

## Dataset stats

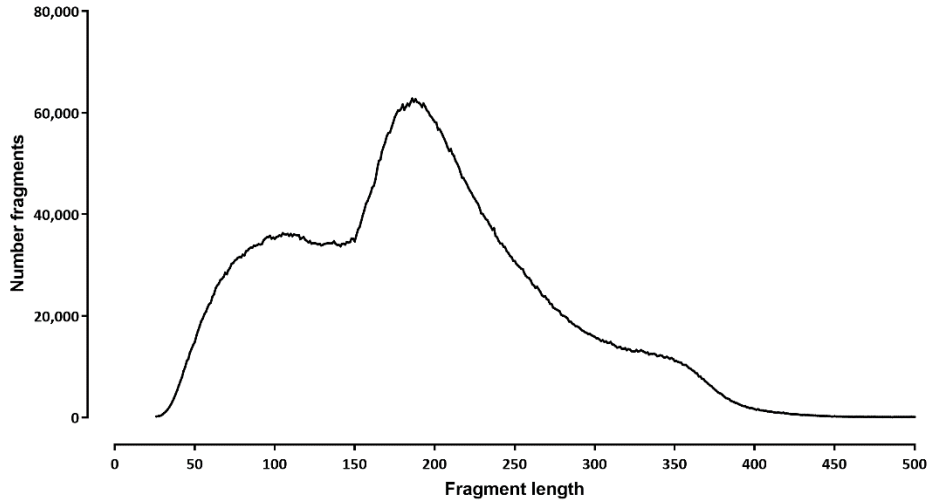
Species	#	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 noBL NumPeaks	MACS2 noBL RPM	Read Length	Unique	Raw fragments	Alignment fraction
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_ACTTGA	0.74	53,519	315,967	53,049	306,739	2x25	20,696,852	13,310,406	0.78
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_TTAGGC	0.83	45,605	297,427	45,212	288,160	2x25	18,838,322	12,740,316	0.74
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_ATCACG	0.97					2x25	16,680,248	9,917,125	0.84
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_CAGATC	0.97					2x25	16,001,638	9,574,535	0.84
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_ACTTGA	0.75	37,499	292,348	37,356	284,000	2x25-maxFL120	4,626,646	13,310,406	0.17
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_TTAGGC	0.84	32,721	264,161	32,580	255,956	2x25-maxFL120	3,682,142	12,740,316	0.14
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_ATCACG	0.98					2x25-maxFL120	1,090,998	9,917,125	0.06
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_CAGATC	0.98					2x25-maxFL120	2,235,440	9,574,535	0.12
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_ACTTGA	0.74	40,591	304,251	40,212	295,672	2x25-minFL150	14,080,428	13,310,406	0.53
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-CTCF_AUPT0_L1_TTAGGC	0.84	36,279	286,315	35,953	277,712	2x25-minFL150	13,431,296	12,740,316	0.53
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_ATCACG	0.97					2x25-minFL150	14,851,214	9,917,125	0.75
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test1-H3K27me3_ATY4L_L1_CAGATC	0.97					2x25-minFL150	12,673,924	9,574,535	0.66

### Notes:

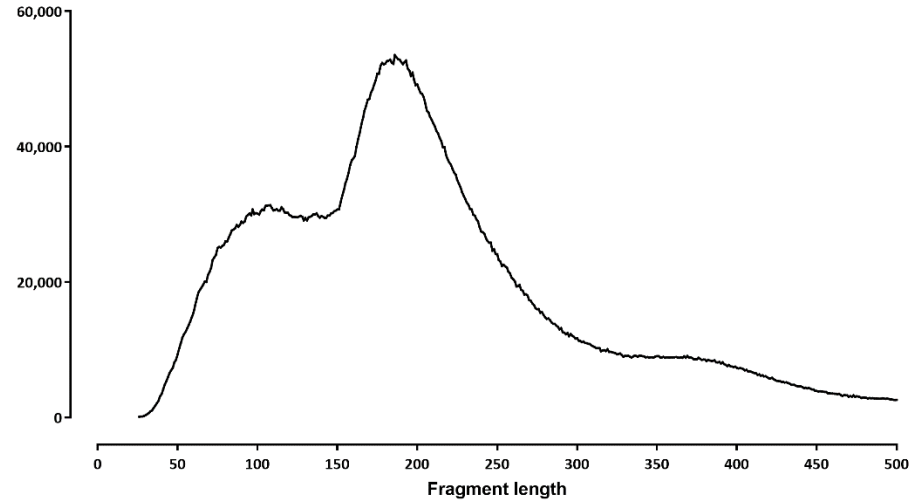
1. in a number of external CUT&RUN datasets we have observed a huge fraction of reads coming from blacklisted regions. This is not the case here, which is good
2. “maxFL120” means including only fragments shorter than 120bp
3. “minFL150” means including only fragments longer than 150bp

