

**1)HiC Explorer**

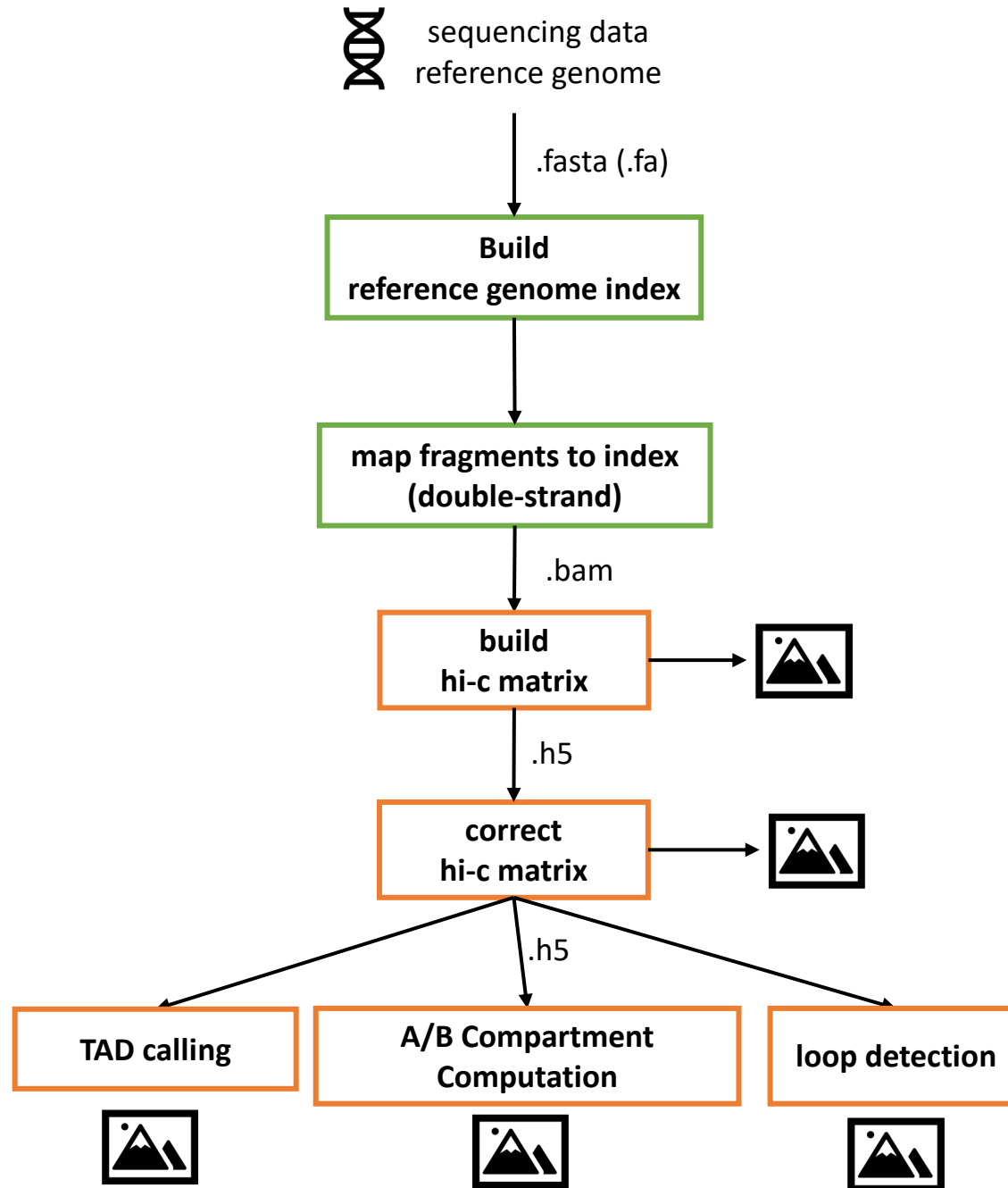
**2)HiC DC+**

**109753144**

**陳韋翰**

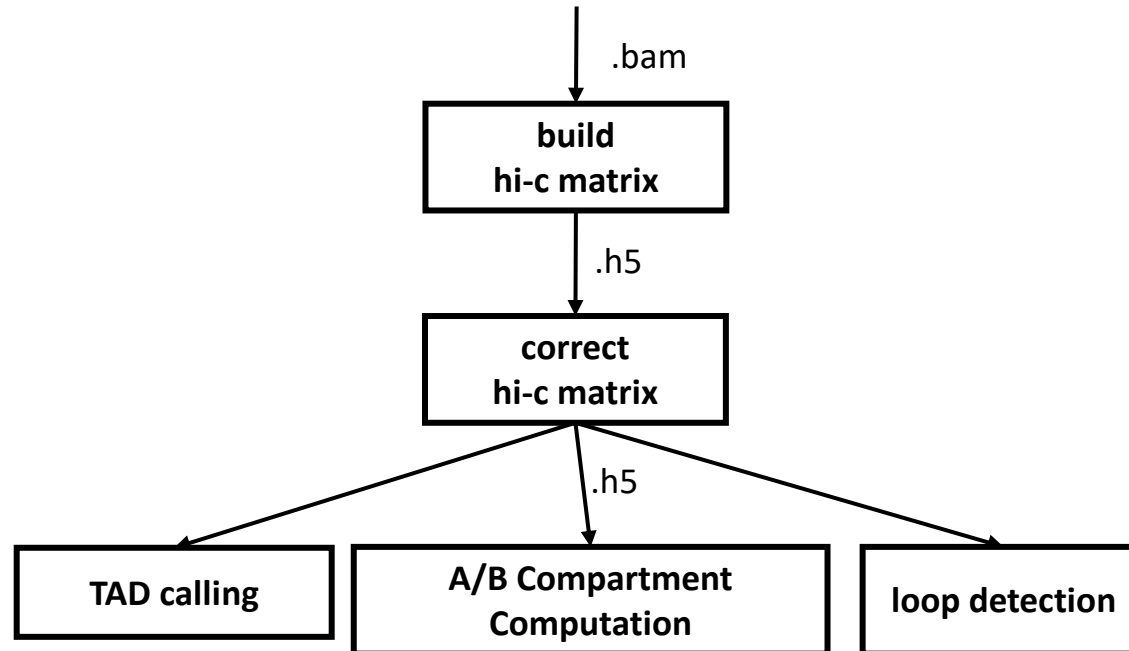
# HiCExplorer

*Drosophila melanogaster* (dm3)



