Report CORIANDR: ChrOmosomal abeRration Identifier AND Reporter in R

09 Dezember, 2020

unique_reads	897816
average_length	149.281
unique_mapped_reads	1749945
SAMPLE_ID	98217.new
gender	M

Calculated numerical karyotype:

add(1)(q25.2q25.2)

add(3)(p22.3p22.3)

del(3)(p21.32p21.32)

del(3)(p14.3p14.3)

add(3)(q25.31q25.31)

del(5)(q33.2q33.2)

del(7)(q21.11q36.3)

del(9)(q22.1q22.1)

del(11)(q14.2q14.2)

del(12)(q13.2q13.2)

del(16)(p11.2p11.1)

del(16)(q11.2q11.2)

add(18)(q12.2q12.2)

add(21)(q21.3q21.3)

Genes affected by CNVs*:

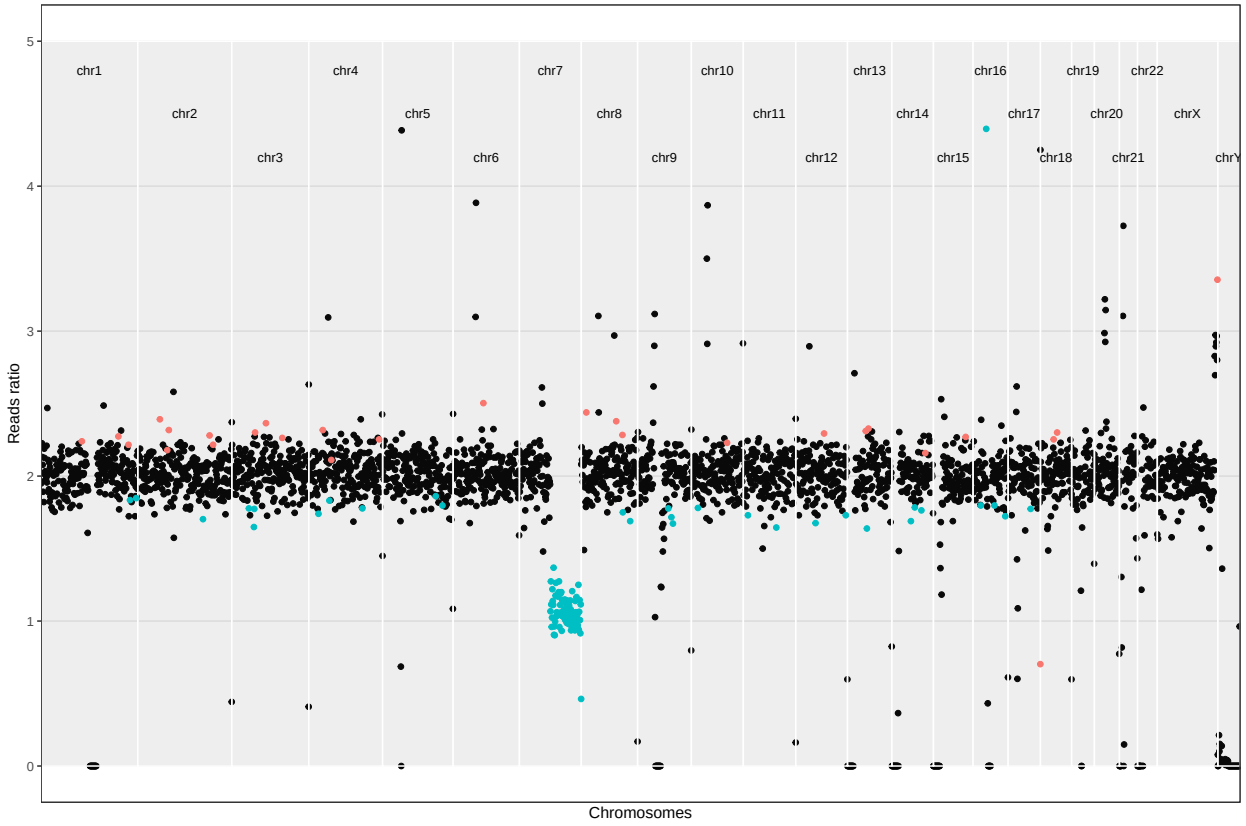
id	sym	bol chr	sta	rt end	abe	rration
5025	ENSG00000069248	NUP133	chr1	229440259	229508341	del
23074	ENSG00000019991	HGF	chr7	81699010	81770438	del
23552	ENSG00000105851	PIK3CG	chr7	106865278	106908980	del
23659	ENSG00000105976	MET	chr7	116672196	116798386	del
23865	ENSG00000128602	SMO	chr7	129188633	129213545	del
24082	ENSG00000157764	BRAF	chr7	140719327	140924928	del
24217	ENSG00000197993	KEL	chr7	142941114	142962363	del
24328	ENSG00000055130	CUL1	chr7	148697914	148801110	del
24329	ENSG00000106462	EZH2	chr7	148807383	148884321	del
24436	ENSG00000106615	RHEB	chr7	151466012	151520120	del

id	sym	bol chr	sta	rt end	abe	rration
24449	ENSG00000055609	KMT2C	chr7	152134922	152436005	del
51230	ENSG00000108375	RNF43	chr17	58352500	58417595	del

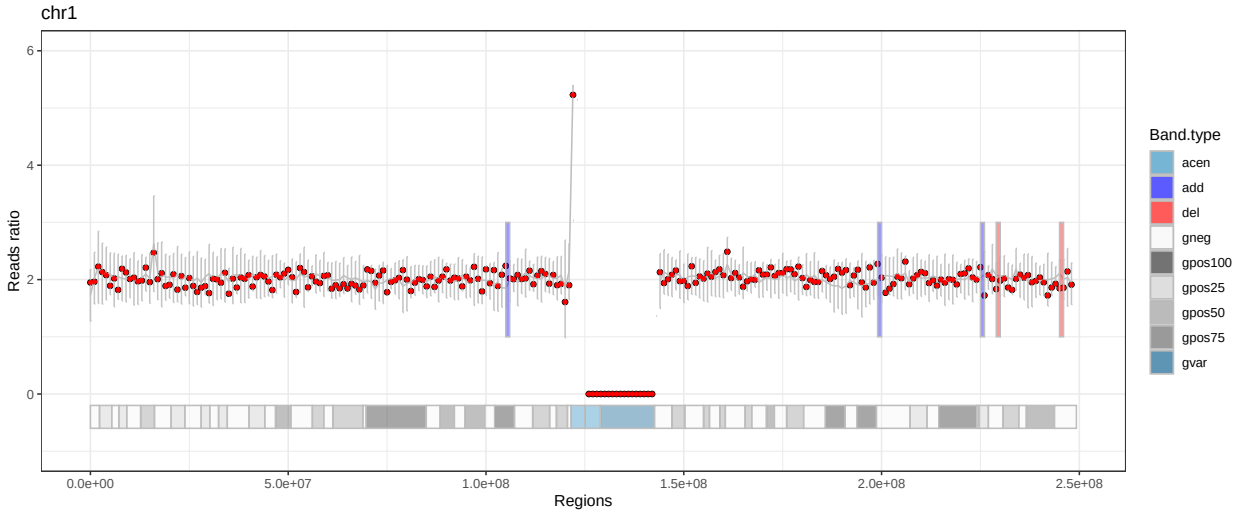
Bailey et al. (2018): Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell 173 (2), 371-385.e18. DOI: 10.1016/j.cell.2018.02.060.;

