Table S4. Significant differentially expressed genes ($p < 0.05$; FC* > 1.5): R88 treated vs R88 AI-2 and AHLs untreated, 37°C.

ID	*p* value	*q* value	FC	qRT-PCR	Gene	Gene function	Process	COG	COG function categories
YPO3954	0.002285581	0.172345563	2.639792		*gntT, usgA, g*	Putative gluconate permease	Transport/binding Carbohydrates,organic acids and alcohol	COG2610	GE
fruA	0.001035183	0.149305096	2.568186		*fruA, ptsF*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohols		
YPO1299	0.002544894	0.172345563	2.559725	2.96	*fruK, fpk*	1-phosphofructokinase	Glycolysis	COG1105	G
YPO3953	0.0001616	0.117718871	2.394082			Putative gluconokinase	Degradation of carbon compounds	COG3265	G
YPO1298	0.001743415	0.159979859	2.245886		*fruB, fruF, fp*	Bifunctional fructose-specific PTS IIA/HPr protein	Transport/binding Carbohydrates,organic acids and alcohol	COG1762	GT
YPO1300	0.003666333	0.181747668	2.158039		*fruA, ptsF*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohol	COG1299	G
YPO3644	0.00456205	0.191937387	2.090911		*cspa1*	Major cold shock protein Cspa1	Adaptions and atypical conditions	COG1278	K
YPO1994	0.005104302	0.192240271	2.062667			Hypothetical protein	Unknown		
YPO3643	0.000338717	0.149305096	2.029521		*cspa2*	Major cold shock protein Cspa2	Adaptions and atypical conditions	COG1278	K
YPO0003	0.006498704	0.207919903	2.006115		*asnA*	Aspartate-ammonia ligase	Aspartate family biosynthesis	COG2502	E
YPO1993	0.030901545	0.272926836	1.991723			Putative dehydrogenase	Unknown	COG1028	IQR
YPO1222	1.24692E-05	0.038941811	1.972102		*ompC, meoA,*	Outer membrane protein C, porin	Cell envelop	COG3203	M
ompC	0.002095443	0.172214519	1.894964		*ompC, meoA,*	Outer membrane protein C, porin	Cell envelop		
YPO2659	0.02018705	0.269745289	1.776597		*cspB*	Cold shock protein	Adaptions and atypical conditions	COG1278	K
YPO1659	0.007923744	0.221321263	1.721679			Hypothetical protein	Unknown	COG1028	IQR
YPO1301	0.007902523	0.221321263	1.670796	2.09	*psaE*	Putative regulatory protein	Broad regulatory functions	COG0745	TK
YPO1995	0.02564657	0.272926836	1.661964			Hypothetical protein	Unknown		
YPO4064	0.002657749	0.172345563	1.649216			Hypothetical protein	Unknown		
pla	0.000188468	0.117718871	1.639186	3.04	*pla*				
YPO1618	0.011300444	0.243342439	1.603999			Hypothetical protein	Unknown	COG1028	IQR
YPO1398	0.000452953	0.149305096	1.598395		*cspB*	Cold shock-like protein	Adaptions and atypical conditions	COG1278	K
YPO1435	0.009704892	0.237066633	1.570666		*ompA, tolG,*	Putative outer membrane porin A protein	Cell envelop	COG2885	M
YPO2180	0.000877937	0.149305096	1.555349		*adhE, ana*	Aldehyde-alcohol dehydrogenase	Fermentation	COG1012	C
YPO3901	0.014515089	0.25814246	1.538026		*ilvG*	Acetolactate synthase isozyme II large subunit	Pyruvate family biosynthesis	COG0028	EH
YPO0630	0.028558296	0.272926836	1.526076			Conserved hypothetical protein	Unknown	COG3531	O
YPO4084	0.010968843	0.243342439	1.50471		*ibpB, hslS, ht*	Heat shock protein	Adaptions and atypical conditions	COG0071	O
YPO0992	0.01691141	0.263207317	-1.52364		*iucC*	Putative siderophore biosynthesis protein IucC	Iron uptake		
YPO0800	0.007937132	0.221321263	-1.55909			Putative exported protein	Membranes, lipoproteins and porins	COG0491	R
YPO1499	0.032334818	0.272926836	-1.56174			Putative membrane protein	Membranes, lipoproteins and porins	COG0477	GEPR
YPO3788	0.000930148	0.149305096	-1.6284		*metE*	5-methyltetrahydropteroyltriglutamate--homocyst e	Aspartate family biosynthesis	COG0620	E

* FC = Fold Change