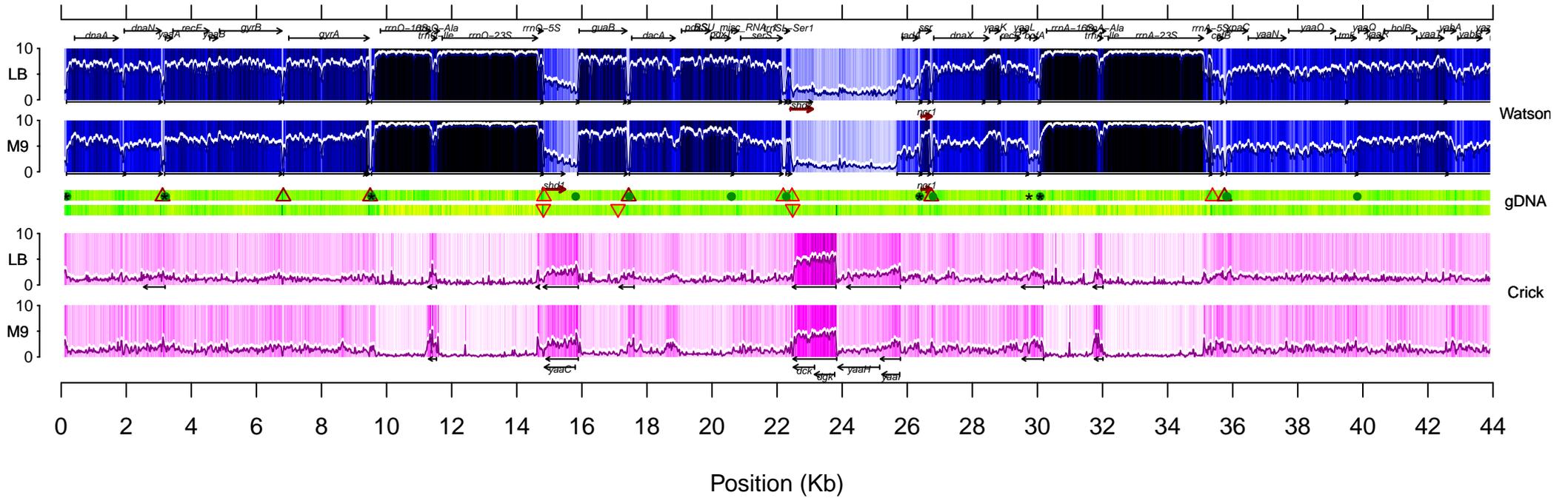


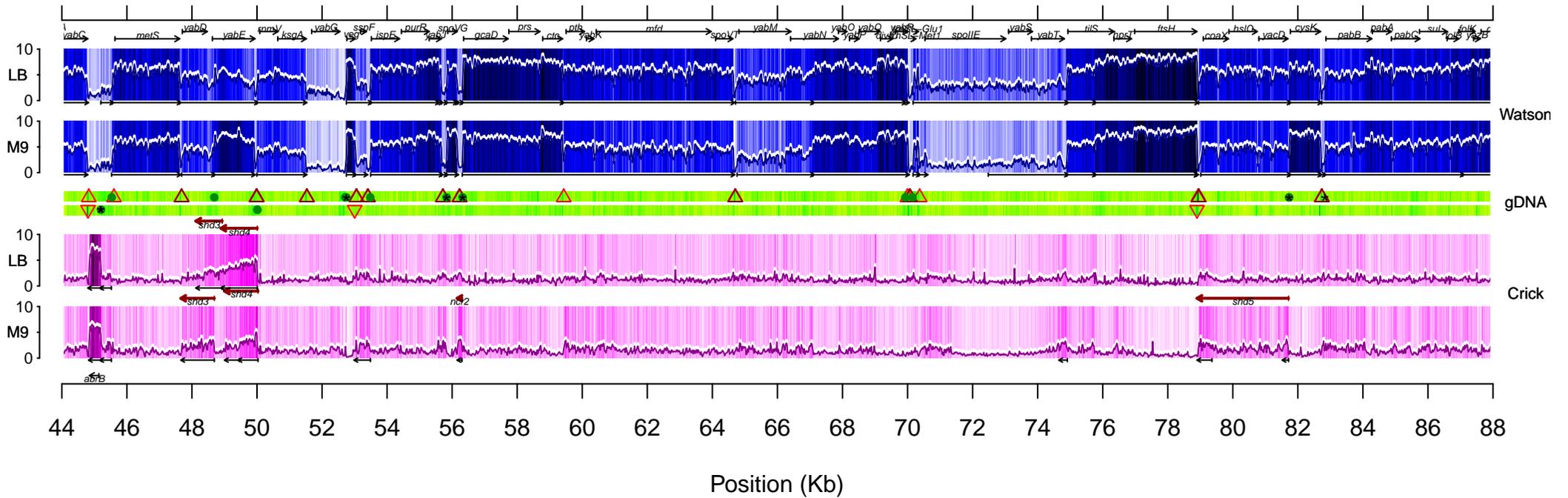
Figure S2

The following pages show the level of expression along the genome of *Bacillus subtilis* when growing on rich (LB) and minimal (M9) medium. The signal from genomic DNA hybridized to the same tiling chip (Rasmussen *et al.*, 2009) is also shown. Each page contains two similar plots each presenting ~44 Kb of the genome. The two blue bands show the expression in LB and M9 respectively on the positive strand, the two magenta bands show the minus strand. The darker the color the higher the expression in the given position. On top of the bands the expression level is plotted as a scaled version (0-10) of the log₂ to the fold change (signal/background signal). In the middle of each plot the gDNA signal is shown for both strands, here the color scale is yellow-green-black, where black is low and yellow is high. Along the genome, in all 6 bands in the same positions, white regions indicate regions where the recent re-sequencing of the genome (AL009126.3) have shown either inserts or regions with very low similarity to the last version (see Rasmussen *et al.*, 2009). Annotated genes are shown as black arrows in the top and the bottom of each plot (annotation from AL009126.3), indicating genes on the positive and negative strand respectively. New genes are shown as red arrows below (+ strand) and above (- strand) each band. Both predicted and experimentally verified terminators and sigma-factor binding sites are shown on top of the gDNA bands. Dark red triangles: Experimentally verified terminators, red triangles: Predicted terminators, stars: Experimentally verified sigma-factor binding sites, green dots: Predicted sigma-factor binding sites.

