Report CORIANDR: ChrOmosomal abeRration Identifier AND Reporter in R

09 Dezember, 2020

unique_reads	2729209
average_length	150.12
unique_mapped_reads	5066331
SAMPLE_ID	17839.muenchen
gender	M

Calculated numerical karyotype:

add(1)(q11q11)

add(1)(q21.1q21.1)

add(5)(p15.1p15.1)

del(12)(q23.2q23.2)

add(18)(q23q23)

add(Y)(q12q12)

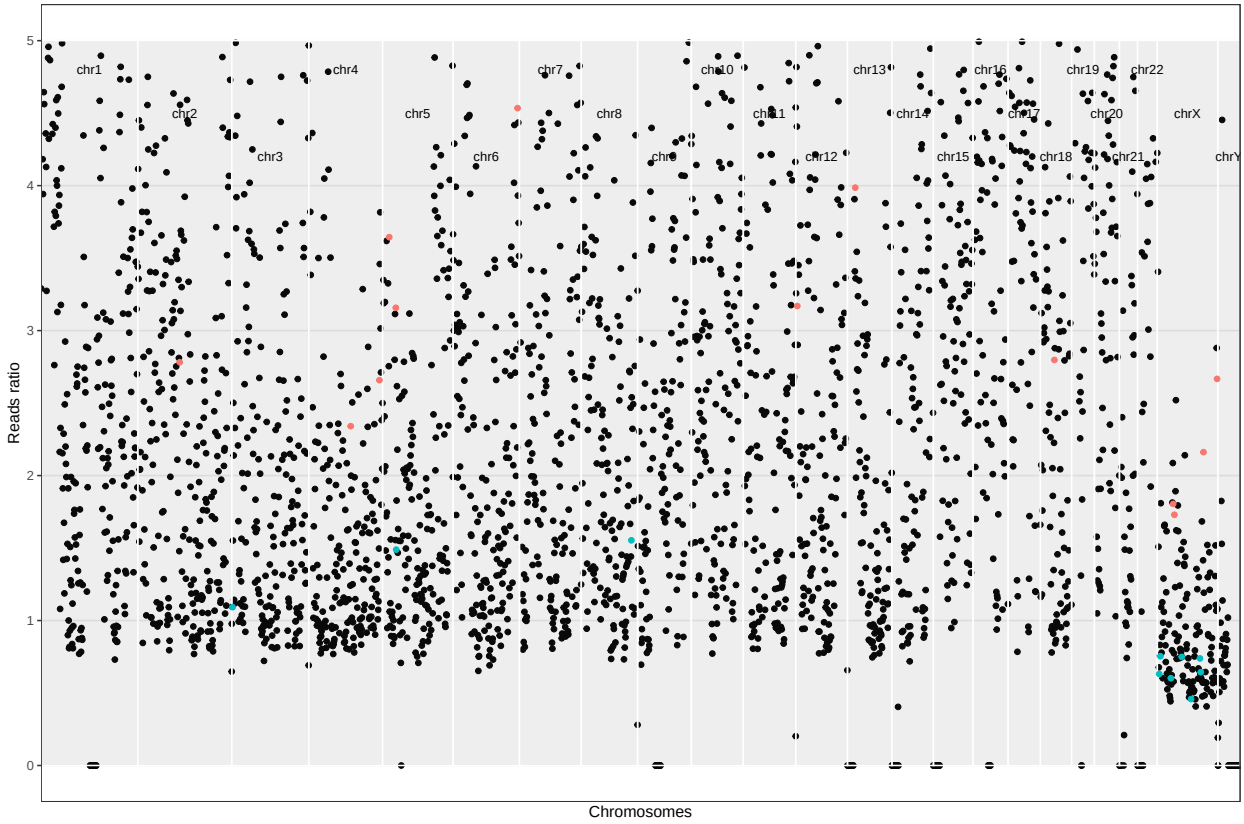
Genes affected by CNVs*:

id	sym	bol chr	sta	rt end	abe	rration
16045	ENSG00000168685	IL7R	chr5	35852695	35879603	del
40605	ENSG00000121741	ZMYM2	chr13	19958670	20091829	amp
40632	ENSG00000150457	LATS2	chr13	20973036	21061586	amp
250501	ENSG00000124486	USP9X	chrX	41085445	41236579	amp
250551	ENSG00000215301	DDX3X	chrX	41333284	41364472	amp
251001	ENSG00000147050	KDM6A	chrX	44873177	45112602	amp
268991	ENSG00000196924	FLNA	chrX	154348524	154374638	amp

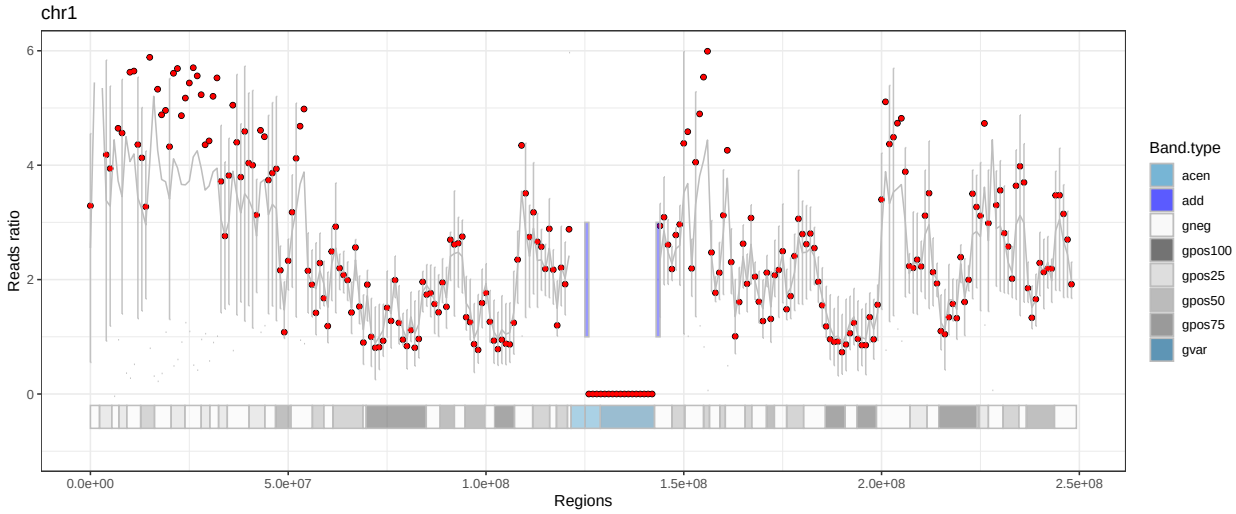
Bailey et al. (2018): Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell 173 (2), 371-385.e18. DOI: 10.1016/j.cell.2018.02.060.;

