

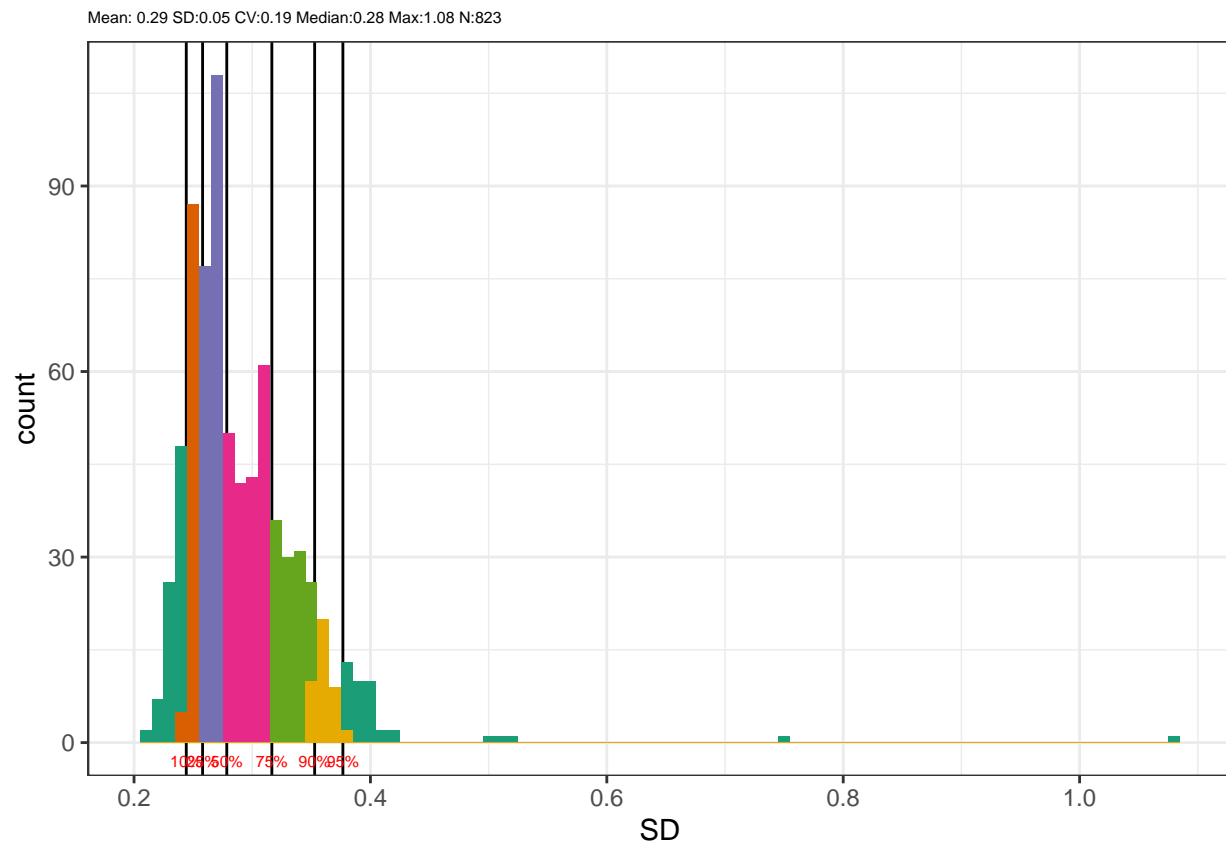
# Analysis of CNV around RHT for QC

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This notebook is to look at some examples of lines where calling the CNV may be troublesome, based on the dispersion

Out of 823 lines, 5 have an  $\sigma > 0.45$ . We consider lines above the threshold as noisy.