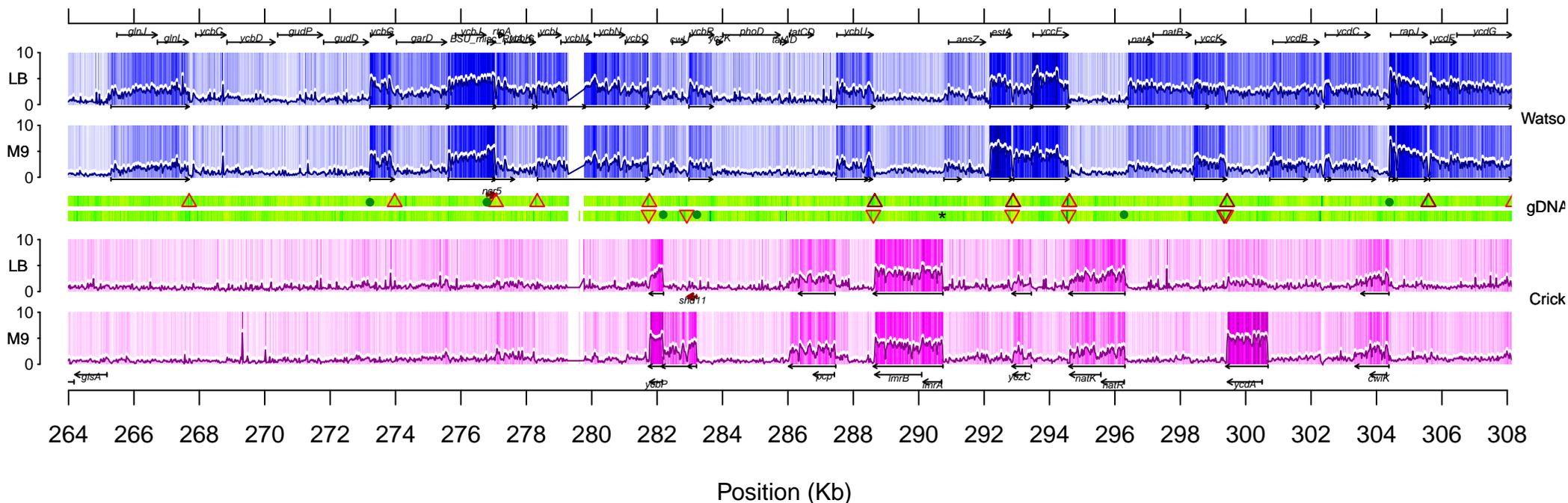
0 – 44 Kb



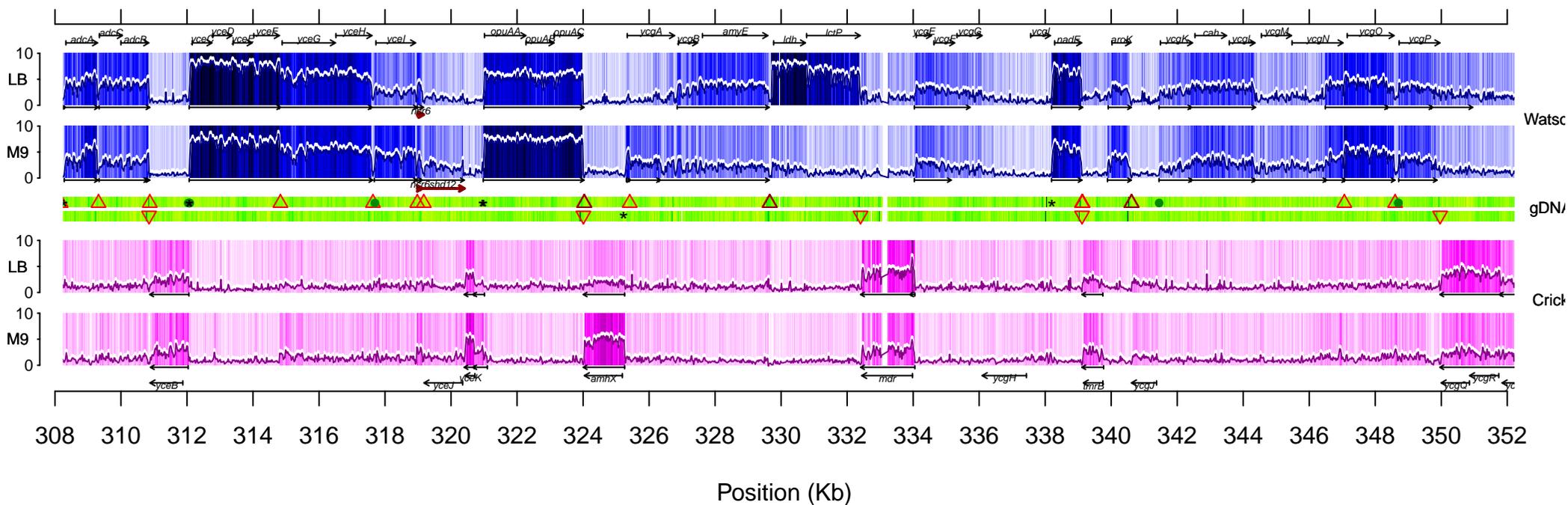
44 – 88 Kb



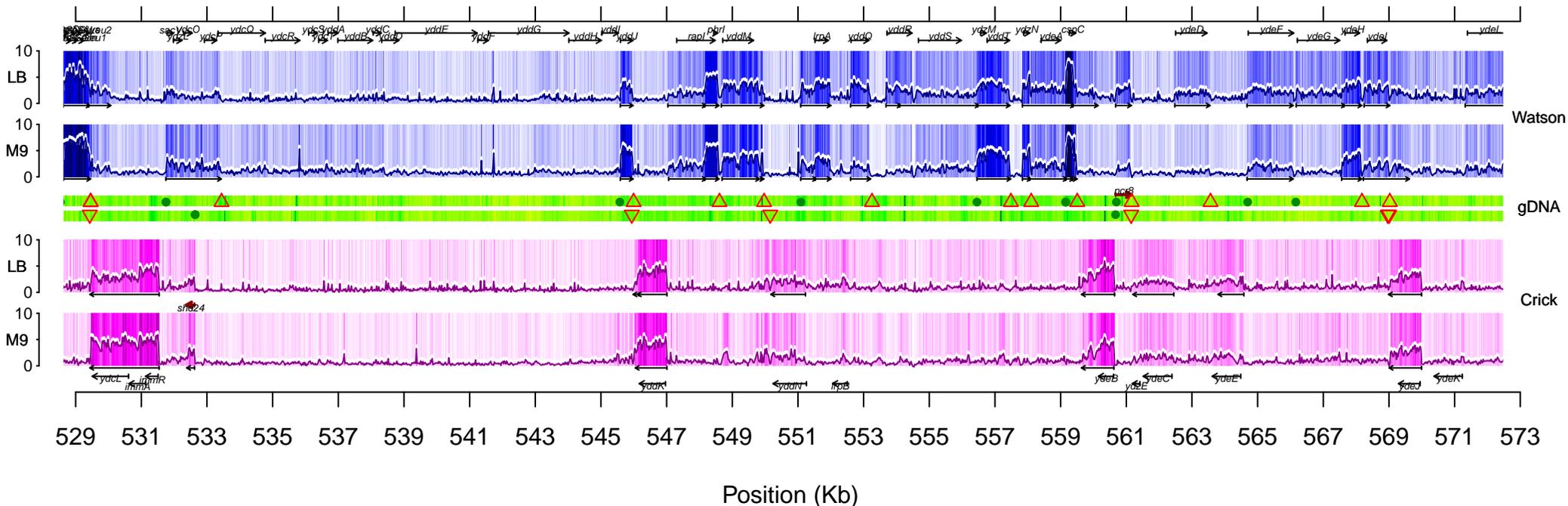
264 – 308 Kb



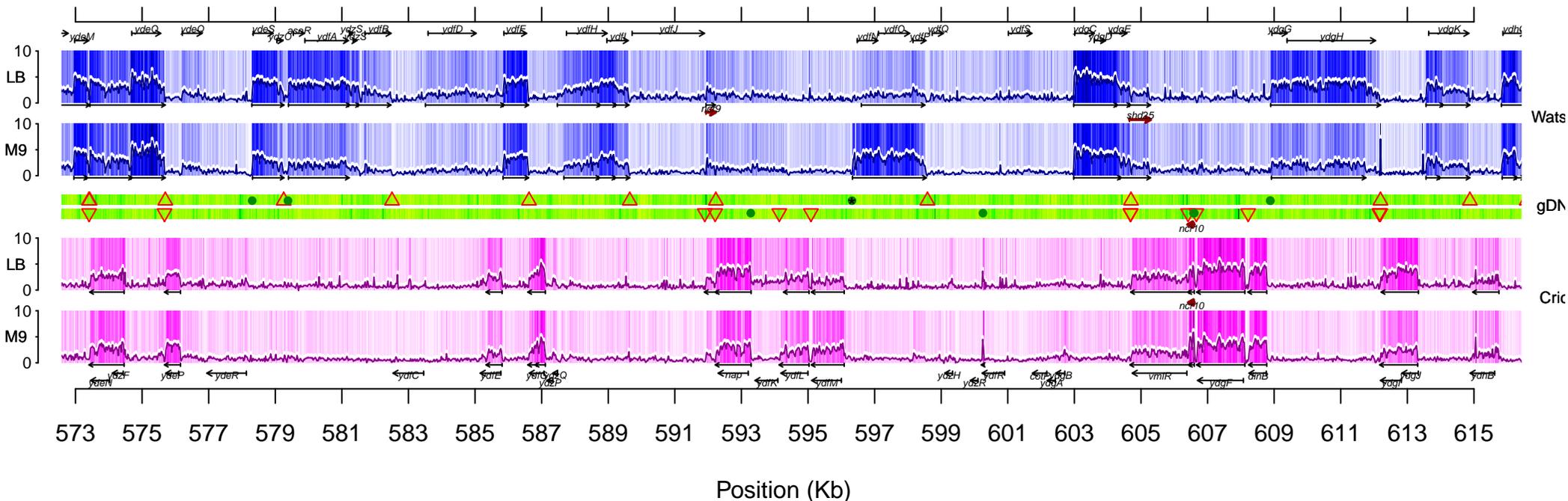
308 – 352 Kb



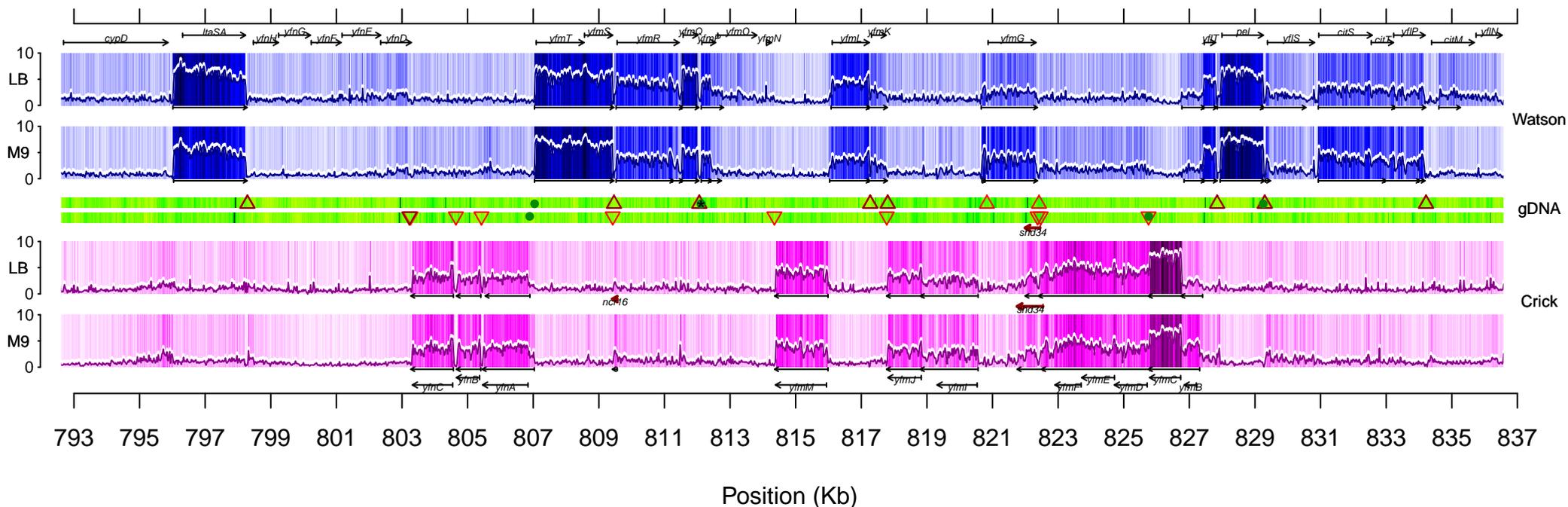
529 – 573 Kb



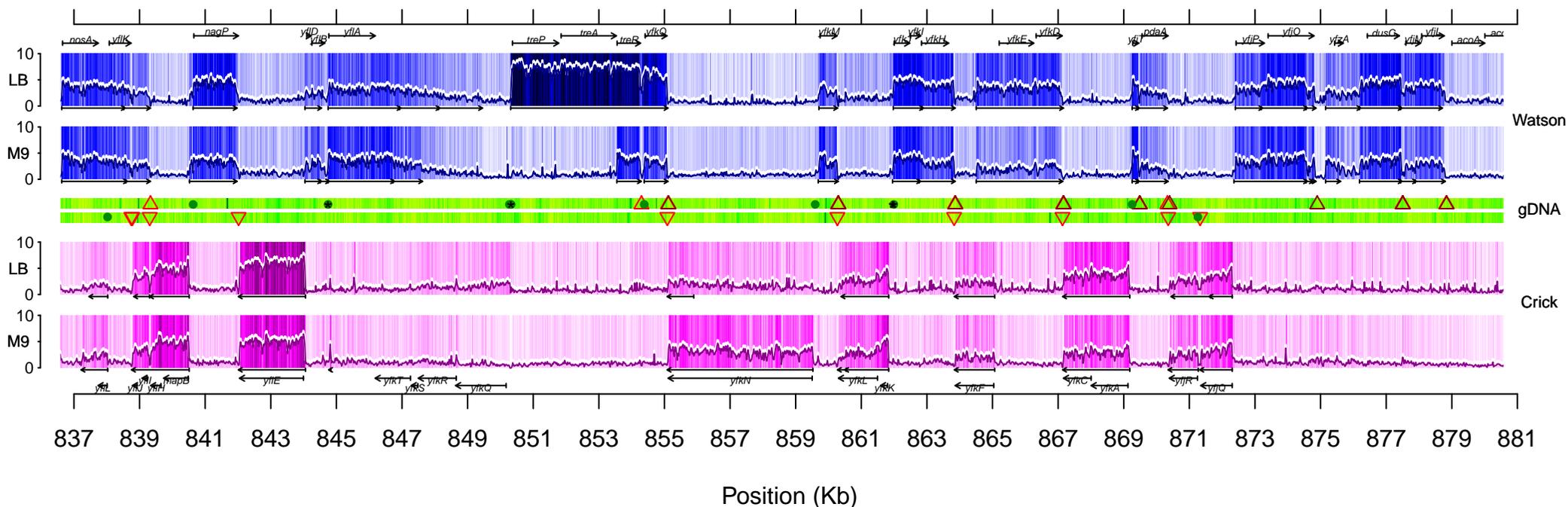
573 – 616 Kb



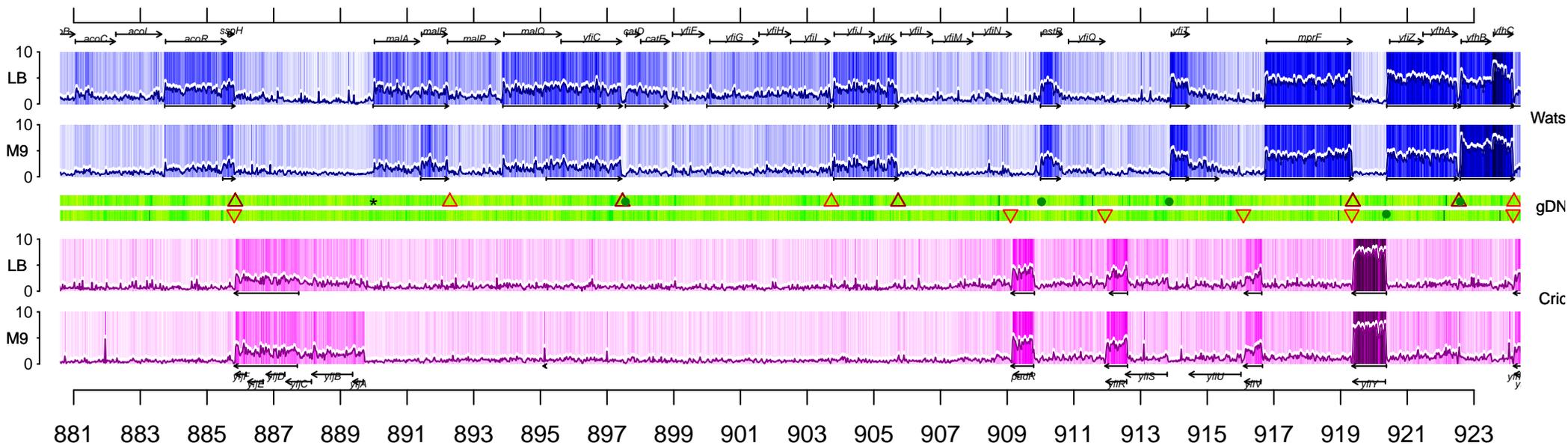
793 – 837 Kb



837 – 881 Kb

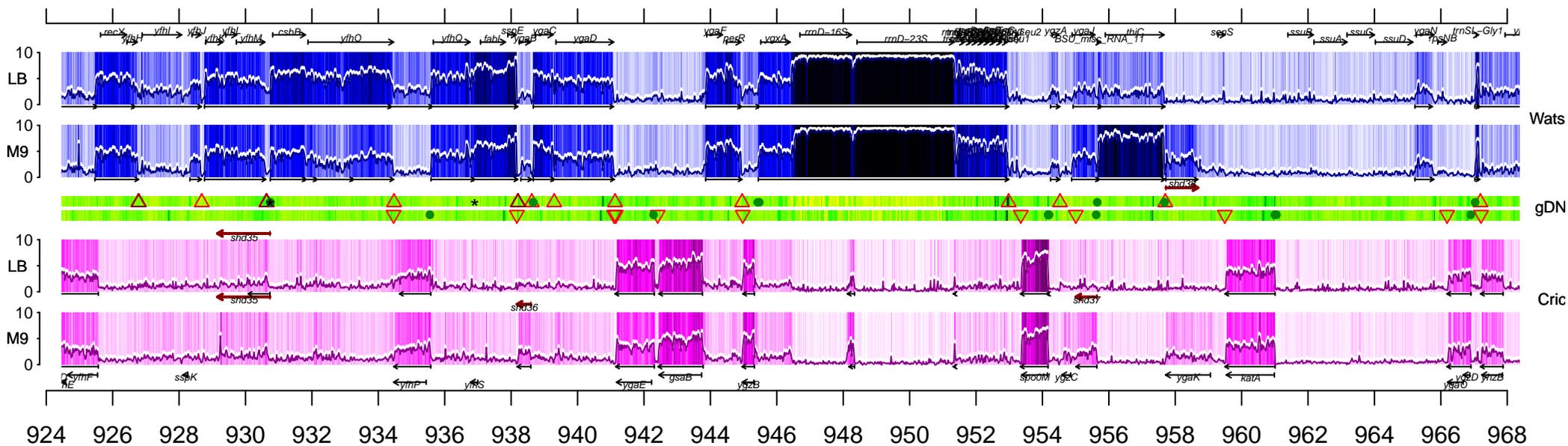


881 – 924 Kb



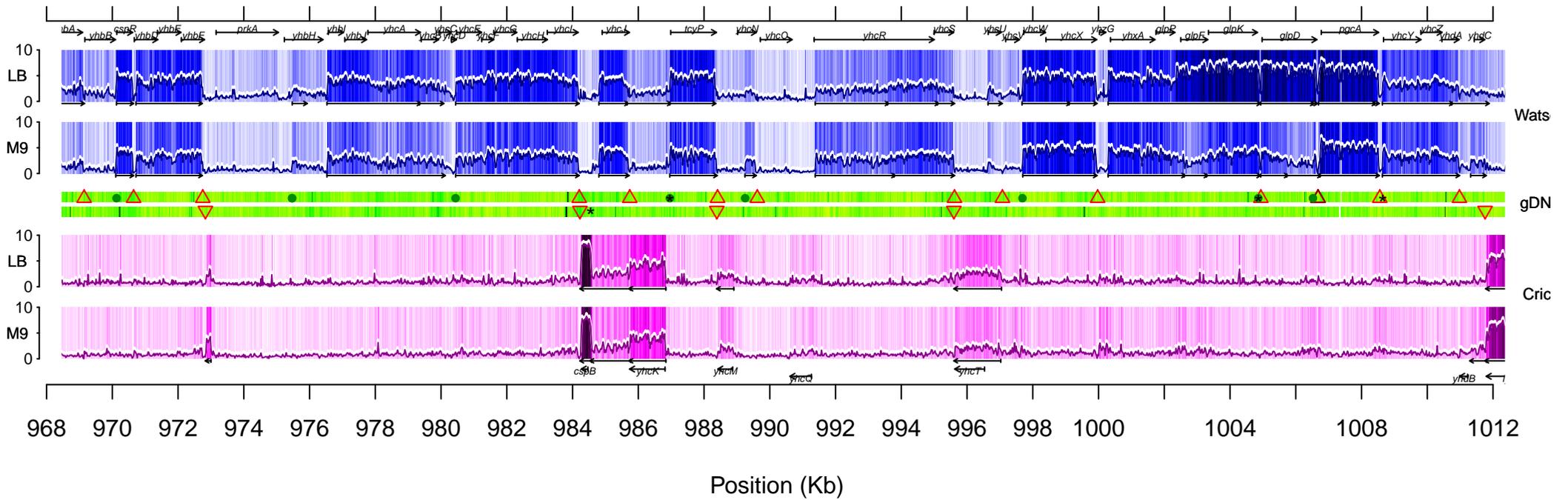
Position (Kb)

924 – 968 Kb

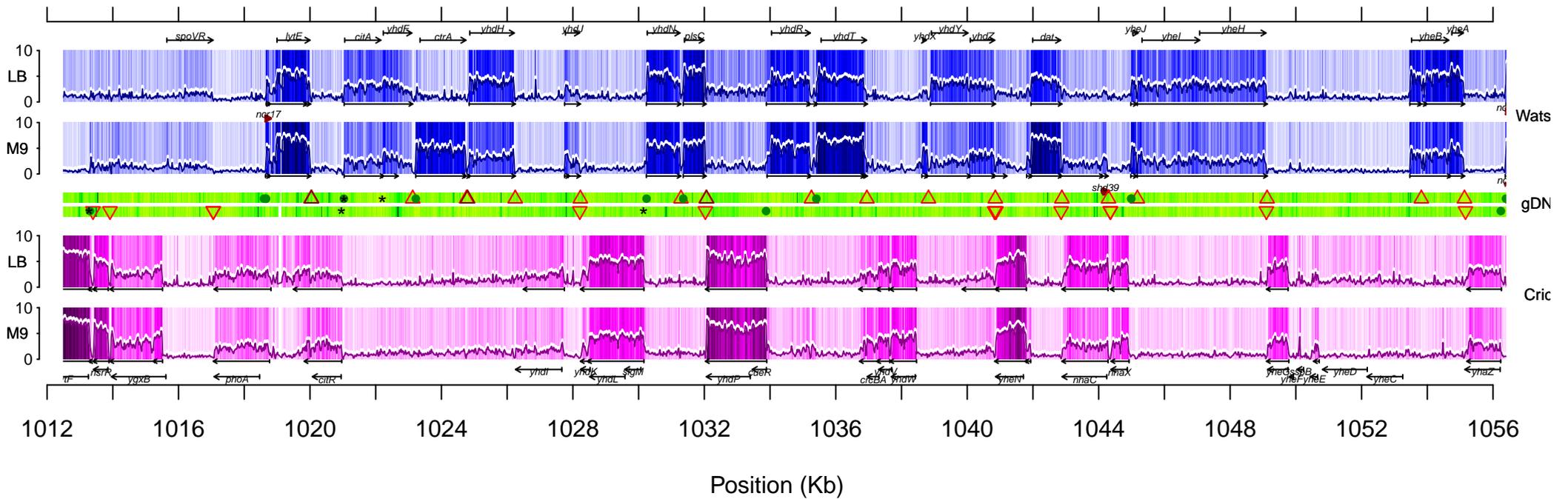


Position (Kb)