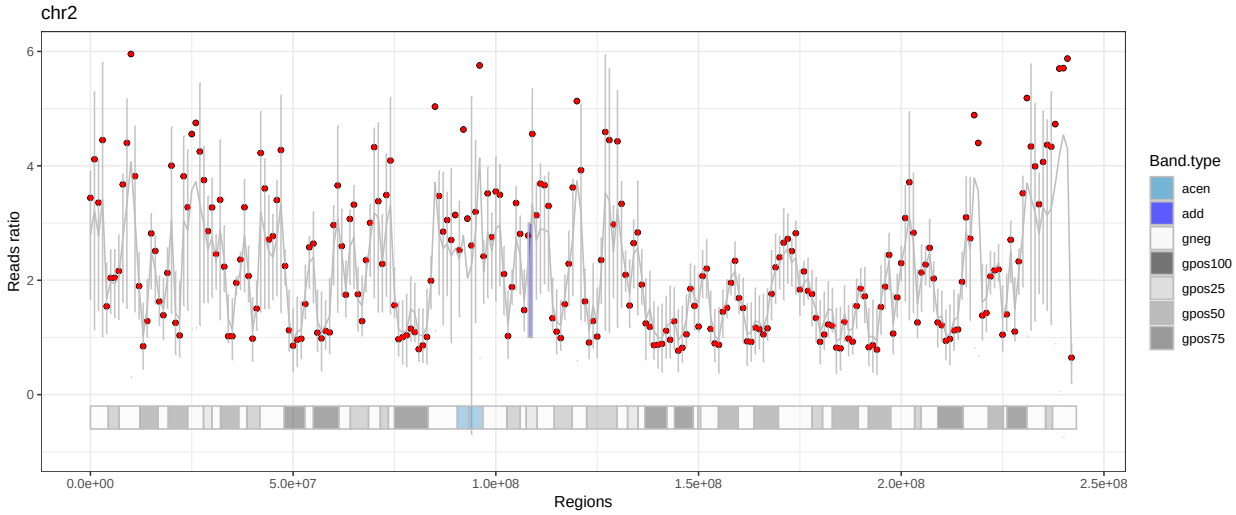
Papaemmanuil et al. (2016): Genomic Classification and Prognosis in Acute Myeloid Leukemia. The New England journal of medicine 374 (23), S. 2209–2221. DOI:10.1056/NEJMoa1516192.

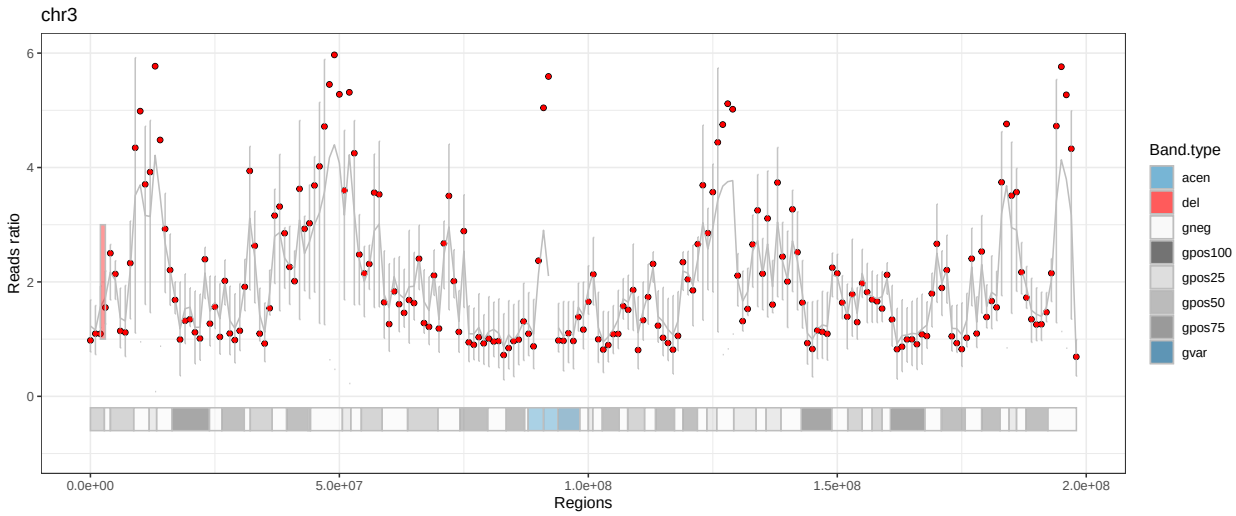
Karyotype overview:

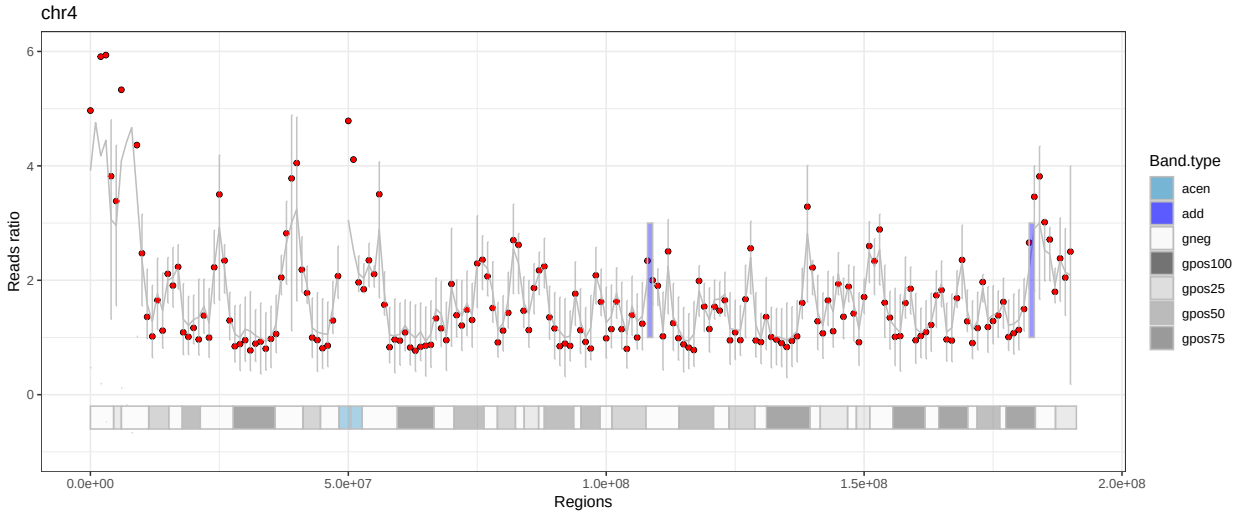


Chromosome Plots:





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Reads ratio
Regions
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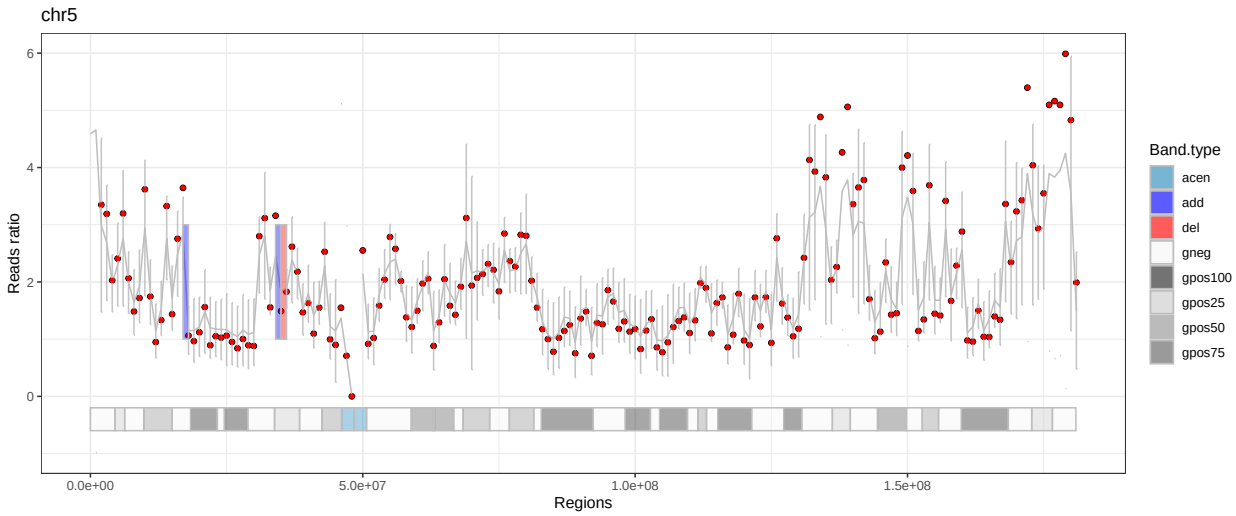
1.0e+08
1.5e+08
2.0e+08
Band.type
acen
add
gneg
gpos100
gpos25
gpos50
gpos75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Reads ratio
Regions
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1.0e+08
1.5e+08
Band.type
acen
add
del
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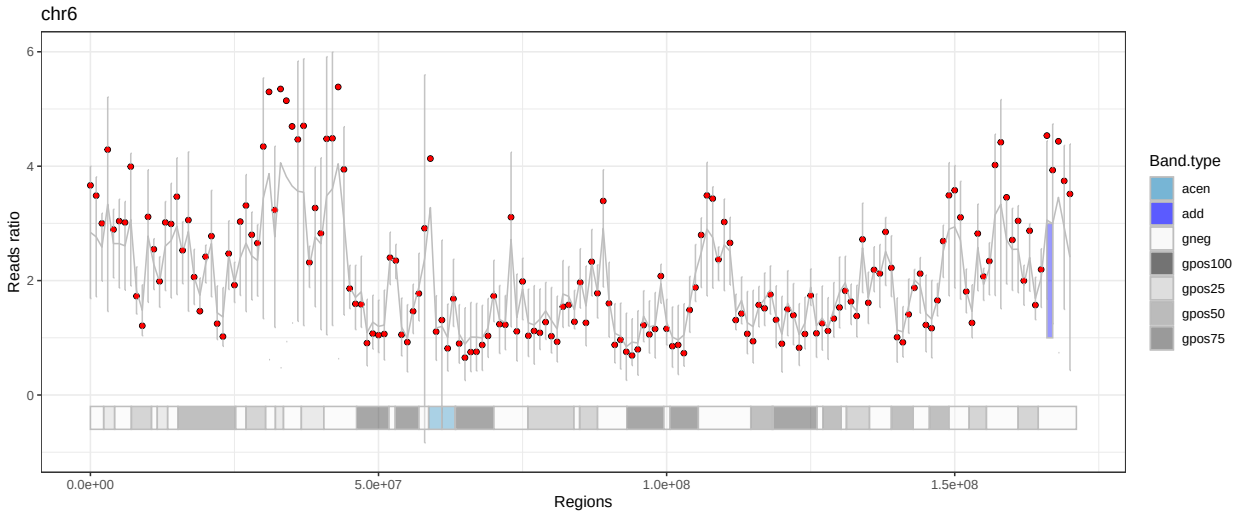
gpos100
gpos25
gpos50
gpos75


