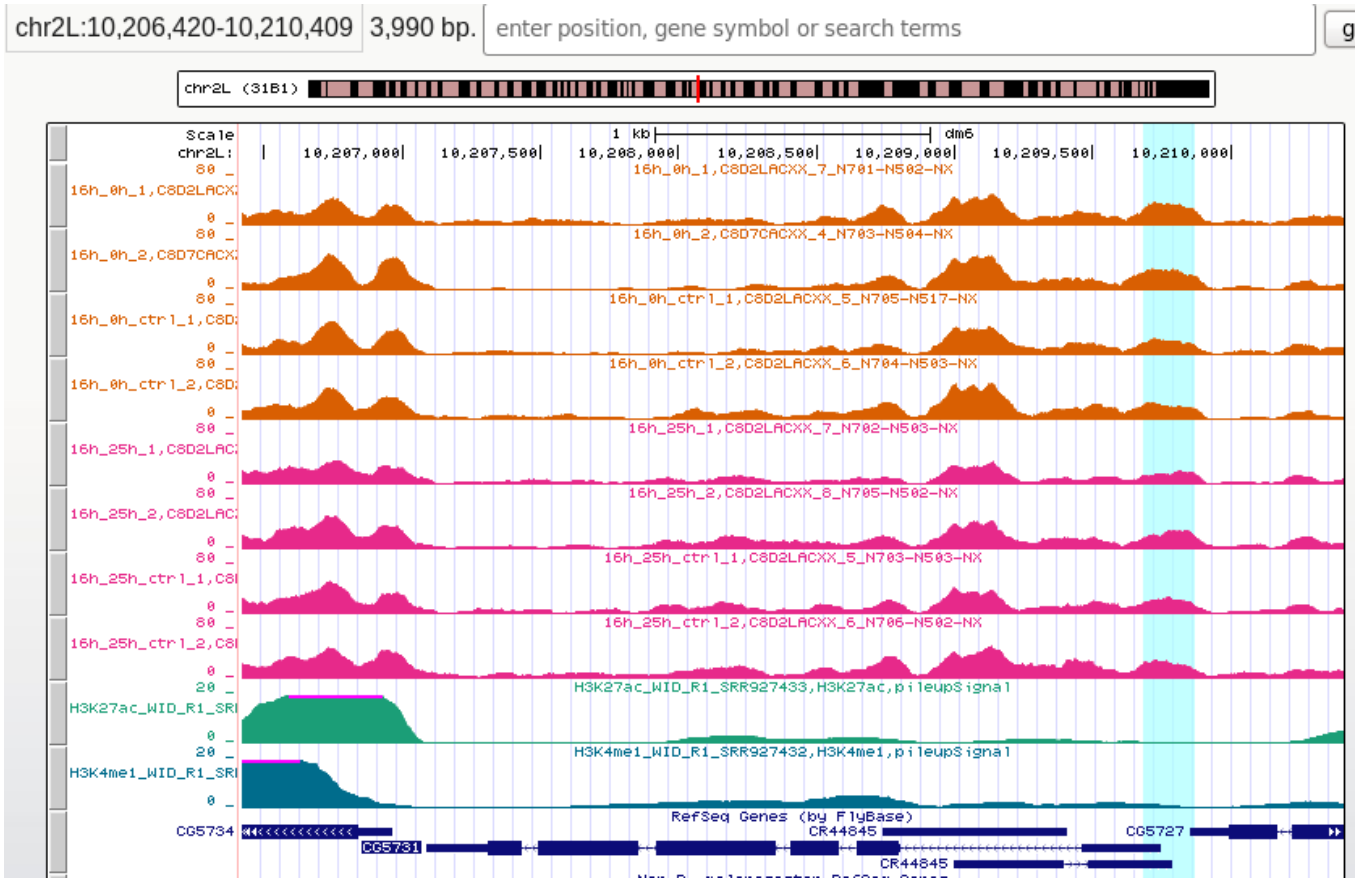
Number of peaks in the TSS of 48 downregulated genes

meta-gene	0h-ctrl-1	0h-ctrl-2	0h-treat-1	0h-treat-2	25h-treat-1	25h-treat-2
CR43767-ncRNA-FBgn0264267	0	0	0	1	0	0
CG3355-mRNA-FBgn0031619	3	2	4	2	3	3
CG5731-mRNA-FBgn0032192	0	0	1	1	0	0
NimC2-mRNA-FBgn0028939	2	1	1	1	2	1
CG44476-mRNA-FBgn0265669	2	2	1	3	2	2
CR43144-ncRNA-FBgn0262620	3	2	2	3	1	3
CR43242-ncRNA-FBgn0262887	2	3	1	2	1	2
Prosalpha1-mRNA-FBgn0263121	2	3	2	3	2	2
CG18853-mRNA-FBgn0042173	4	4	3	4	3	5
sut2-mRNA-FBgn0028562	1	1	2	1	1	1
Obp44a-mRNA-FBgn0033268	1	0	0	1	0	0
Lcp1-mRNA-FBgn0002531	3	2	1	2	1	3
Lcp2-mRNA-FBgn0002533	2	1	0	1	0	2
Spn47C-mRNA-FBgn0033574	1	1	0	0	1	0
Cpr49Ac-mRNA-FBgn0033725	1	2	2	2	2	2
CG8157-mRNA-FBgn0034010	0	0	0	2	1	1
CG34193-mRNA-FBgn0085222	1	1	0	2	1	1
Cpr57A-mRNA-FBgn0034517	2	3	2	3	2	2
CG9344-mRNA-FBgn0034564	4	4	4	3	3	3

