@bernatgel

karyoploteR

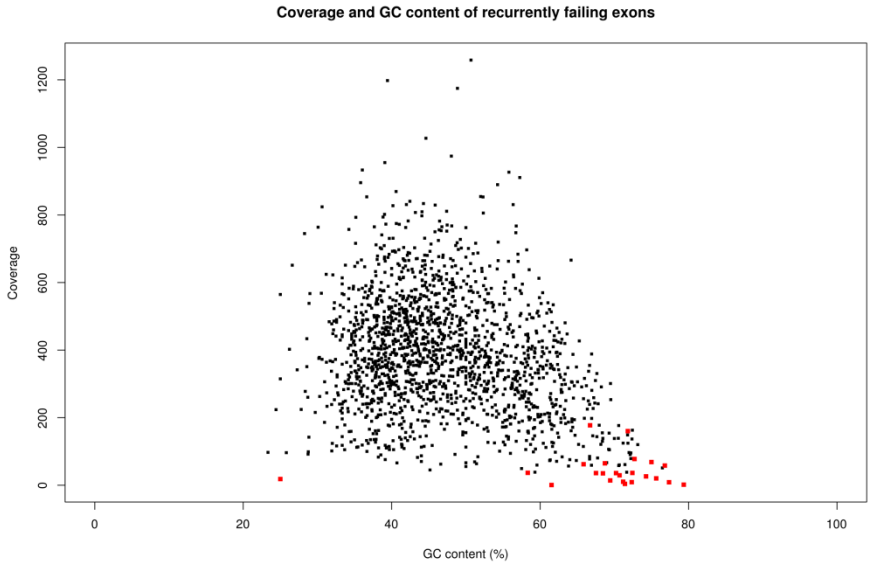
plot any data on any genome

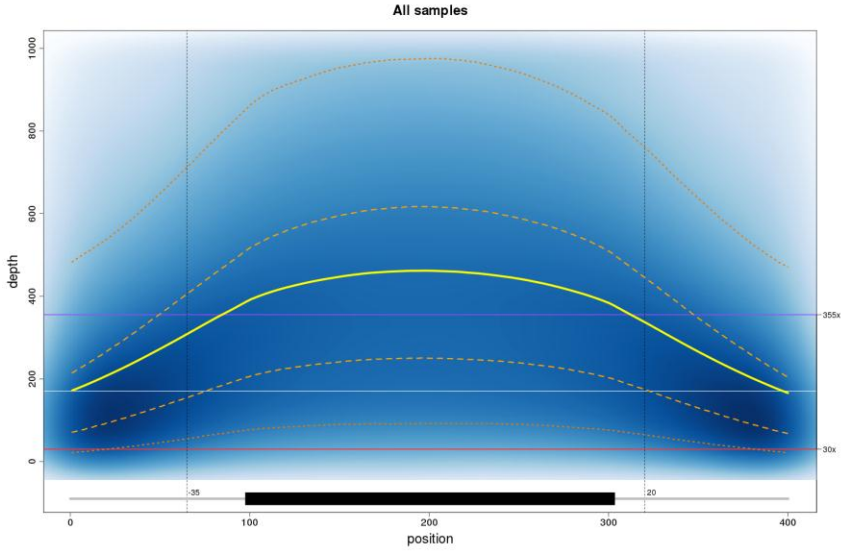
Bernat Gel
IGTP, Badalona, Spain

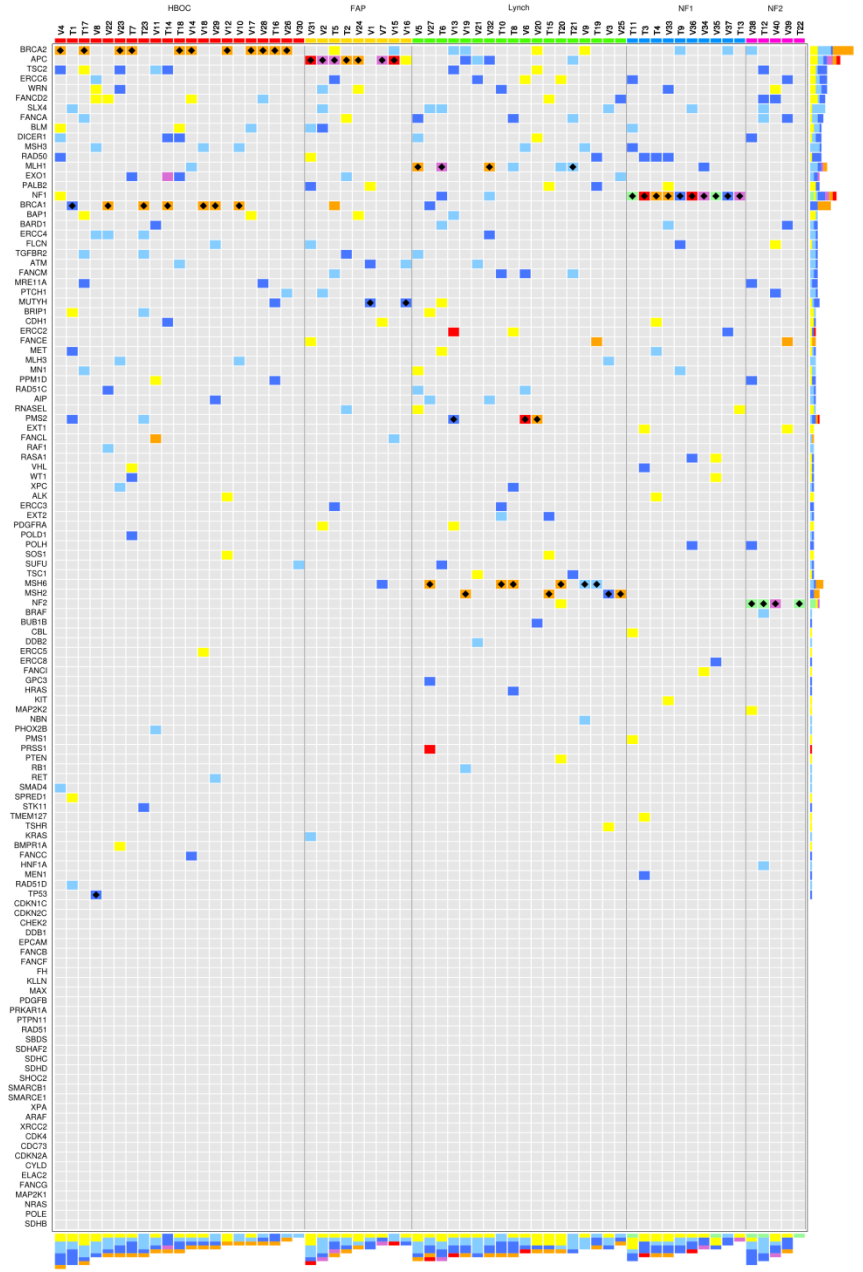
PMPPC
Program for Predictive and Personalized Medicine of Cancer

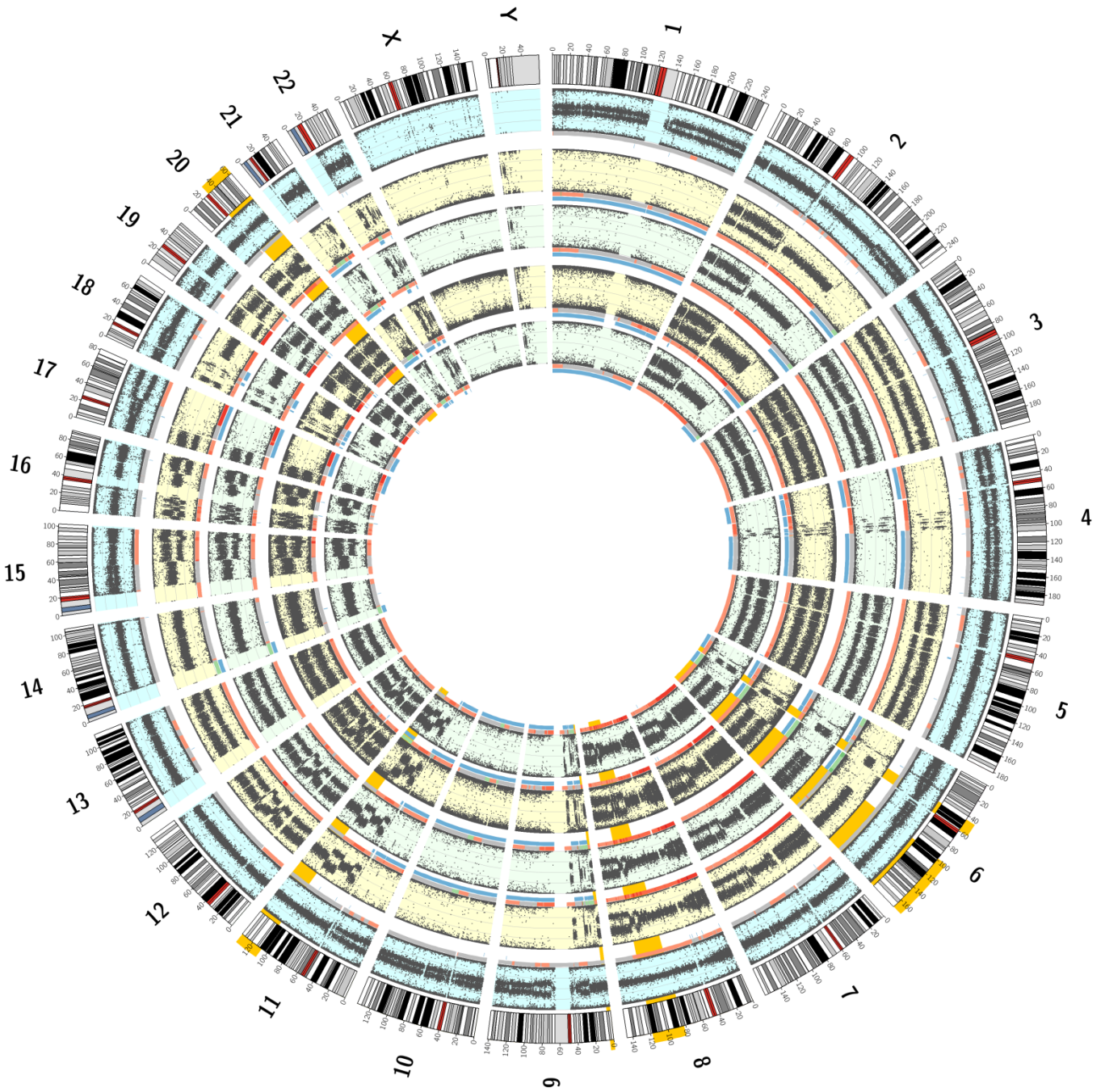
IGTP
Germans Trias i Pujol Research Institute