# HiCExplorer

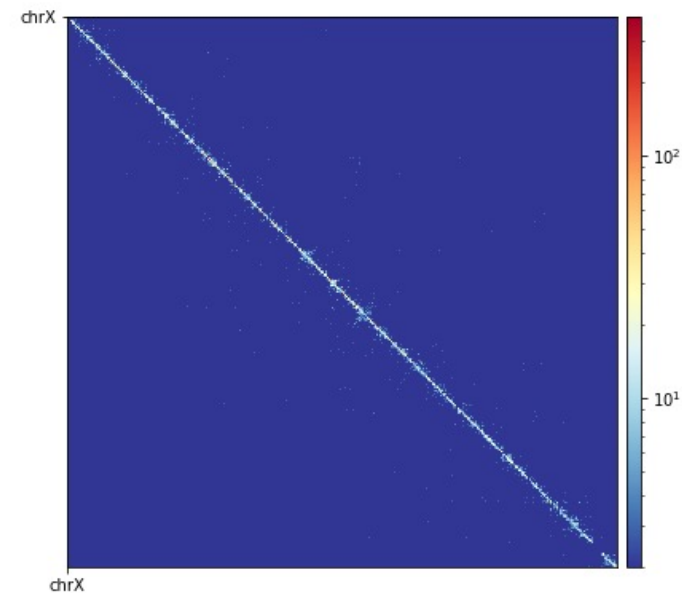
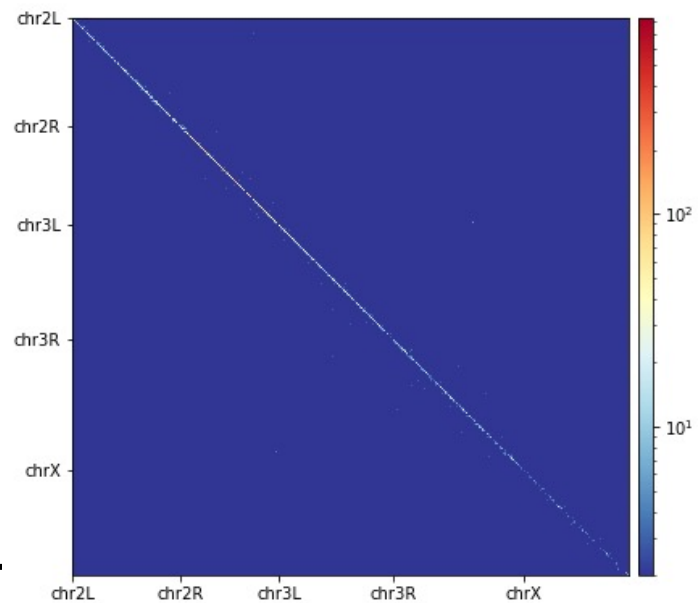
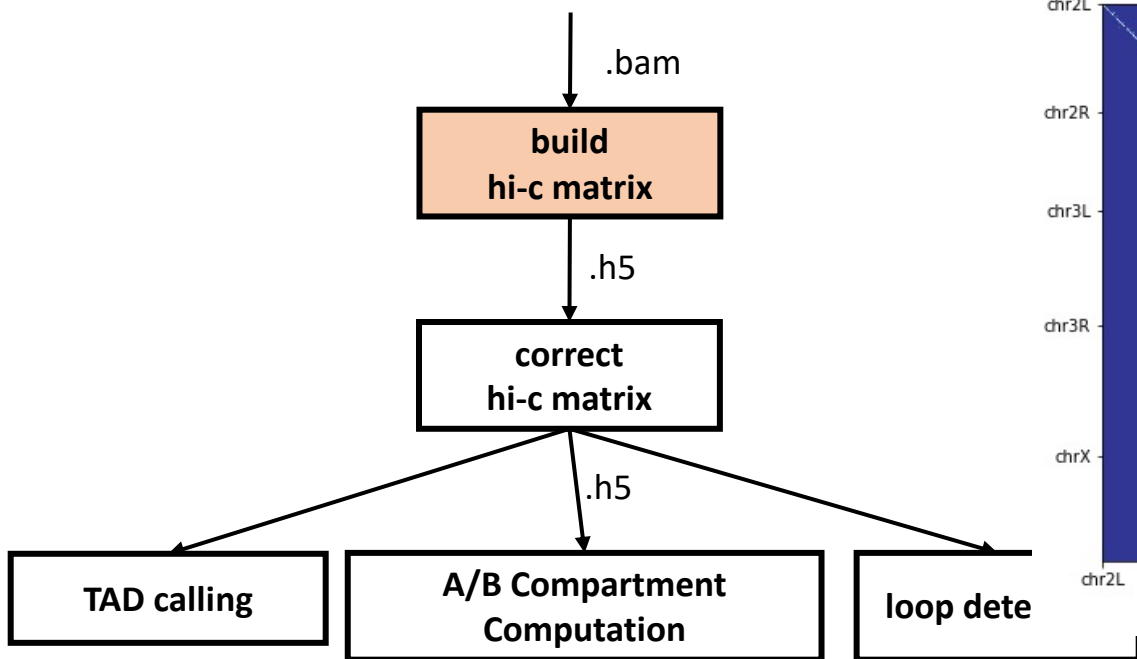
Drosophila melanogaster (dm3)



# HiCExplorer

Drosophila melanogaster (dm3)

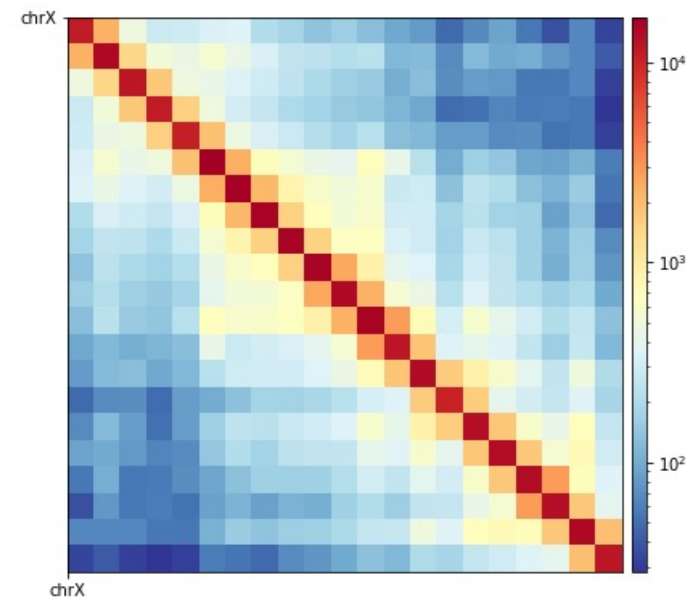
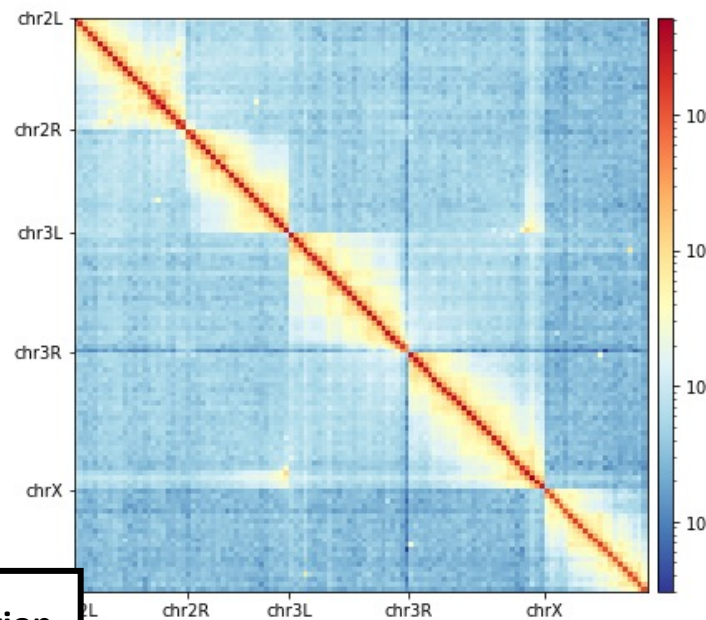
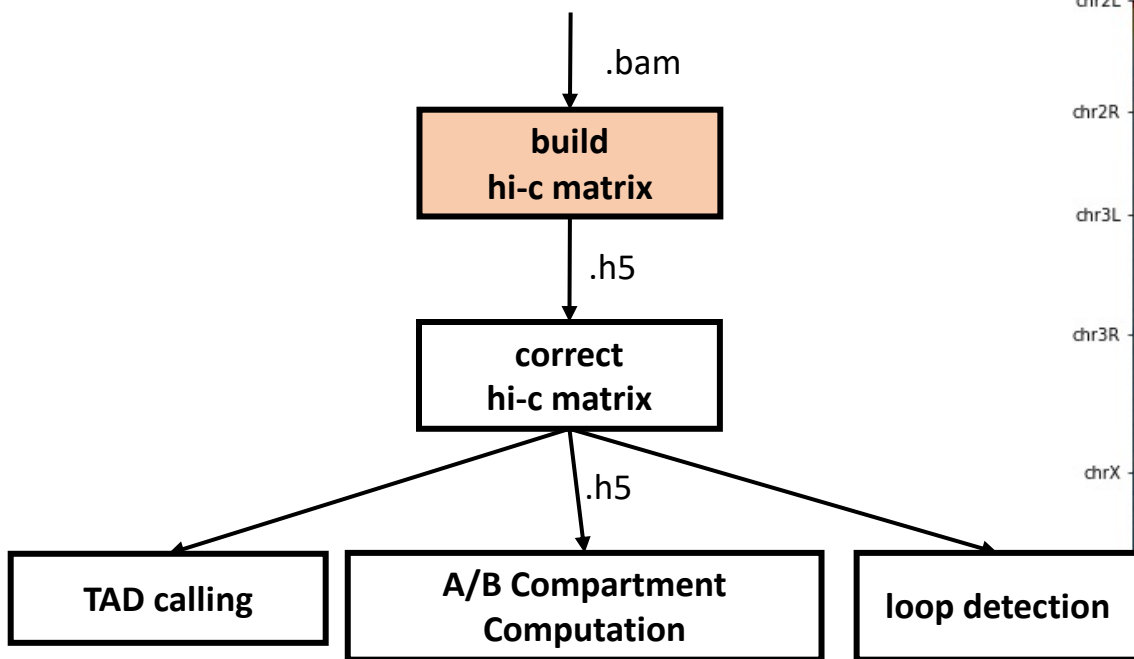
bin size : 10k