CG5731-mRNA-FBgn0032192



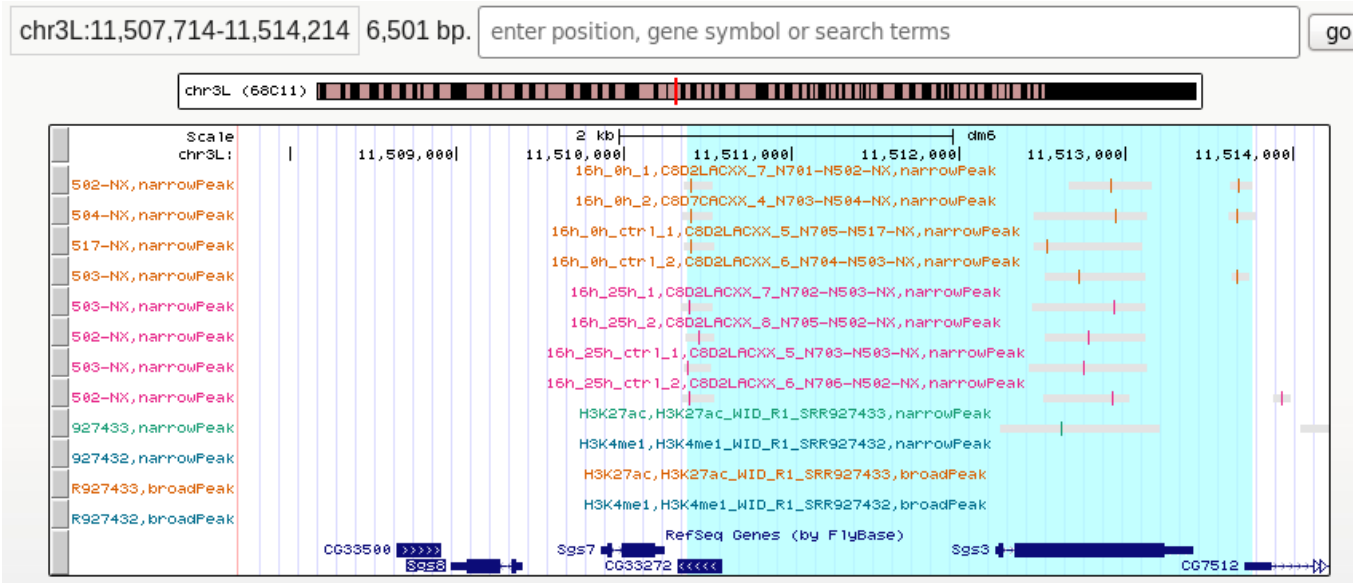
CG5731-mRNA-FBgn0032192



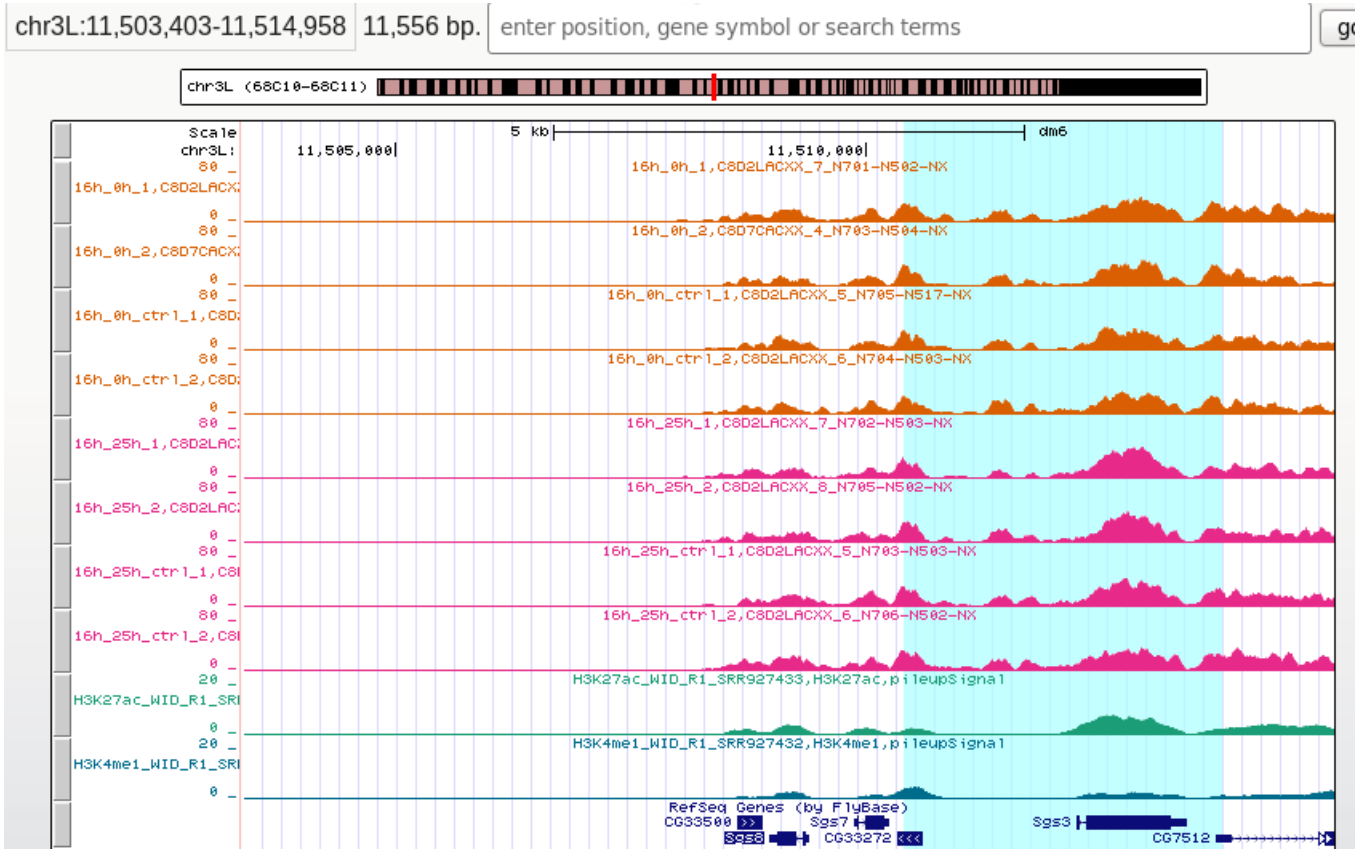
Number of peaks in the TSS of 48 downregulated genes

meta-gene	0h-ctrl-1	0h-ctrl-2	0h-treat-1	0h-treat-2	25h-treat-1	25h-treat-2
CG34206-mRNA-FBgn0085235	1	0	1	2	1	1
CG4250-mRNA-FBgn0034761	1	2	0	1	2	1
CG9192-mRNA-FBgn0035193	2	1	1	2	1	1
Drsl5-mRNA-FBgn0035434	2	4	3	3	2	3
Zasp66-mRNA-FBgn0035917	0	0	1	0	0	0
Hsp67Bb-mRNA-FBgn0001228	1	1	0	1	0	0
CR43482-pseudogene-FBgn0263493	4	6	4	5	5	4
Cpr67Fa2-mRNA-FBgn0036109	1	1	0	2	0	2
Sgs8-mRNA-FBgn0003378	2	2	3	3	2	2
CG34244-mRNA-FBgn0085273	2	1	1	2	3	2
CG13064-mRNA-FBgn0040796	2	1	1	2	1	2
Oat-mRNA-FBgn0022774	1	1	0	2	1	1
Cpr78E-mRNA-FBgn0037114	2	0	0	1	2	2
CG11370-mRNA-FBgn0037181	1	1	0	0	2	1
CG14664-mRNA-FBgn0040682	2	2	1	2	1	3
CG2663-mRNA-FBgn0037323	0	1	1	1	1	1
CG43060-mRNA-FBgn0262362	3	2	1	2	1	1
CG8369-mRNA-FBgn0040532	2	2	3	3	4	3
CG3397-mRNA-FBgn0037975	0	0	0	1	1	0
NijC-mRNA-FBgn0038079	2	2	3	3	3	1
CR43166-ncRNA-FBgn0262722	3	2	2	2	2	2
CG13641-mRNA-FBgn0039239	1	0	0	2	0	1
Ef1alpha100E-mRNA-FBgn0000557	2	1	2	3	1	2
18SrRNA:CR41548-rRNA-FBgn0085802	3	3	4	3	4	4
CR43461-ncRNA-FBgn0263415	2	3	3	3	3	3
CG15345-mRNA-FBgn0040928	4	3	4	3	3	3
CG9686-mRNA-FBgn0030158	1	1	1	2	1	1
roX2-ncRNA-FBgn0019660	1	2	3	1	0	2
CG33502-mRNA-FBgn0053502	1	1	2	1	3	1