DATA


Coverage and GC content of recurrently failing exons
Coverage
GC content (%)
0
200
400
600
800
1000
1200
0
20
40
60
80
100


All samples
depth
position
355x
30x
-35
20
0
200
400
600
800
1000
0
100
200
300
400


HBOC
FAP
Lynch
NF1
NF2
BRCA2
APC
TSC2
ERCC6
WRN
FANCD2
SLX4
FANCA
BLM
DICER1
MSH3
RAD50
MLH1
EXO1
PALB2
NF1
BRCA1
BAP1
BARD1
ERCC4
FLCN
TGFBR2
ATM
FANCM
MRE11A
PTCH1
MUTYH
BRIP1
CDH1
ERCC2
FANCE
MET
MLH3
MN1
PPM1D
RAD51C
AIP
RINASEL
PMS2
EXT1
FANCL
RAF1
RASA1
VHL
WT1
XPC
ALK
ERCC3
EXT2
PDGFRA
POLD1
POLH
SOS1
SUFU
TSC1
MSH6
MSH2
NF2
BRAF
BUB1B
CBL
DDB2
ERCC5
ERCC8
FANCI
GPC3
HRAS
KIT
MAP2K2
NBN
PHOX2B
PMS1
PRSS1
PTEN
RB1
RET
SMAD4
SPRED1
STK11
TMEM127
TSHR
KRAS
BMPR1A
FANCC
HNF1A
MEN1
RAD51D
TP53
CDKN1C
CDKN2C
CHEK2
DDB1
EPCAM
FANCB
FANCF
FH
KLLN
MAX
PDGFB
PRKAR1A
PTPN11
RAD51
SBDS
SDHAF2
SDHC
SDHD
SHOC2
SMARCB1
SMARCE1
XPA
ARAF
XRCC2
CDK4
CDC73
CDKN2A
CYLD
ELAC2
FANCG
MAP2K1
NRAS
POLE
SDHB


1
2
3
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7
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11
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13
14
15
16
17
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19
20
21
22
X
Y

We wanted

Flexible

Data agnostic

Genome agnostic

Customizable

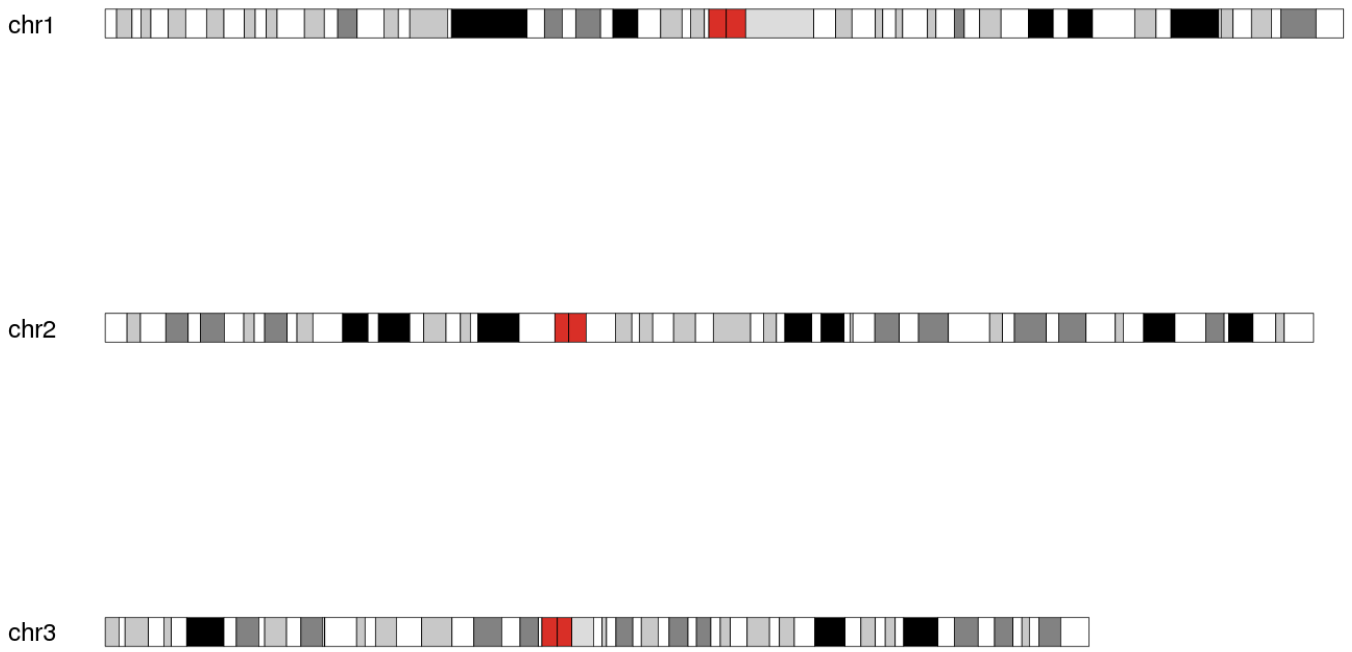
Only plotting

karyoploteR

… in R!!!!

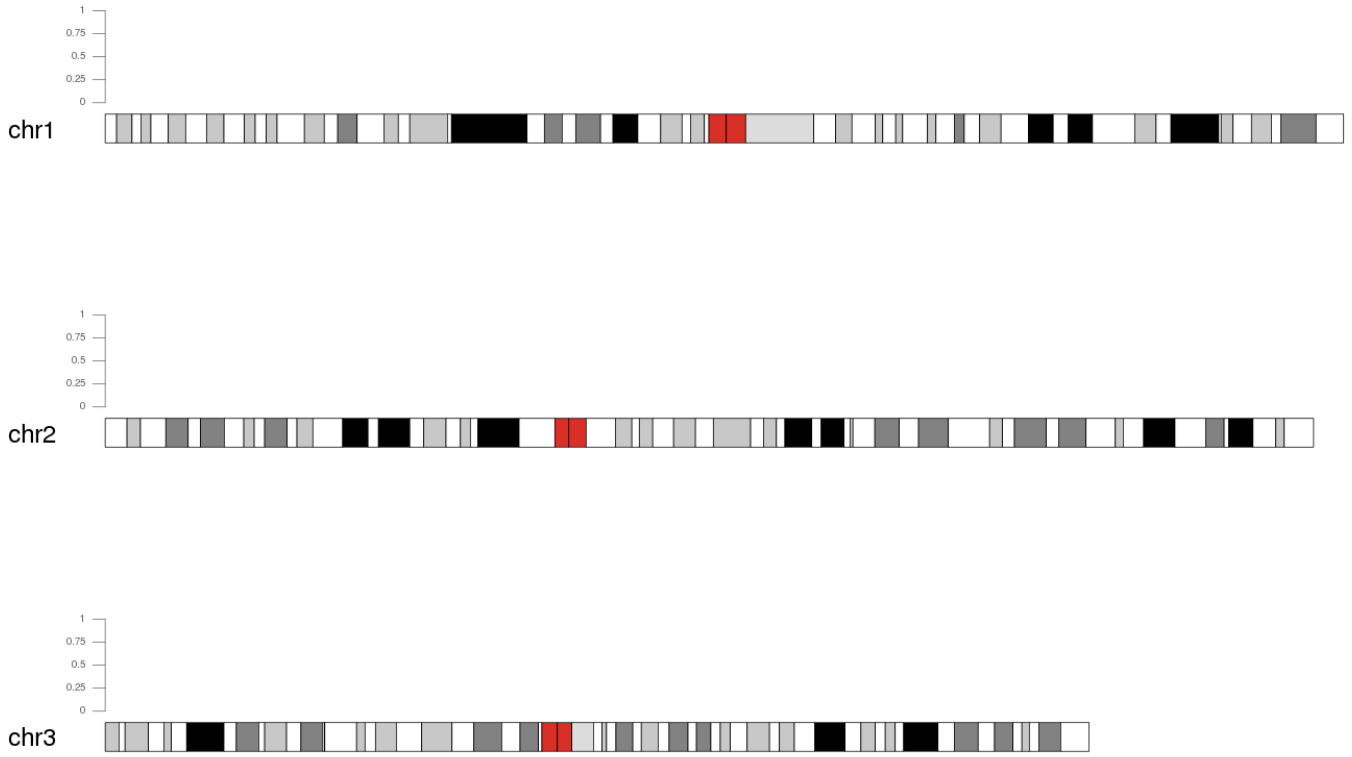
Inspired in R base graphics

plotKaryotype()



