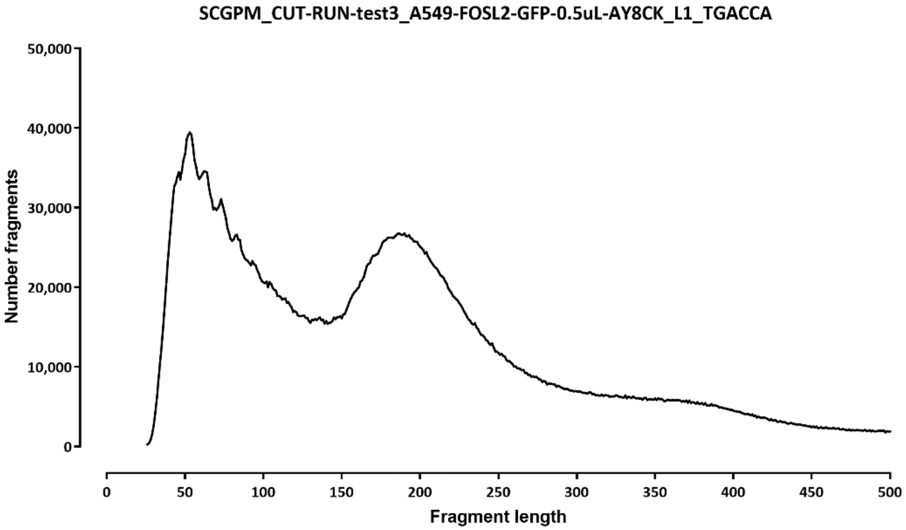
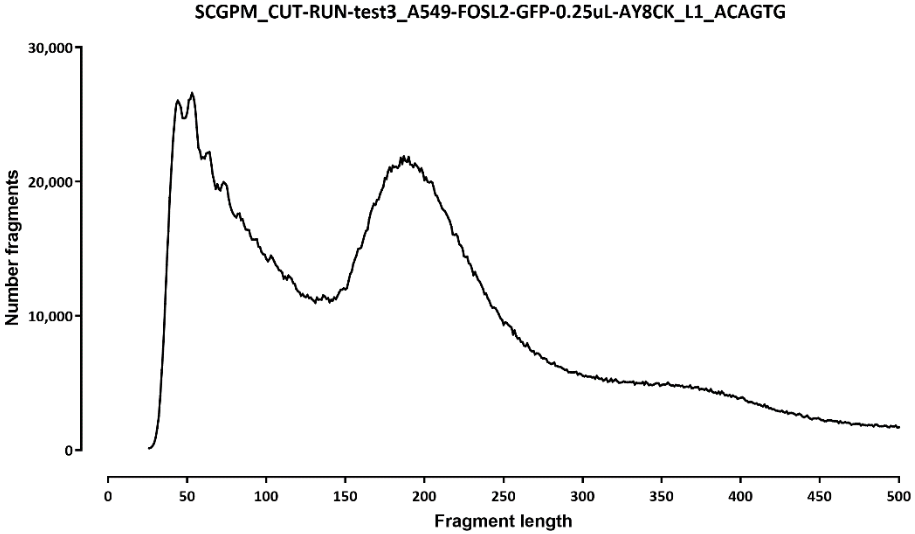
Dataset stats

Species	#	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 noBL NumPeaks	MACS2 noBL RPM	Read Length	Unique	Raw fragments	Alignment fraction
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.25uL-AY8CK_L1_ACAGTG	0.82	28,523	341,514	28,368	333,938	2x25	9,995,714	6,158,716	0.81
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.25uL-AY8CK_L1_ACAGTG	0.81	30,922	425,817	30,833	419,065	2x25-maxFL120	3,160,192	6,158,716	0.26
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.25uL-AY8CK_L1_ACAGTG	0.85	18,250	256,044	18,138	249,030	2x25-minFL150	6,173,684	6,158,716	0.50
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.5uL-AY8CK_L1_TGACCA	0.88	33,922	327,251	33,680	318,951	2x25	12,992,012	8,519,150	0.76
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.5uL-AY8CK_L1_TGACCA	0.85	40,788	423,992	40,653	416,583	2x25-maxFL120	4,618,096	8,519,150	0.27
Homo sapiens hg19-male	SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.5uL-AY8CK_L1_TGACCA	0.92	19,867	231,779	19,705	224,004	2x25-minFL150	7,445,120	8,519,150	0.44