Sgs8-mRNA-FBgn0003378



Sgs8-mRNA-FBgn0003378



Intersection ATACseq peaks and histones

H3K4me1

mark	nb-narrowPeaks	nb-broadPeaks
H3K4me1	21555	6411

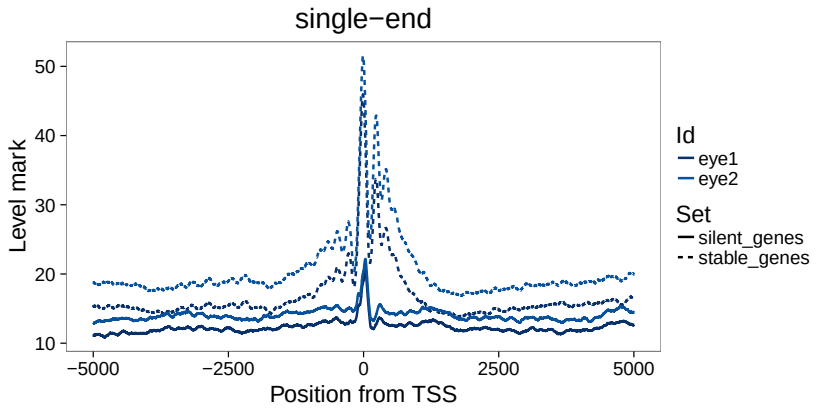
sample	nb-shared-narrowPeaks	nb-shared-broadPeaks
16h-0h-1	13354	10635
16h-0h-2	14626	11689
16h-0h-ctrl-1	13897	10804
16h-0h-ctrl-2	13228	10488
16h-25h-1	12894	10265
16h-25h-2	13393	10653
16h-25h-ctrl-1	13402	10653
16h-25h-ctrl-2	13319	10526

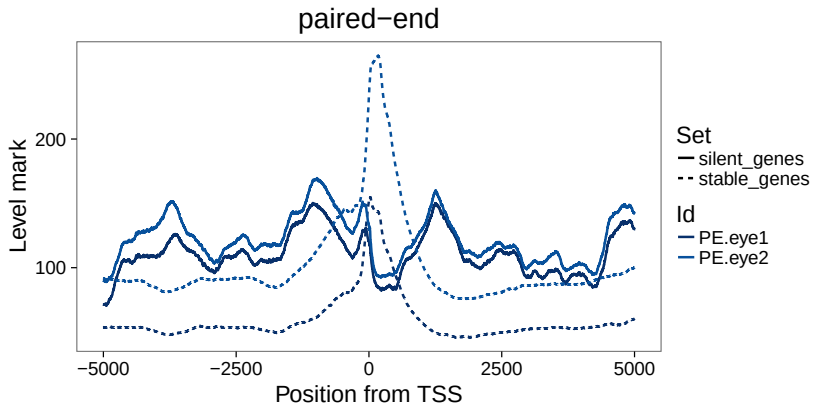
H3K27ac

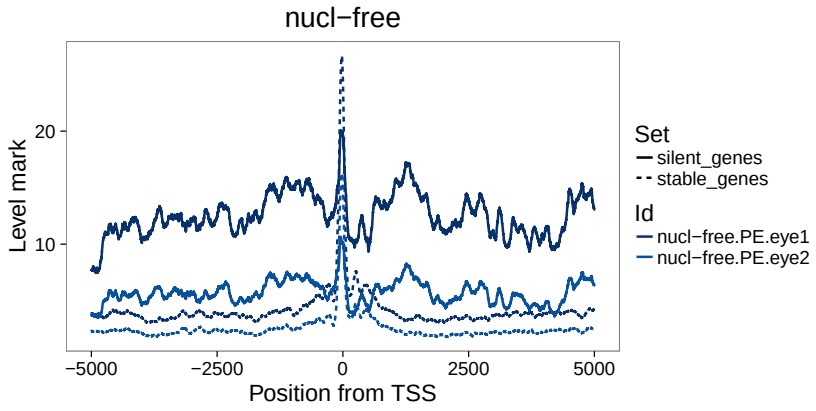
mark	nb-narrowPeaks	nb-broadPeaks
H3K4me1	30969	6053

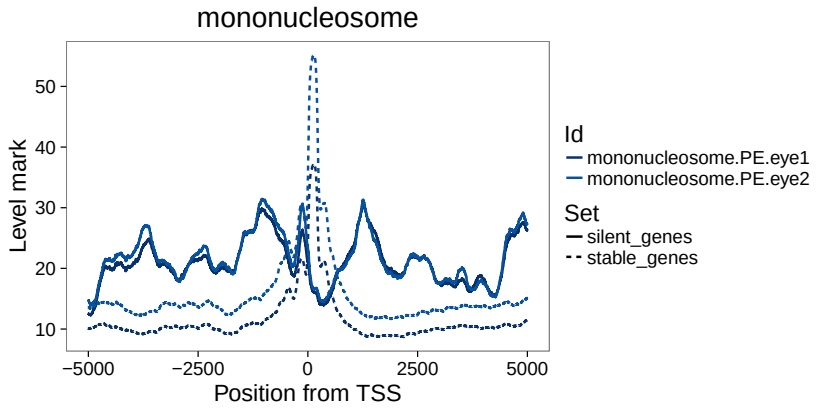
sample	nb-shared-narrowPeaks	nb-shared-broadPeaks
16h-0h-1	12639	6516
16h-0h-2	13793	7120
16h-0h-ctrl-1	13530	6806
16h-0h-ctrl-2	12596	6477
16h-25h-1	13351	6763
16h-25h-2	13418	6747
16h-25h-ctrl-1	13330	6716
16h-25h-ctrl-2	12945	6619

