**Figure 5 – Foreign genes are contained in scaffolds confirmed by multiple datasets.**

14 next-generation sequencing read datasets, originating from 4 independent sequencing projects, were mapped against **(A)** Bemm et al.’s and **(B)**  Koutsovoulos et al.’s assembly and visualized using Anvi’o (Delmont *et al.,* 2015). Tracks showing coverage of moleculo long-read (LR), Pacbio, and short-insert library reads (UNC 300, 500, & 800) from our original study (Boothby *et al.,* 2015) are colored blue. Tracks showing coverage by genomic reads from (Koutsovoulos *et al.,* 2016) are colored purple. Tracks showing coverage by genomic and pooled RNAseq reads generated by Dr. Kazuharu Arakawa are colored green. The track showing coverage by pooled RNAseq reads generated by Dr. Itai Yanai is colored yellow. Black tick-marks in the outer rings indicate scaffolds that contain foreign sequences identified using the method indicated in parentheses. Highlighted in red are scaffolds that are covered by genomic reads originating from only 1 group’s sequencing effort. Highlighted in orange are scaffolds covered by 2 of 3 groups genomic reads.