# Fragment length distribution:

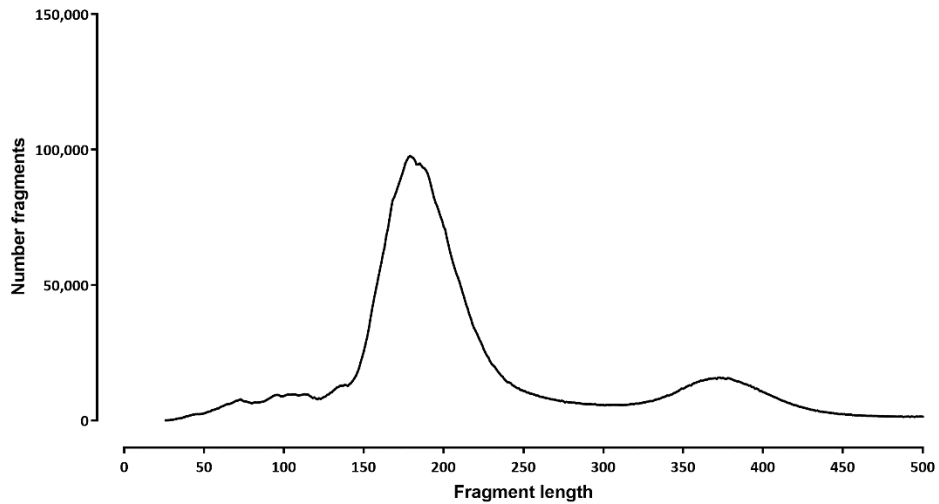
SCGPM\_CUT-RUN-test1-CTCF\_AUPT0\_L1\_ACTTGA



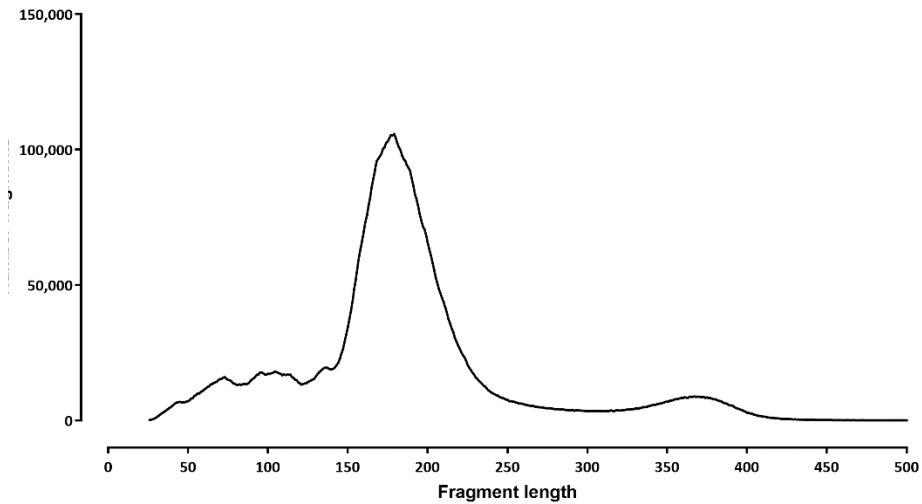
SCGPM\_CUT-RUN-test1-CTCF\_AUPT0\_L1\_TTAGGC



