

Supplemental Figure Legends

FIG S1. Confirmation of mutant survival and growth. Following Ham's F12 survival and RnP growth assays, 2 μ l of each culture was plated on Blood Agar plates to ensure optical density did in fact correlate with bacterial survival and that the culture was not contaminated. In this example, wild type (WT) bacteria that were capable of growth in RnP media given any of the single purine bases listed, but did not survive for 48 hours when grown in 0.1% catalase. Δ *guaA* was capable of survival in media containing guanine or guanosine and Δ *guaB* was capable of survival on xanthine, guanine, or guanosine.

FIG S2. Sequence alignment of *purD* genes. Genes were compared between *Escherichia coli*, *Campylobacter jejuni*, and *Helicobacter pylori* (Genbank accession numbers are GI:16131835, GI:218562862, and GI:208433042, respectively). Highlighted residues indicate P-loop and ATP binding sites. Figure adapted from Sampei *et al.*, Crystal structures of glycinamide ribonucleotide synthetase, PurD, from thermophilic eubacteria, *Journal of Biochemistry*, 2010, 148(4), 429-38, by permission of Oxford University Press.

FIG S3. Cladogram of epsilon proteobacteria. Cladogram for the order of campylobacterales (generated via PATRIC multi-gene phylogenetic tree viewer). Species are listed in order of similarity at the genome level. Species are labeled according to the presence or absence of three purine salvage pathway associated genes: *deoD*; purine nucleoside phosphorylase, *guaC*; GMP reductase, and *gpt*; guanine phosphoribosyltransferase. Those species lacking more than 4 of the 10 *pur* genes

required for inosine monophosphate (IMP) production and thereby, *de novo* purine nucleotide biosynthesis, are highlighted in grey.

FIG S4. Alternate potential metabolic pathways by which *H. pylori* is capable of generating GMP and AMP from the single purine source, adenine. (A) Base pathway for adenine processing. Pathway thermodynamics assuming (B) strong APRTase activity coupled with an adenine deaminase and (C) weak APRTase activity coupled with an adenosine deaminase. Steps are described in text.

TABLE S1. Primers used in this study.