# HiCExplorer

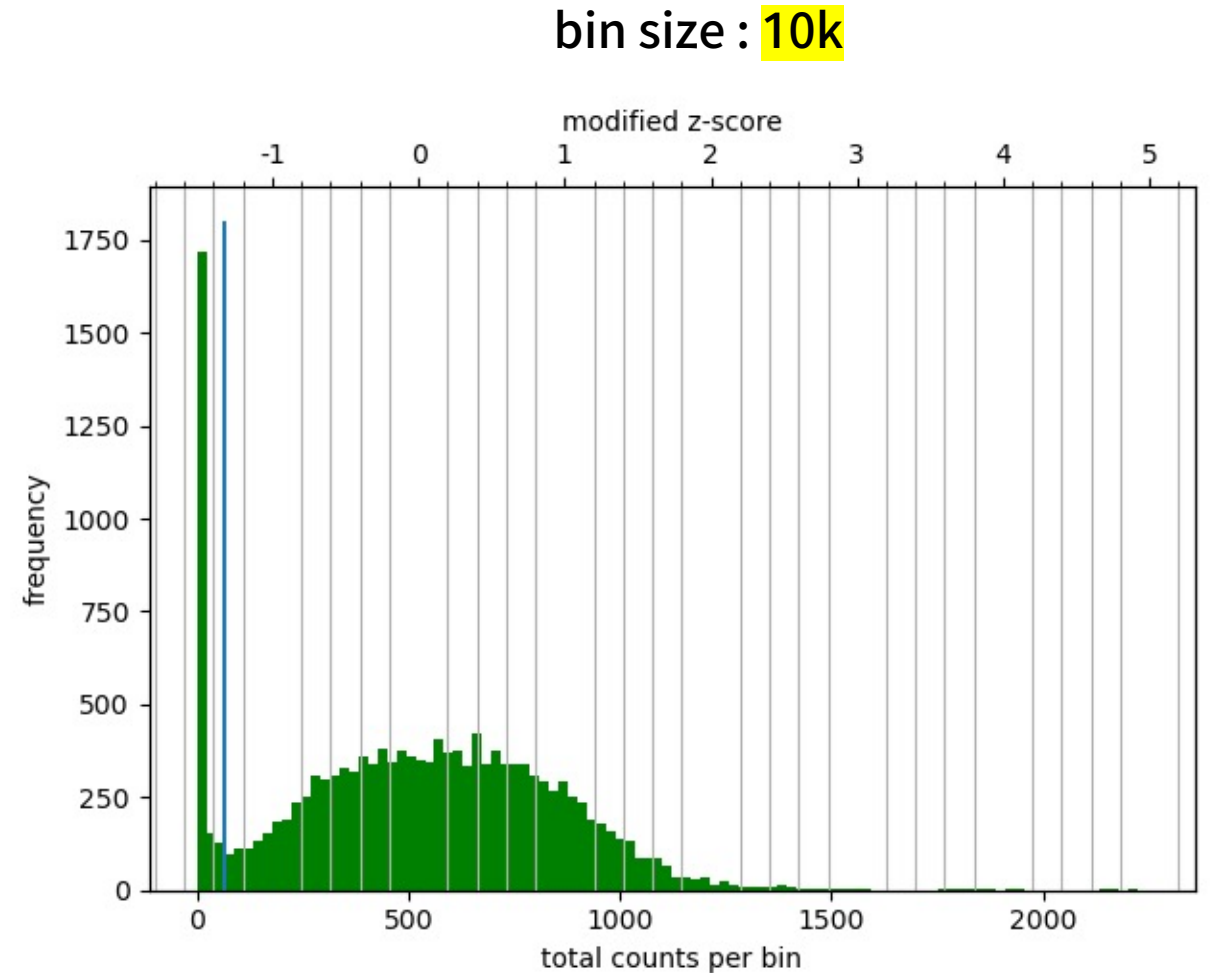
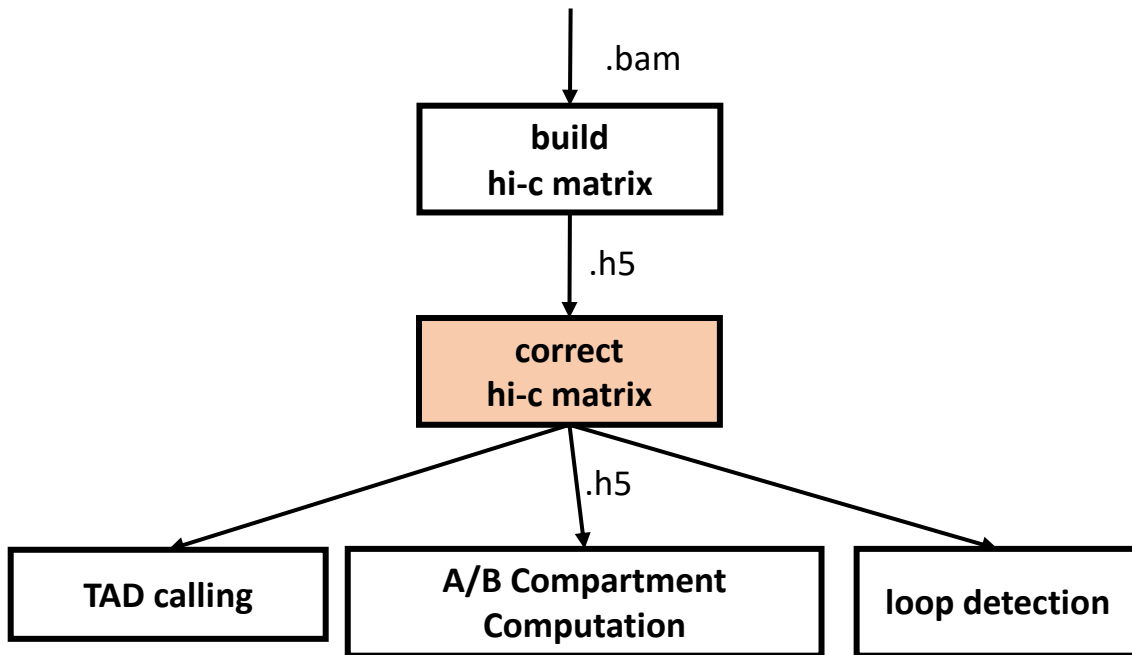
Drosophila melanogaster (dm3)

bin size : 1M



# HiCExplorer

Drosophila melanogaster (dm3)

