

MAPPING STATS, *S.cerevisiae* CHIP SAMPLES ONLY

Species	#	Complexity	MACS2 NumPeaks	MACS2 RPM	MACS2 PseudoRep NumPeaks	MACS2 RPM	NSC	RSC	QC	Read Length	Unique	Multi	Raw fragments
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L65_MS521_AB101_GFP-NLS-V5	0.68								2x36	23,080,984		14,809,015
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L66_MS529_AB101_WHI5-V5	0.67	287	53,340						2x36	26,585,258		17,119,001
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L67_MS527_AB101_STB1-V5	0.67	384	73,912						2x36	26,251,504		16,476,649
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L68_MS522_AB101_SWI4-V5	0.66	372	128,638						2x36	25,325,600		15,909,901
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L69_MS524_AB101_SWI6-V5	0.64	466	692,720						2x36	27,924,198		17,829,144
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L70_MS528_AB101_BCK2-V5	0.68	226	72,461						2x36	22,793,478		14,290,468
<i>Saccharomyces cerevisiae sacCer3</i>	2019-08-12-190722L71_MS523_AB101_MBP1-V5	0.68	665	134,528						2x36	23,911,870		15,103,878

Note: peaks were called with the GFP sample as control (I assumed this is why it was done)

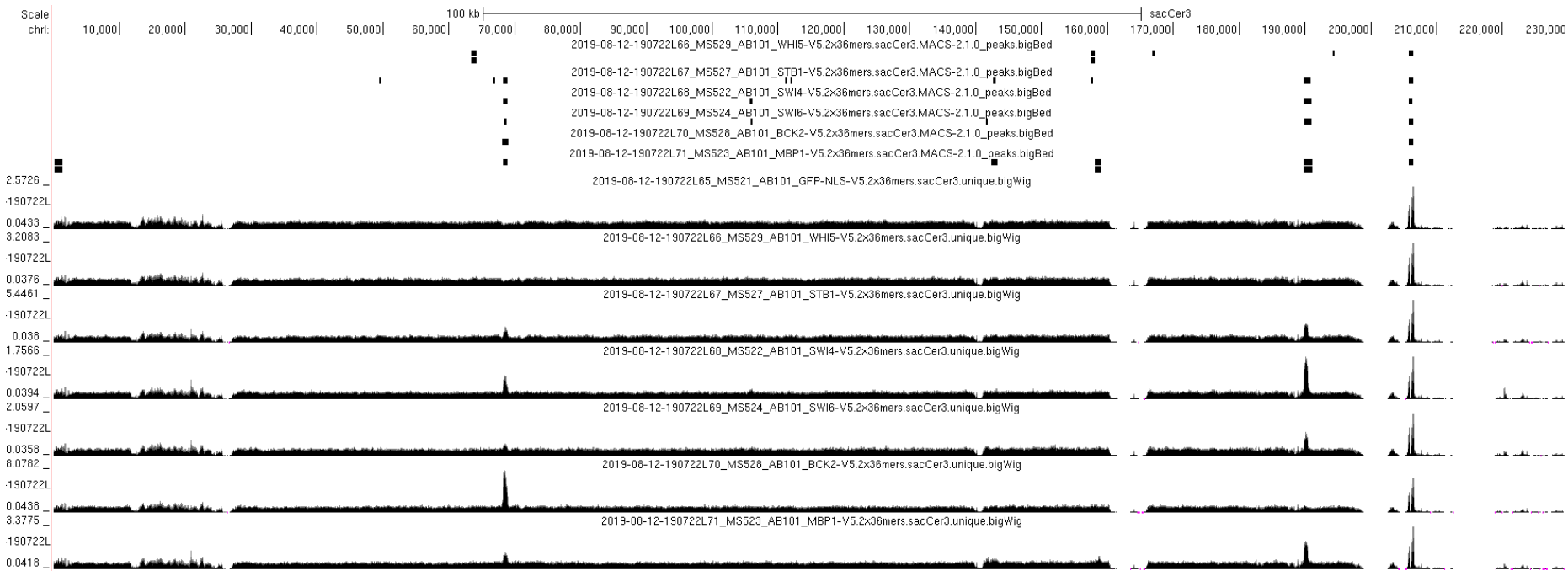
PEAK OVERLAP

- 2019-08-12-190722L66_MS529_AB101_WHI5-V5
- 2019-08-12-190722L67_MS527_AB101_STB1-V5
- 2019-08-12-190722L68_MS522_AB101_SWI4-V5
- 2019-08-12-190722L69_MS524_AB101_SWI6-V5
- 2019-08-12-190722L70_MS528_AB101_BCK2-V5
- 2019-08-12-190722L71_MS523_AB101_MBP1-V5