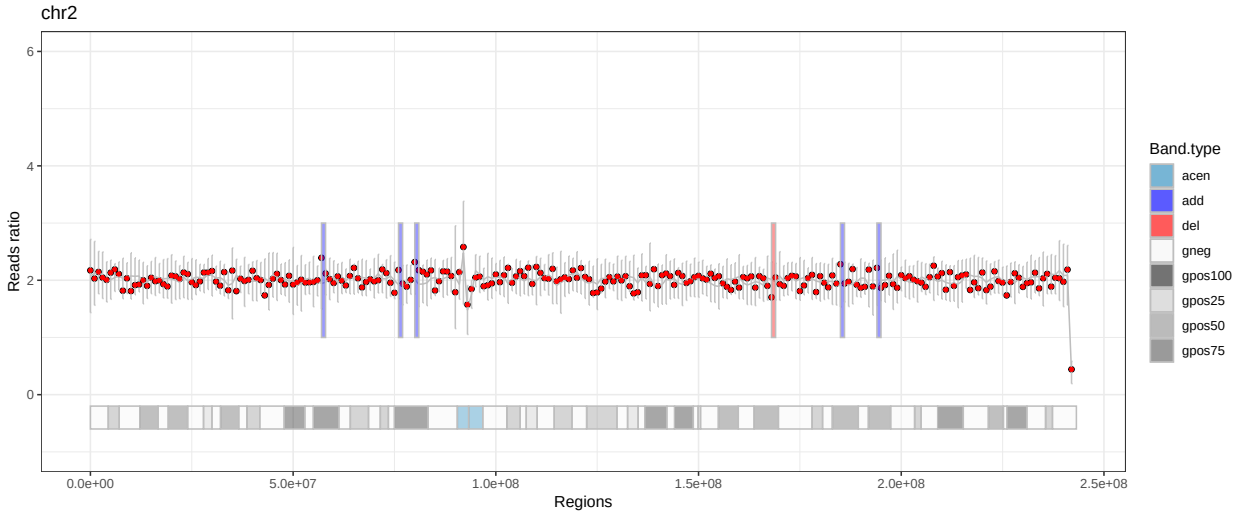
Papaemmanuil et al. (2016): Genomic Classification and Prognosis in Acute Myeloid Leukemia. The New England journal of medicine 374 (23), S. 2209–2221. DOI:10.1056/NEJMoa1516192.

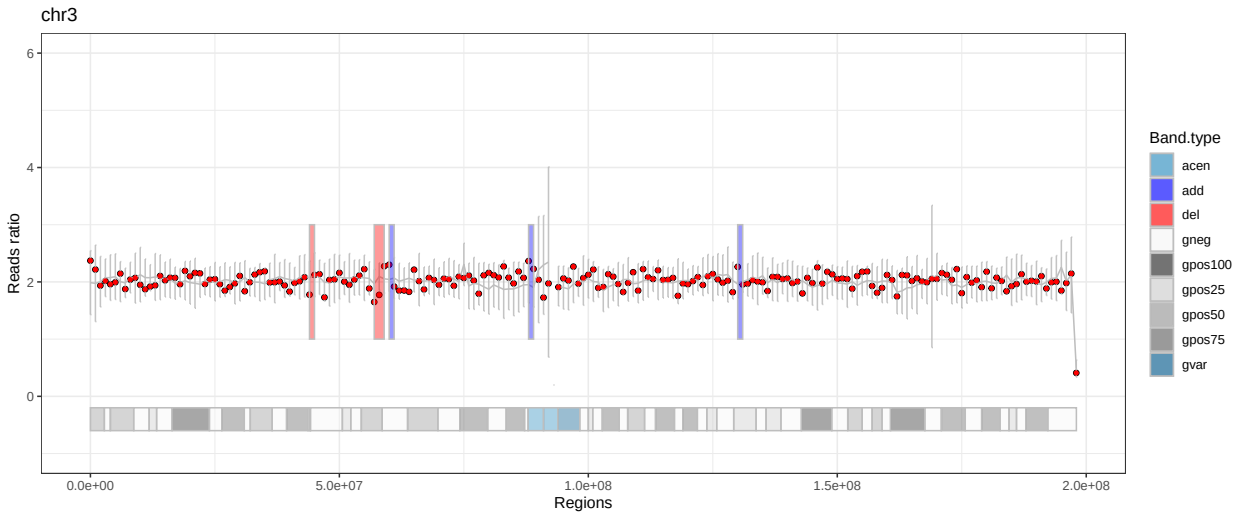
Karyotype overview:

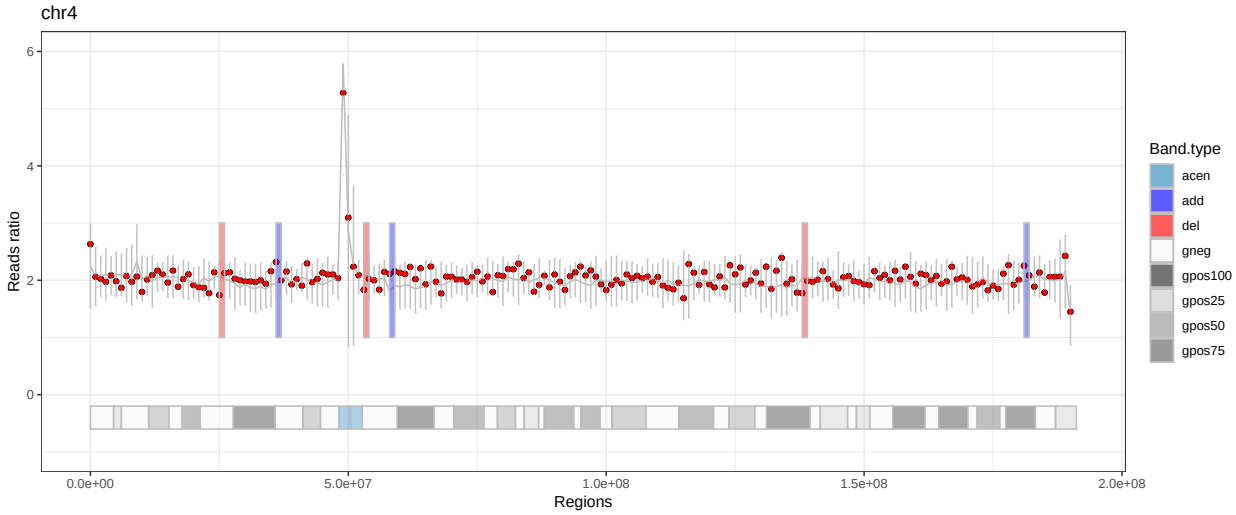


Chromosome Plots:





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Reads ratio
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4
2
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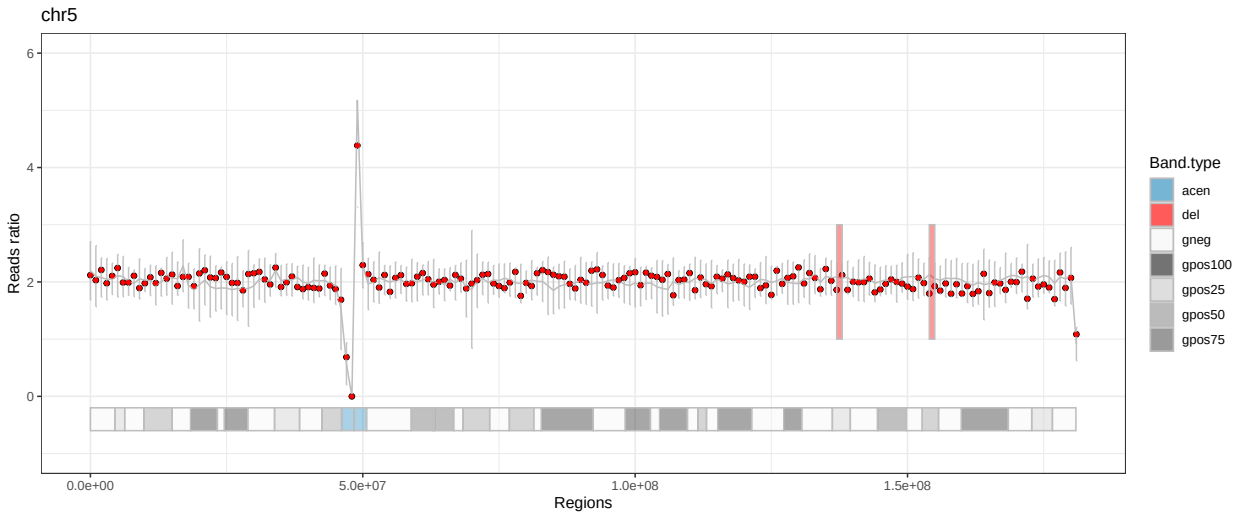
0.0e+00
5.0e+07
1.0e+08
1.5e+08
2.0e+08
Regions
Band.type
acen
add
del
gneg
gpos100
gpos25
gpos50
gpos75


chr5
Reads ratio
6
4
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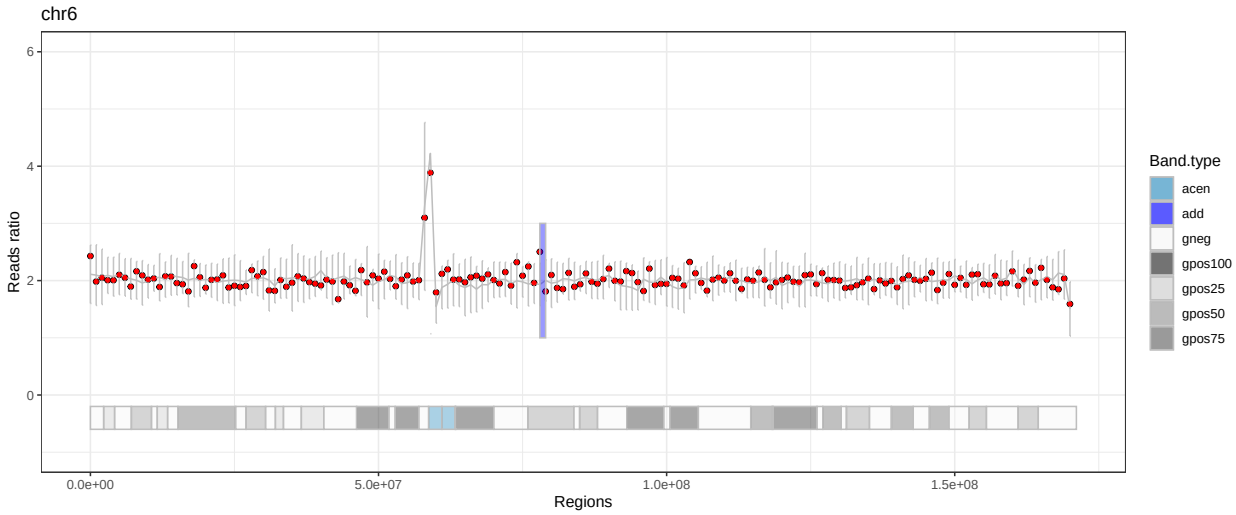
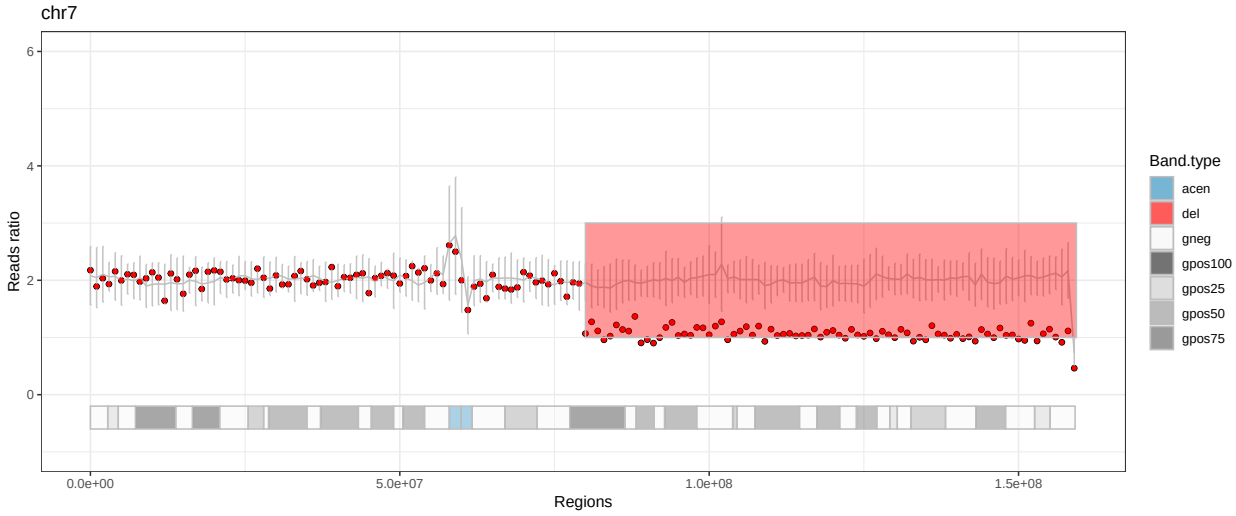
0
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Regions
Band.type
acen
del
gneg
gpos100
gpos25
gpos50
gpos75


chr6
Reads ratio
6
4
2
0
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Regions
Band.type
acen
add
gneg
gpos100
gpos25
gpos50
gpos75


