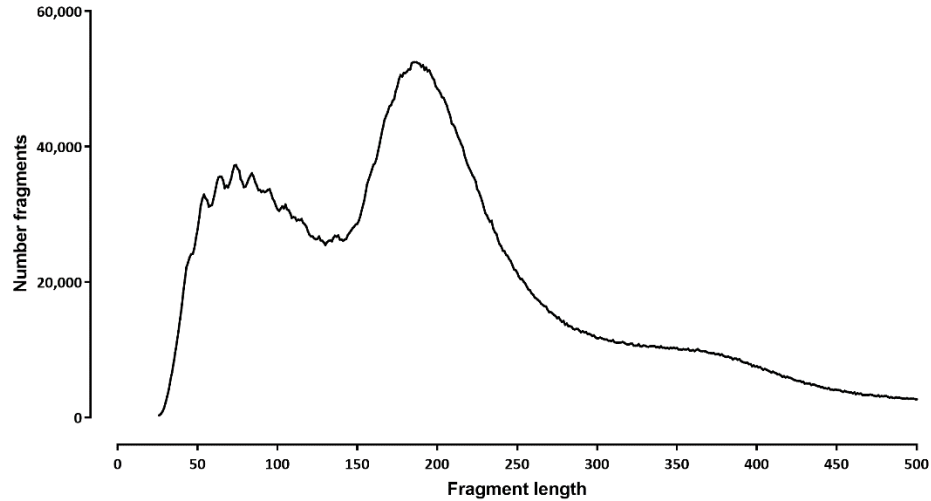


Dataset stats

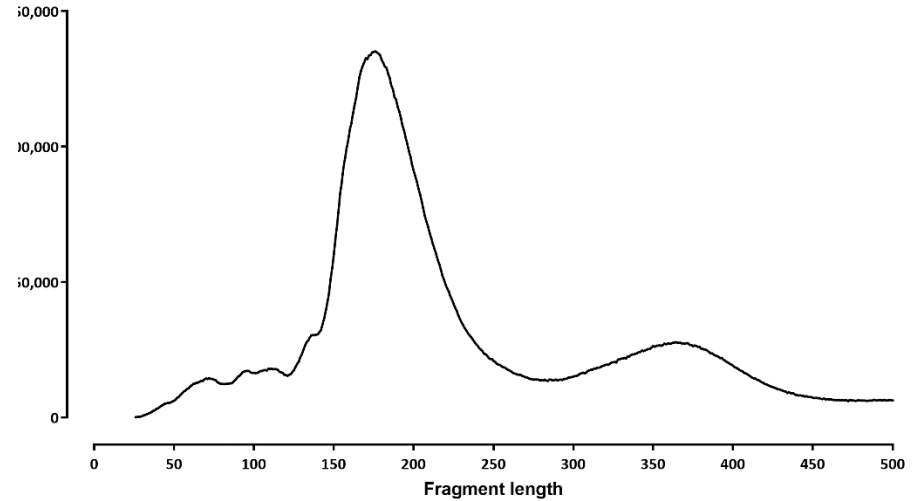
Species	#	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 noBL NumPeaks	MACS2 noBL RPM	Read Length	Unique	Raw fragments	Alignment fraction
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-FOSL2-GFP-ATWJL_L1_GCCAAT	0.83	43,275	358,158	43,029	348,547	2x25	19,882,234	11,903,934	0.84
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-FOSL2-GFP-ATWJL_L1_GCCAAT	0.83	43,561	422,574	43,414	412,859	2x25-maxFL120	5,233,868	11,903,934	0.22
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-FOSL2-GFP-ATWJL_L1_GCCAAT	0.85	31,037	298,799	30,844	289,984	2x25-minFL150	13,105,348	11,903,934	0.55
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-H3K4me1-ATWJL_L1_CGATGT	0.94	53,467	169,952	53,421	169,634	2x25	30,056,250	17,187,817	0.87
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-H3K4me1-ATWJL_L1_CGATGT	0.98	3,534	14,513	3,525	14,326	2x25-maxFL120	2,136,256	17,187,817	0.06
<i>Homo sapiens</i> hg19-male	SCGPM_CUT-RUN-test2_A549-H3K4me1-ATWJL_L1_CGATGT	0.94	49,537	157,670	49,489	157,370	2x25-minFL150	26,231,238	17,187,817	0.76

Fragment length distribution:

