SUPPORTING INFORMATION

In *Salmonella enterica,* the pathogenicity island 2 (SPI-2) regulator PagR regulates its own expression and the expression of a five-gene operon that encodes transketolase C

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Running title: PagR regulates the synthesis of transketolase C

AUTHOR CONTRIBUTIONS

A.R.P., R.D.M., and J.C.E.-S. conceptualized the project, designed the research, analyzed data, wrote the first draft of the paper; A.R.P. performed most of the experiments. J.A.B. assisted in the performance of experiments and edited the paper. J.C.E.-S obtained funding for the performance of the work.

SUPPORTING FIGURES

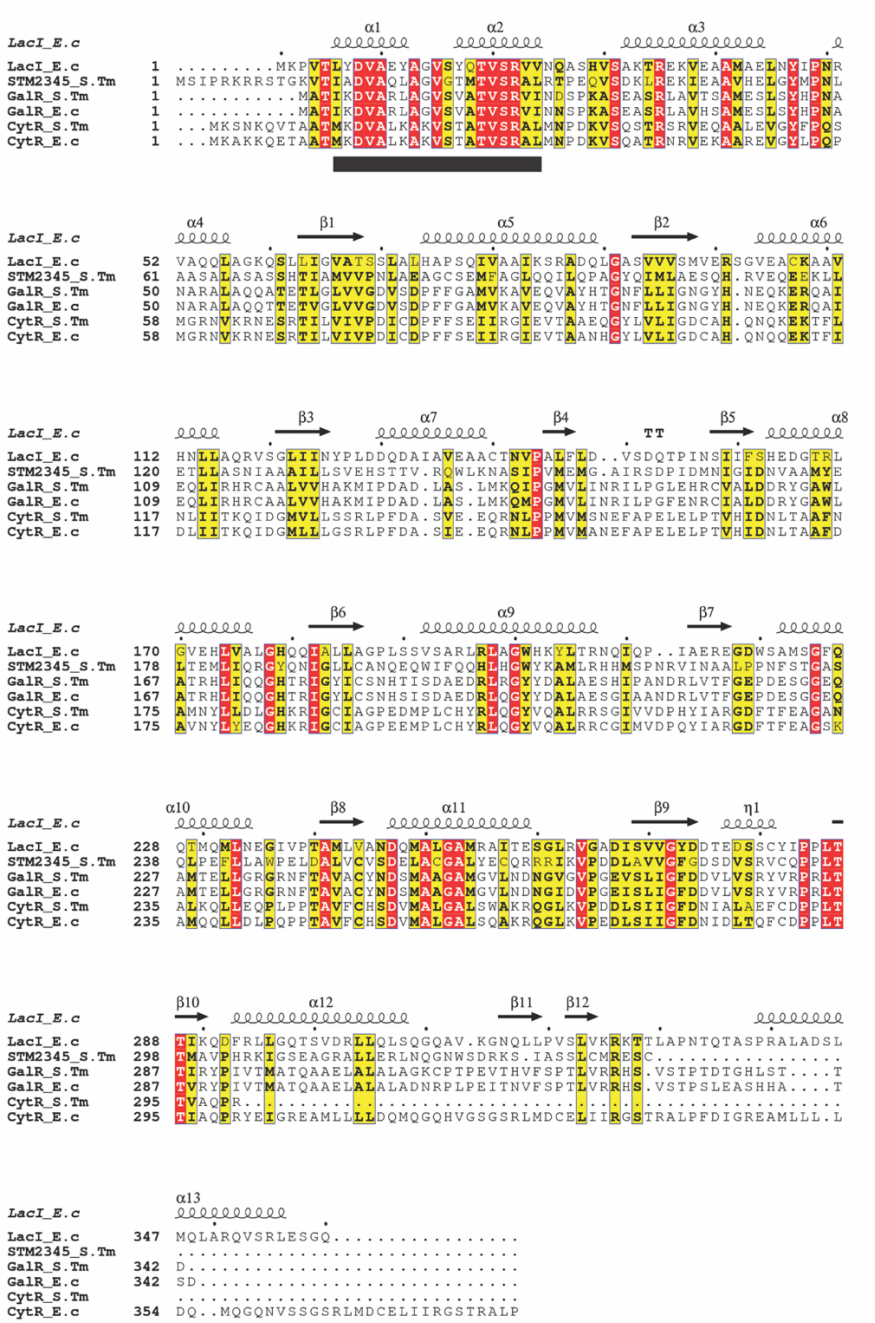


Figure S1. PagR alignment with LacI/GalR family members. PagR was aligned to various LacI/GalR family members from *S.* Typhimurium and *E. coli* MG1655 with Clustal Omega and visualized with ESPript 3.0. The secondary structure of LacI was imported from PDB entry 4RZS. The black bar spans the LacI/GalR family helix-turn-helix DNA binding motif, as defined elsewhere (Weickert and Adhya, 1992), for which PagR shares a high degree of identity and similarity to *bona fide* LacI/GalR family members