chr6
Reads ratio
Regions
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5.0e+07
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1.5e+08
Band.type
acen
add
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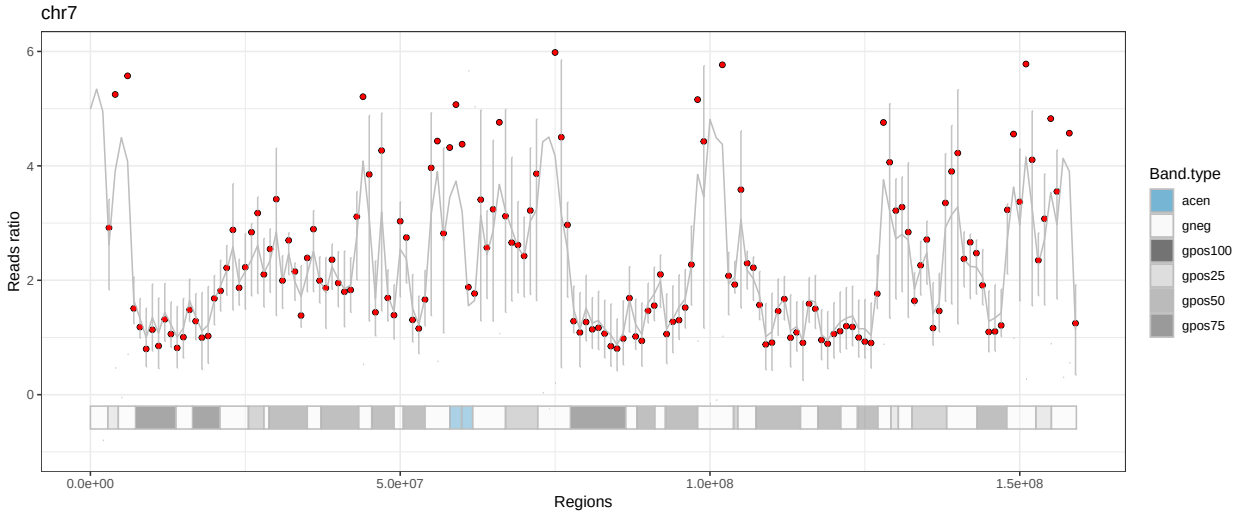
gpos50
gpos75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Reads ratio
Regions
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5.0e+07
1.0e+08
1.5e+08
Band.type
acen
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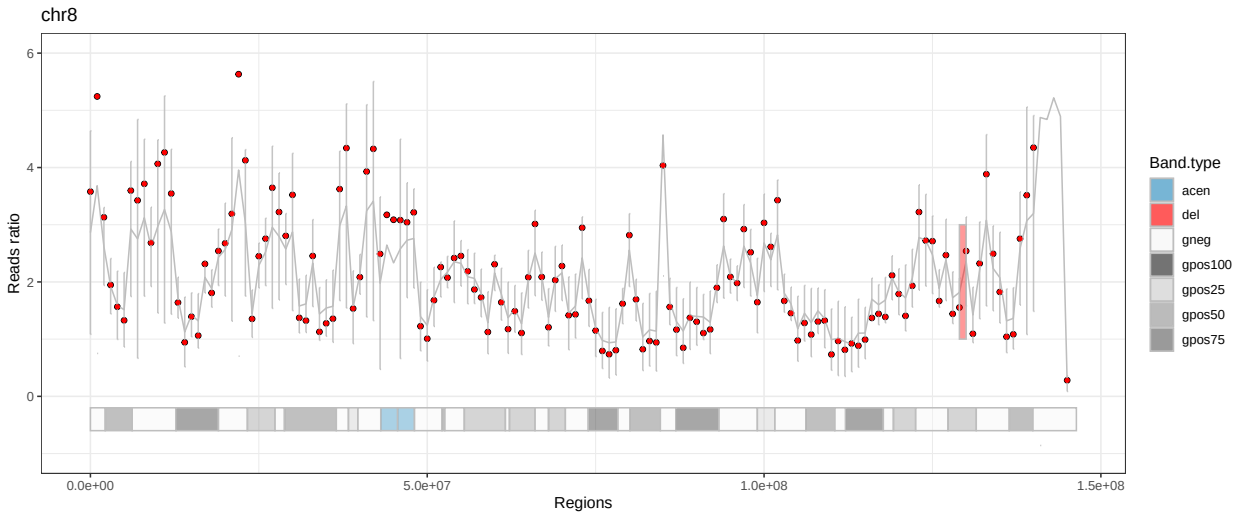
gpos75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Reads ratio
Regions
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1.5e+08
Band.type
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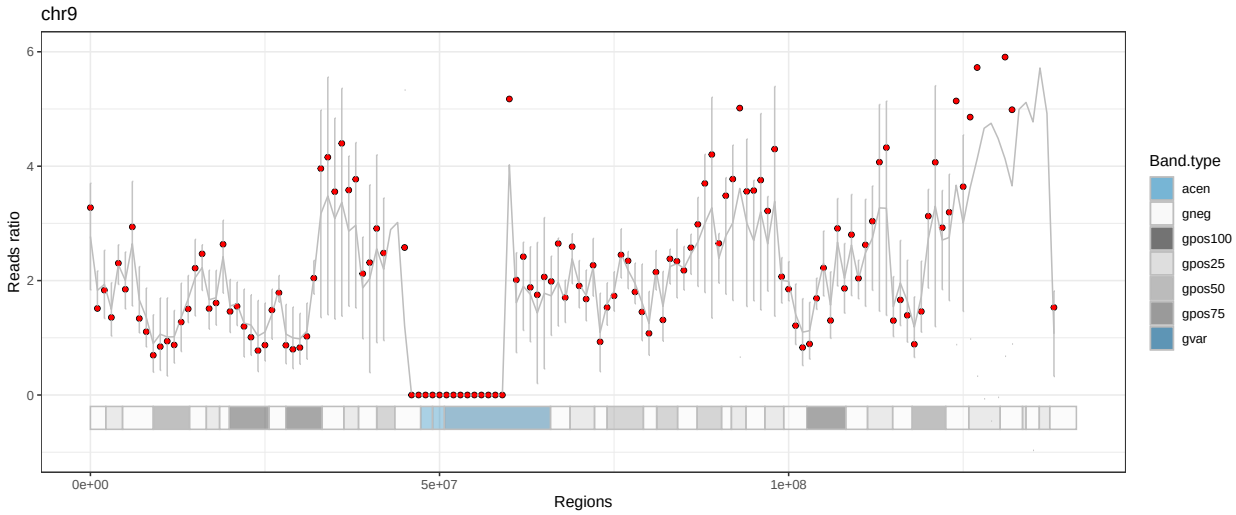
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Reads ratio
Regions
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Band.type
acen
gneg
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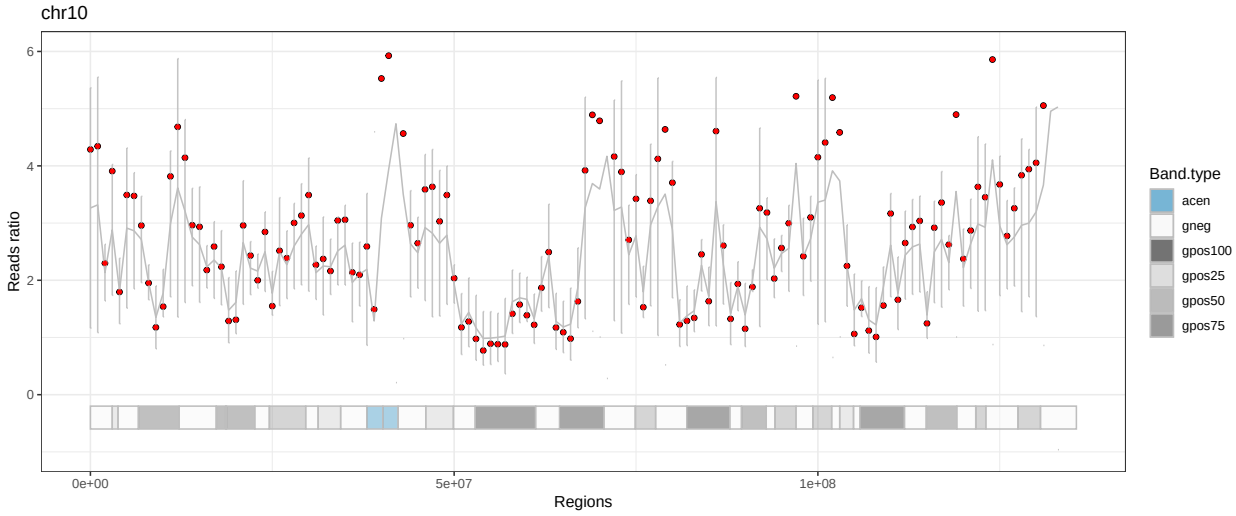