SCGPM_CUT-RUN-test2_A549-FOSL2-GFP-ATWJL_L1_GCCAAT



SCGPM_CUT-RUN-test2_A549-H3K4me1-ATWJL_L1_CGATGT



Overlap with ChIP-seq peaks and CTCF motifs:

number peaks

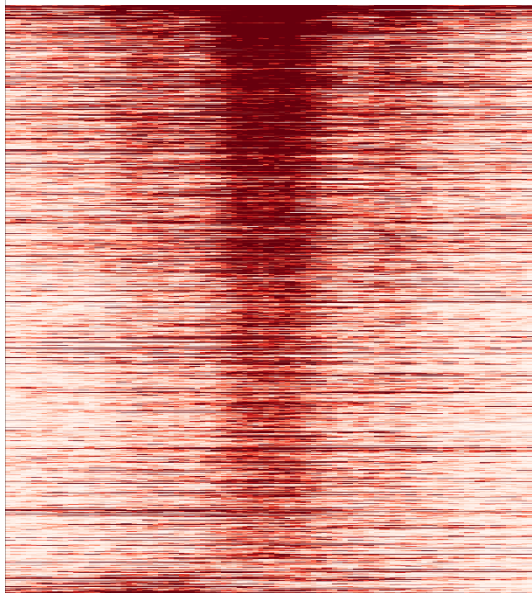
	ChIP peak		no ChIP peak	
	motif	no motif	motif	no motif
A549-FOSL2-HA-ENCFF374ZCG	18,729	14,625	0	0
GCCAAT	14,147	8,243	6,345	14,540
GCCAAT.maxFL120bp	11,350	8,977	3,963	19,271
GCCAAT.minFL150bp	11,751	7,006	3,666	8,614

fraction

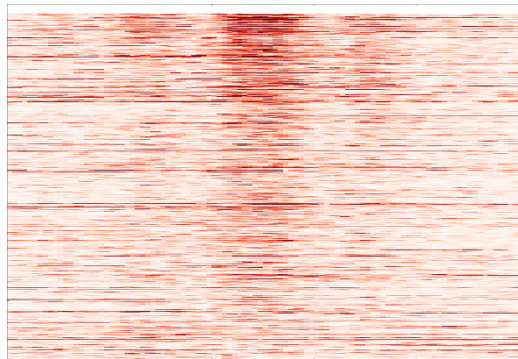
	ChIP peak		no ChIP peak		fraction	
	ChIP peak	no ChIP peak	motif	no motif	motif	no motif
A549-FOSL2-HA-ENCFF374ZCG	1.00	0.00	0.56	0.44	n/a	n/a
TTAGGC	0.52	0.48	0.63	0.37	0.30	0.70
TTAGGC.maxFL120bp	0.47	0.53	0.56	0.44	0.17	0.83
TTAGGC.minFL150bp	0.60	0.40	0.63	0.37	0.30	0.70

