Figure S1

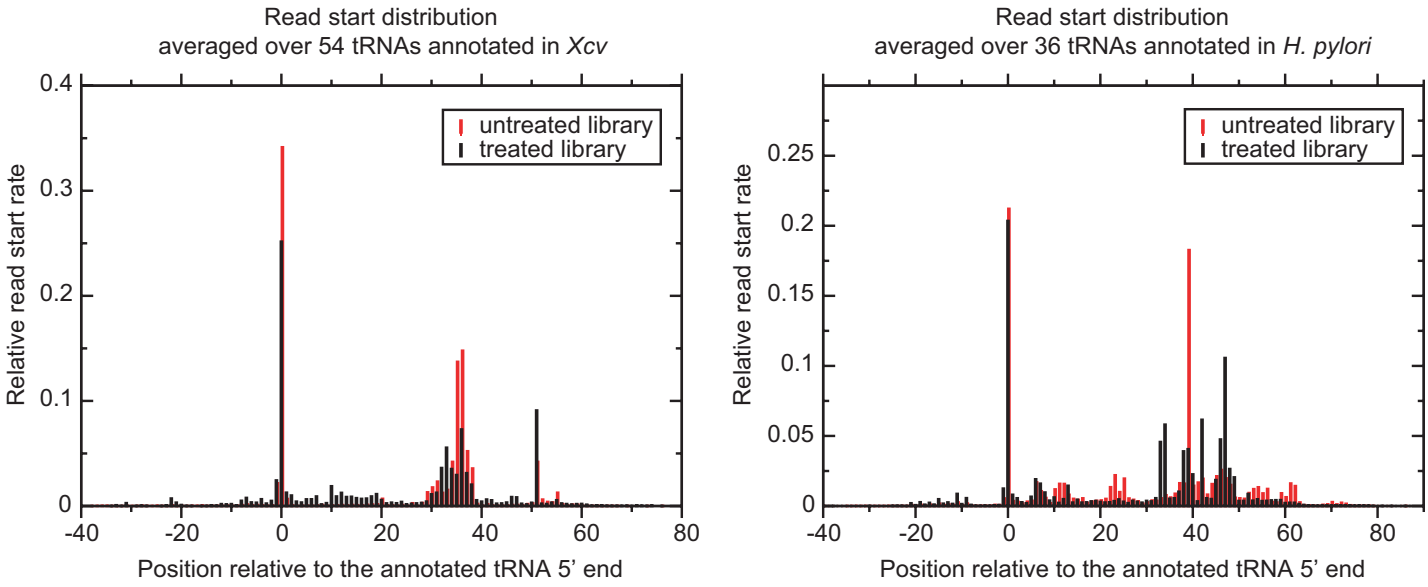

Figure S1. Averaged distribution of read starts across all annotated tRNA loci in *Xcv* and *H. pylori*, respectively. For each library, the number of read starts at any position was normalized to the total number of reads that map to tRNAs. Position 0 indicates the 5‘ ends of annotated tRNA genes and corresponds to the RNase P processing site. Although treated libraries (black) show a relative reduction of read start rates compared to untreated RNA-seq libraries (red), tRNA expression is still detected in the enriched libraries. TSSs of tRNAs are expected to be located upstream of position 0.