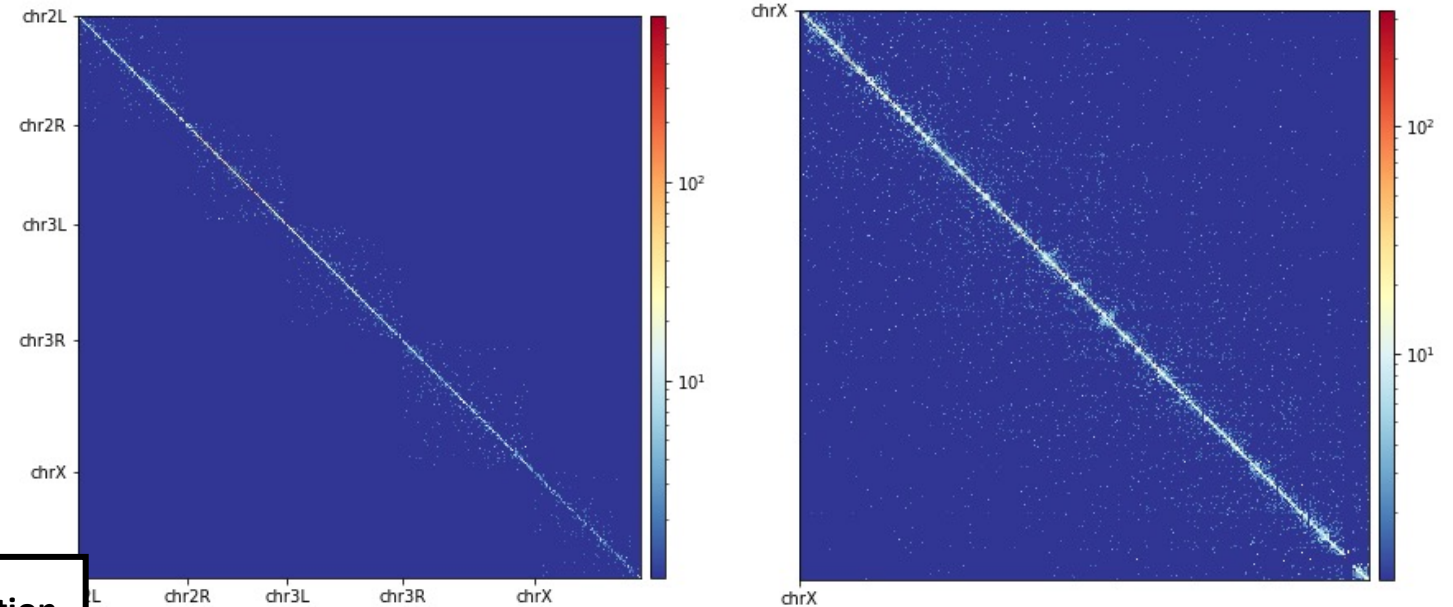
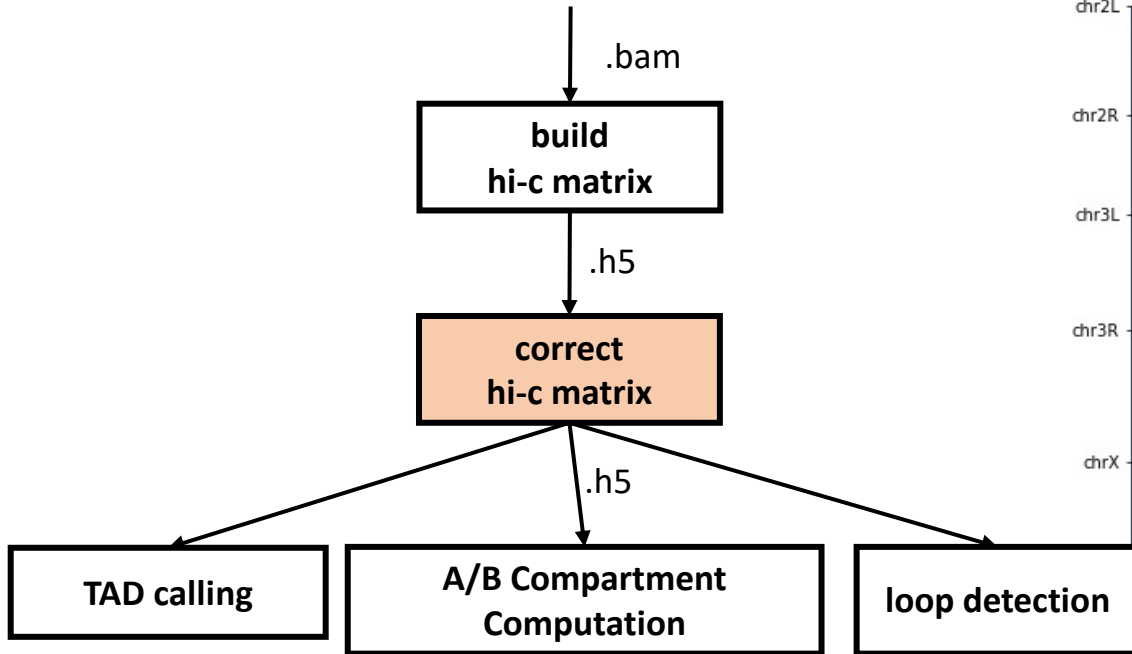


Remove bins of low coverage to -1.6  
Remove bins of large coverage to 1.8

# HiCExplorer

Drosophila melanogaster (dm3)

bin size : 10k

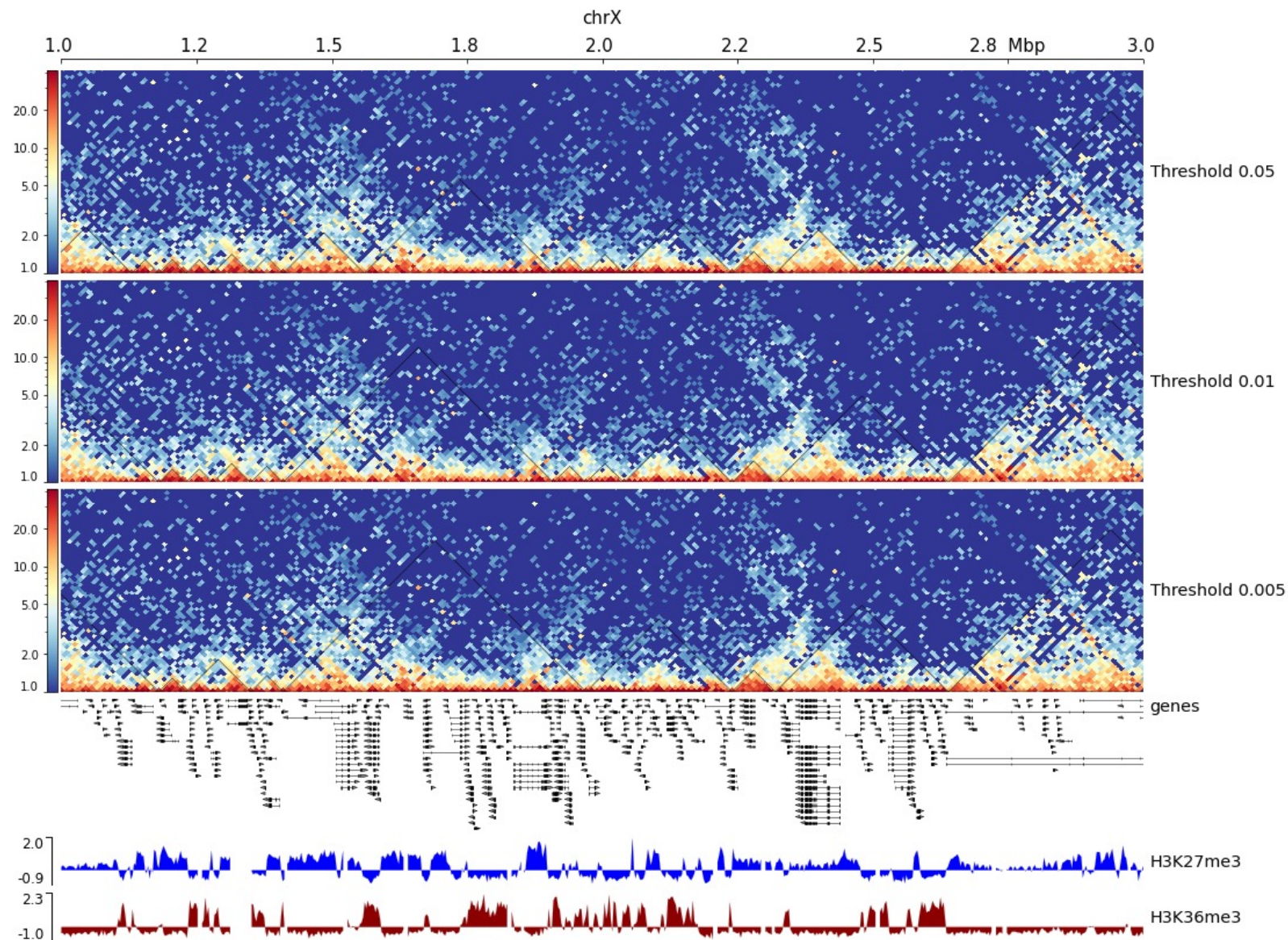
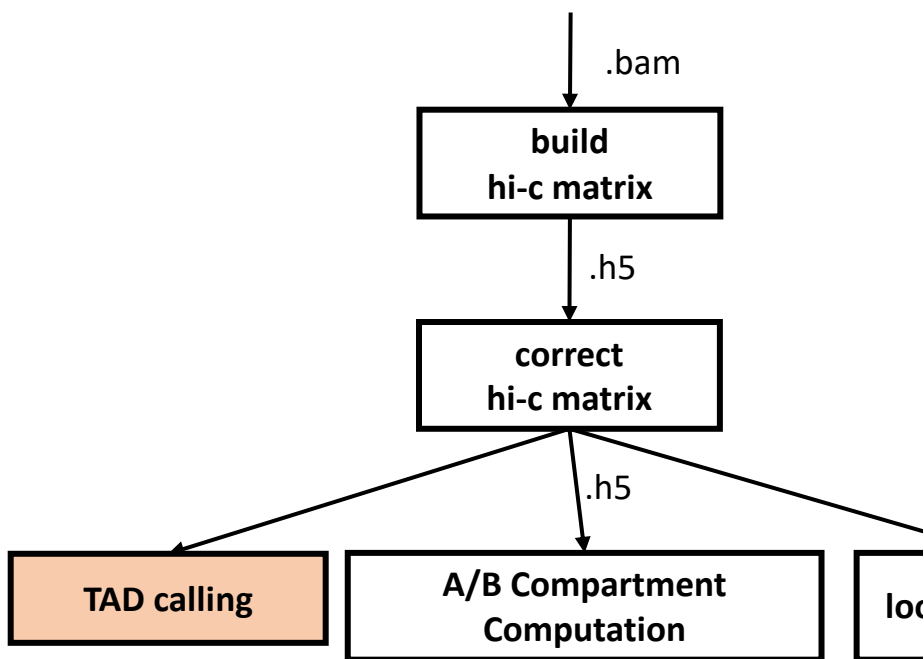


