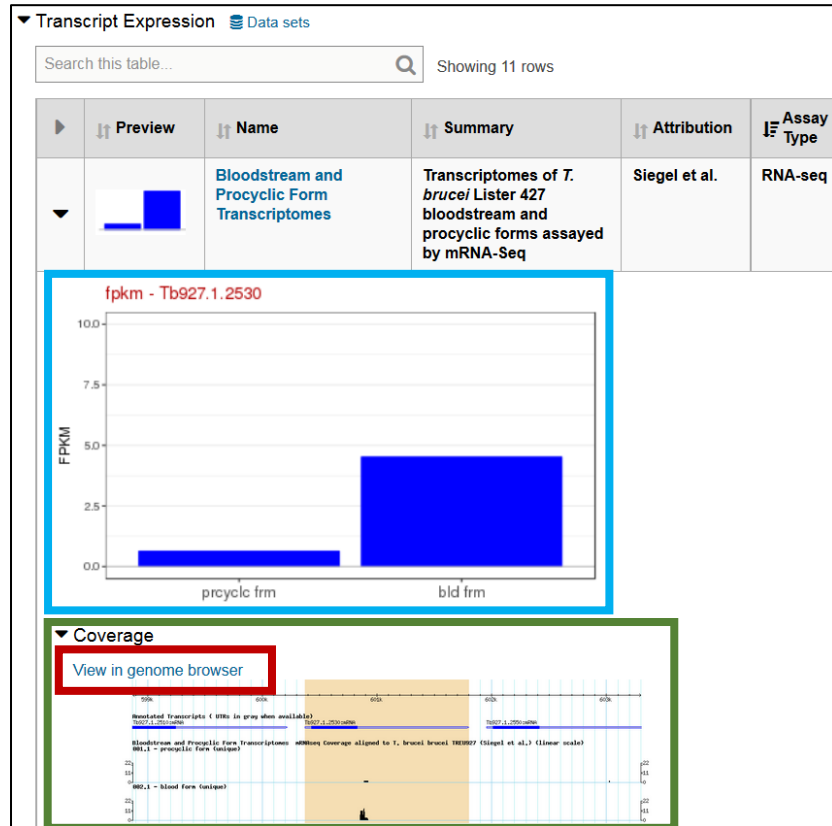
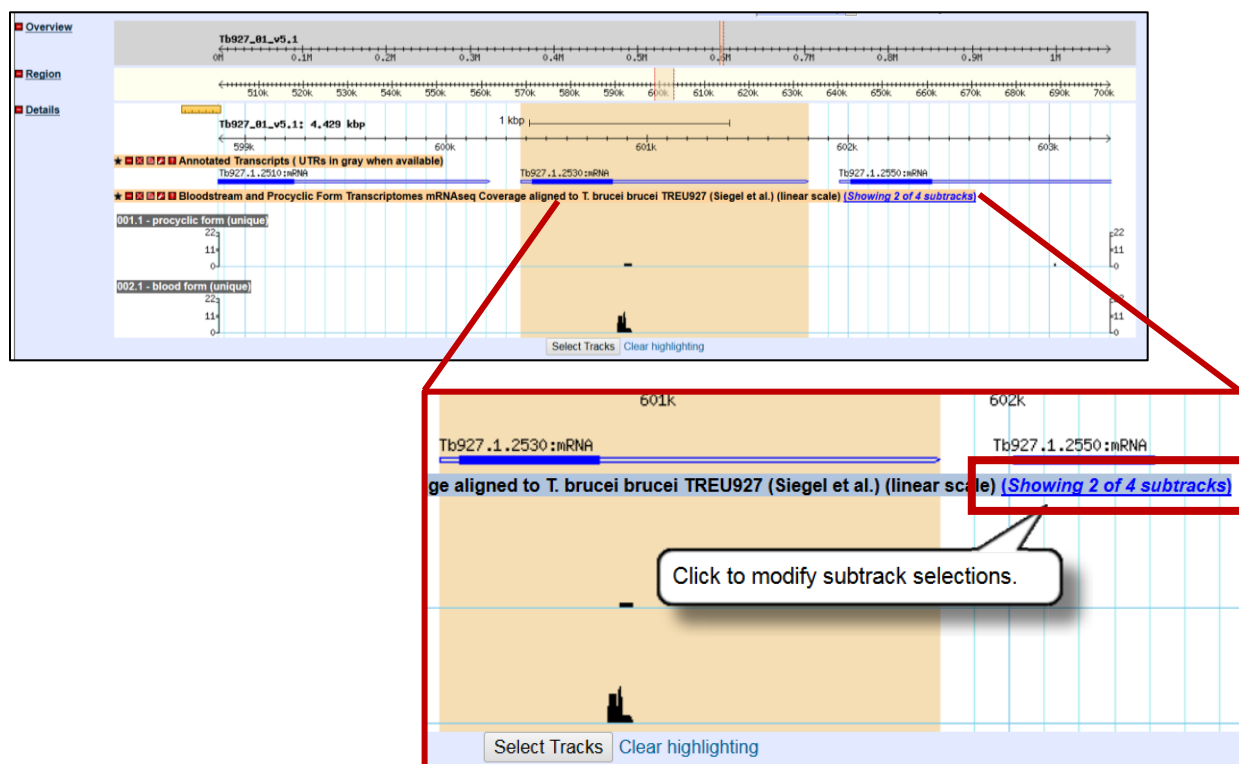