SCGPM\_CUT-RUN-test1-H3K27me3\_ATY4L\_L1\_ATCACG



SCGPM\_CUT-RUN-test1-H3K27me3\_ATY4L\_L1\_CAGATC



## Overlap with ChIP-seq peaks and CTCF motifs:

**number peaks**

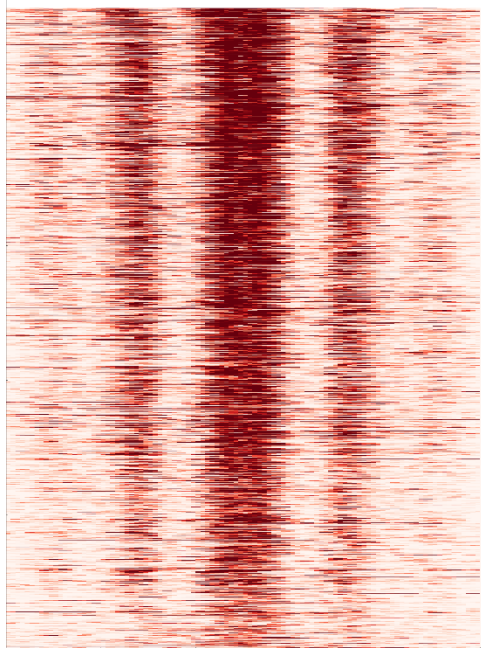
	ChIP peak		no ChIP peak	
	motif	no motif	motif	no motif
ENCODE A549 CTCF	39,669	7,106	-	-
ACTTGA	29,650	5,376	5,325	13,168
ACTTGA.maxFL120bp	20,710	3,098	2,048	11,643
ACTTGA.minFL150bp	24,321	5,645	3,276	7,349
TTAGGC	28,644	4,318	4,283	8,360
TTAGGC.maxFL120bp	18,679	2,822	1,770	9,450
TTAGGC.minFL150bp	23,663	4,791	2,796	5,029

**fraction**

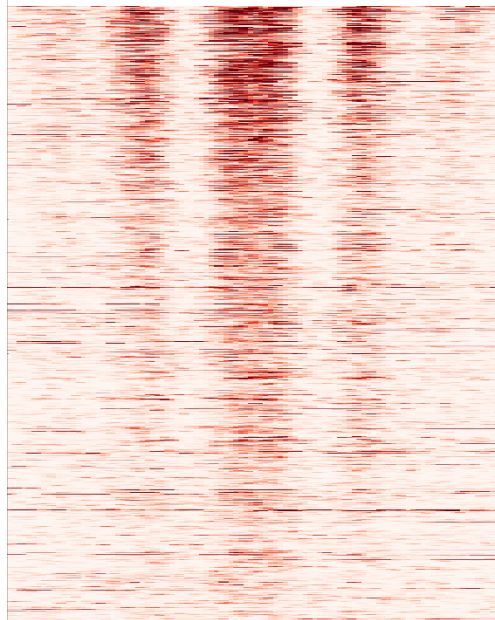
	ChIP peak	no ChIP peak	ChIP peak		no ChIP peak	
			motif	no motif	motif	no motif
ENCODE A549 CTCF	1.00	0.00	0.85	0.15	n/a	n/a
ACTTGA	0.65	0.35	0.85	0.15	0.29	0.71
ACTTGA.maxFL120bp	0.63	0.37	0.87	0.13	0.15	0.85
ACTTGA.minFL150bp	0.74	0.26	0.81	0.19	0.31	0.69
TTAGGC	0.72	0.28	0.87	0.13	0.34	0.66
TTAGGC.maxFL120bp	0.66	0.34	0.87	0.13	0.16	0.84
TTAGGC.minFL150bp	0.78	0.22	0.83	0.17	0.36	0.64