Remove bins of low coverage to -1.6  
Remove bins of large coverage to 1.8



# HiCExplorer

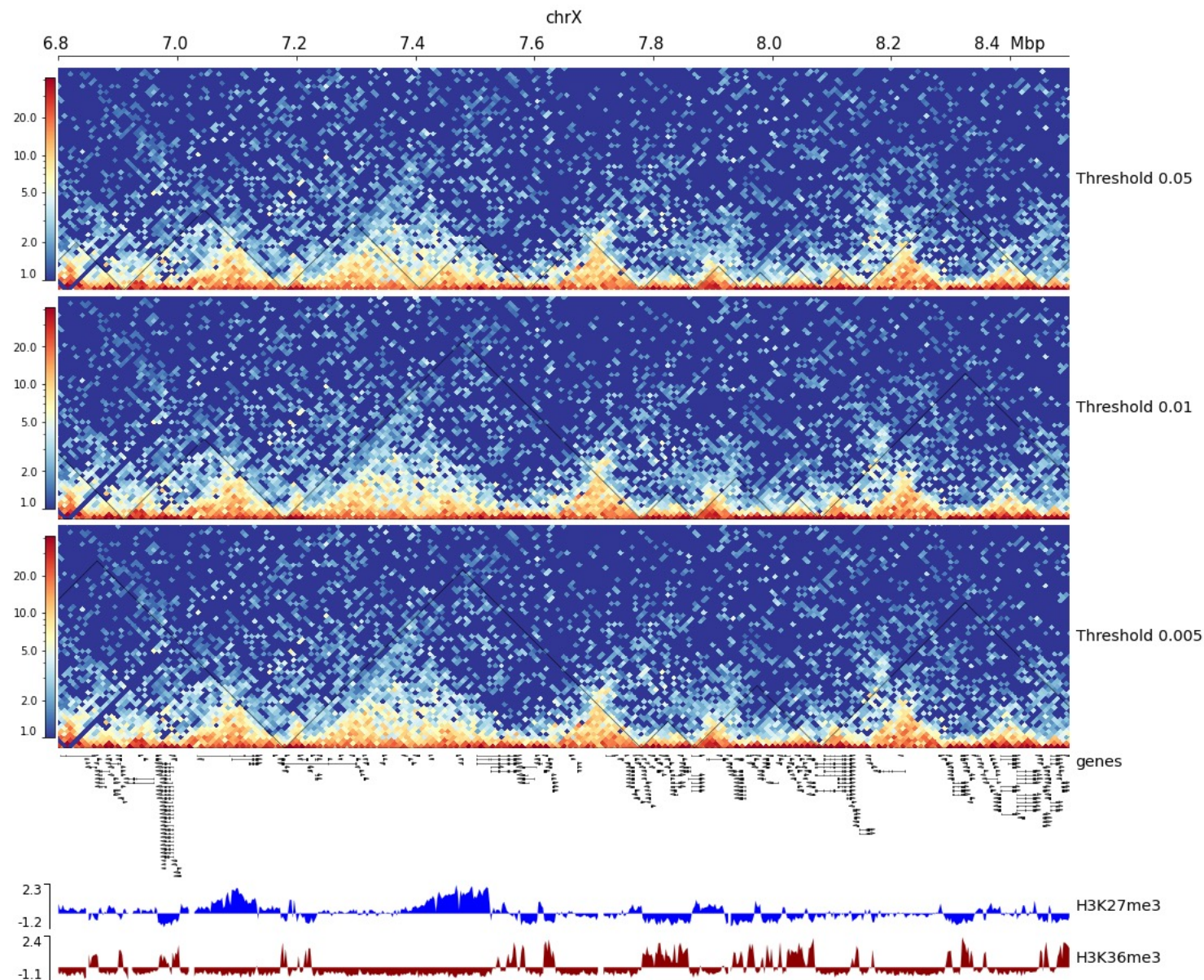
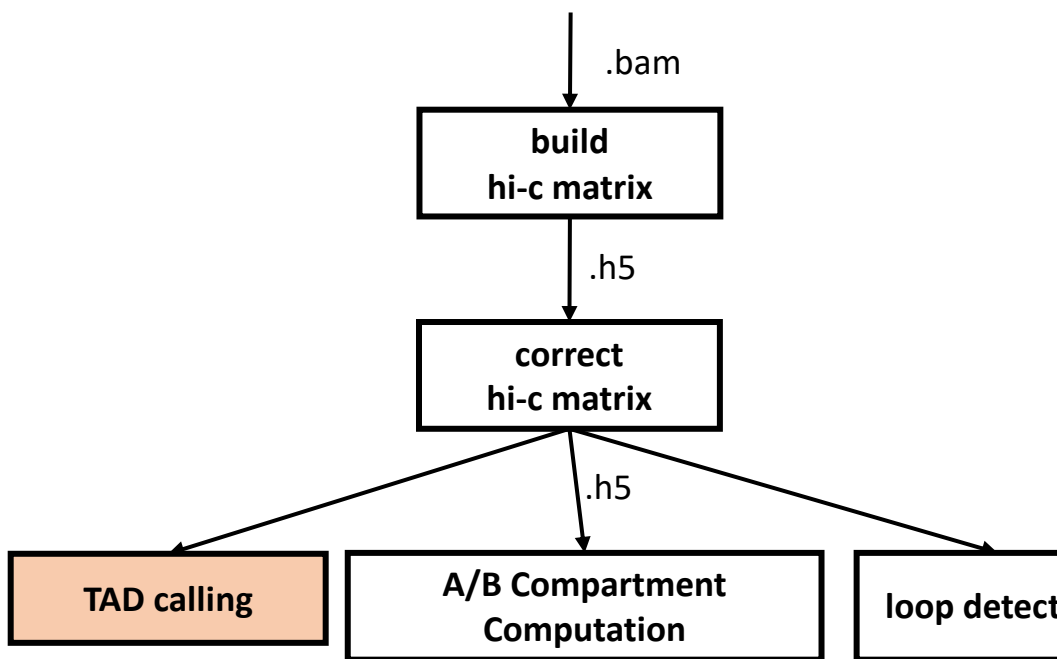
*Drosophila melanogaster* (dm3)





