COV2HTML: Adding Statistic Results

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/

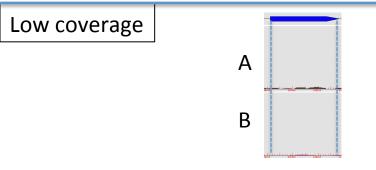
COV2HTML use the coverage file from MAP2COV software

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.

Statistics issues found using coverage views



Side	coverage



_	Condition	Counts (triplicates)	Ratio	pvalue
	Α	22 ; 17 ; 30	107	0,0000214
	В	0;0;0	107	0,0000214

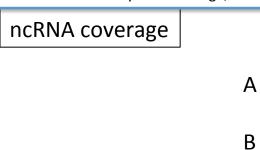
Condition	Counts (triplicates)	Ratio	pvalue		
Α	1;3;2 0,002		1,56e ⁻⁵⁶		
В	1784 ; 1616 ; 1704	0,002	1,306		

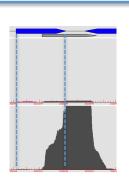
Α

В

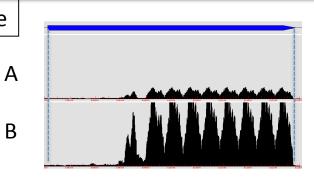
Statistics: high ratio and low variability, this gene is highly significative **Visualisation**: very low coverage, need validation

Statistics: high ratio and low variability, this gene is highly significative **Visualisation**: coverage from promotor of next gene





Repeat	coverage



Condition	Counts (triplicates)	Ratio	pvalue		
Α	3;3;6	0,013	3.42e ⁻³⁷		
В	369 ; 310 ; 403	0,013	3,420		

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

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

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

ID A1 A2 A3 A4 B1 B2 B3 B4 A B FC pvalue significant

Creation of the statistical results file

The file must be a tabulated format text file with the following columns: gene identifier ('ID'), each condition numbered per replicate (e.g. 'A1, A2, A3, A4, B1, B2, B3, B4'), each condition normalized value (e.g. 'A, B'), the fold change value ('FC'), the pvalue ('pvalue') and a significativity column with 0 or 1 value ('significant'). Column 'ID', 'A', 'B', 'FC' and 'pvalue' are mandatory. If significant column is not present, pvalue <= 0,05 are considered as significative. For stranded experiments you have to add sense + results and single line with « END_STRAND+ » then add sense - results and finish the file by « END_STRAND- »

Example with 2 conditions (RpoS, WT) and 3 replicates

ID	RpoS1	RpoS2	RpoS3	WT1	WT2	WT3	RpoS	WT	FC	pvalue
STM14 0001	32	11	37	14	6	4	27	8	3.43	0.01
STM14_0002	62	55	64	25	26	33	60	28	2.15	0.02
STM14_0048	9	5	11	54	44	52	9	50	0.17	0.04
END_STRAND+										
STM14_0001	1	1	1	2	1	1	1	1	1.00	1.00
STM14_0002	1	2	2	1	2	2	2	2	1.00	1.00
STM14_0048	1	2	1	2	1	3	1	2	1.00	1.00
END_STRAND-										