## Overlap with ChIP-seq peaks, profile around peaks, ACTTGA

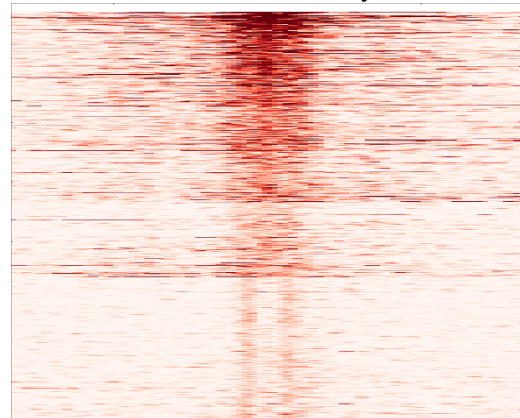
common sites



ChIP-only sites



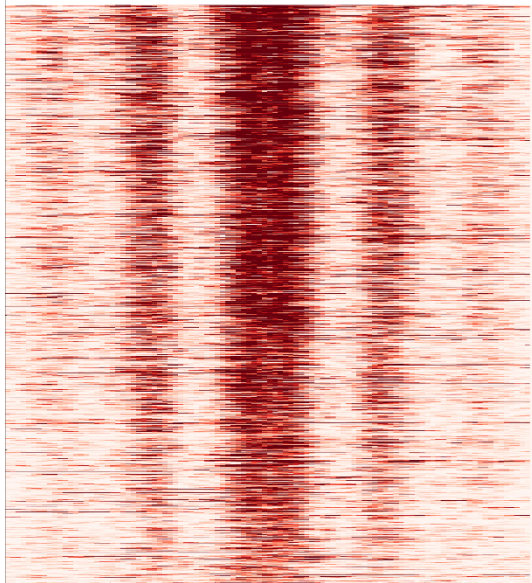
CUT&RUN only sites



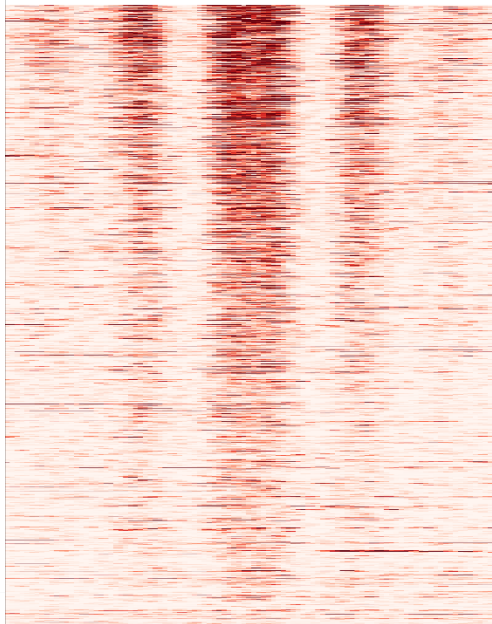
Note: usually the ChIP-only sites are about the same proportion but they show very little signal in CUT&RUN. Here it seems to be more of an issue with having to optimized the peak calling