Eye

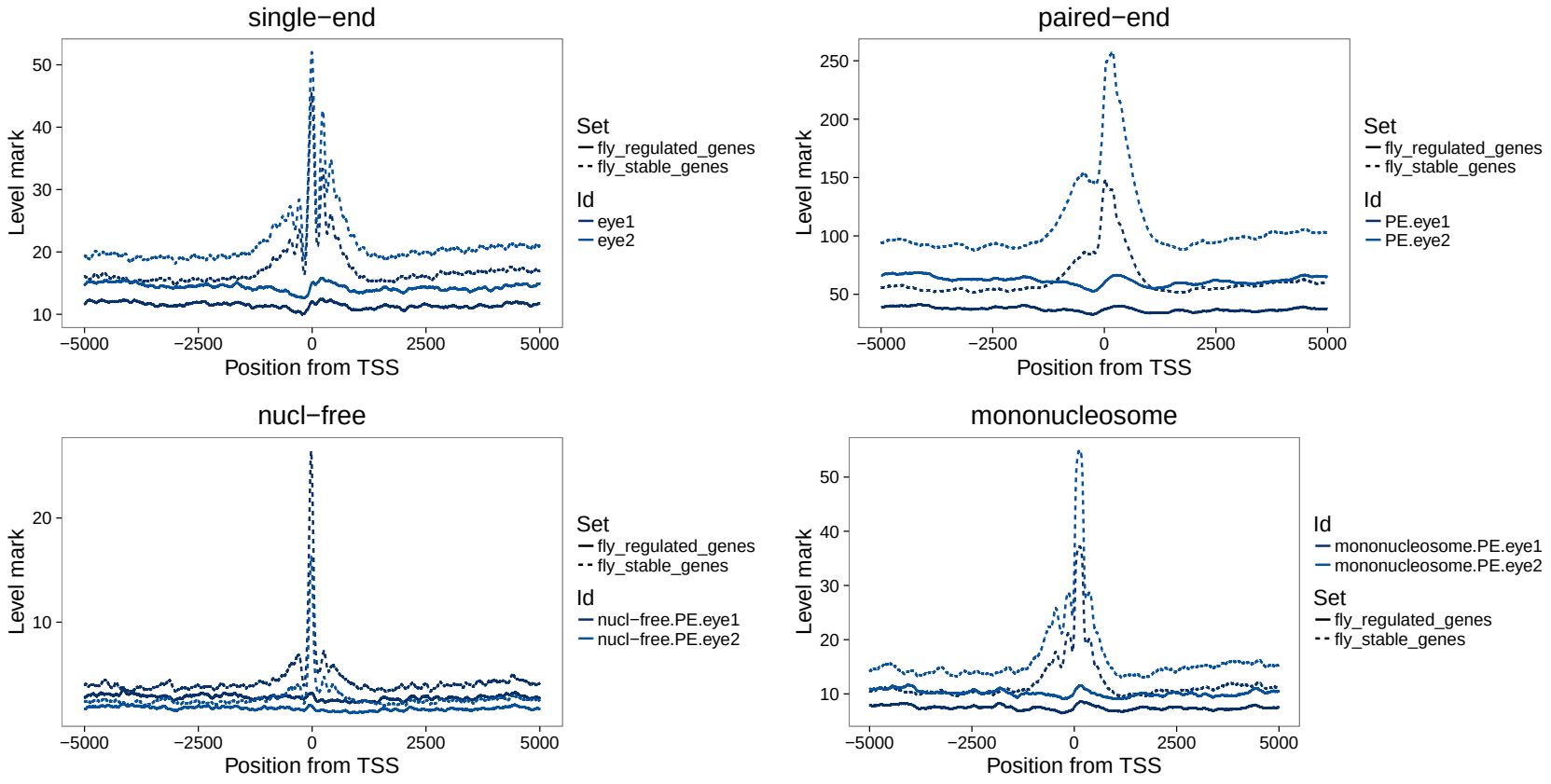

single−end
Level mark
50
40
30
20
10
−5000
−2500
0
2500
5000
Position from TSS
Id
eye1
eye2
Set
silent_genes
stable_genes


paired−end
Level mark
200
100
−5000
−2500
0
2500
5000
Position from TSS
Set
silent_genes
stable_genes
Id
PE.eye1
PE.eye2

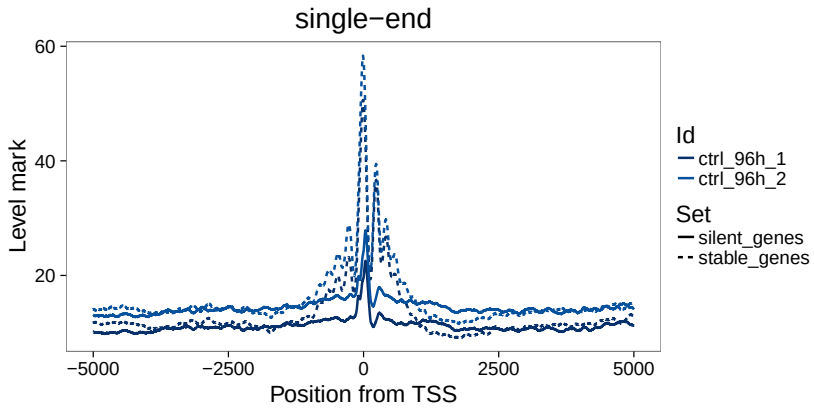

nucl−free
Level mark
20
10
−5000
−2500
0
2500
5000
Position from TSS
Set
silent_genes
stable_genes
Id
nucl−free.PE.eye1
nucl−free.PE.eye2

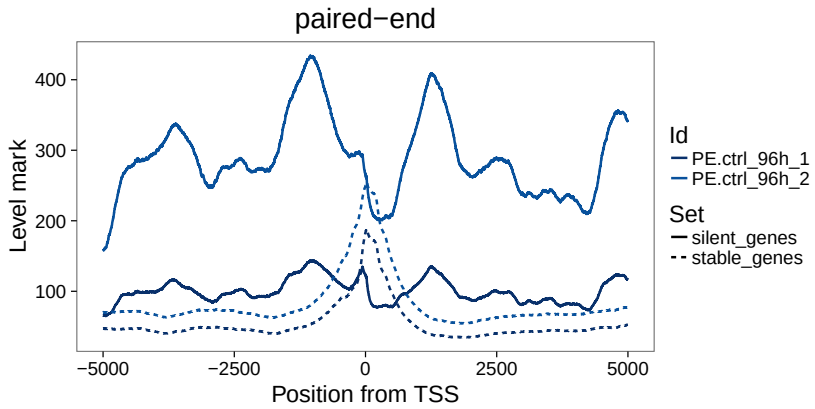

mononucleosome
Level mark
50
40
30
20
10
−5000
−2500
0
2500
5000
Position from TSS
Id
mononucleosome.PE.eye1
mononucleosome.PE.eye2
Set
silent_genes
stable_genes

