

Supplementary Table and Figures

Supplementary Table 1. The ChIP-exo detected the PunR occupied an ~200 bp region in the promoter/ intergenic region for the listed genes.

Supplementary data. RNA-Seq measured differentially expressed genes in the presence and absence of 2.5 mM adenosine compared for *E. coli* MG1655 wild type strain.

Supplementary Figure 1. The genome context analysis of the *ydhC-ydhB* genes. Orthologous genes are marked by arrows of the same color and labeled according to their functional annotations: 3-PunC (YdhC), 1-PunR (YdhB), 2-PurR (purine nucleotide synthesis repressor).

Supplementary Figure 2. Multiple alignments of intergenic regions of the *ydhC/ydhB* genes in various groups of Enterobacteria and *Pseudomonas* spp. Gene coding regions are shown in red capital letters. Location of predicted PunR binding site is highlighted in yellow. The predicted -35 and -10 promoter elements of *punC* are underlined.

Supplementary Figure 3. The EMSA binding assay for PunR. The fluorescently labelled DNA pre-incubated for 1 hour with PunR and separated on 6% polyacrylamide gel. The lines -1, 2, 3 represent 1.5, 0.8, 0 microM of PunR incubated with the negative control – GguR- regulator fluorescently labelled DNA sequence in the presence of 1mM adenine. The lines 4, 5, 6, 7 represent PunR-predicted labelled DNA sequence incubated with PunR -0, 0.4, 0.8 and 1.5 microM in the presence of 1 mM adenine and lines 8, 9, 10 are PunR pre-incubated with the predicted PunR DNA-binding site at the 1, 0.5, 0 microM in the presence of 10 mM adenine. The Tris-Glycine running buffer, pH 8 supplemented with 0.25 mM adenine.

Supplementary Figure 4. The phenotypes of the *E. coli* BW25113 and *punC* knockout strains in the Biolog plate PM1 using M9 medium (PM1- carbon sources). The Omnilog measured growth curves for *E. coli* BW25113 and *punC* knockout strains on 2-deoxy-adenosine, adenosine, D-glucose, D-sorbitol, D-glucuronate, D-xylose. The Biolog plate PM1 contains 95 different carbon sources: L-arabinose, N-acetyl-D-glucosamine, D-saccharic acid, succinate, D-galactose, L-aspartate, L-proline, D-alanine, D-trehalose, D-mannose, dulcitol, D-serine, D-sorbitol, glycerol, L-fucose, D-glucuronate, D-gluconate, D,L-glycerol-phosphate, D-xylose, L-lactate, formate, D-mannitol, L-glutamate, D-glucose-phosphate, D-galactonate-lactone, D,L-malate, D-ribose, Tween 20, L-rhamnose, D-fructose, acetate, D-glucose, maltose, melibiose, thymidine, L-asparagine, D-aspartate, D-glucosaminic acid, 1,2-propandiol, Tween 40, α -keto-glutarate, α -keto-butyrate, α -Methyl-galactoside, D-lactose, lactulose, sucrose, uridine, L-glutamine, m-Tartrate, D-glucose-1-phosphate, D-fructose-6-phosphate, Tween 80, α -hydroxy-glutarate-lactone, α -hydroxy-butyrate, β -methyl-D-glucoside, adonitol, maltotriose, 2-Deoxy-adenosine, adenosine, glycyl-L-aspartate, citrate, Myo-inositol, D-threonine, fumarate, bromo-succinate, propionate, mucic acid, glycolate, glyoxylate, D-cellobiose, inosine, glycyl-L-glutamate, tricarballylate, L-serine, L-threonine, L-alanine, L-alanyl-glycine, acetoacetate, N-acetyl-D-mannosamine, mono-methyl-succinate, methyl-pyruvate, D-malate, L-malate, glycyl-L-proline, p-hydroxy-phenylacetate, m-hydroxy-phenylacetate, tyramine, D-psicose, L-lyxose, glucuronamide, pyruvate, L-galactonate- γ -lactone, D-galacturonate, phenylethylamine, 2-aminoethanol.

