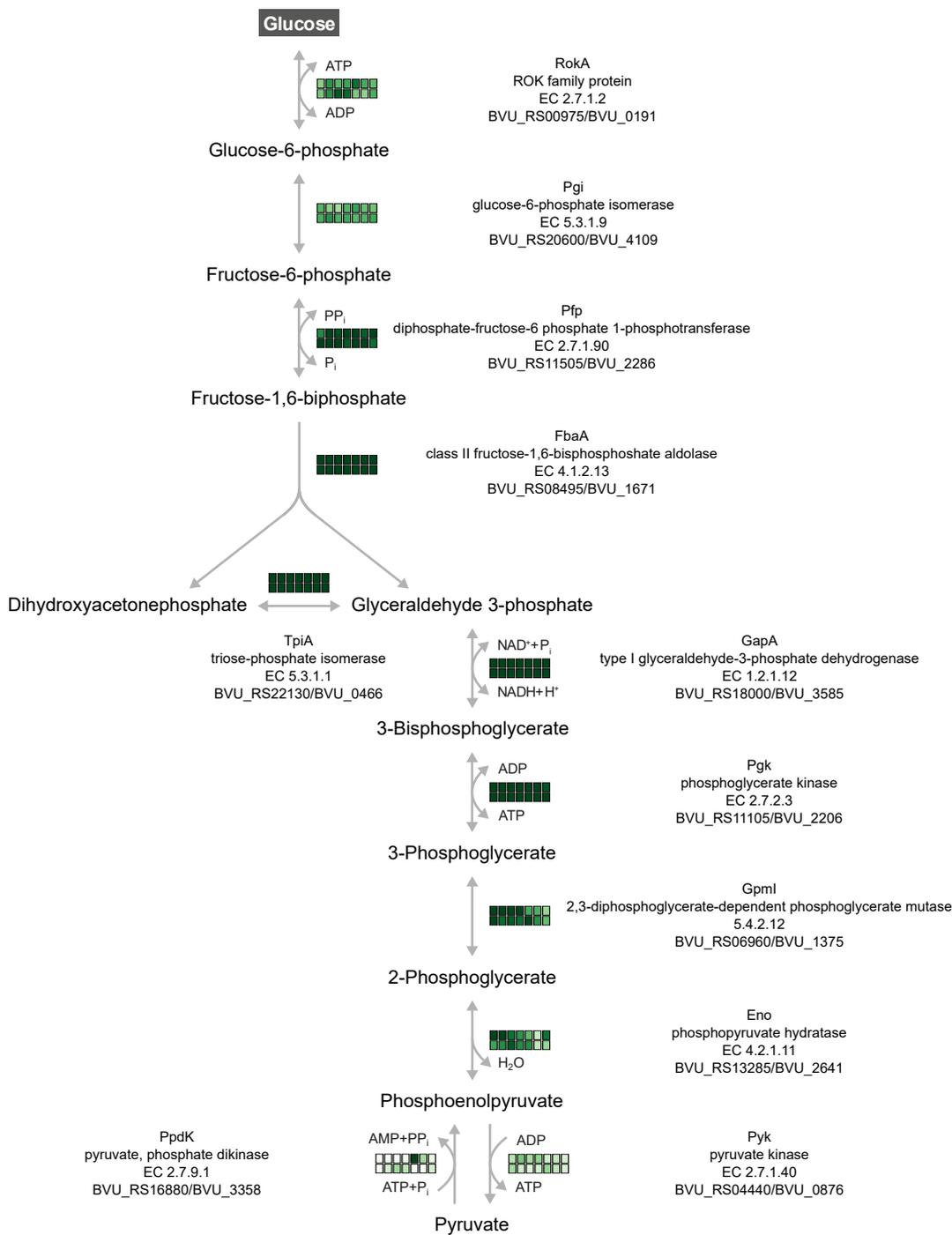
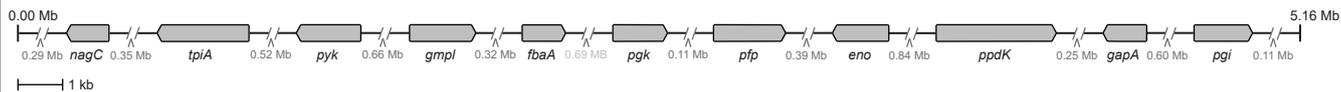


