Table 5. Glycolysis, PTS, mixed acid fermentation, TCA cycle, and detoxification genes

Gene	$E(g)$*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
Glycolysis										
Glucokinase (glk)[†]	(0.50)	(0.65)	(0.98)	(0.75)	1.30	(0.78)	1.50	(0.51)	(0.94)	1.17
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
6-phosphofructokinase (pfk)	(0.89)	(0.71)	1.09	1.07	1.76	1.43	1.78	(0.56)	(0.97)	1.60
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)
Triosephosphate isomerase (tpi)	1.48	(0.96)	1.61	1.68	1.92	1.59	1.93	1.73	1.21	1.60
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) (pmg)	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
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										
PTS system, IIA component (cellobiose-specific or lactose-specific)	(0.74) (0.61)	(0.81) (0.78)	1.15 1.11 etc	1.21 1.14 etc	(0.97)	(0.77) (0.69) (0.63)	(0.79) (0.73) etc	(0.72)	(0.98) (0.92)	(0.65)
PTS system, IIB component (cellobiose-specific)[‡]	(0.79) (0.61)	(0.75) (0.74)	1.08 (1.05) etc	1.12 1.06 etc	1.19	(0.86) (0.75)	(0.80) (0.78)	—	(1.04)	(0.64)
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	—
PTS system, IIABC component (trehalose-, sucrose-, or β-glucosides-specific)	(0.45) (0.44) (0.41)	(0.74) (0.72) etc	1.73 (0.81)	1.78 (0.77) etc	(0.65) (0.48)	(0.57) (0.43) (0.33)	1.84 (0.58) (0.47)	(0.50) (0.40)	1.20 1.04	(0.92) (0.58)
PTS system, IIA component (mannitol-specific)	—	(0.86)	—	—	(0.63)	—	(0.63)	(0.84)	1.05	—
PTS system, IIA component (mannitol/fructose-specific)	—	—	(0.71) (0.68) (0.64)	(0.75) (0.71) etc	—	—	(0.57)	—	1.11	—
PTS system, IIAB component (mannose-specific or fructose-specific)	(0.62)	—	1.36 (1.05) (0.73)	1.26 (1.10) (0.84)	1.45	1.67	1.17 1.14 (0.58)	—	—	(0.82) (0.71) (0.70)
PTS system, IIBC components (mannitol-specific)	(0.52)	(0.75)	(0.49)	(0.48)	—	—	(0.66)	(0.62)	1.15	—

Gene	*E*(*g*)*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
PTS system, IIC component (mannose-specific or fructose-specific)	(0.55)	—	1.23 1.20	1.28 1.16	1.98	1.91	1.60 (0.70)	—	—	1.06 (0.91)
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 (fructose-specific)	(0.87) (0.41)	1.04	(0.77) (0.76) etc	1.01 (0.81) etc	(0.75)	(0.73)	1.69 (0.79)	(0.84) (0.43)	1.16	(0.87)
PTS system, component IIA (glucose-specific)	(0.70)	—	(0.68)	(0.83)	(0.61)	—	—	(1.00)	(0.96) (0.90) (0.85)	1.12
PTS system, IIABC components (mostly glucose-specific or acetylglucosamine-specific)	(0.80) (0.45) (0.52)	1.29 (0.73) (0.74)	—	—	—	—	—	1.59 (0.86) (0.70)	1.20 1.19	(0.77) (0.69)
PTS system, IIB component (galactitol-specific)	(0.95)	—	1.16 (0.90) (0.79)	1.20 (0.86) (0.79)	—	—	—	(0.99)	—	—
PTS system, IIC component (galactitol-specific)	(0.66)	—	1.40 (0.68) (0.64)	1.33 (0.69) (0.67)	—	—	—	(0.46)	—	—
PTS system, IIBC component (lactose-specific)	—	—	—	—	—	1.18	1.15 (0.53)	(0.62)	1.07	—
PTS system, histidine-containing phosphocarrier protein (hpr)	1.50 (0.86)	1.11 (0.97)†	1.31	1.26	1.73	1.50	1.87	1.44	1.18	1.28
PTS system, enzyme I (ptsI)	1.35	(0.94)	1.13	1.22	2.07	1.96	2.31	1.25	1.33	1.78
PTS system, IIABC components	—	—	—	—	—	(0.60)	2.43	—	—	(0.80)
PTS system, IIB component	—	—	(0.86) (0.82)	1.03 (0.95) etc	—	—	(0.67)	—	—	—
PTS system, IIB component	—	—	(0.81)	(0.93)	—	1.06	(0.74)	—	—	(0.76)
PTS system, IIC component	—	—	(0.63)	(0.69)	—	—	1.91	—	—	(0.93)
PTS system, IID component	—	—	(0.58)	(0.62)	—	—	2.12	—	—	—
Putative PTS system, IIA component	—	—	—	—	—	(0.55)	(0.66)	—	1.06	—
Putative PTS system, IIB component	—	—	—	—	—	(0.71)	1.57 1.39	—	1.09	—
Putative PTS system, IIC component	—	—	—	—	—	(0.58)	2.13	—	(0.84)	—
Putative PTS system, membrane component	—	—	—	—	—	1.12	(0.76)	—	—	—
Fermentation										
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