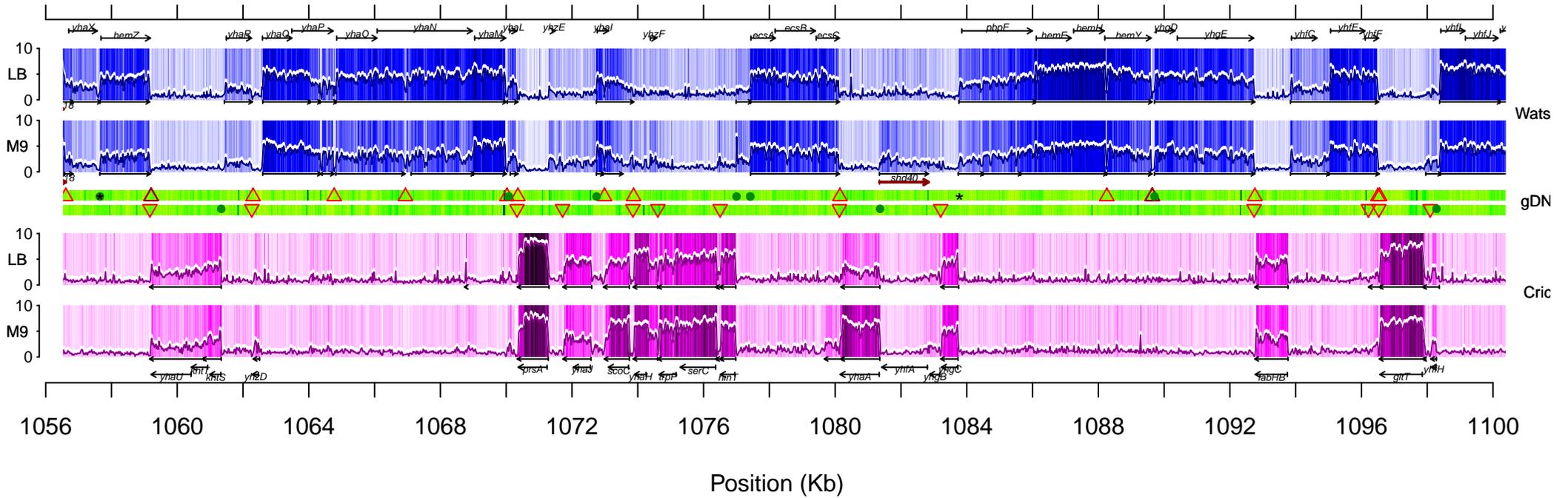
968 – 1012 Kb



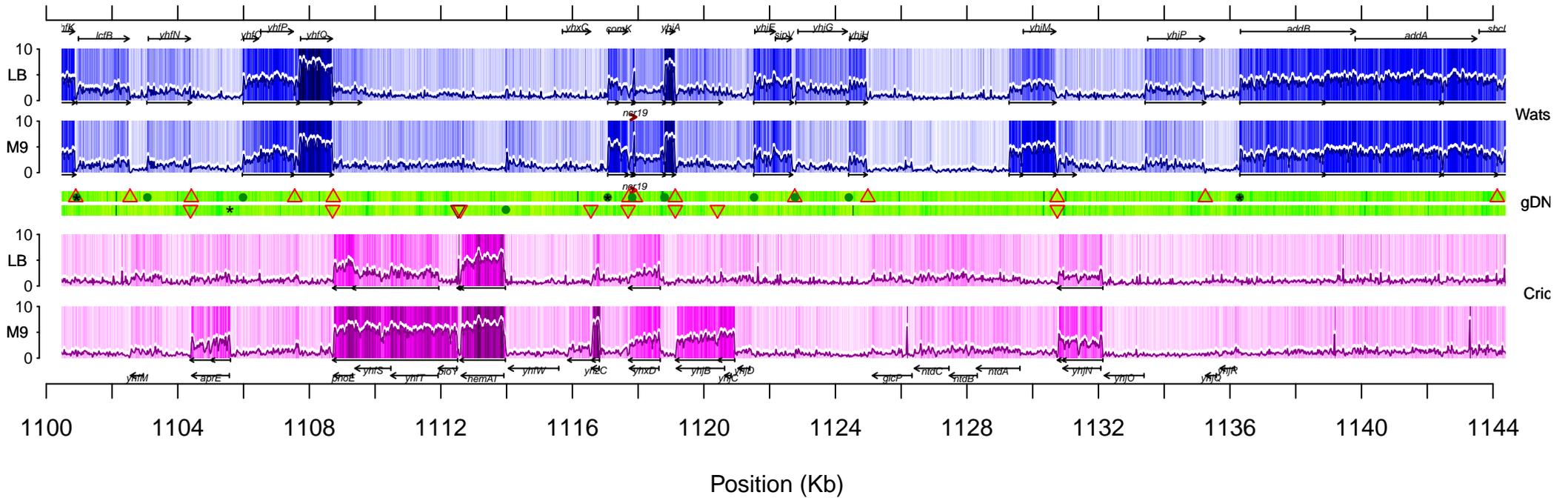
1012 – 1056 Kb



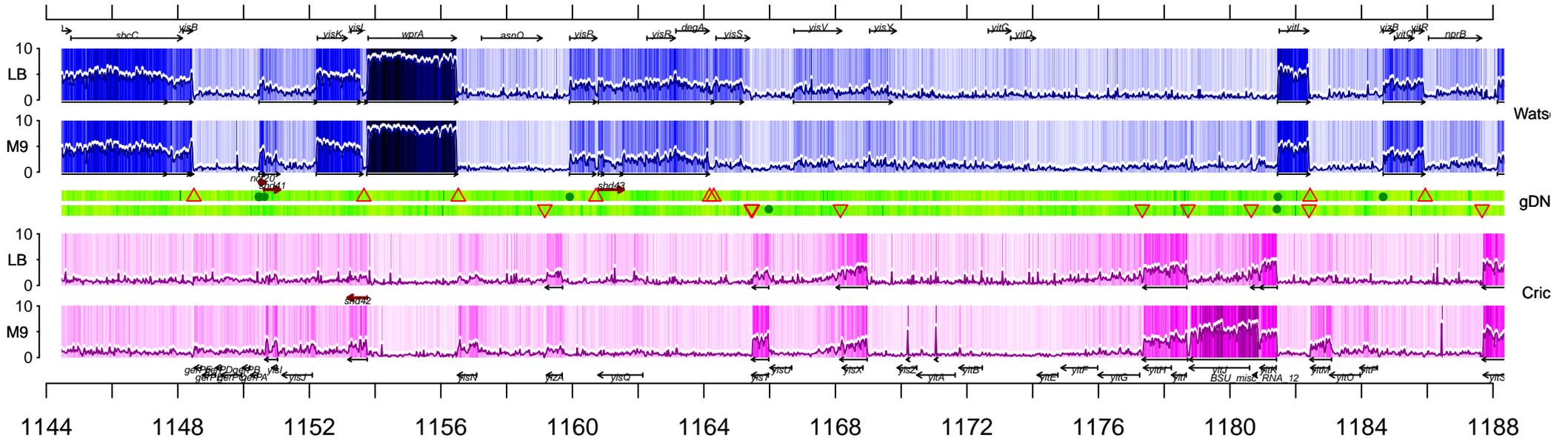
1056 – 1100 Kb



1100 – 1144 Kb

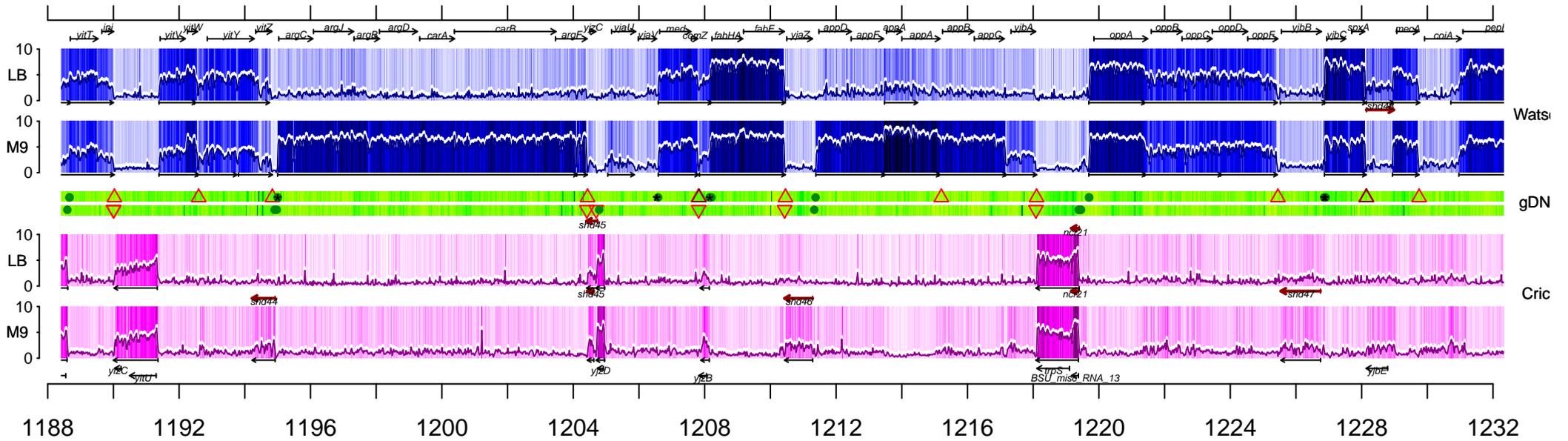


1144 – 1188 Kb



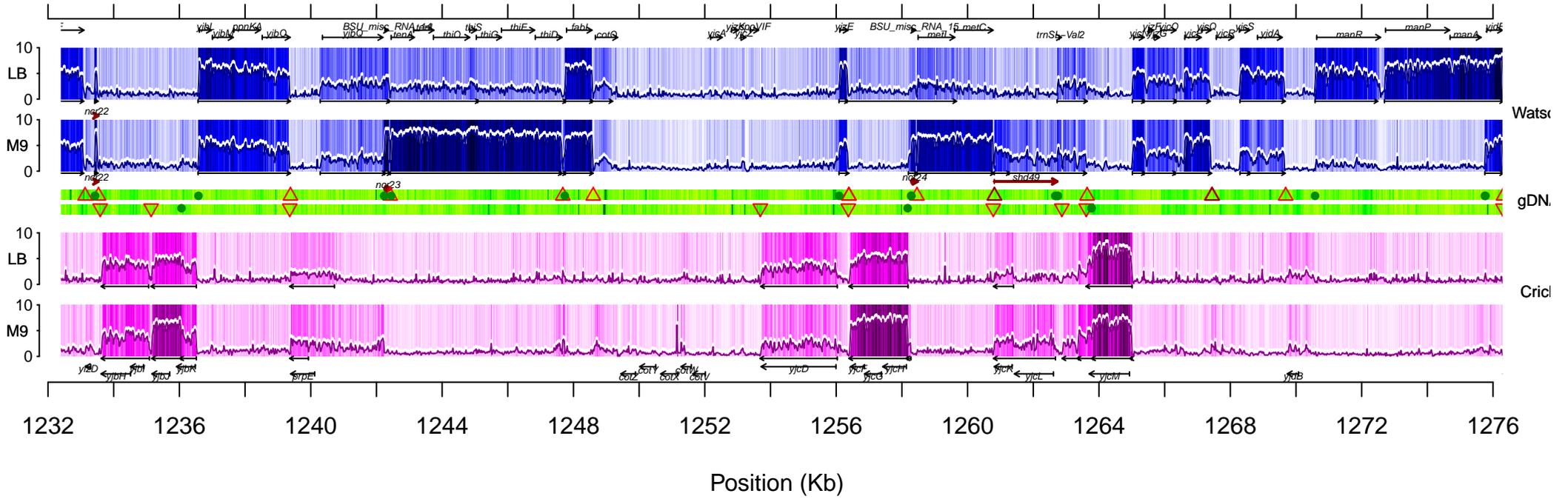
Position (Kb)

1188 – 1232 Kb

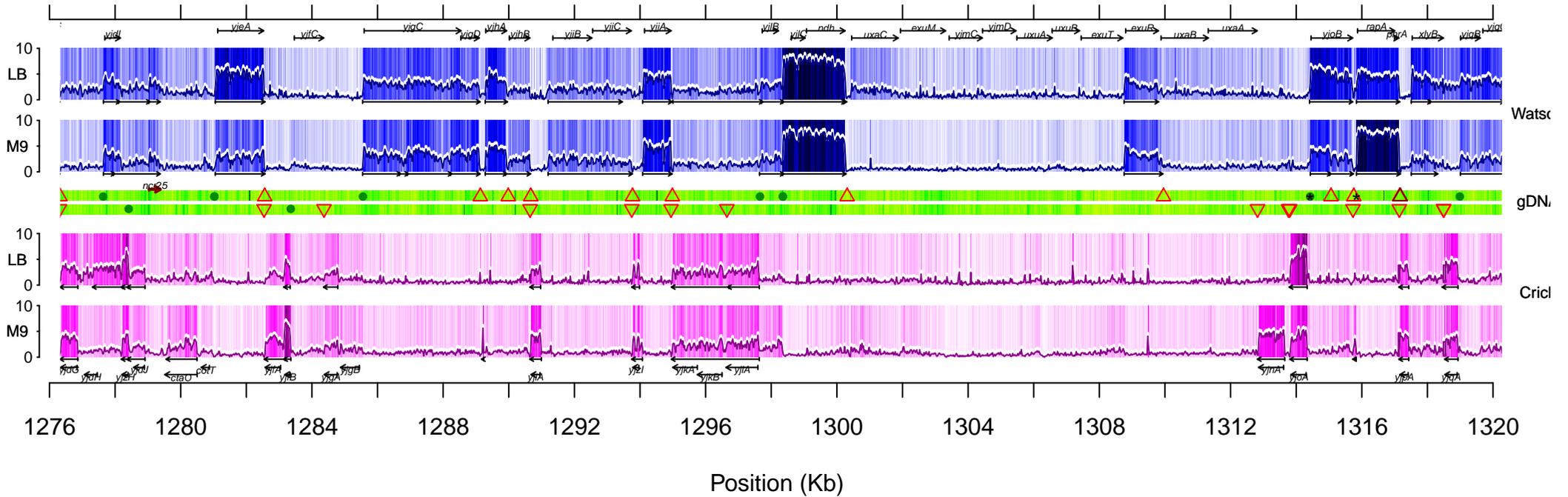


Position (Kb)