Fragment length distribution:



SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.5uL-AY8CK_L1_TGACCA



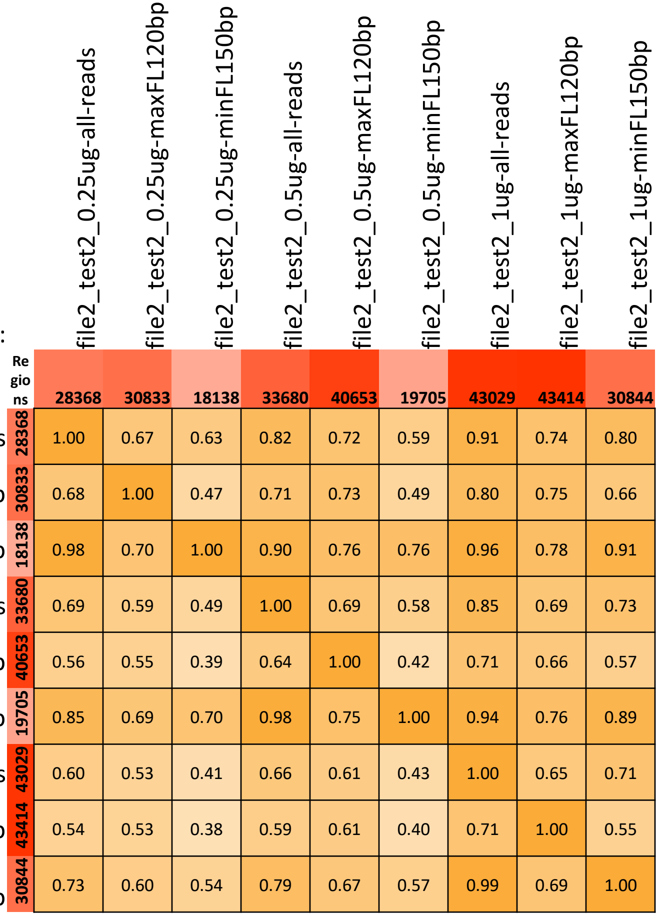
SCGPM_CUT-RUN-test3_A549-FOSL2-GFP-0.25uL-AY8CK_L1_ACAGTG

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**
A549-eGFP-FOSL2-Snyder-IDR	22,880	11,950	**0**	**0**
CUT&RUN-1uL	14,147	8,243	6,345	14,540
CUT&RUN-1uL.maxFL120bp	11,350	8,977	3,963	19,271
CUT&RUN-1uL.minFL150bp	11,751	7,006	3,666	8,614
CUT&RUN-0.25uL	11,459	6,472	3,006	7,586
CUT&RUN-0.25uL.maxFL120bp	9,968	7,504	2,620	10,830
CUT&RUN-0.25uL.minFL150bp	8,088	5,042	1,315	3,805
CUT&RUN-0.5uL	12,472	7,088	4,131	10,231
CUT&RUN-0.5uL.maxFL120bp	11,619	8,328	4,192	16,649
CUT&RUN-0.5uL.minFL150bp	8,542	5,389	1,538	4,398