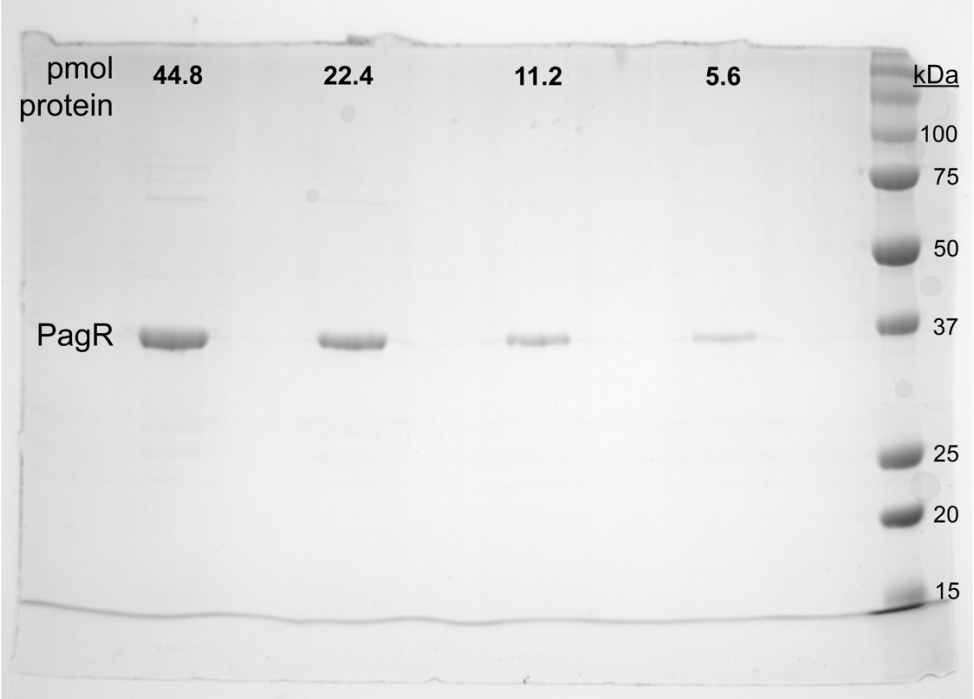


Figure S2. PagR purified to >95% homogeneity. PagR was purified as described under *Experimental procedures* for Electrophoretic Mobility Shift Assays and DNase 1 footprinting. Serial 1:2 dilutions of the final preparation were electrophoresed through a 12% acrylamide denaturing gel, and percent purity of the 44.8 pmol lane was calculated using the TotalLab TL 100 program. Valley to valley background correction was employed, and the final percent purity of PagR was calculated to be 97%.