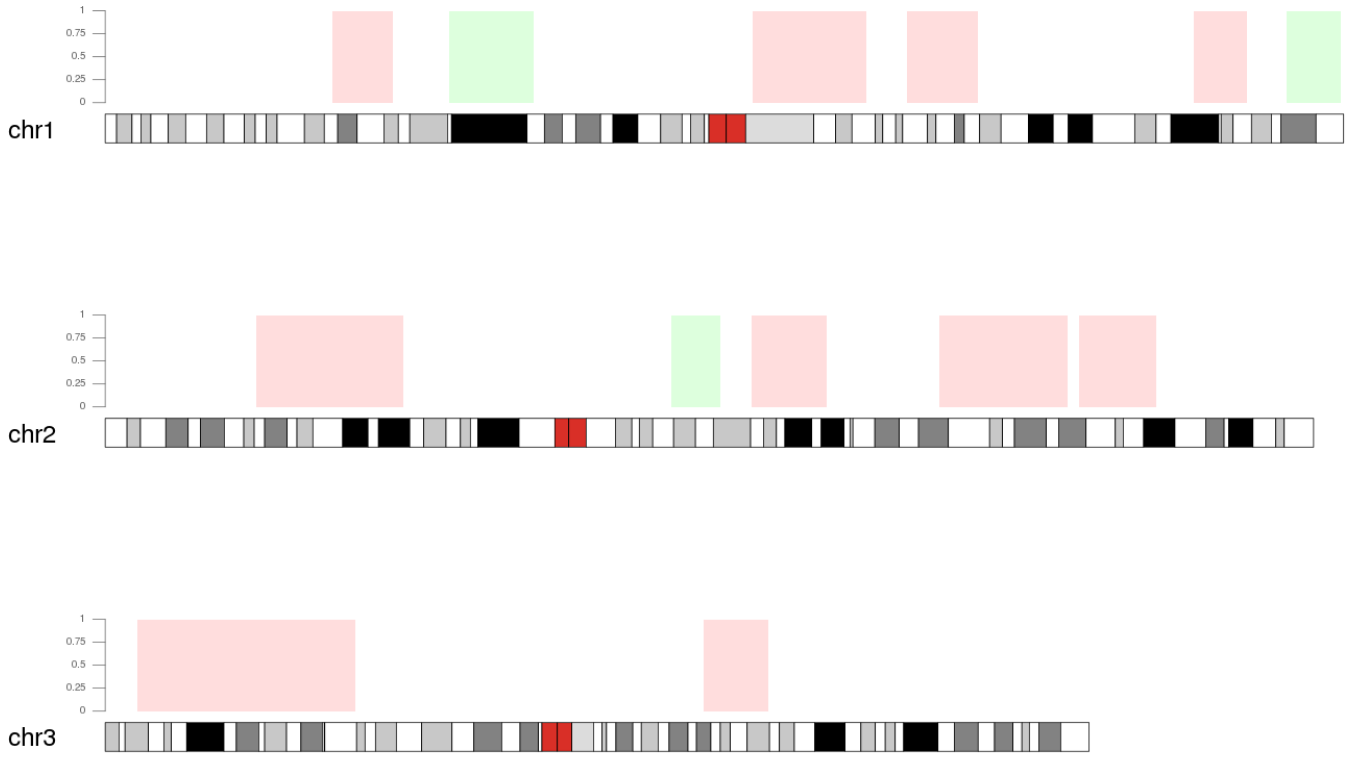
Inspired in R base graphics

kpAxis()



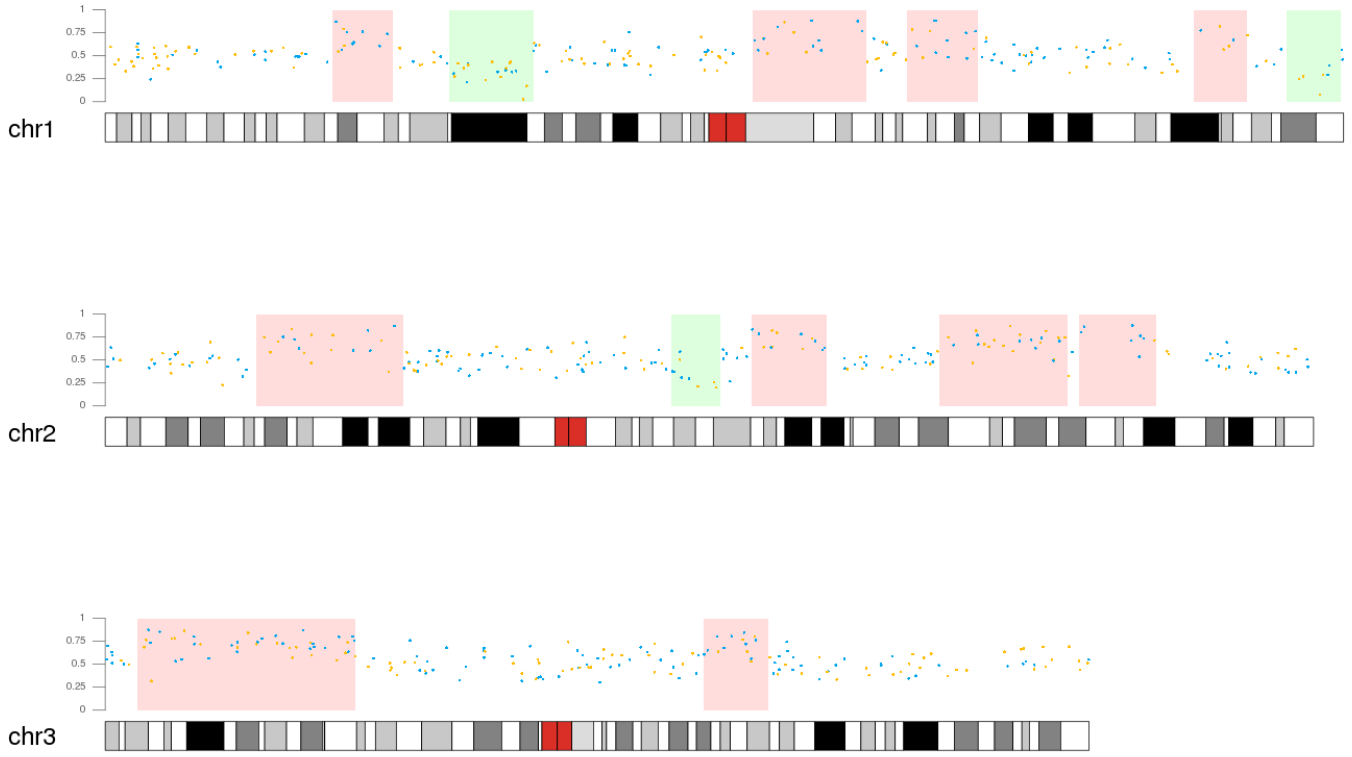
Inspired in R base graphics

kpRect()



