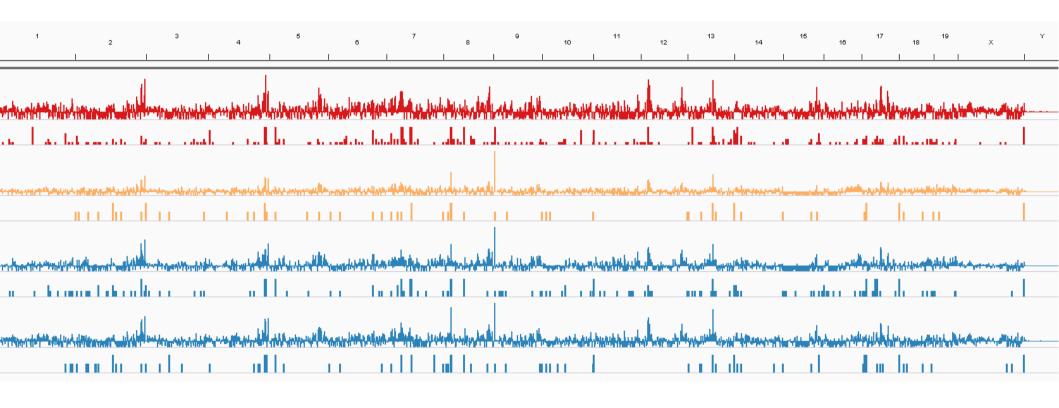
Régions IGV d'intérêt

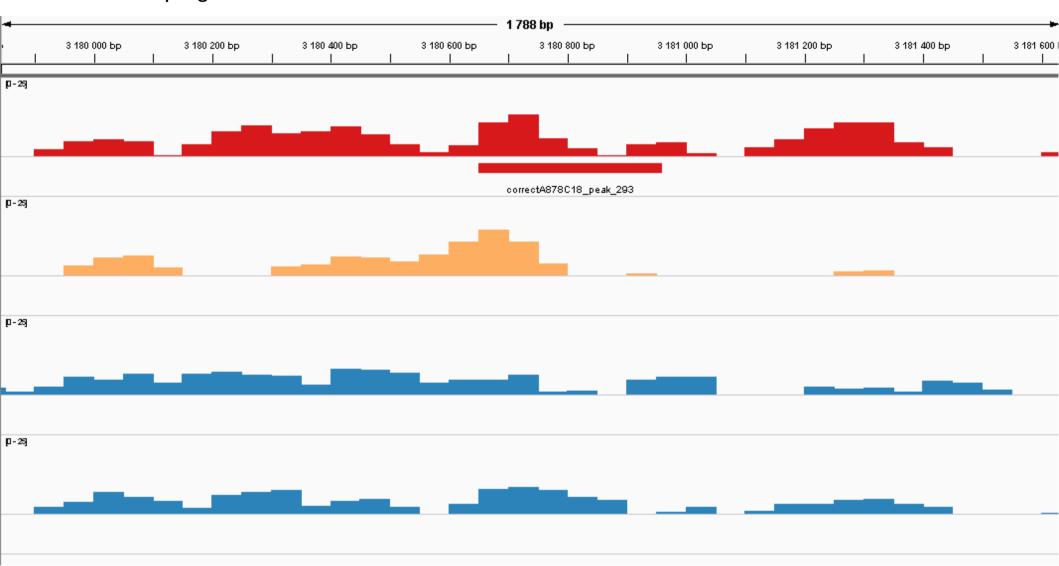


Gain de marquage

	chipseqK9_HD1 hr2 chr13 chr18 chr6 chr11 chr11 chr12 chr16 chr17 chr17 chr17 chr17 chr18 chr19 chr																																			
			chr6	chr11	chr11	chr12	chr16	chr17	chr17	chr17	chr18	chr19	chr19	chr19	chr19	chr1	chr1	chr2	chr2	chr3	chr3	chr6	chr6	chr6	chr8	chr8				chr9	chr9	chr5	chr19		chr18	chr15
Celf2	Ssbp2	Sral	Cadps2	Egfr	Gabrp	Nova1	Hira	Nrxn1	Msh2	Thada	Toergl	Cptla	Duft	Tdrd1	Afap112	Sgk3	Ccdc93	Fam107b	Lypd6b	Ndst3	Slc44a5	Abcg2	Art4	Rassf8	Proz	Adam18	x <u>s</u>	Slc10a7	Maml2	Td12	Mel	Gm9758	Nrxm2	Scaper	Cfap53	Pphln1
p-28	p-28j	p-28	p-28j	p-28j	p-28	D-2SJ	p-28	p-28	p-28	p-283	p-25j	p-28	p-28J	p-28J	p-28j	p-28	p-28J	p-28J	p-283	D-28	p-28j	p-28	[D-28]	D-28	[D-28]	p-25j	p-28	p-28	D-23	D-28	p-25	D-28	p-2sj	p-28j	p-28	p-28j
•	1	•	- 1	1	•	•	•			•	1	•	•	1	•	•		•	•		1	•		•	•	•	•	•	1	•	•	•	1.1	•	•	