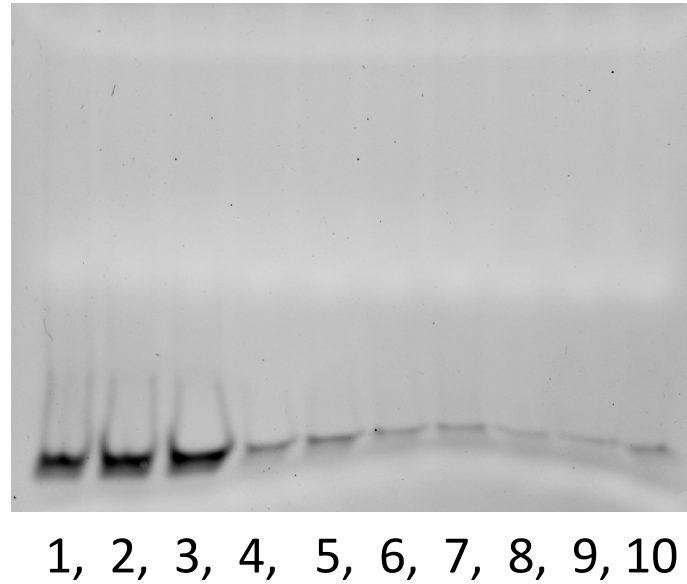


Fig S3. The EMSA assay for the fluorescently labeled DNA pre-incubated 1 hour with PunR and separated on 6% polyacrylamide gel. The lines -1, 2, 3 represent 1.5, 0.8, 0 microM of PunR pre-incubated 1 hour with the negative control - GguR labeled DNA GTTGT(A/C)N(G/T)ACAAC from (Ref) in the presence of 1mM adenine . The lines 4, 5, 6, 7 represent pre-incubated PunR-predicted labeled DNA with PunR-0, 0.4, 0.8 and 1.5 microM in the presence of 1 mM adenine and lines 8, 9, 10 are PunR pre-incubated with the predicted DNA-binding site at the 1, 0.5, 0 microM in the presence of 10 mM adenine. The Tris-Glycine running buffer contains 0.25 mM adenine.

ydhC knockout strain

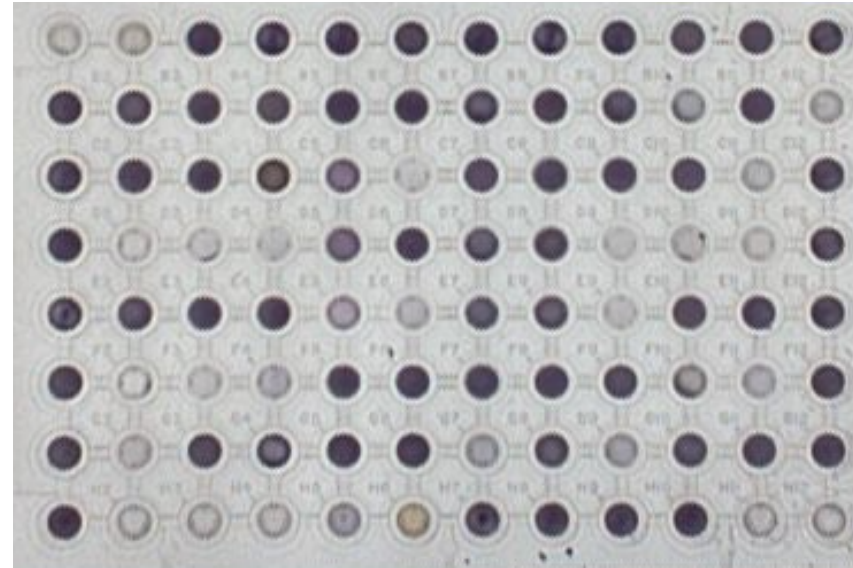
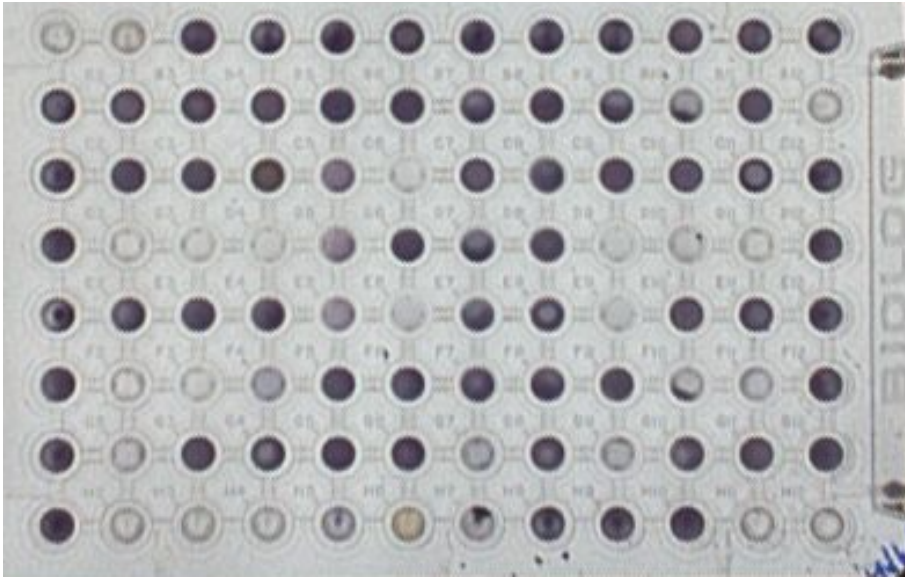