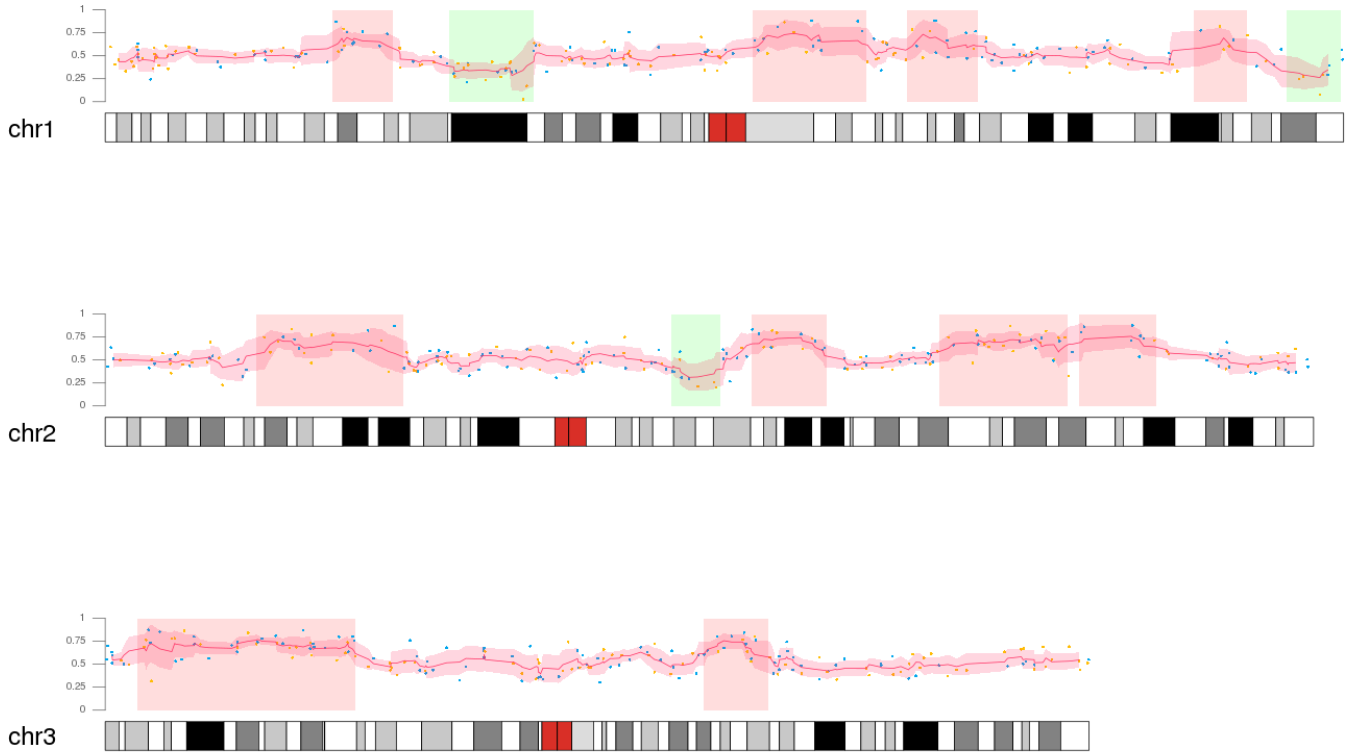
Inspired in R base graphics

kpPoints()



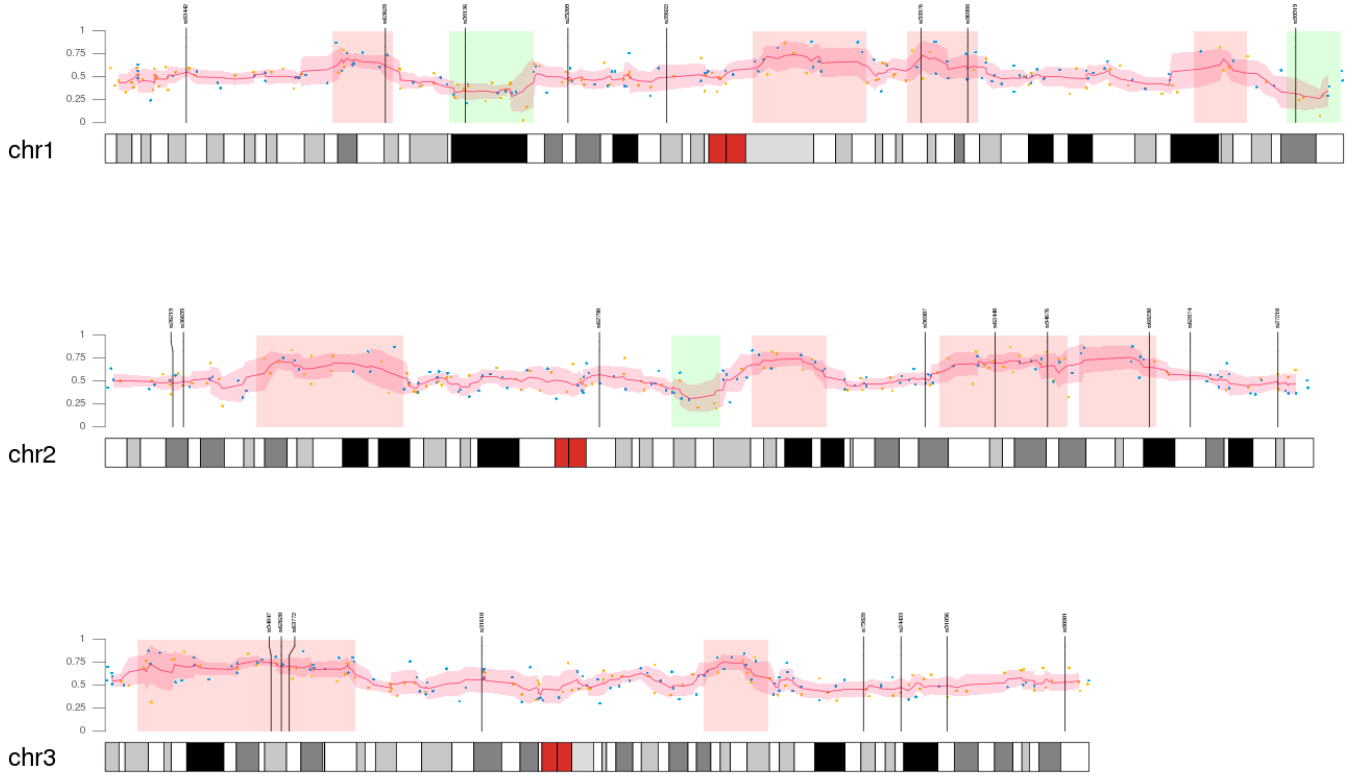
Inspired in R base graphics

kpLines()



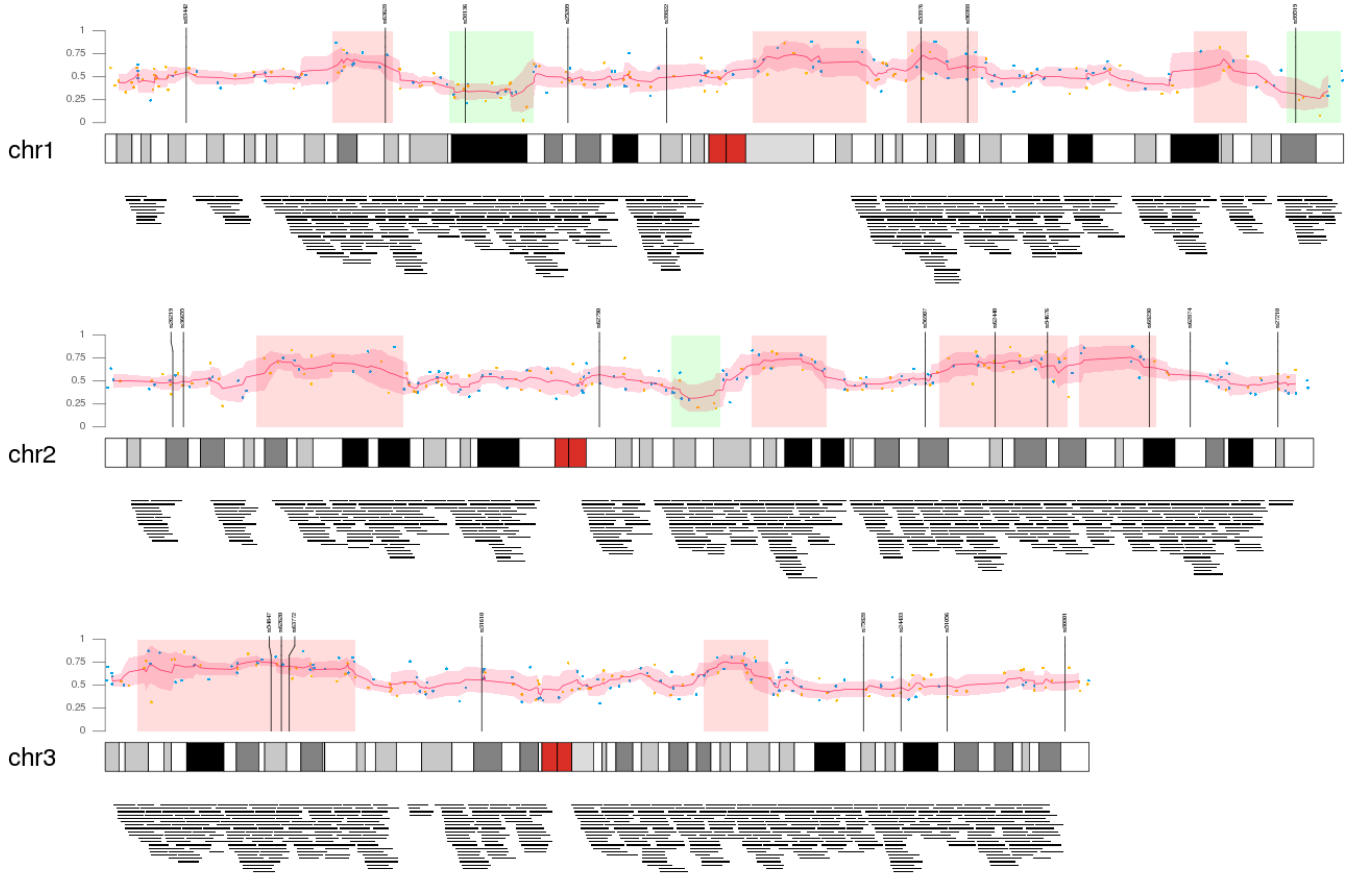
Inspired in R base graphics

kpPlotMarkers()



