Supplemental Figure Legends

FIG S1. Confirmation of mutant survival and growth. Following Ham's F12 survival and RnP growth assays, 2 μl 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 mulit-gene phylogentic 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.

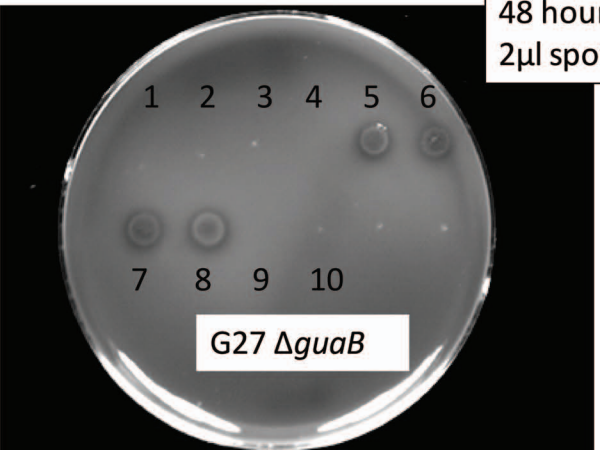
FIG S4. Alternate potential metabolic pathways by which *H. pylori* is capable of generating GMP and AMP from the single purine source, adenine. **(A)** Base pathway for adenine processing. Pathway thermodynamics assuming **(B)** strong APRTase activity coupled with an adenine deaminase and **(C)** weak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

TABLE S1. Primers used in this study.

Primer	sequence
guaA P1	GTTTGAAATGTTGCGTGGGG
guaA P2	ATCCACTTTTCAATCTATATCAATCAGCTGTGTGTATTGGC
guaA P3	CCCAGTTTGTCGCACTGATAAAGTGAGCGGTATCAATAGGG
guaA P4	CAATATCTTCTAAGATAGCC
guaA seq F	TATAATACCCAATCAATGCG
guaA seq R	AAATTCAAATTCAAATACCC
guaA int F	ATTGCGCGATTGAAAACGGC
guaA int R	TTGATCACTTTTGAAGGCCC
guaB-P1a	TTGATGGGGTTCGTTACGGG
guaB-P2a	ATCCACTTTTCAATCTATATCAAACGCTGGACTTTCTAGGC
guaB-P3a	CCCAGTTTGTCGCACTGATAATAGAAATCACTAGCGCGGGG
guaB-P4a	GCTCCAGCTAGCCGTAGGGG
guaB-seqF	GCCTTGAAAGAAATGGGGC
guaB-seqR	GCGAGATGATCTCAATAGGG
guaB int - F	TTTGAGTAAAAAAGTGGGCG
guaB int - R	TCATCACGCTTGATGCCCCC
guaBF+rdx5`	CGGTCATTACATGCAAAATCATTTTGTCTTAAGCAGTGGG
guaBR+kamF	TTGGCGTATAACATAGTATCGTGAAAAAGTTTCTCTAAGCC
P1 guaC	TTATTACCTATCAAAACCGC
P2 guaC	ATCCACTTTTCAATCTATATCCGTATCGCACTCTGAACGGC
P3 guaC	CCCAGTTTGTCGCACTGATAACAATCTCCTATGCAGGCGGG
P4 guaC	ACAAGTAGAAGCGTTAGGGG
guaC seq - F	ATCGCTCAAATCGCCTTCGG
guaC seq - R	AAAGGAAAGGTTTGAGCGCG
guaC int - F	ATGCAAACAATCATCAACCG
guaC int - R	AGCGTGTCTTTTAATGAGCC
guaCF+rdx5`	CGGTCATTACATGCAAAATCAAAGCGTATTGATCTTGCCC
guaCR+kamF	TTGGCGTATAACATAGTATCGAACCATTCTTTCTGCTTCGC
purA - P1	TCTTAGCAGCGCTGTTAAGG
purA - P2	ATCCACTTTTCAATCTATATCACAATTTTTCCTTTCCCCTC
purA - P3	CCCAGTTTGTCGCACTGATAATATTGAAAAAGAAGTGGGGG
purA - P4	TTCTACGCATGCAAGCCCCC
purA seq F	GCTTTGGCATTCAAGTGGGC
purA seq R	CATTGCAACAATTCTTGCGC
purA int - F	TACCATTGTGCATAAGGGGG
purA int - R	GAGTAGGCTTTCGTGATGCC
purB- P1	TATCATGGCAAGCCATGGGG
purB - P2	ATCCACTTTTCAATCTATATCGTTTGCTCATTCCATAGGGC
purB - P3	CCCAGTTTGTCGCACTGATAATTACACTAAAAATGTGGGGG
purB - P4	TTGGCCATAAAGAGAGGCGC
purB seq F	GGCTCTACGCCATTAGGGGC
purB seq R	ATCCCCAGATTGAACCCGGC
purB int - F	GATTGTGAAAAAATCTGCGC
purB int - R	TATTCTCGCTCAATATGGGG
purD - P1	AGTCTCTACGCATTTGGTGG
purD - P2	ATCCACTTTTCAATCTATATCTGAGCCAAAGCATACTCTCG