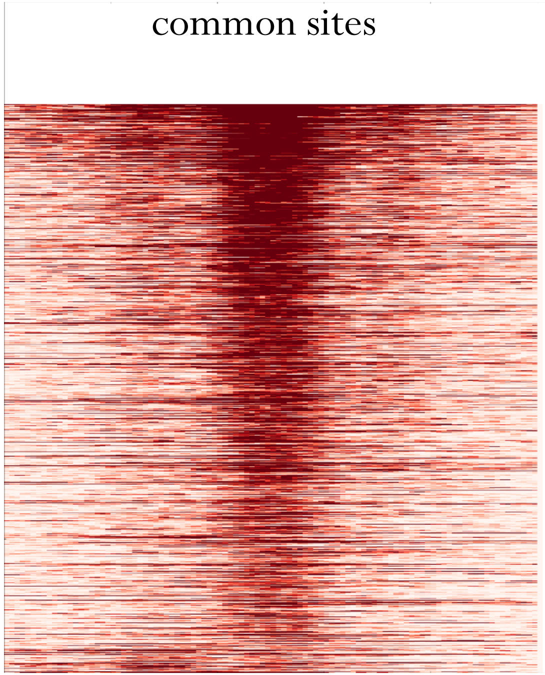
	fraction					
	ChIP peak	no ChIP peak	ChIP peak		no ChIP peak	
			motif	no motif	motif	no motif
A549-FOSL2-HA-ENCFF374ZCG	1.00	0.00	0.56	0.44	n/a	n/a
A549-eGFP-FOSL2-Snyder-IDR	1.00	0.00	0.66	0.34	n/a	n/a
TTAGGC	0.52	0.48	0.63	0.37	0.30	0.70
TTAGGC.maxFL120bp	0.47	0.53	0.56	0.44	0.17	0.83
TTAGGC.minFL150bp	0.60	0.40	0.63	0.37	0.30	0.70
	0.63	0.37	0.64	0.36	0.28	0.72
	0.57	0.43	0.57	0.43	0.19	0.81
	0.72	0.28	0.62	0.38	0.26	0.74
	0.58	0.42	0.64	0.36	0.29	0.71
	0.49	0.51	0.58	0.42	0.20	0.80
	0.70	0.30	0.61	0.39	0.26	0.74

Overlap with 1ug CUT&RUN

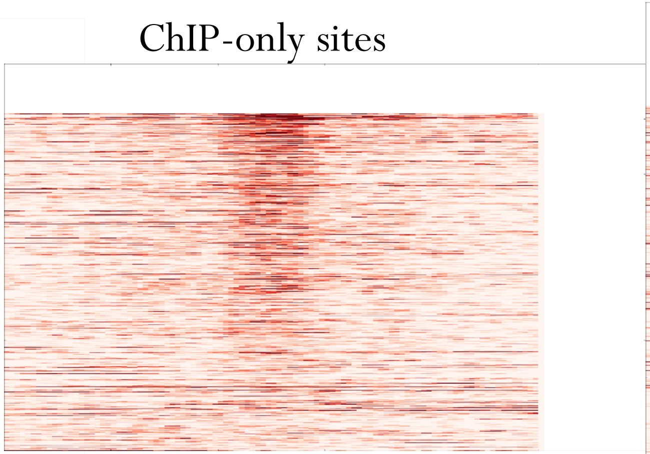


#DataSet:		file2_test2_0.25ug-all-reads	file2_test2_0.25ug-maxFL120bp	file2_test2_0.25ug-minFL150bp	file2_test2_0.5ug-all-reads	file2_test2_0.5ug-maxFL120bp	file2_test2_0.5ug-minFL150bp	file2_test2_1ug-all-reads	file2_test2_1ug-maxFL120bp	file2_test2_1ug-minFL150bp
	Regions	**28368**	**30833**	**18138**	**33680**	**40653**	**19705**	**43029**	**43414**	**30844**
test2_0.25ug-all-reads	**28368**	1.00	0.67	0.63	0.82	0.72	0.59	0.91	0.74	0.80
test2_0.25ug-maxFL120bp	**30833**	0.68	1.00	0.47	0.71	0.73	0.49	0.80	0.75	0.66
test2_0.25ug-minFL150bp	**18138**	0.98	0.70	1.00	0.90	0.76	0.76	0.96	0.78	0.91
test2_0.5ug-all-reads	**33680**	0.69	0.59	0.49	1.00	0.69	0.58	0.85	0.69	0.73
test2_0.5ug-maxFL120bp	**40653**	0.56	0.55	0.39	0.64	1.00	0.42	0.71	0.66	0.57
test2_0.5ug-minFL150bp	**19705**	0.85	0.69	0.70	0.98	0.75	1.00	0.94	0.76	0.89
test2_1ug-all-reads	**43029**	0.60	0.53	0.41	0.66	0.61	0.43	1.00	0.65	0.71
test2_1ug-maxFL120bp	**43414**	0.54	0.53	0.38	0.59	0.61	0.40	0.71	1.00	0.55
test2_1ug-minFL150bp	**30844**	0.73	0.60	0.54	0.79	0.67	0.57	0.99	0.69	1.00