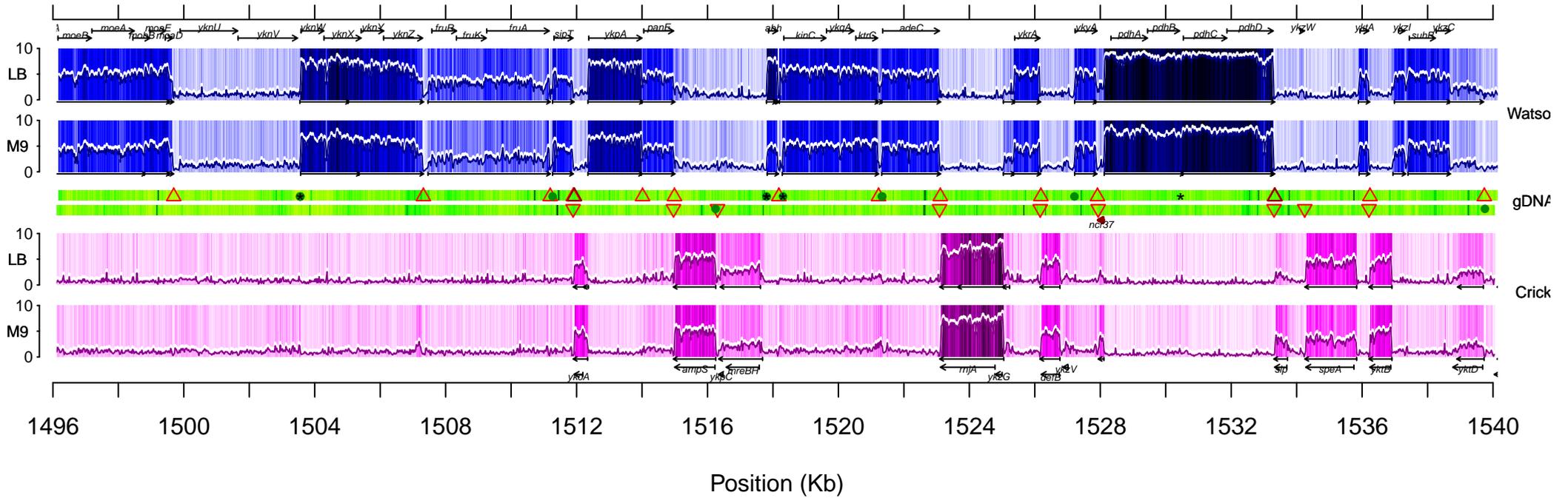
1232 – 1276 Kb



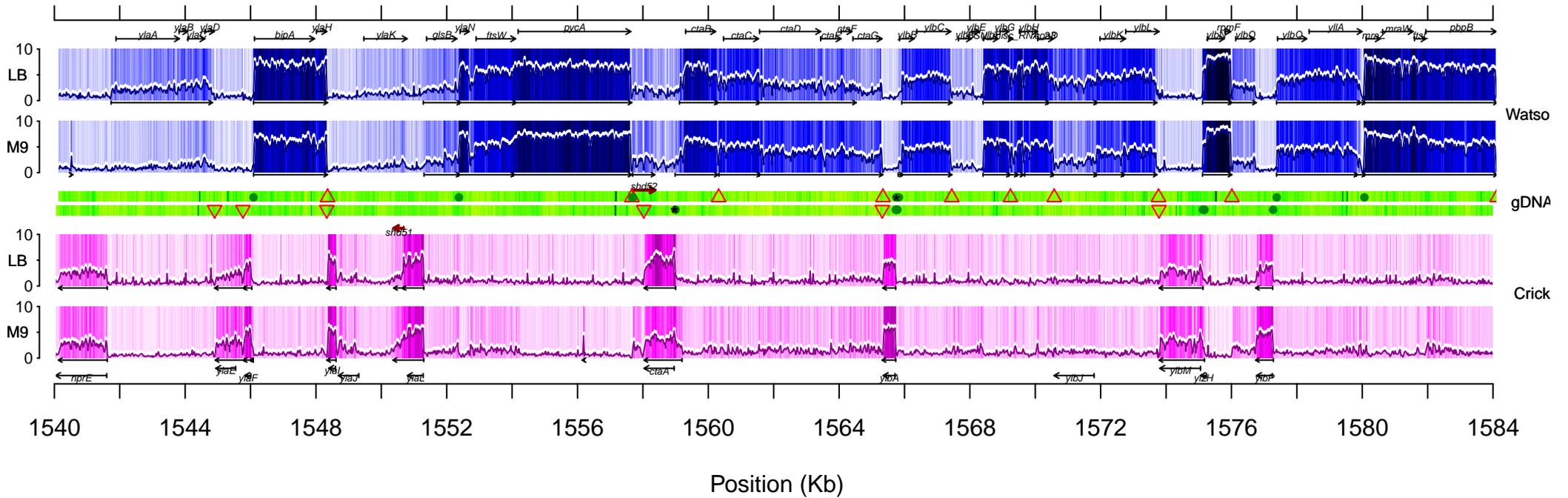
1276 – 1320 Kb



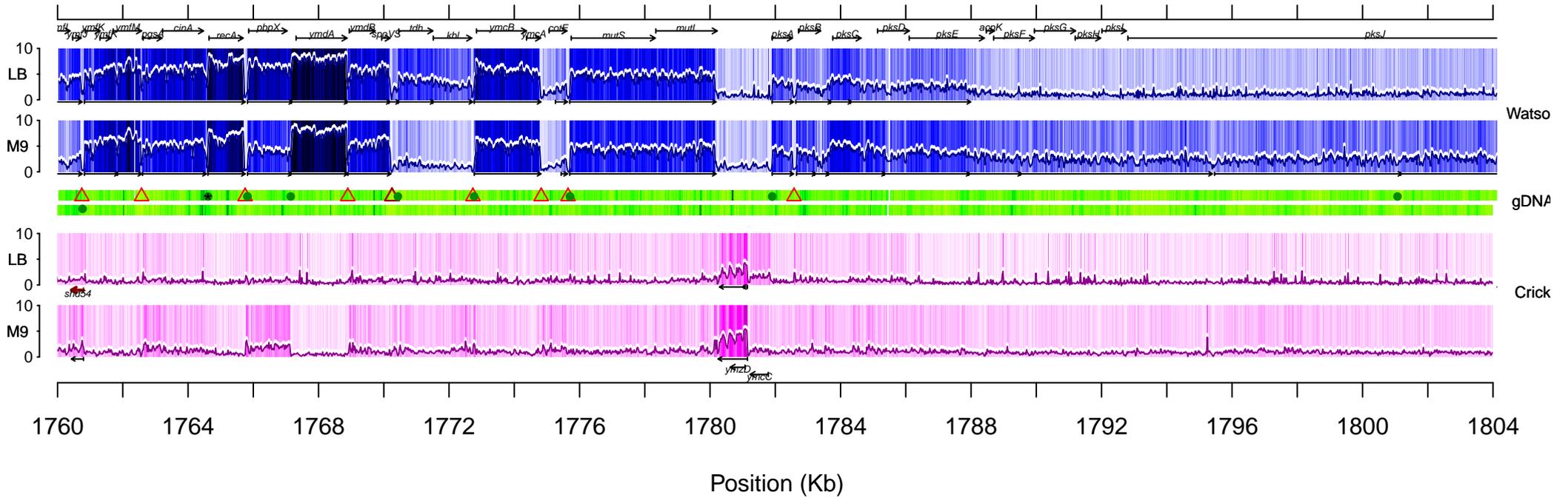
1496 – 1540 Kb



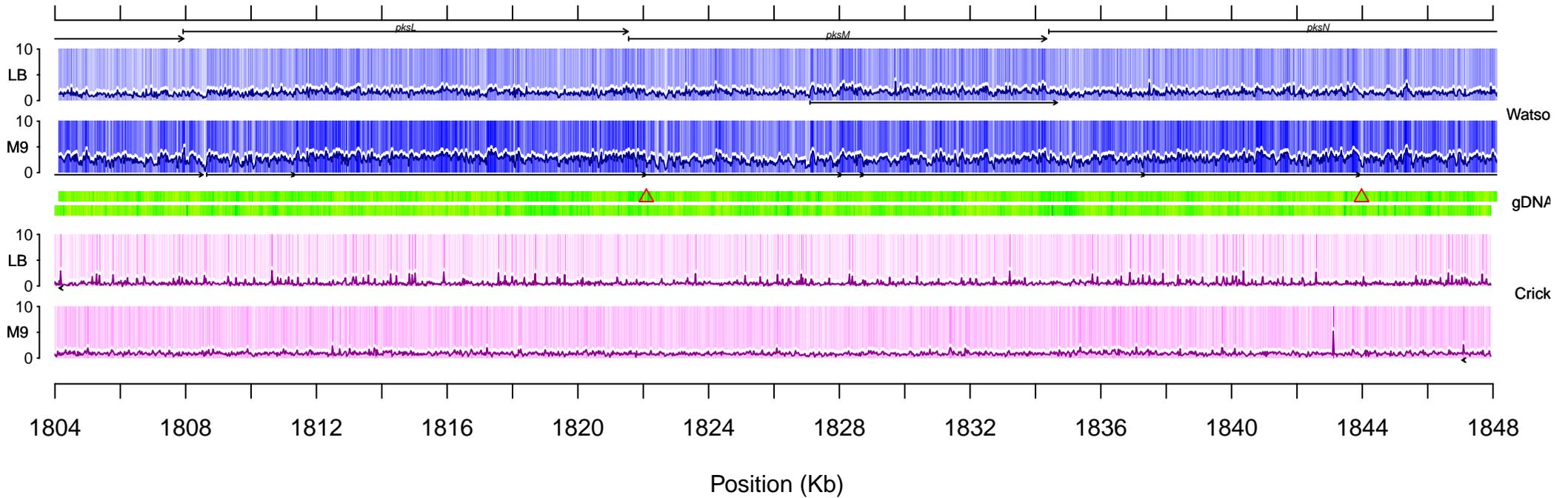
1540 – 1584 Kb



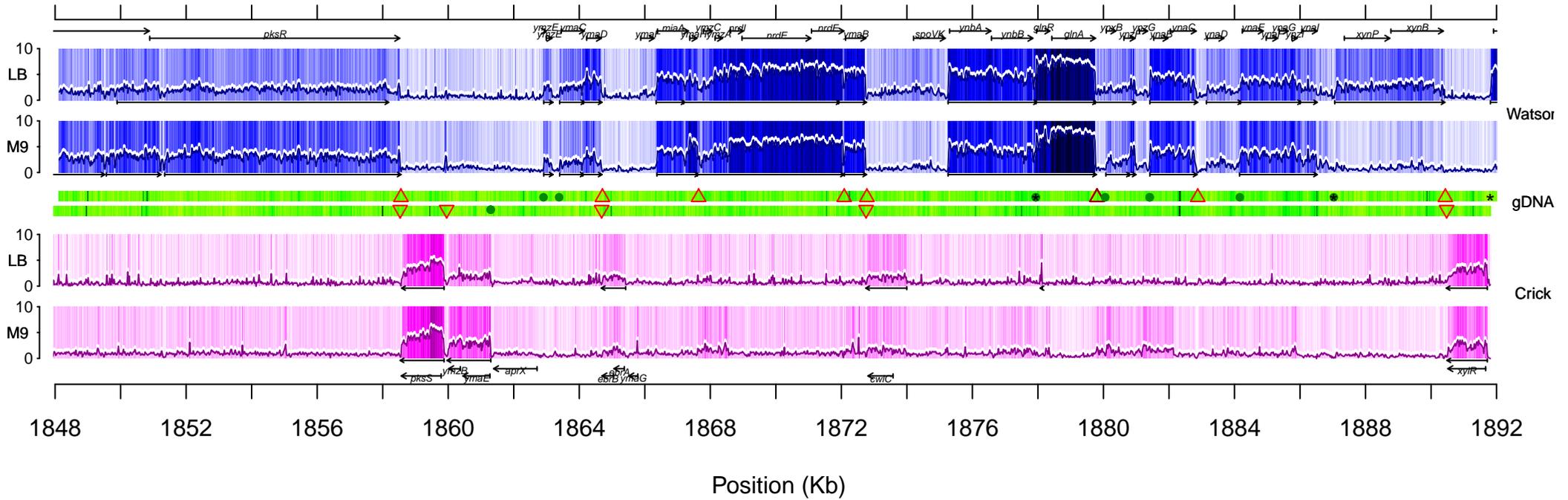
1760 – 1804 Kb



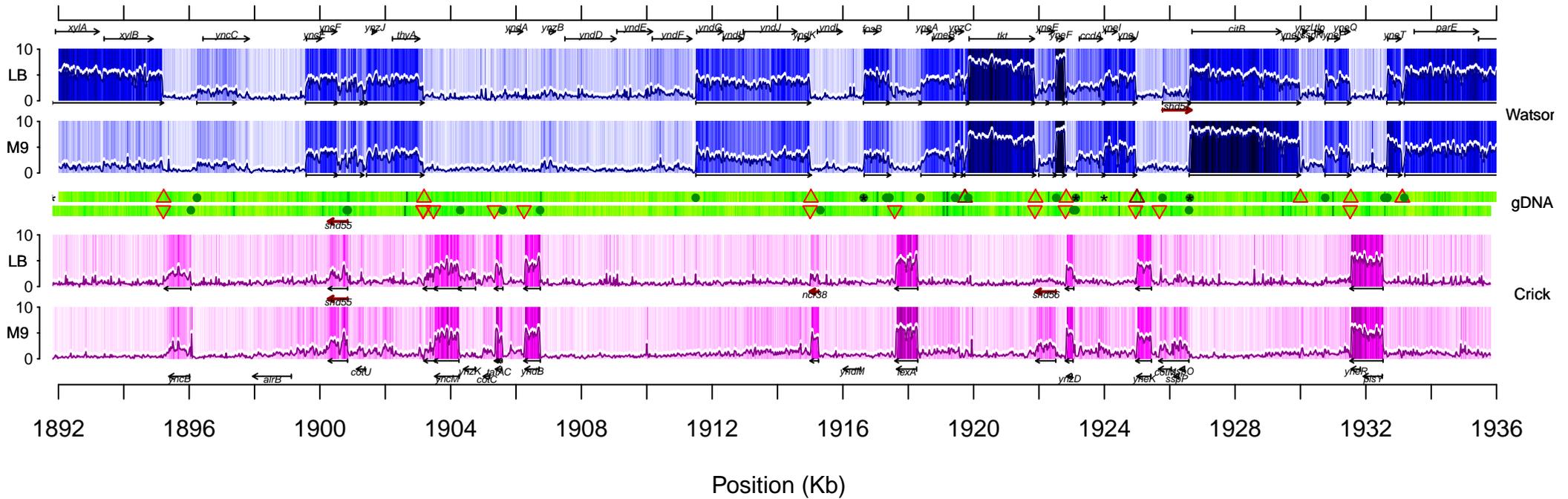
1804 – 1848 Kb



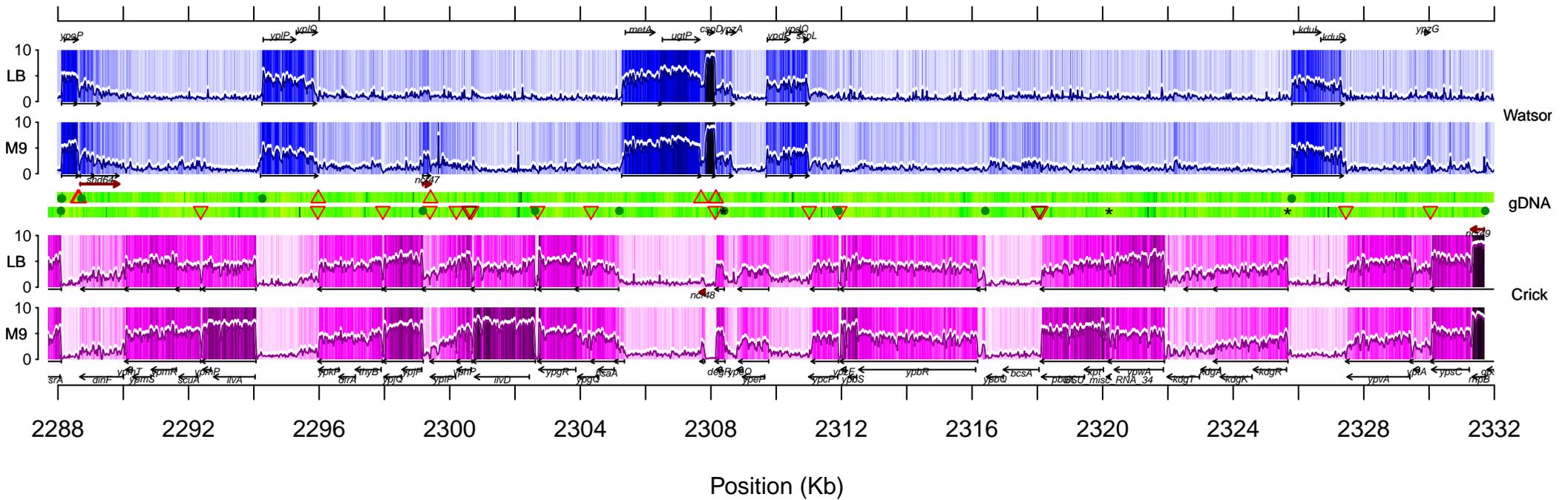
1848 – 1892 Kb



