

# Global analysis of CNV

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## Warning in valid.GenomicRanges.seqinfo(x, suggest.trim = TRUE): GRanges object contains 4 out-of-bounds
## chr1B_part2, chr2B_part2, chr4B_part1, and chrUn. Note that ranges
## located on a sequence whose length is unknown (NA) or on a circular
## sequence are not considered out-of-bound (use seqlengths() and
## isCircular() to get the lengths and circularity flags of the underlying
## sequences). You can use trim() to trim these ranges. See
## ?`trim,GenomicRanges-method` for more information.
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First we want to explore some lines.





























































































































