Fig.S3. The H-NS and Hha binding signals in and around the genes up-regulated in both *hha*/*ydgT* and *hns*/*stpA* mutant cells

Fig.S3A. H-NS binding in“intergenic” region

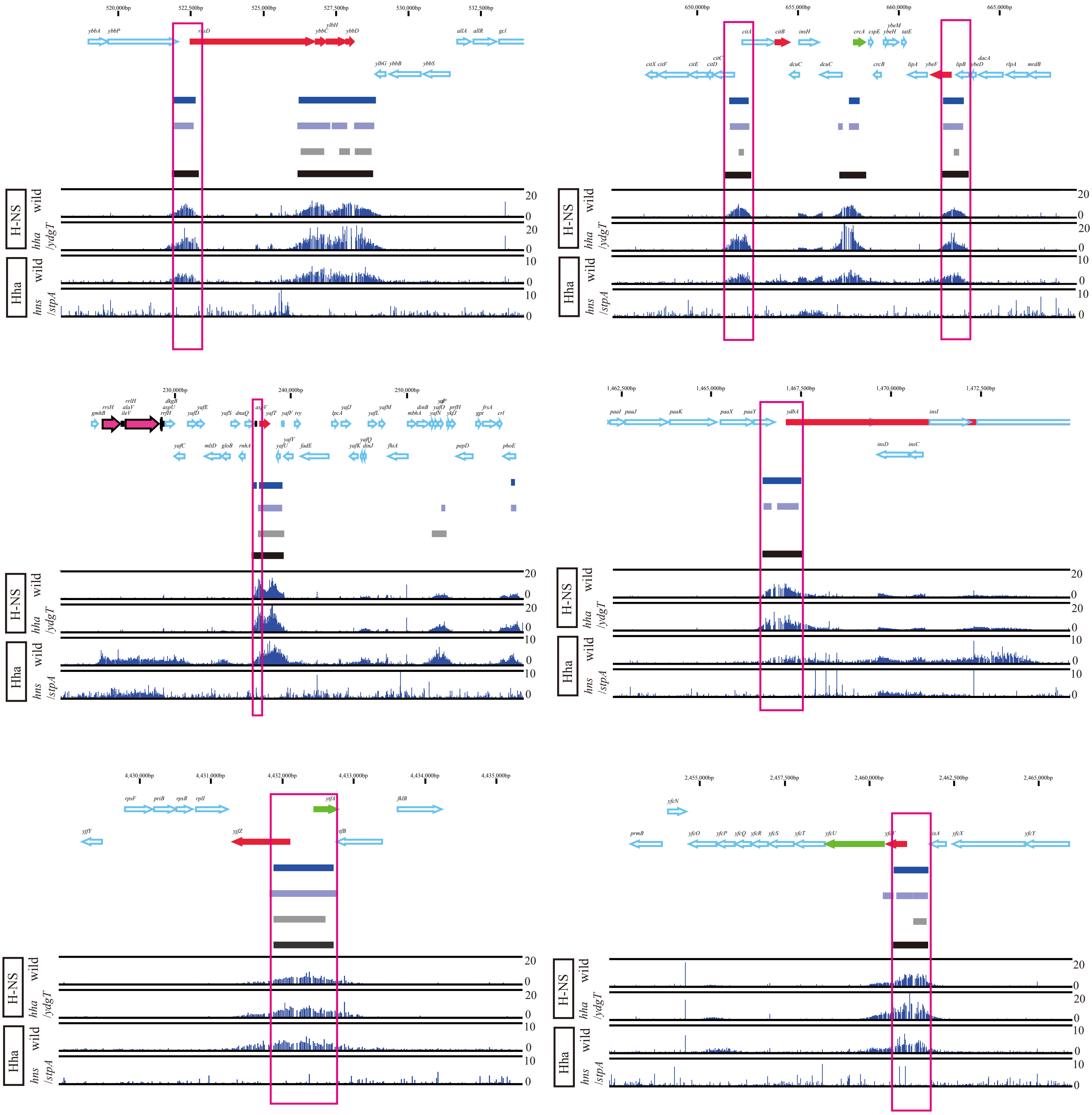

Fig.S3A. continued

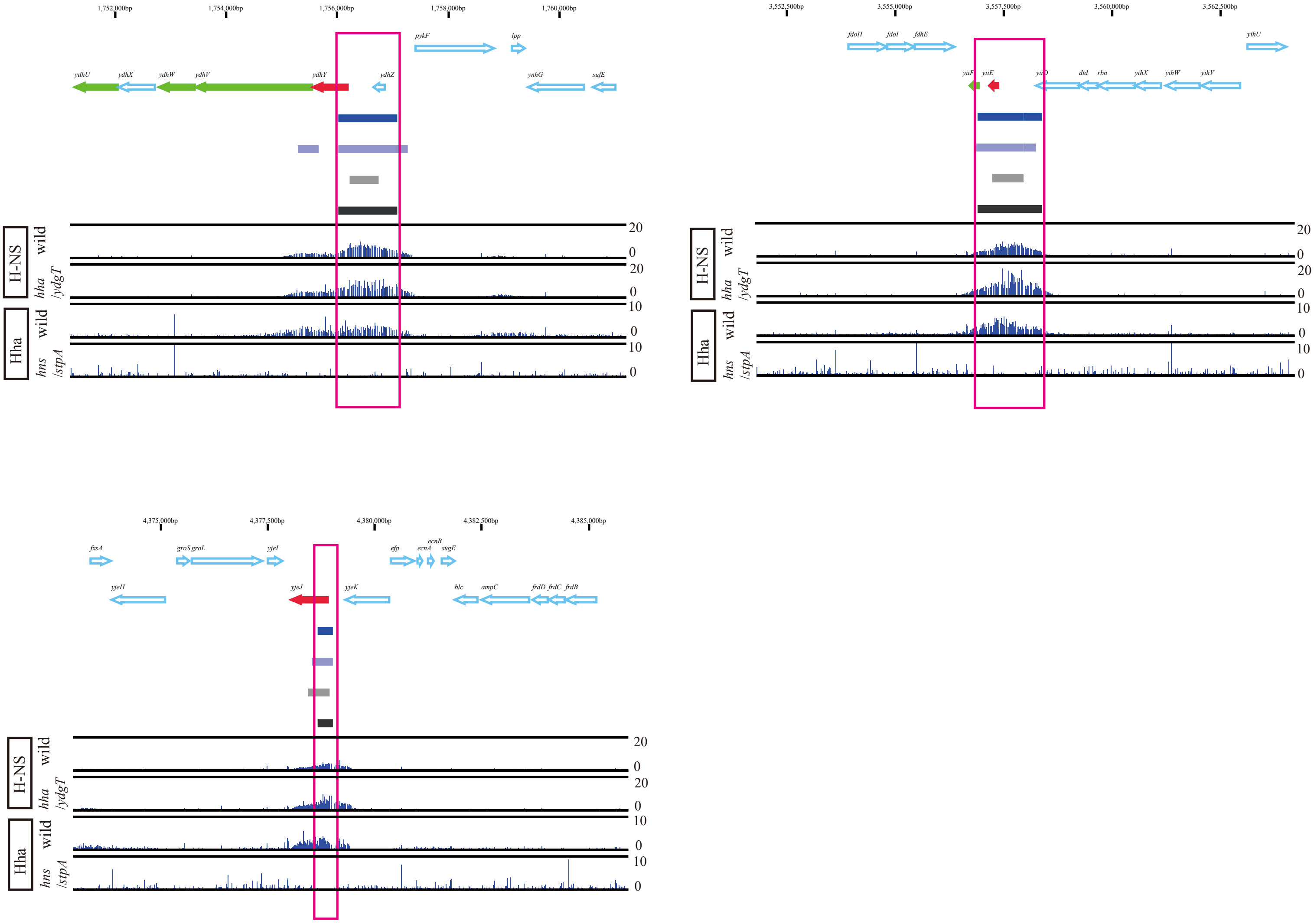

Fig.S3B. H-NS binding on single “coding” sequence

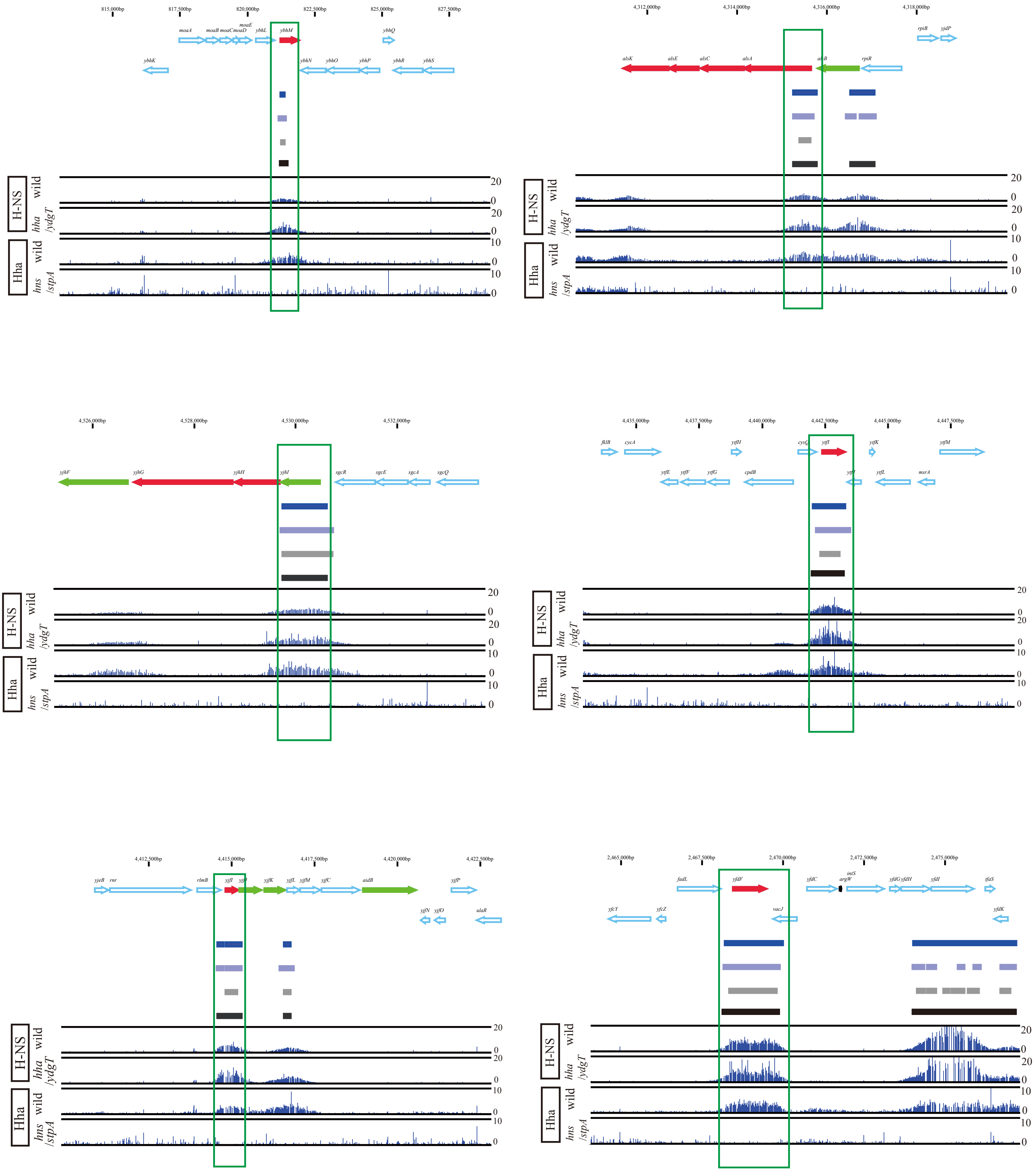

