

COV2HTML: Adding Statistic Results

COV2HTML is a free interactive display of read alignments
It has been developed by the Laboratoire Pathogénèse des
Bactéries Anaérobies of the Institut Pasteur.

<http://cov2html.sourceforge.net/>

COV2HTML use the coverage file from MAP2COV software

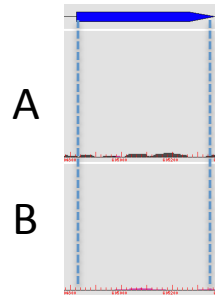
A web version* is currently accessible at

<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.*

Statistics issues found using coverage views

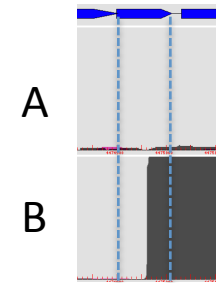
Low coverage



Condition	Counts (triplicates)	Ratio	pvalue
A	22 ; 17 ; 30	107	0,0000214
B	0 ; 0 ; 0		

Statistics: high ratio and low variability, this gene is highly significant
Visualisation: very low coverage, need validation

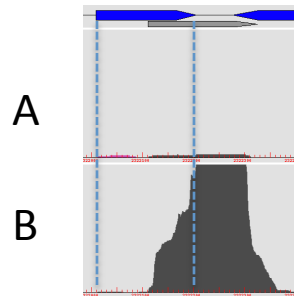
Side coverage



Condition	Counts (triplicates)	Ratio	pvalue
A	1 ; 3 ; 2	0,002	1,56e ⁻⁵⁶
B	1784 ; 1616 ; 1704		

Statistics: high ratio and low variability, this gene is highly significant
Visualisation: coverage from promoter of next gene

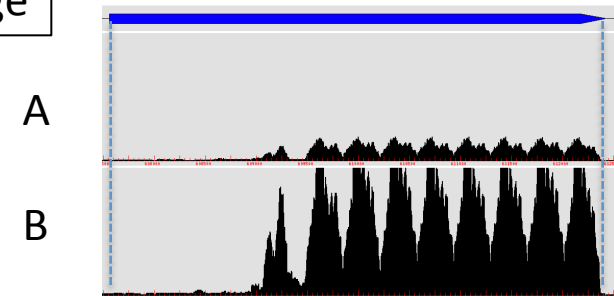
ncRNA coverage



Condition	Counts (triplicates)	Ratio	pvalue
A	3 ; 3 ; 6	0,013	3,42e ⁻³⁷
B	369 ; 310 ; 403		

Statistics: high ratio and low variability, this gene is highly significant
Visualisation: coverage from ncRNA

Repeat coverage



Condition	Counts (triplicates)	Ratio	pvalue
A	141 ; 188 ; 181	0,029	2,14e ⁻²⁵
B	5034 ; 7589 ; 4909		

Statistics: high ratio and low variability, this gene is highly significant
Visualisation: coverage from repeat region (another gene repeats)

