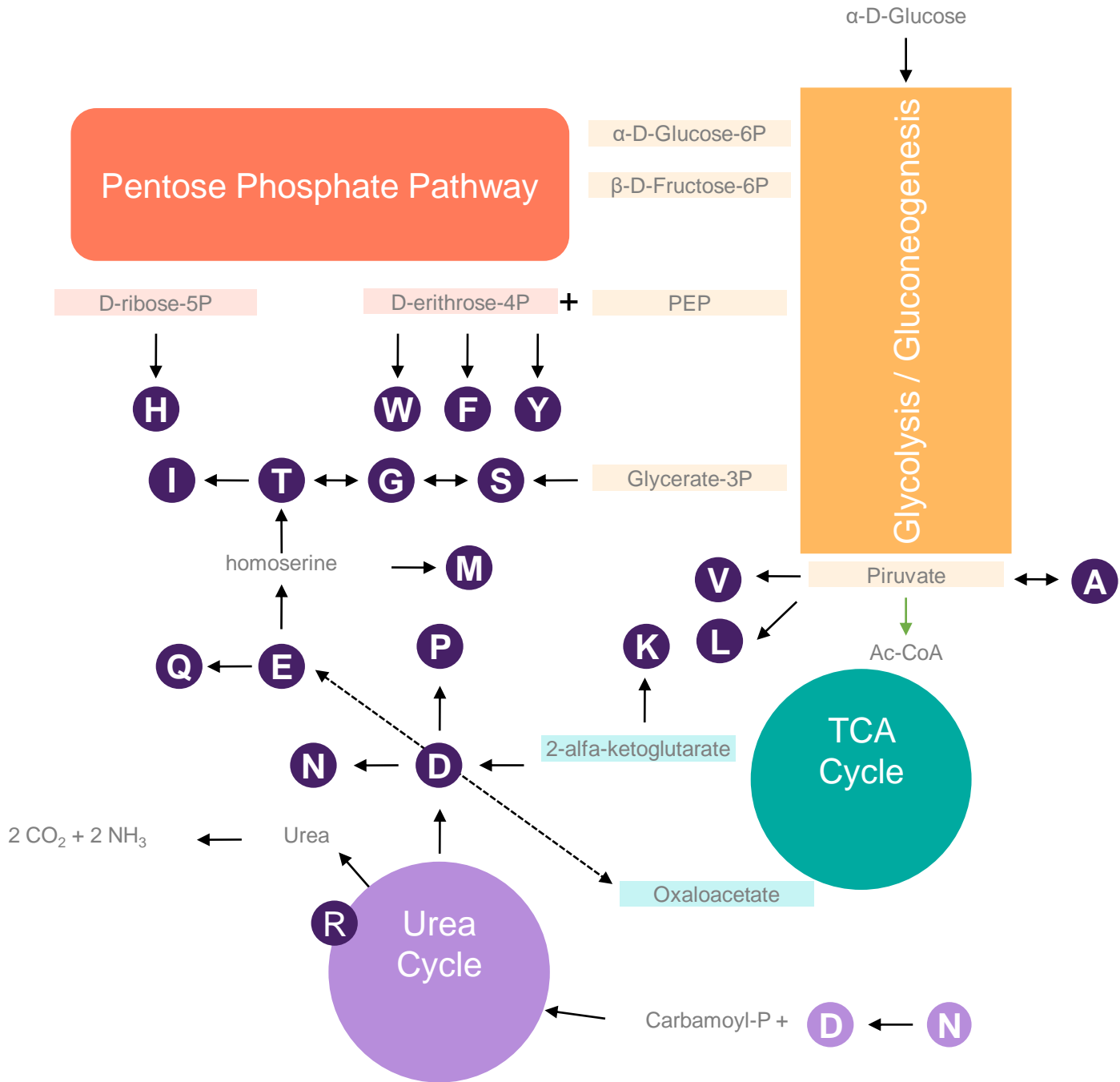


A) Supplementary Figure 1: Carbon and Nitrogen metabolism



Supplementary Figure 1: A) Central Carbon and Nitrogen metabolism. Yellow: Glycolysis and Gluconeogenesis. Red: Pentose phosphate Pathway, Light Blue: Tricarboxylic Acid Cycle (TCA), Light Purple: Urea Cycle. Purple: Amino acids synthesized in *I. terricola*. Compound in shaded boxes are colored according to the pathway that produce them. Abbreviations: P: Phosphate, G3P: Glycerate-3-Phosphate, PEP: Phosphoenolpyruvate, Ac-coA: Acetyl coenzyme A. **B)** *I. terricola* genes involved in the analyzed metabolic pathways (next page)

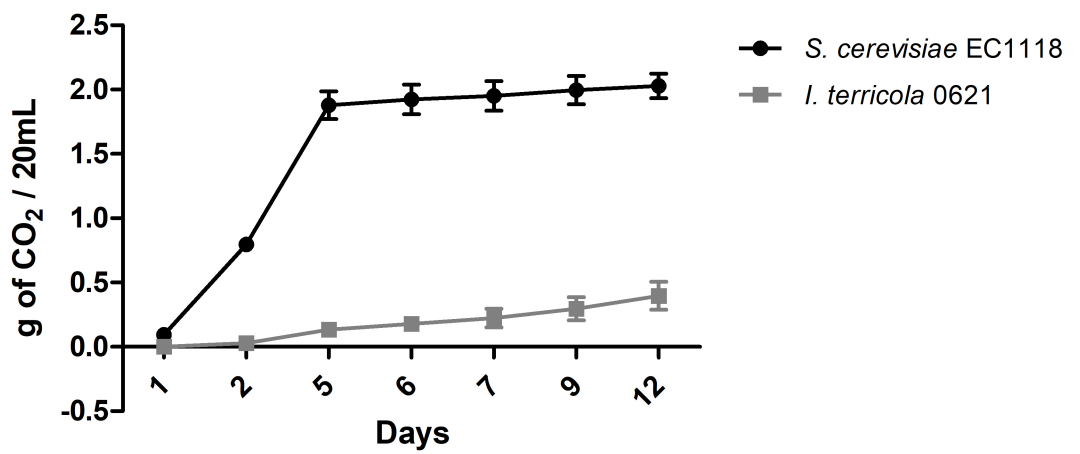
B)