Fig.S3C. H-NS binding on multiple “coding” sequences

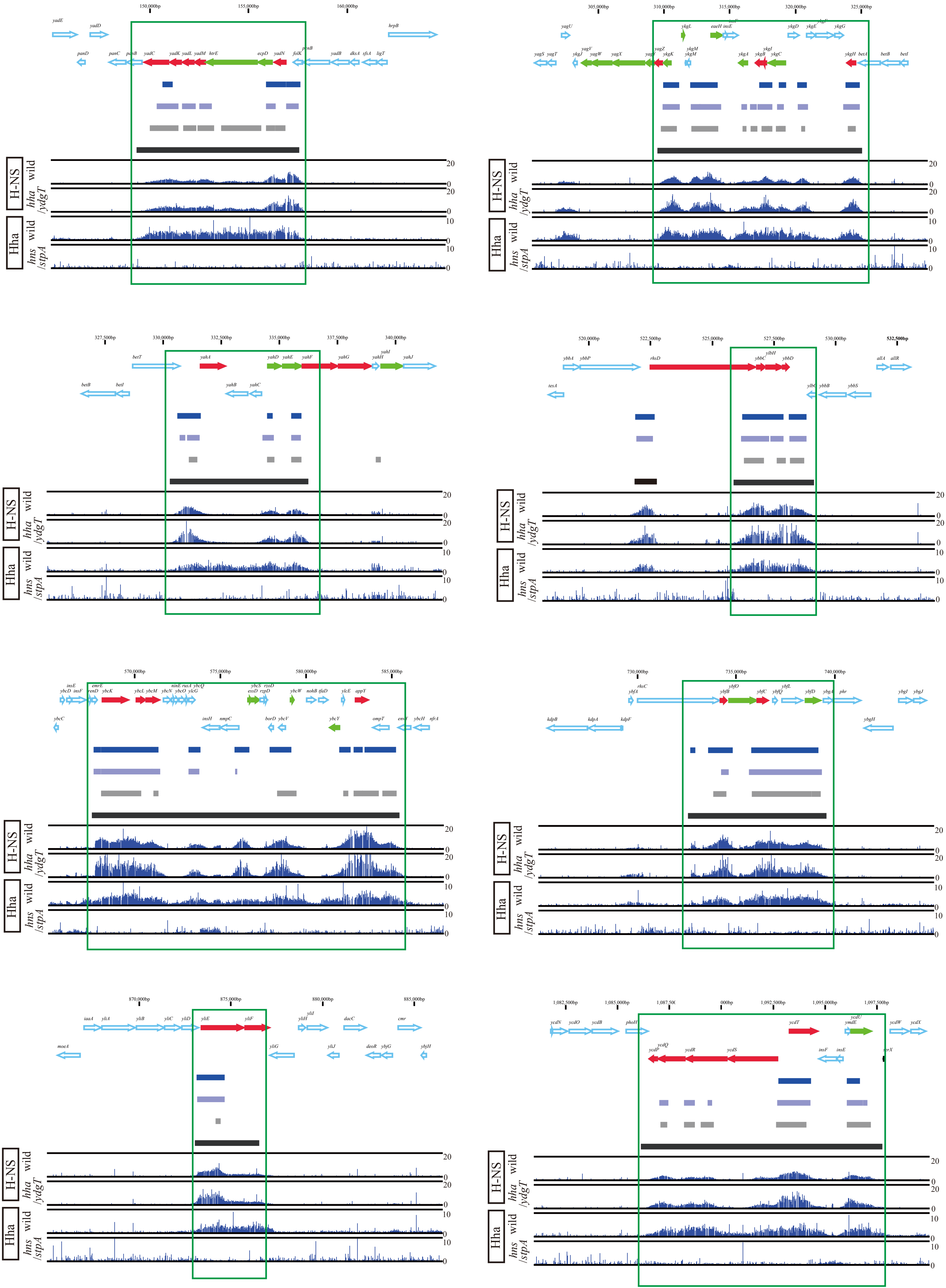

Fig.S3C. continued

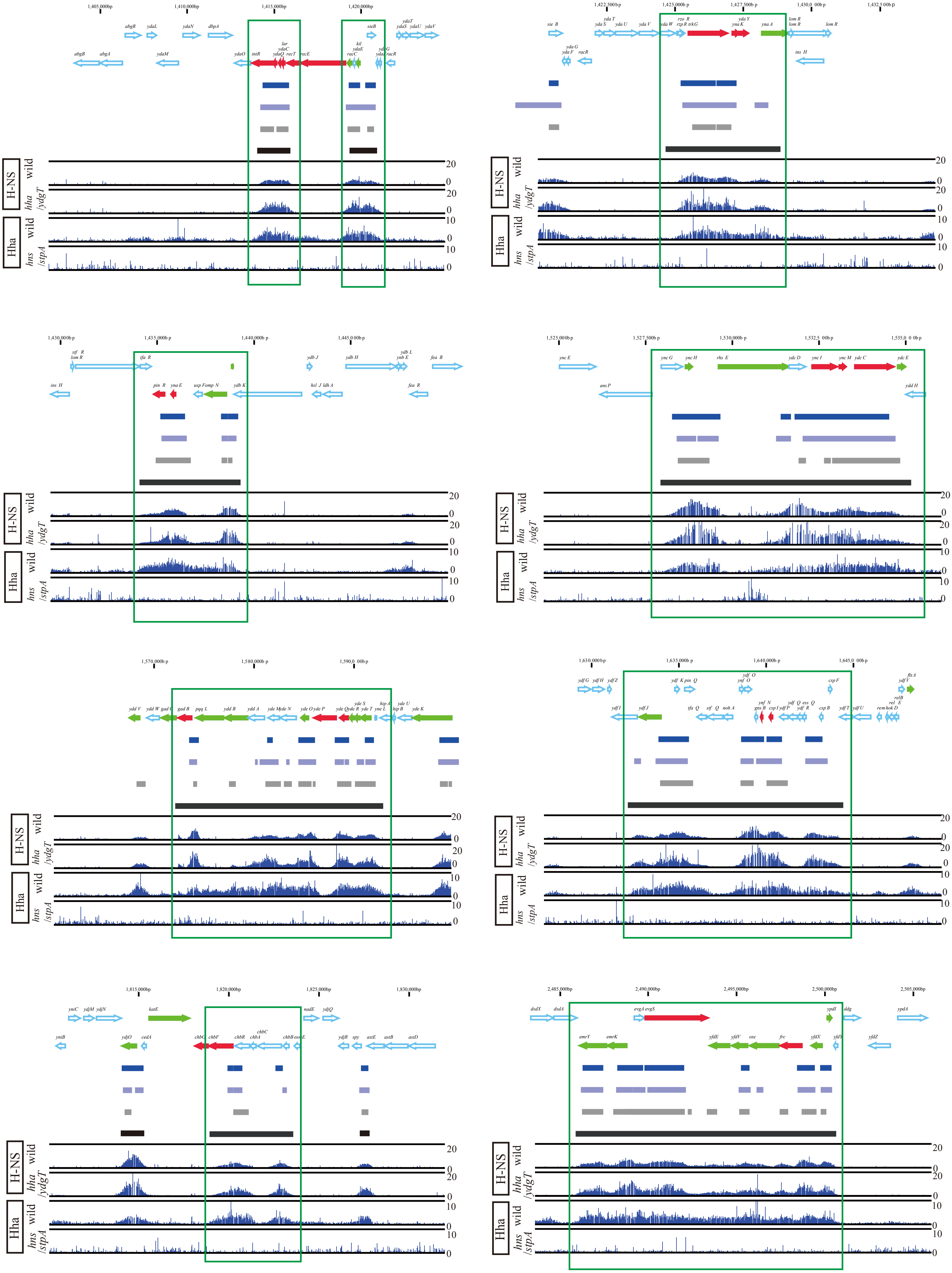

Fig.S3-5

Fig.S3C. continued

