Table 4. Top 20 PHX genes from genomes of G^{+}_{low} bacteria

Gene	*E*(*g*)*									
	BACSU	BACHA	LISIN	LISMO	LACLA	STRPY	STRPN	STAAU	CLOAC	CLOPE
RPs										
RP L1 (rplA)	1.91	1.55	2.05	2.03	2.00	1.95	2.11	2.12	1.18	1.71
RP L2 (rplB)	2.02	1.69	1.92	1.85	2.09	2.16	2.33	1.70	1.40	1.52
RP L3 (rplC)	1.78	1.60	1.44	1.42	1.71	1.73	1.87	1.59	1.30	1.85
RP L4 (rplD)	1.98	1.67	1.69	1.73	1.70	1.71	1.91	1.46	1.23	1.24
RP L5 (rplE)	1.92	1.35	1.34	1.36	1.79	1.69	2.17	1.79	1.52	1.72
RP L6 (rplF)	1.68	1.43	1.55	1.42	1,83	2.09	2.15	1.76	1.12	1.73
RP L13 (rplM)	1.91	1.39	1.75	1.77	1.95	1.67	1.91	1.87	1.33	1.47
RP L14 (rplN)	1.98	1.43	1.30	1.37	1.51	1.69	1.89	1.70	1.08	1.24
RP L15 (rplO)	1.83	1.58	1.78	1.52	2.05	1.31	2.13	1.44	1.09	1.70
RP L16 (rplP)	1.90	1.49	1.66	1.68	1.67	1.85	1.89	1.42	1.09	1.43
RP L17 (rplQ)	1.87	1.51	1.69	1.72	2.31	—	1.83	2.03	1.18	1.23
RP L19 (rplS)	1.84	1.62	1.54	1.60	1.90	1.76	1.99	1.71	1.38	1.55
RP L20 (rplT)	1.57	1.54	1.38	1.42	1.57	1.72	2.15	1.80	1.24	1.96
RP S1 (rpsA)	1.20	(1.01)	(0.90)	1.17	2.14	2.32	2.31	(0.80)	(0.74)	(0.76)
RP S2 (rpsB)	1.84	1.47	1.72	1.67	2.37	2.03	2.30	2.09	1.33	1.58
RP S3 (rpsC)	1.87	1.48	1.69	1.70	2.17	1.96	2.10	1.83	1.21	1.99
RP S4 (rpsD)	1.94	1.61	1.84	1.82	2.09	2.12	2.33	2.11	1.19	1.67
RP S5 (rpsE)	1.89	1.35	1.61	1.52	1.82	1.97	1.86	2.01	1.30	1.51
RP S6 (rpsF)	1.67	1.36	1.39	1.50	1.82	2.00	1.78	1.86	(1.06)	1.54
RP S7 (rpsG)	1.73	1.45	1.49	1.49	1.98	1.95	2.12	1.63	1.30	1.27
RP S8 (rpsH)	1.51	1.47	1.28	1.21	2.07	1.56	2.09	1.60	1.19	1.51
RP S9 (rpsI)	1.51	1.53	1.86	1.87	1.52	1.92	1.87	2.36	1.42	1.46
RP S12 (rpsL)	1.84	1.51	1.38	1.39	1.73	1.68	2.11	1.67	1.20	1.29
RP S13 (rpsM)	2.02	1.38	1.93	1.86	1.59	1.72	1.95	1.86	1.27	1.23
TFs										
Translation elongation factor G (fus)	2.34	1.77	2.34	2.31	2.46	2.16	2.47	2.64	1.45	2.08
Translation elongation factor Ts (tsf)	1.75	1.44	1.98	2.33	1.41	1.87	2.35	2.11	1.31	1.62
Translation elongation factor Tu (tuf)	1.97	1.50	2.00	1.92	1.91	1.96	2.06	2.09	1.14	1.42 1.42
Translation initiation factor IF-2 (infB)	(0.79)	(0.77)	1.06	1.23	1.65	(0.56)	1.04	1.00	(1.04)	2.04
RNA polymerase β-subunit (rpoB)	1.49	1.19	2.37	2.19	1.87	1.72	1.83	1.67	(0.98)	1.62
RNA polymerase β'-subunit (rpoC)	1.76	1.54	2.39	2.26	2.02	1.72	1.77	1.55	1.19	1.53
GTP-binding protein TypA/BipA	1.11	(0.78)	1.91	2.09	1.95	1.46	1.98	(0.97)	1.18	1.45
Chaperones										
HSP 60 (groEL)	1.87	1.79	1.91	1.89	1.23	(0.86)	1.08	1.19	1.45	(0.71)
HSP70 (dnaK)	1.83	1.14	2.25	2.17	2.08	2.25	2.43	2.21	1.38	2.19
Trigger factor (tig)	1.85	1.53	2.02	1.81	1.86	1.55	2.55	2.02	1.42	1.60
Glycolysis										
Glucose-6-phosphate isomerase (pgi)	(0.92)	(0.93)	1.67	1.77	2.13	1.57	2.46	1.33	1.28	1.74
Fructose-1,6-bisphosphate aldolase (fba)	1.99 (0.59)	1.20 (0.83)	1.71 (0.67) (etc.)	1.70 (0.59) (etc.)	2.08	2.07	2.15	2.00	1.20 (0.86)	1.52 (0.71)
fructose-bisphosphate aldolase homolog (SAV2606)	—	—	—	—	—	—	—	1.95	—	—
Glyceraldehyde-3-phosphate dehydrogenase (gap)	1.80 (0.48)	1.53 (0.70)	1.77	1.72	1.95 1.04	2.13	2.08	2.12 (0.69)	1.27	1.48
Phosphoglycerate kinase (pgk)	1.34	1.09	2.08	2.02	2.30	2.18	2.24	1.86	1.34	1.65
Phosphoglycerate mutase (gpmA)	(0.70)	—	(0.93)	(1.04)	2.27	1.88	1.94	(0.79)	(0.95)	—
Phosphoglycerate mutase (2,3-bisphosphoglycerate-independent) (pgm)	1.08	(0.88)	1.97	1.98	—	—	—	1.15	1.29	1.80
Enolase (eno)	1.92	1.61	1.83	1.92	1.96 (0.49)	2.17	2.24	2.12	1.26	1.51