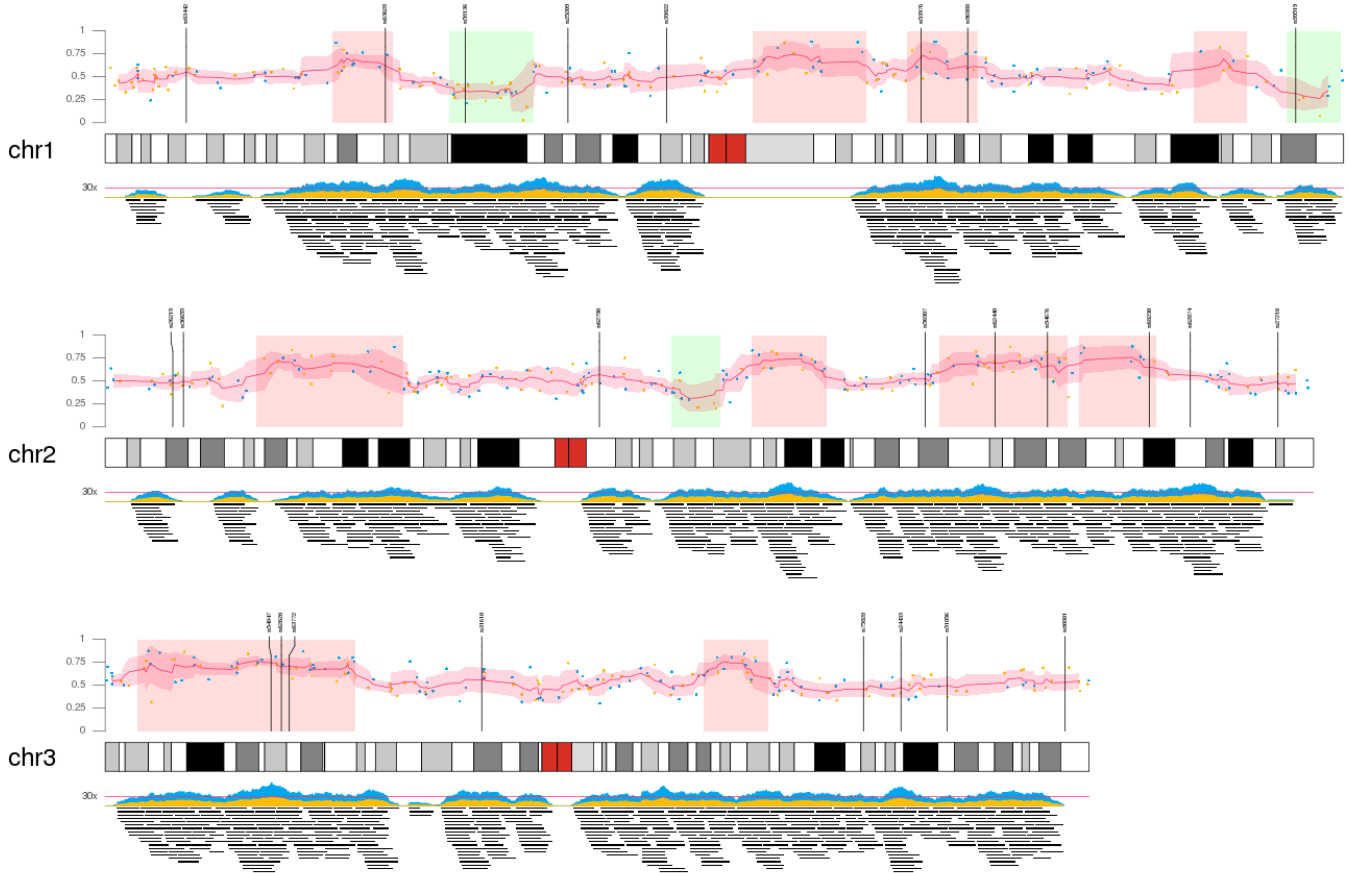
Inspired in R base graphics

kpPlotRegions()



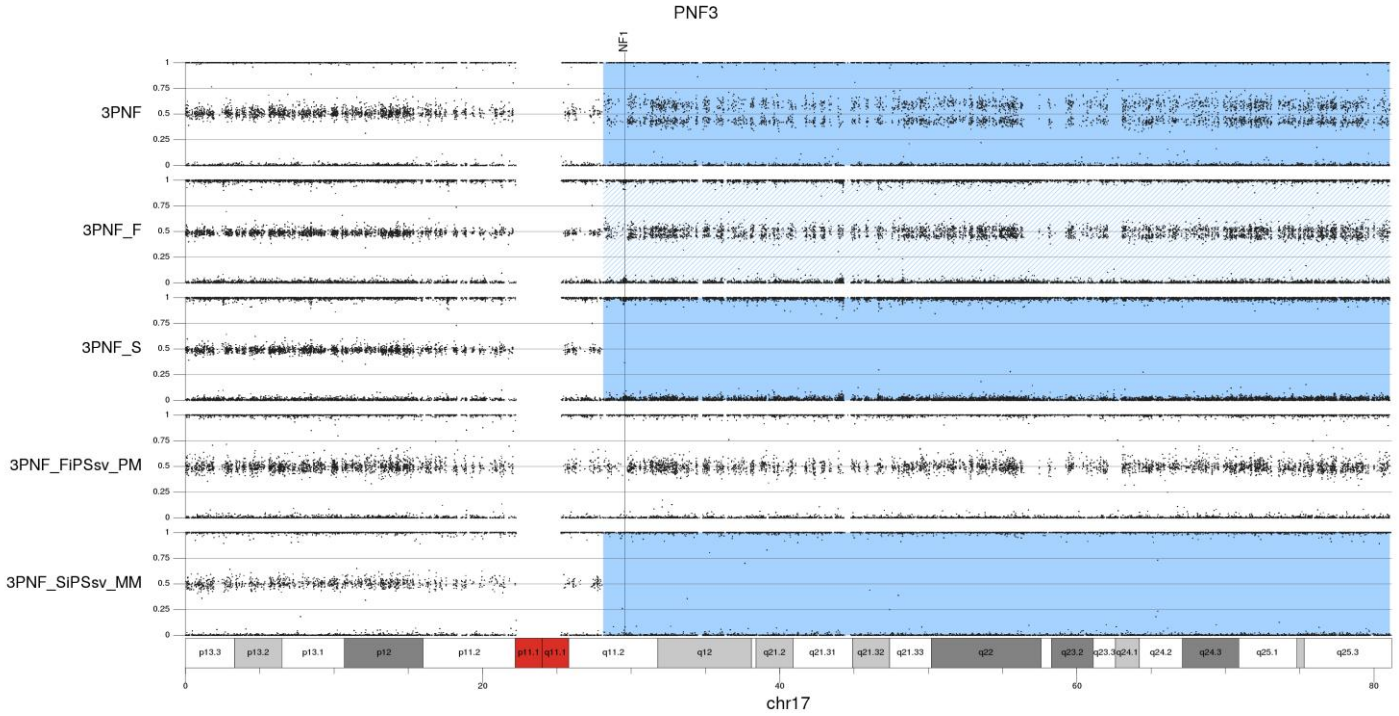
Inspired in R base graphics

kpPlotCoverage()



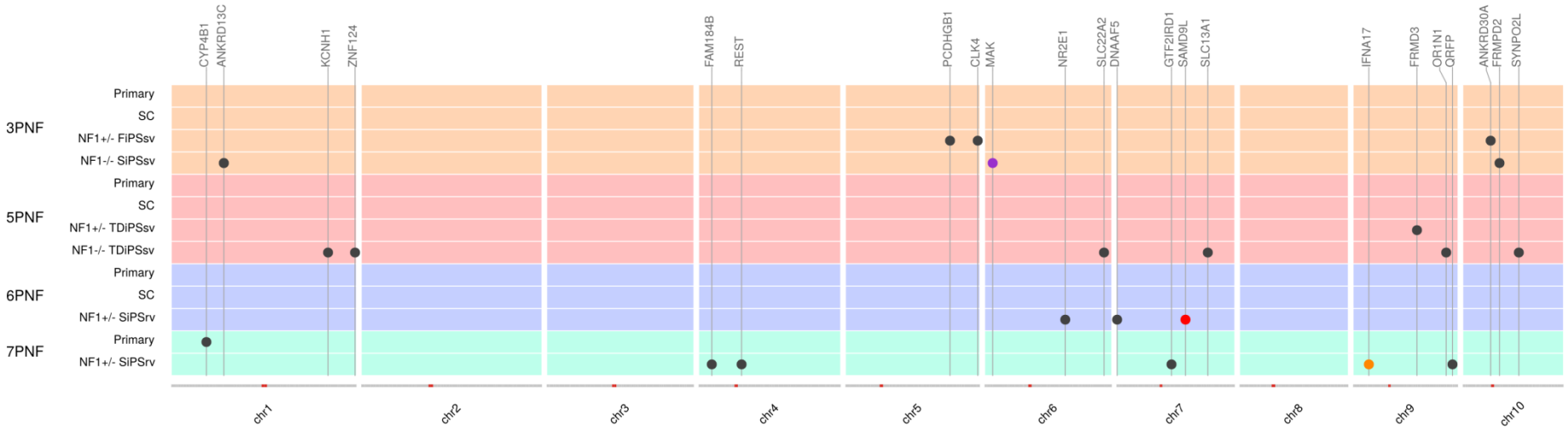
Data Agnostic

kpPoints()



