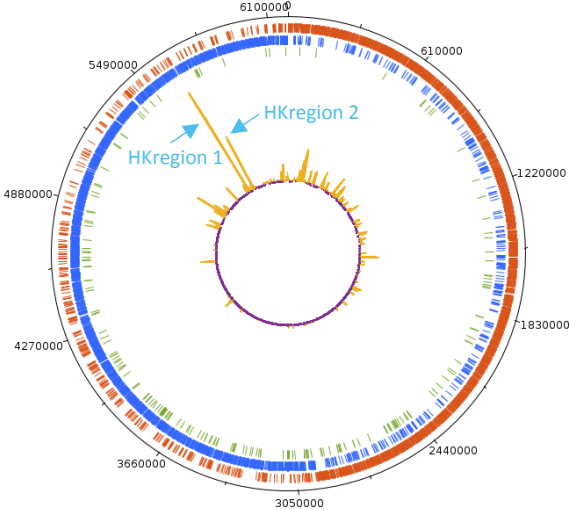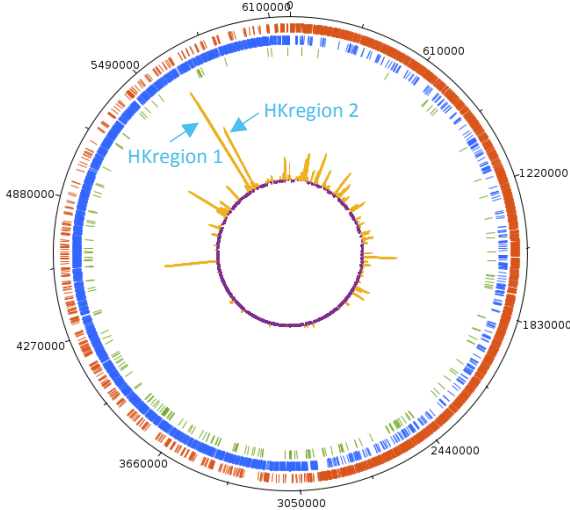# Additional file 4: Circular plots showing average coverage of the genome by RNA-Seq reads in all six time points
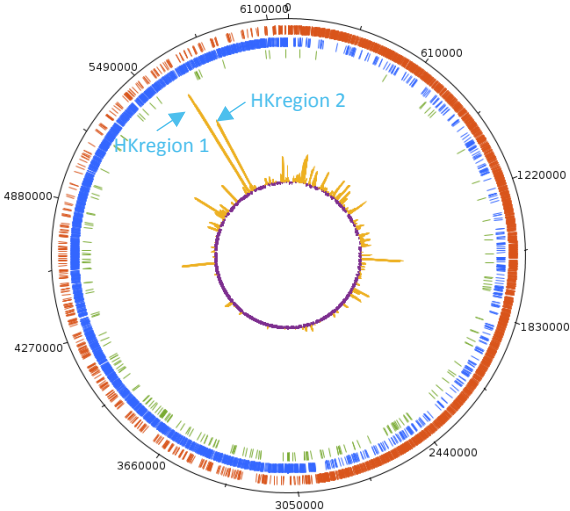
The outermost and the second outermost circles represent positions of genes on the forward (red) and reverse (blue) strands respectively. The third circle (green) stands for pseudogenes. The yellow peak and shading area represents transcription greater than the average and violet lower than average. Floating window of 10,000 bp with step of 200 bp was used to render the shading area.
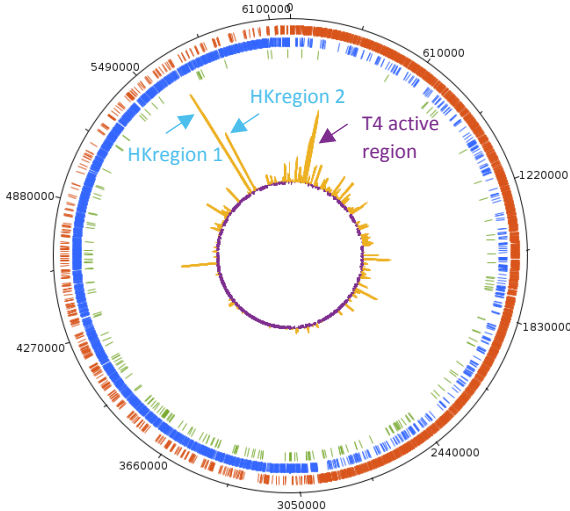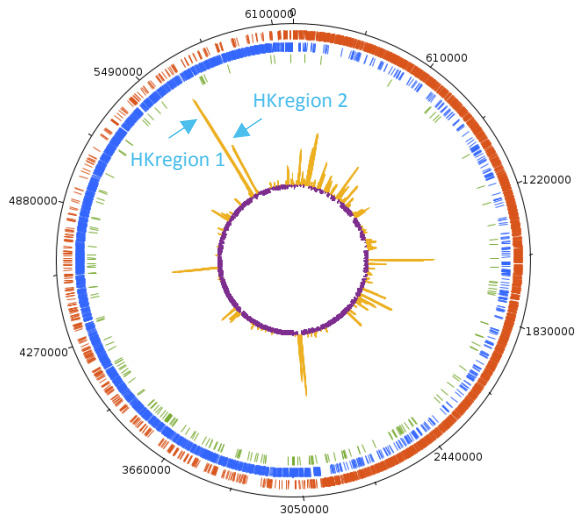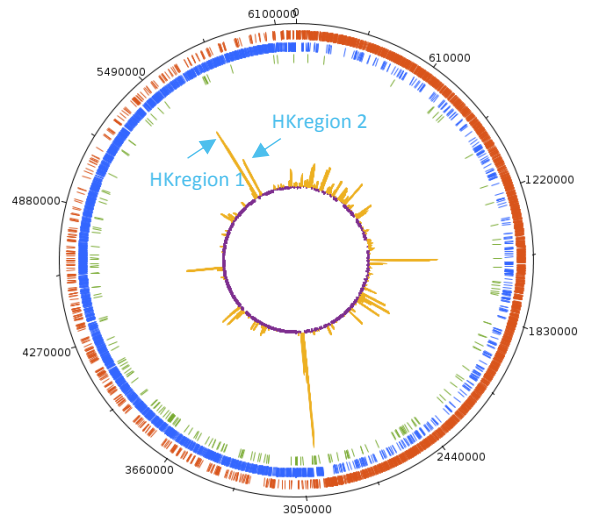

T1 (3.5h)

T2 (6h)

T3 (8.5h)

T4 (13h)

T5 (18h)   T6 (23h)