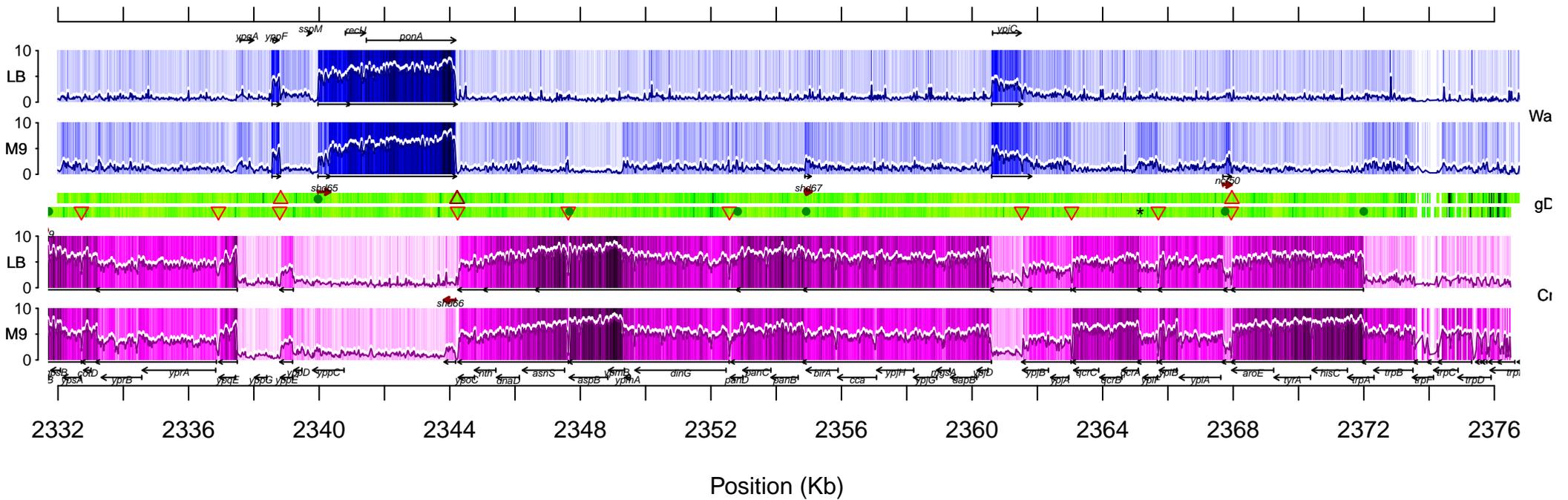
1892 – 1936 Kb



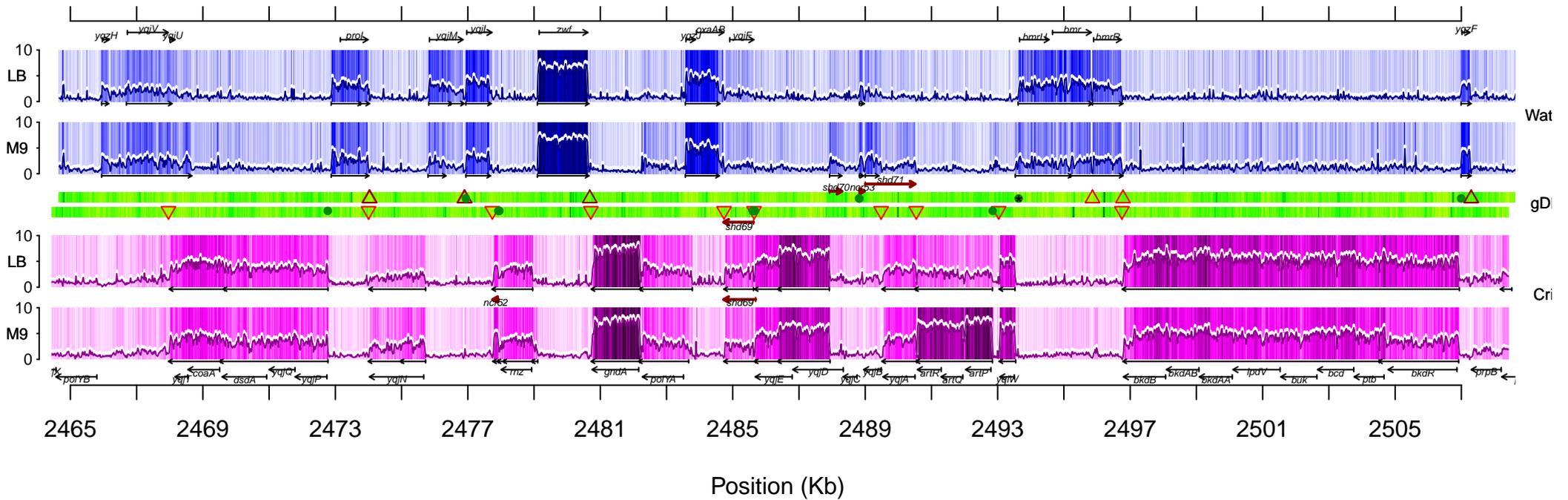
2288 – 2332 Kb



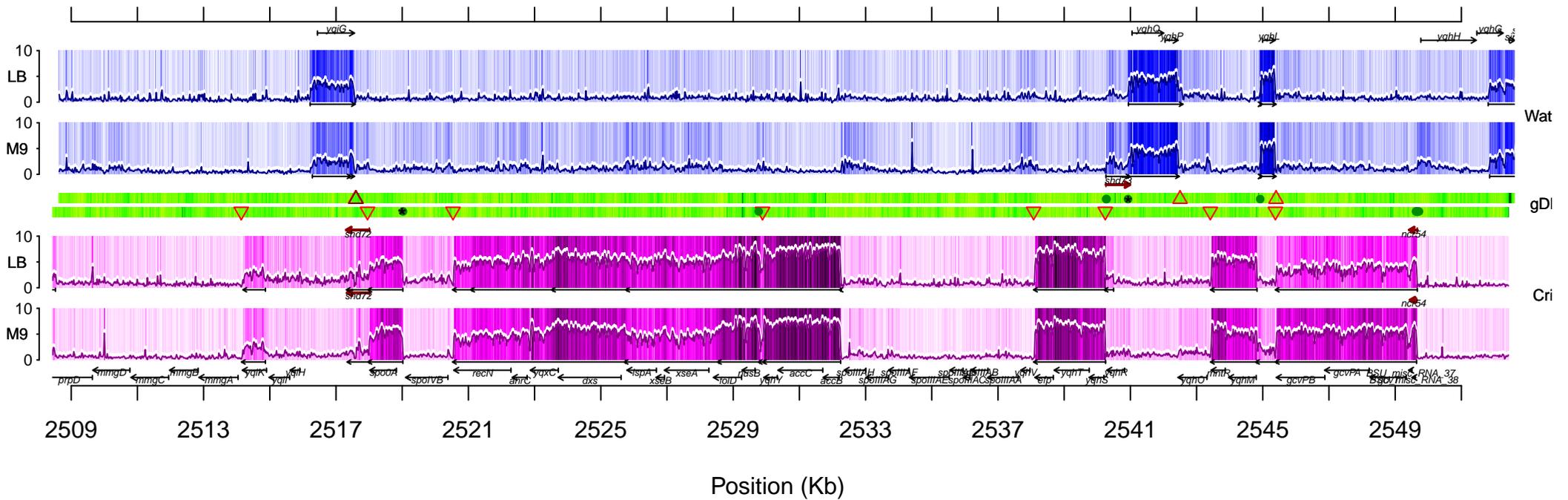
2332 – 2376 Kb



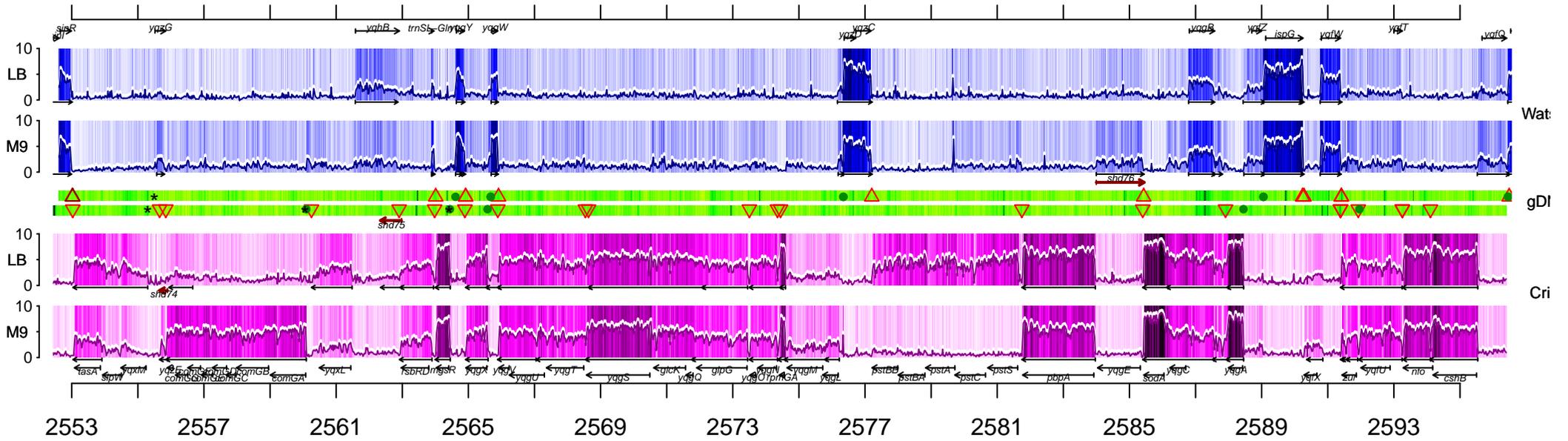
2465 – 2508 Kb



2509 – 2552 Kb

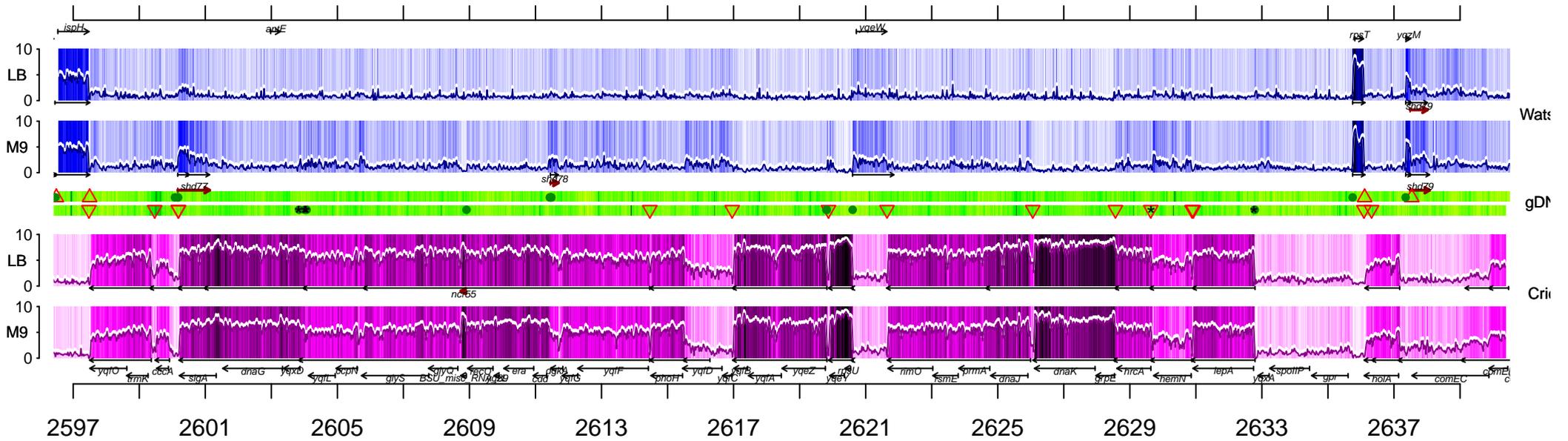


2553 – 2596 Kb



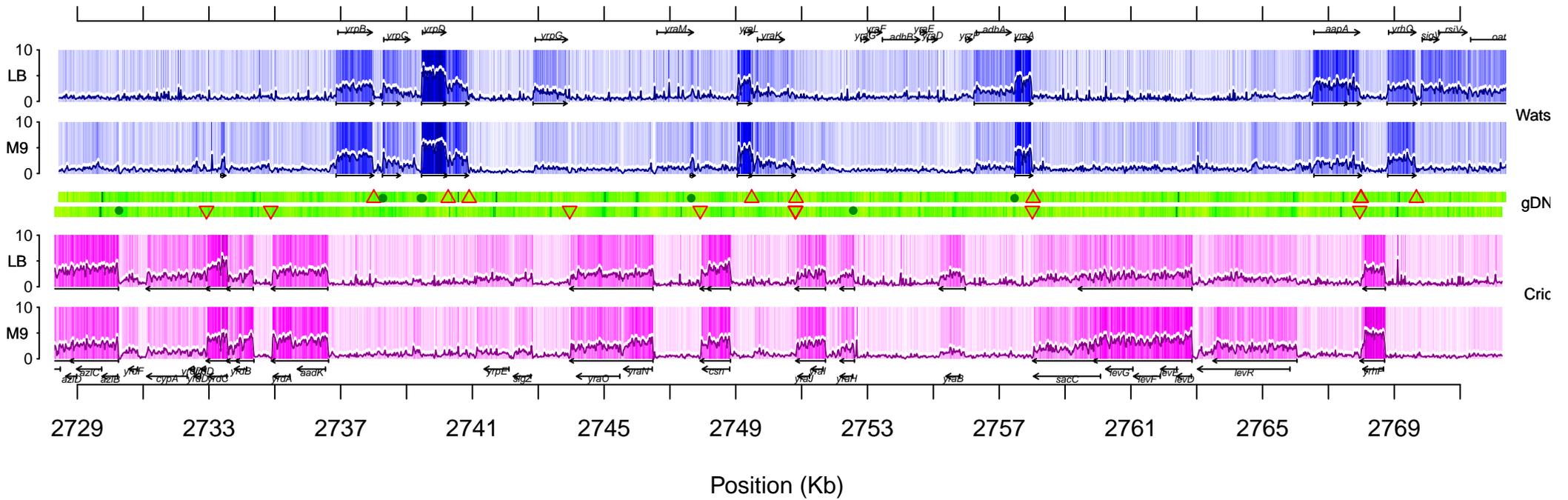
Position (Kb)

2597 – 2640 Kb

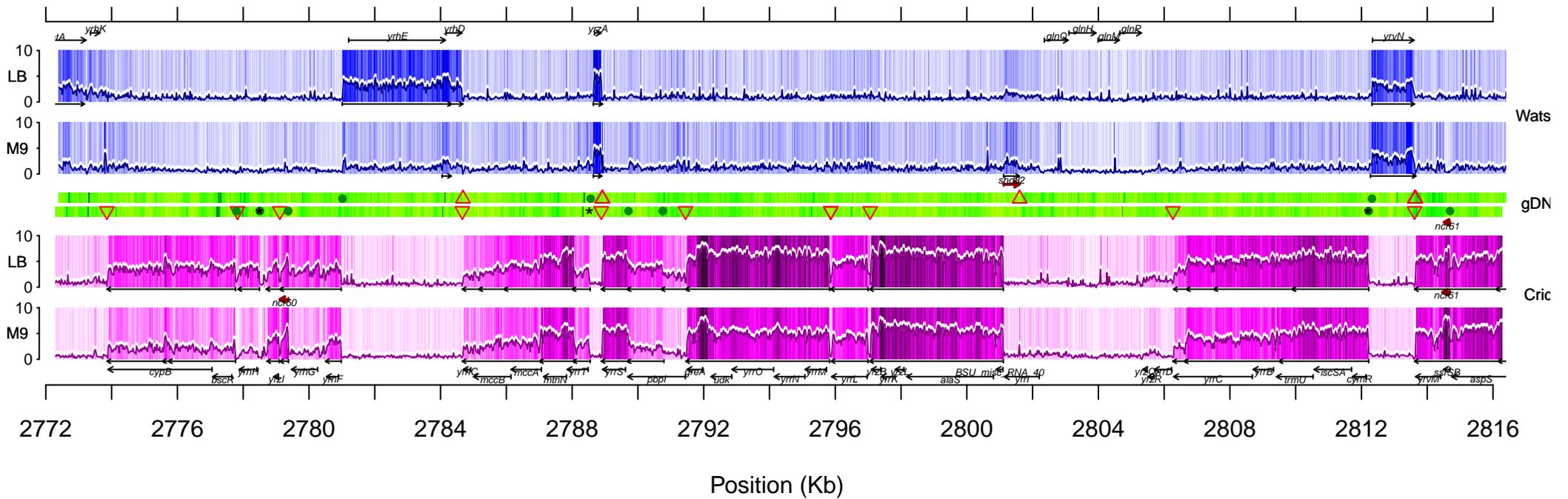


Position (Kb)