gpos75
gvar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Reads ratio
0
2
4
6
0e+00
5e+07
1e+08
Regions
Band.type
acen
gneg
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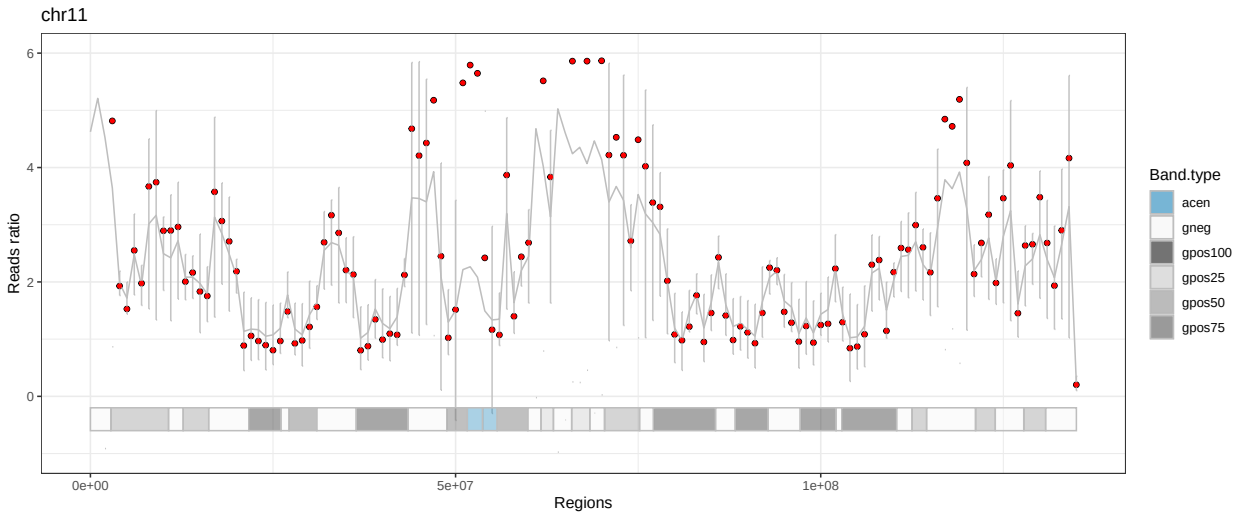
gpos25
gpos50
gpos75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Reads ratio
0
2
4
6
0e+00
5e+07
1e+08
Regions
Band.type
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gneg
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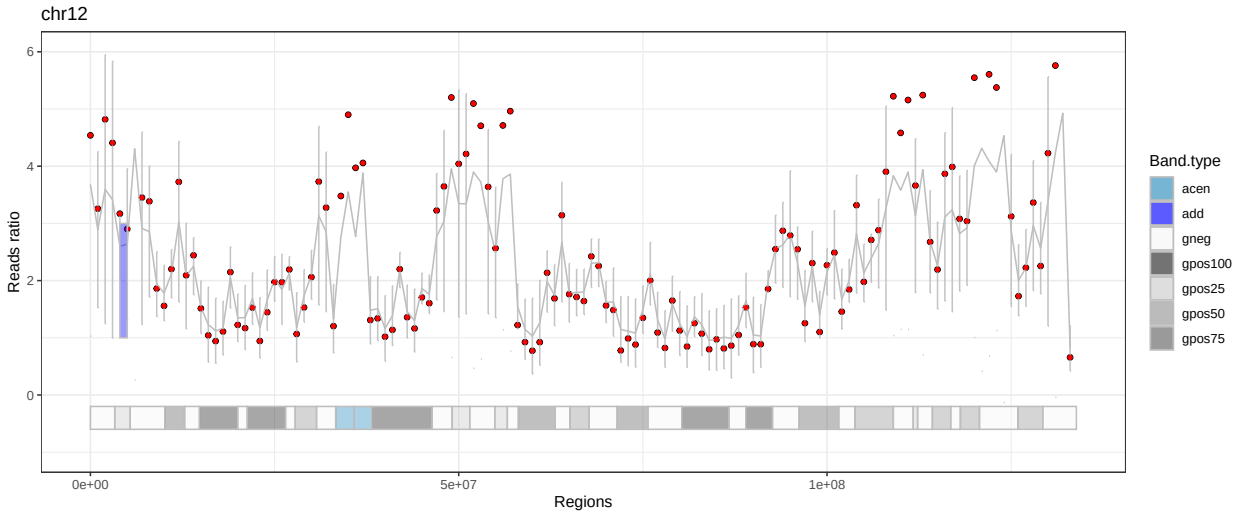
gpos25
gpos50
gpos75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Reads ratio
0
2
4
6
0e+00
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1e+08
Regions
Band.type
acen
add
gneg
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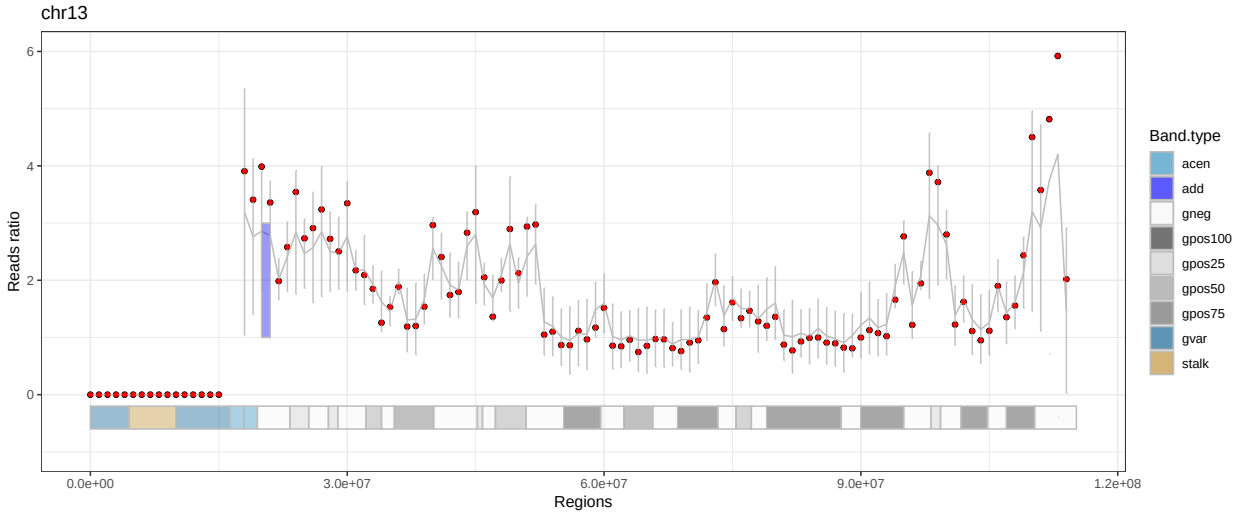
gpos50
gpos75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Reads ratio
Regions
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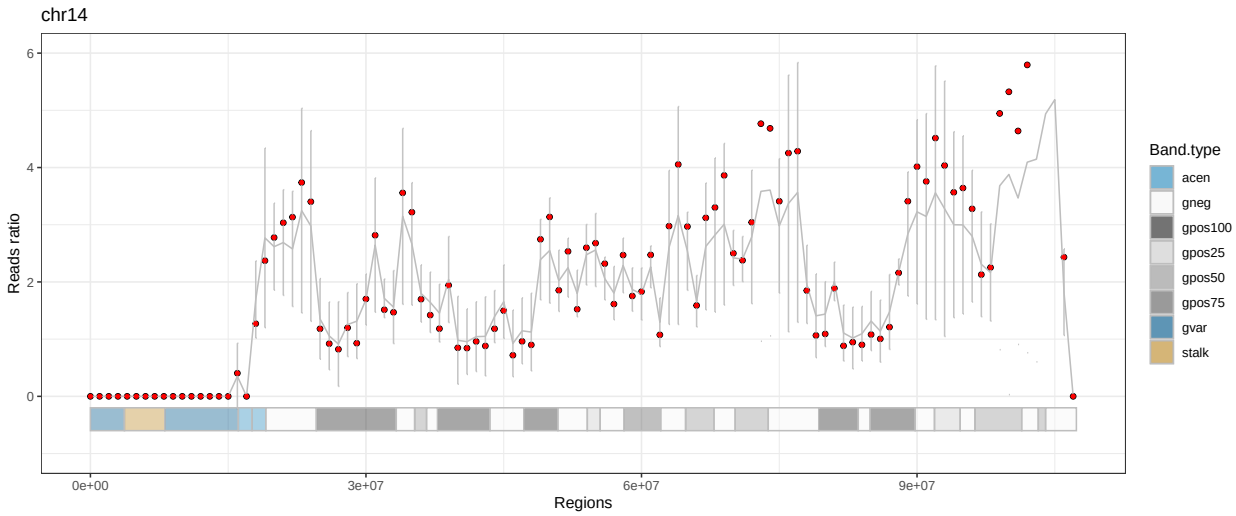
3.0e+07