purD - P3	CCCAGTTTGTCGCACTGATAATTGAAGGCATGTTTTATCGC
purD - P4	TAAAATAGCCCTACTGGGGC
purD seq F	CTTTTTGATGAGCCGG
purD seq R	CTACAAACCATAAAAAGGGG
purD int - F	TGGCACTCAAGATTTAGGCG
purD int - R	AGAAAAAGTTTGCAGGAGCG
surE - P1	TTTTAAGCGCTAATGGGGGG
surE - P2	ATCCACTTTTCAATCTATATCATGCCTTTTGCATGGTAGCC
surE - P3	CCCAGTTTGTCGCACTGATAAAAACCATGCCTCTATCACGC
surE - P4	AGCGTAATAATCCGTAGGGG
surE seq - F	AAACGCTTTATTAGAAAGCC
surE seq - R	AAAATTTGCTCGCTAAAGCC
surE int - F	AAATCTATGTGGTCGCCCCC
surE int - R	GTCTGTCTTCATTTTCGCGC
gpt - P1	AACACCACAAGCTACACCGC
gpt - P2	ATCCACTTTTCAATCTATATCTTGTTTGACTAATTCCAAGC
gpt - P3	CCCAGTTTGTCGCACTGATAAATGGATTGATTTCTTTTGGG
gpt - P4	GAGCATTTTTGGTTACAGCC
gpt seq F	TTGGAGGGAGTCAAAAAGCG
gpt seq R	ATGAGCTAGAATCTTGAGCG
gpt int - F	GTGTGCGTGATGCGAGGGGG
gpt int - R	ATCGGCTTTGTATTTCGCGC
apt - P1	ACAGAATTTGAACAAGGCCG
apt - P2	ATCCACTTTTCAATCTATATCGTCTTTCACTTCTCTGATGC
apt - P3	CCCAGTTTGTCGCACTGATAATCCAACTTTTAGAAGAACGC
apt - P4	TCTTCTCCTAAATACCACGC
apt - seq F	CTAATGTCTTGTGCTTGGGC
apt - seq R	GTAATATTAGCGCATAAGGG
apt - int F	ATTCAAAGATATTACCACGC
apt - int R	TATGCATTCAGCTTGTAGGG
apt-F + rdx5'	CGGTCATTACATGCAAAATCACAGAATTTGAACAAGGCCG
apt-R + kan F	TTGGCGTATAACATAGTATCGTATTCTTCCAAAATTCACCC
deoD - P1	ATATTTACGCCCATGTGGGG
deoD - P2	ATCCACTTTTCAATCTATATCATTGAGGATAAAAATCGCCG
deoD - P3	CCCAGTTTGTCGCACTGATAACTTAAGCCCTAAAGAAAGGG
deoD - P4	GCATGCAAGAGTGATGCCGC
deoD seq - F	CATTGAAGAAAAGCAAGGCG
deoD seq - R	CTTCACCGATTTGATAACCC
deoD int - F	ATGCGGCGATCCCTTAAGGG
deoD int - R	GATTAAGTGATCCGAAACCG
deoD- P2(Kan)	TTGGCGTATAACATAGTATCGATTGAGGATAAAAATCGCCG
deoD- P3(Kan)	TAGTACCTAGATTTAGATGTCCTTAAGCCCTAAAGAAAGGG
apt - P2(Kan)	TTGGCGTATAACATAGTATCGGTCTTTCACTTCTCTGATGC
apt - P3(Kan)	TAGTACCTAGATTTAGATGTCTCCAACTTTTAGAAGAACGC
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	TTGGCGTATAACATAGTATCGTTAGCGACCGGAGATTGGCG
Ec hptR + kanf	TTGGCGTATAACATAGTATCGTTACTCGTCCAGCAGAATCA
E.c. gpt F	ATGAGCGAAAAATACATCGT
E.c. gpt R	TTAGCGACCGGAGATTGGCG
E.c. hpt F	ATGGTTAGAGATATGAAACA
E.c. hpt R	TTACTCGTCCAGCAGAATCA
rdxA_P1.1	GAGTTATTTTTTATGGGCGG
rdxA_P4.1	TCTCAAGCCTTAATCGATCG
rdxA seq F	AGCCAGATAGCCAAATGGGG
rdxA seq R	GAAACGCTTGAAAACACCCC