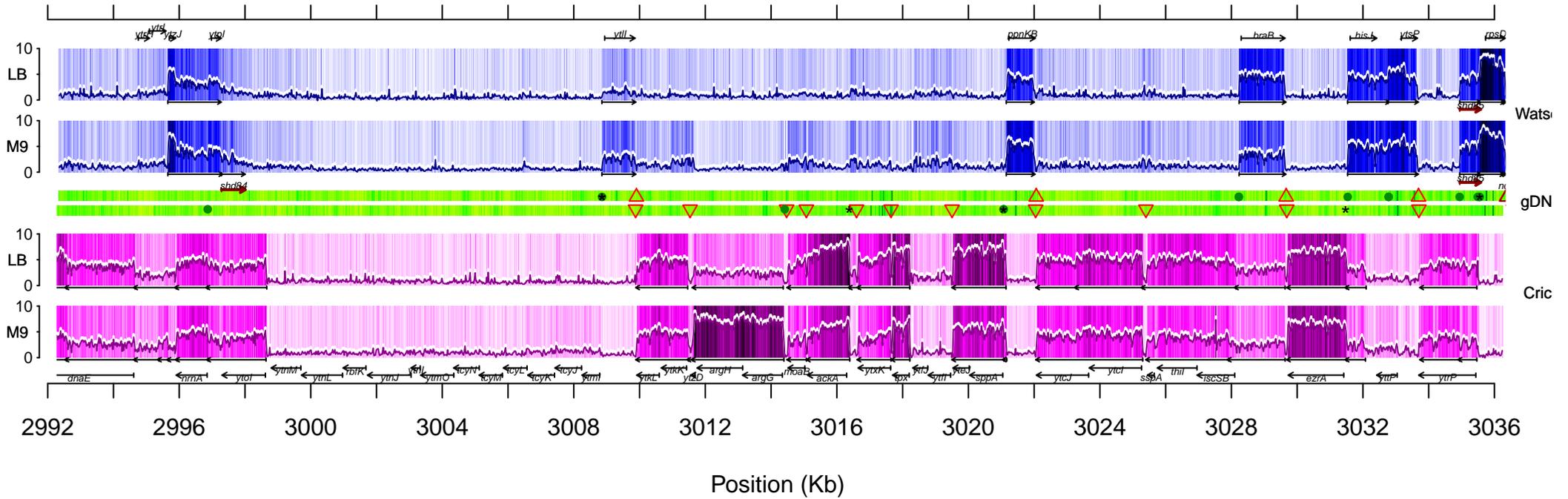
2729 – 2772 Kb



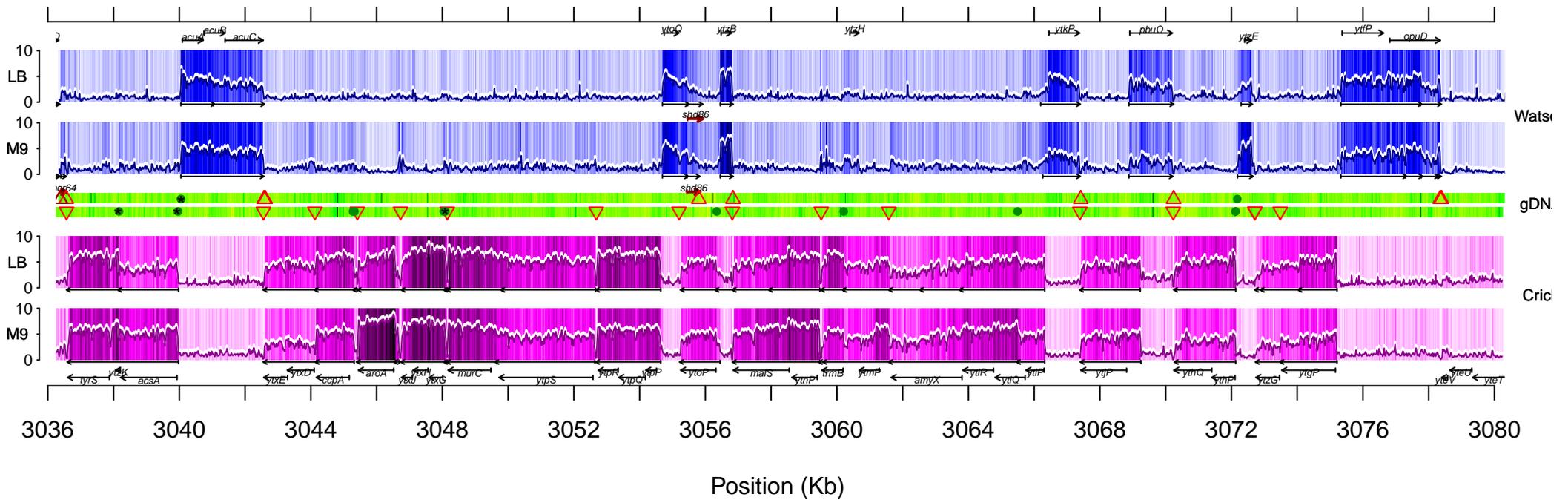
2772 – 2816 Kb



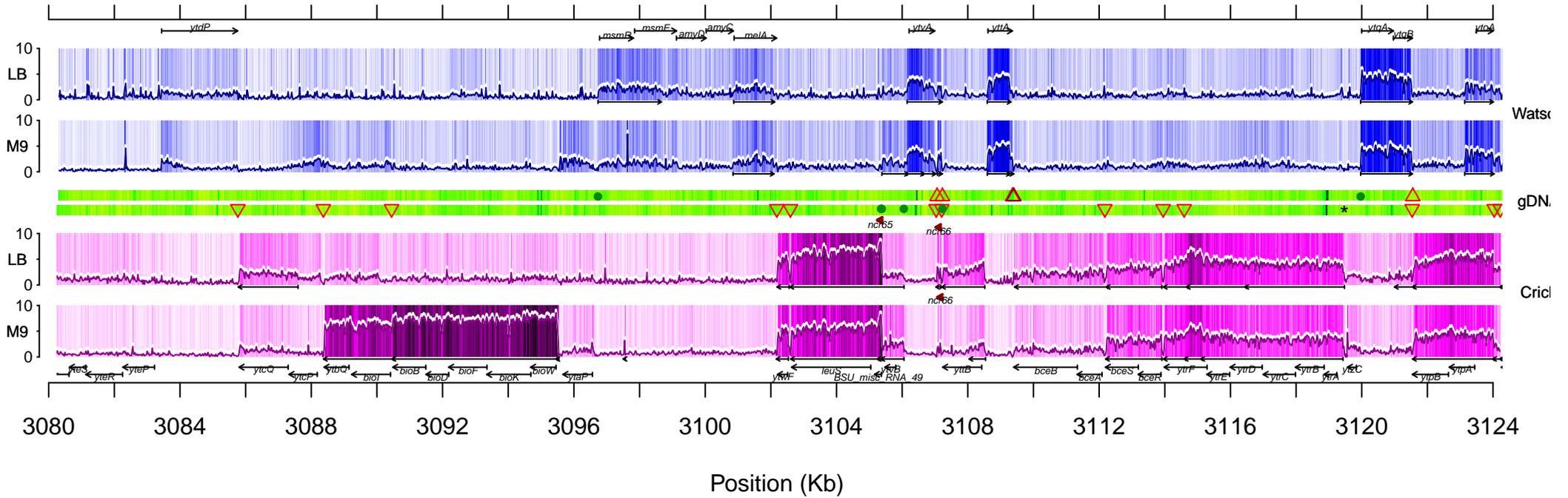
2992 – 3036 Kb



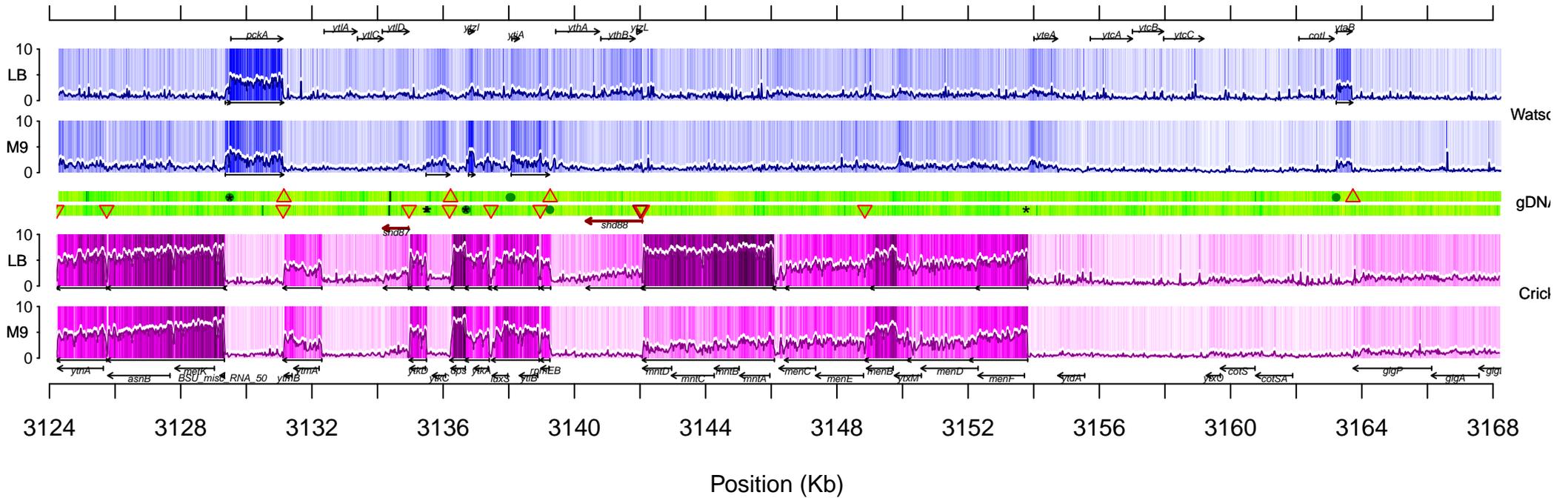
3036 – 3080 Kb



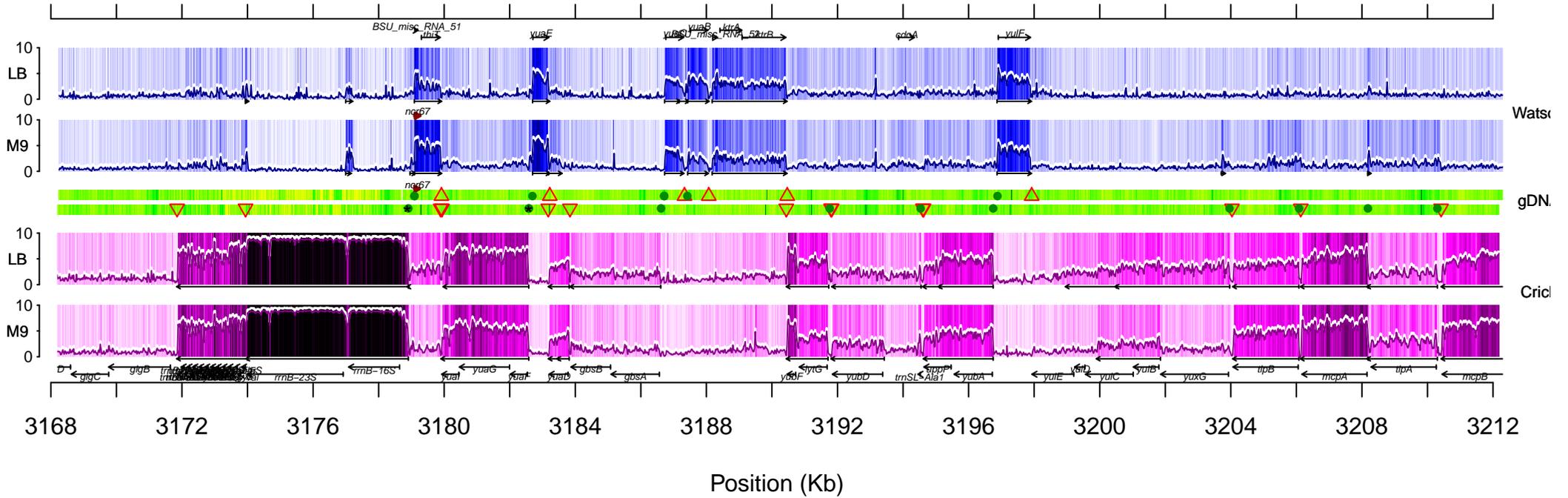
3080 – 3124 Kb



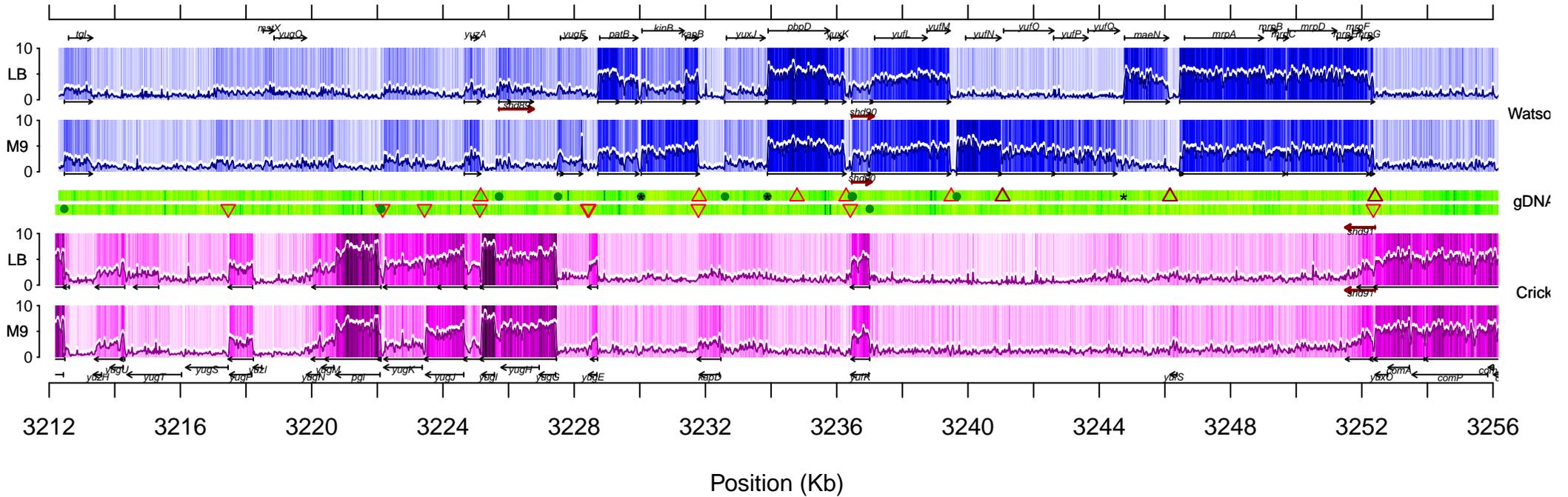
3124 – 3168 Kb



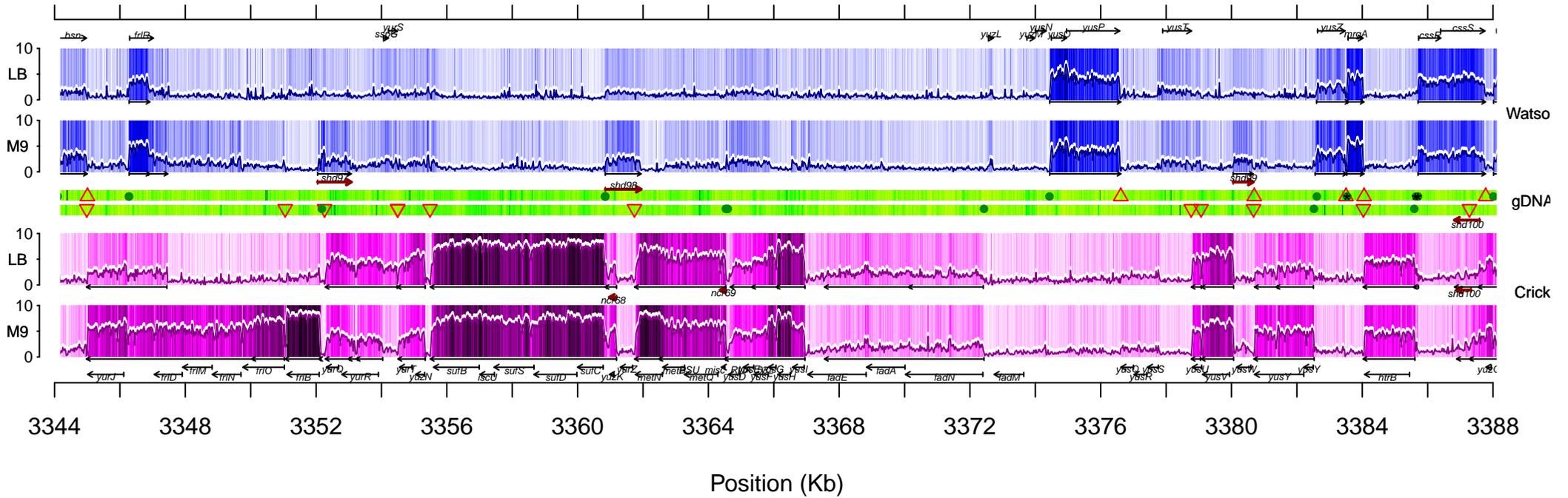
3168 – 3212 Kb



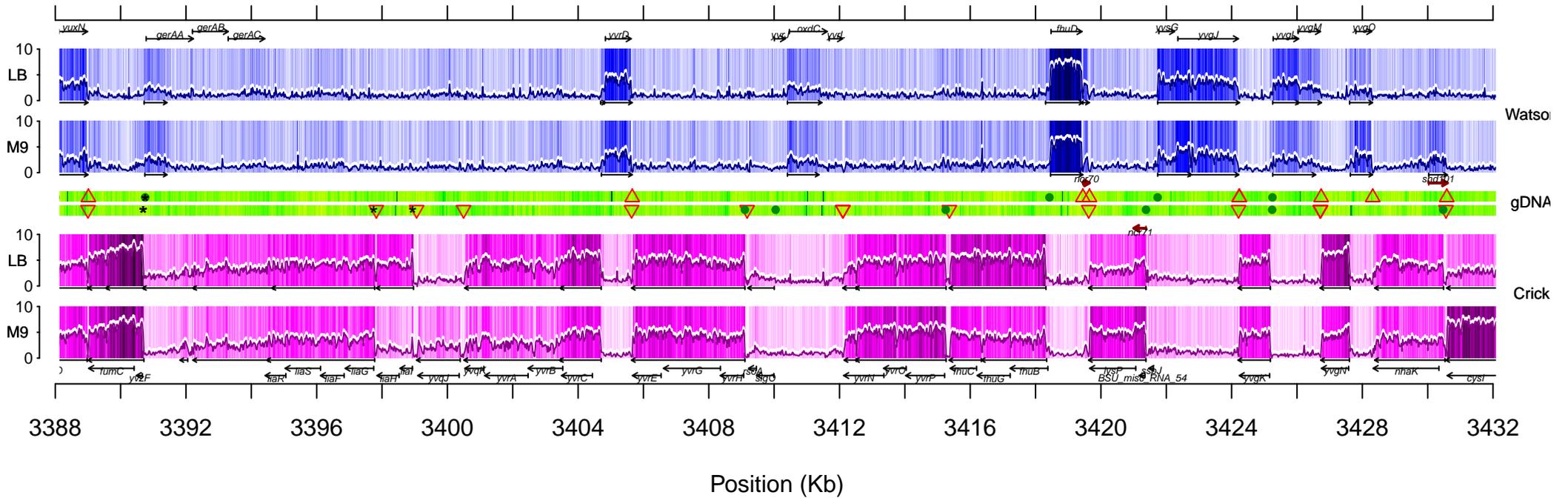