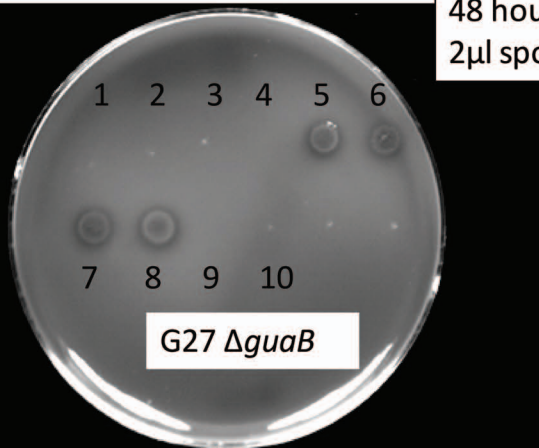
Primer	sequence
guaA P1	GTTTGAAATGTTGCGTG GGG
guaA P2	<u>ATCCACTTTTCAATCTATATCAATCAGCTGTGTGTATTGGC</u>
guaA P3	<u>CCCAGTTTGTGCGACTGATAAAGTGAGCGGTATCAATAGGG</u>
guaA P4	CAATATCTTCTAAGATAGCC
guaA seq F	TATAATACCCAATCAATGCG
guaA seq R	AAATTCAAATTCAAATACCC
guaA int F	ATTGCGCGATTGAAAACGGC
guaA int R	TTGATCACTTTTGAAGGCC
guaB-P1a	TTGATGGGGTTCGTTACGGG
guaB-P2a	<u>ATCCACTTTTCAATCTATATCAAACGCTGGACTTTCTAGGC</u>
guaB-P3a	<u>CCCAGTTTGTGCGACTGATAATAGAAATCACTAGCGCGGGG</u>
guaB-P4a	GCTCCAGCTAGCCGTAGGGG
guaB-seqF	GCCTTGAAAGAAATGGGGC
guaB-seqR	GCGAGATGATCTCAATAGGG
guaB int - F	TTTGAGTAAAAAAGTGGGCG
guaB int - R	TCATCACGCTTGATGCCCC
guaBF+rdx5'	<u>CGGTCATTACATGCAAAATCATTGTTGTCTTAAGCAGTGGG</u>
guaBR+kamF	<u>TTGGCGTATAACATAGTATCGTGAAAAAGTTTCTCTAAGCC</u>
P1 guaC	TTATTACCTATCAAAACCGC
P2 guaC	<u>ATCCACTTTTCAATCTATATCCGTATCGCACTCTGAACGGC</u>
P3 guaC	<u>CCCAGTTTGTGCGACTGATAACAATCTCCTATGCAGGCGGG</u>
P4 guaC	ACAAGTAGAAGCGTTAGGGG
guaC seq - F	ATCGCTCAAATCGCCTTCGG
guaC seq - R	AAAGGAAAGGTTTGAGCGCG
guaC int - F	ATGCAAACAATCATCAACCG
guaC int - R	AGCGTGTCTTTAATGAGCC
guaCF+rdx5'	<u>CGGTCATTACATGCAAAATCAAAGCGTATTGATCTTGCCC</u>
guaCR+kamF	<u>TTGGCGTATAACATAGTATCGAACCATTCTTTCTGCTTCGC</u>
purA - P1	TCTTAGCAGCGCTGTTAAGG
purA - P2	<u>ATCCACTTTTCAATCTATATCACAATTTTCCCTTTCCCCTC</u>
purA - P3	<u>CCCAGTTTGTGCGACTGATAATATTGAAAAAGAAGTGGGGG</u>
purA - P4	TTCTACGCATGCAAGCCCC
purA seq F	GCTTTGGCATTCAAGTGGGC
purA seq R	CATTGCAACAATTCTTGCGC
purA int - F	TACCATTGTGCATAAGGGGG
purA int - R	GAGTAGGCTTTCGTGATGCC
purB- P1	TATCATGGCAAGCCATGGGG
purB - P2	<u>ATCCACTTTTCAATCTATATCGTTTGCTCATTCCATAGGGC</u>
purB - P3	<u>CCCAGTTTGTGCGACTGATAATTACACTAAAAATGTGGGGG</u>
purB - P4	TTGGCCATAAAGAGAGGCGC
purB seq F	GGCTCTACGCCATTAGGGGC
purB seq R	ATCCCAGATTGAACCCGGC
purB int - F	GATTGTGAAAAAATCTGCGC
purB int - R	TATTCTCGCTCAATATGGGG
purD - P1	AGTCTCTACGCATTTGGTGG
purD - P2	<u>ATCCACTTTTCAATCTATATCTGAGCCAAAGCATACTCTCG</u>

purD - P3 CCCAGTTTGTGCGCACTGATAATTGAAGGCATGTTTTATCGC
 purD - P4 TAAATAGCCCTACTGGGGC
 purD seq F CTTTTTGATGAGCCGG
 purD seq R CTACAAACCATAAAAAGGGG
 purD int - F TGGCACTCAAGATTTAGGCG
 purD int - R AGAAAAAGTTTGCAGGAGCG
 surE - P1 TTTTAAGCGCTAATGGGGGG
 surE - P2 ATCCACTTTTTCAATCTATATCATGCCTTTTGCATGGTAGCC
 surE - P3 CCCAGTTTGTGCGCACTGATAAAAACCATGCCTCTATCACGC
 surE - P4 AGCGTAATAATCCGTAGGGG
 surE seq - F AAACGCTTTATTAGAAAGCC
 surE seq - R AAAATTTGCTCGCTAAAGCC
 surE int - F AAATCTATGTGGTCGCCCG
 surE int - R GTCTGTCTTCATTTTCGCGC
 gpt - P1 AACACCACAAGCTACACCGC
 gpt - P2 ATCCACTTTTTCAATCTATATCTTGTGGTACTAATTCCAAGC
 gpt - P3 CCCAGTTTGTGCGCACTGATAAATGGATTGATTTCTTTGGG
 gpt - P4 GAGCATTTTTGGTTACAGCC
 gpt seq F TTGGAGGGAGTCAAAAAGCG
 gpt seq R ATGAGCTAGAATCTTGAGCG
 gpt int - F GTGTGCGTGATGCGAGGGGG
 gpt int - R ATCGGCTTTGTATTTTCGCGC
 apt - P1 ACAGAATTTGAACAAGGCCG
 apt - P2 ATCCACTTTTTCAATCTATATCGTCTTTCATTCTCTGATGC
 apt - P3 CCCAGTTTGTGCGCACTGATAATCCAACCTTTTAGAAGAACGC
 apt - P4 TCTTCTCCTAAATACCACGC
 apt - seq F CTAATGTCTTGTGCTTGGGC
 apt - seq R GTAATATTAGCGCATAAGGG
 apt - int F ATCAAAGATATTACCACGC
 apt - int R TATGCATTGAGCTTGTAGGG
 apt-F + rdx5' CGGTCATTACATGCAAAATCACAGAATTTGAACAAGGCCG
 apt-R + kan F TTGGCGTATAACATAGTATCGTATTCTTCCAAAATTCACCC
 deoD - P1 ATATTTACGCCCATGTGGGG
 deoD - P2 ATCCACTTTTTCAATCTATATCATTGAGGATAAAAATCGCCG
 deoD - P3 CCCAGTTTGTGCGCACTGATAACTTAAGCCCTAAAGAAAGGG
 deoD - P4 GCATGCAAGAGTGATGCCCG
 deoD seq - F CATTGAAGAAAAGCAAGGCG
 deoD seq - R CTTACCGATTTGATAACCC
 deoD int - F ATGCGGCGATCCCTTAAGGG
 deoD int - R GATTAAGTGATCCGAAACCG
 deoD- P2(Kan) TTGGCGTATAACATAGTATCGATTGAGGATAAAAATCGCCG
 deoD- P3(Kan) TAGTACCTAGATTTAGATGTCCTTAAGCCCTAAAGAAAGGG
 apt - P2(Kan) TTGGCGTATAACATAGTATCGGTCTTTCATTCTCTGATGC
 apt - P3(Kan) TAGTACCTAGATTTAGATGTCCTCAACTTTTAGAAGAACGC
 surE - P2(Kan) TTGGCGTATAACATAGTATCGATGCCTTTTGCATGGTAGCC
 surE - P3(Kan) TAGTACCTAGATTTAGATGTCAAACCATGCCTCTATCACGC
 RDX5`F TGGTAGTTGTTTCGTTAGGG
 RDX5`R GATTTTGCATGTAATGACCG
 RDX3`F+kamR TAGTACCTAGATTTAGATGTCGCTCAAATGCTTGGCG
 RDX3`R CACAACCAAGTAATCGCATC
 KAMF-E1 CGATACTATGTTATACGCCAA
 KAMR-E2 GACATCTAAATCTAGGTACTA
 Hp gptF+ rdx5' CGGTCATTACATGCAAAATCAACACCACAAGCTACACCGC
 Hp gptR+ kanF TTGGCGTATAACATAGTATCGACATCACCTCTGAATCCACC

Ec gptR + kanf	<u>TTGGCGTATAACATAGTATCG</u> TTAGCGACCGGAGATTGGCG
Ec hptR + kanf	<u>TTGGCGTATAACATAGTATCG</u> T TACTCGTCCAGCAGAATCA
E.c. gpt F	ATGAGCGAAAAATACATCGT
E.c. gpt R	TTAGCGACCGGAGATTGGCG
E.c. hpt F	ATGGTTAGAGATATGAAACA
E.c. hpt R	T TACTCGTCCAGCAGAATCA
rdxA_P1.1	GAGTTATTTTTTATGGGCGG
rdxA_P4.1	TCTCAAGCCTTAATCGATCG
rdxA seq F	AGCCAGATAGCCAAATGGGG
rdxA seq R	GAAACGCTTGAAAACACCCC