[D-28]	p-28j	p-29	[D-25]	[D-25]	p-29	p-28j	p-25j	[D-25]	D-25j	p-28j	p-28j	p-25j	[D-25]	[D-25]	p-28j	p-29	[D-28]	[D-25]	p-29	p-29	p-29	[D-25]	p-29	[D-25]	[D-25]	p-29	p-29	p-28	[D-25]	[D-25]	p-29	p-25j	p-29	p-29	p-29	p-29
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[D-2S]	p-2sj	p-2sj	p-28j	p-2sj	p-28j	p-28j	D-2SJ	p-2sj	p-29	[D-28]	[D-25]	p-2sj	p-28j	p-2sj	[D-28]	p-2sj	[D-28]	p-2sj	p-2sj	p-2sj	p-2sj	p-29	D-25j	p-29	p-29	p-29	p-2sj	p-29	p-29	p-29	p-29	D-28j	p-29	p-28j	D-25j	p-29
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p-25j	p-29	[D-25]	p-25j	p-25j	[D-25]	p-29	p-25j	p-28j	[D-25]	p-28j	p-25j	[D-25]	p-25j	p-29	p-25	p-28j	p-28j	p-29	p-28j	p-29	p-25j	p-28	p-25j	p-25j	p-25j	[D-25]	p-29	p-29	p-28j	p-2sj	p-25j	p-25j	p-25j	[D-25]	[D-25]	[D-25]
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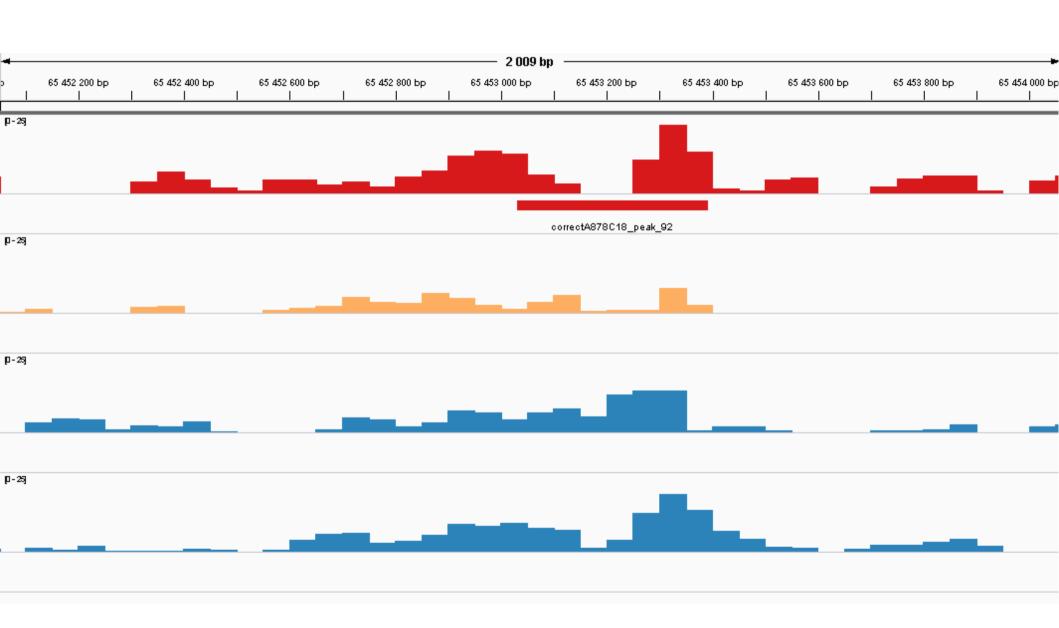
chr4:3,179,843-3,181,633

