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).