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



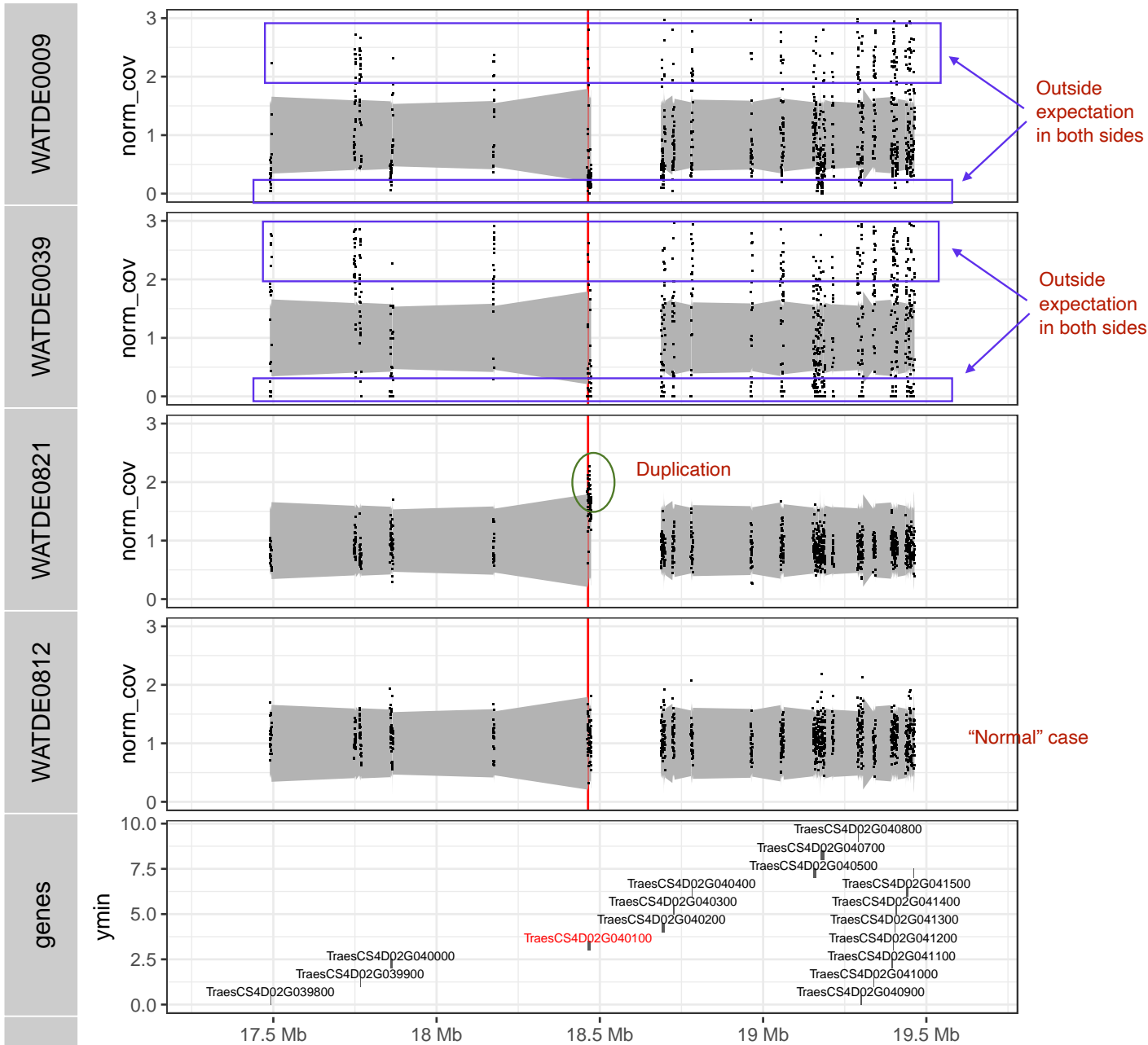
	line	SD
25	WATDE0009	0.7529014
54	WATDE0039	1.0792827
71	WATDE0056	0.5134964
75	WATDE0060	0.5173301
104	WATDE0090	0.4956258

## Details for TraesCS4D02G040100

To showcase the issues with the 5 noisy lines, we have a closer look at TB1-4D. The ribbon is showing the area  $\pm 3\sigma$  across each particular window. The dots that are outside the ribbon represent windows that are candidates to be considered a CNV, as they are outside the 99% expectation, assuming a normal distribution.

