COV2HTML: RNA coverage visualization guide

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.*

ENTER your Analysis (title) :	
Condition A ⬜	Condition B ⬜
(Choose File) no file selected	(Choose File) no file selected
(Choose File) no file selected	(Choose File) no file selected
(Choose File) no file selected	(Choose File) no file selected
(Choose File) no file selected	(Choose File) no file selected
STATISTICS (Optionnal) (Choose File) no file selected	
(ENTER ANALYSIS IN DATABASE)	

ENTER your Analysis

The title should be chosen to describe analysis carefully as there is no link between coverage files and experiments. A label of 4 characters could also be attached to each condition and numbered per replicate. Two conditions can be compared with a maximum of 4 replicates per condition. Finally a statistical results file could also be integrated using a tabulated format text file.

http://mmonot.eu/COV2HTML/connexion.php

VIEW an Analysis
---------- YOUR Analysis ---------- ⬍
---------- TUTORIAL Data ---------- ⬍
---------- REMOVE Analysis ---------- ⬍

VIEW an Analysis

Analysis is saved in the "YOUR Analysis" down-drop list of the
« connexion.php » page. As there is no login requirement, analysis is
linked to a cookie created in the web browser for 2 years. Case studies
are available in the "TUTORIAL Data" down-drop list. Finally a remove
analysis button is present to erase one or all of the analysis attached to
the computer's browser.

http://mmonot.eu/COV2HTML/connexion.php
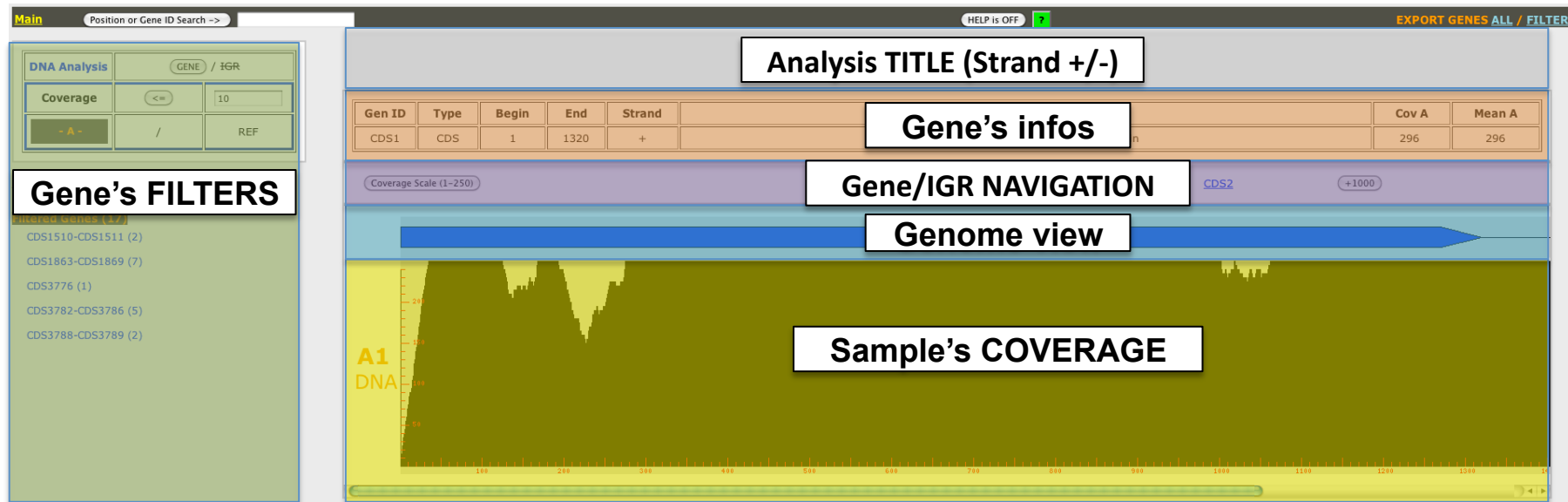
COV2HTML Visualization

[Grey box] At the top the analysis title and the genomic strand. [Orange box] The selected gene or IGR informations (gene ID or IGR ID, position, strand, type and product) and coverage for each replicates, the mean value per conditions and the ratio of conditions A/B. [Yellow box] The analysis condition and replicate genomic coverage views. One graphical bar (one pixel) represents a genomic base coverage. [Blue box] Genetic elements in a genomic view, blue color for all except rRNA and tRNA which are in red. [Purple box] Navigation tools within genome. Current gene or IGR surround with link to the previous and next one. A Y-axis zoom button, to change coverage scale from 1-250 to 1-2500 (10x). [Green box] Gene or IGR filters to analyse coverage data.

RNA Analysis	GENE / ~~IGR~~	
Coverage	>=	10
- A -	/	REF

COV2HTML RNA one condition
From up to bottom: (i) Select the genetic elements using the swich button from gene to IGR analysis. (ii) Filter genetic elements by their coverage value either lower or upper a desired value (switch ">=" to "<"). Filters results are displayed below the filter box.

COV2HTML RNA two conditions
From up to bottom: (i) Select the genetic elements using the swich button from gene to IGR analysis. (ii) Filter genetic elements by their coverage value either lower or upper a desired value (switch "<=" to ">"). (iii) Balance the mean coverage of each sample using the standardize button (iv) Analysis of genetic elements coverage value from one condition (blue rectangle): "A" or "B" or (v) Filter fold change differences between the two conditions "A / B" by setting the minimum coverage value (threshold) assigned to genetic elements before ratio calculation (red rectangle). Filters results are displayed below the filter box. If statistical results are present, 'Standardization' is replace by 'Statistics' and 'threshold' option disapears.