Gain de marquage

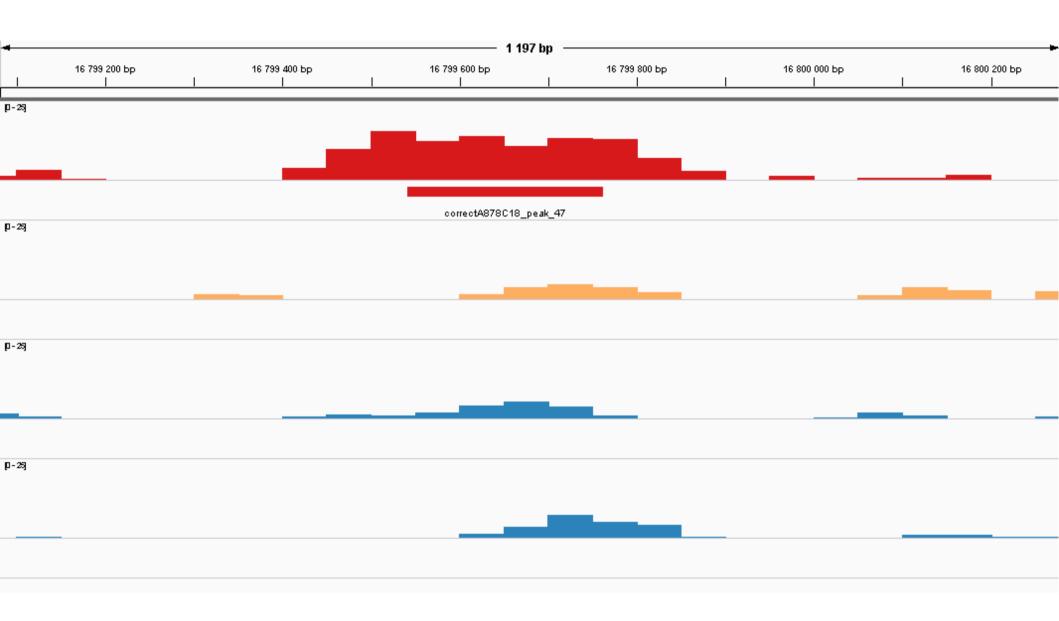


chr13:65,452,051-65,454,062

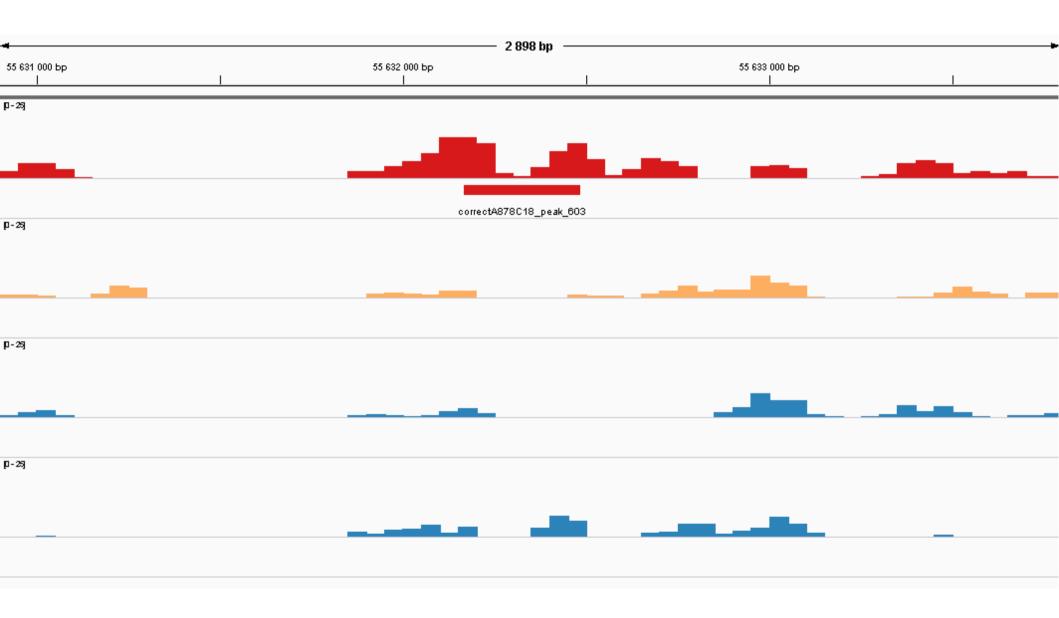
Gain de marquage



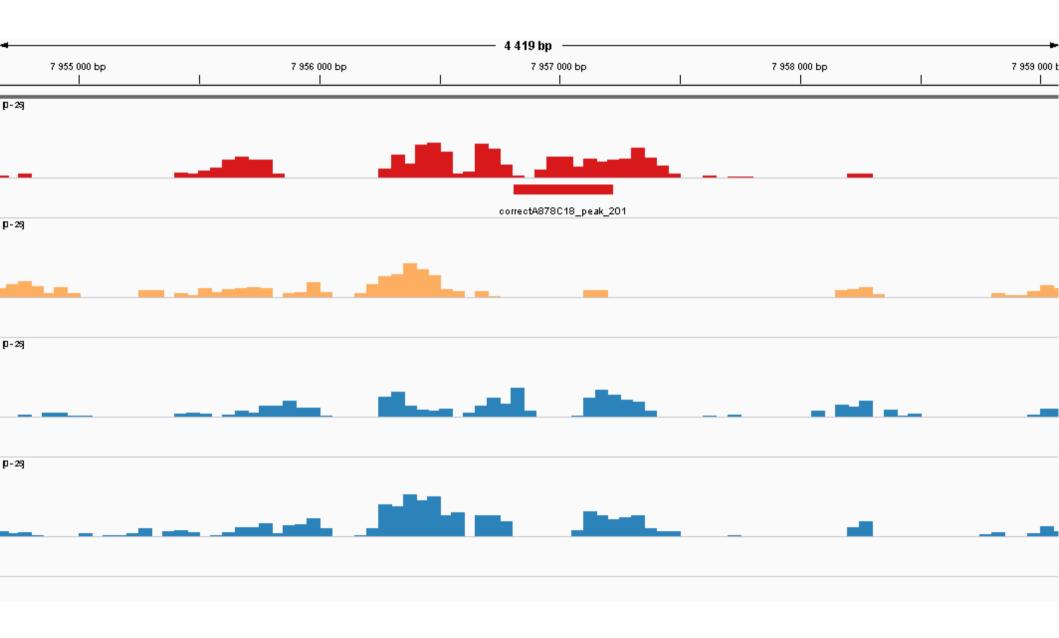