chr7
Reads ratio
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4
2
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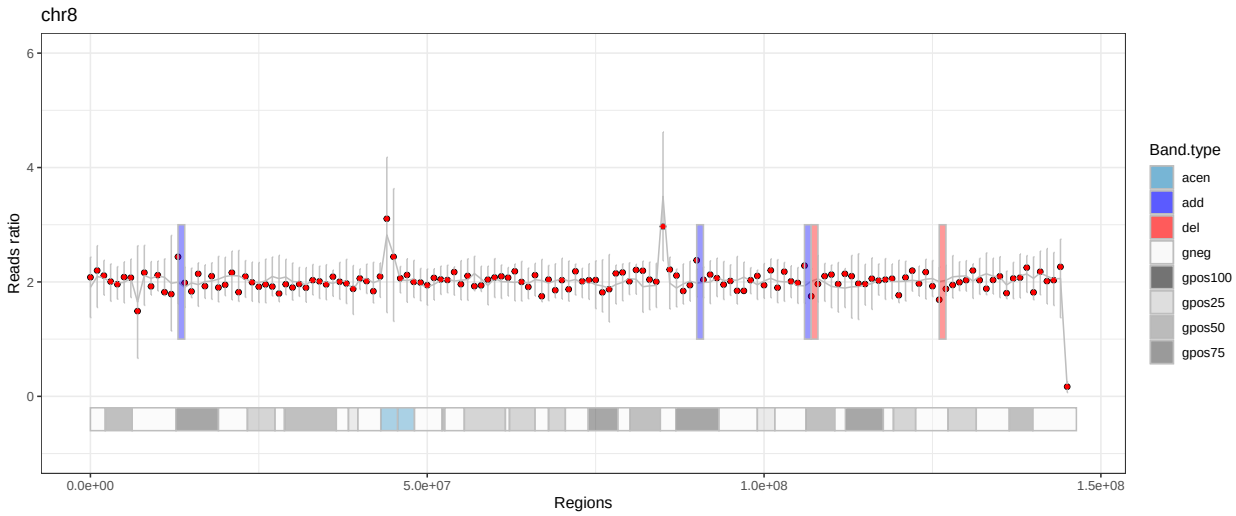
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Regions
Band.type
acen
del
gneg
gpos100
gpos25
gpos50
gpos75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Reads ratio
6
4
2
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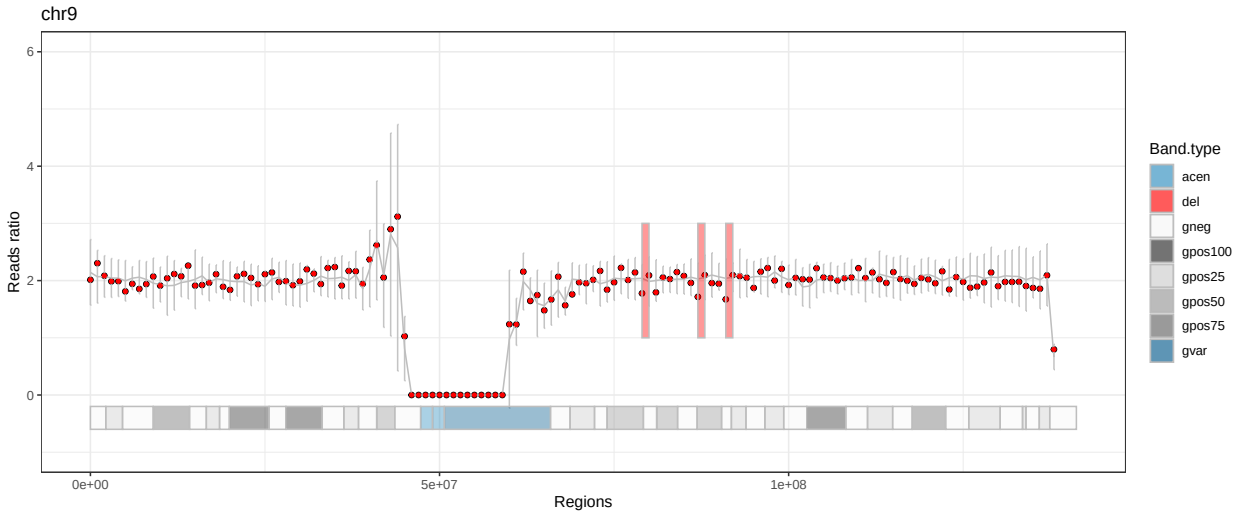
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Regions
Band.type
acen
add
del
gneg
gpos100
gpos25
gpos50
gpos75


chr9
Reads ratio
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4
2
0
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Regions
Band.type
acen
del
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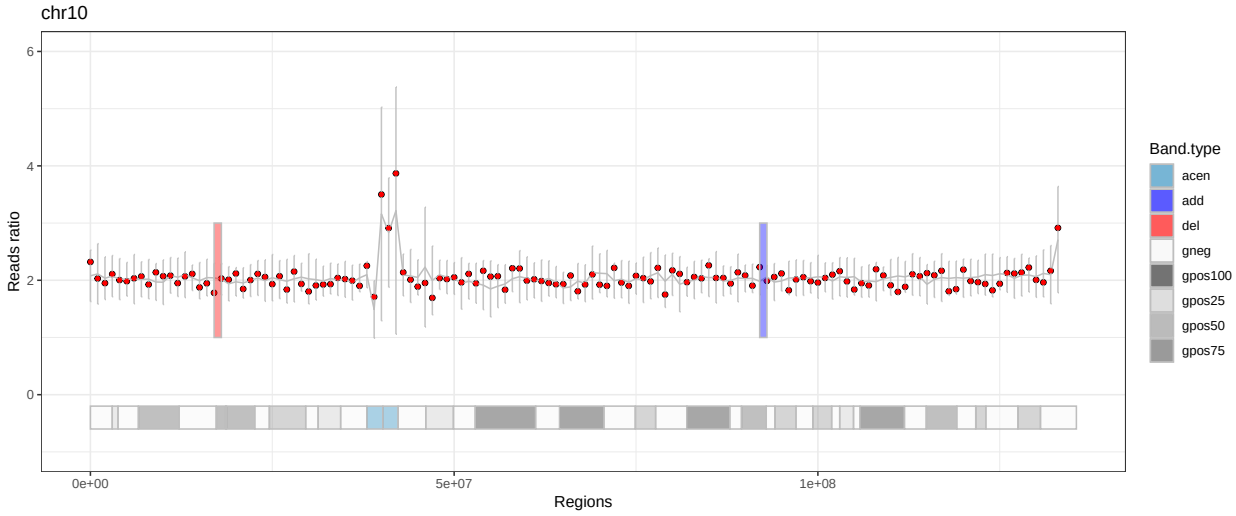
gpos25
gpos50
gpos75
gvar