Figure S2

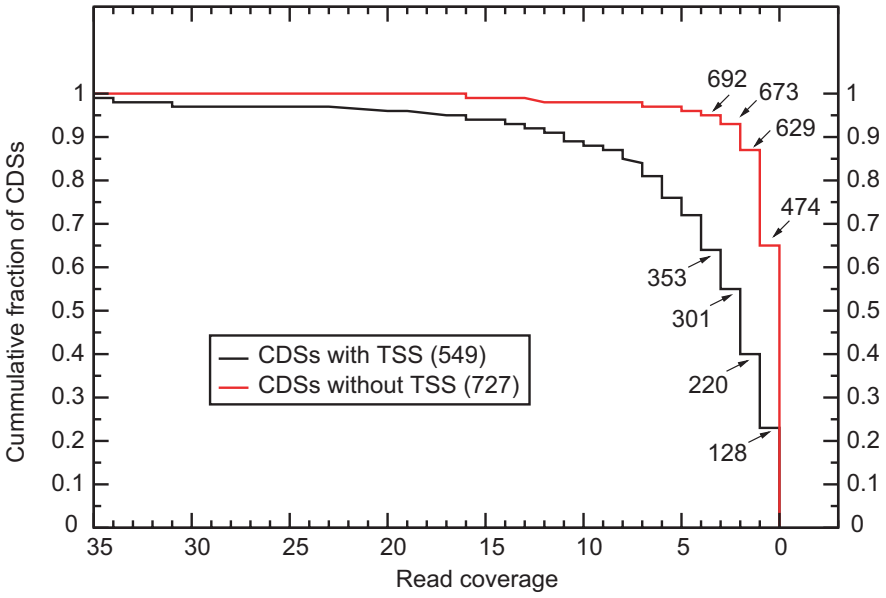

Figure S2. Coverage of CDSs with and without assigned TSSs in *Xcv*. The plot displays the coverage of the first 100 nt of selected CDSs that are assumed to possess an own promoter since upstream genes are encoded on the opposite strand. The y-axis indicates the cummulative fraction of CDSs that exhibit a certain coverage in each data set. Numbers of CDSs with 0- up to 4-fold coverage are given at the corresponding positions within the plot. A successful TSS annotation depends on coverage. CDS without annotated TSS exhibit an overall lower coverage than CDSs with assigned TSS.

Figure S3 (Continued)