Ara	Glc	Gal	Xyl	Fru	Man	Lac	Sac	Rha	Fuc	α-Glc	β-Glc
				n.d.							
				12.5							
				25.0							
				37.5							
				≥50.0							

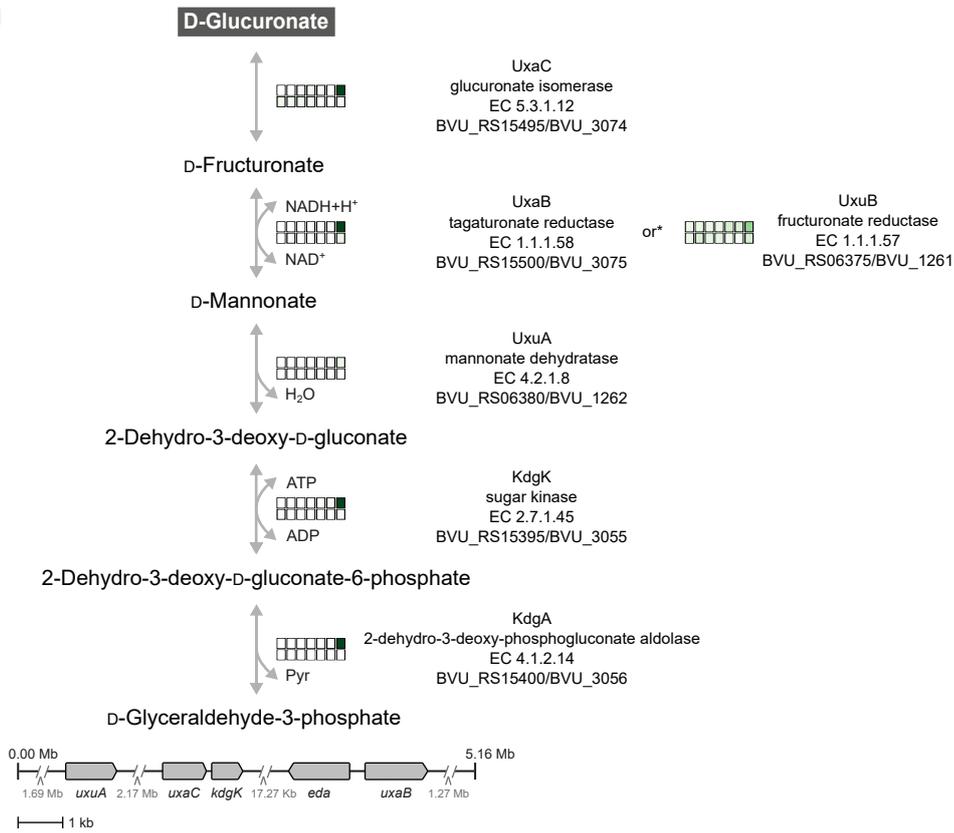
f



Ara	Glc	Xyl	Gal	Mal	Fru	Lac	Man	Sac	Rha	dCyd	Fuc	Xln	GlcA
													n.d.
													12.5
													25.0
													37.5
													≥50.0