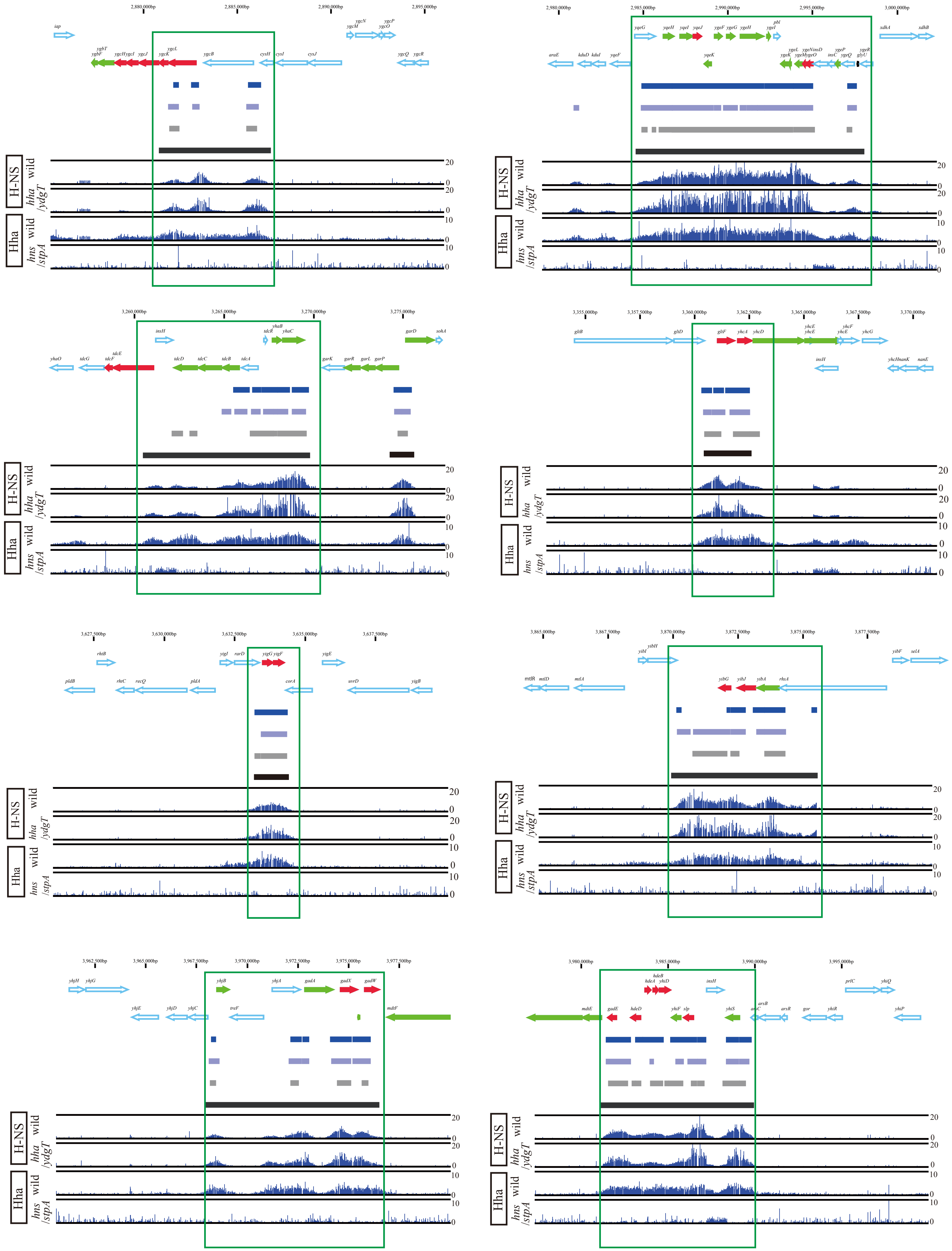

Fig.S3-6

Fig.S3C. continued

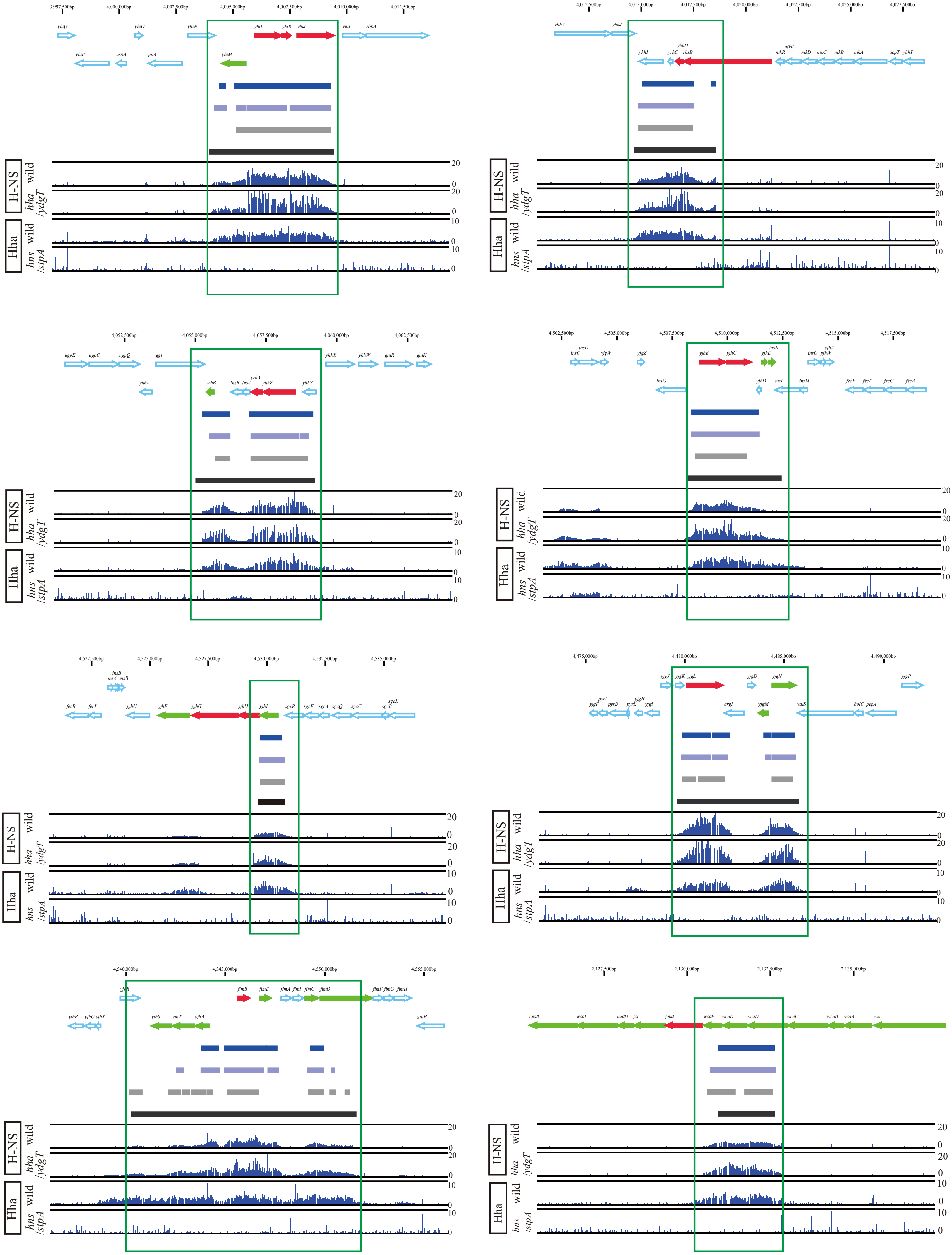

Fig.S3C. continued

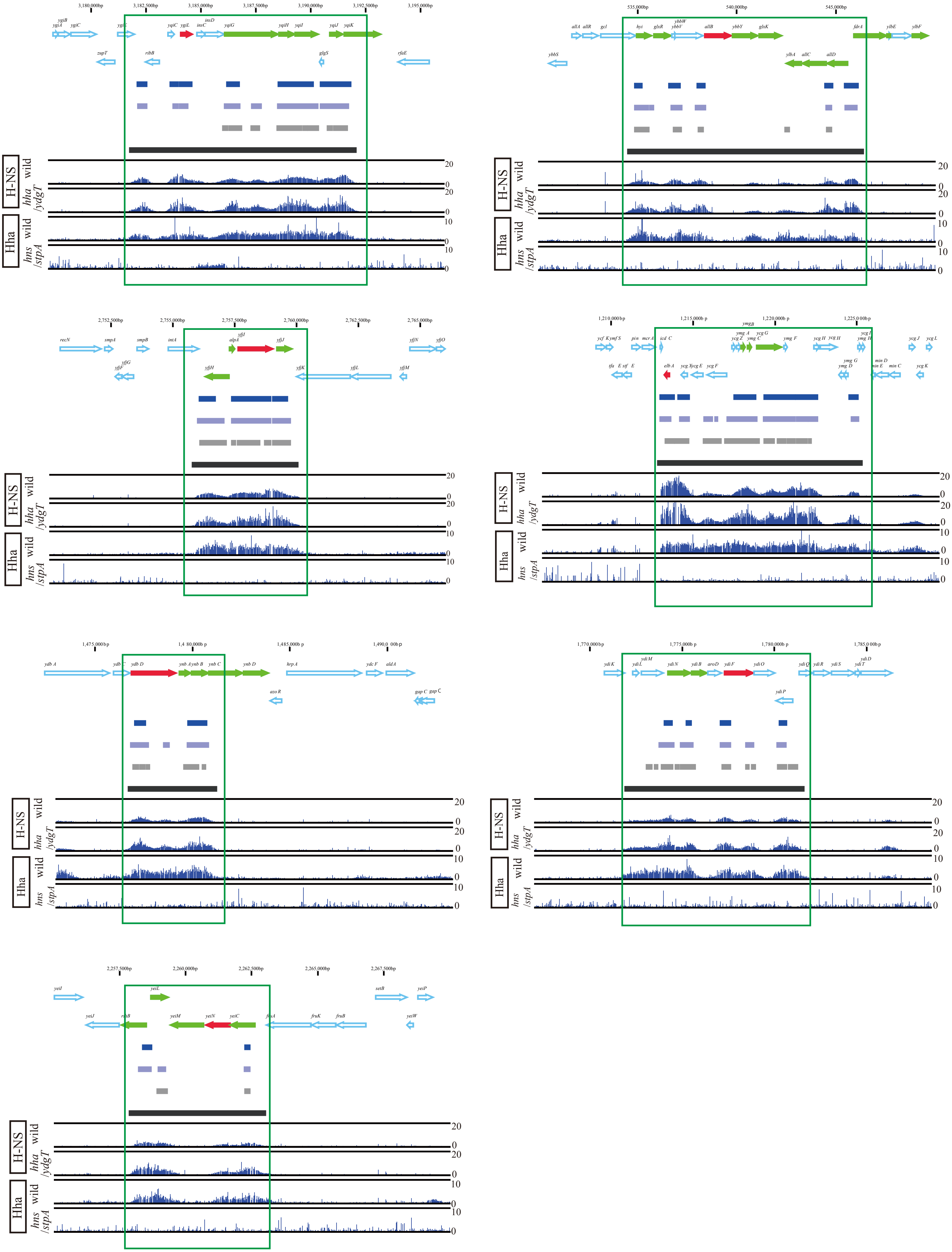