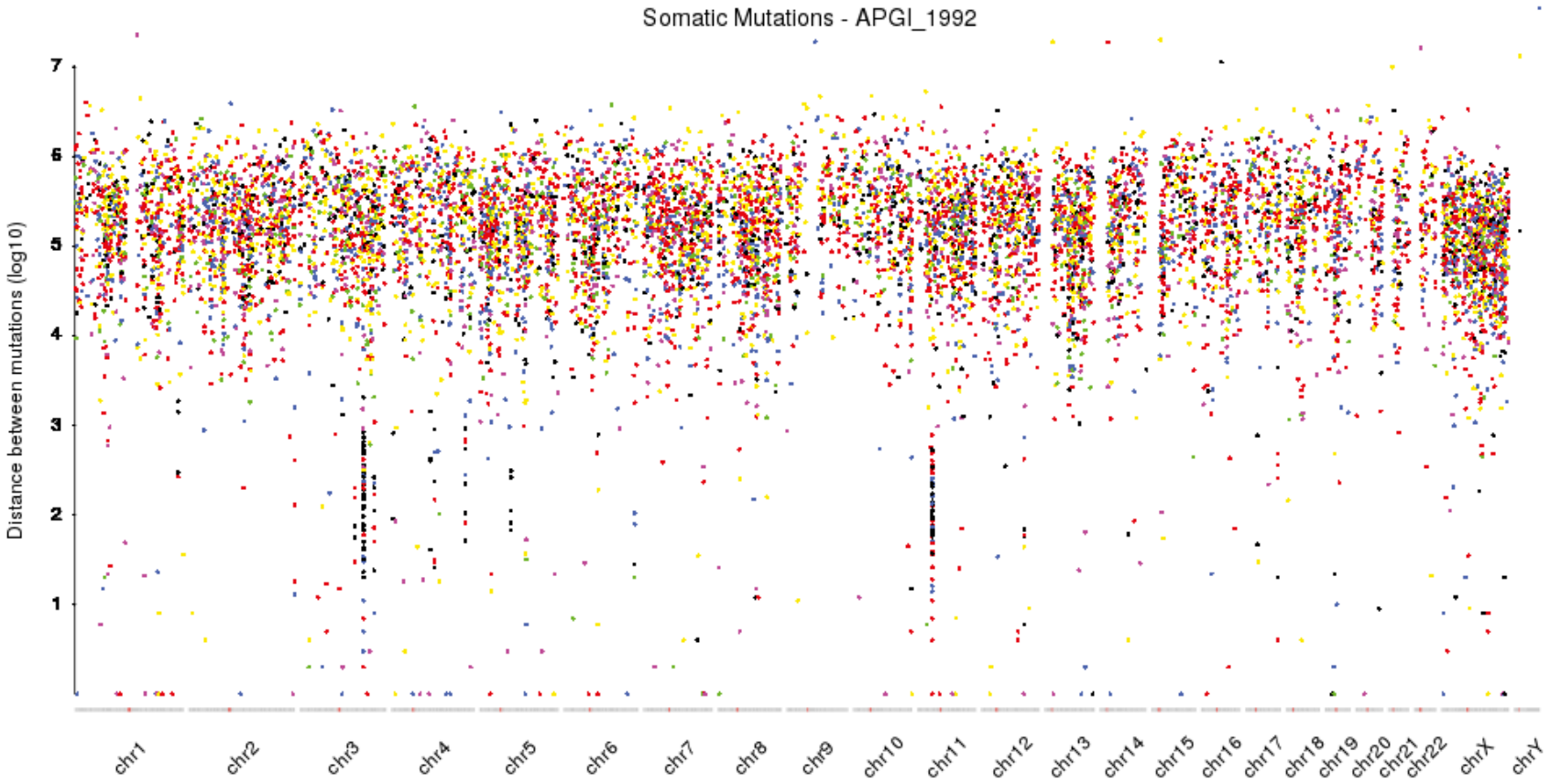
Data Agnostic

kpPoints()



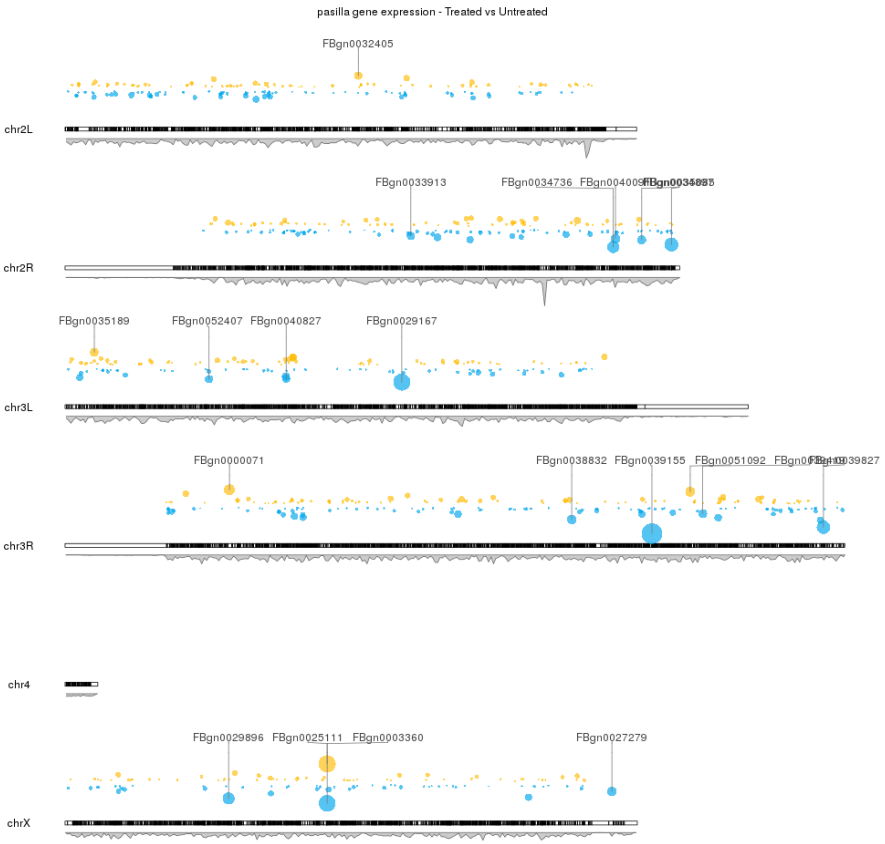
Data Agnostic

kpPoints()



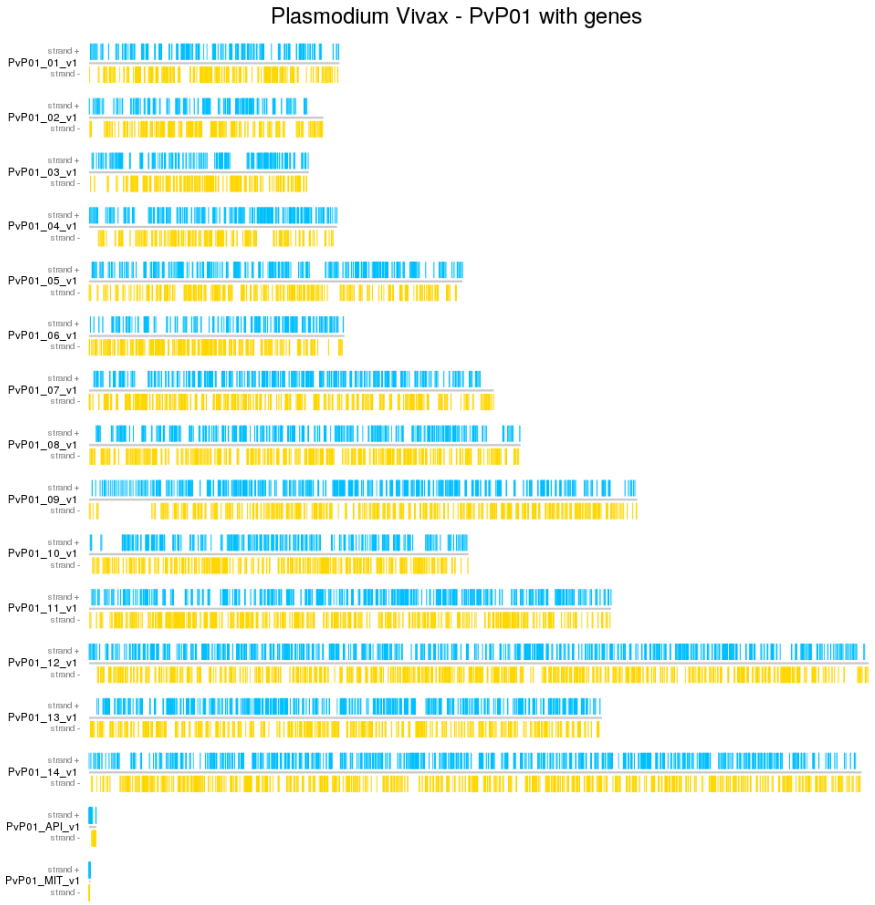
Genome Agnostic

plotKaryotype(genome='dm9')



