

Global analysis of CNV

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We want to explore how the details of the called CNVs

There are 290,248 CNV events in the dataset. This analysis contains 15 lines

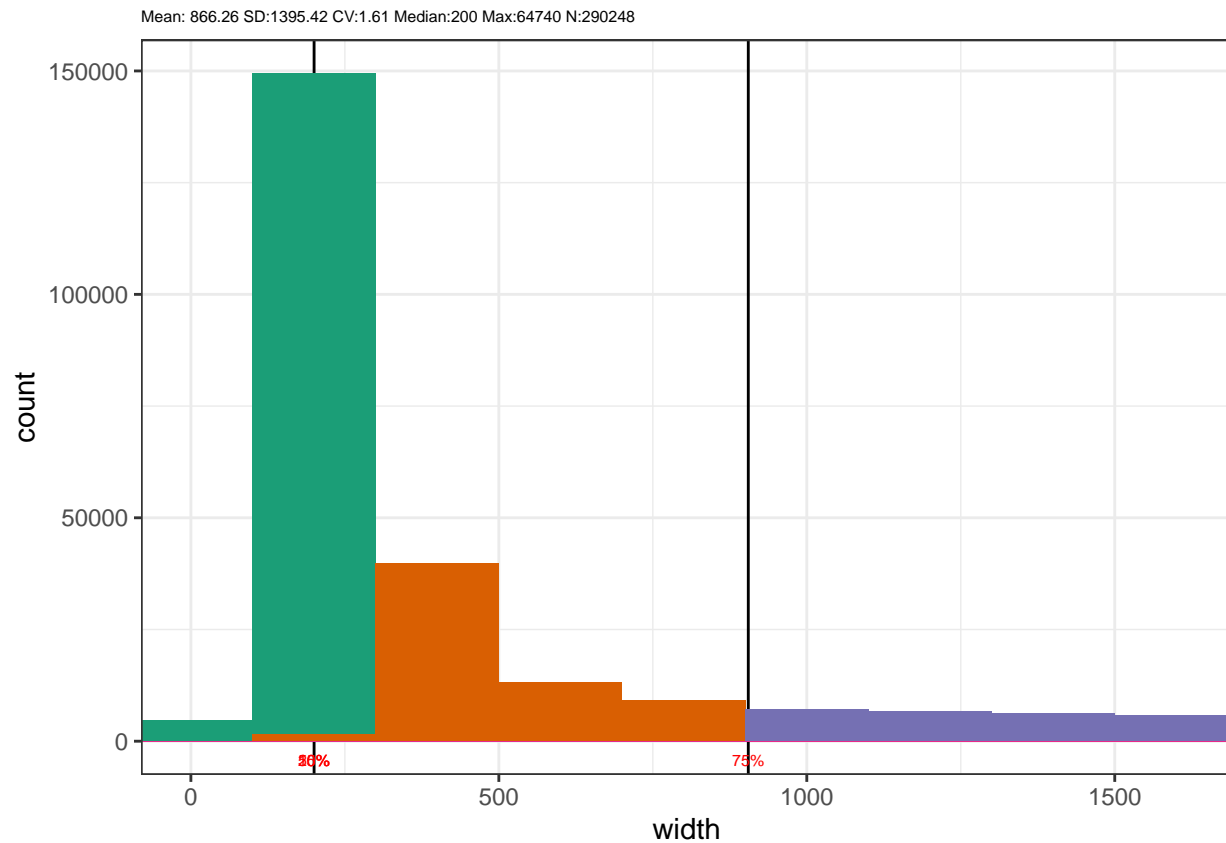
First we want to get an idea of the distribution of the deletion sizes.

```
kable(head(cnvs))
```

seqnames	start	end	width	strand	norm_cov	cnv_level	line	max_gap
chr1A_part1	1610157	1610356	200	*	0.0000000	0	B1190023.1	10
chr1A_part1	2393686	2394485	800	*	0.0000000	0	B1190023.1	10
chr1A_part1	2436043	2437842	1800	*	0.0266237	0	B1190023.1	10
chr1A_part1	2472568	2475367	2800	*	0.0170682	0	B1190023.1	10
chr1A_part1	2520813	2521012	200	*	0.0000000	0	B1190023.1	10
chr1A_part1	2557847	2558046	200	*	0.0000000	0	B1190023.1	10

```
plotHistogram(cnvs_df, column="width", binwidth=200)
```

```
## Warning: Use of `quantiles$value` is discouraged. Use `value` instead.
```