48 hour 2mL cultures from 12 well plates:
2µl spotted

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

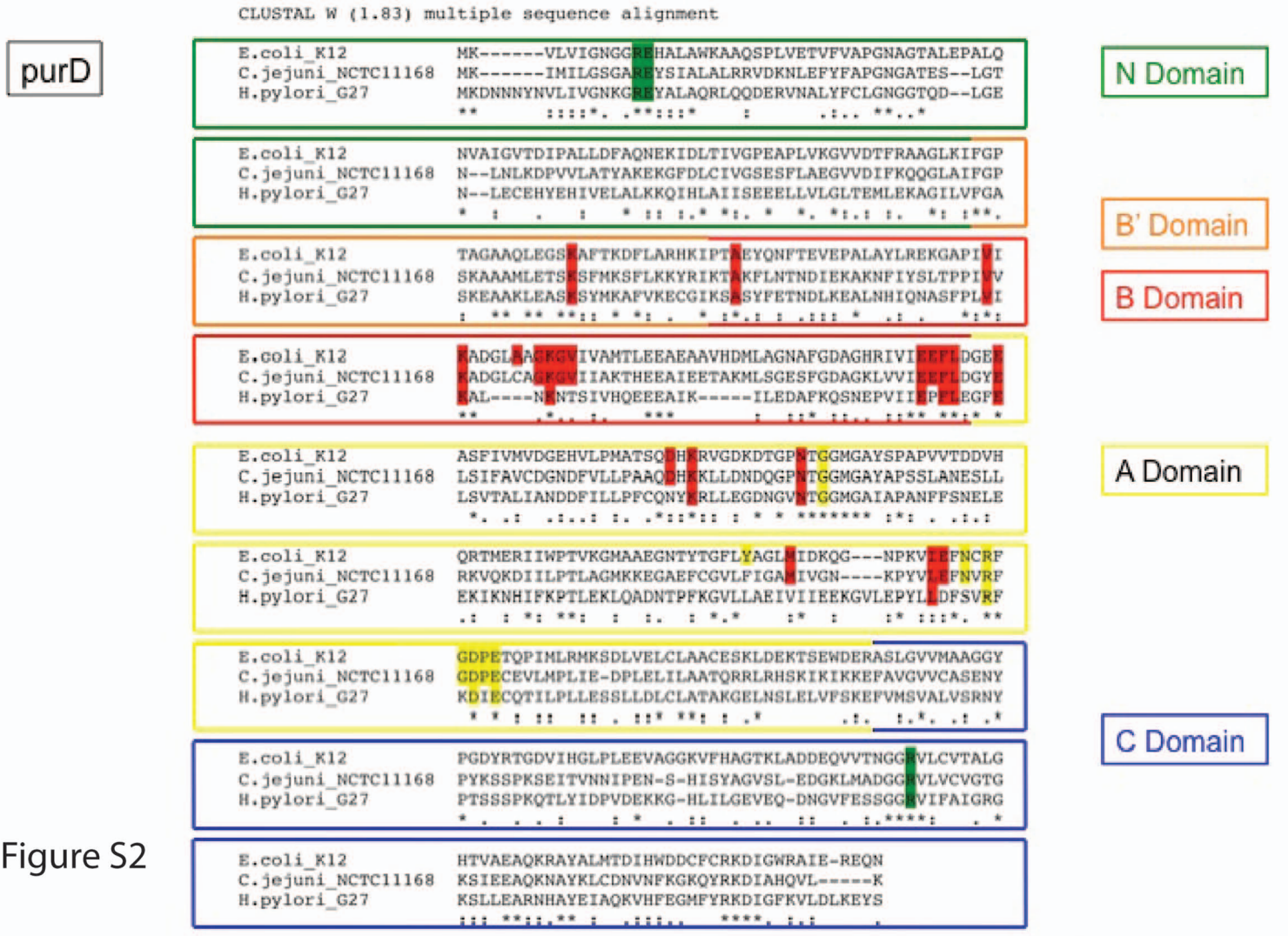
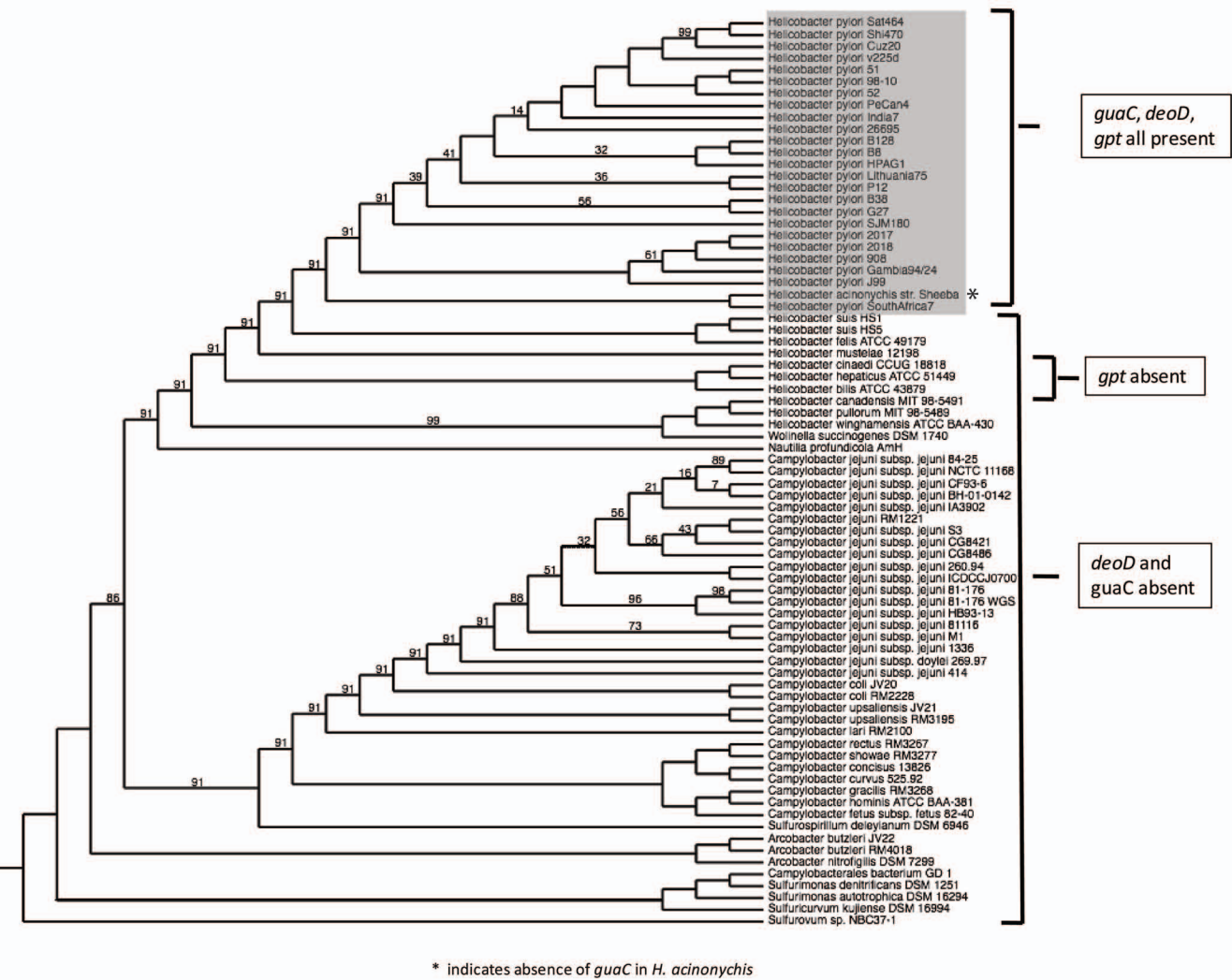