Genome Agnostic

plotKaryotype(genome=pvivax)



Genome Agnostic

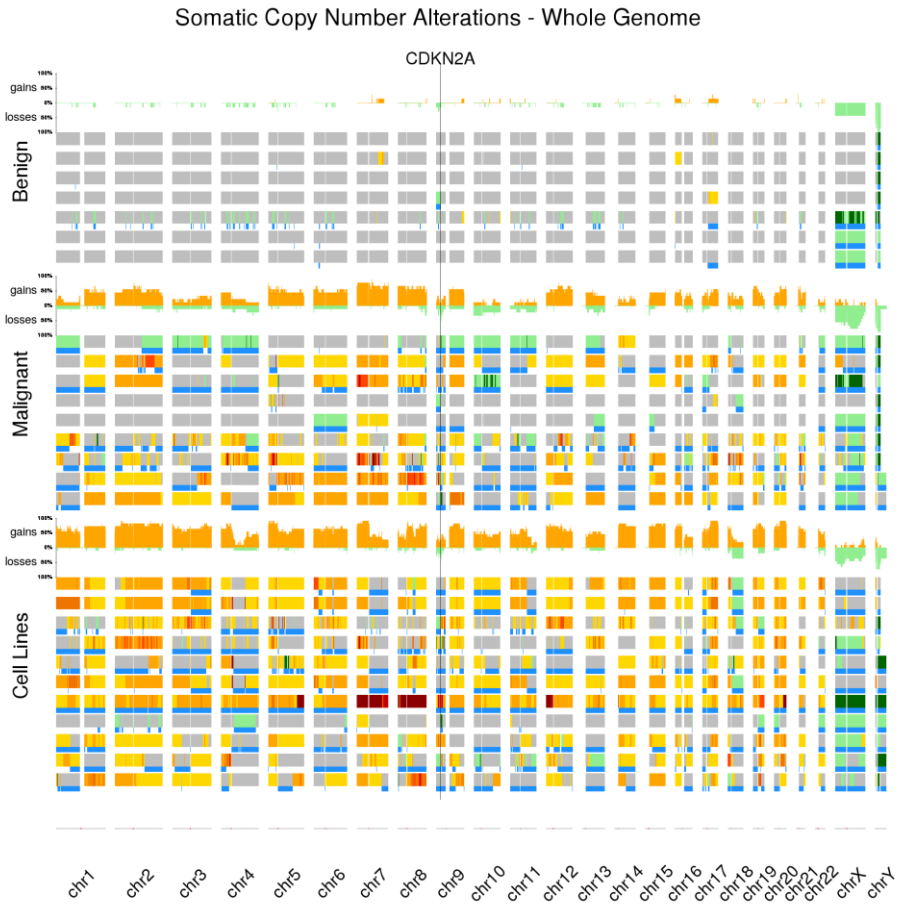
Small cache included

BSgenome

GRanges ⟵ **Custom Genomes!**

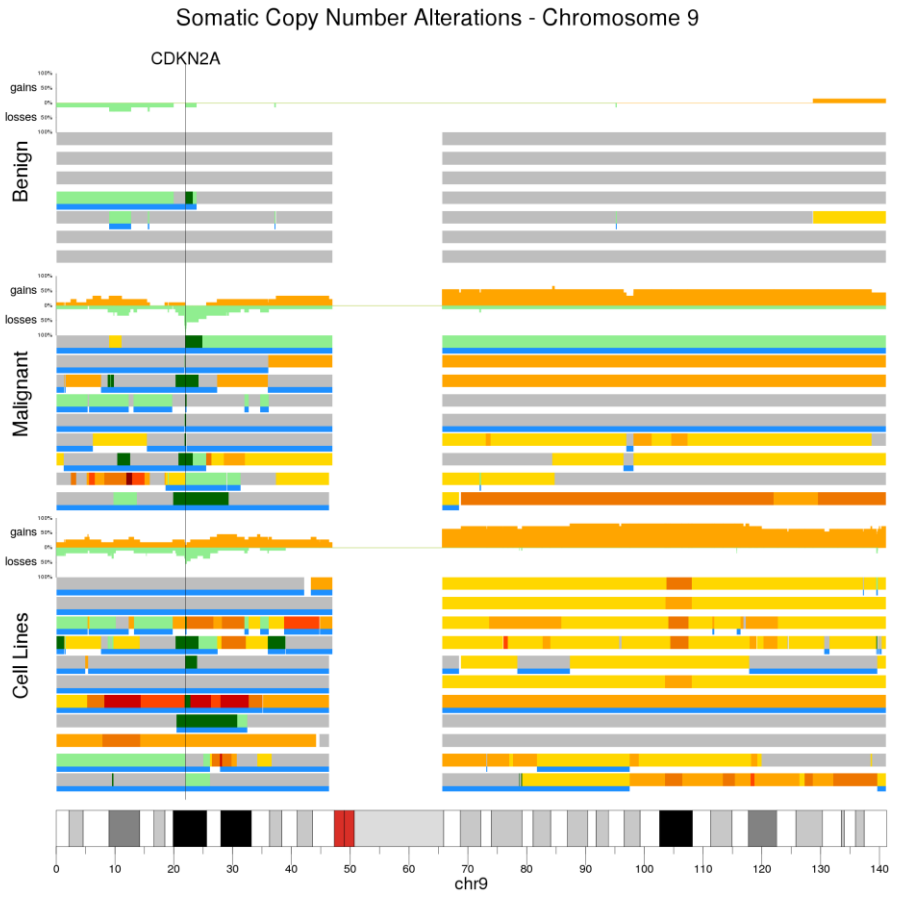
Getting closer…

plotKaryotype()



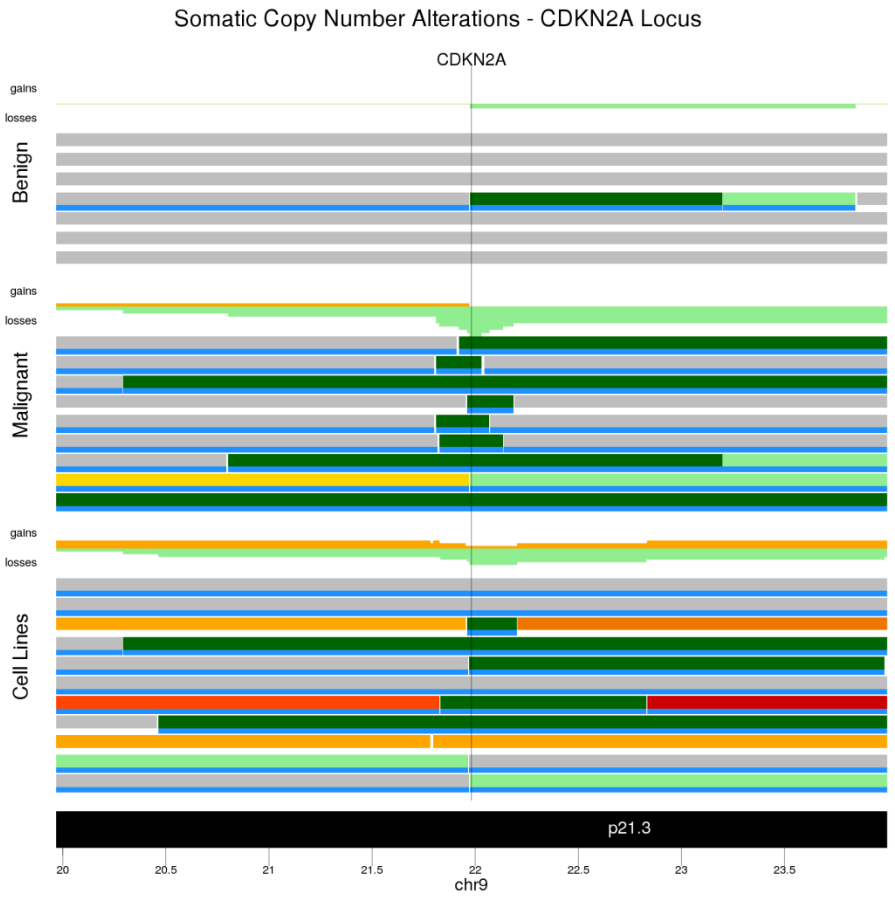
Getting closer…

plotKaryotype(chromosomes='chr9')