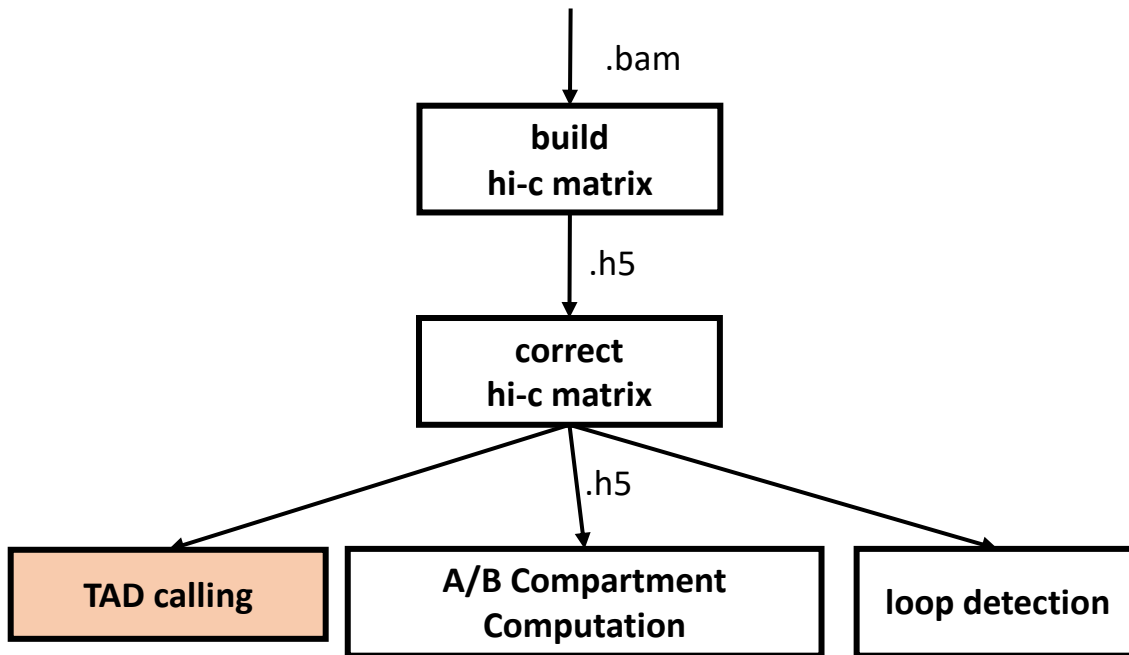
# HiCExplorer

*Drosophila melanogaster* (dm3)



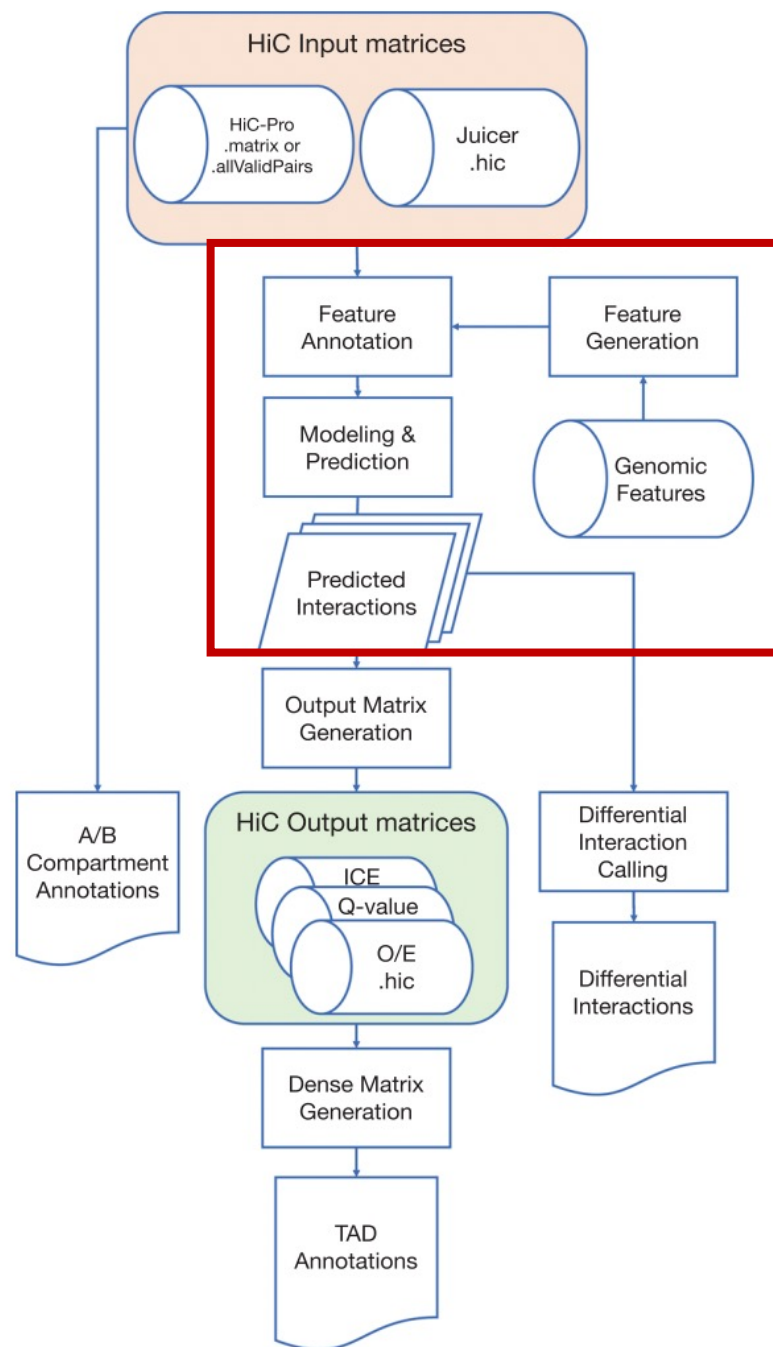
# HiCExplorer

Drosophila melanogaster (dm3)



```
49 [hic matrix]
50 file = ../contact_matrix/correct_10k_dm3.h5
51 title = Threshold 0.005
52 depth = 750000
53 transform = log1p
54 file_type = hic_matrix
55
56 [tads]
57 file = correct_10k_dm3_thr0.005_domains.bed
58 file_type = domains
59 border_color = black
60 color = none
61 overlay_previous = share-y
62
63 [spacer]
64 height = 0.2
65
66 [genes]
67 file = ../extend_data/dm3_genes.bed
68 title = genes
69 color = black
70 height = 4
71 labels = true
72 file_type = bed
73
74 [spacer]
75 height = 0.2
76
77 [bigwig]
78 file = ../extend_data/H3K27me3.bw
79 title = H3K27me3
80 color = blue
81 height = 1.5
82 file_type = bigwig
```

# HiC DC+



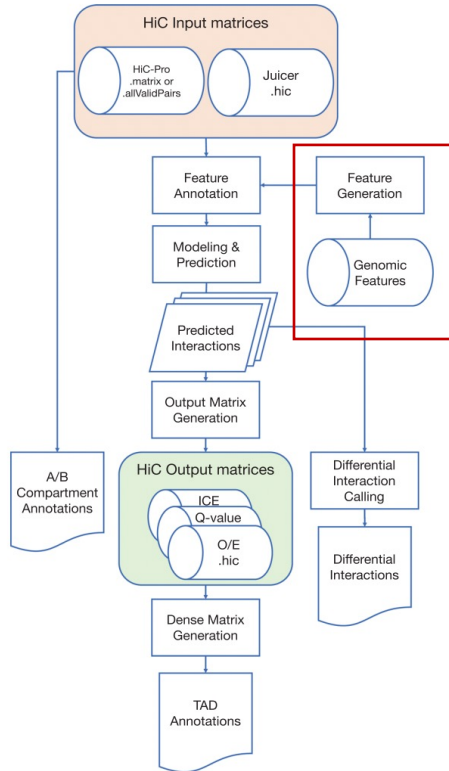
call significant interactions

GSE63525 (hg19)



# HiC DC+

GSE63525 (hg19)



