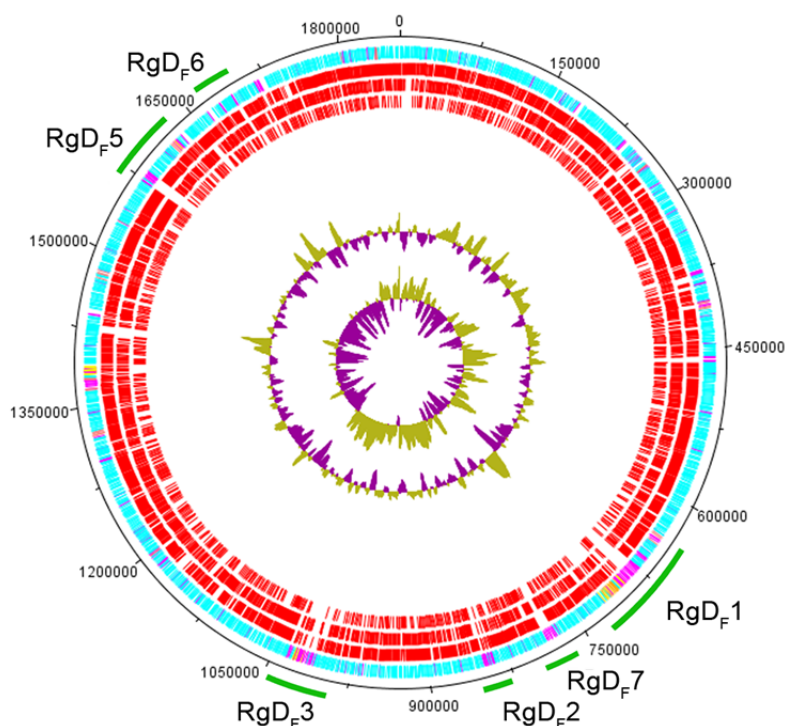


Additional file 7



Map of RgD_F in *H. influenzae* type f KR494 genome in relative to closely-related human *Haemophilus* species. Circular representation of protein conservation between Hif KR494 and reference species was visualized using DNA plotter. From the outside in, the outer circle shows the genome length of Hif KR494 with position markers. The second circle shows the total ORFs of KR494 genome predicted on both forward and reverse strands. Common and unique ORFs in relative to the reference species are colored in blue and magenta, respectively. Phage-related ORFs are marked in yellow and orange. The third to fifth circles represent the distribution of individual ORF with high homology ($\geq 85\%$ identity) (in red) to the corresponding ORF in reference species *H. aegyptius* ATCC11116, *H. haemolyticus* M21639 and *H. parainfluenzae* ATCC33392, respectively. Gaps between the conserved ORFs represent RD between Hif KR494 and the compared species and were denoted as RgD_F1 to RgD_F7 (marked with green lines). GC plot and GC skew of KR494

genome are shown in the sixth and seventh circle, respectively. Genome of Hif KR494 was less conserved with *H. aegyptius*, *H. haemolyticus* and *H. parainfluenzae* at the RgD_F1, 2, 3, 5, 6 and 7. RgD_F7 comprises *xylFGH* and *xylAB* operons (HifGL_000770-HifGL_000777) that are involved in xylose uptake and metabolism through the pentose phosphate pathway. This indicated that *H. aegyptius*, *H. haemolyticus* and *H. parainfluenzae* lacked a xylose metabolism system that is, however, conserved in *H. influenzae*.