Fig. S4 The phenotype of the *E. coli* BW25113 NC and *punC* knockout strains in PM1.

b_number	The nearest gene
b0591	fepD
b1200	dhaR
b1241	adhE
b1499	ydeO
b1521	uxaB
b1638	pdxH
b1658	purR
b1659	ydhB
b1844	exoX
b2448	yffQ
b2632	yfjP
b2956	yggM
b3092	uxaC
b3175	secG
b3321	rpsJ

Table S1. The ChIP-exo detected the PunR occupied an 200bp region in the promoter/intergenic. Region for the listed genes.

- 548.115.peg.1014 Enterobacter aerogenes strain CAV1320
- 883121.3.peg.2572 Klebsiella oxytoca 10-5246
- 1286170.3.peg.1018 Raoultella ornithinolytica B6
- 575.4.peg.1602 Raoultella planticola strain CHB
- 640131.3.peg.2253 Klebsiella variicola At-22
- 1134687.3.peg.2478 Klebsiella michiganensis strain SA2
- 701347.4.peg.2203 Enterobacter cloacae SCF1
- 1697388.3.peg.3561 Enterobacter tabaci strain CCUG 72520
- 290338.8.peg.1409 Citrobacter koseri ATCC BAA-895
- 546.84.peg.3727 Citrobacter freundii strain FDAARGOS_61
- 500640.5.peg.1436 Citrobacter youngae ATCC 29220
- 67829.4.peg.3727 Citrobacter murlinae strain P080C CL
- 295319.15.peg.1525 Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150
- 12149.1.peg.1388 Salmonella bongori 12149
- 1095768.3.peg.1306 Enterobacter sp. JC163