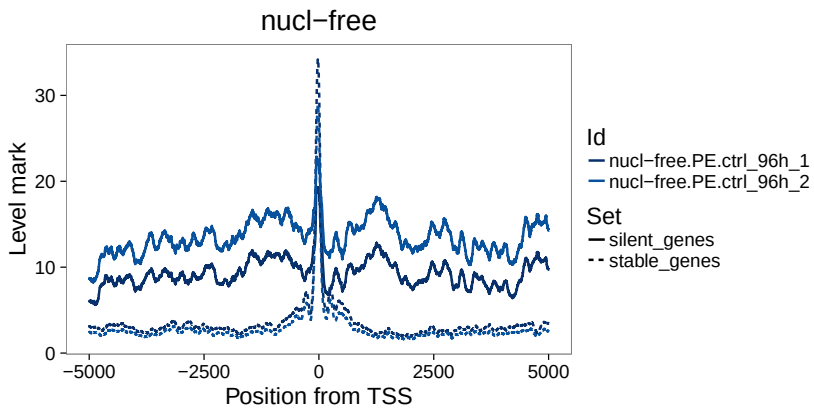
Eye NG stable regulated

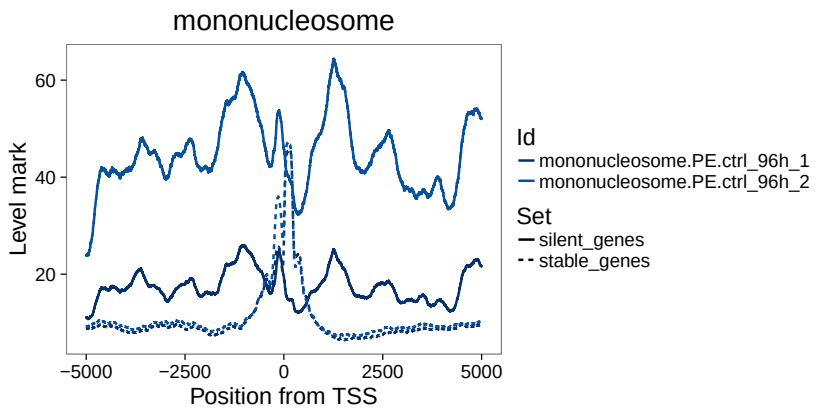


Wing 96h control

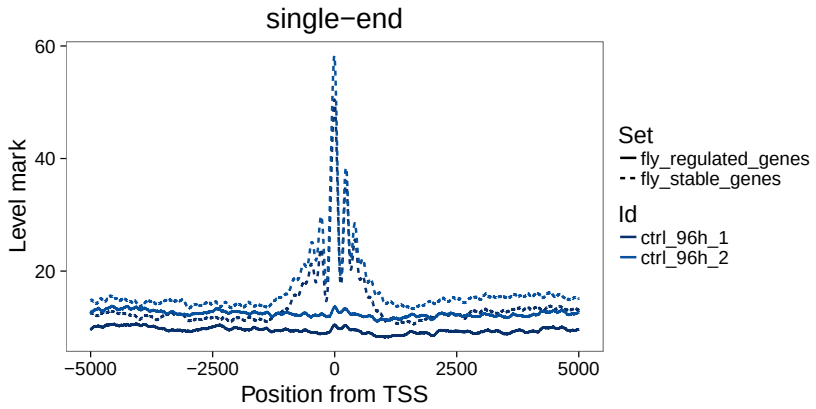


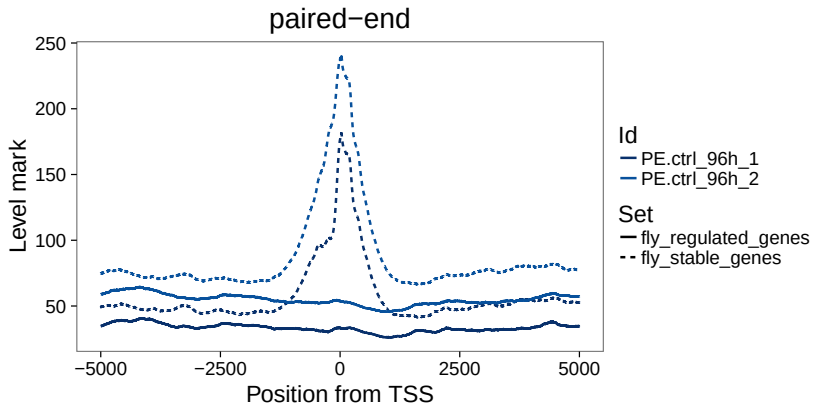


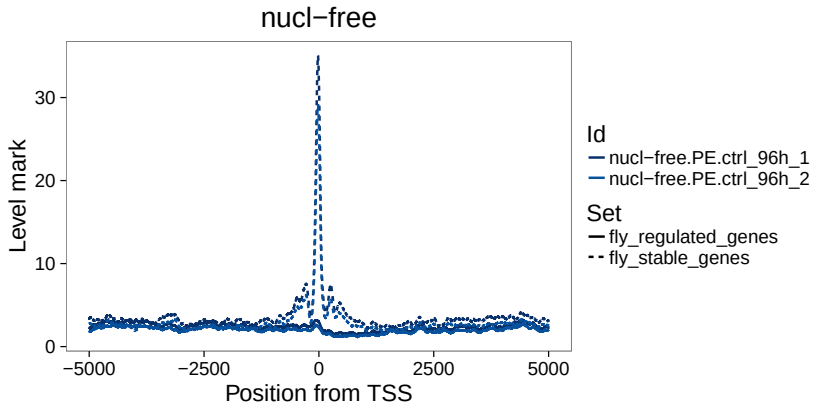


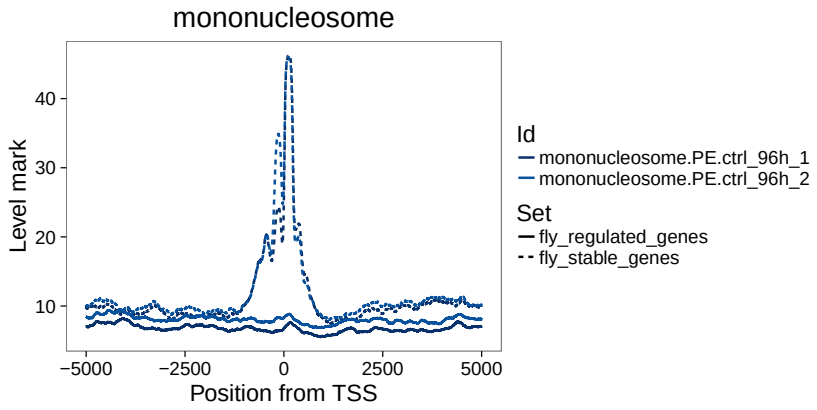


