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.