I. terricola genes identified for each pathway

PPP		2-oxoglutarate → Lys		Glycolysis /Gluconeogenesis **	
K01810, GPI	g605	K01655, LYS20/21	g4734/g5134	K00844	g2005, g2787, g4909
K00036, G6PD	g3099	K17450, ACO2	g684	K01810	g605
K01057, PGLS	g3547, g4225	K01705, LYS4	g2208	K00850/K03841	g1705, g3386 / g4264
K00033, PGD	g1946	K05824, LYS12	g4420	K01624	g1321
K01807, RPIA	g4477	K00838, ARO8	g3918	K01803	g3893
K00615, TKT	g4646	K00143, LYS2	g587	K00134	g3139
K00616, TAL	g2259	K00293, LYS9	g220	K00927	g3492
K01783, RPE	g1689	K00290, LYS1	g436/g4389	K01834	g1932, g4184
D-Ribose → His		2-oxoglutarate → Glu		K01689	g2780
K00948, PRS	g404.t1, g1347, g1845, g1304	K14454, AAT2	g4066	K00873	g2715
K00765, HIS1	g4841	K00814, ALT2	g794	K01610	g1925
K14152, HIS4	g2145	Glu ↔ Gln		Pyruvate → Ac-CoA	
K01814, HIS6	g3855	K01915, GLN1	g1129	K00161	g4948
K01663, HIS7	g4688	K00264, GLT1	g54	K00162	g3010
K01693, HIS3	g3908	Glycerate-3P → Ser+ Cys *		K00627	g639
K00817, HIS5	g4782	K00058, SER3	g3290	K00382	g1027
K04486, HIS2	g2380	K00831, SER1	g3596	TCA Cycle	
K14152, HIS4	g2145	K01079, SER2	g1390	K01681, ACO1	g1922
D-erythrose-4P + PEP → Trp/Phe/Tyr		K00640, cysE	NONE	K00031, IDP1/2/3	g1982, g4702
K01626, ARO3/4	g4684, g4762	K01738, CYSK	g2254/g2308	K00030, IDH1/2	g2401, g4445
K13830, ARO1	g2689	Ser → Gly		K00164, KGD1	g1571
K01736, ARO2	g706	K00600, SHM1/2	g4154/g2346	K00658, KGD2	g5206
K01850, ARO7	g1239	Gly → Thr		K00382, LPD1	g1027
K00211, TIR1	g4942	K01620, GLY1	g3759/g2731	K01899, LSC1	g497
K04518, PHA2	g3081	Thr → Ile		K01900, LSC2	g3200
K00838, ARO8	g3918	K01754, ILV1	g3230	K00234, SDH1	g2117
K01657, TRP2	g3815	K01652, ILV2	g1670	K00235, SHD2	g726
K00766, TRP4	g4004	K01653, ILV6	g4567	K00236, SDH3	g1211
K01817, TRP1	g4859	K00053, ILV5	g3960	K00237, SDH4	g118
K01656, TRP3	g3554	K01687, ILV13	g1493	K01679, FUM1	g2216
H01694, TRP5	g2949	K00826, BAT1/2	g1059/g1532	K00026, MDH1/2/3	g129, g3383, g3469
Pyruvate → Oxaloacetate		Glu → Pro		K01647, CIT1/2/3	g689.t1
K01658, PYC1/2	g827	K00931, PRO1	g4792	Pyruvate → Ala	
Oxaloacetate → Asp		K00147, PRO2	g1710	K00814, ALT1/2	g749
K14454, AAT2	g4066	K00286, PRO3	g1616	Pyruvate → Val / Leu	
Asp → Asn		Glu → Ornithine		K01652, ILV2	g1670
K01953, ASN1/26	g4176	K00618, ARG2	g1621	K01653, ILV6	g4567
Asp → Homoserine		K12659, ARG56	g5220	K00053, ILV5	g3960
K00928, HOM3	g3615	K00818, ARG8	g313	K01687, ILV3	g1439
K00133, HOM2	g2826	K00620, ARG7	g2819	K01649, LEU4/9	g4736/g5118
K00003, HOM6	g898	Urea Cycle (Ornithine → Arg)		K01702, LEU1	g1428
Homoserine → Thr		K00611, ARG3	g4010	K00052, LEU2	g1818
K00872, THR1	g322	K01940, ARG1	g598	K00826, BAT1/2	g1059/g1532
K01733, THR4	g2190	K01755, ARG4	g2561	Carbamoyl-phosphate synthesis	
Homoserine → Met		K01476, CAR1	g2848	K01965, CPA2	g3970
K00641, MET2	g4031	Urea → CO ₂ + NH ₃		K01966, CPA1	g5075
K01739, STR2	g1207/g2083	K14541, DUR1	g1379	K11541, URA2	g4466
K01760, DTR3	g1439			2 ATP + L-glutamine + hydrogencarbonate + H ₂ O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate	
K00549, MET6	g3817				

*: Gene in red could not be identified

**: genes catalyzing the reverse reactions of gluconeogenesis are shown in yellow



Supplementary Figure 2: **Fermentation assay.** Grams (g) of CO₂ produced by *S. cerevisiae* EC1118 (black) or *I. terricola* 0621 (gray), during Viura must fermentation