Overlap with ChIP-seq peaks, profile around peaks, FOSL2

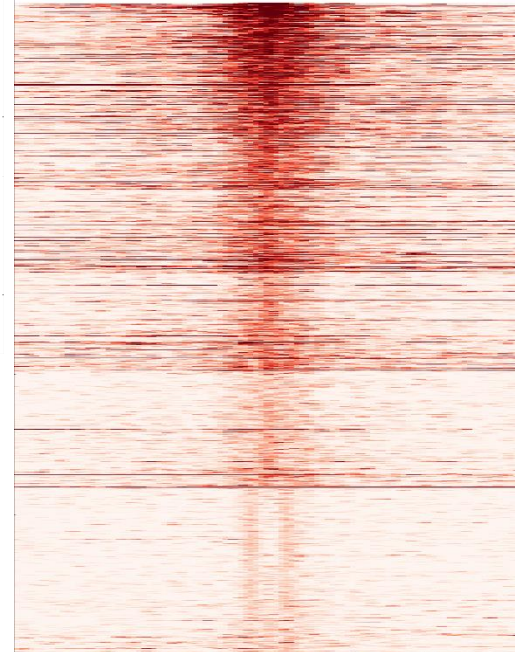
common sites



ChIP-only sites



CUT&RUN only sites

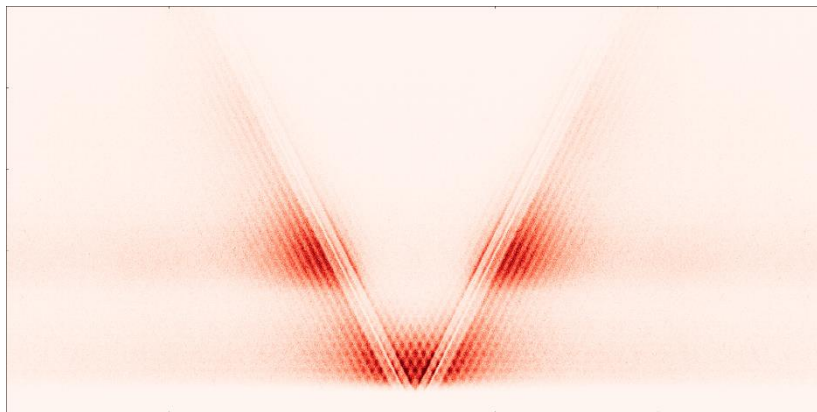


CTCF ACTTGA

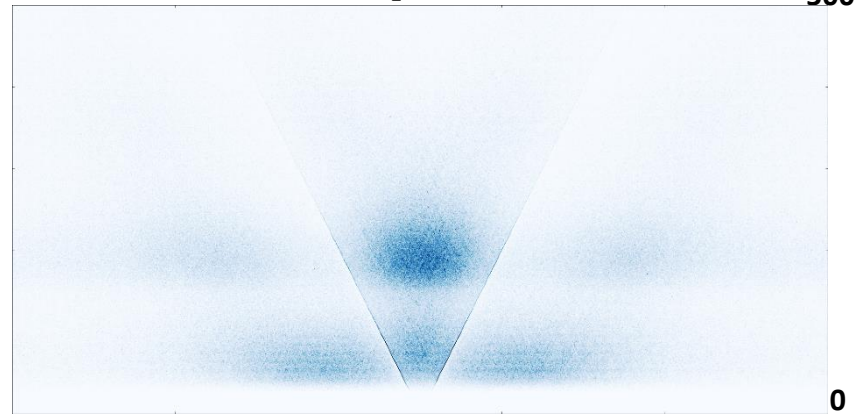
motif-centered

MACS2 peak call-centered

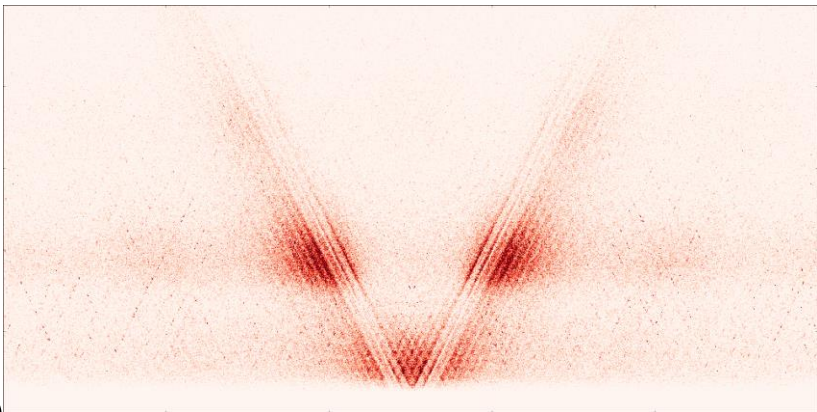
ChIP-common sites
with motif



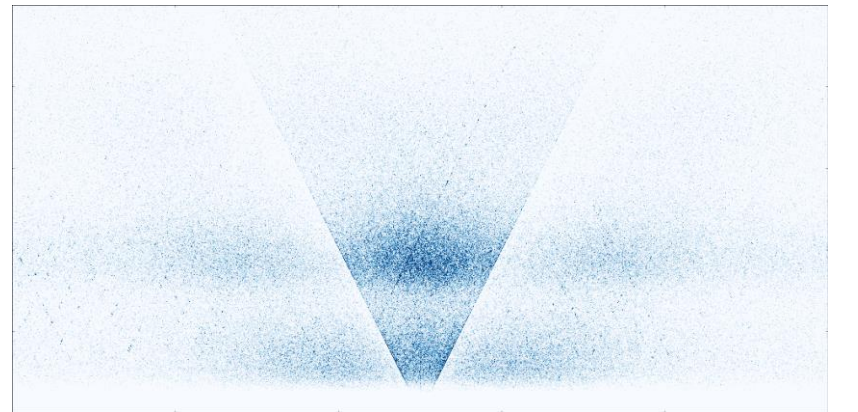
ChIP-common sites
with motif



CUTnRUN-only sites
with motif



CUTnRUN-only sites
no motif



Overlap with CHIP-seq peaks and CTCF motifs:

number peaks

	CHIP peak		no CHIP peak	
	motif	no motif	motif	no motif
A549-eGFP-FOSL2-Snyder-IDR	22,880	11,950	0	0
GCCAAT	15,090	7,938	6,278	14,845
GCCAAT.maxFL120bp	11,898	8,827	3,415	19,421
GCCAAT.minFL150bp	12,417	6,991	3,000	8,629

fraction

	CHIP peak	no CHIP peak	CHIP peak		no CHIP peak	
			motif	no motif	motif	no motif
A549-eGFP-FOSL2-Snyder-IDR	1.00	0.00	0.66	0.34	n/a	n/a
TTAGGC	0.52	0.48	0.66	0.34	0.30	0.70
TTAGGC.maxFL120bp	0.48	0.52	0.57	0.43	0.15	0.85
TTAGGC.minFL150bp	0.63	0.37	0.64	0.36	0.26	0.74