Table S3. Significant differentially expressed genes ($p < 0.05$; FC* > 1.5): R88 treated vs R88 AI-2 untreated, 37°C.

ID	*p* value	*q* value	FC	qRT-PCR	Gene	Gene function	Process	COG	COG function categories
YPO4086	0.004658066	0.159506831	1.715835	2.21		Putative lipoprotein	Membranes, lipoproteins and porins		
YPO1828	0.028092755	0.233063202	1.525161		*fliH, fla BIII, fla A*	Flagellar assembly protein FliH	Chemotaxis and mobility	COG1317	NU
YPO0285	0.000165303	0.056605044	-1.50757			Conserved hypothetical protein	Unknown		
YPO3518	0.022173535	0.213040384	-1.51301			Putative exported protein	Membranes, lipoproteins and porins	COG0214	H
YPO0295	0.000298356	0.072559933	-1.52776		*terA*	Putative tellurite resistance protein	Drug/analogue sensitivity	COG2310	T
YPO0292	0.004568822	0.158887026	-1.53818			Conserved hypothetical protein	Unknown		
YPO2855	0.013920316	0.193296993	-1.53941			Putative protease	Degradation of Proteins, peptides and glycopeptides	COG0826	O
terA	0.000324803	0.072559933	-1.56612		*terA*	Putative tellurite resistance protein	Drug/analogue sensitivity		
YPO1383	0.011113428	0.191141134	-1.57491		*pflB, pfl*	Formate acetyltransferase 1	Anaerobic respiration	COG1882	C
YPO3454	0.004381917	0.158887026	-1.61656		*nrdD*	Anaerobic ribonucleoside-triphosphate reductase	2 -deoxyribonucleotide biosynthesis	COG1328	F
YPO3786	0.000344331	0.072559933	-1.62515		*udp*	Uridine phosphorylase	Salvage of nucleosides and nucleotides	COG2820	F
YPO1512	0.014758559	0.193296993	-1.63101		*cdd*	Cytidine deaminase	Salvage of nucleosides and nucleotides	COG0295	F
YPO1304	0.00161006	0.145277514	-1.69029		*psaB*	Chaperone protein PsaB precursor	Chaperones, chaperonins, heat shock	COG3121	NU
YPO1307	0.000424341	0.073287293	-1.69605			Putative membrane protein	Membranes, lipoproteins and porins	COG2855	S
ompC	0.018767438	0.204017789	-1.74124		*ompC, meoA, par*	Outer membrane protein C, porin	Cell envelop		
YPO0293	0.00587751	0.162871375	-1.76156			Conserved hypothetical protein	Unknown		
YPO0284	0.001067248	0.120900811	-1.7889			Conserved hypothetical protein	Unknown	COG0702	MG
YPO0276	0.008402046	0.174475422	-1.79176			Putative LysR-family transcriptional regulator	Broad regulatory functions	COG0583	K
YPO2693	0.00734691	0.163670303	-1.85688		*ybfA*	Putative membrane protein	Membranes, lipoproteins and porins	COG0628	R
YPO1298	0.002276456	0.145277514	-1.90522		*fruB, fruF, fpr*	Bifunctional fructose-specific PTS IIA/HPr protei	Transport/binding Carbohydrates,organic acids and alcoho	COG1762	GT
YPO1222	0.003901307	0.158887026	-1.94352		*ompC, meoA, par*	Outer membrane protein C, porin	Cell envelop	COG3203	M
fruA	0.009707368	0.17861306	-1.98457		*fruA, ptsF*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohols		
YPO0286	0.002492486	0.145277514	-1.98576			Putative coproporphyrinogen III oxidase	Heme and porphyrin Biosynthesis	COG0635	H
YPO1300	0.008130419	0.171898598	-2.01013		*fruA, ptsF*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcoho	COG1299	G
YPO2012	0.004051819	0.158887026	-2.04419			Putative membrane protein	Membranes, lipoproteins and porins		
YPO1299	0.005868601	0.162871375	-2.11404		*fruK, fpk*	1-phosphofructokinase	Glycolysis	COG1105	G
YPO1303	0.000372753	0.072938539	-2.14384	-2.44	*psaA*	pH 6 antigen precursor (antigen 4) (adhesin)	Surface polysaccharides, lipopolysaccharides and antigens		
focA	0.000725086	0.104544025	-2.16799		*focA*	Putative formate transporter 1	Transport/binding Carbohydrates,organic acids and alcohols		
YPO2705	0.000164739	0.056605044	-2.2646			Conserved hypothetical protein	Unknown	COG3445	R
YPO1384	2.28847E-06	0.006269157	-2.31012		*focA*	Putative formate transporter 1	Transport/binding Carbohydrates,organic acids and alcoho	COG2116	P
YPO1661	0.007309608	0.163670303	-2.71475		*mgtB*	Mg(2+) transport ATPase protein B	Pathogenicity	COG0474	P
YPO3279	8.54569E-06	0.011705253	-3.36121	-4.9	*yfiA*	Putative sigma 54 modulation protein	Broad regulatory functions	COG1544	J

* FC = Fold Change