Gene	$E(g)$*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
Pyruvate kinase (pykA)	1.18	(0.76)	2.38	2.17	2.25	2.04	2.28	1.70	1.29 1.29	1.68 (0.83)
PTS enzymes										
Phosphotransferase enzyme IIC component (cellobiose-specific)	(0.57) (0.46) (0.45)	(0.57)	2.06 1.16 (etc.)	2.05 1.32 (etc.)	1.32 1.10 (0.47)	(0.55)	(1.01)† (0.60) (0.49)	—	1.24	—
Phosphotransferase system component IID (mannose-specific) (manN)	—	—	1.26 1.23	1.47 1.09	1.85	2.15	1.54	—	—	1.27 1.04
PTS system, IIABC components‡	—	—	—	—	—	(0.60)	2.43	—	—	(0.80)
PTS system, phosphoenolpyruvate-protein phosphotransferase (ptsI, ptsA)	1.35	(0.94)	1.13	1.22	2.07	1.96	2.31	1.25	1.33	1.78
mannose-specific PTS system component IIC (ptnC, manM)	(0.55)	—	1.23 1.20	1.28 1.16	1.98	1.91	1.60	1.91	—	1.06
Pyruvate dehydrogenase, pyruvate oxidase										
pyruvate dehydrogenase E1 β-subunit (pdhB)	1.91	1.31	1.72	1.75	1.06	—	—	1.81	—	—
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (pdhC)	2.05	1.48	1.79	1.81	(0.94)	—	—	1.43	—	—
Dihydrolipoamide dehydrogenase E3 subunit of pyruvate dehydrogenase (pdhD)	2.14	1.55	1.98	1.80	1.09	—	—	2.05	—	—
Pyruvate oxidase	(0.47)	—	(0.86)	1.03	(0.47)	—	2.48	(0.66)	—	—
Fermentation and anaerobic respiration										
Pyruvate formate-lyase (formate acetyltransferase) (pflB, pflA)	—	—	2.40 1.98	2.49 2.09	1.78	2.32	2.87	2.09	(0.98)	1.92
L-lactate dehydrogenase (ldh)	(0.76)	(0.69)	1.63	1.53	2.26 (0.45) (0.44)	1.72	2.30	(0.90) (0.88)	(0.94) (0.80)	(0.78)
Alcohol-acetaldehyde dehydrogenase (adhE)	—	—	2.08	2.14	1.44	—	2.22	(0.56)	—	2.00
Beta-hydroxybutyryl-CoA dehydrogenase, NAD-dependent (CAC2708)	(0.52)	(0.81) (0.71) (0.68)	—	—	—	—	—	—	1.44	1.55
Butyryl-CoA dehydrogenase (CAC2711)	(0.56) (0.48) (0.41)	(0.66) (0.63) (0.62)	—	—	—	—	—	—	1.44	1.70 (0.66)
Pyruvate ferredoxin oxidoreductase (CAC2229, CPE2061)	—	—	(0.51)	(0.45)	(0.40)	—	—	—	1.43 1.07	2.05
Putative NADH dehydrogenase (yjlD, ndh, nox))	1.87 (0.42)	1.07	2.02 (0.92)	1.76 1.09	1.29 (0.66)	—	—	1.87	—	—
NADH oxidase (nox)	—	—	—	—	(0.35)	1.46	2.36	—	—	—
Electron transfer flavoprotein alpha-subunit (etfA, fixB)	(0.59)	(0.67)	—	—	—	—	—	—	1.37 (0.98)	1.12 (0.56)
Use of alternative carbon sources										
Tagatose 1,6-diphosphate aldolase (lacD)	—	—	1.22	1.20	—	(1.05) (0.51)	1.85	1.93	—	—
Altronate oxidoreductase (yjmI)	(0.46)	(0.56)	—	—	—	—	—	—	1.36	—
Glucuronate isomerase (uxaC)	(0.38)	(0.69)	—	—	(0.28)	—	—	—	1.35	(0.45)
Detoxification										
Alkyl hydroperoxide reductase subunit C (ahpC)	1.66	—	—	—	(0.74)	1.27	—	2.02	—	(0.94)
Amino acyl-tRNA synthetases										
isoleucine-tRNA synthetase (ileS)	(0.78)	(0.63)	1.16	1.14	(0.97)	(0.65)	1.84	(0.92)	—	
isoleucine-tRNA synthetase (ileS)	—	—	—	—	—	—	—	—	1.02	1.89
asparagine-tRNA synthetase (asnS)	(0.83)	(0.53)	(1.00)	1.08	1.16	(1.05)	1.32	(0.96)	1.17	1.88
lysine-tRNA synthetase (lysS)	1.09	(0.59)	(1.07)	1.34	1.61	1.09	1.73	(0.75)	(0.93)	1.87
glycine-tRNA synthetase, class II (GRS1)	—	—	—	—	—	—	—	1.46	1.06	1.84
Amino acid biosynthesis										