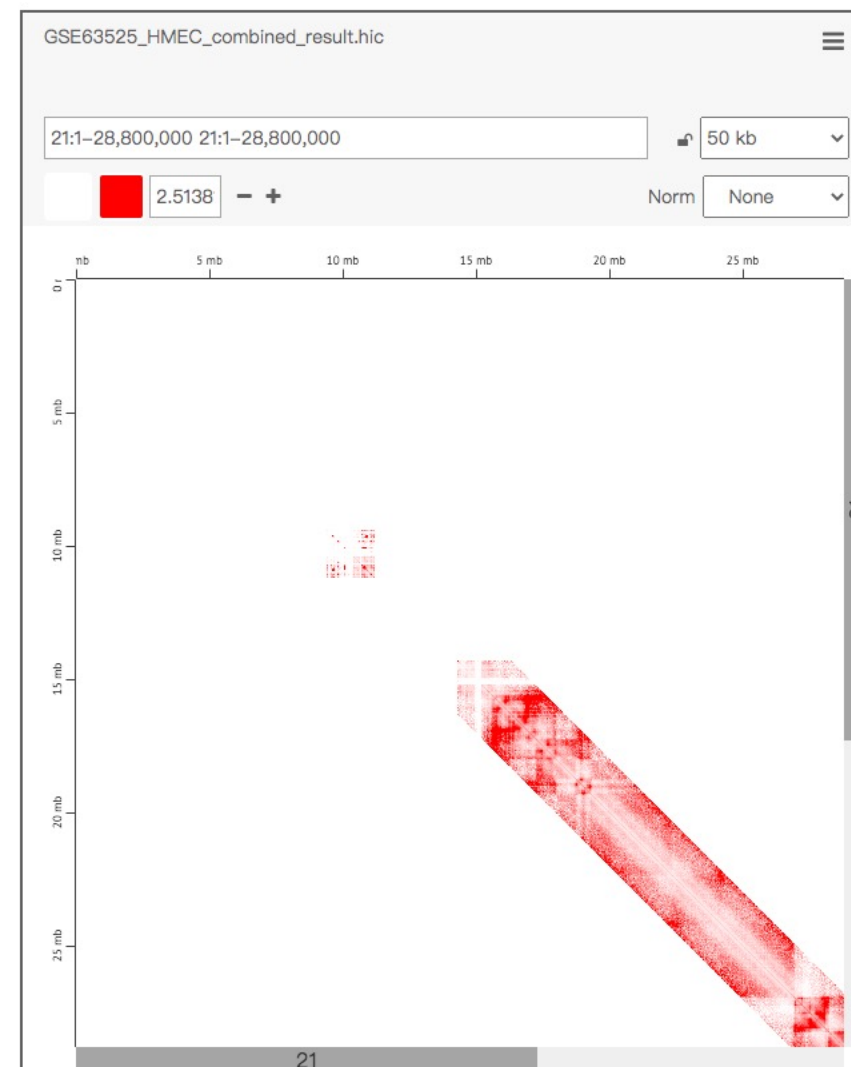
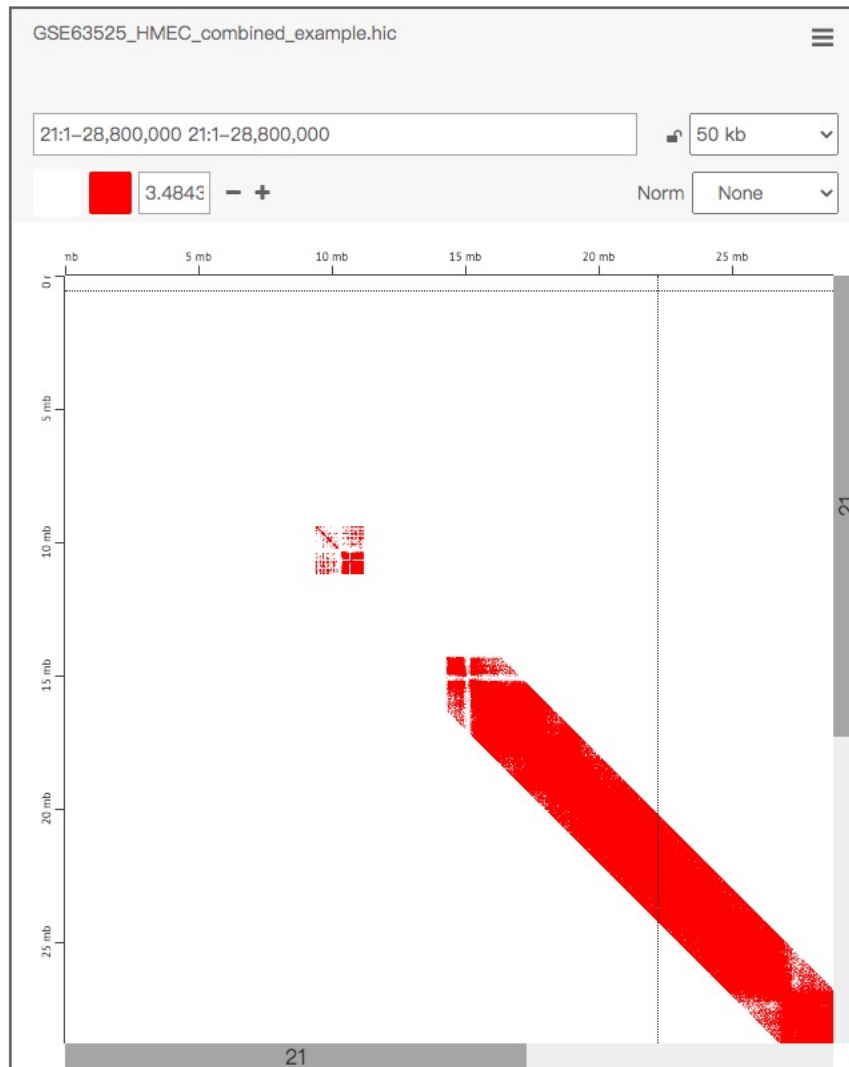
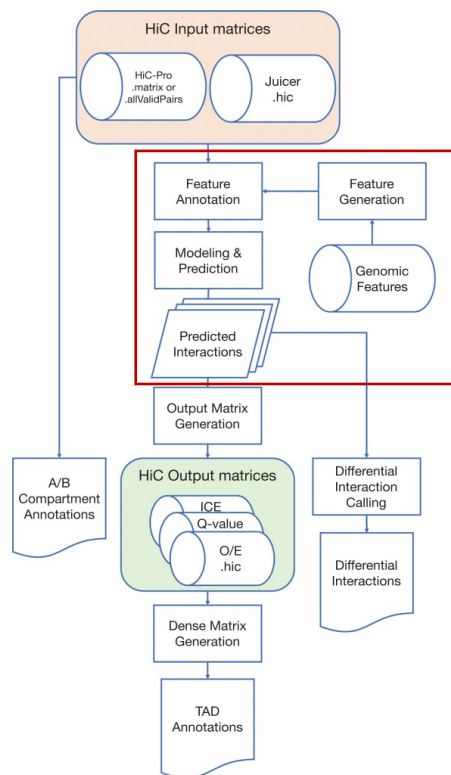
	bins	gc	map	len
1:	chr22-49850001-49900000	0.4833	0	49875
2:	chr22-49900001-49950000	0.5126	0	47521
3:	chr22-49950001-50000000	0.5139	0	46220
4:	chr22-50000001-50050000	0.5472	0	48270
5:	chr22-50050001-50100000	0.5241	0	49289
6:	chr22-50100001-50150000	0.5014	0	49584
7:	chr22-50150001-50200000	0.5466	0	48171
8:	chr22-50200001-50250000	0.5232	0	47970
9:	chr22-50250001-50300000	0.4675	0	49242
10:	chr22-50300001-50350000	0.6117	0	41993
11:	chr22-50350001-50400000	0.1997	0	49875
12:	chr22-50400001-50450000	0.3623	0	47683
13:	chr22-50450001-50500000	0.5526	0	49544
14:	chr22-50500001-50550000	0.5126	0	49105
15:	chr22-50550001-50600000	0.4790	0	49875
16:	chr22-50600001-50650000	0.6103	0	49700
17:	chr22-50650001-50700000	0.5927	0	49531
18:	chr22-50700001-50750000	0.6473	0	49469
19:	chr22-50750001-50800000	0.5409	0	49669
20:	chr22-50800001-50818468	0.4792	0	7806

**construct\_features :**

finds all restriction enzyme cutsites of a given genome and genome version and computes **GC content**, **mappability** (if a relevant .bigWig file is provided) and **effective fragment length** for uniform bin