6.0e+07
9.0e+07
1.2e+08
Band.type
acen
add
gneg
gpos100
gpos25
gpos50
gpos75
gvar
stalk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Reads ratio
Regions
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Band.type
acen
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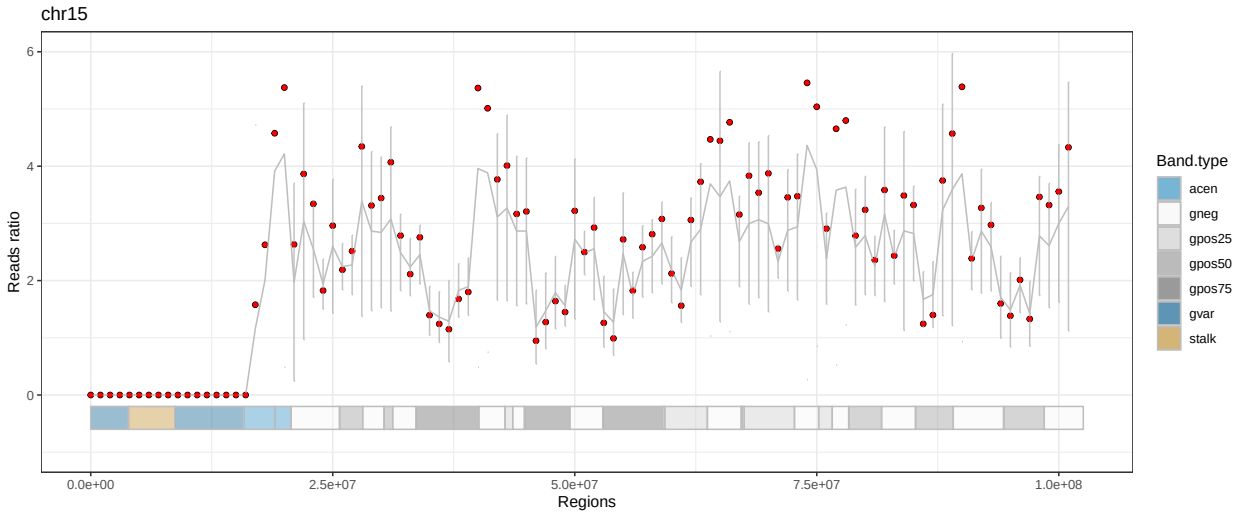
gpos75
gvar
stalk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Reads ratio
Regions
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2.5e+07
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7.5e+07
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Band.type
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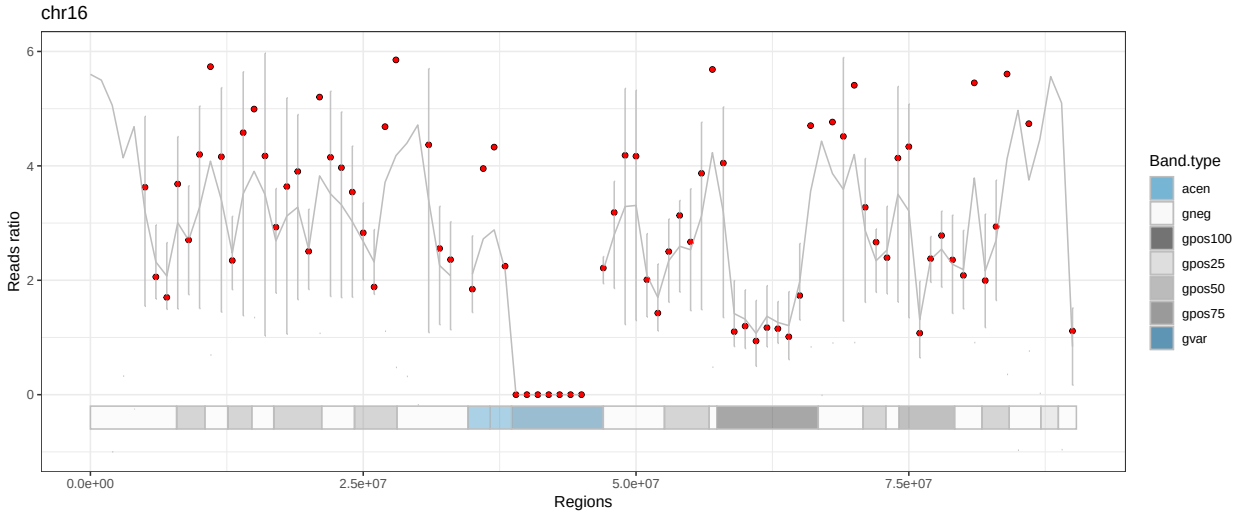
gneg
gpos25
gpos50
gpos75
gvar
stalk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Reads ratio
Regions
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7.5e+07
Band.type
acen
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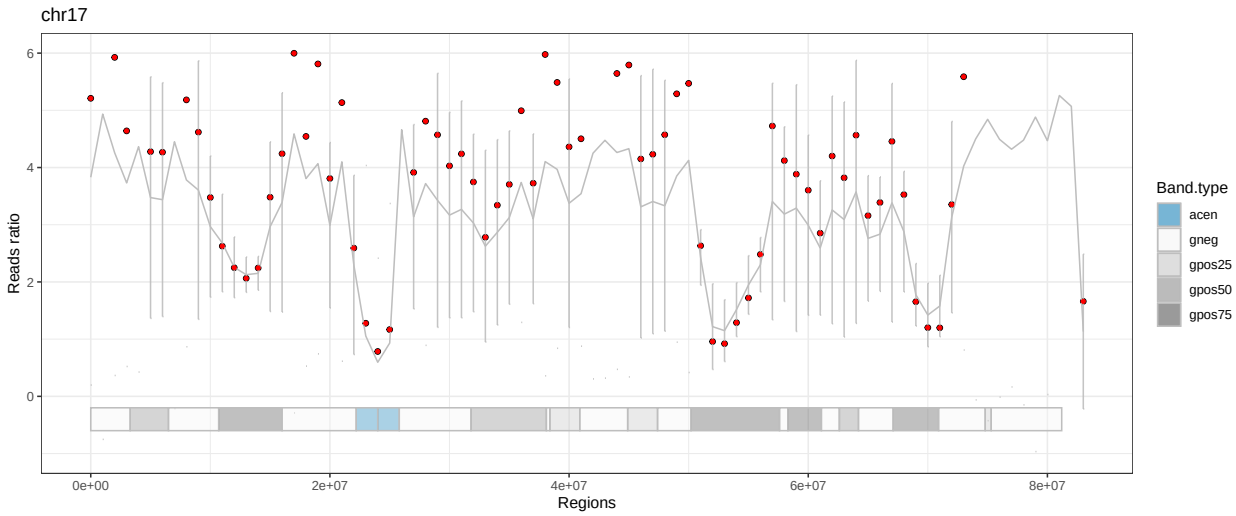
gpos50
gpos75
gvar