1. The gene page [Expression graph](#) and [Coverage Section](#) represent unique reads. To view non-unique reads click on the [‘View in genome browser’](#) link and turn on the non-unique subtracks



2. Open the Subtracks dialog box by clicking the [‘Showing # of # subtracks’](#) link in the track title.



3. Turn on non-unique subtracks individually (check box in first column) or as a group ('All on' link in first column header). Then choose 'Change' to view the new subtrack configuration. If needed, adjust the y-axis scaling with the track configuration tool (wrench icon that appears before the track title).

The image shows a multi-step process for configuring and viewing subtracks in a genome browser.

Step 1: Subtrack Configuration Table

Select	:selected	Alignment	Display_name	Sample	Type
All off All on	All ▾	All ▾	All ▾	All ▾	All ▾
<input checked="" type="checkbox"/>	1	unique	001.1 - procyclic form (unique)	1_procyclic_form	Coverage
<input checked="" type="checkbox"/>	1	unique	002.1 - blood form (unique)	1_blood_form	Coverage
<input type="checkbox"/>		non-unique	001.0 - procyclic form (non-unique)	1_procyclic_form	Coverage
<input type="checkbox"/>		non-unique	002.0 - blood form (non-unique)	1_blood_form	Coverage

Buttons: ☐ Semi-transparent overlap

Step 2: Visualization

The visualization shows four subtracks: 001.1 - procyclic form (unique), 001.0 - procyclic form (non-unique), 002.1 - blood form (unique), and 002.0 - blood form (non-unique). A red arrow points from the 'Change' button in the configuration table to the track configuration tool.

Step 3: Track Configuration Tool

Bloodstream and Procyclic

Bloodstream and Procyclic Form Transcriptomes mRNAseq Coverage aligned to *T. brucei brucei* TREU927 (0 bp)
(Currently showing 4.429 kbp)

Spacing: Expand & Label ▾

Shape: wiggle_xyplot (default) ▾

plot style: histogram (default) ▾

Set colors automatically: ☐

Switch colors when value crosses: none ▾

Fill color: Dynamically calculated (default) ▾

Line color: black (default) ▾

Y-axis scaling: scale to local min/max (default) ▾

Show variance band: fixed

Height: scale to SD multiples
scale to local min/max (default)
scale to chromosome min/max
scale to genome min/max
clip to +/- SDs shown below

Apply config when view between: