Genes and Pathways	ME3880	TH2746	ME12612	ME12173	TE4605	ME6381	ME8366	TH2747	TH3004	TH0989	TH2519	TE1800	TH4590	ME2014	ME12657	TE1301	TH4093	ME30509	TH4820
Central carbon metabolism																			
Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	0.78	0.89	0.89	0.67	1	0.89	0.78	1	0.89	1	0.67	0.89	1	0.89	0.56	1	0.89	0.56	0.33
Glycolysis (Entner-Doudoroff pathway)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Pentose phosphate pathway (Pentose phosphate cycle)	0.86	0.71	0.71	0.71	0.86	0.57	0.71	1	0.86	1	0.71	0.86	1	0.86	0.57	1	0.71	0.29	0.43
Pyruvate oxidation, pyruvate => acetyl-CoA	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Citrate cycle (TCA cycle, Krebs cycle)	0.63	0.88	1	0.38	0.75	0.63	0.88	0.88	0.88	0.75	1	1	0.88	0.63	0.75	1	0.5	0.25	0.25
Other carbohydrate and carbon metabolism																			
Galactose degradation to glycerate-3P	0.5	0.75	0.75	0.25	0.75	0.5	0.5	1	0.75	1	0.5	0.5	0.75	0.25	0.25	0.5	0.75	0.25	0.5
Rhamnose degradation	1	1	0.75	0.5	0.5	0.5	0.5	1	1	1	0.75	1	0.75	0.5	0.5	0.5	1	0.5	0.75
Fucose degradation	1	0.75	0.75	0.25	0.75	0.5	0.75	1	0.75	0.75	0.5	0.75	0.75	0.75	0.5	0.75	1	0.75	0.75
L-Arabinose degradation to xylulose-P for pentose pathway	1	1	0	0	0.67	0.33	0.33	1	1	1	0	0	0.33	0	0	0	0.67	0.33	0.33
Xylose degradation	1	1	1	1	1	0.5	1	1	1	1	0.5	1	1	1	1	1	0.5	1	1
D-Galacturonate degradation to pyruvate & D-glyceraldehyde 3P	(0)	(0)	(0)	(0)	0.8	0.2	(0)	0.6	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
D-Glucuronate degradation to pyruvate and D-glyceraldehyde 3P	0	0.6	0.4	0.4	0.6	0	0.2	0.6	0.8	0.6	0.6	0.8	0.6	0.2	0.4	0.4	0.6	0.4	0.8
Mannose degradation to glucose-P	0.5	1	1	1	1	1	1	1	1	1	1	1	1	1	0.5	0.5	1	0.5	1
Lactaldehyde degradation to pyruvate (Aerobic)	1	1	0.33	1	0.33	0.33	1	1	1	0.67	0.33	0.33	1	0.33	0.33	0.33	0.67	0.67	0.67
Fatty acid biosynthesis	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Glycogen biosynthesis from alpha-D-glucose-6P via ADP-D glucose	0.75	0.25	0.75	0.75	0.75	0.5	1	1	0.75	1	0.5	0.5	1	1	1	1	0.5	0	0.75
Glyoxylate cycle	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Ethylmalonyl pathway, alternative to glyoxylate cycle	0	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hydrogenase																			
Iron-only [FeFe]-hydrogenase	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	1	1
[NiFe]-hydrogenase																			
Group 1 [NiFe]-hydrogenase, H2 uptake	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Group 2 [NiFe]-hydrogenase, H2 sensing	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0
Group 3 [NiFe]-hydrogenase, NAD(P)-reducing	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0
Group 4 [NiFe]-hydrogenase, H2 evolving	0	1	0	0	0	0	0	1	0	1	0	0	0.5	0	0	0	1	1	1
Fermentation																			
Pyruvate to acetate via acetyl-coA	1	1	0.67	0.67	0.33	0.33	1	1	1	0.67	0.33	0.33	1	0.67	0.67	0.67	1	1	1
Pyruvate to propanoate	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Pyruvate to succinate	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Pyruvate to butanoate	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Pyruvate to butanol	0.71	0.71	0.71	0.29	1	0.71	0.57	0.43	0.43	0.43	0.57	0.57	1	0.57	0.57	0.57	0.43	0.43	0.43