chr11:16,799,081-16,800,279 - EGFR - ENSMUSG00000020122



chr9:55,630,896-55,633,798 - Scaper - ENSMUSG00000034007



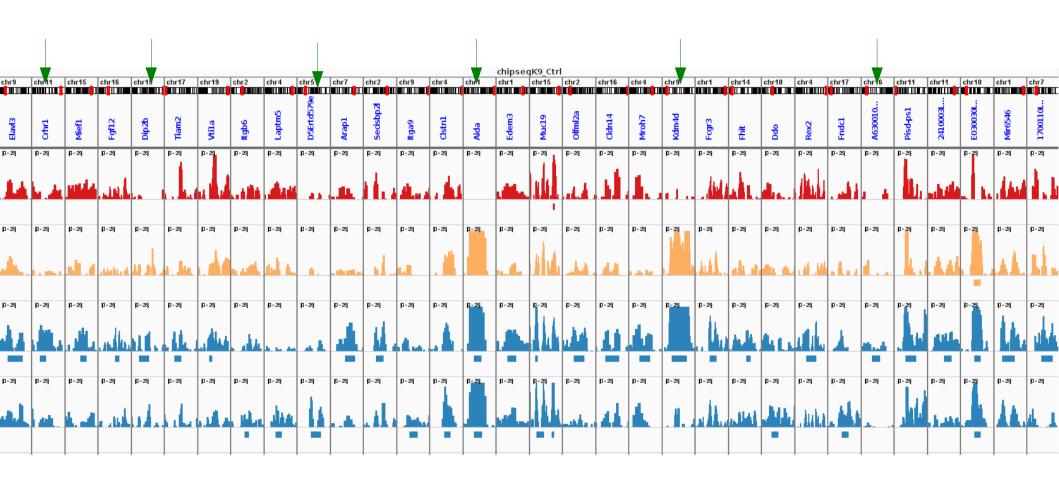
chr17:7,954,661-7,959,086 - Rsph3a - ENSMUSG0000007347