Wing 96h control NG stable regulated

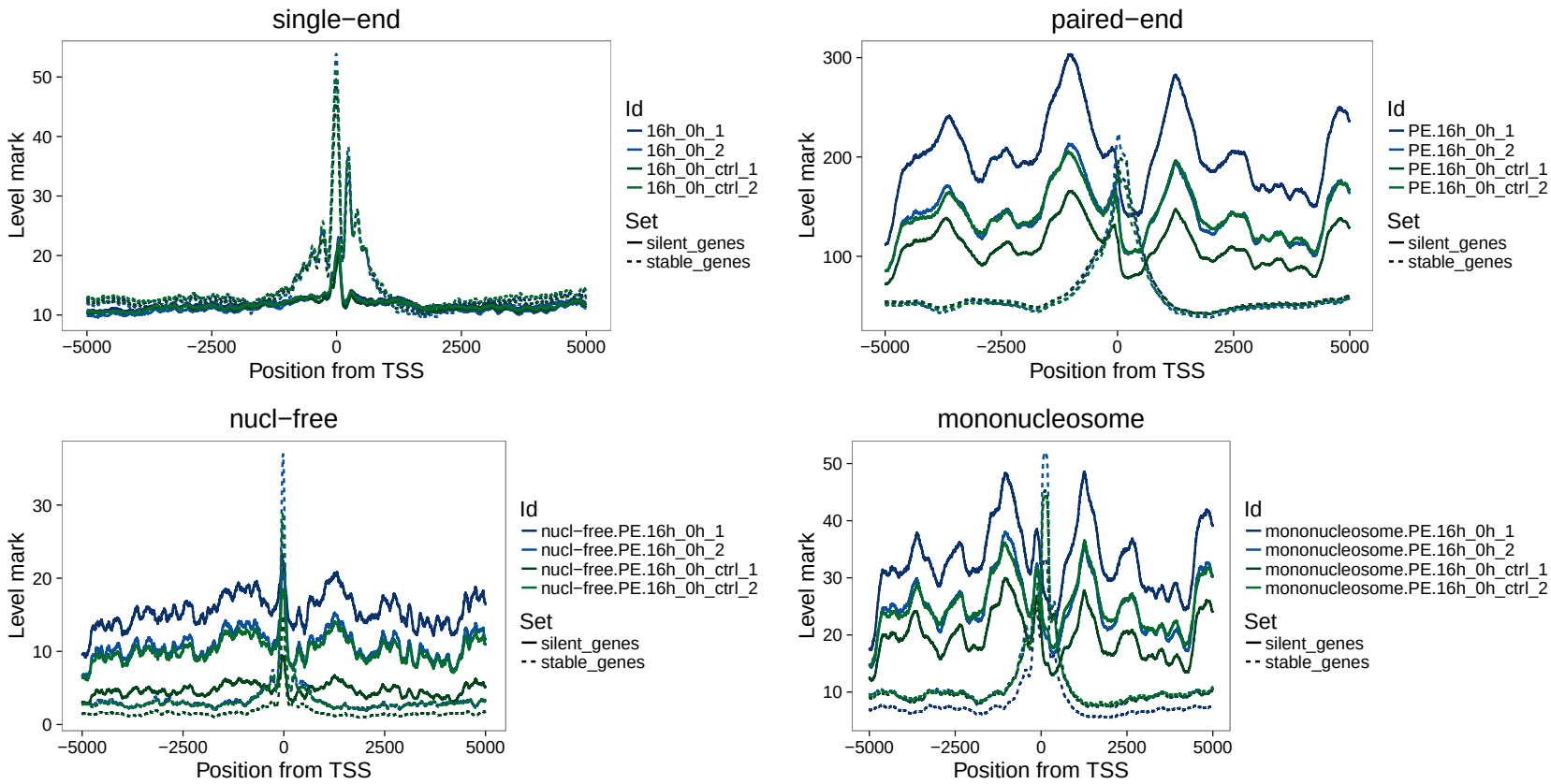




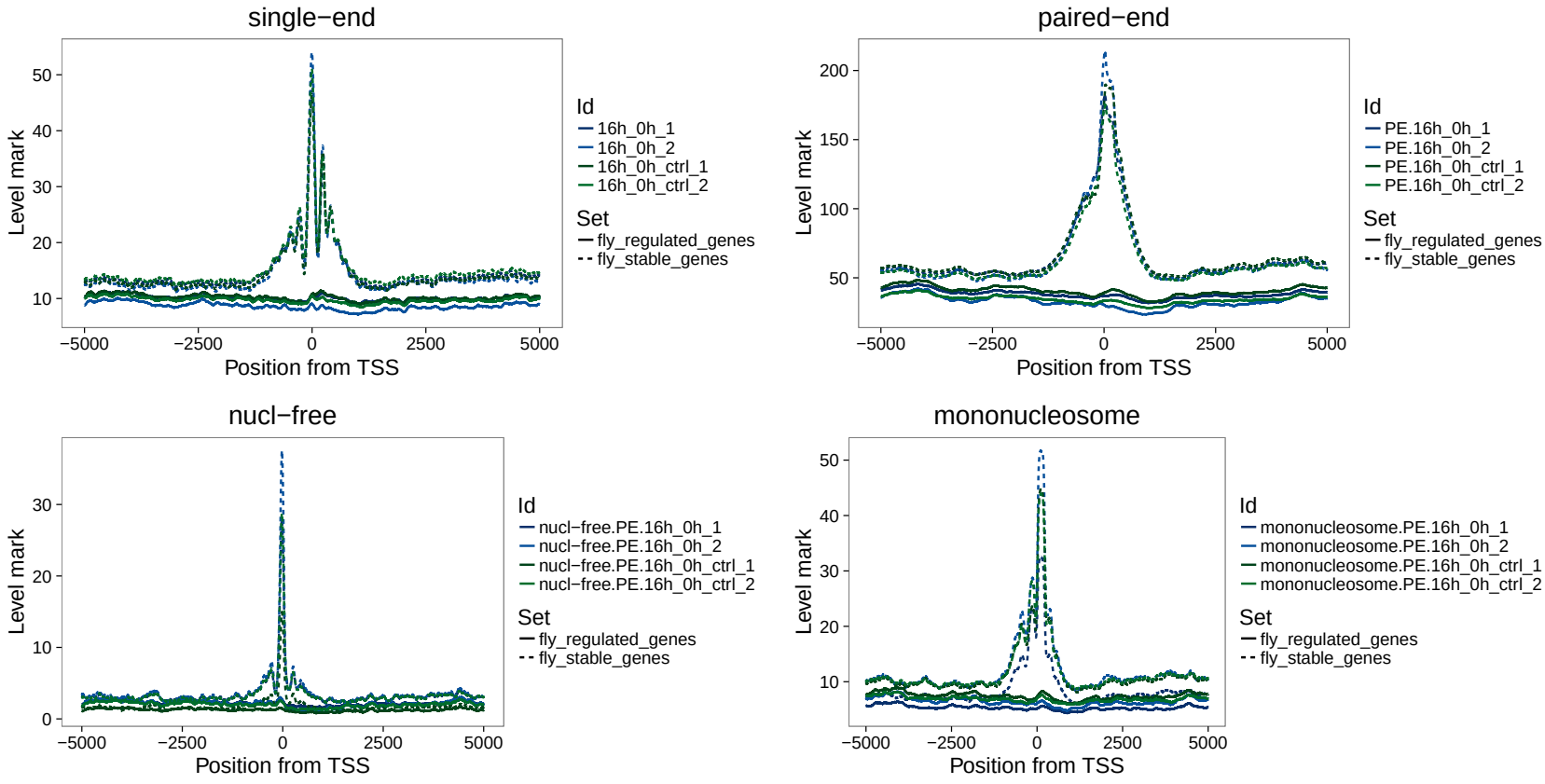




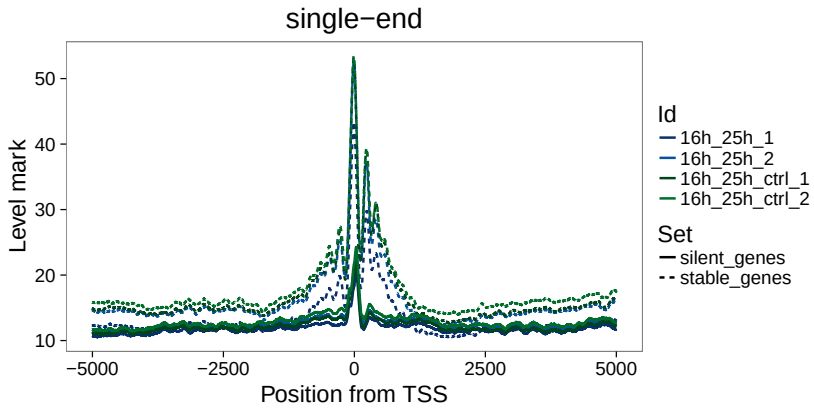
Wing 0h control and treatment

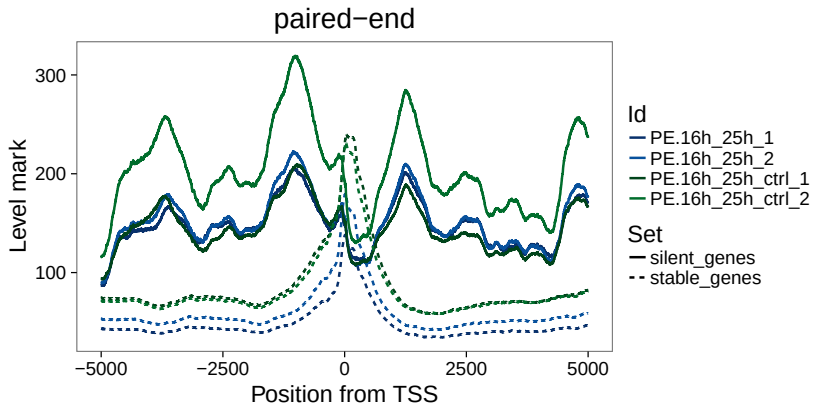


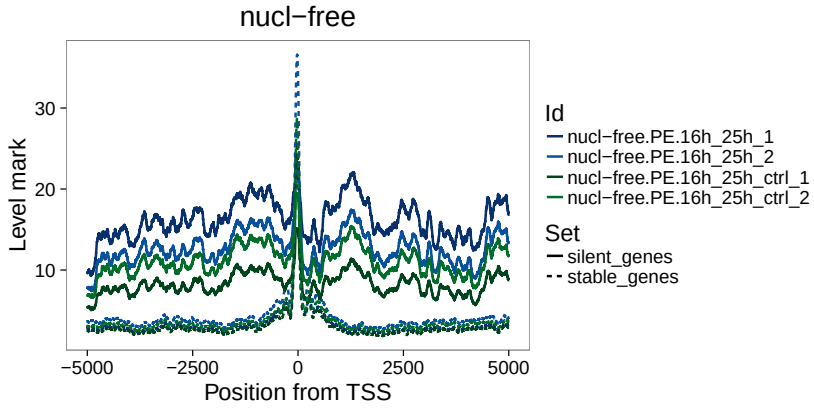
Wing 0h control and treatment NG stable regulated