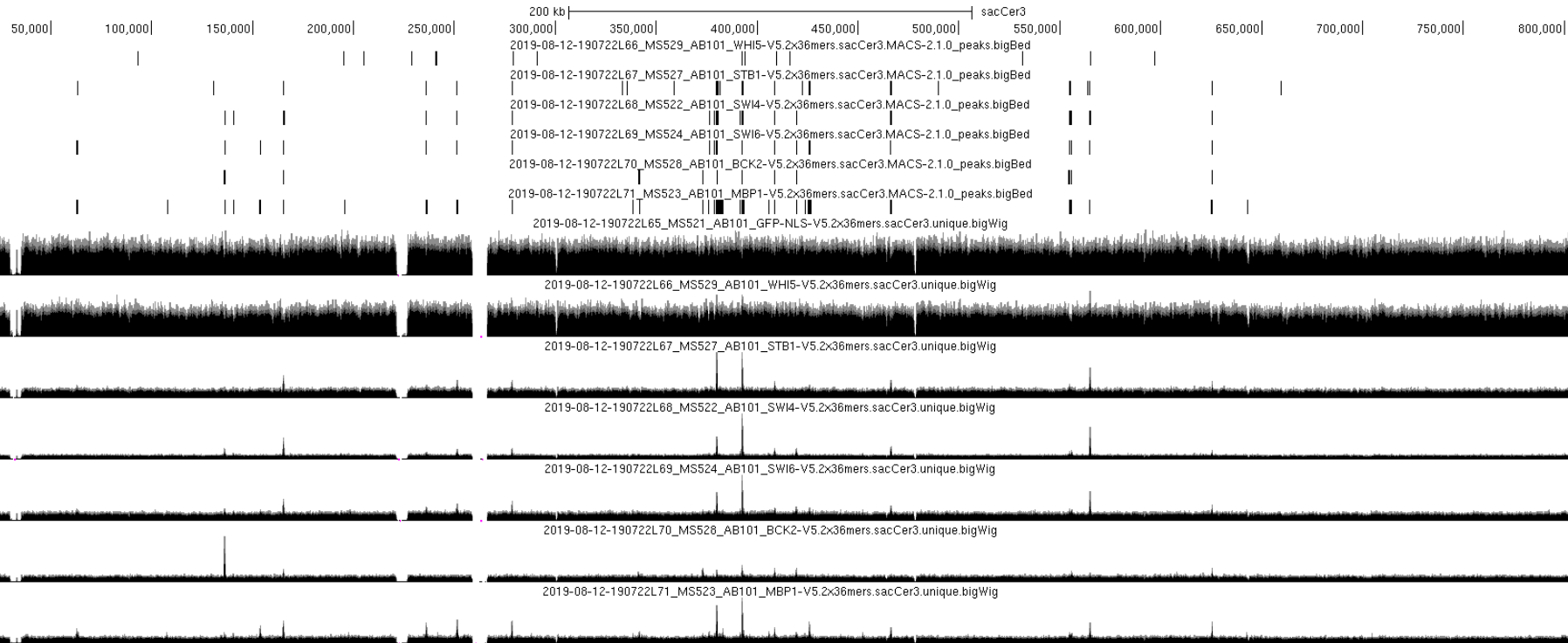
#DataSet:

	287	384	372	466	226	665
287	1.00	0.32	0.25	0.25	0.19	0.34
384	0.23	1.00	0.63	0.70	0.40	0.76
372	0.19	0.68	1.00	0.80	0.48	0.88
466	0.14	0.56	0.61	1.00	0.56	0.76
226	0.23	0.65	0.70	0.82	1.00	0.81
665	0.18	0.54	0.57	0.60	0.36	1.00

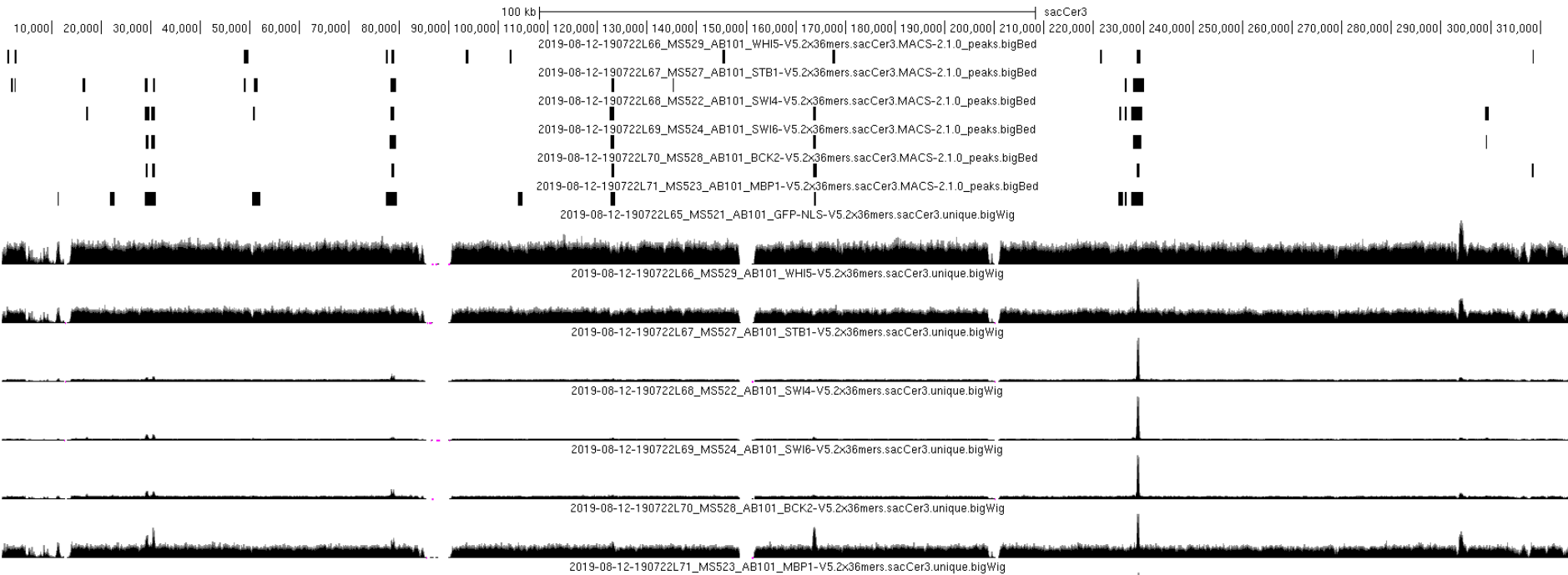
chr1



chr11



chrIII



chrIV

