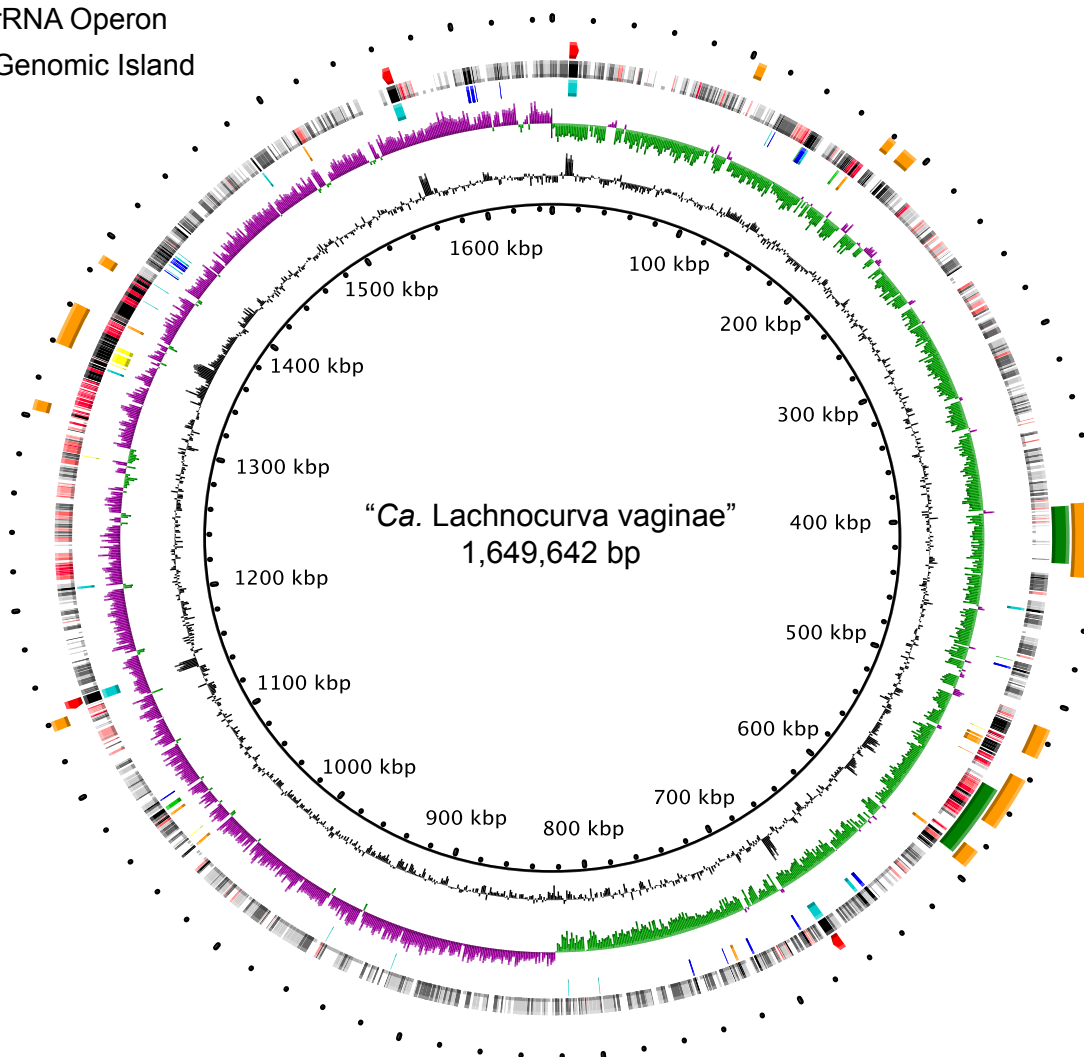


- Ring 1: Base position
- Ring 2: GC Content
- Ring 3: GC Skew(+ / -)
- Ring 4: Best Blast hit if match to close relatives > 80% ID
 - Shuttleworthia satelles*
 - Lachnobacterium bovis*
 - Mageeibacillus indolicus*
 - Lachnospiraceae* bacterium 2_1_46FAA
 - Clostridiales* bacterium KA00274
- Ring 5: Best Blast hit if match to *Clostridiales* > 80% ID
 - Clostridiales*, > 80% ID
 - Clostridiales*, > 60% ID
 - Clostridiales*, > 40% ID
 - Not *Clostridiales*, > 80% ID
 - Not *Clostridiales*, > 60% ID
 - Not *Clostridiales*, > 40% ID
- Ring 6: ■ Phage
■ rRNA Operon
- Ring 7: ■ Genomic Island



Supplemental Figure 2. Circle plot of “*Ca. Lachnocurva vaginae*” cMAG with best blast hits indicated as either *Clostridiales* or not (Ring 5). If hit is within *Clostridiales* and >80% ID, specific taxon of close relatives is indicated in Ring 4. Included BLAST hits covered at least 80% of the query gene.