chr17
Reads ratio
Regions
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2e+07
4e+07
6e+07
8e+07
Band.type
acen
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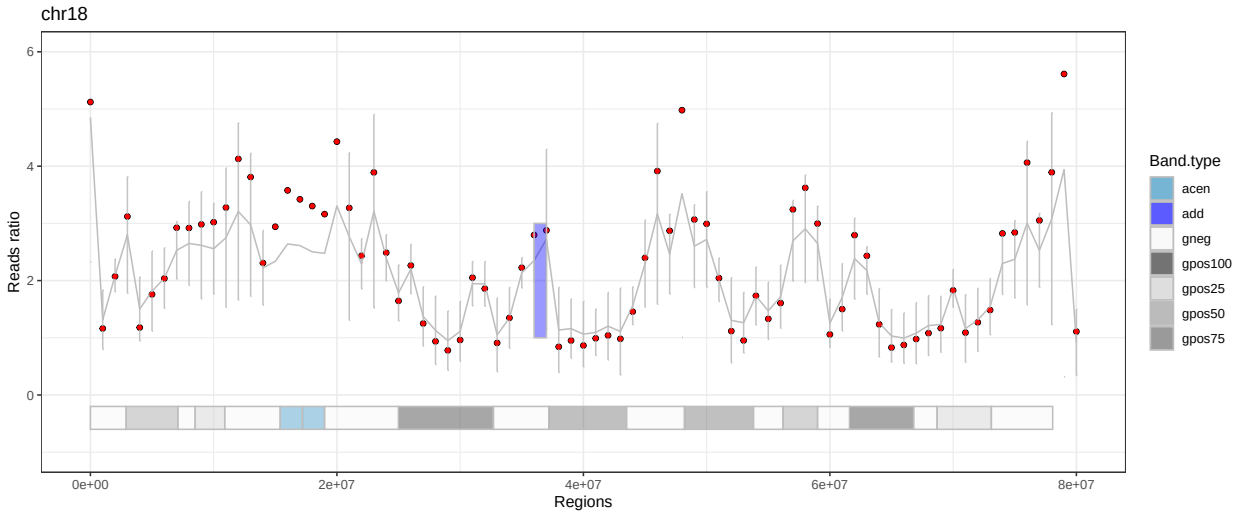
gpos50
gpos75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Reads ratio
Regions
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4e+07
6e+07
8e+07
Band.type
acen
add
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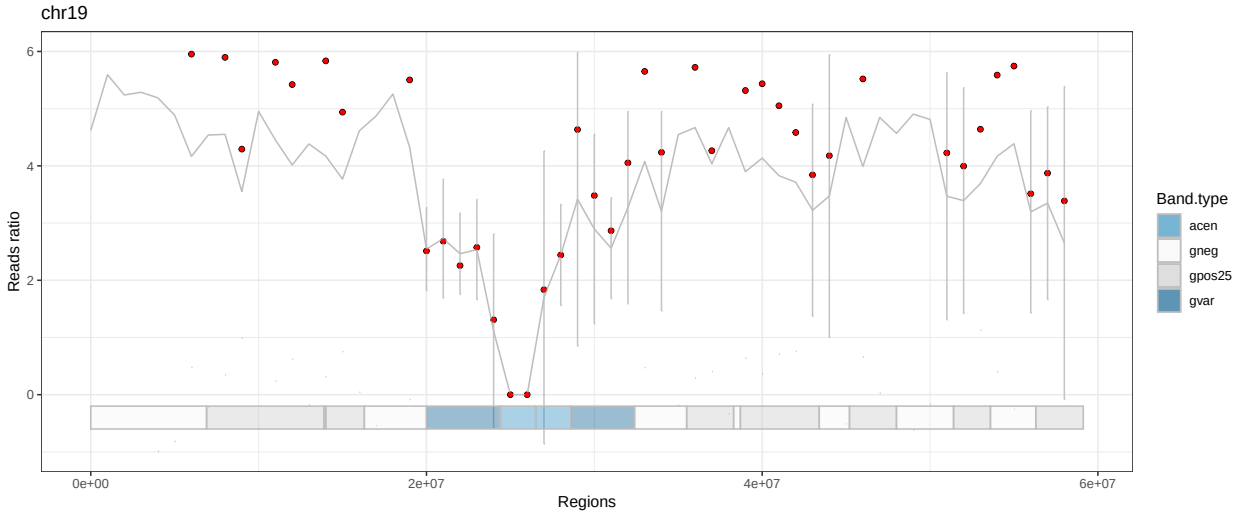
gpos50
gpos75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Reads ratio
Regions
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4e+07
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Band.type