# HiC DC+

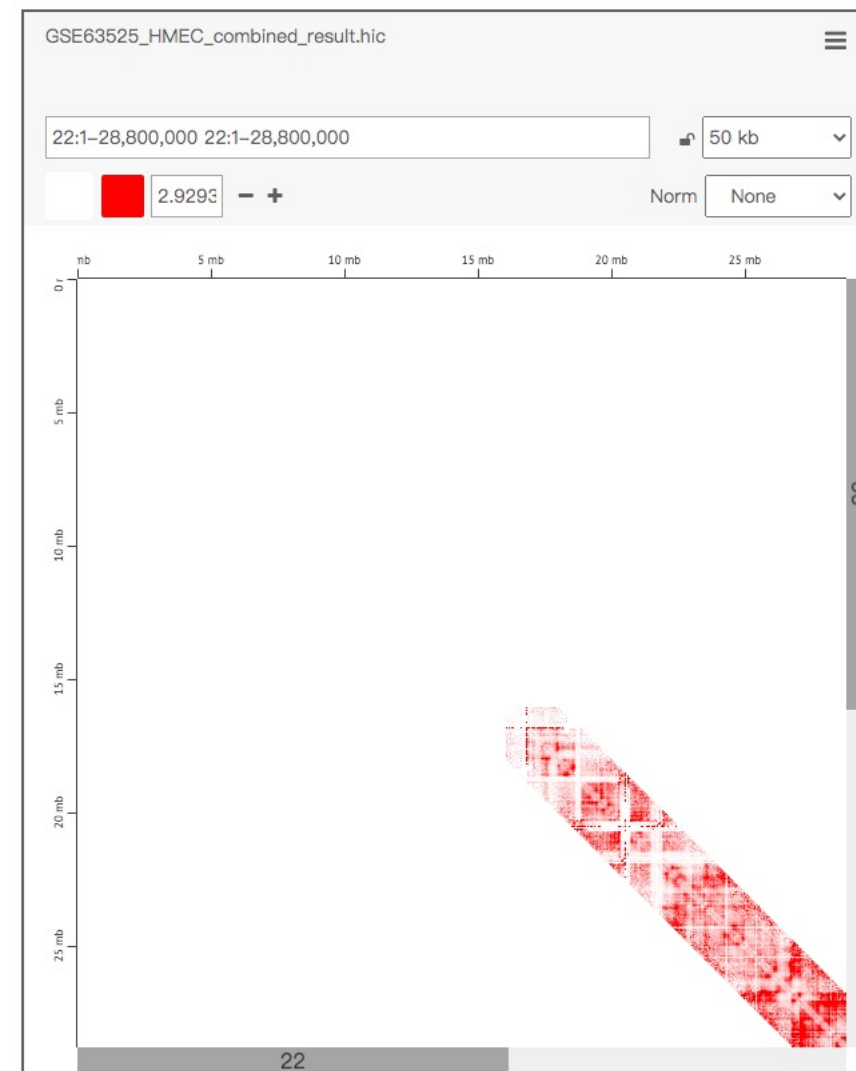
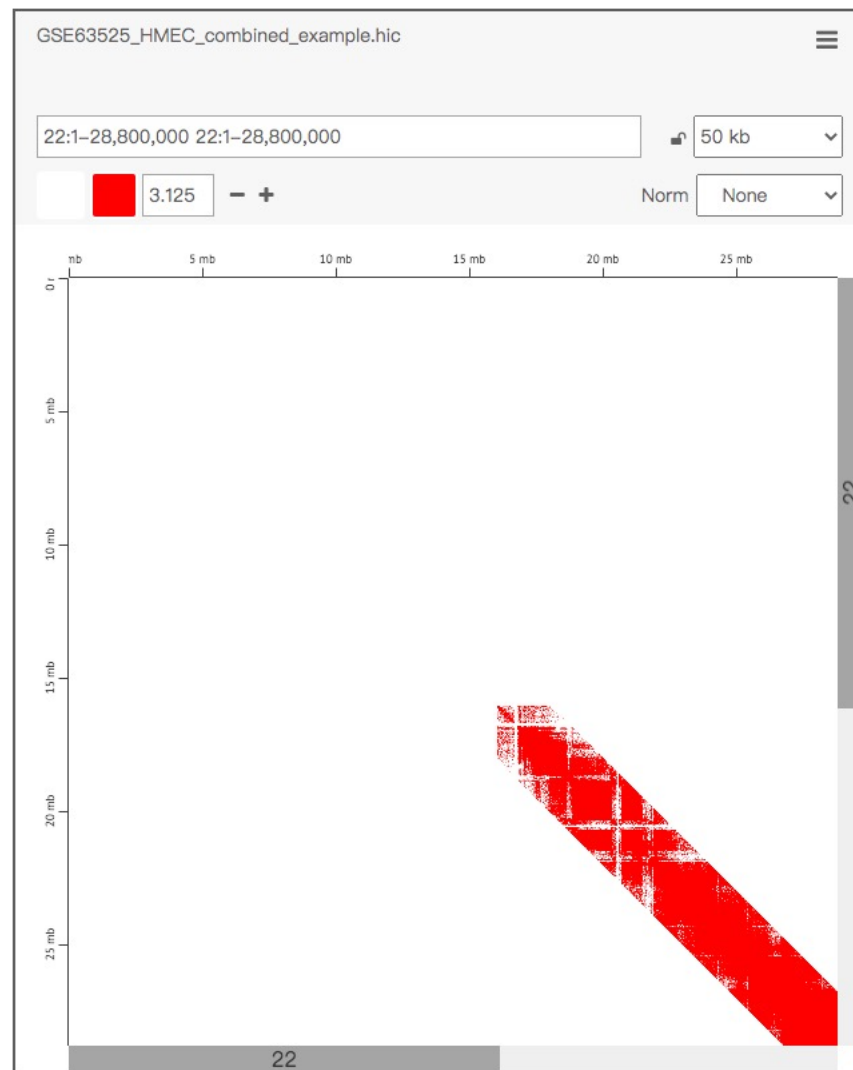
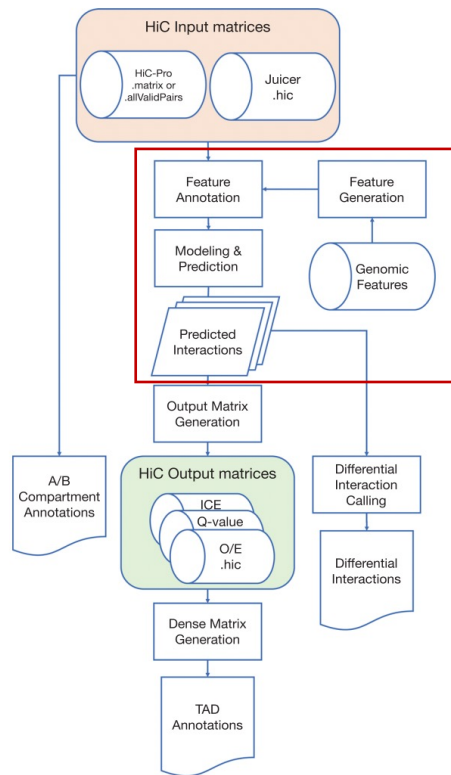
GSE63525 (hg19)



chr21

# HiC DC+

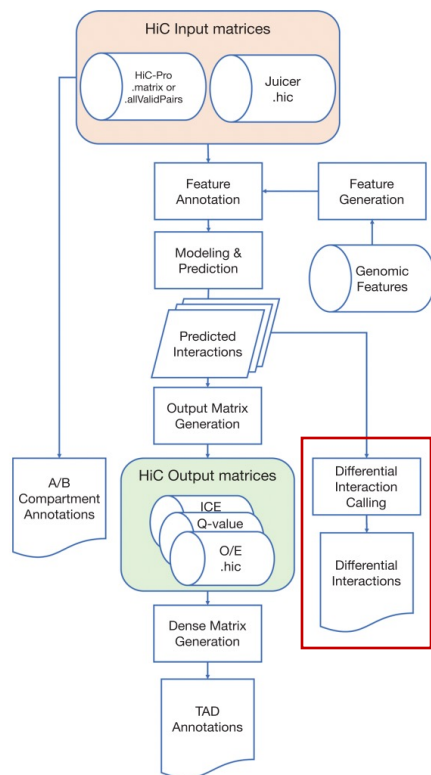
GSE63525 (hg19)



chr22

# HiC DC+

GSE131651 (hg38)



## diff\_analysis\_example

diff\_chr21\_PCA.pdf

diff\_chr22\_PCA.pdf

diff\_resTKOoverNSD2\_chr21.txt.gz

diff\_resTKOoverNSD2\_chr22.txt.gz

dispersionplot.pdf

geomean\_sizefactors\_chr21.pdf

geomean\_sizefactors\_chr22.pdf

plotMA\_TKOoverNSD2\_chr21.pdf

plotMA\_TKOoverNSD2\_chr22.pdf

sizefactors\_chr21.pdf

sizefactors\_chr22.pdf



# HiC DC+