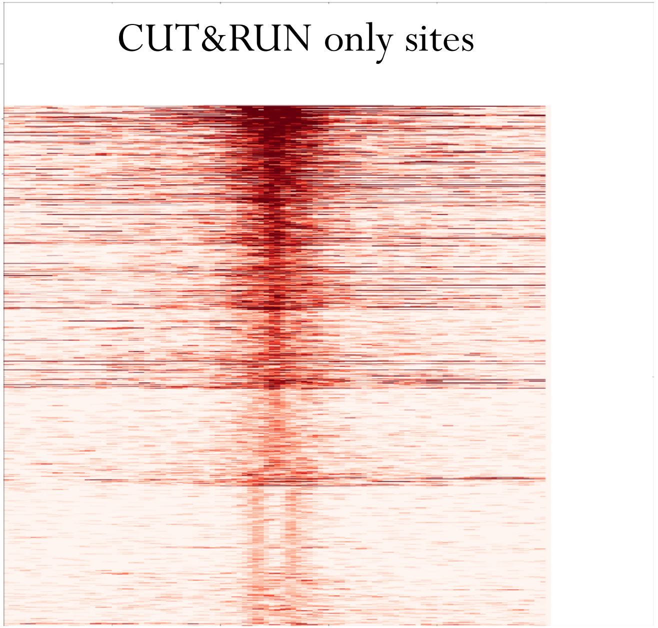
Overlap with ChIP-seq peaks, profile around peaks, FOSL2 , 0.5ug