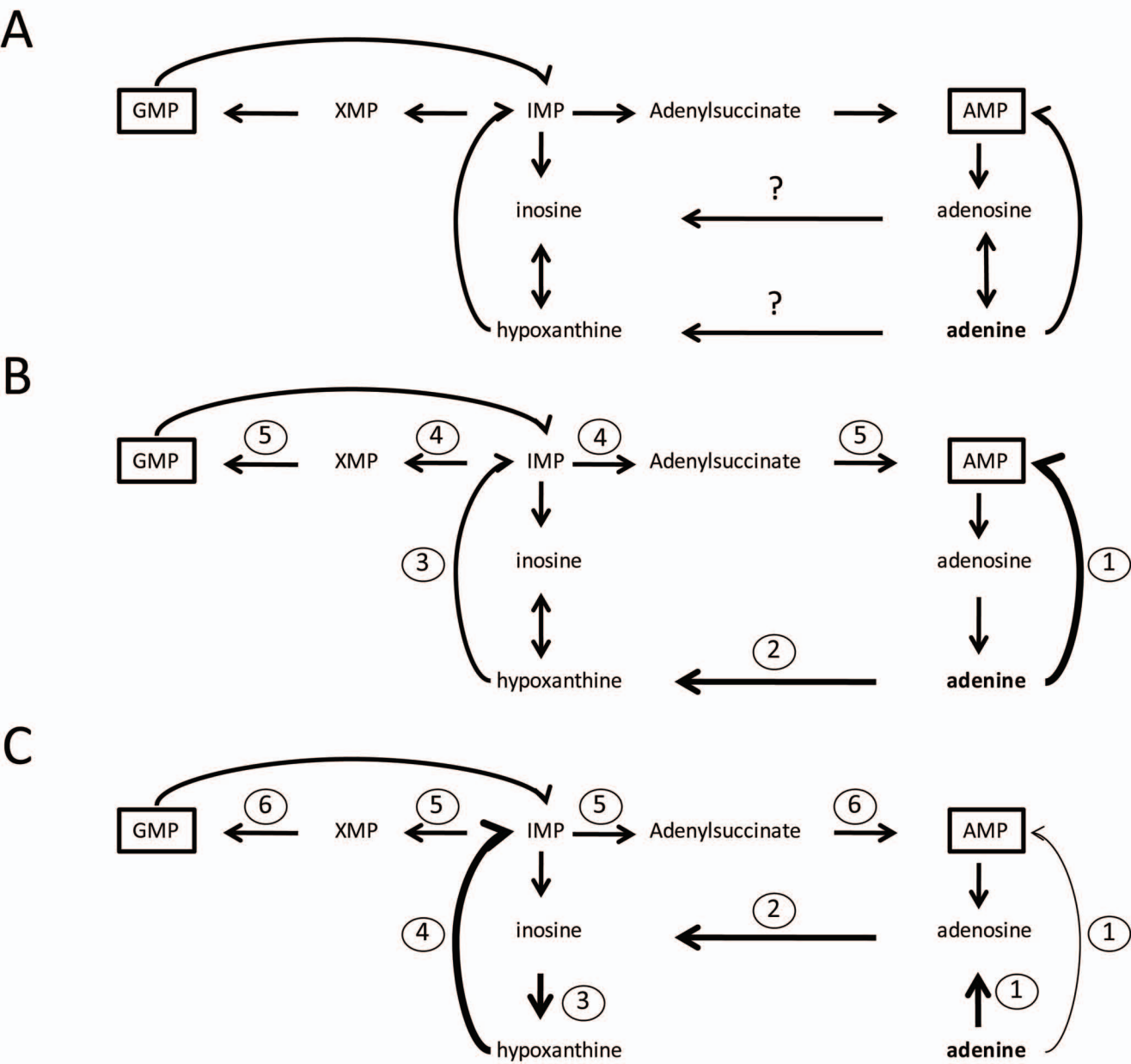


Figure S2

figure adapted from ; Sampei *et al.* 2010



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


A
GMP
XMP
IMP
Adenylsuccinate
AMP
inosine
adenosine
hypoxanthine
adenine
?
?
B
GMP
XMP
IMP
Adenylsuccinate
AMP
inosine
adenosine
hypoxanthine
adenine
5
4
4
5
3
1
2
C
GMP
XMP
IMP
Adenylsuccinate
AMP
inosine
adenosine
hypoxanthine
adenine
6
5
5
6
4
2
1
3
1