3212 – 3256 Kb



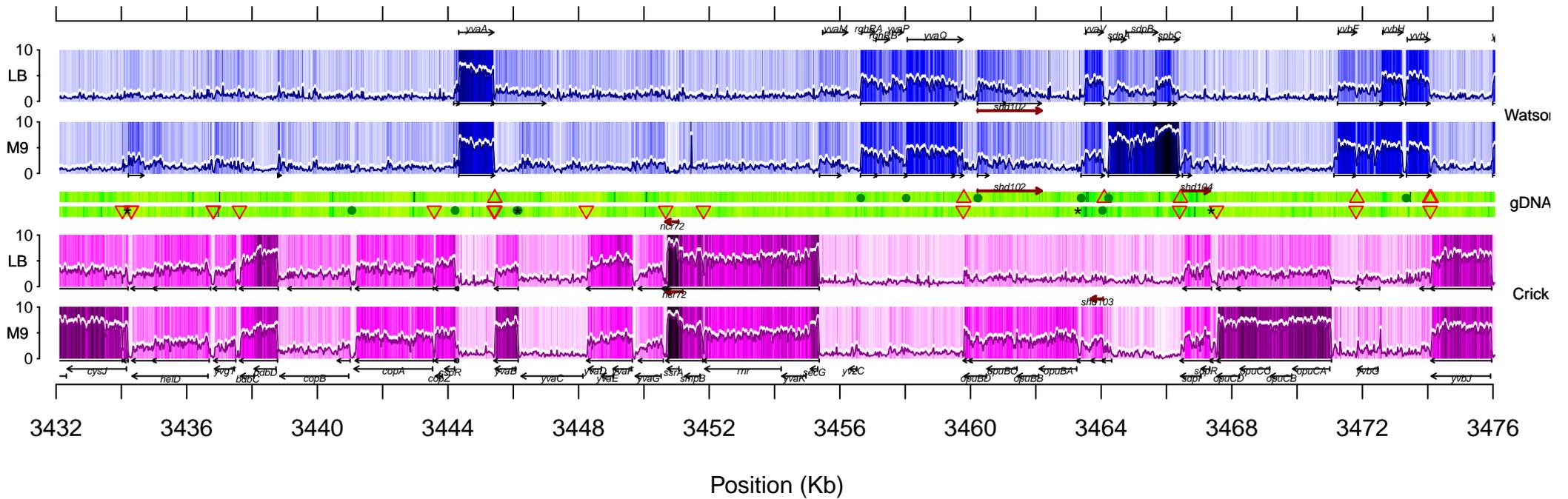
3344 – 3388 Kb



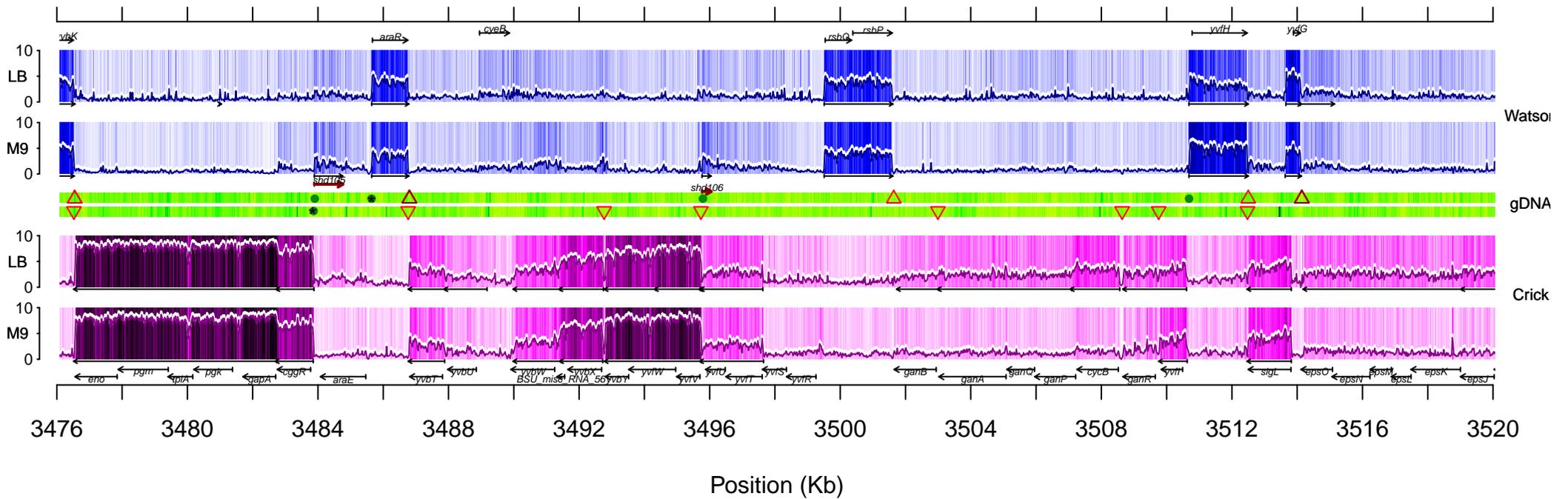
3388 – 3432 Kb



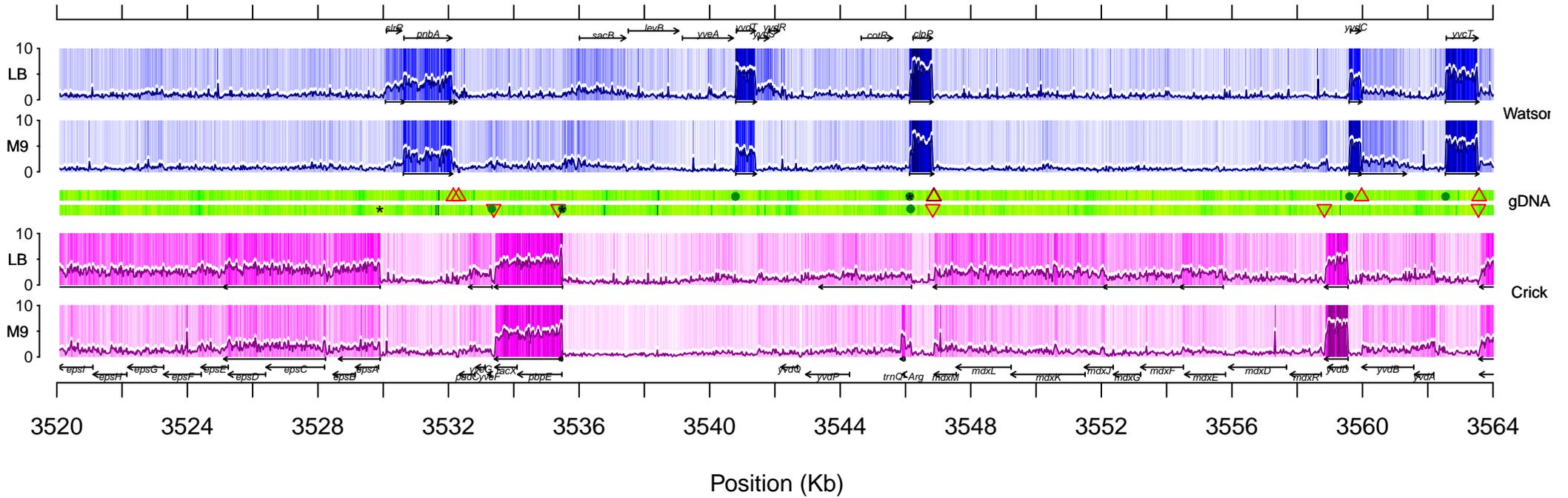
3432 – 3476 Kb



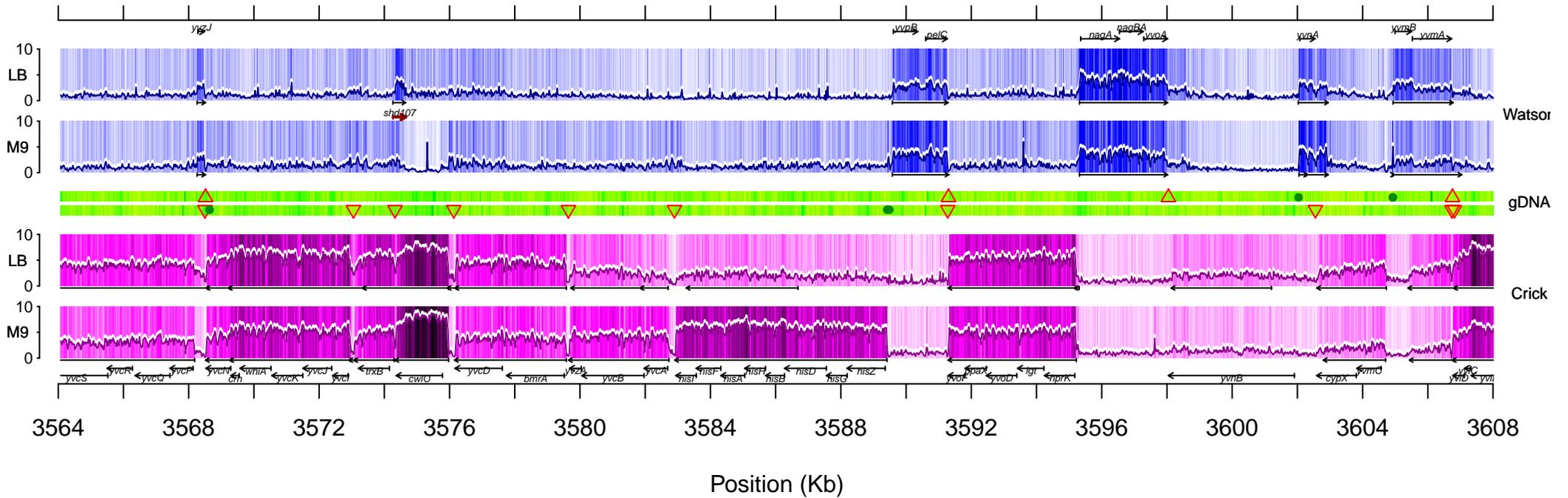
3476 – 3520 Kb



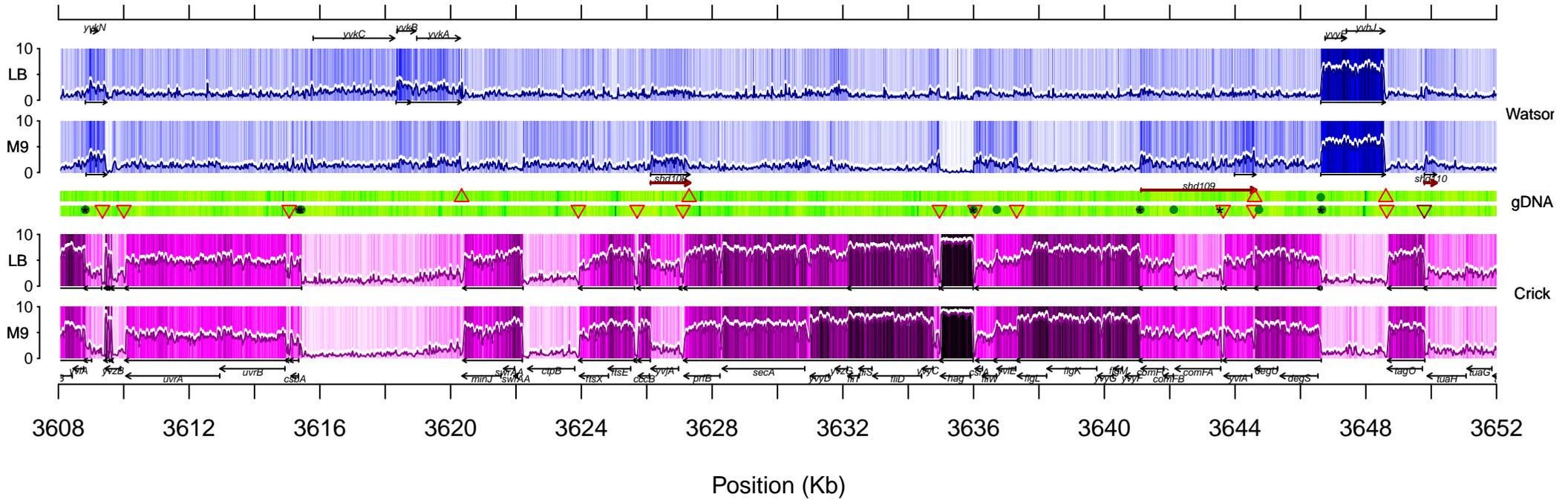
3520 – 3564 Kb



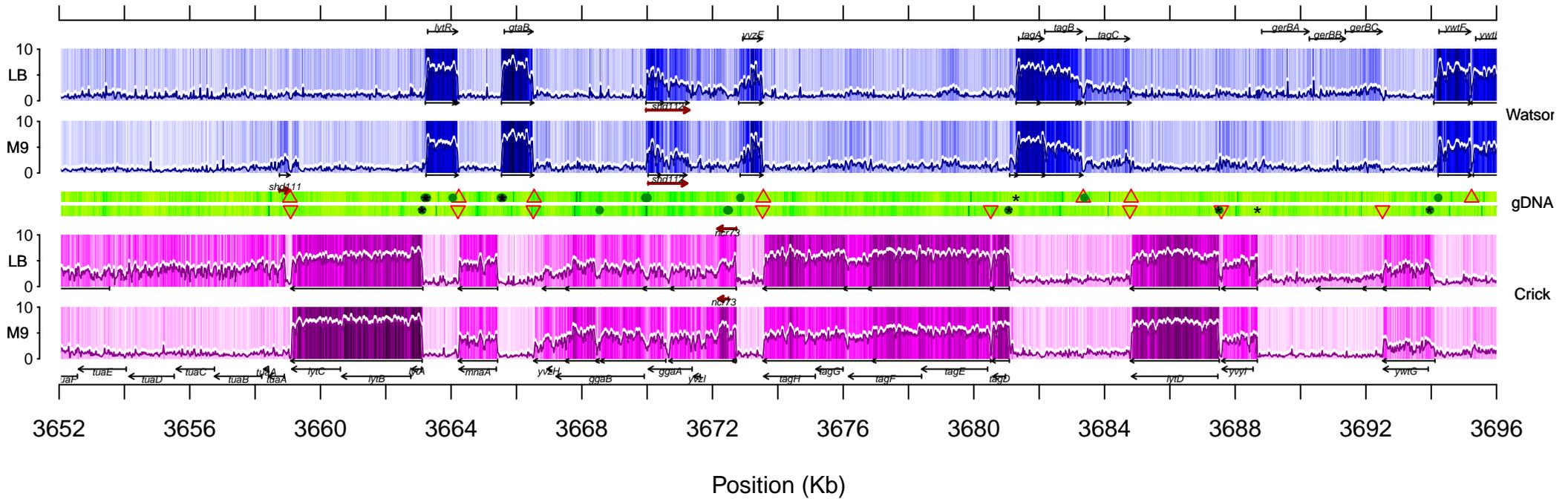
3564 – 3608 Kb



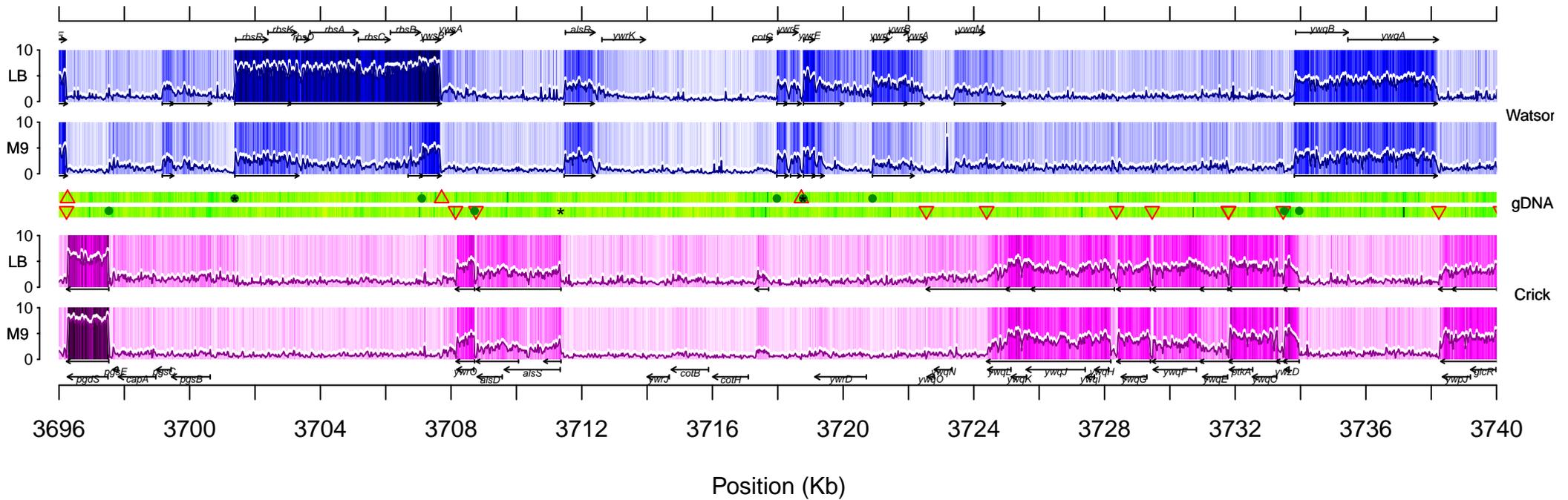
3608 – 3652 Kb