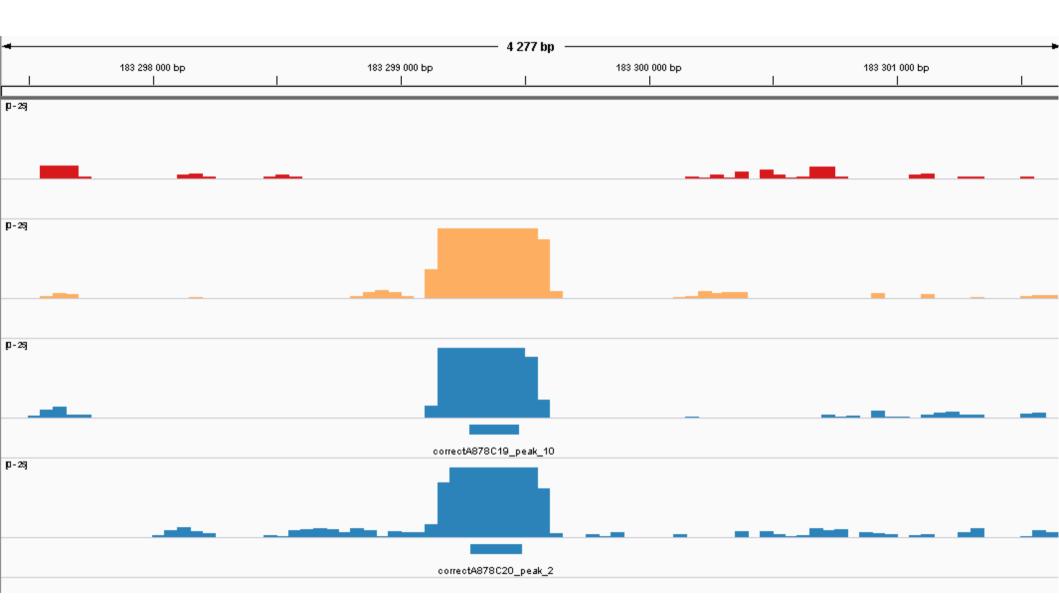
Perte de marquage

Beaucoup moins clair !!!