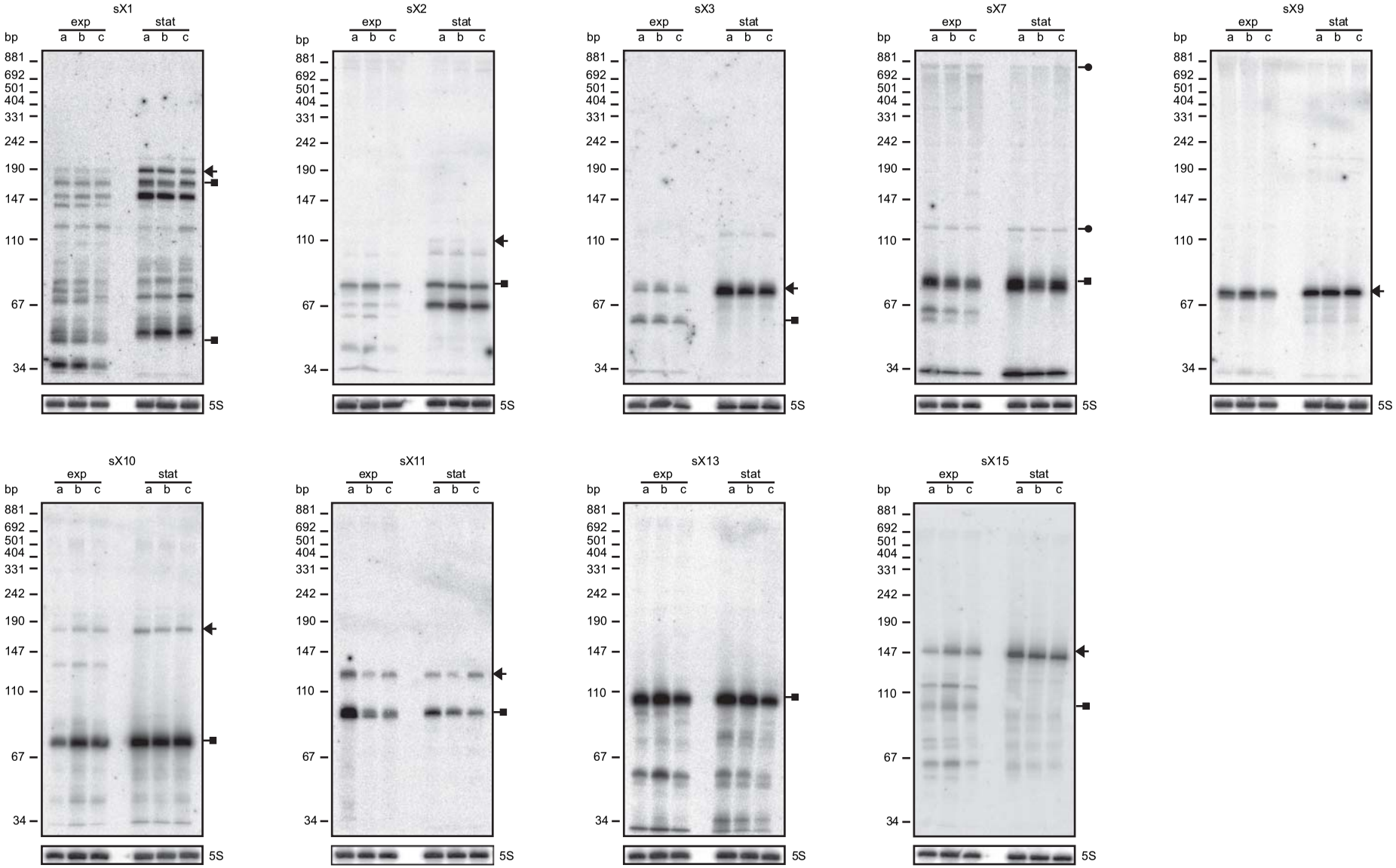

Figure S3

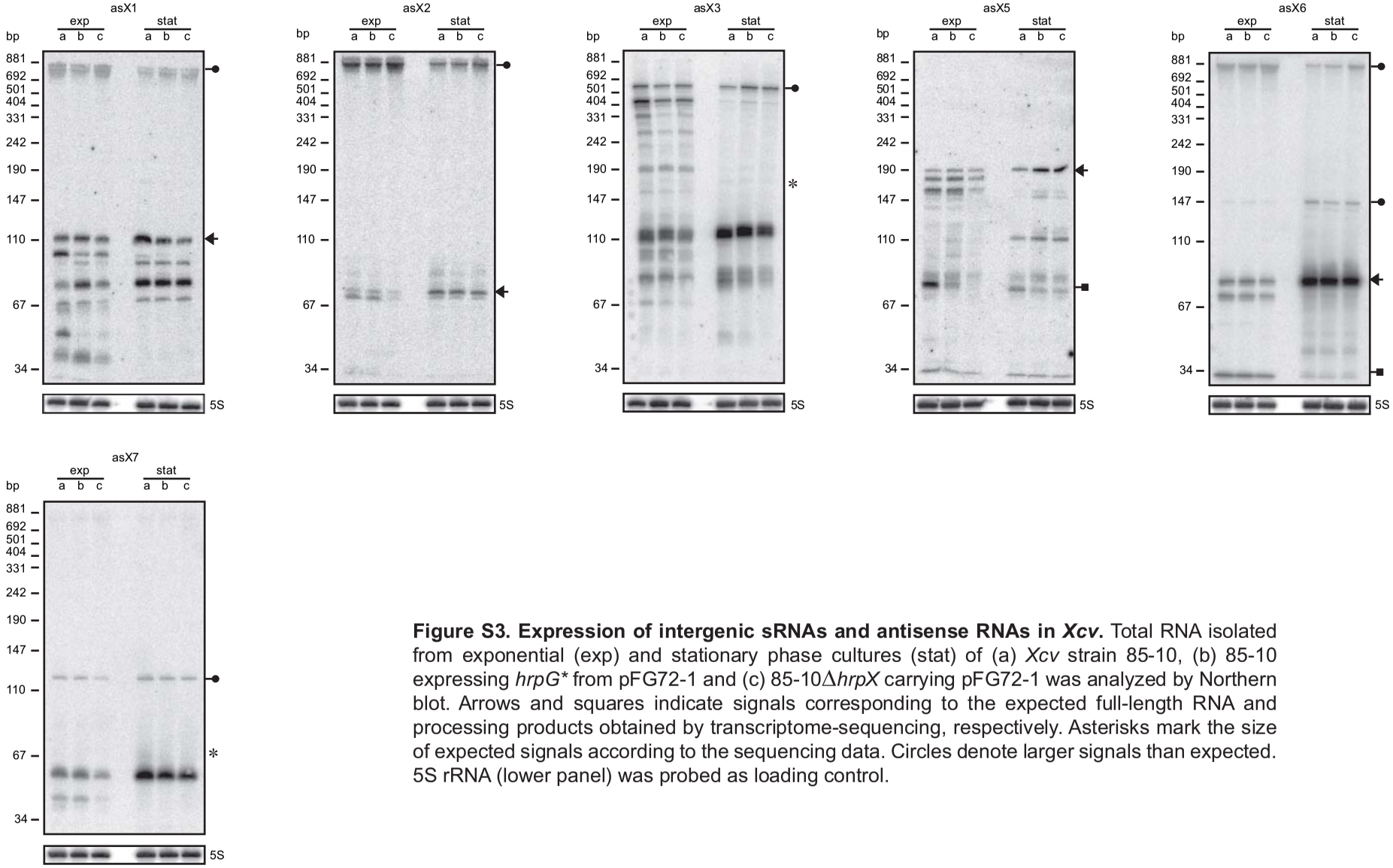

Figure S3. Expression of intergenic sRNAs and antisense RNAs in *Xcv*. Total RNA isolated from exponential (exp) and stationary phase cultures (stat) of (a) *Xcv* strain 85-10, (b) 85-10 expressing *hrpG** from pFG72-1 and (c) 85-10Δ*hrpX* carrying pFG72-1 was analyzed by Northern blot. Arrows and squares indicate signals corresponding to the expected full-length RNA and processing products obtained by transcriptome-sequencing, respectively. Asterisks mark the size of expected signals according to the sequencing data. Circles denote larger signals than expected. 5S rRNA (lower panel) was probed as loading control.

Figure S4

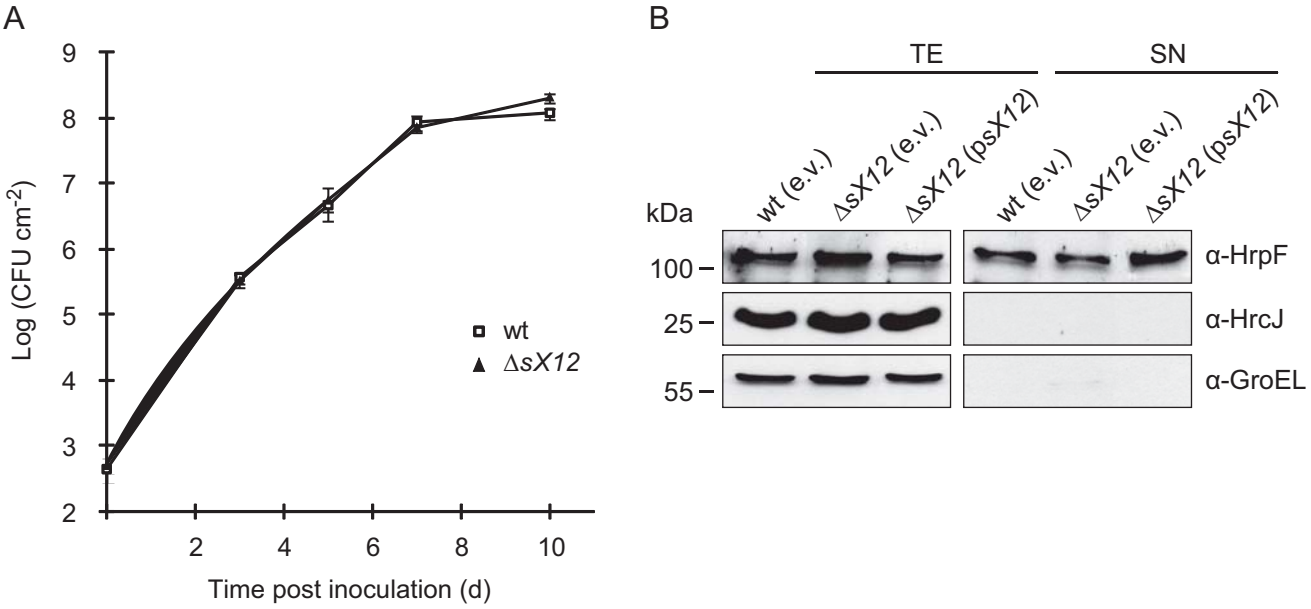

Figure S4. Deletion of *sX12* does not affect *in planta* growth and type III secretion. A. *In planta* growth of an *sX12* mutant strain. *Xcv* wild type strain 85-10 (wt) and an *sX12* deletion mutant (Δ*sX12*) were inoculated at a density of 10^4 CFU ml^{-1} into leaves of susceptible ECW pepper plants. Bacterial growth was determined over a period of 10 days. Data points indicate the mean of three samples from three different plants. Error bars represent standard deviations. B. Analysis of type III secretion. *Xcv* strain 85-10 carrying empty vector pLAFR6 [wt (e.v.)], an *sX12* deletion mutant [Δ*sX12* (e.v.)] and a complemented strain [Δ*sX12* (p*sX12*)] were incubated in secretion medium. The respective strains additionally express *hrpG** from pFG72-1. Total protein extracts (TE) and culture supernatants (SN) were analyzed by immunoblotting using antibodies directed against HrpF, HrcJ and GroEL.