

## **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.

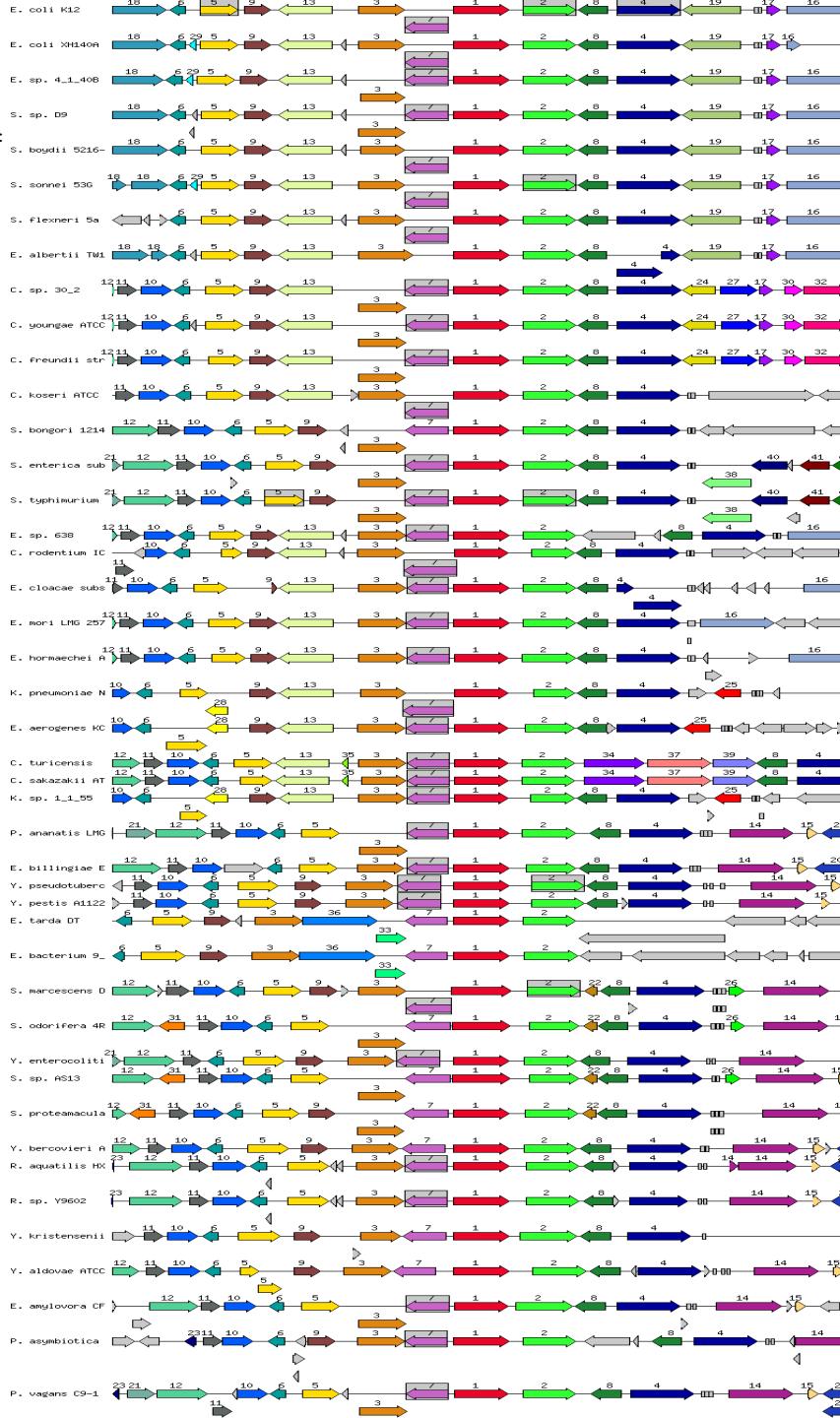
**Supplementary Figure 1. The genome context analysis of the *ydhC-ydhB* genes.** Orthologous genes are marked by arrows of the same color and labeled according to their functional annotations: 3-PunC (YdhC), 1-PunR (YdhB), 2-PurR (purine nucleotide synthesis repressor).

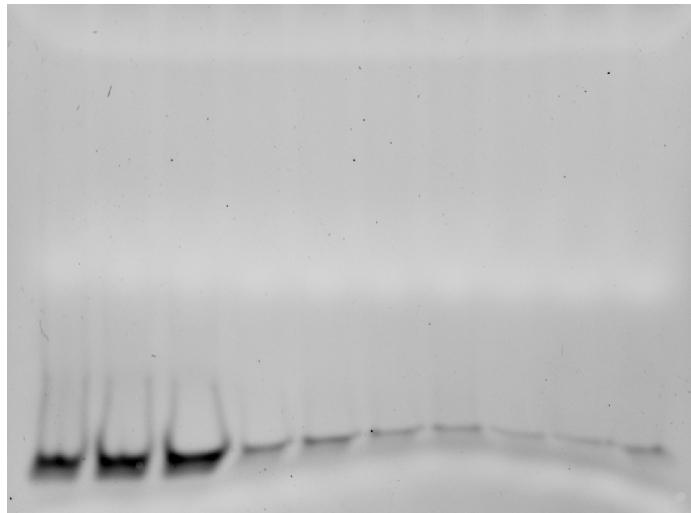
**Supplementary Figure 2. Multiple alignments of intergenic regions of the *ydhC/ydhB* genes in various groups of Enterobacteria and *Pseudomonas* spp.** Gene coding regions are shown in red capital letters. Location of predicted PunR binding site is highlighted in yellow. The predicted -35 and -10 promoter 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-glucosamine, 1,2-propandiol, Tween 40,  $\alpha$ -keto-glutarate,  $\alpha$ -keto-butyrate,  $\alpha$ -Methyl-galactoside, D-lactose, lactulose, sucrose, uridine, L-glutamine, m-Tartrate, D-glucose-1-phosphate, D-fructose-6-phosphate, Tween 80,  $\alpha$ -hydroxy-glutarate-lactone,  $\alpha$ -hydroxy-butyrate,  $\beta$ -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- $\gamma$ -lactone, D-galacturonate, phenylethylamine, 2-aminoethanol.

**Fig. S1** The identifications for the genes encoding (marked by arrows):  
1-YdhC, 7-YdhB, 3-PurR





1, 2, 3, 4, 5, 6, 7, 8, 9, 10

**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

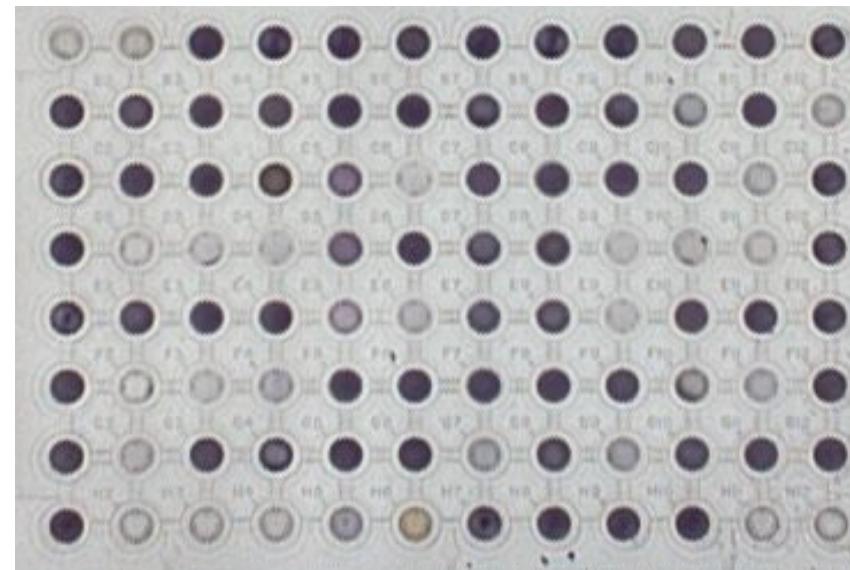
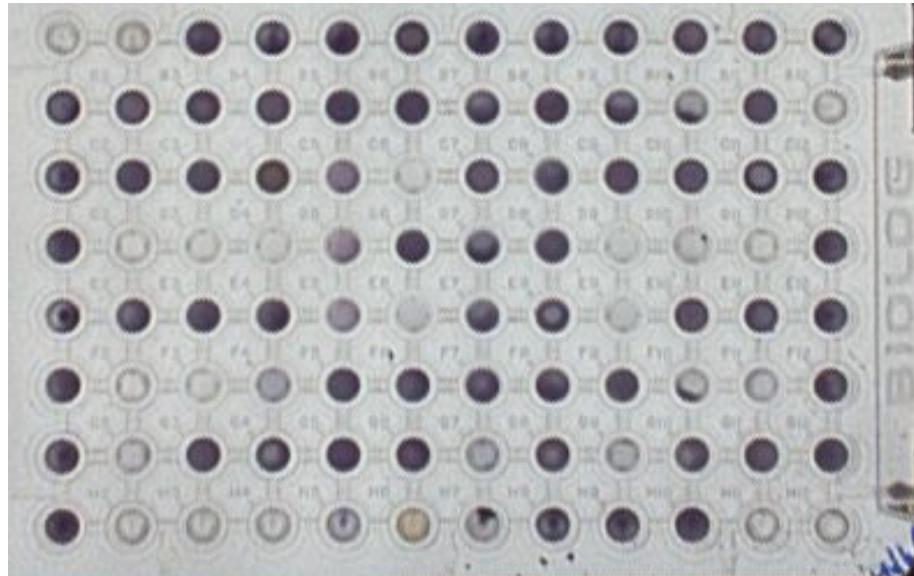


Fig. S4 The phenotype of the *E. coli* BW25113 NC and *punC* knockout strains in PM1.

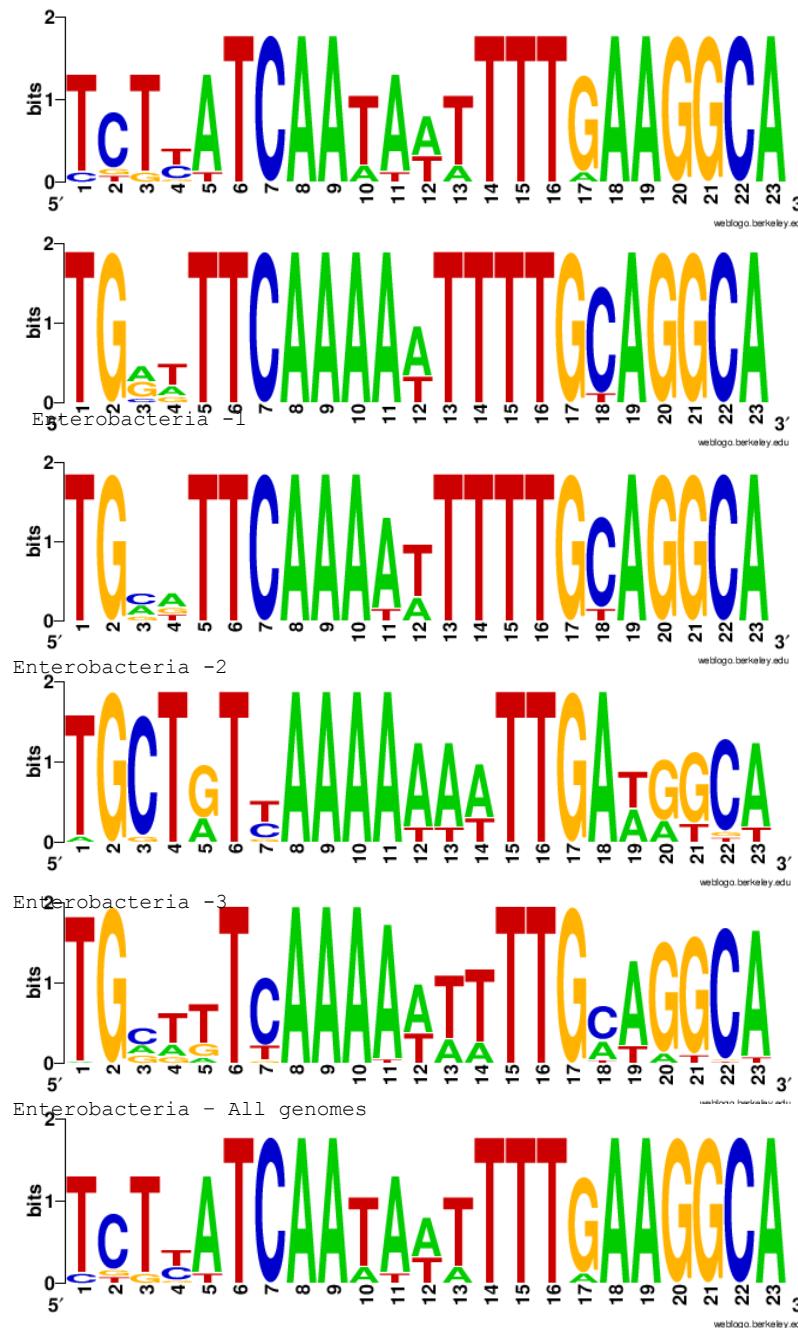
b_number	The nearest gene
b0591	fepD
b1200	dhaR
b1241	adhE
b1499	ydeO
b1521	uxaB
b1638	pdxH
b1658	purR
b1659	ydhB
b1844	exoX
b2448	yffQ
b2632	yfjP
b2956	yggM
b3092	uxaC
b3175	secG
b3321	rpsJ