48 hour 2mL cultures from 12 well plates:
2 μ l spotted



1,2, RnP + catalase
3,4, RnP + hypoxanthine
5,6, RnP + xanthine
7,8, RnP + guanine
9,10, RnP + adenine

purD

E.coli_K12 MK-----VLVIGNGGEEHALAWKAAQSPLVETVVFVAPGNAGTALEPALQ
 C.jejuni_NCTC11168 MK-----IMILGSGAEEYSIALALRRVVDKNLEFYFAPGNNGATES--LGT
 H.pylori_G27 MKDNNNYYNVLIVGNKGEYALAQRLQQDERVNALYFCLNGGGTQD--LGE
 ** : : : : : . * : : : : : : : : : : * : : *

N Domain

E.coli_K12 NVAIGVTDIPALLDFAQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGP
 C.jejuni_NCTC11168 N--LNLKDPVVLATYAKEKGFDLICIVGSESFLEAGVVDFIFKQQGLAIFGP
 H.pylori_G27 N--LECEHYEHIVELALKKQIHLAIISEBELLVGLTEMLEKAGILVFGA
 * : : : : : : : : : : * : : : : * * * * * * * * * : : : * : *

B' Domain

E.coli_K12 TAGAAQLEGSVAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVI
 C.jejuni_NCTC11168 SKAAAMLETSVFMKSFLLKRYRIKTKPLNTNDIEKAKNFYISLTPPIIV
 H.pylori_G27 SKAAAKLEASVSYMKAFVKECGEKSIVSYFETNDLKEALNHIIQNASPFLVI
 : * * * * : : : * * : . * : * : : : : : : : * : . : . * : : :

B Domain

E.coli_K12 MADGLASAKGVIVAMTLEEAEEAVHDMLAGNAFGDAGHRIVIVKFDLGEV
 C.jejuni_NCTC11168 MADGLCAGKGVIIAKTHEEAIEETAKMLSGESFGDAGKLVVIVKFDLGEV
 H.pylori_G27 MAL----NNTSIVHQEEEAIK-----ILEDAFKQSNPEVIIKFDLGEV
 ** : : * * : : : * * * : : : : : : : * : : * : : : : * * * * *

E.coli_K12 ASFIVMVDGEHVLPMASTQVHVRVGDKDTGPIVGGMGAYSPAPVVTDVH
 C.jejuni_NCTC11168 LSIFAVCDGNDFVLLPAACVHKLDDNDQGPVGGMGAYAPSSLANESLL
 H.pylori_G27 LSVTALIANDDFILLPFCQNYRLEEGDNGVIVGGMGAIAPANFFSNELE
 * . : : : . : : : : . * : : : : : * * * * * * * * * : : : * : :

A Domain

E.coli_K12 QRTMERIIWPTVKGMAAEGNTYTGFLYAGLVLDKQG---NPKVIKFNCRF
 C.jejuni_NCTC11168 RKVQKDIILPTLAGMKKEGAEFCGVLFIGAVVGN----KPYVIVFNVRF
 H.pylori_G27 EKIKNHIFKPTLEKLDQADNTPFKGVLLAEIVIIIEKGVLEPYLIDFSVRF
 . : : * : * * : : : . : . : * * : * : : * : : : : * * *

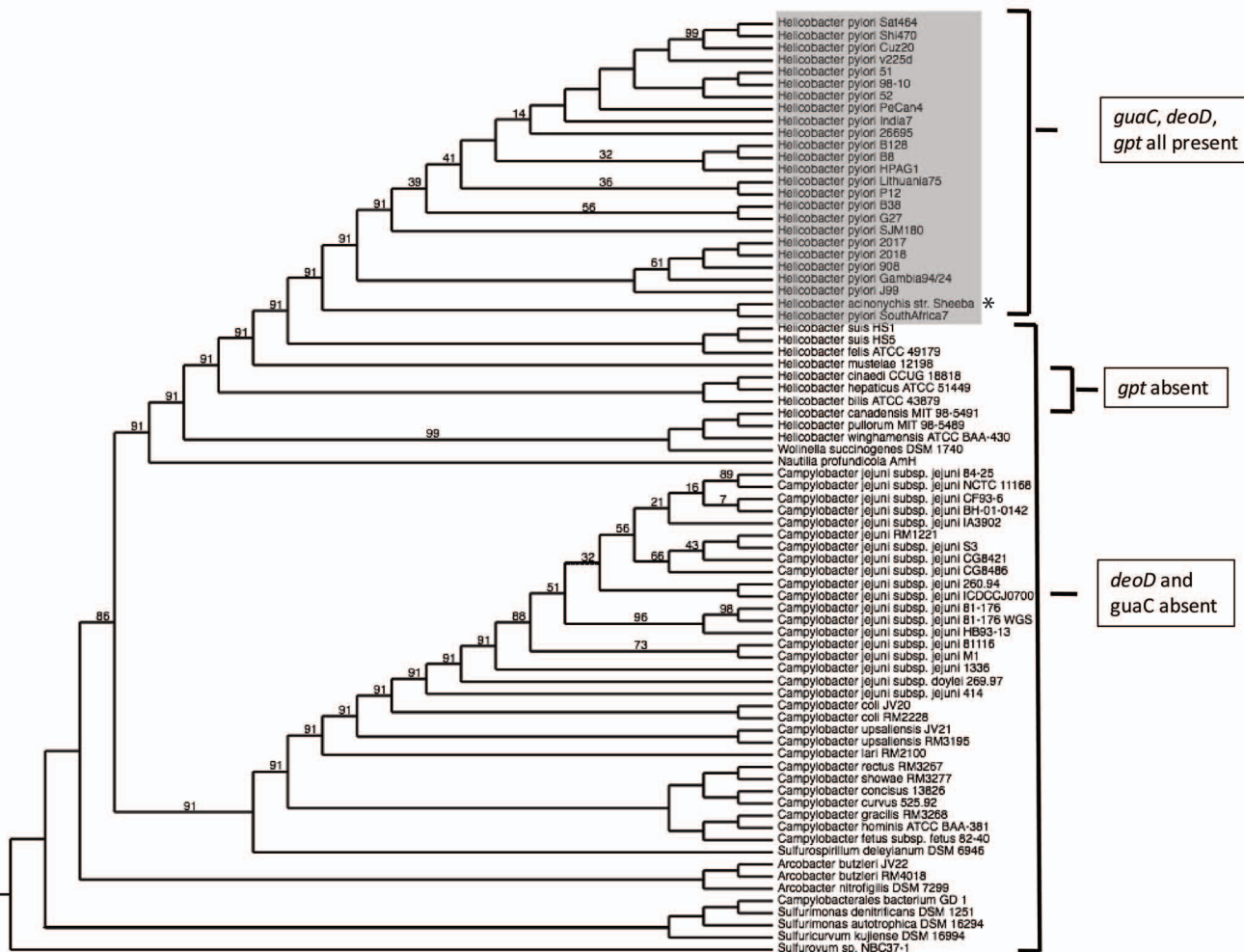
E.coli_K12 GDPEVQPIMLRMKSDLVELCLAACESKLDEKTSSEWDERASLGVVMAAGGY
 C.jejuni_NCTC11168 GDPECEVLMPLIE-DPLELILAATQRRLRHSKIKIKKEFVAVGVVCASENY
 H.pylori_G27 KDIECQTILPLESLLDLCLATAKGEINSLVLSFVMSVALVSRNY
 * * * : : : : : . * * * * : : * * . : . : . * * : : *

