Table S2: Genomic markers of CUE or CUE temperature sensitivity  $(Q_{10})$  identified in exploratory and complete glucose datasets and confirmed by their presence as correlates of efficiency in the microcosms dataset or for at least two of the three remaining substrates in the liquid culture assays. Markers are included when the slopes were either both positive or both negative for the two datasets at an alpha of 0.05.

validation method	Temperature/ temperature range (°C)	corelation	КО
microcosms	15	negative	K09474 - acid phosphatase (class A) K01625 - 2-dehydro-3-deoxyphosphogluconate aldolase /
	25	negative	(4S)-4-hydroxy-2-oxoglutarate aldolase K00809 - deoxyhypusine synthase K02167 - TetR/AcrR family transcriptional regulator,
		positive	transcriptional repressor of bet genes K09815 - zinc transport system substrate-binding protein
other substrates	15	negative	K01733 - threonine synthase K07095 - uncharacterized protein K14441 - ribosomal protein S12 methylthiotransferase K01752 - L-serine dehydratase
		positive	K02016 - iron complex transport system substrate-binding protein K02072 - D-methionine transport system permease protein K03786 - 3-dehydroquinate dehydratase II K03825 - putative acetyltransferase
			K05596 - LysR family transcriptional regulator, chromosome initiation inhibitor K09780 - Uncharacterized protein K12256 - putrescine—pyruvate transaminase
	20	negative positive	K14441 - ribosomal protein S12 methylthiotransferase K03442 - small conductance mechanosensitive channel
	25	positive	K0342 - Sinar Conductance mechanosensitive channel K0864 - glycerol kinase K02013 - iron complex transport system ATP-binding protein K02015 - iron complex transport system permease protein K02342 - DNA polymerase III subunit epsilon K05846 - osmoprotectant transport system permease protein
microcosms		negative	K01638 - malate synthase [EC:2.3.3.9] K07222 - putative flavoprotein involved in K+ transport K02536 - UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.191]
	15-20	positive	K03560 - biopolymer transport protein TolR K06168 - tRNA-2-methylthio-N6-dimethylallyladenosine synthase [EC:2.8.4.3] K07023 - putative hydrolases of HD superfamily K08191 - MFS transporter, ACS family, hexuronate transporter K09747 - uncharacterized protein K11085 - ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3]
	15-25	negative	K01638 - malate synthase [EC:2.3.3.9] K02283 - pilus assembly protein CpaF K00389 - putative membrane protein
	20-25	negative	K00508 - linoleoyl-CoA desaturase [EC:1.14.19.3] K01858 - myo-inositol-1-phosphate synthase [EC:5.5.1.4]
		positive	K09764 - uncharacterized protein K02049 - NitT/TauT family transport system ATP-binding protein K07240 - chromate transporter
other substrates	15-20	positive	K08151 - MFS transporter, DHA1 family, tetracycline resistance protein
	20-25		K03417 - methylisocitrate lyase [EC:4.1.3.30] K19294 - alginate O-acetyltransferase complex protein AlgI