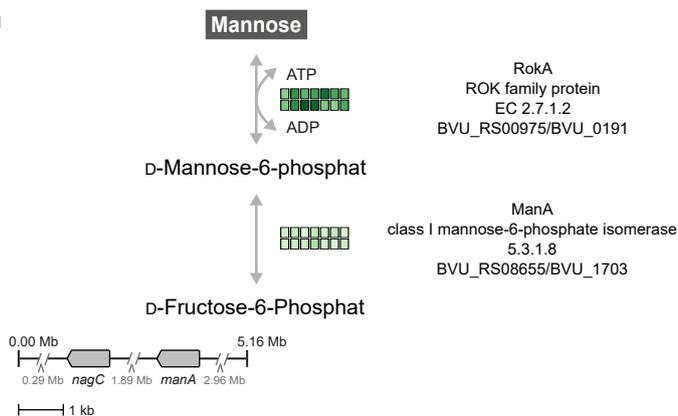
g



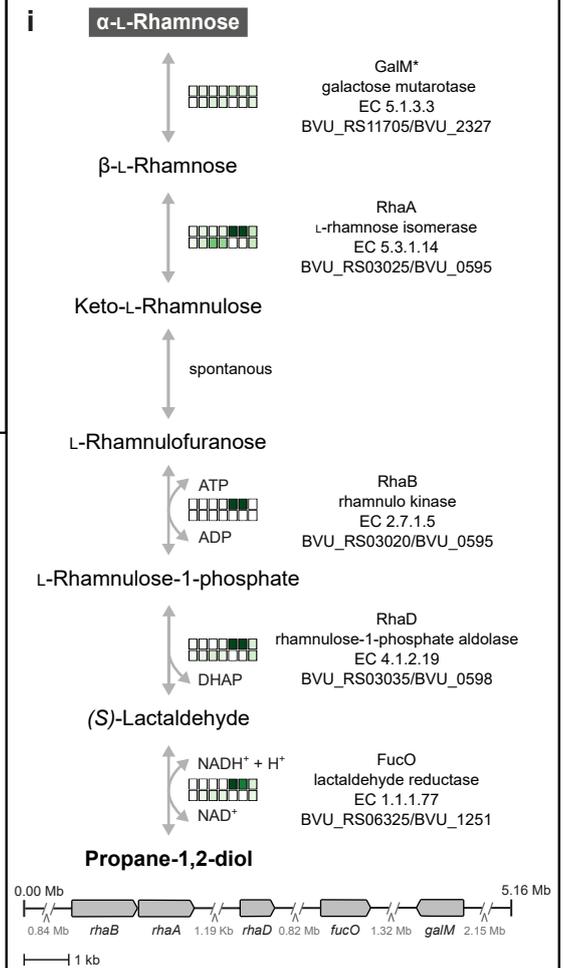
Ara	Glc	Xyl	Gal	Man	Fru	Lac	Rha	qCyc	Fuc	Xln	GlucA
											n.d.
											12.5
											25.0
											37.5
											≥50.0

* UxaB: slightly divergent functional prediction, specifically detected in glucuronate adapted cells;
UxuB: fitting functional prediction, not specifically detected, lower peptide count

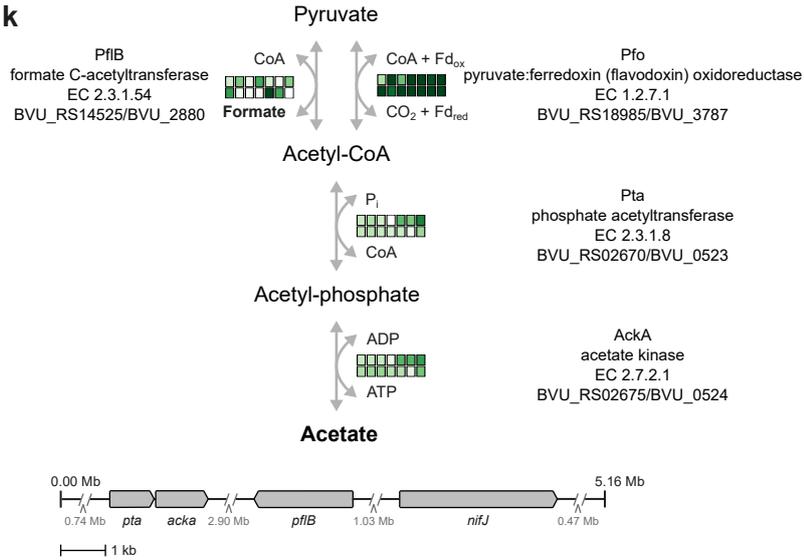
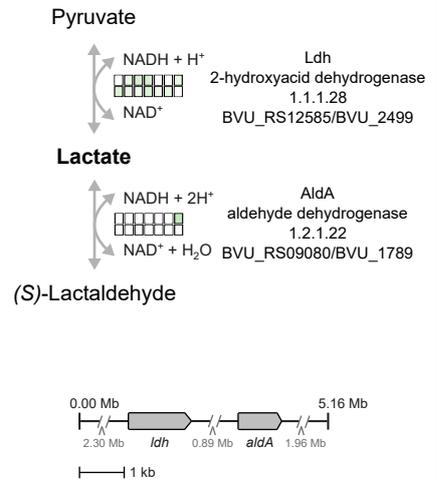
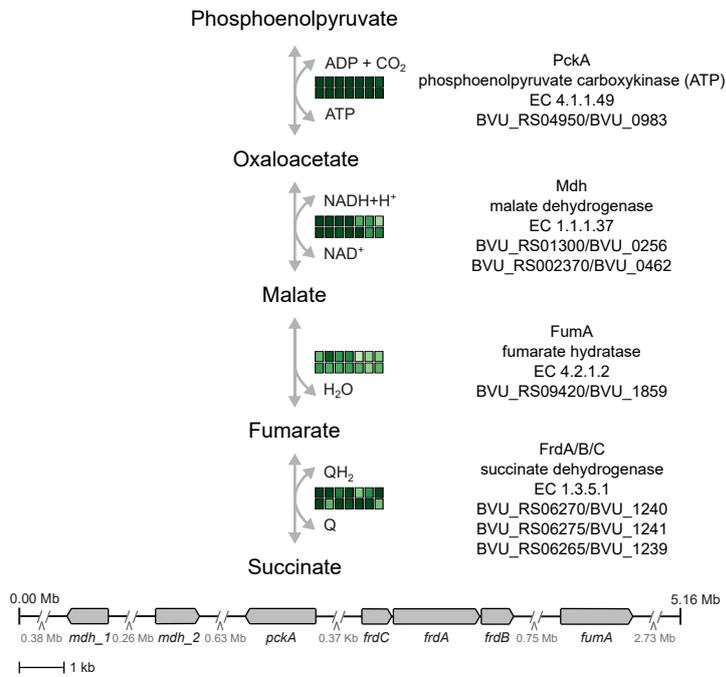
h