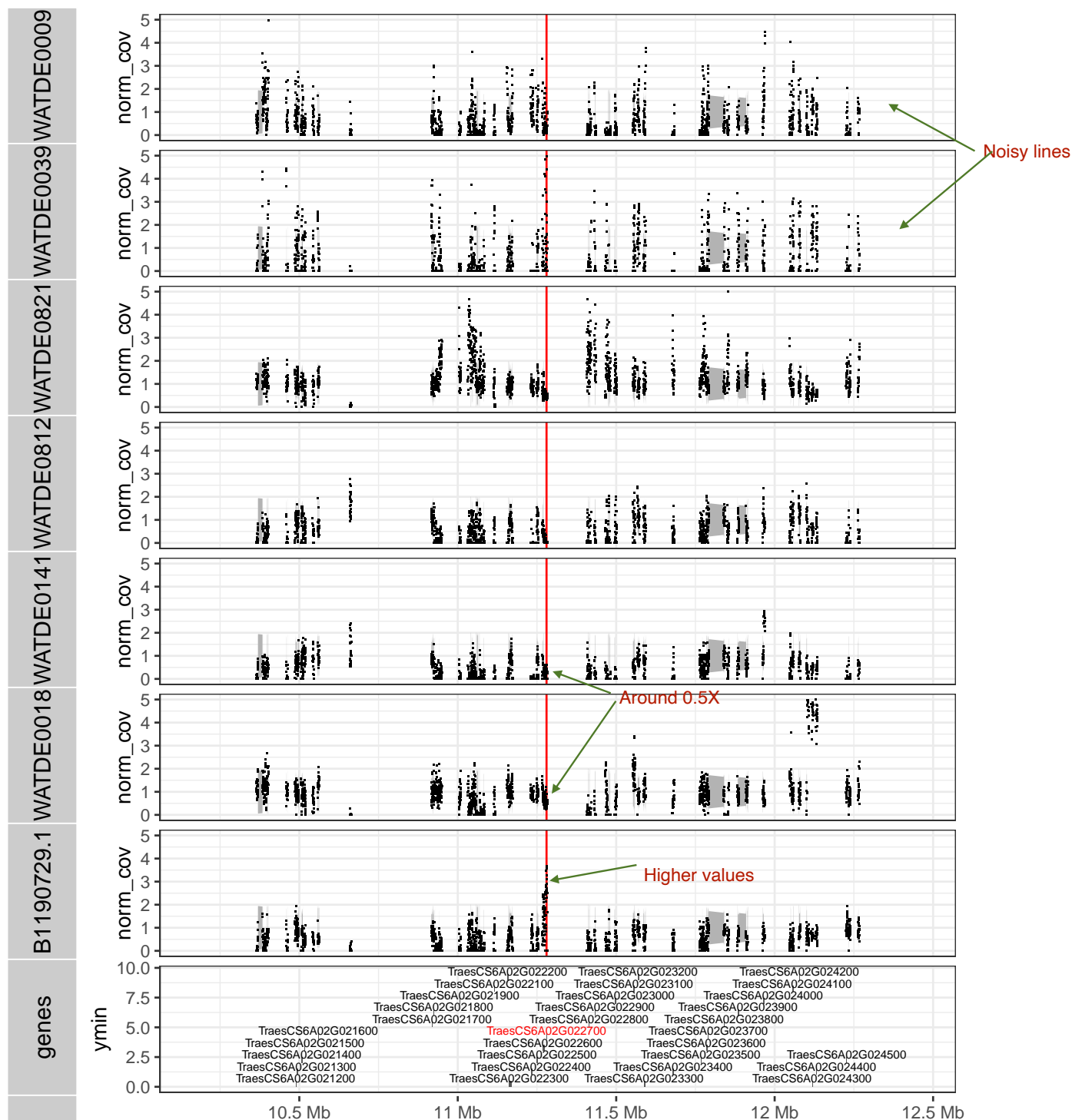
In this example, lines WATDE0009 and WATDE0039 are considered as noisy. Naively, one would think that there are plenty of candidates for CNV on those lines. However, the fact that the values oscillate above and below the region of the expected distribution suggests that these calls are noisy. Line WATDE0821 seems to have some duplications. We can call this because the normalised coverage is, in general, over the expected dispersion, without any value close to 0. Furthermore, the windows outside the gene seem quite stable. Line WATFE812 doesn't seem to have anything abnormal, which should be how most of the lines look.

This is relevant because in some of the previous heatmaps this line is shown as having CNV.



### Some examples around TraesCS6A02G022700

The gene `TraesCS6A02G022700` is reported has missing copies in the Chinese Spring reference. We picked this because we wanted to see if we observe this gene has some variation. Again, the lines `WATDE0009` and `WATDE0039` show a lot of variation, so this is consistent with the noise being noisy. Line `B1190729.1` seems to have higher coverage, which is expected. Lines `WATDE0018` and `WATDE0141` have a lower coverage, but it doesn't go to 0. This may be a case where there is a single copy, in a region that is collapsed in the assembly.



## Details for TraesCS6A02G022700, to show change in real coverage

To look if the change in global coverage in regions that are repetitive can be detected only from the raw coverage, but not from the normalised values, we explored in more detail lines B1190729.1, 'WATDE0018 and WATDE0141.

WATDE0141 and WATDE0018 seems like having the same raw dispersion of raw coverage in the highlighted region, but a normalised coverage around and below 0.5.

This may indicate that the assembly is collapsing two copies, but this samples only have one copy of the gene.

B1190729.1 Seems to have more coverage in that region, so it may be that the line has more than the 2 expected collapsed copies from the reference.