Fig.S3D. H-NS binding on both “intergenic” region and “coding” sequence

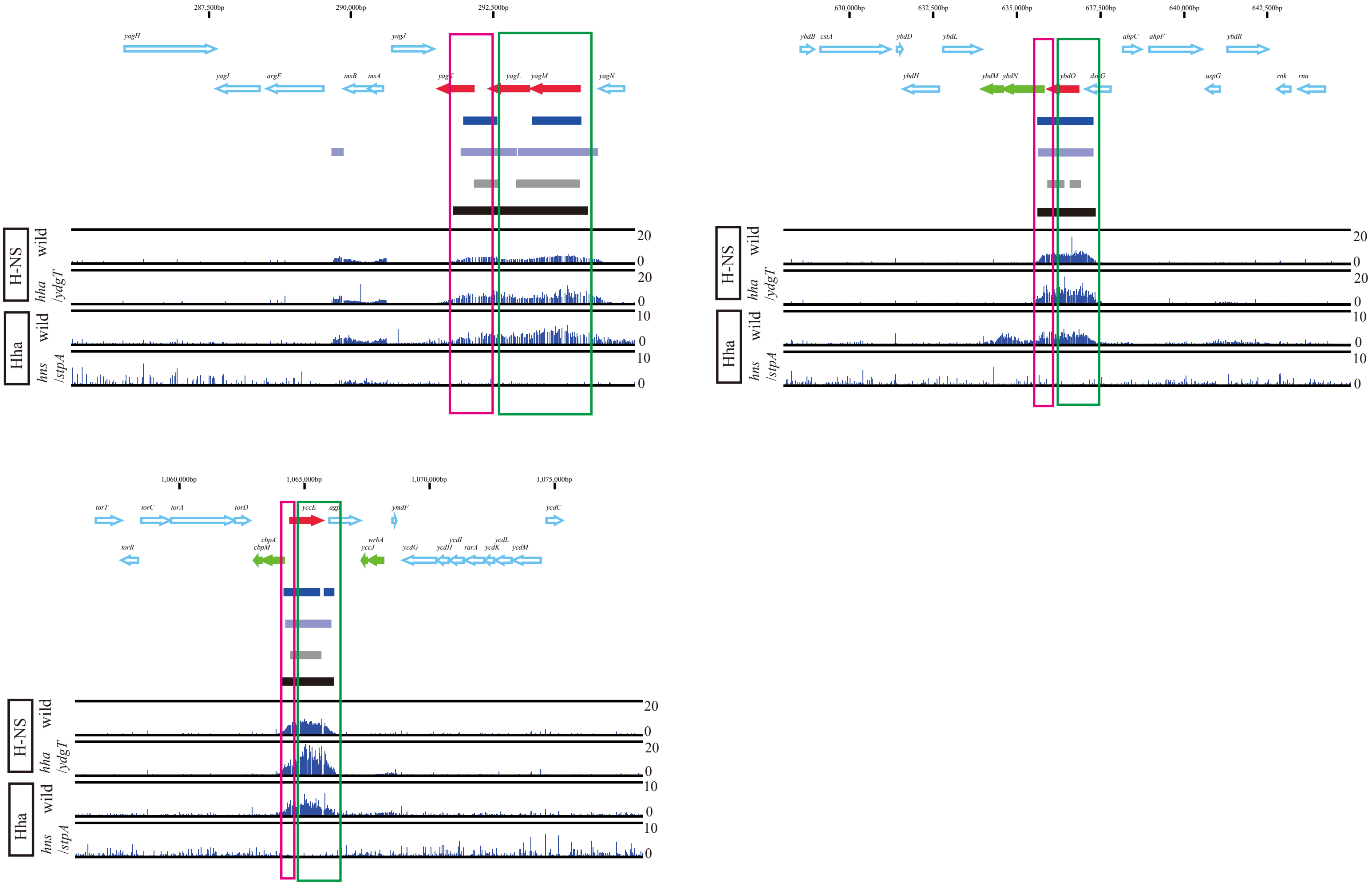

Fig. S3. The H-NS and Hha binding signals in and around the genes up-regulated in both *hha/ydgT* and *hns/stpA* mutant cells

H-NS and Hha binding profiles in and around all genes up-regulated in both *hha/ydgT* mutant and *hns/stpA* mutant cells are shown. The localizations of H-NS binding signals were classified as “intergenic” (A), “coding (single)” (B), coding (multiple)” (C), and both “coding” and “intergenic” (D).

“Intergenic” and “coding” H-NS binding regions are shown by red and green boxes, respectively. H-NS and Hha binding signals are shown as in Fig. S1, except that results of only one experiment for each strain are shown.