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

Fig. S2 Multiple alignments of intergenic regions of the *ydhC/ydhB* genes in various groups of Enterobacteria

Enterobacteriaceae - 1							
83333.1.peg.1645	Escherichia coli K12	500640.5.peg.1436	Citrobacter youngae ATCC 29220				
457401.3.peg.399	Escherichia sp. 4_1_40B	701347.4.peg.2203	Enterobacter cloacae SCF1				
216599.12.peg.1710	Shigella sonnei 53G	1265617.3.peg.1260	Salmonella enterica subsp. enterica serovar Agona st				
1038844.18.peg.786	Escherichia coli O104:H4 str. TY-2482	36.H.00					
556266.3.peg.160	Shigella sp. D9	35703.16.peg.2786	Citrobacter amalonaticus strain YG6				
622.8.peg.966	Shigella dysenteriae CDC 74-1112	12149.1.peg.1388	Salmonella bongori 12149				
300268.11.peg.1907	Shigella boydii Sb227	575.4.peg.1602	Raoultella planticola strain CHB				
373384.11.peg.1943	Shigella flexneri 5 str. 8401	571.108.peg.202	Klebsiella oxytoca strain CAV1335				
208962.36.peg.1645	Escherichia albertii strain EC06-170	1286170.3.peg.1018	Raoultella ornithinolytica B6				
290338.8.peg.1409	Citrobacter koseri ATCC BAA-895	1134687.3.peg.2478	Klebsiella michiganensis strain SA2				
1173691.3.peg.3874	Citrobacter sp. A1	936565.3.peg.5502	Klebsiella sp. OBRC7				
1288347.3.peg.145	Citrobacter freundii GTC 09479	ydhC <-					
500640.5.peg.1436	GGCCCCGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATcatcattctcttttttagcagtaga-----acaatGccgct						
290338.8.peg.1409	GGCCCCGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATcatcattctcttttttagcagtaga-----acaatgccgt						
83333.1.peg.1645	GACCCGCCAACAGACTAAAAACCCCTTCCCAGGGTGCATcatcattctcttttgcgct-----actataga-----acaatgccgt						
457401.3.peg.399	GACCCGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATcatcattctcttttgcgct-----actataga-----acaatgccgt						
1038844.18.peg.786	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
556266.3.peg.160	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
216599.12.peg.1710	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
373384.11.peg.1943	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
622.8.peg.966	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
300268.11.peg.1907	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
208962.36.peg.1645	AACCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATgtatatt-ctctaattctcaattaa-----acaccggccca						
1265617.3.peg.1260	GACCGGCTAACAGACTAAAAACCCCTTCCCAGGGTGCATatgtt-tctcttttatcagacag-----acattgtcgca						
12149.1.peg.1388	GACCGGCTAACAGACTAAAAACCCCTTCCCAGGGTGCATatgtt-tctcttttatcagacag-----acattgtcgca						
35703.16.peg.2786	GCCCTGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATatgtt-tctcttttatcagacag-----acattgtcgca						
575.4.peg.1602	GTCCCGCCAGCCACACTAAAAACCCCTTCCCAGGGTGCATacattctctt-----atagatgcag-----gtatgtcgca						
1286170.3.peg.1018	GTCCCGCCAGCCACACTAAAAACCCCTTCCCAGGGTGCATacattctctt-----atagatgcag-----gtatgtcgca						
1134687.3.peg.2478	GGCCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATacattctctt-----atagatgcag-----gtacgtggcgca						
936565.3.peg.5502	GTCCAGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATacattctctt-----atagatgcag-----gtacgtggcgca						
571.108.peg.202	GTCCCGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATatattctcttttagtgcag-----gtacgtggcgca						
701347.4.peg.2203	AGCCCTGCCAGCCAGACTAAAAACCCCTTCCCAGGGTGCATcgtattctcattctcgatgtgcaggtttcaggcgt-----*						