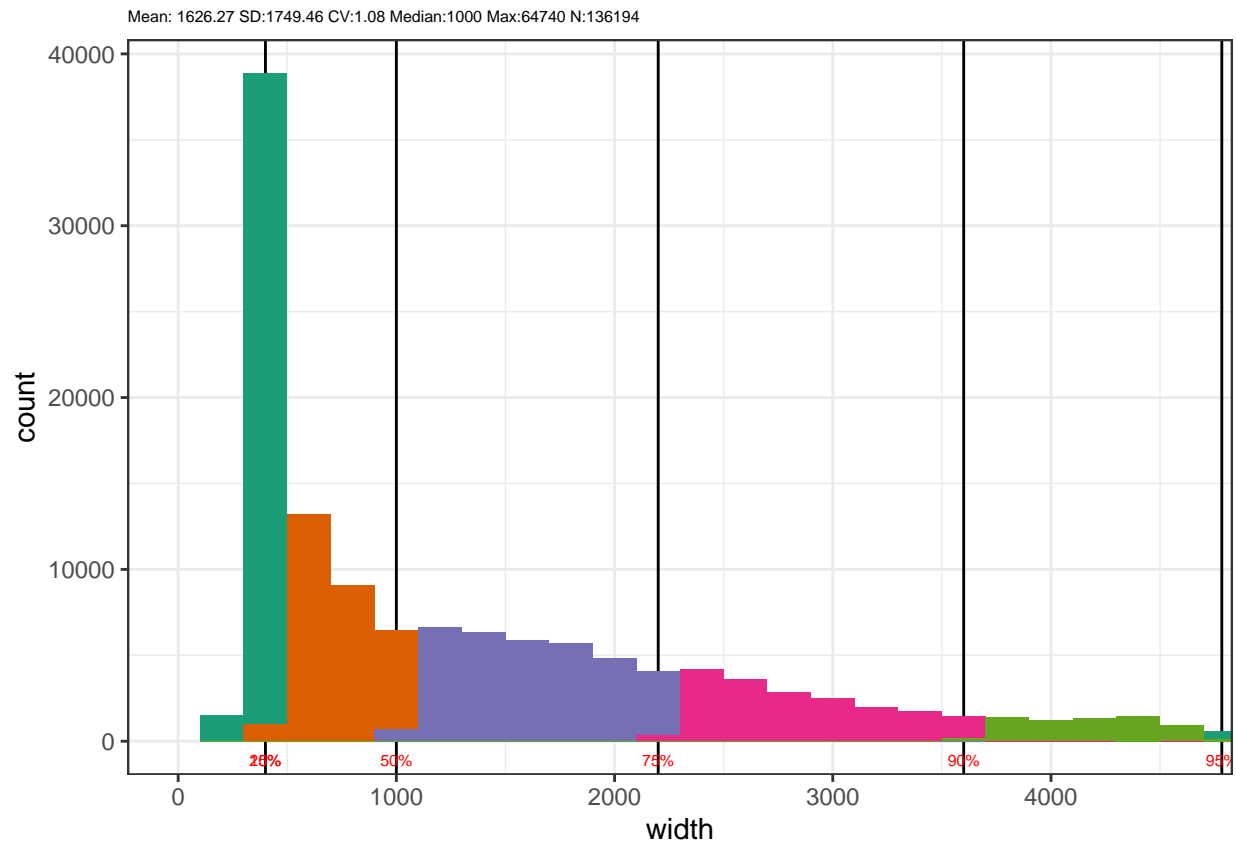


Most of them are under 1,500, however there are 52,481 larger than 1,500 (18.08 %).