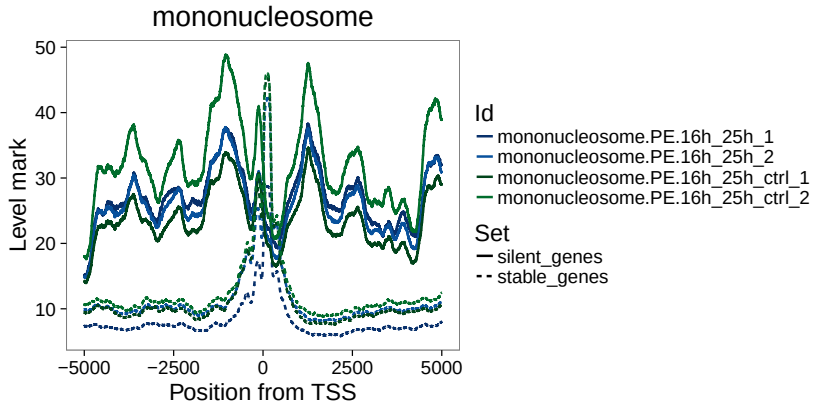


Wing 25h control and treatment

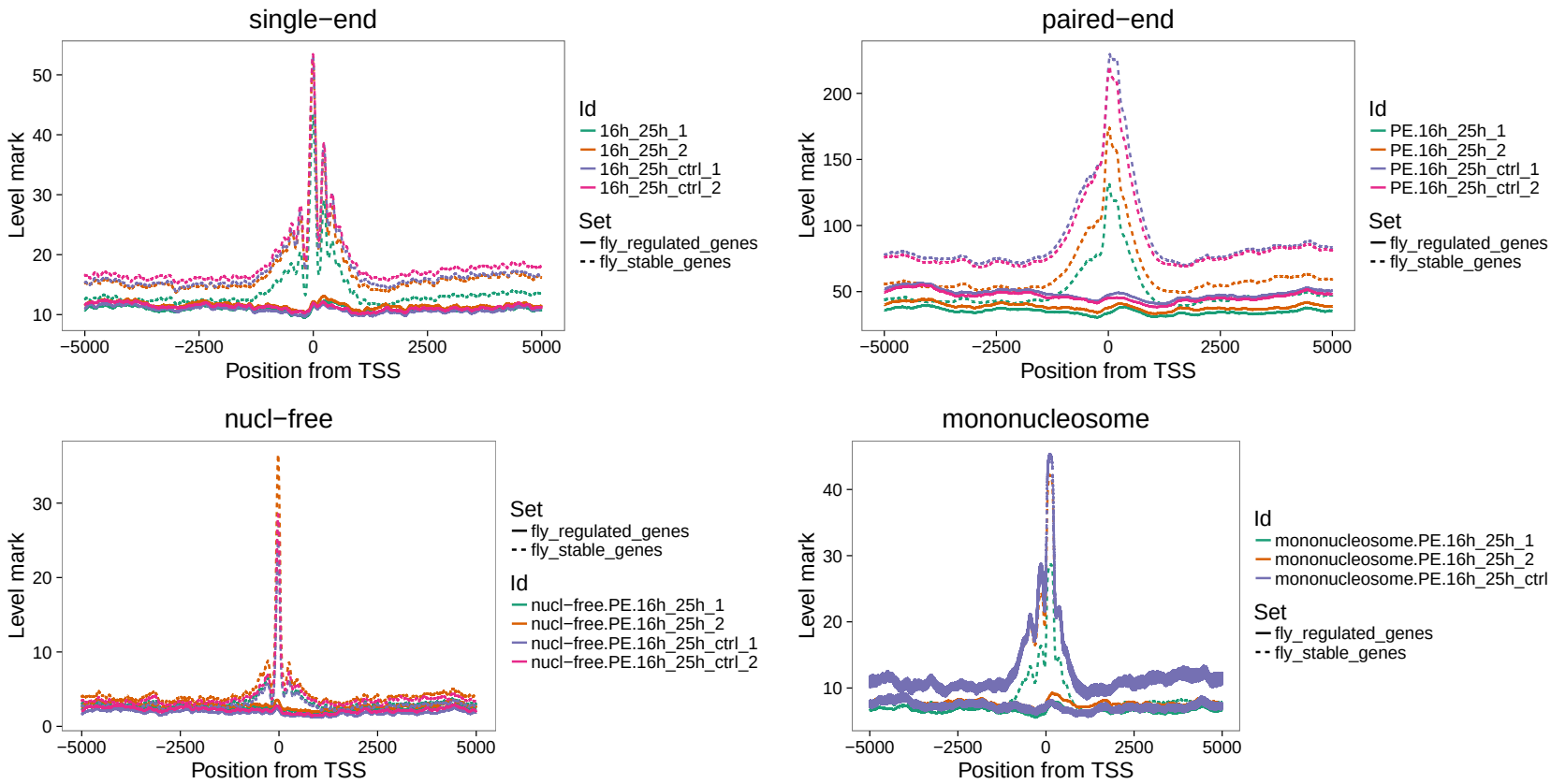




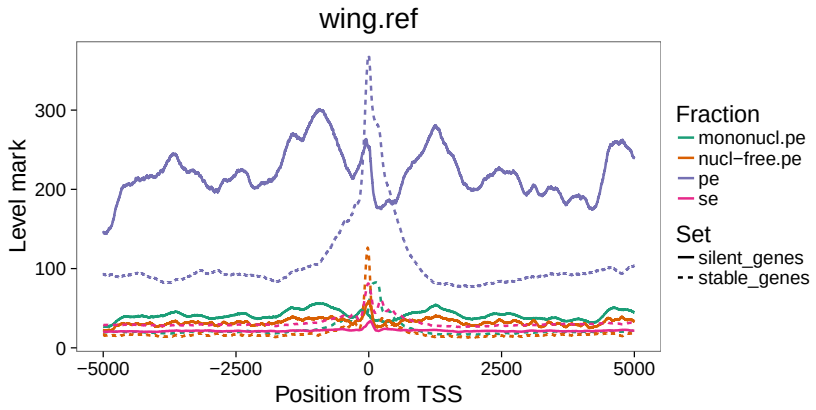


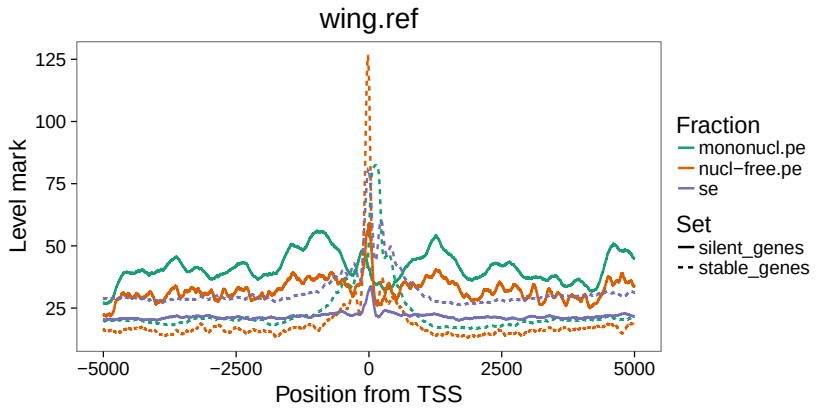


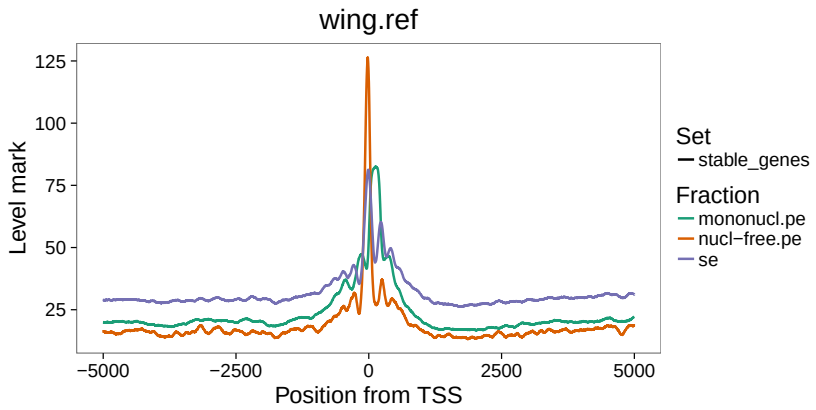
Wing 25h control and treatment NG stable regulated