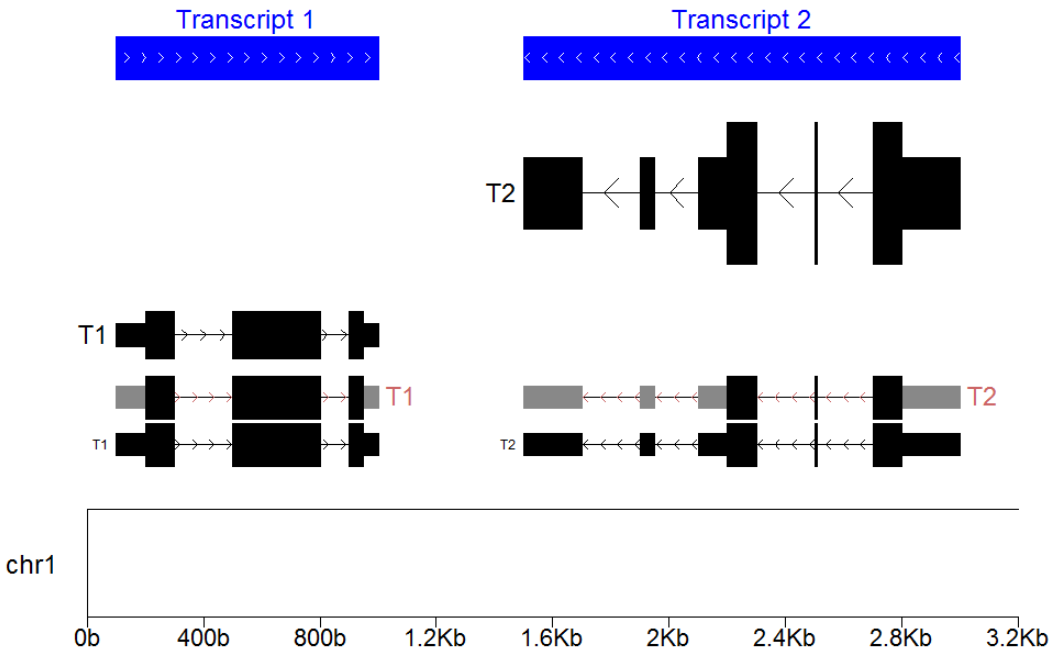
Getting closer…

plotKaryotype(zoom=cdkn2a.region)



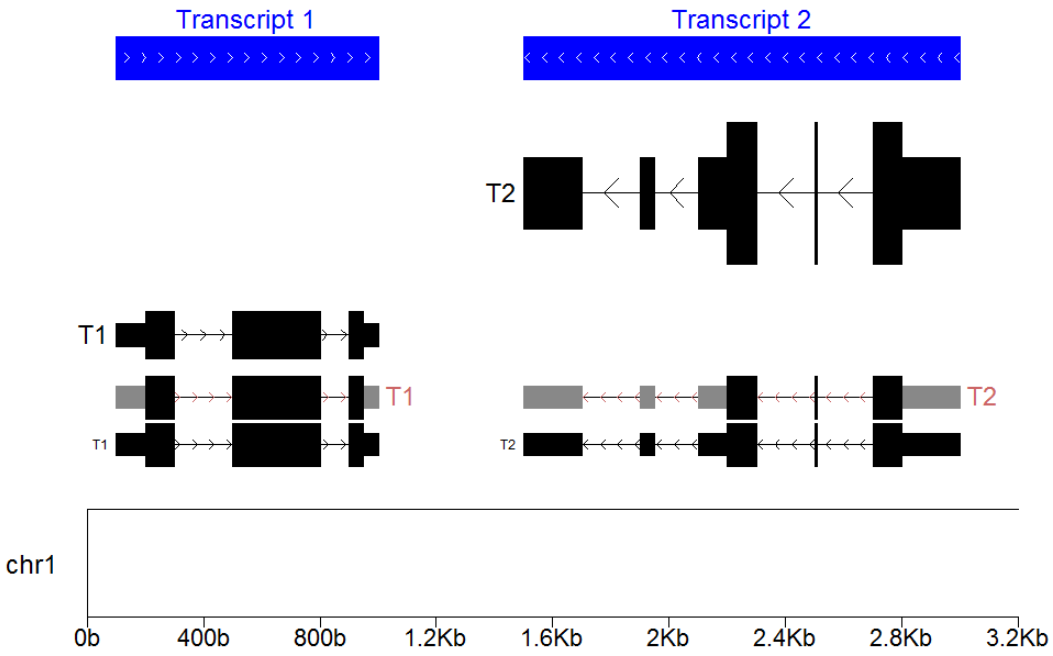
Genes and transcripts

kpPlotTranscripts()



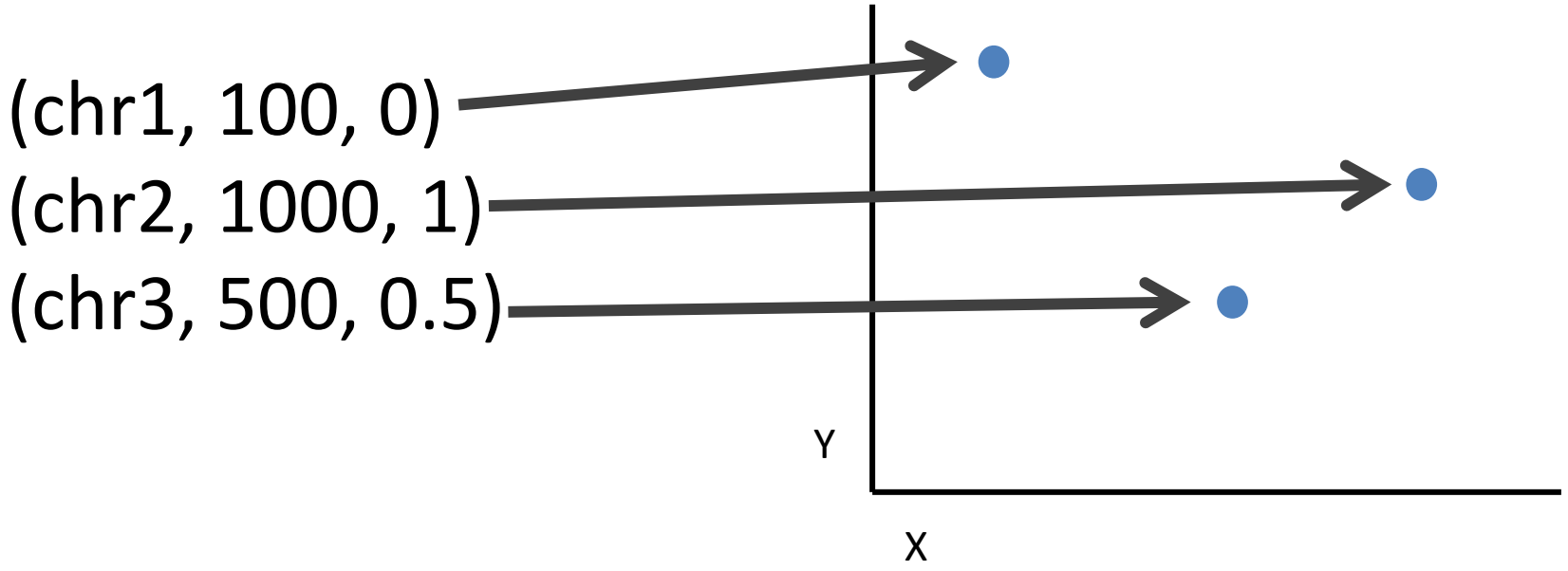
Genes and transcripts

kpPlotGenes(data=TxDb)



Implementation

Coordinate Change Function



Tutorial & Examples

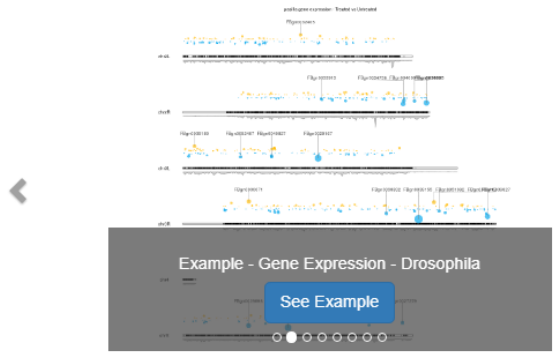
https://bernatgel.github.io/karyoploter_tutorial/

karyoploteR

A tutorial and a set of examples on using the R/Bioconductor package karyoploteR to plot whole genomes with arbitrary data on them

Getting Started | Citing | Tutorial | Examples

karyoploteR is an R package to create karyoplots, that is, representations of whole genomes with arbitrary data plotted on them. It is inspired by the R base graphics system and does not depend on other graphics packages. The aim of karyoploteR is to offer the user an easy way to plot data along the genome to get broad genome-wide view to facilitate the identification of genome wide relations and distributions.



karyoploteR is based on base R graphics and mimicks its interface. You first create a plot with a call to the `plotKaryotype` function and then sequentially call a number of plotting functions (`kpLines`, `kpPoints`, `kpBars` ...) to add data to the genome plot.

karyoploteR is a plotting tool and only a plotting tool. That means that it is not able to download or retrieve any data. The downside of this is that the user is responsible of getting the data into R. The upside is that it is not tied to any data provider and thus can be used to plot genomic data coming from anywhere. The only exception to this are the ideograms cytobands, that by default are plotted using predownloaded data from UCSC.

karyoploteR is useful in any situation where a general genome-wide view of data is desirable. It can be used to plot somatic copy-number changes (SCNA) in cancer genomes obteined from exome, aCGH or SNP-array data; to plot the global BAM coverage from a WGS experiment; to create manhattan plots from GWAS studies; to create rainfall plots to detect kataegis. Since it is not tied to any data type or source, karyoploteR can be used to plot almost anything on a genome-wide scale.

karyoploteR

plot any data on any genome

https://github.com/bernatgel/karyoploteR

https://bernatgel.github.io/karyoploter_tutorial/

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