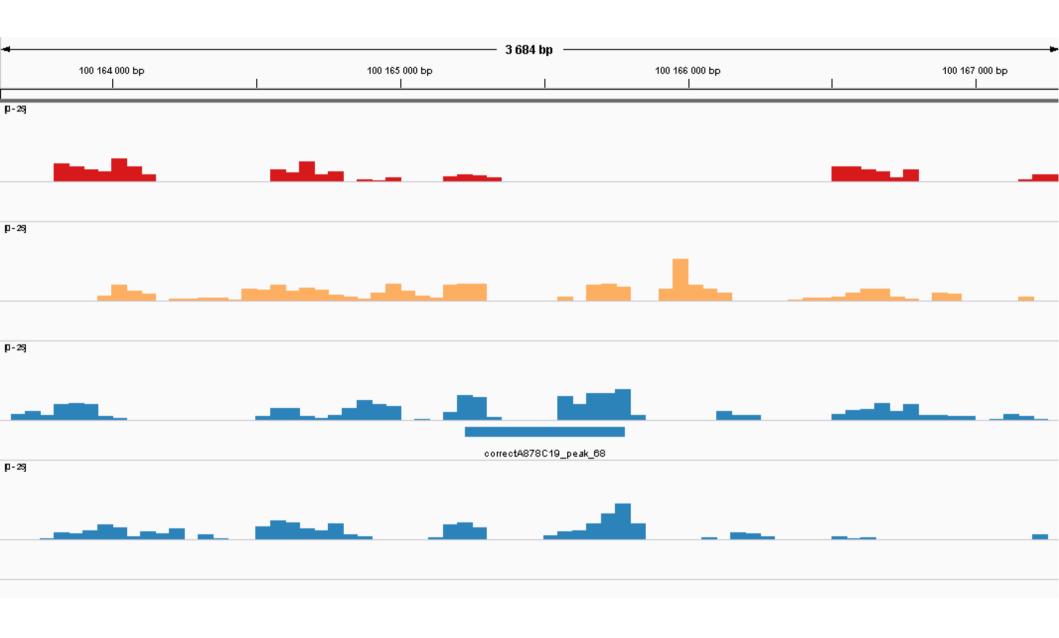
Signal global



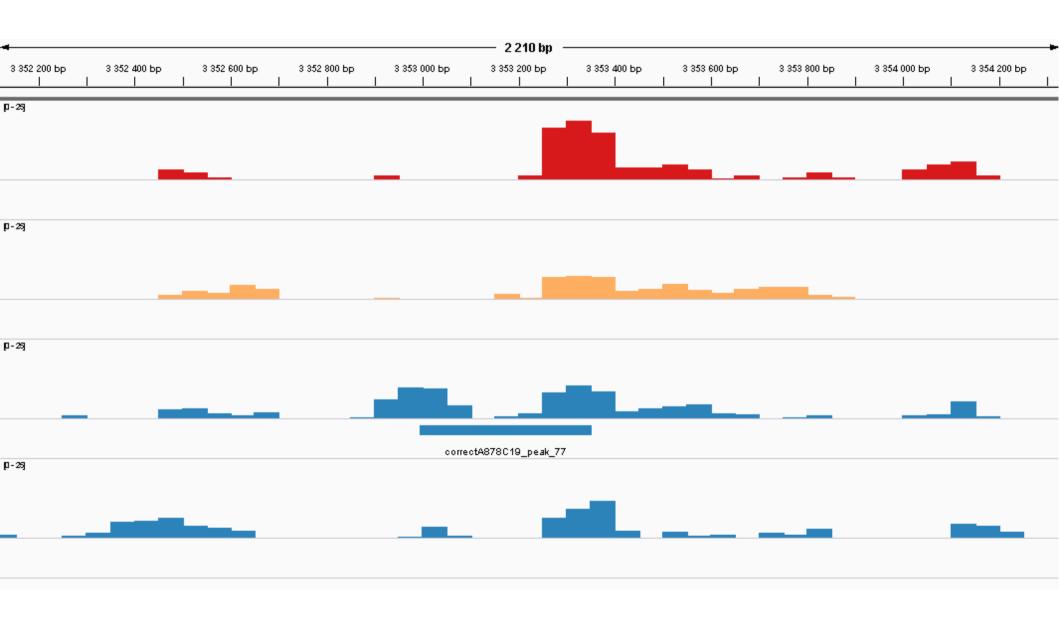
Chr1:183,297,387-183,301,671 - Aida - ENSMUSG00000042901



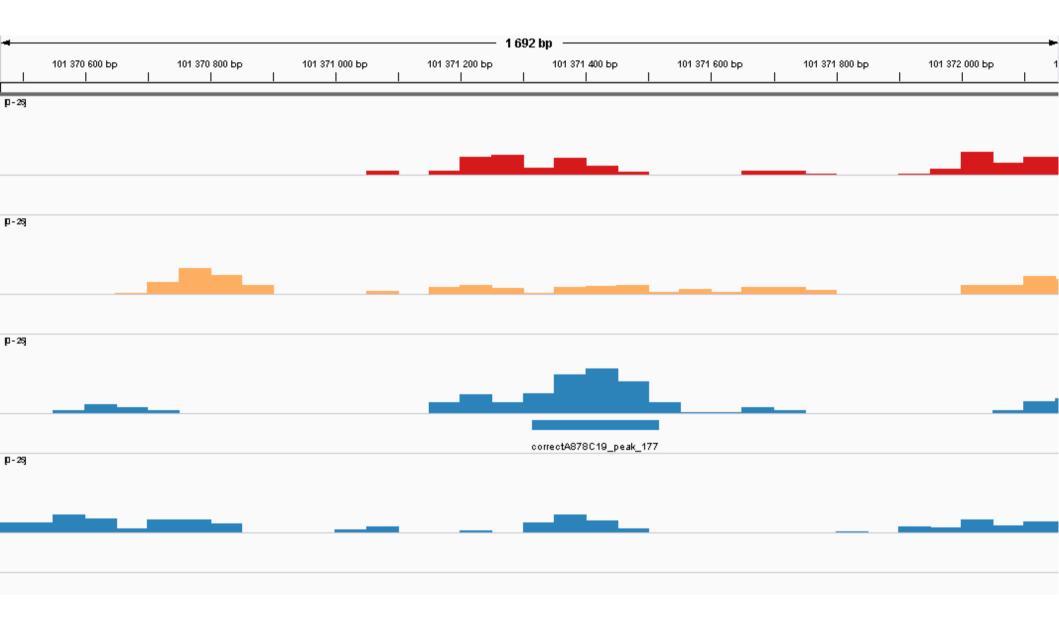
Chr15:100,163,608-100,167,297 - Dip2b - ENSMUSG00000023026