1028307.3.peg.3552	Enterobacter aerogenes KCTC 2190
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 muriiniae 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  
ATCCTTACAGGGTCATcgtcatttcatt-ctcgtgcaggtttcaggcagtggcccgagtgtag  
ATCCTTCTGGGTTGCATgttttattctct-gaggaggcaggttacgt-----tggcccgagtgtag  
ATCCCTCCCAGGGTGTGCATaacgttctttactgtatgcaggatgatga-----tgcccgagagtgtag  
ATCCCTCCCAGGGTGTGCATaacgttctttactgtatgcaggatgatga-----tgcccgagagtgtag  
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ACCCTTCCAGGGTGCATCATcattcttctt----ttacaatagaacaa-----tgccgctgagtgtag  
ACCCTTCCAGGGTGCATCATcattcttttt--taagcagtaaaacag-----tgtcccgagagtgtag  
AACCTTCCAGGGTGCATattgtttctttt--ccagaagaagacat-----tgccgctgagtgtag  
AACCTTCCAGGGTGCATattgtttctttc--ttatcagacagacat-----tgtcccgagagtgtag  
AACCTTCCAGGGTGCATattgtttctttt--ttatcaaacagacac-----tgcccgagagtgtag  
ACCCTTCCAGGGTGCATggt-aaaatctttttt--taatgctataacag-----ggctcccgagtgtagaa

*ydhB* binding site  $\Rightarrow$  *ydhB*

ggagtgcattctggct**tgtgaa**acgtaatatttgcagaatgggtccaaaattttgcaggcagatt**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcagatgcatccaaattttgcaggcagaac**ATGTGGTC**  
ggagtgtaatccgc**tgtgaa**acgctatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgtaatccgc**tgtgaa**acgctatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctggct**tgtgaa**acgtaatatttgcacatgcattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgtaattcacgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgtaaatttcgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgtaggcagact**ATGTGGTC**  
ggagtgtaaatttcgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgtaaatttcgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgtaaatttcgc**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagaat**ATGTGGTC**  
ggagtgcattctgtg**tgtgaa**acgtaatatttgcattactgattccaaaattttgcaggcagatt**ATGTGGTC**

**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 bercoieri</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</i> <i>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