common sites



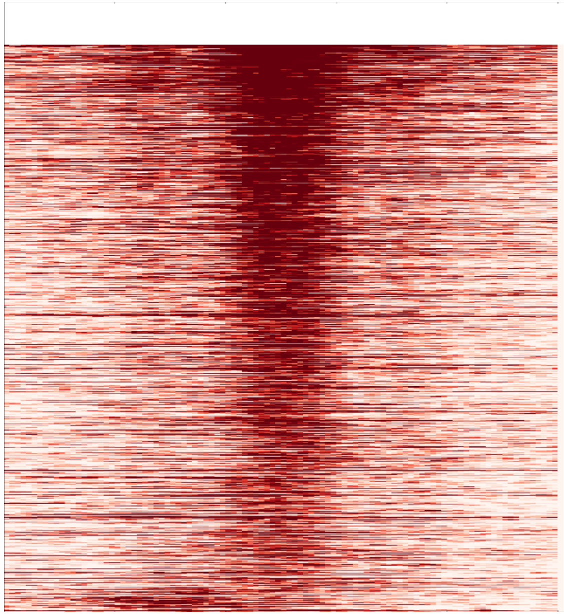
ChIP-only sites



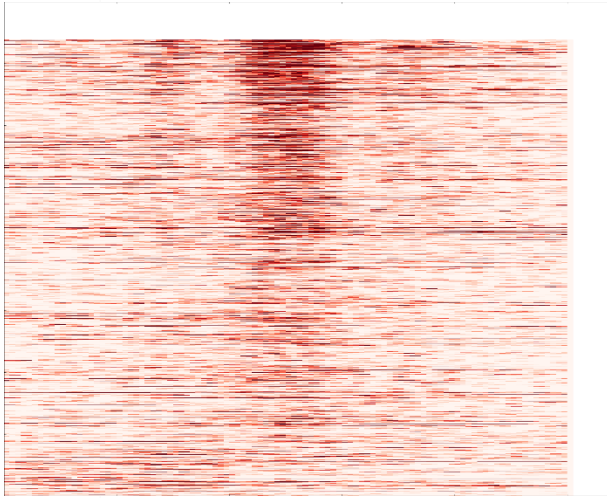
CUT&RUN only sites

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

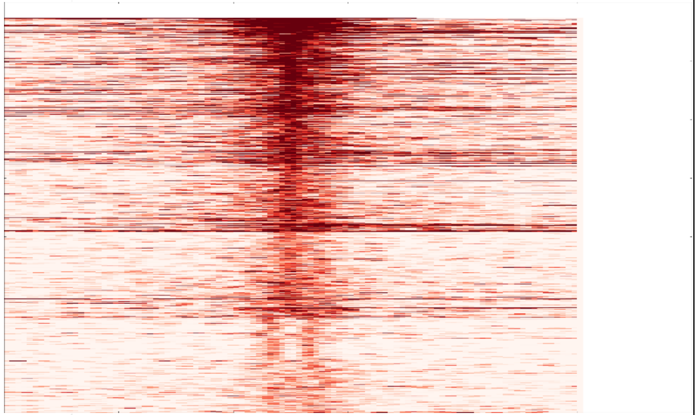
common sites



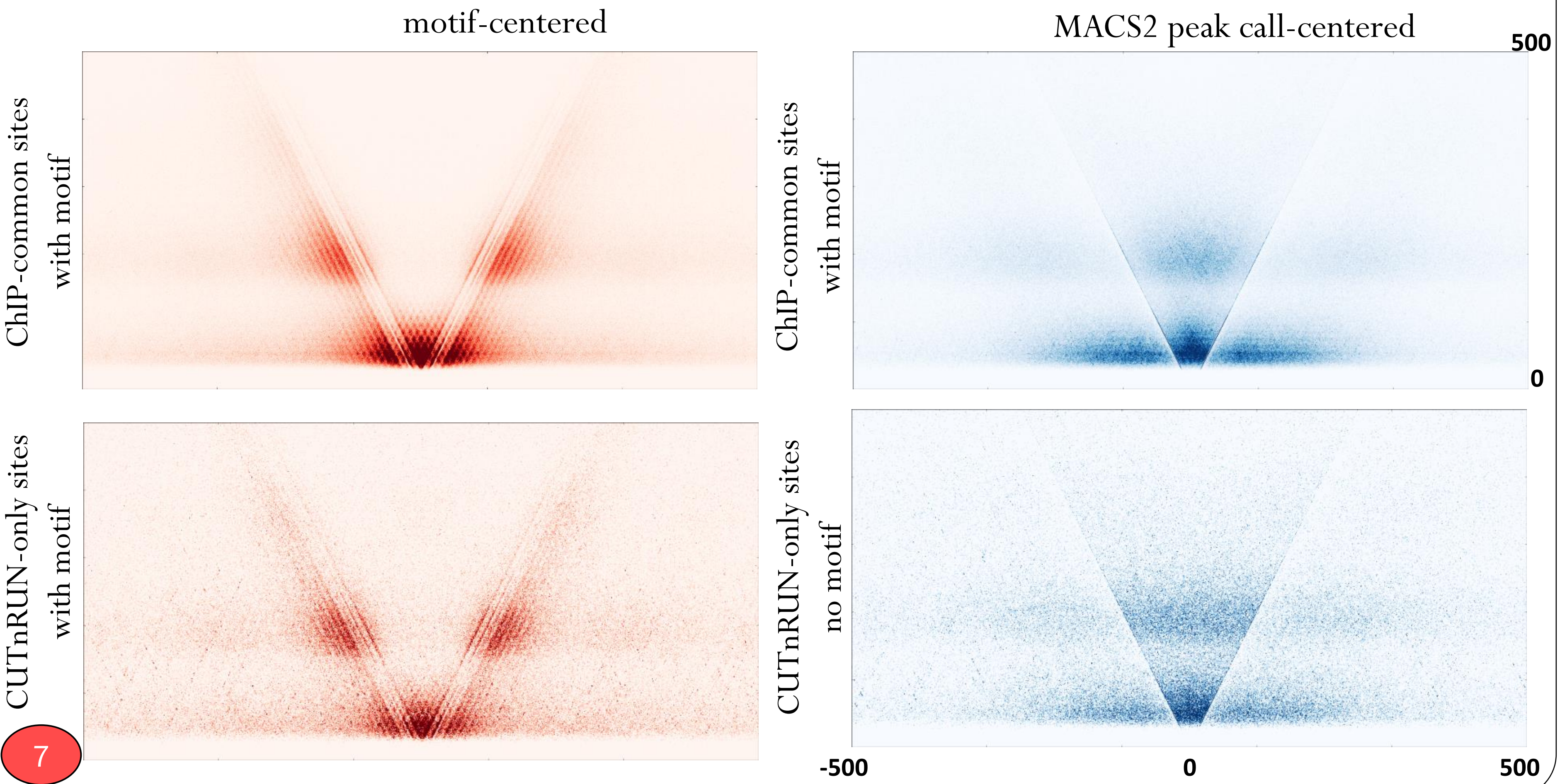
ChIP-only sites



