COV2HTML: Adding Normalisation Factors

COV2HTML is a free interactive display of read alignments
It has been developed by the Laboratoire Pathogenèse des
Bactéries Anaérobies of the Institut Pasteur.
http://cov2html.sourceforge.net/

COV2HTML use the coverage file from MAP2COV software

A web version* is currently accessible at

http://mmonot.eu/COV2HTML

*This website is free and open to all users without any login requirement
but is limited to 10 megabases genome for performance reason.*

2 conditions (RpoS, WT) with 3 replicates (RpoS1, RpoS2, RpoS3, WT1, WT2, WT3)
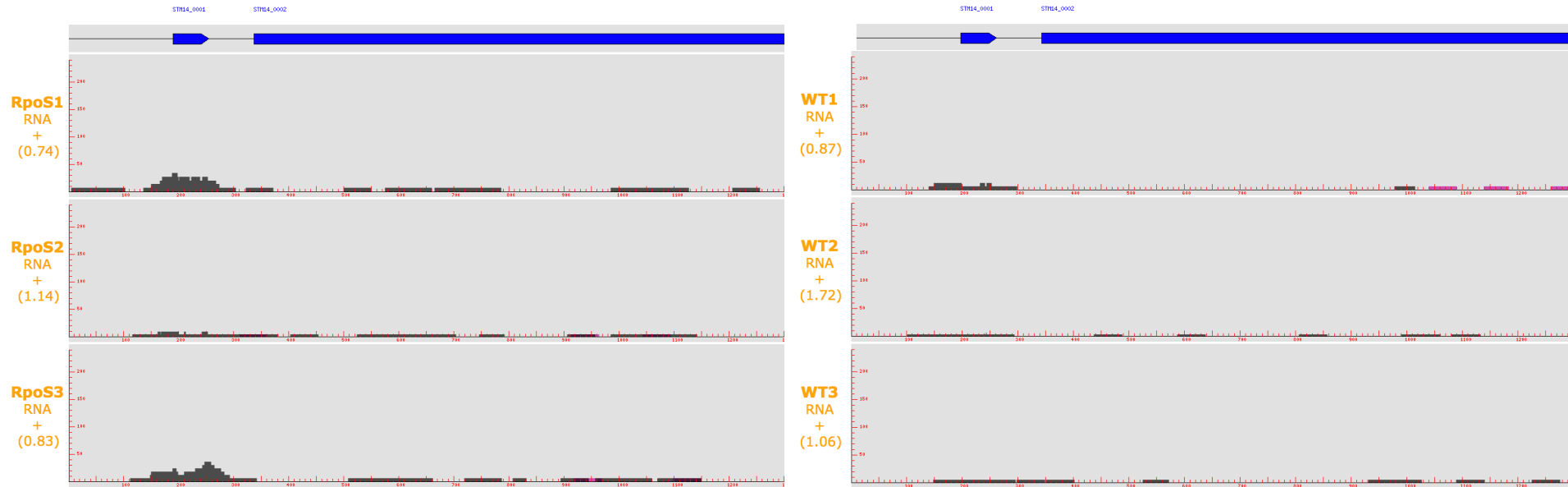
Normalisation Factors applied on coverage views

Normalization aims at correcting systematic technical biases in the data, in order to make coverage comparable across samples. It computes a scaling factor for each sample. Normalized factors are obtained by dividing raw read counts by the scaling factor associated with the sample they belong to. Scaling factors around 1 mean no normalization is performed. Scaling factors lower than 1 will produce normalized coverage higher than raw ones, and the other way around*.

https://github.com/PF2-pasteur-fr/SARTools

RpoS1	0.74
RpoS2	1.14
RpoS3	0.83
WT1	0.87
WT2	1.72
WT3	1.06