chr17:3,352,117-3,354,329 - Tiam2 - ENSMUSG00000023800

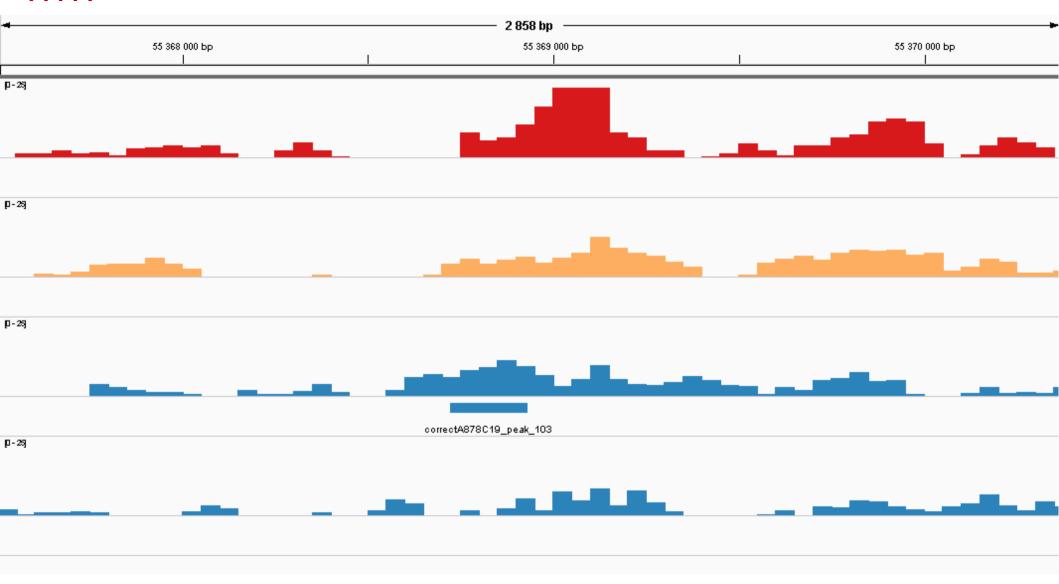


chr7:101,370,464-101,372,157 - Arap1 - ENSMUSG00000032812



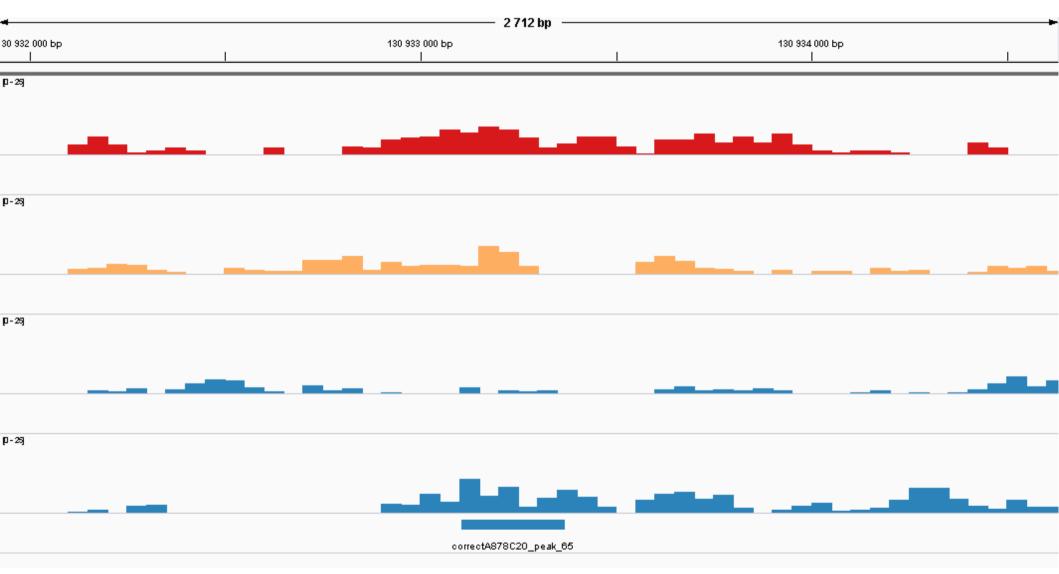
chr19:55,367,507-55,370,368 - Vti1a - ENSMUSG00000024983

?????



chr4:130,931,919-130,934,635 - Laptm5 - ENSMUSG00000028581





Régions neutres