chr10
Reads ratio
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2
4
6
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Regions
Band.type
acen
add
del
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gpos25
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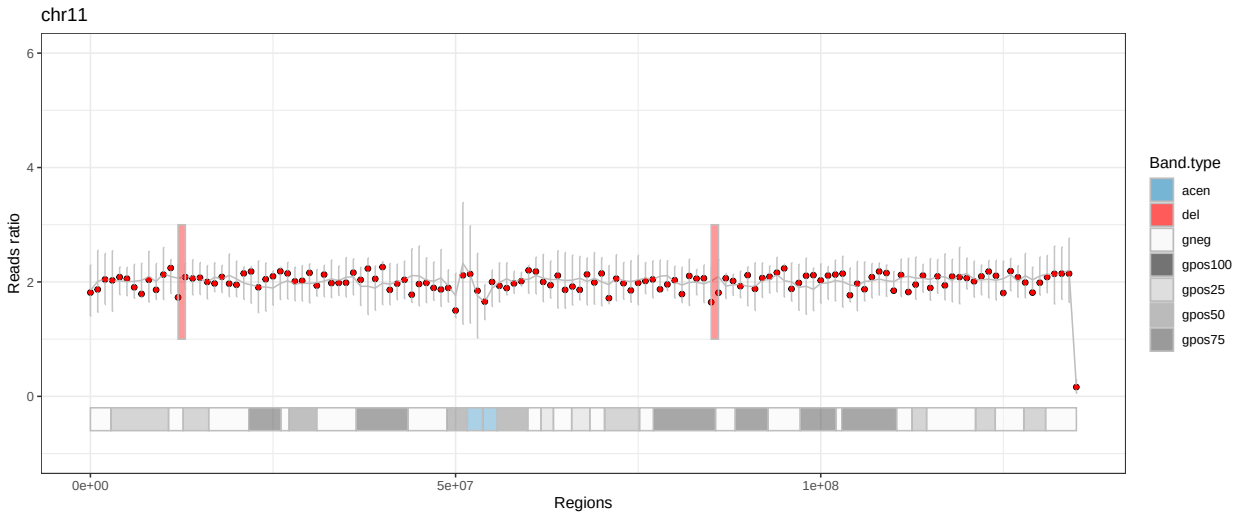
gpos75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Reads ratio
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2
4
6
0e+00
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1e+08
Regions
Band.type
acen
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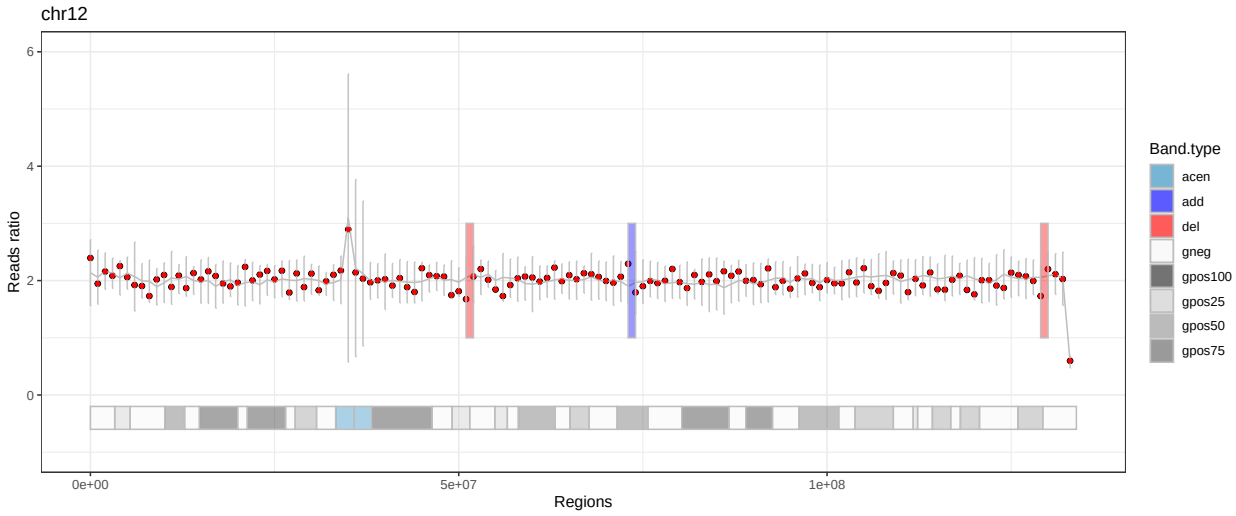
gneg
gpos100
gpos25
gpos50
gpos75


chr12
Reads ratio
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2
4
6
0e+00
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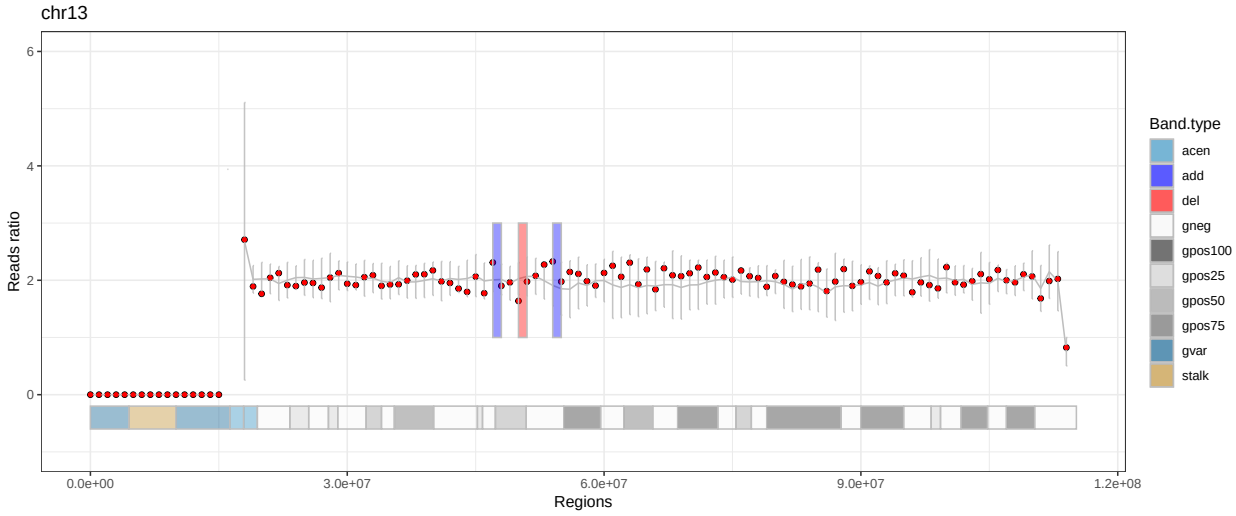
1e+08
Regions
Band.type
acen
add
del
gneg
gpos100
gpos25
gpos50
gpos75