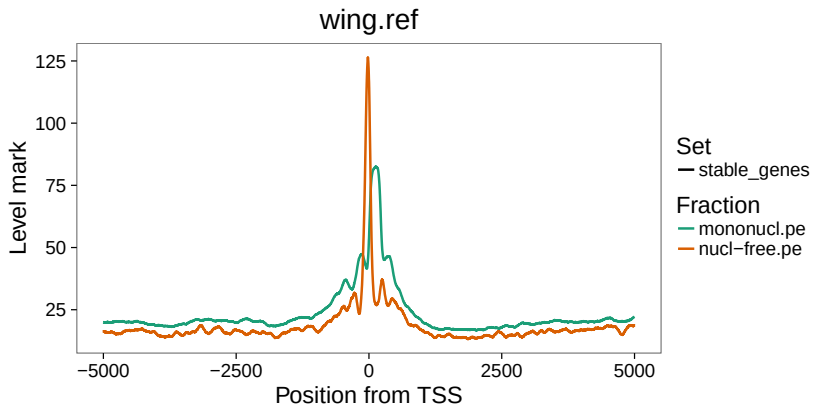
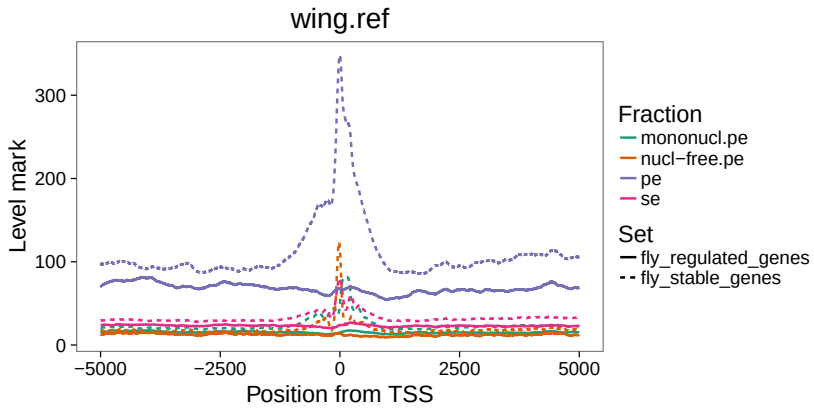
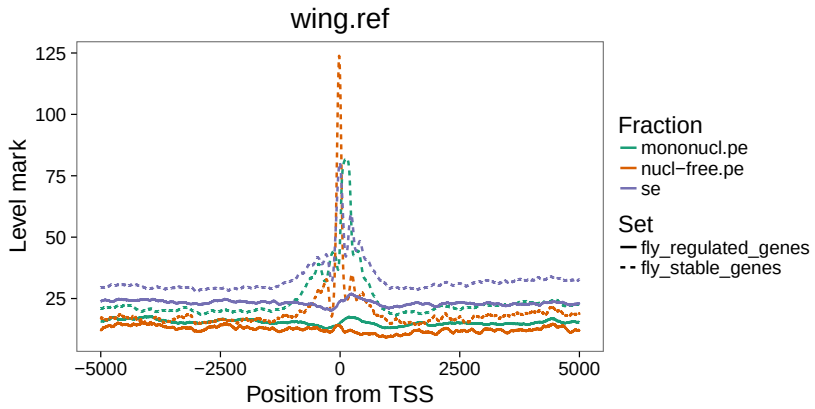
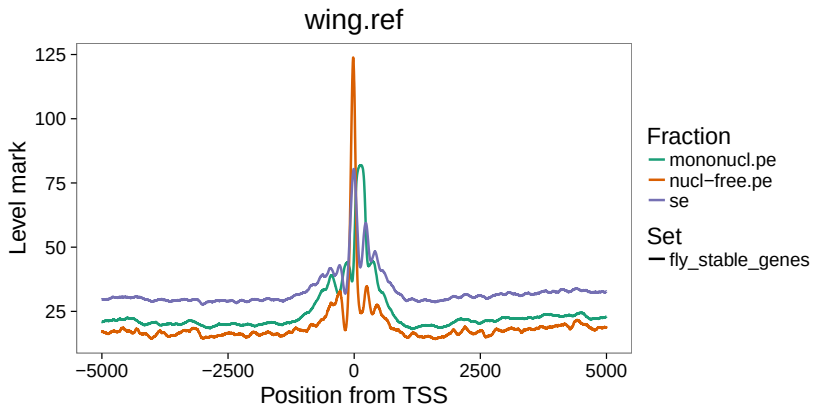
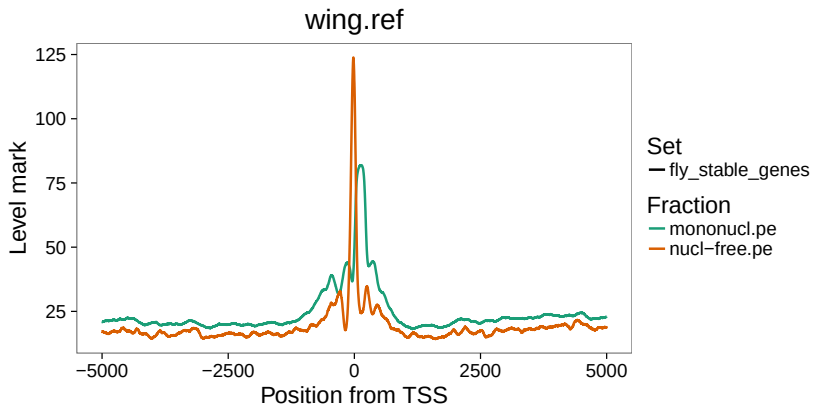


Wing reference









Wing reference - NG genes