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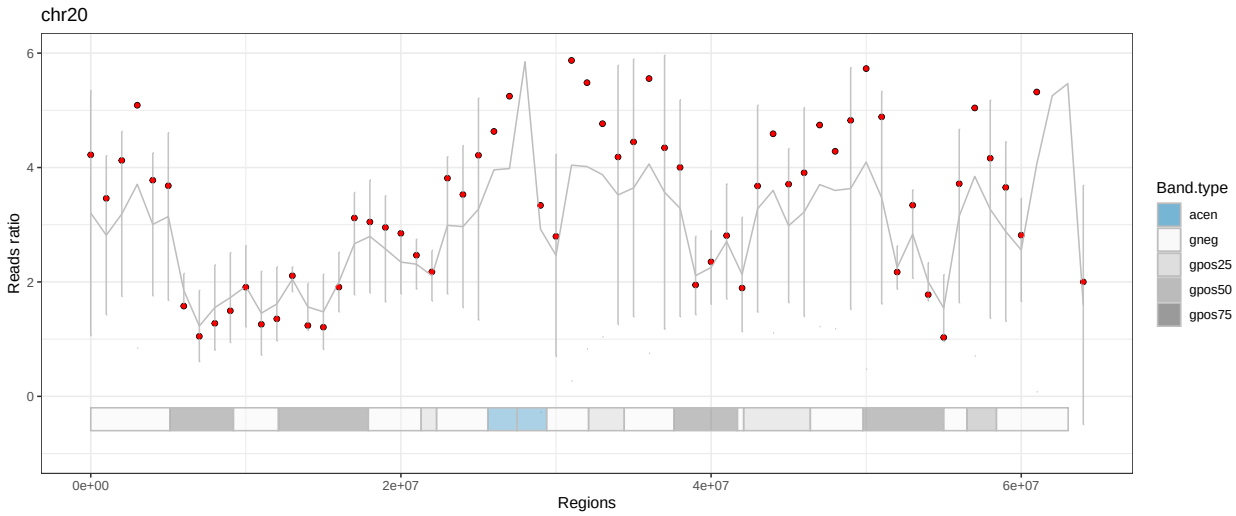
gneg
gpos25
gvar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Regions
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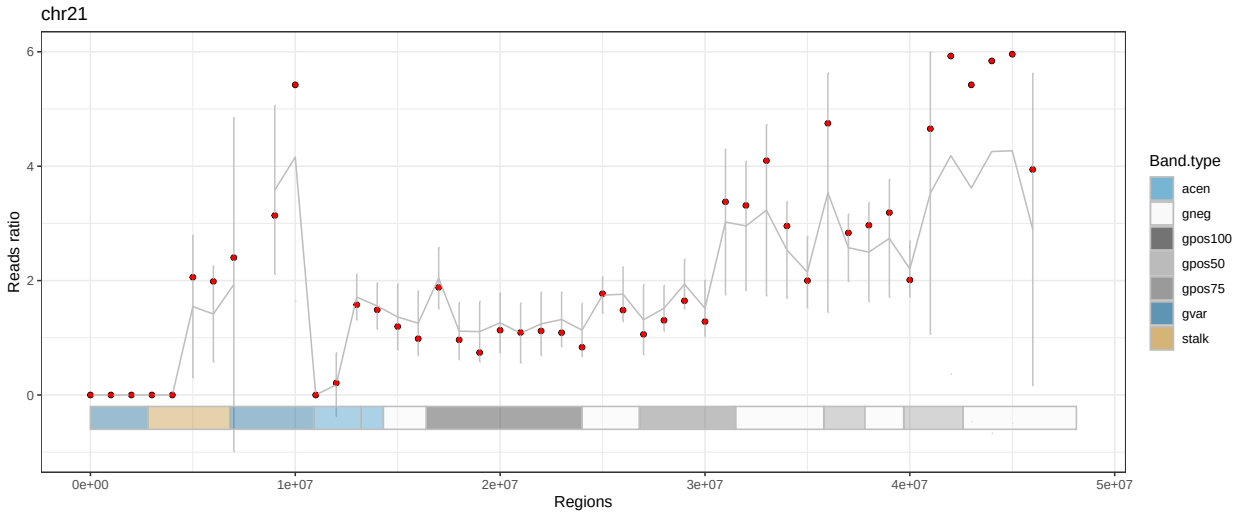
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Reads ratio
Regions
0e+00
1e+07
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4e+07
5e+07
Band.type
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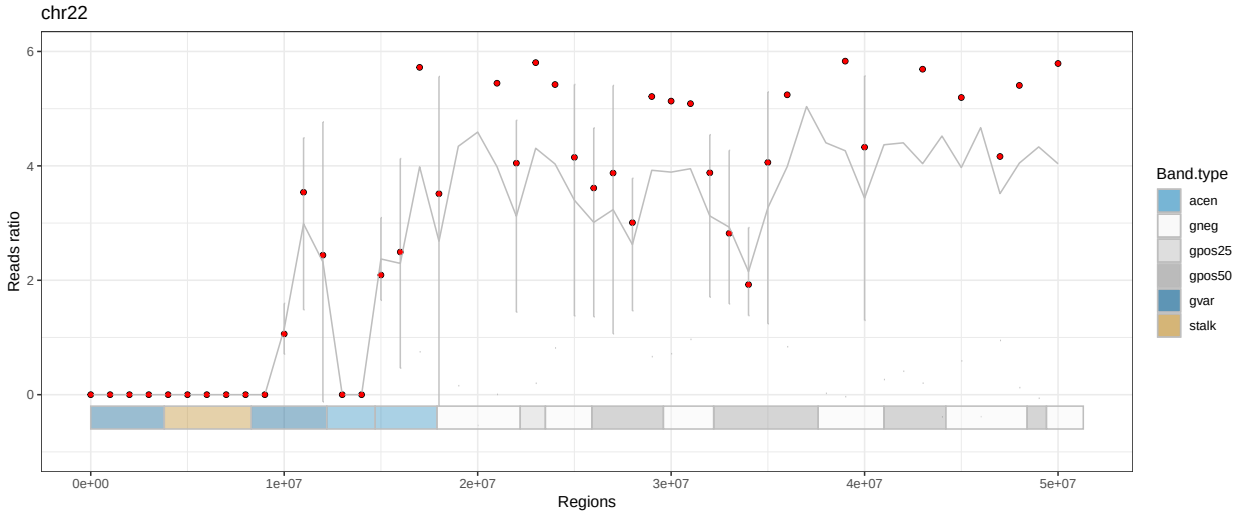
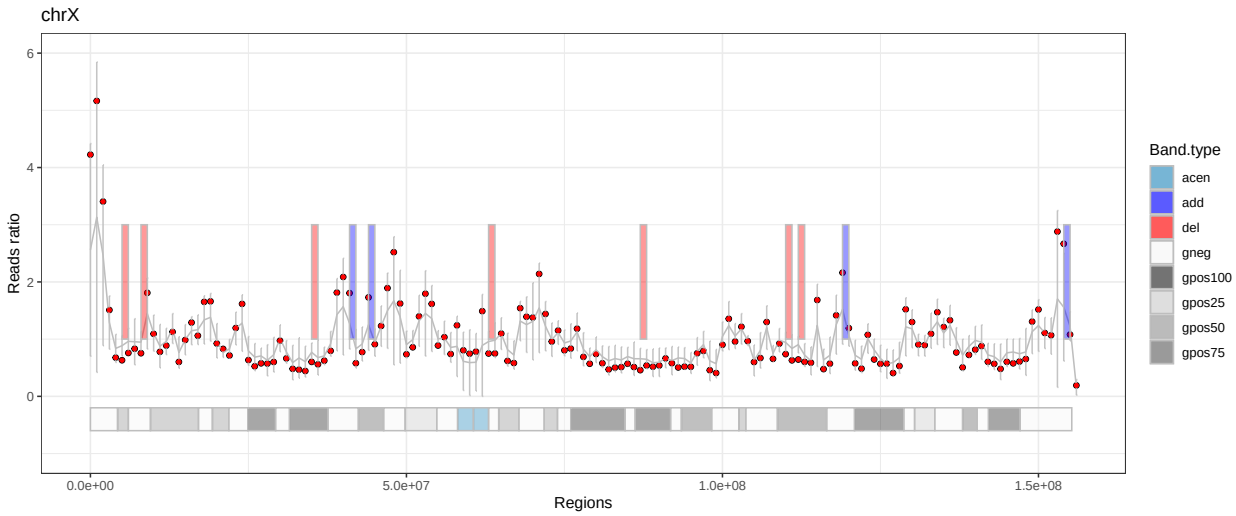
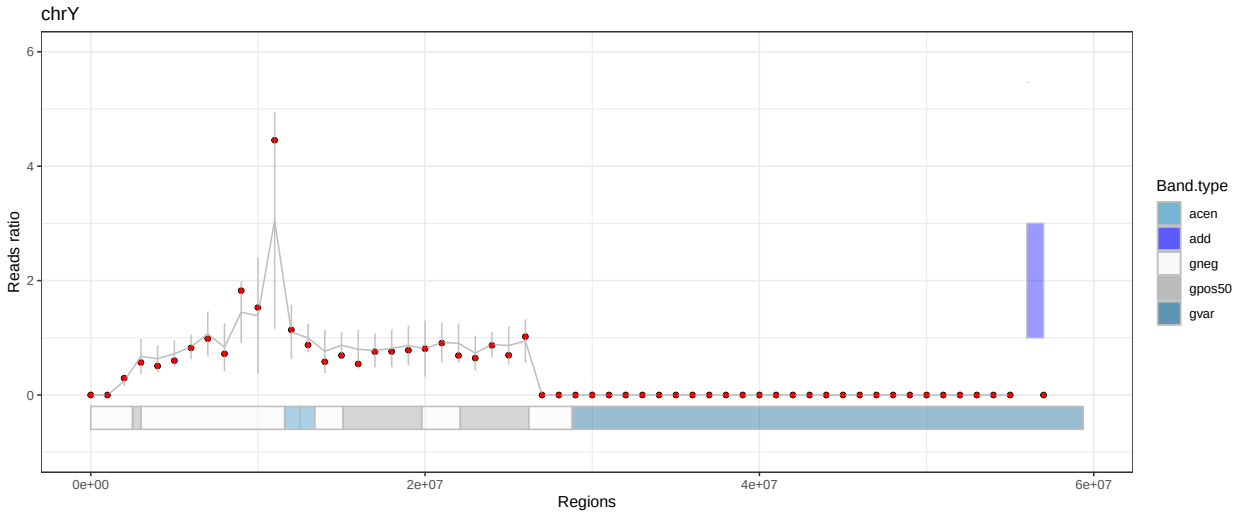
gneg
gpos100
gpos50
gpos75
gvar
stalk







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).