ydhC <-

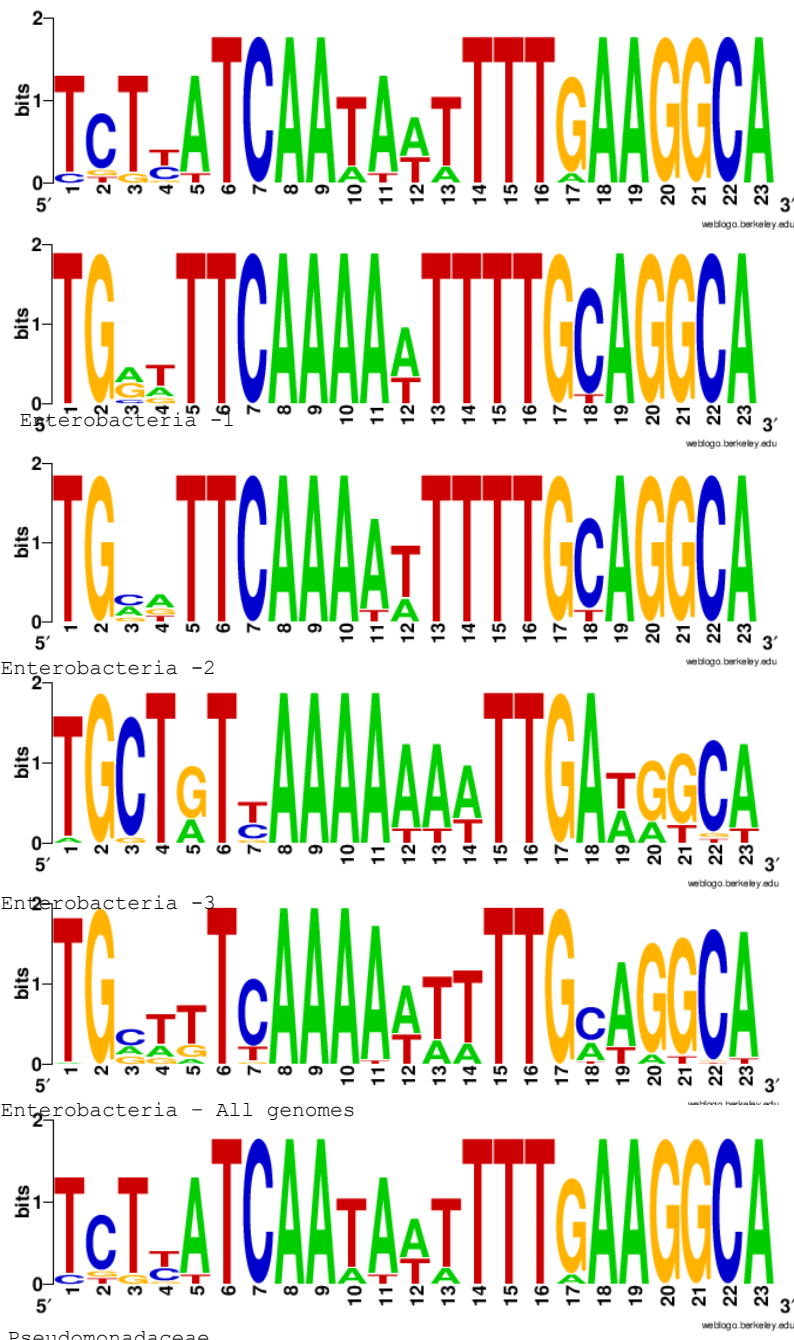
-10

ATCCTTTTACCAGGTTGCATcgtcatttctcatt-ctcgttgcagggttccagttcagtcgccgcagagtgtag
 ATCCTTTTCTGGGTTGCATtgttttattctcct-gaggaggcagggttacgt-----tggcgcagagtgtag
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 AACCTTTTCCAGGTTGCATaattgtttctctt---ttatcaaacagacac-----tgccgcagagtgtag
 ACCCTTTTCCAGGTTGCATgggt-aaatctctt---taatgctgataaacag-----ggctccagagtctaa
 *

-35

YdhB binding site -> ydhB

ggagtgcacacctggctt**gttgaa**acgctaattattgtcgaa**tgggttcaaaat**tttgcaggcagatt**ATGTGGTCGAGA**
 ggagtgcacaaagcggct**gttgaa**acgctaattattgtcgagtgcattcaaaat**tttgcaggcagaac**ATGTGGTCGAGA
 ggagtgcacaaagcggct**gttgaa**acgctaattattgtcgagtgcattcaaaat**tttgcaggcagaac**ATGTGGTCGAGA
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Enterobacteriaceae - 3

630.33.peg.1425	<i>Yersinia enterocolitica</i> strain ATCC 9610
393305.7.peg.2324	<i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081
349966.5.peg.542	<i>Yersinia frederiksenii</i> ATCC 33641
28152.3.peg.1198	<i>Yersinia kristensenii</i> strain ATCC 33639
349965.6.peg.1196	<i>Yersinia intermedia</i> ATCC 29909
349967.4.peg.1011	<i>Yersinia mollaretii</i> ATCC 43969
527004.3.peg.123	<i>Yersinia rohdei</i> ATCC 43380
349968.5.peg.69	<i>Yersinia bercovieri</i> ATCC 43970
502800.6.peg.2008	<i>Yersinia pseudotuberculosis</i> YPIII
1084234.3.peg.4018	<i>Yersinia pestis</i> biovar <i>Orientalis</i> str. AS200901509
29486.45.peg.499	<i>Yersinia ruckeri</i> strain Big Creek 74
291112.3.peg.2119	<i>Photorhabdus asymbiotica</i>
615.109.peg.2214	<i>Serratia marcescens</i> strain UCI88
768490.3.peg.2144	<i>Serratia</i> sp. AS12
614.9.peg.259	<i>Serratia liquefaciens</i> strain FDAARGOS_125
667129.3.peg.3101	<i>Serratia odorifera</i> DSM 4582
399741.7.peg.2234	<i>Serratia proteamaculans</i> 568
82996.16.peg.4145	<i>Serratia plymuthica</i> strain A153
47917.12.peg.3337	<i>Serratia fonticola</i> strain GS2

Pseudomonadaceae

746360.3.peg.1750	Pseudomonas fluorescens WH6
1038924.3.peg.1593	Pseudomonas fluorescens SS101
321846.3.peg.1569	Pseudomonas simiae strain WCS417
1144885.3.peg.4026	Pseudomonas sp. R81
1037911.3.peg.1617	Pseudomonas fluorescens A506
96901.3.peg.1676	Pseudomonas synxantha BG33R
216595.4.peg.1849	Pseudomonas fluorescens SBW25
1125977.3.peg.5361	Pseudomonas sp. PAMC 25886
294.123.peg.1588	Pseudomonas fluorescens strain UK4
882211.3.peg.4099	Pseudomonas deceptionensis strain DSM 26521