# Overlap with ChIP-seq peaks, profile around peaks, TTAGGC

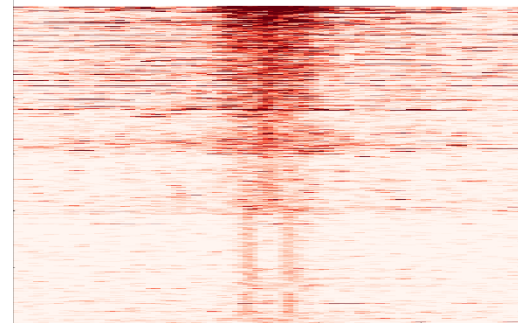
common sites



ChIP-only sites



CUT&RUN only sites

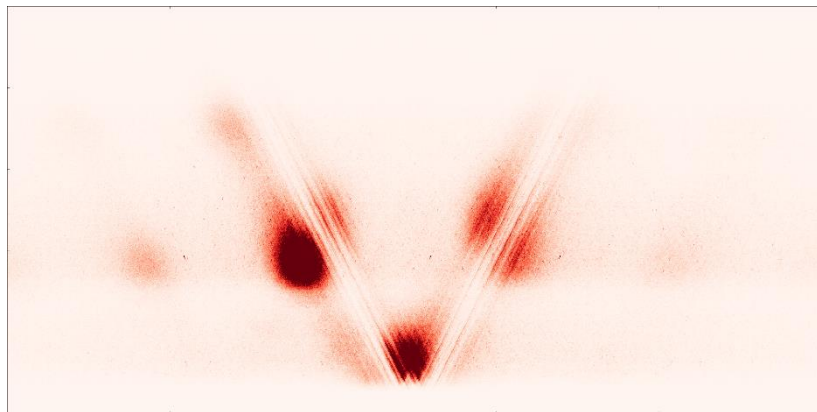


CTCF ACTTGA

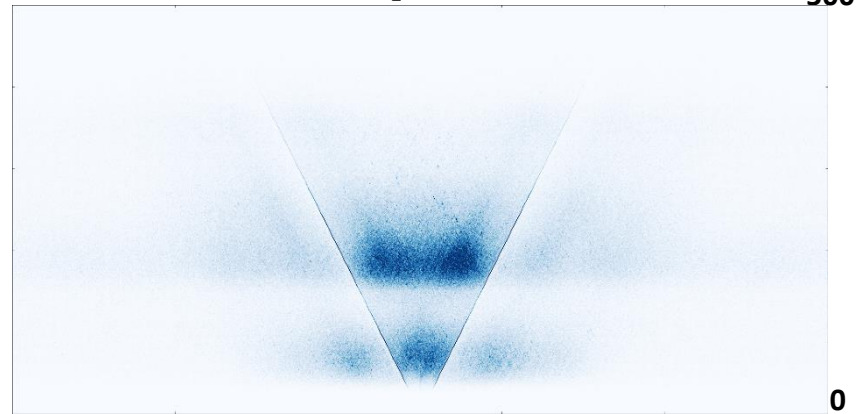
motif-centered

MACS2 peak call-centered

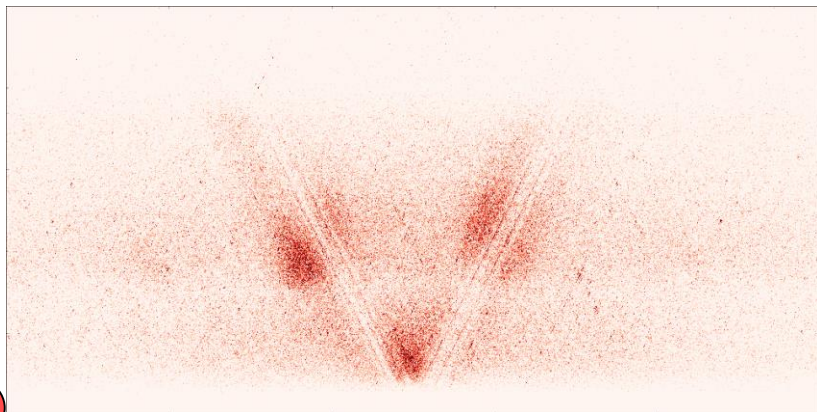
ChIP-common sites  
with motif



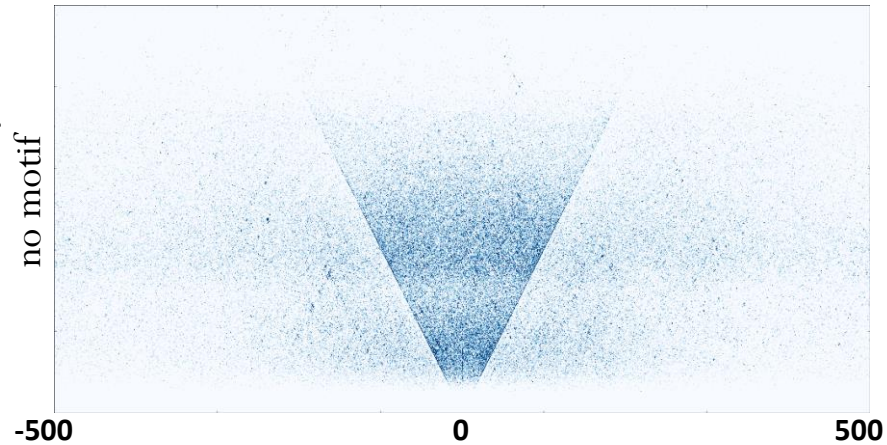
ChIP-common sites  
with motif



CUTnRUN-only sites  
with motif



CUTnRUN-only sites  
no motif

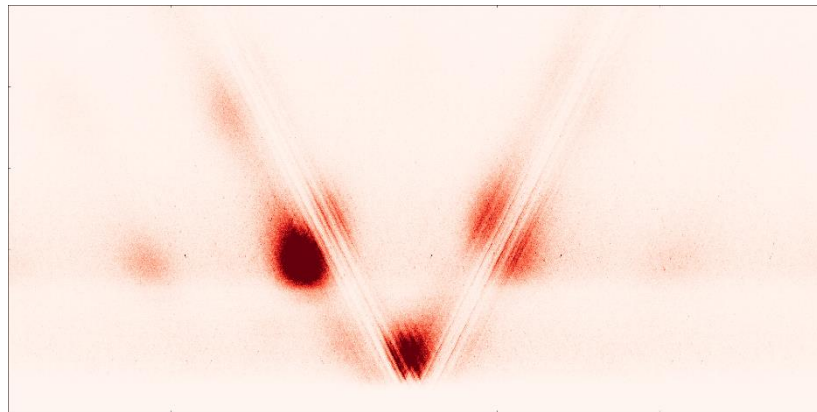


# CTCF TTAGGC

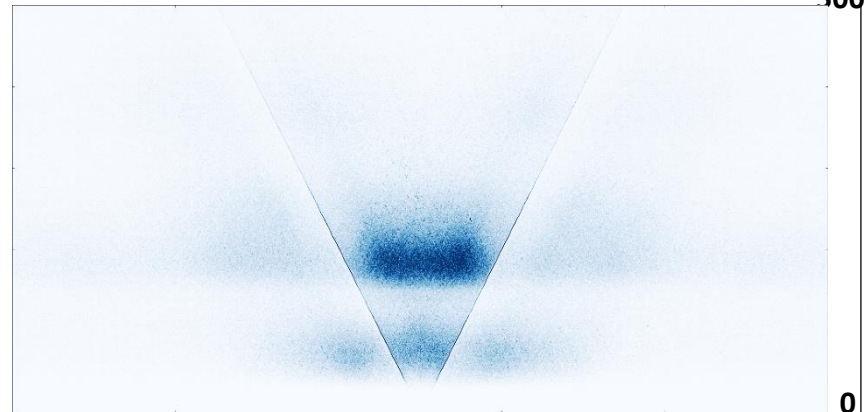
motif-centered

MACS2 peak call-centered

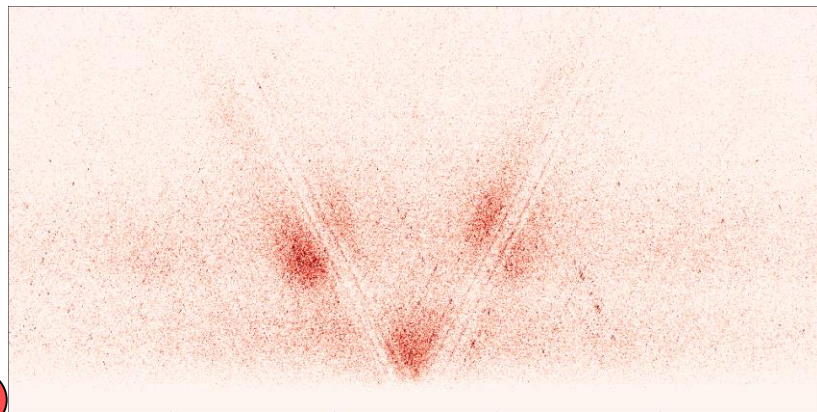
ChIP-common sites  
with motif



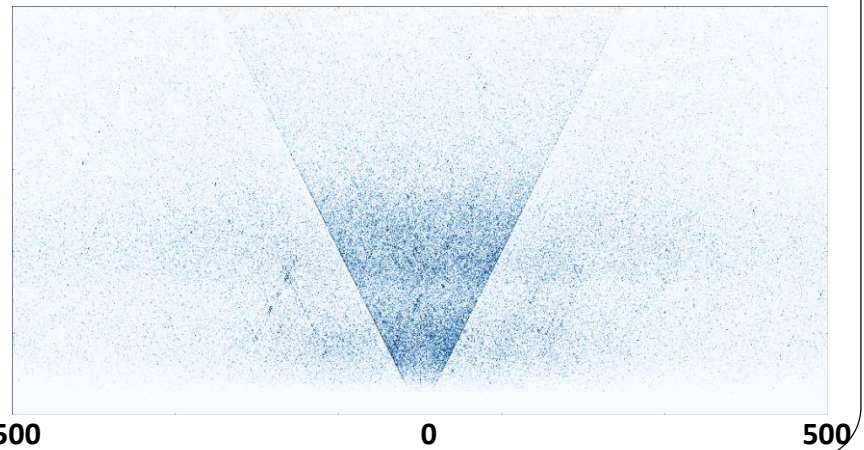
ChIP-common sites  
with motif



CUTnRUN-only sites  
with motif



CUTnRUN-only sites  
no motif



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