The minimum size that we have in this dataset is 200bp, so if we filter “unique” events out. This filter leaves 136,194 (46.92 %) events The distribution is the following distribution:

```
plotHistogram(non_singletons_cnvs, column="width", binwidth=200)
```

```
## Warning: Use of `quantiles$value` is discouraged. Use `value` instead.
```

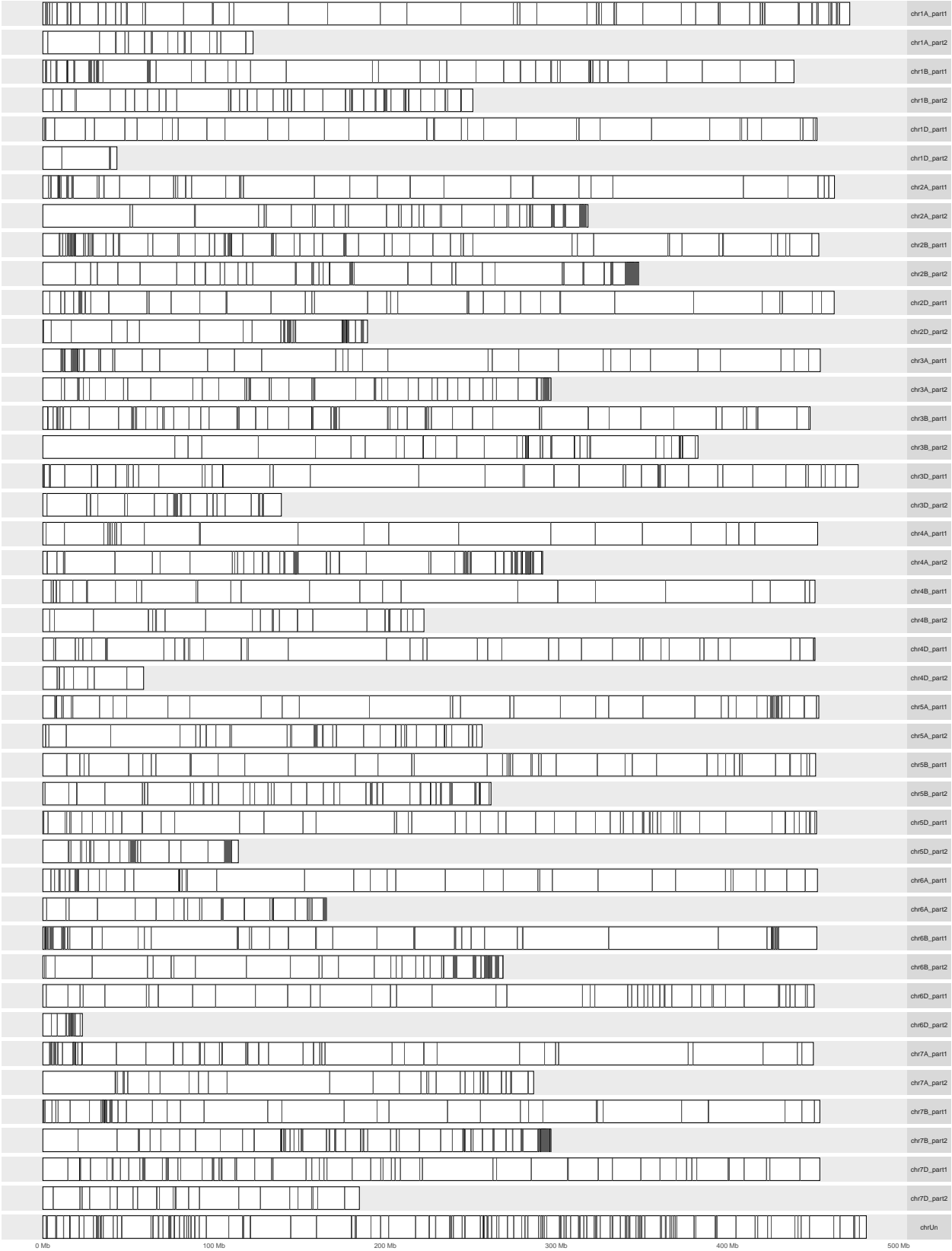


We want to look how one of the lines look randomly

```
plotCnvsInLine(non_singletons_cnvs_gr)
```

```
## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.
## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.
```

WATDE0821 CNV: 0



```
plotCnvsInLine(non_singletons_cnvs_gr, cnv_level=2)
```

```
## Scale for 'x' is already present. Adding another scale for 'x', which will  
## replace the existing scale.  
## Scale for 'x' is already present. Adding another scale for 'x', which will  
## replace the existing scale.
```

WATDE0821 CNV: 2