C Domain

E.coli_K12 PGDYRTGDVVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGIVLVCVTALG
 C.jejuni_NCTC11168 PYKSSPKSEITVNNIPEN-S-HISYAGVSL-EDGKLMADGGIVLVCVGTG
 H.pylori_G27 PTSSSPKQTLYIDPVDEKKG-HLLLGEVEQ-DNGVFESSGGIVIFALGRG
 * . . . : : : * . : : : . . . : : . : : * * * * : *

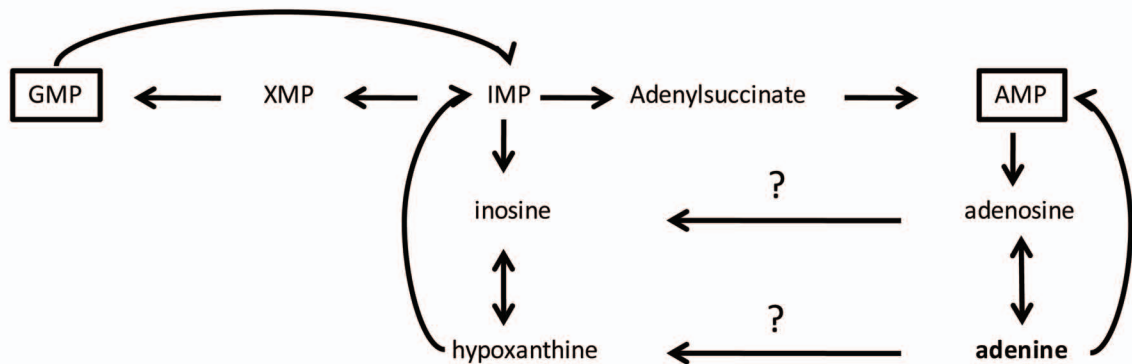
E.coli_K12 HTVAEAQKRAYALMTDIHWDDCFCRCKDIGWRAIE-REQN
 C.jejuni_NCTC11168 KSIEEAQKNAYKLCDNVNPKGKQYRKDIAHQVL-----K
 H.pylori_G27 KSLLEARNHAYEIAQKVHFEQMPYRKDIGFKVLDLKEYS
 : : : * : : : * * : : : : : : * * * * : : : *

Figure S2

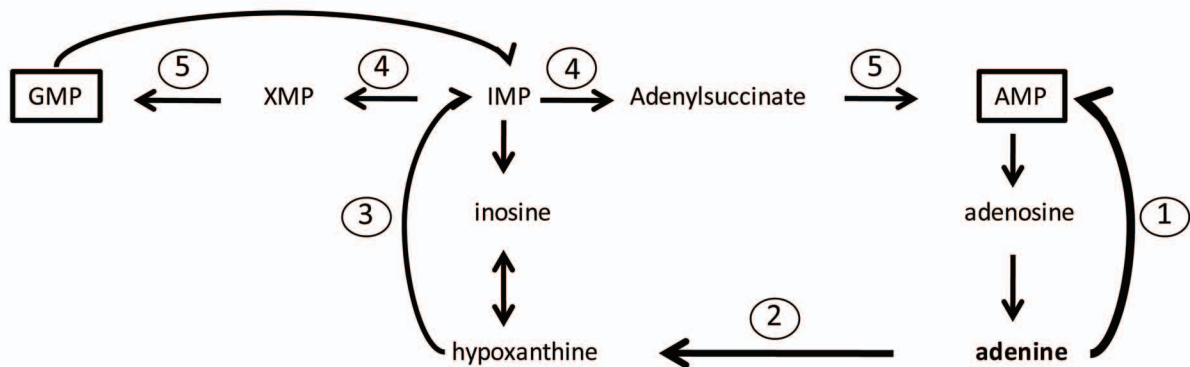


* indicates absence of *guaC* in *H. acinonychis*

A



B



C