Gene	*E*(*g*)*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
Ketol-acid reductoisomerase (ilvC)	1.03	1.59	1.16	1.27	(0.79)	—	2.11	(1.06)	1.04	—
Methionine synthase (metE)	(0.72)	(0.88)	(0.56)	(0.61)†	(0.44)	—	2.44	1.34	—	—
Nucleotide biosynthesis										
inositol-monophosphate dehydrogenase (guaB)	1.12	(0.73)	(0.90)	(0.87)	(0.92)	(0.99)	(0.98)	1.17	1.35	1.14
GMP synthetase (guaA)	1.31	(0.82)	1.20	1.14	1.62	1.17	1.59	1.28	1.05	1.79
Flagella										
Flagellin (flaA, hag)	1.83 1.69	1.43 (0.90)	2.04	2.09	—	—	—	—	1.36 (0.89) (0.80)	—
Transporters										
Permease of the Na+:galactoside symporter family (CAC0694, yjmB)	(0.46)	—	—	—	—	—	—	—	1.47	—
ABC-type dipeptide/oligopeptide/nickel transport system (oppA)	(0.75)	—	2.04	2.08	—	—	—	—	1.18	—
ABC transporter, substrate-binding protein (SP0092)	—	(0.63)	(0.83)	(0.82)	(0.68)	(0.80)	2.73	—	—	1.54
Oligonucleotide ABC transporter (BH0031)	—	1.78 (0.66) (etc.)	—	—	—	—	—	—	—	—
Oligopeptide ABC transporter (CAC3643)	(0.58) (0.49)	(0.76)	(0.69)	(0.75)	(0.69)	—	—	(0.51)	1.42 (1.06)	(0.65)
sugar ABC transporter (msmX, msmK)	(0.51)	1.23	1.95	1.94	1.21	(0.72)	2.40	(0.49)	(0.93)	1.35
Glycogen degradation										
Glycogen phosphorylase (glgP)	(0.39)	(0.52)	—	—	(0.42)	1.27	2.88	—	(0.90)	(0.57) (0.43)
Phosphoglucomutase	(0.54)	(0.64)	(0.44)	(0.56)	—	(0.84)	2.46	—	—	—
Other										
P60 extracellular protein, invasion-associated (iap)	—	—	2.16	1.76	—	—	—	—	—	—
Hypothetical protein (CPE1232)	—	—	—	—	—	—	—	—	1.35	2.00
Hypothetical protein (CPE1233)	—	—	—	—	—	—	—	—	1.30	1.90
Transcriptional pleiotropic regulator of transition state genes (abrB)	1.49	1.52	(0.90)	(0.71)	—	—	—	—	1.24 1.17 (1.03)	x
Conserved lipoprotein (lin2786, lmo2637)	—	—	1.91	1.92	—	—	—	—	—	—
Outer membrane lipoprotein (plp)	—	—	—	—	(0.62) (0.38)	(0.62)	2.38	—	—	—
Secretory antigen precursor SsaA homolog (ssaA)	—	—	—	—	—	—	—	2.03 1.19 (1.04)	—	—
Cellulase CelE ortholog, dockerin domain (CAC0561)	—	—	—	—	—	—	—	—	1.35	—
Probable manganase-dependent inorganic pyrophosphatase	1.47	—	(0.95)	1.18	1.57	(0.85)	1.64	1.24	1.18	1.84

Included are all genes ranking among the top 20 PHX genes in any of the eight genomes (underlined if among top 10) and their homologs in other genomes even if they are not among the top 20.

*Numbers in parentheses indicate the gene is not PHX; –, the gene does not have a homolog in the genome; etc., more than three homologs; x, PHX status not evaluated due to length <80 codons.

†PA gene.

‡All genomes have homologs of PTS system IIABC components but of lower similarity (≈30%). Those listed exhibit high mutual similarity (>50%).