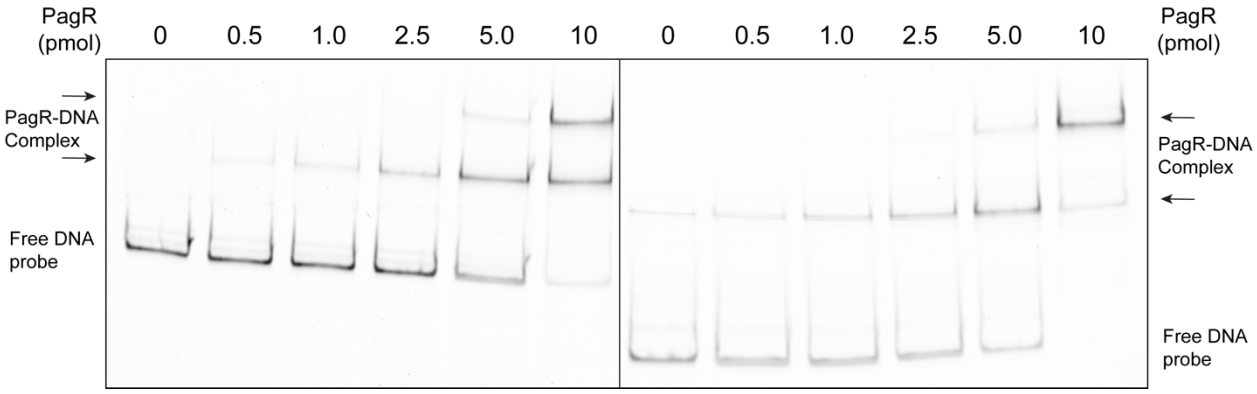


Figure S3. PagR generates the same banding pattern when assayed against two probes of the *stm2344 – pagR* promoter region. Electrophoretic Mobility Shift Assays against the probe spanning 2,457,048 nt to 2,457,454 nt of the chromosome (left box, shown in Fig. 4) and the probe spanning from 2,457,048 nt to 2,457,339 nt of the chromosome (right box, used for DNase footprinting in Fig. 6). A low amount (0.5 pmol) of fluorescent DNA probe was used for each assay. There are two clear mobility shifts for both probes, even with 20:1 PagR:probe ratio.

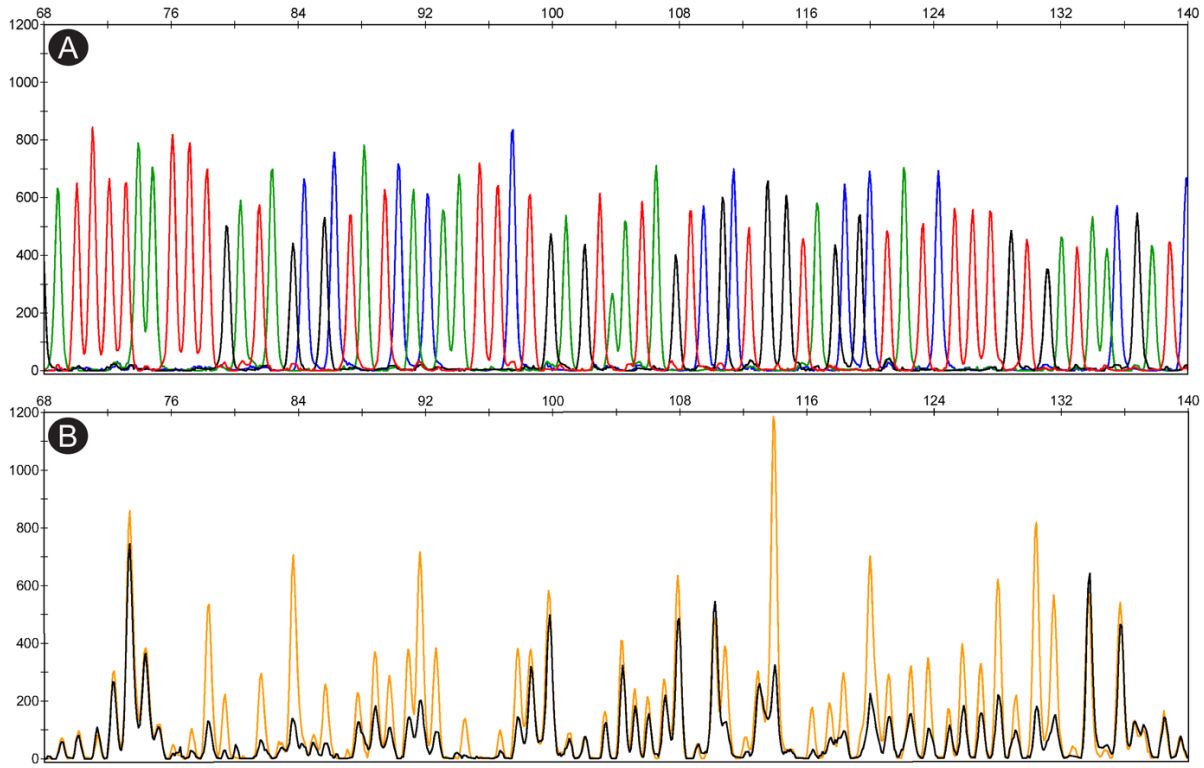


Figure S4. Identification of PagR binding sites in the promoter region of the *stm2344-stm2340* operon. A. Combined electropherograms from dideoxy termination Sanger sequencing of the *stm2344* promoter. Each trace is colored based on traditional presentation of BigDye termination: adenine is green, thymine is red, cytosine is blue, and guanine is black. **B.** DNase I digestion of $P_{stm2344}$ with (black trace) or without (orange trace) PagR present. Protected bases were identified by aligning the sequencing traces (**A**) with the digestion traces (**B**).

References

WEICKERT, M. J. & ADHYA, S. 1992. A family of bacterial regulators homologous to Gal and Lac repressors. *J. Biol. Chem.,* 267**,** 15869-15874.