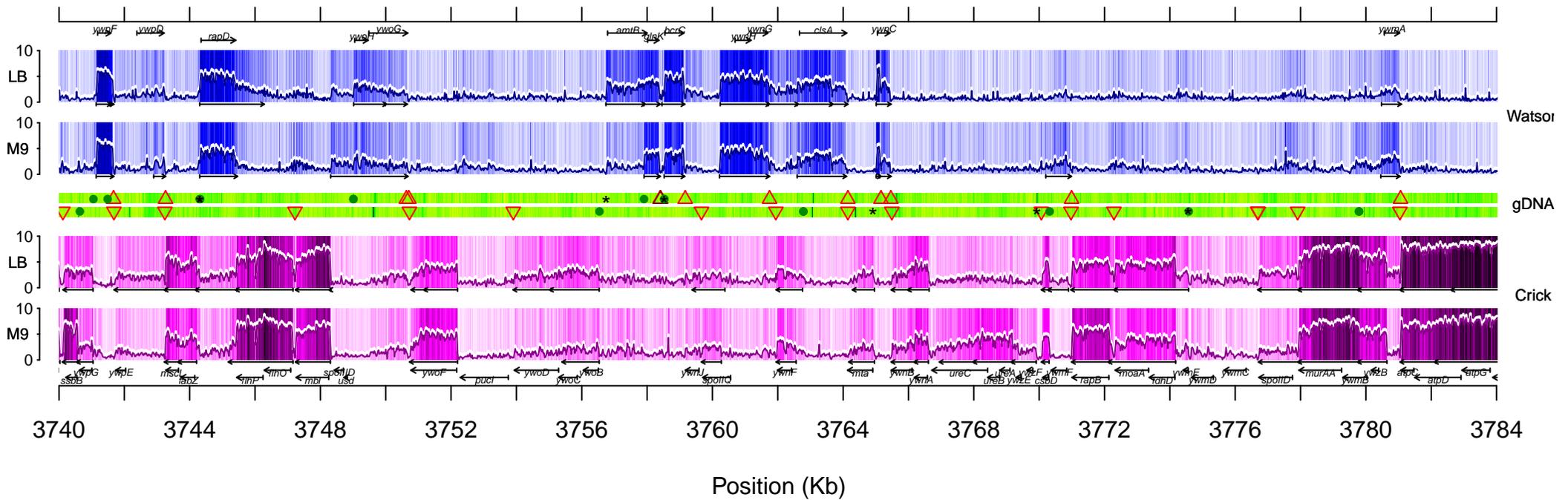
3652 – 3696 Kb



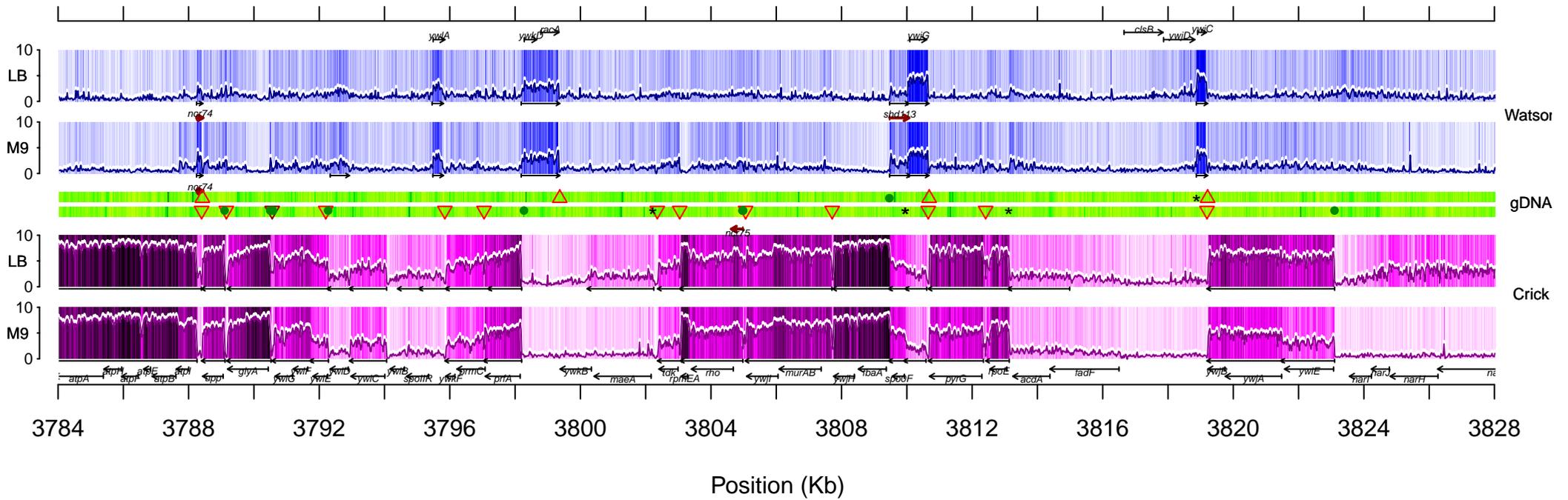
3696 – 3740 Kb



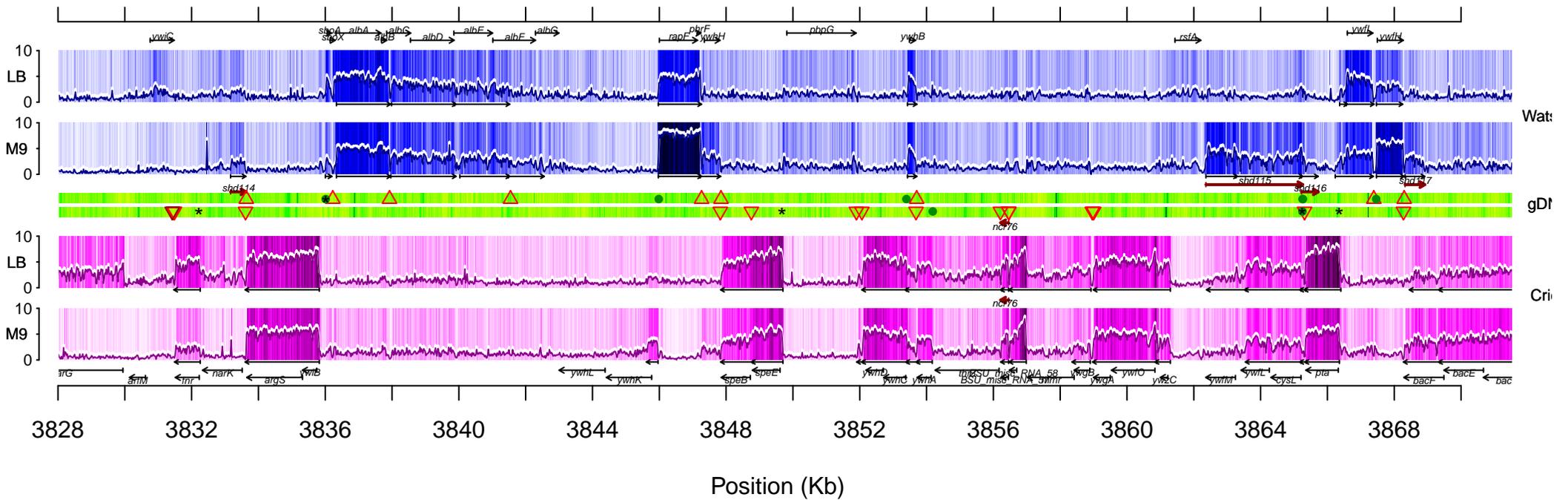
3740 – 3784 Kb



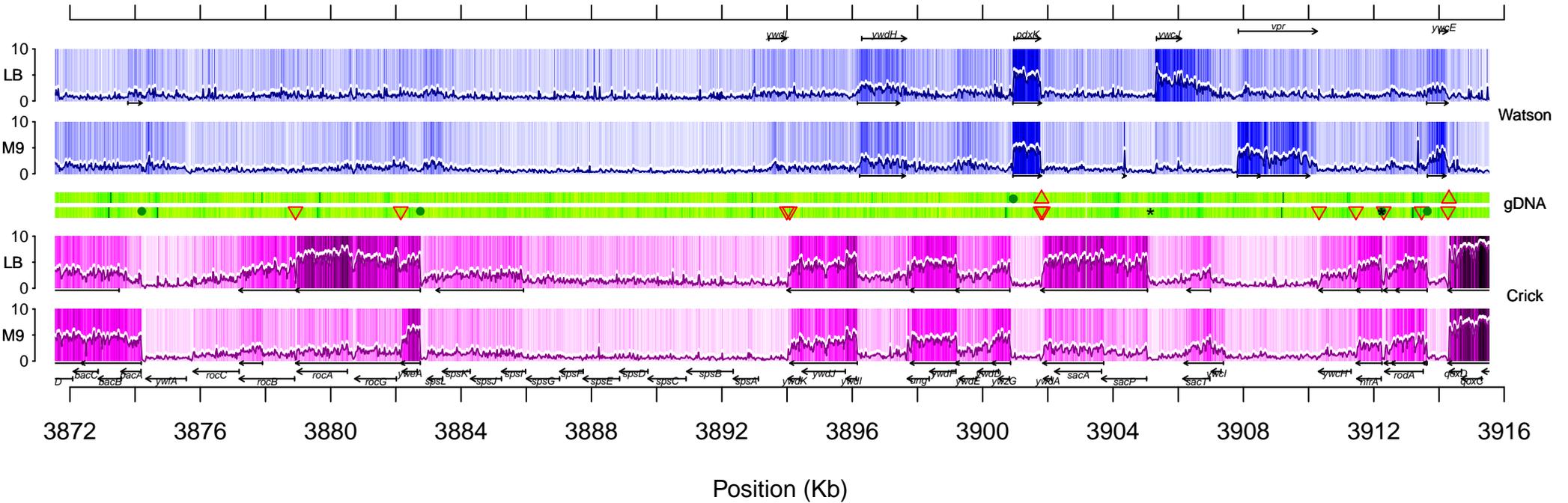
3784 – 3828 Kb



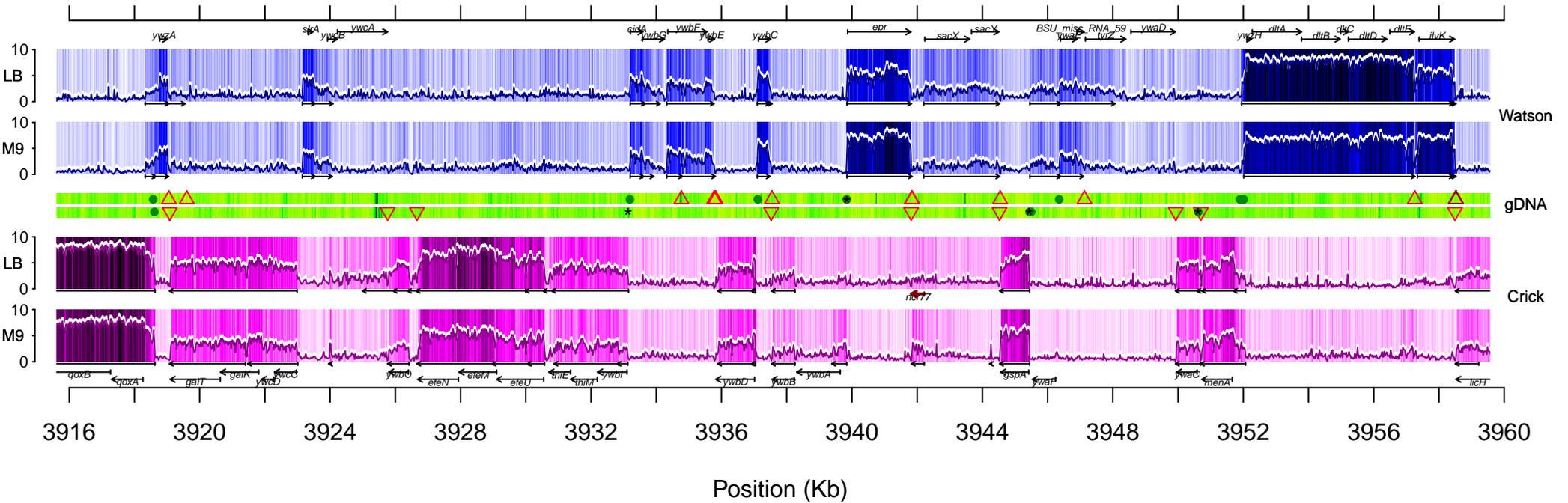
3828 – 3871 Kb



3872 – 3916 Kb

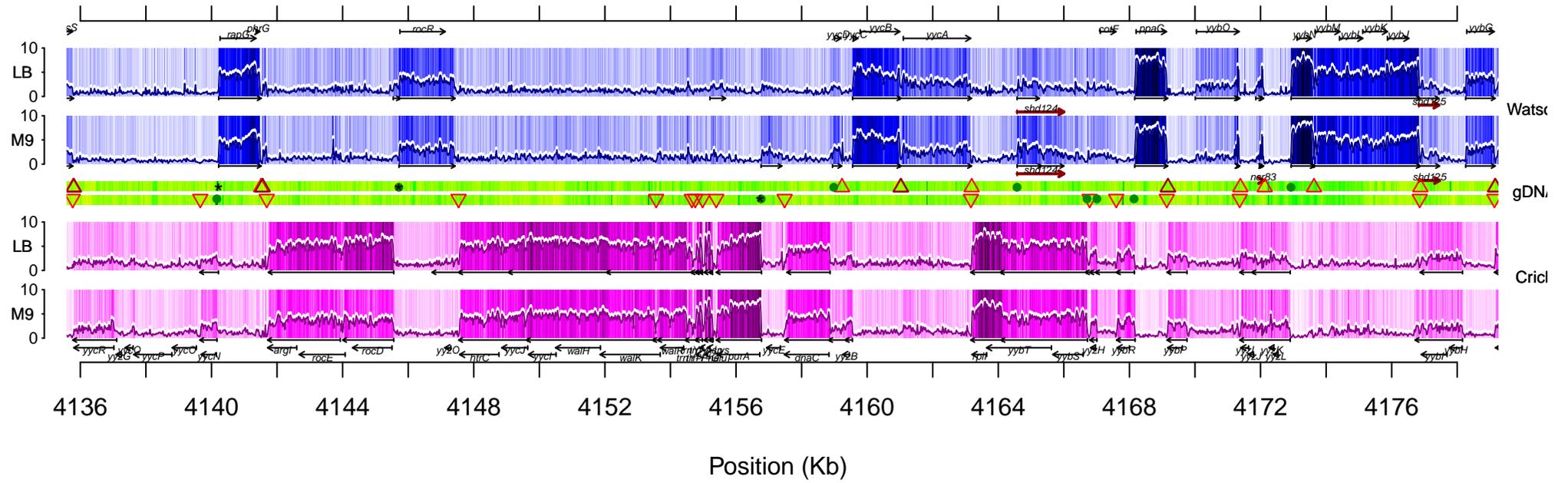


3916 – 3960 Kb



4136 – 4179 Kb

log₂ foldchange



4179 – 4216 Kb

log₂ foldchange