chr13
Reads ratio
Regions
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3.0e+07
6.0e+07
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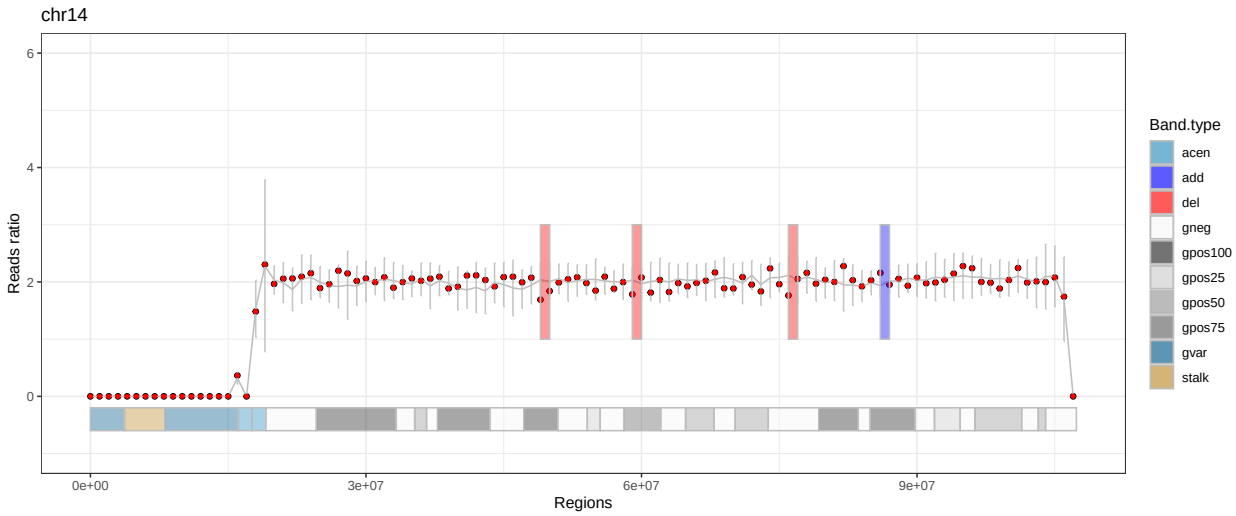
Band.type
acen
add
del
gneg
gpos100
gpos25
gpos50
gpos75
gvar
stalk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Reads ratio
Regions
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3e+07
6e+07
9e+07
Band.type
acen
add
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gneg
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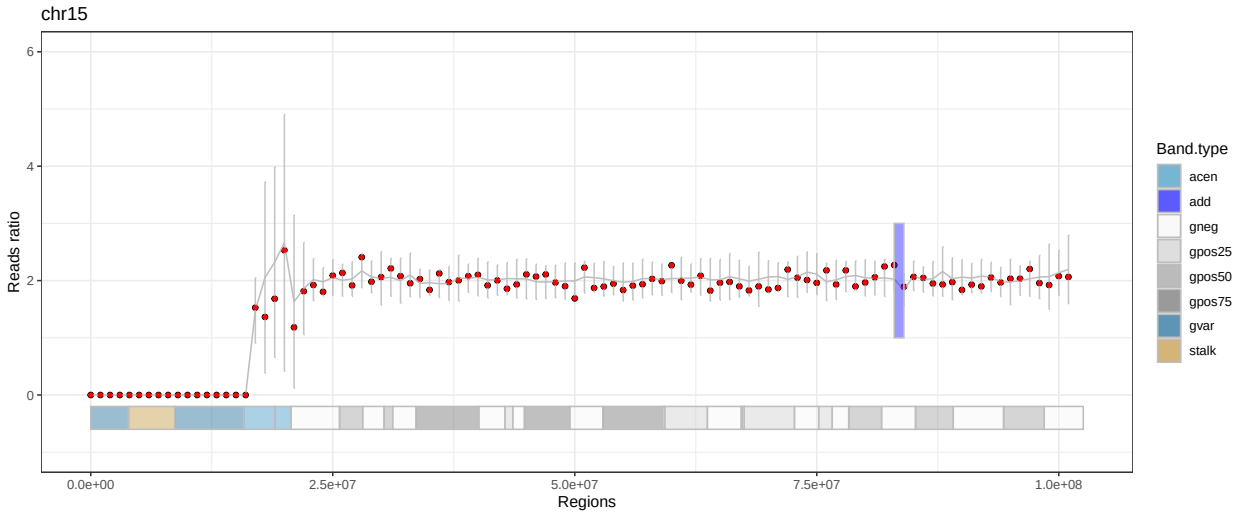
gpos25
gpos50
gpos75
gvar
stalk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Reads ratio
Regions
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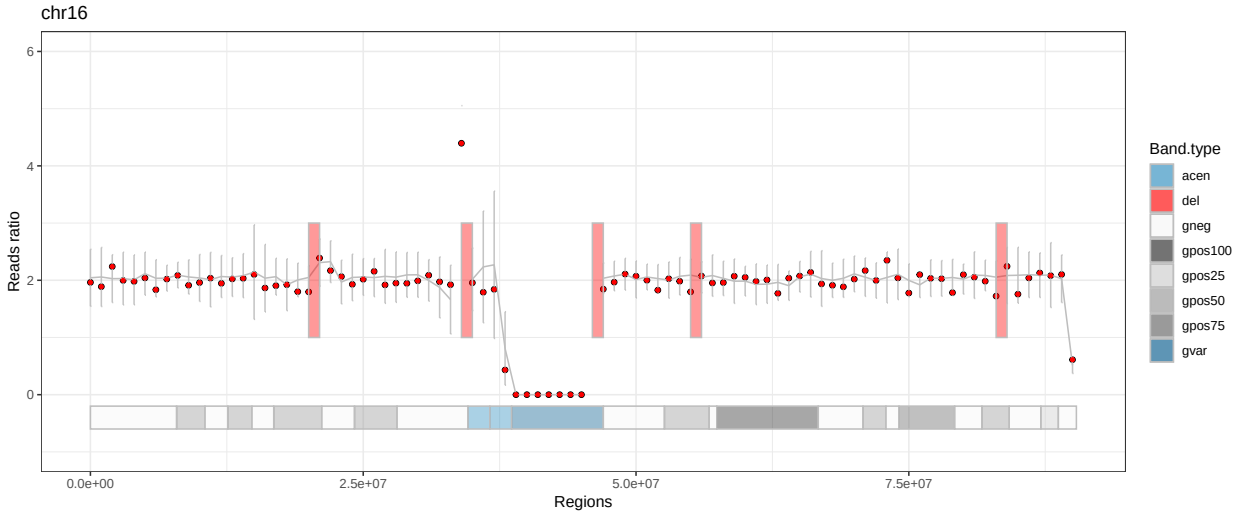
2.5e+07
5.0e+07
7.5e+07
1.0e+08
Band.type
acen
add
gneg
gpos25
gpos50
gpos75
gvar
stalk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Regions
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Band.type
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del
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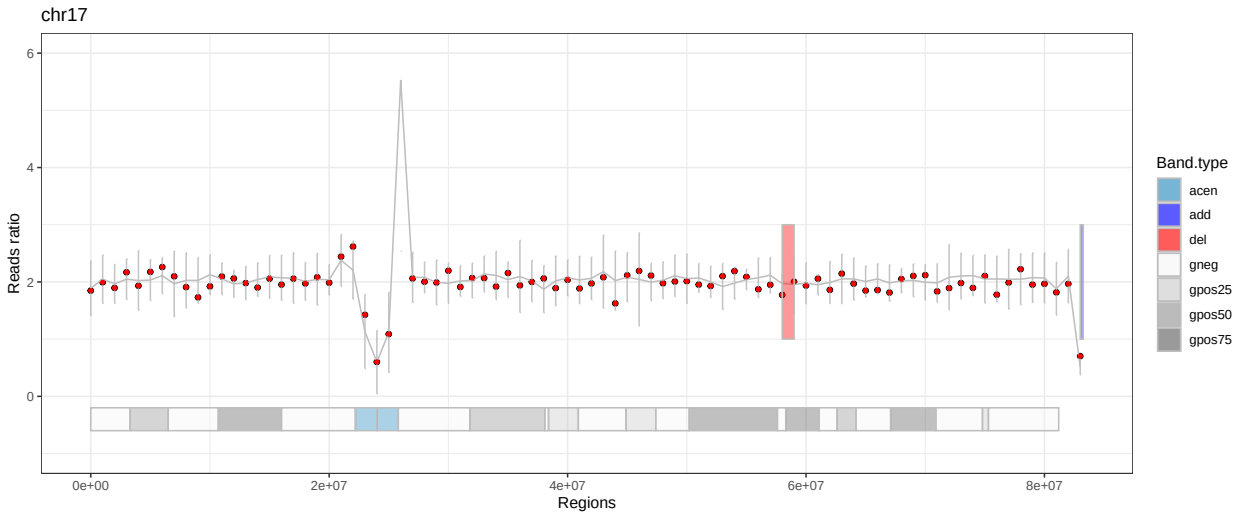
gpos75
gvar


chr17
Reads ratio
Regions
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Band.type
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add
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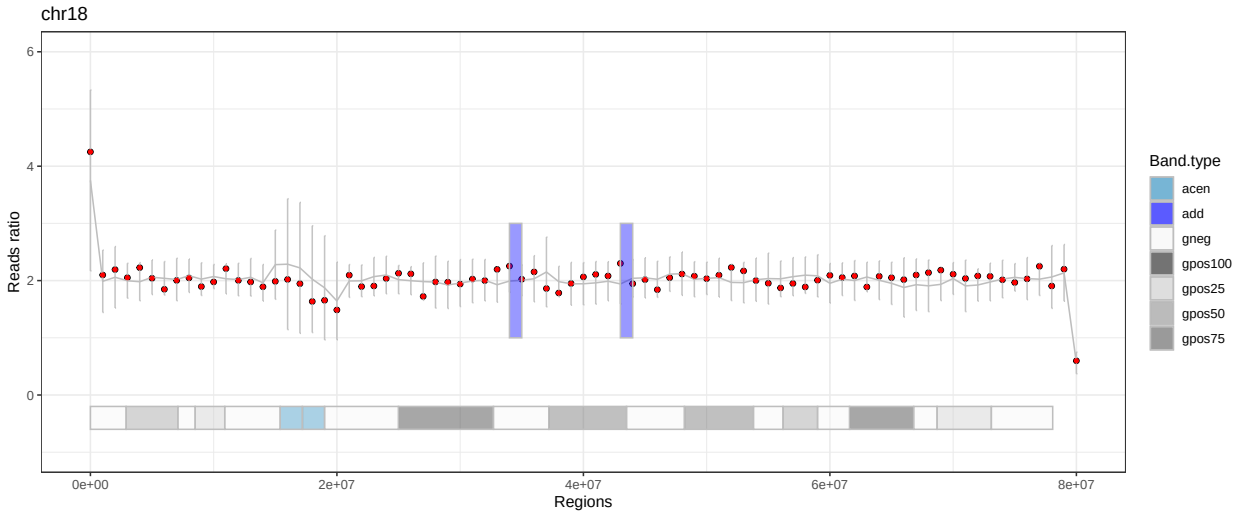
gpos50
gpos75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Reads ratio
Regions
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6e+07
8e+07
Band.type
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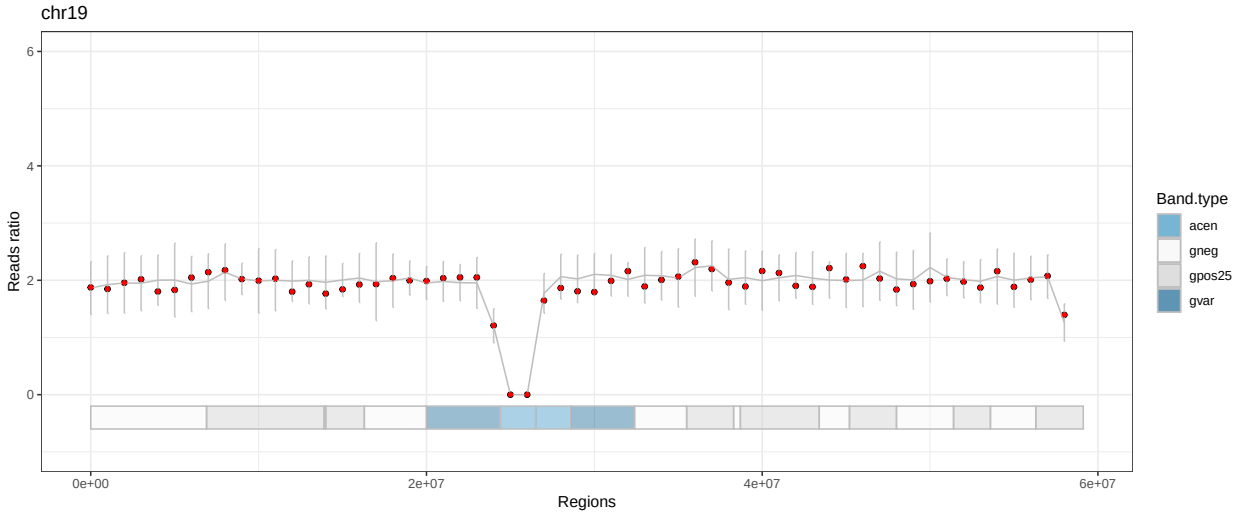
gpos50
gpos75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Reads ratio
Regions
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4e+07
6e+07
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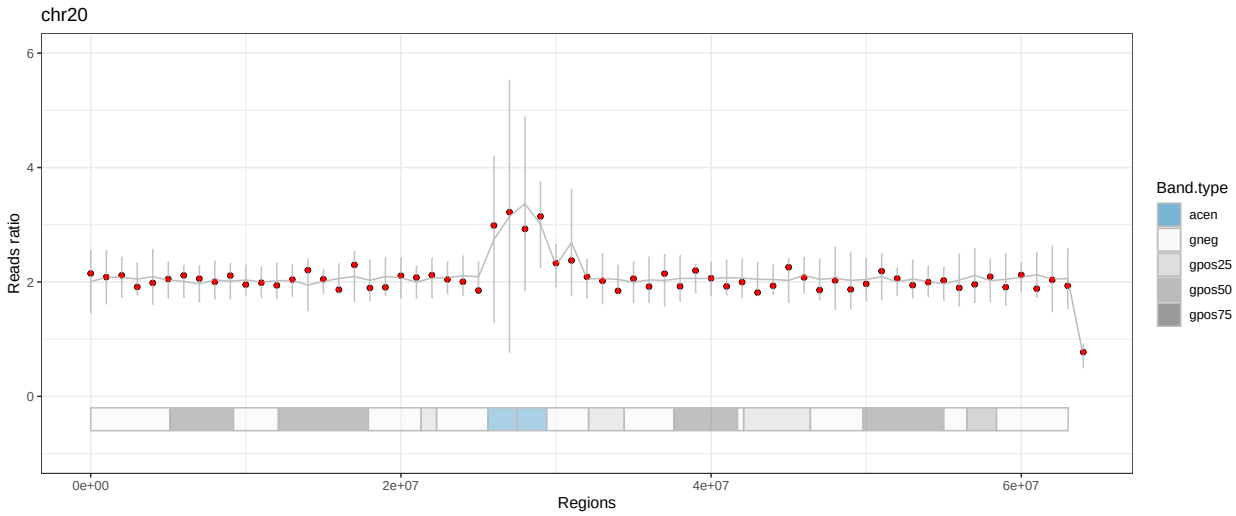
2
4
6
Band.type
acen
gneg
gpos25
gvar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Reads ratio
Regions
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6e+07
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2
4
6
Band.type
acen
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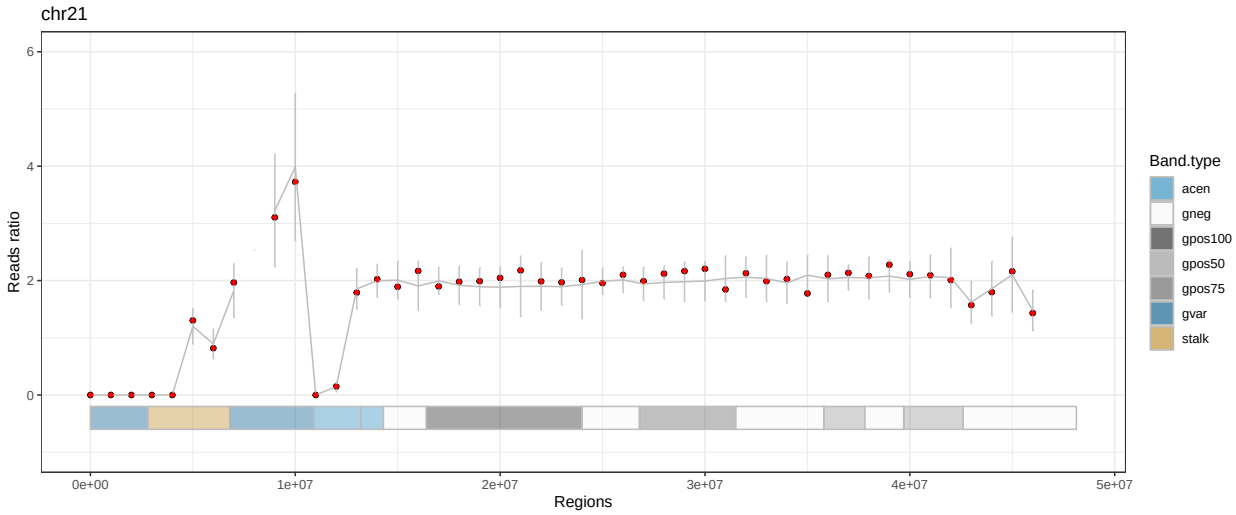
gpos50
gpos75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Reads ratio
Regions
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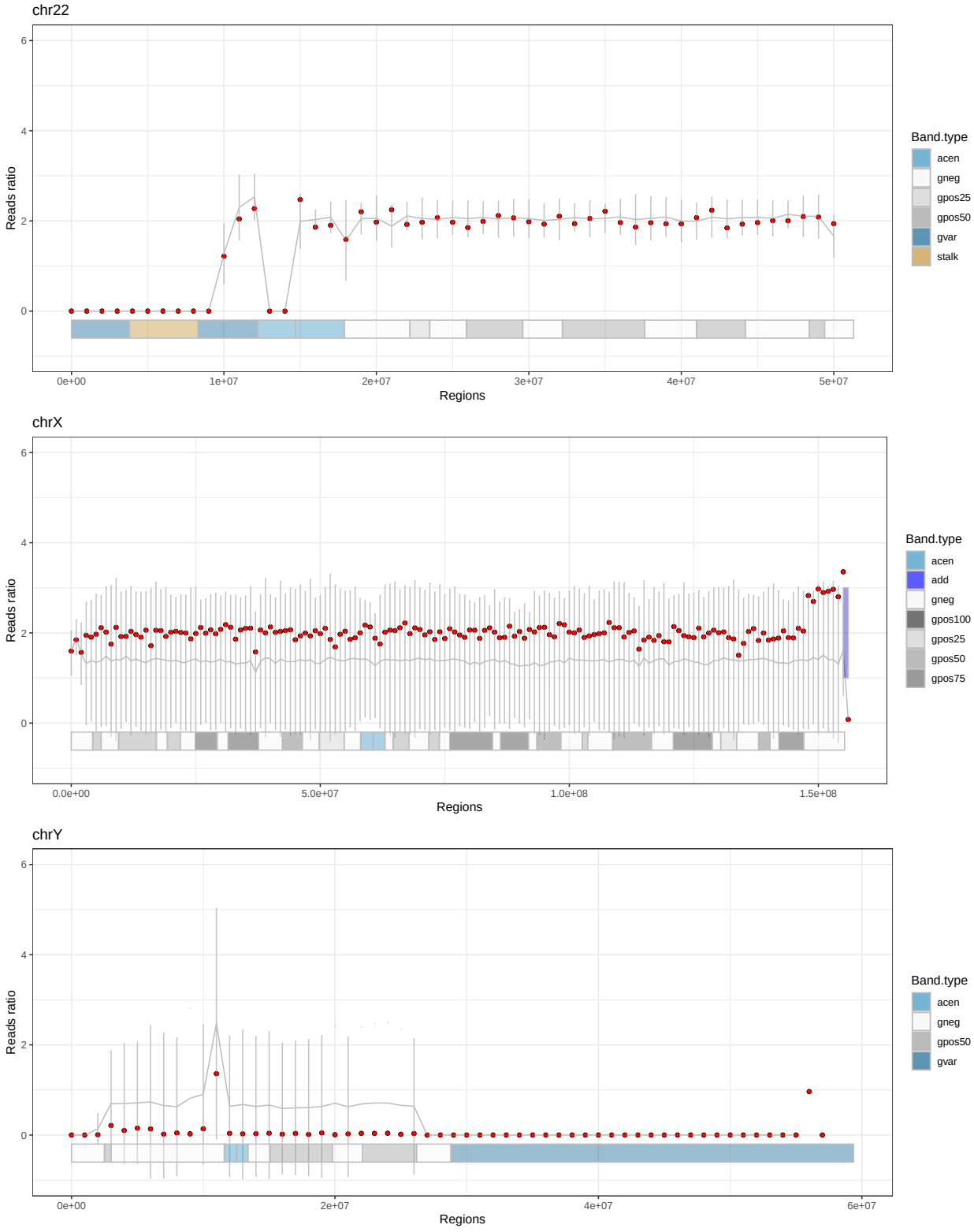
Band.type
acen
gneg
gpos100
gpos50
gpos75
gvar
stalk



The legend contains two characteristics:

1. Giemsa stain results. Recognized stain values: gneg, gpos50, gpos75, gpos25, gpos100, acen,

gvar, stalk.

2. The abnormal regions (add or del).