Pyruvate to ethanol	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Pyruvate to lactate	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0
Pyruvate to acetone	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)	(0)
Nitrogen related																			
Dissimilatory nitrate reduction, nitrate => ammonia	0	0	0	0	0	0	0	0	0	0	0	0	(0)	0	0	0	0	0	(0)
Denitrification, nitrate => nitrogen gas	0	0	0	0	0	0	0	0.25	0.25	0	0	0	0	0	0	0	0	0	0
TMAO (trimethylamine-N-oxide) reductioin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitrification, ammonia => nitrite	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitrogen fixation, nitrogen => ammonia	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0
Assimilatory nitrate reduction, nitrate => ammonia	0	1	0	0	(0)	0	0	0	0	0	0	0	0	0	0	0	(0)	0	(0)
Urease (Urea ==> CO2 + NH3)	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0
Ammonia permease	1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	1	1	0	1
Sulfur related																			
Dissimilatory sulfate reduction, sulfate => H2S	0	(0)	(0)	0	(0)	(0)	(0)	(0)	(0)	(0)	0	0	0.67	0	0	(0)	(0)	(0)	0
Dimethyl sulfoxide (DMSO) reduction	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Polysulfide reduction	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thiosulfate oxidation by SOX complex, thiosulfate => sulfate	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alkanesulfonate oxidation to sulfite	0	0	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0.5	0	0
ABC-type sulfate transport system	0	0.5	0	0	0.75	0	0	1	1	1	0.5	1	0	0	0	0	1	0	0.5
Sulfate permease	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	1	0	0	0
Assimilatory sulfate reduction, sulfate => H2S	0.67	0.67	1	0.67	1	0.67	1	0.67	1	1	0.33	0.33	1	0.33	1	1	0.67	1	0.33
Phosphorus related																			
Alkaline phosphatase	1	1	1	1	0	0	1	0	0	0	0	0	0	1	1	1	1	0	0
High-affinity phosphate specific transport (Pst) system	0	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0
PiT inorganic phosphate transporter, low affinity	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1
Polyphosphate storage and utilization	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
ABC-type phosphonate transport system	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Methylphosphonate degradation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phosphonoacetate degradation	0	1	0	1	1	0	1	1	1	0	0	0	1	0	0	0	0	0	0
Sensitivity and tolorance to oxygen																			
Superoxide dismutase (SOD)	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1
Catalase-peroxidase, katG	0	1	0	1	0	0	0	0	0	1	0	0	1	1	1	1	0	0	0
Oxidative phosphorylation																			
NADH:quinone oxidoreductase (Complex I)	0.64	0.91	0.91	0.73	1	0.73	0.91	1	1	1	0.36	1	1	0.73	0.82	1	0.27	0.18	0.73
Succinate dehydrogenase complex (Complex II)	0.33	1	1	1	1	1	1	0.67	0.67	1	1	1	1	0.67	0	1	0	0	0
Cytochrome bc1 complex (Complex III)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alternative Complex III, ACIII	0.33	1	0.5	0.83	1	0.33	1	1	1	1	0.67	1	1	1	0.83	1	0	0	0
Cytochrome c oxidase, aa3 type (Complex IV)	0	1	0.5	1	1	0.5	1	1	1	1	0	0	1	1	0.5	1	0	0	0
Cytochrome c oxidase, cbb3-type (Complex IV)	0	1	1	0.5	1	0	1	0.5	1	0.5	0.5	1	1	0.5	0.5	0.5	0	0	0
F-type ATPase complex (Complex V)	0	1	0.63	0	1	1	1	1	0.88	1	1	1	1	0.25	0	1	0	0	0