CUT&RUN only sites



FOSL2, 0.25ug



motif-centered

MACS2 peak call-centered

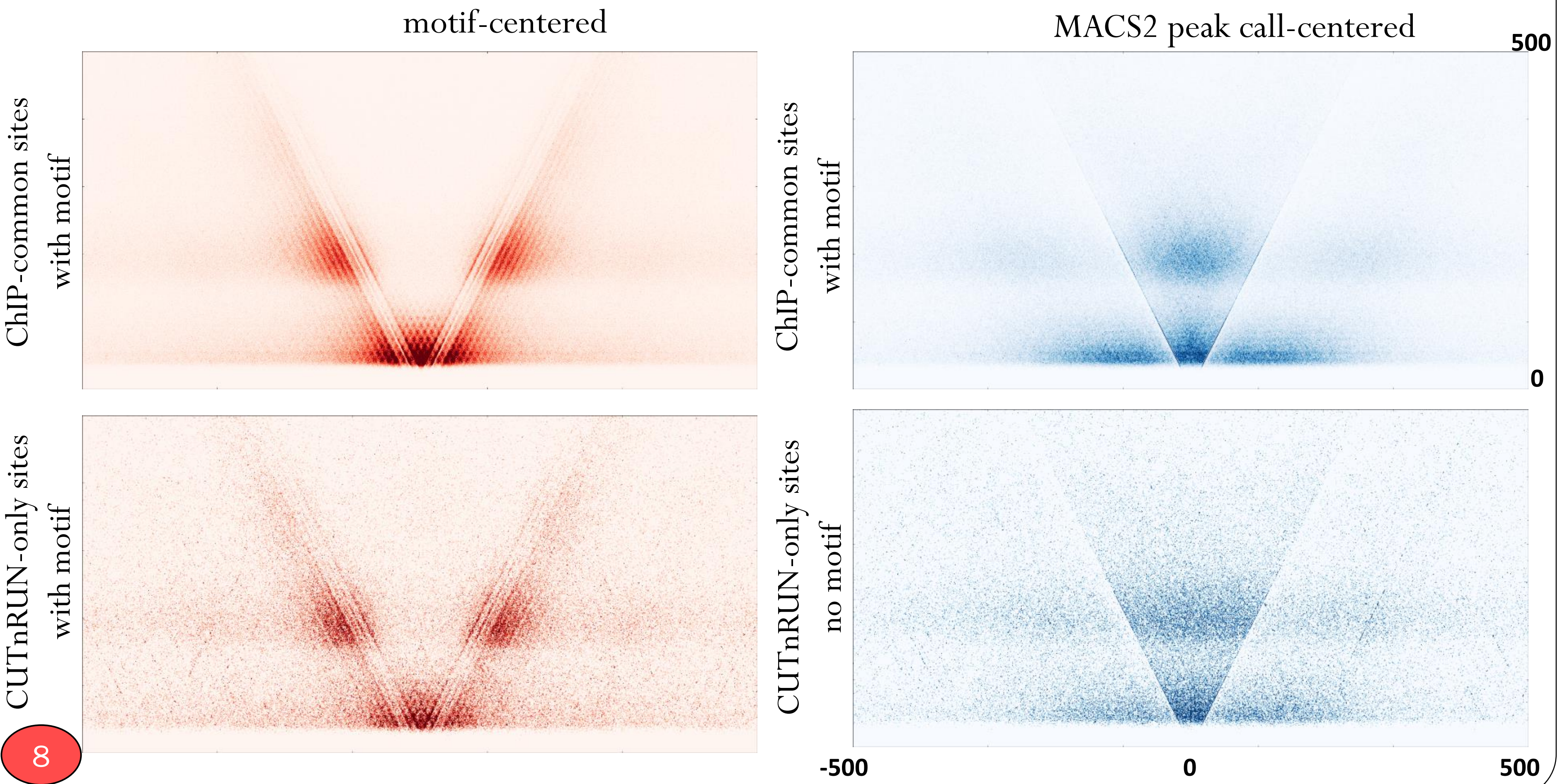
ChIP-common sites with motif

CUTnRUN-only sites with motif

ChIP-common sites with motif

CUTnRUN-only sites no motif

FOSL2, 0.5ug


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
500
0
-500
0
500