i



* specific RhaM (BVU_0150): genome predicted, but not detected

k**l****m**

Ara	Glc
Xyl	Gal
Mal	Fru
Lac	Man
Sac	Rha
αCyc	Fuc
Xih	GlcA
n.d.	
12.5	
25.0	
37.5	
≥50.0	

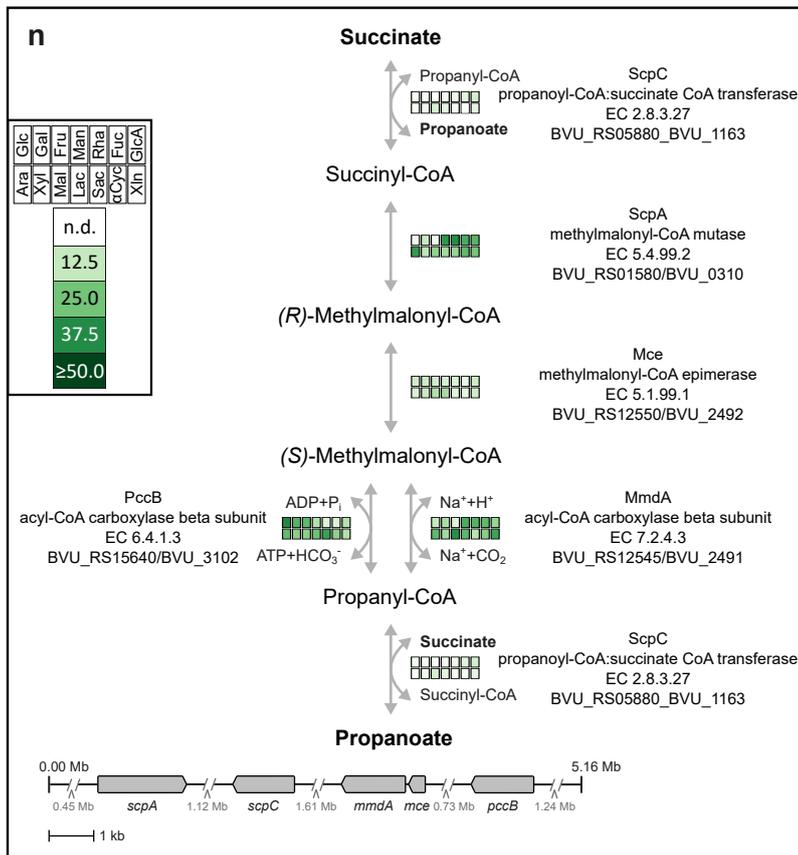


Fig. S2. Substrate-specific and shared details of fermentation network.