Gene	*E*(*g*)*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
Pyruvate:ferredoxin oxidoreductase	—	—	(0.51)	(0.45)	(0.40)	—	—	—	1.43 1.07	2.05
Phosphate acetyltransferase (pta)	1.24	(0.90)	(0.86)	1.18	(0.77)	(0.95)	(0.84)	1.19	1.10	1.43
Acetate kinase (ackA)	1.18	(0.64)	1.67 (0.49)	1.87 (0.47)	(0.75) (0.61)	(0.82)	(0.72)	1.14	1.17	1.23 (0.65)
Alcohol dehydrogenase (adhA)	—	(0.80)	—	—	(0.60)	(0.88)	1.48	(0.94)	—	—
Alcohol dehydrogenase (adhB)	(0.46)	(0.73)	—	—	—	(0.54)	(0.83)	—	1.18	—
Alcohol dehydrogenase (gbsB)	(0.60)	(0.60)	—	—	—	—	(0.60)	—	—	1.66 (0.96) etc
Alcohol-acetaldehyde dehydrogenase (adhE)	—	—	2.08 1.39	2.14 1.44	1.44	—	2.22	(0.56)	—	2.00 (0.85)
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)
Acetolactate synthase small subunit (ilvN)	(0.71)	(0.83)	(0.94)	(1.02)	(0.55)	—	(0.60)	—	(0.78)	—
Malate dehydrogenase (citH)	(0.81)	1.08	—	—	—	—	—	—	—	—
Malate dehydrogenase (malS, mleS)	1.81 (0.47)	—	(0.55)	(0.68)	1.44	—	—	—	(1.01)§ (1.00)§	—
Fumarate reductase flavoprotein subunit (frdC)	—	—	(0.81)	1.16	—	—	—	1.22	—	—
Acetyl-CoA acetyltransferase (mmgA, thiL, fadA)	(0.55) (0.52) (0.45)	(0.69) (0.68) etc	(0.83)	(0.84)	(0.51) (0.49)	(0.75) (0.45)	—	(0.59) (0.47) (0.46)	1.29	(1.01)
3-hydroxybutyryl-CoA dehydrogenase, NAD-dependent (mmgB, fadB, hbd))	(0.52)	(0.81) (0.71) (0.68)	—	—	—	—	—	—	1.44	1.55
3-hydroxybutyryl-CoA dehydratase (crotonase)	(0.58)	(0.81) (0.72)	—	—	—	—	—	—	1.13	(1.01) (0.66)
Butyryl-CoA (acetyl-CoA) dehydrogenase (mmgC, bcd, acdA)	(0.56) (0.54) etc	(0.94) (0.66) etc	—	—	—	—	—	—	1.44	1.70 (0.66)
NADH-dependent butanol dehydrogenase (bdhA)	1.05 (0.68)	(0.66)	(0.61)	(0.72)	—	—	—	—	(0.87) (0.83) (0.76)	(0.52)
Butyrate kinase (buk)	(0.50)	—	(0.71)	(0.59)	—	—	—	—	1.25 (0.82)	(0.84)
TCA cycle										
Citrate synthase (*citA, citZ, mmgD*)	(0.63) (0.57) (0.46)	1.22 (0.63)	(0.77)	(0.73)	—	—	—	(0.51)	—	—

Gene	*E*(*g*)*									
	BACSU	**BACHA**	**LISIN**	**LISMO**	**LACLA**	**STRPY**	**STRPN**	**STAAU**	**CLOAC**	**CLOPE**
Aconitate hydratase (*citB*)	1.08	—	1.05	1.11	(0.37)	—	—	(0.85)	—	—
Isocitrate dehydrogenase (*citC*)	1.33	1.46	(0.95)	(0.92)	(0.45)	—	—	(0.98)	(0.97)	—
Succinyl-CoA synthetase, β-subunit (*sucC*)	(0.63)	1.29	—	—	—	—	—	(0.96)	—	—
Succinyl-CoA synthetase,α-subunit (*sucD*)	(0.67)	1.14	—	—	—	—	—	1.10	—	—
Succinate dehydrogenase, flavoprotein subunit (*sdhA*)	(0.57)	1.30	—	—	—	—	—	(0.74)	—	—
Succinate dehydrogenase, iron-sulfur protein (*sdhB*)	(0.63)	1.02	—	—	—	—	—	(1.00)	—	—
Succinate dehydrogenase, cytochrome b558 subunit (*sdhC*)	(0.64)	1.17	—	—	—	—	—	(0.68)	—	—
Malate dehydrogenase (*citH*)	(0.81)	1.08	—	—	—	—	—	—	—	—
Malate dehydrogenase (malS, mleS)	1.81 (0.47)	—	(0.55)	(0.68)	1.44	—	—	—	(1.01)§ (1.00)§	—
Detoxification										
Superoxide dismutase (sod)	1.64 (0.44)	1.43 (0.52)	1.39	1.39	1.21	(0.74)	1.78	1.43 (0.73)	—	(0.76)
Catalase (Kat)	1.26 (0.43) (0.50)	(0.66) (0.49)	(0.62)	(0.56)	—	—	—	(0.53)	—	—
Alkyl hydroperoxide reductase subunit C (ahpC)	1.66	—	—	—	(0.74)	1.27	—	2.02	—	(0.94)
Alkyl hydroperoxide reductase subunit F (ahpF)	1.04	—	—	—	(0.39)	(0.88)	—	1.10	—	—
2-cys peroxiredoxin	1.40	1.41	(0.67)	(0.75)	—	—	—	—	—	—
Thiol peroxidase (Tpx)	1.03	(0.94)	(0.87)	(0.98)	(0.66)	—	(0.77)	1.05	(0.87)	—
Thioredoxin reductase (trxB)	(0.98)	(0.97)	(0.84)	(0.87)	(0.96)	—	(0.85)	(0.89)	1.04	(0.58) (0.32)

Included are only genes that qualify as PHX in at least one of the genomes.

*Numbers in parentheses indicate the gene is not PHX; –, the gene does not have a homolog in the genome.

†Annotated glucokinase in some genomes but transcriptional regulator NagC in others. Sequence similarity ~40%.

‡Ten homologs are present in each LISMO and LISIN.

§PA gene.