Supplementary Table 2a

The top 10 genes out of 225 significantly up-regulated (p<0.05, fold change>2) genes at 10 min after isooctane treatment: 17 out of 23 genes related to heat shock or iron transport are among the most highly induced genes.

B.No	Gene	*p* value	Fold Change 10min/0min	Gene description	Stress Response
b3686	*ibpB*	0.02	144.1	heat shock protein	Heat Shock
b3687	*ibpA*	0.02	93.5	heat shock protein	Heat Shock
b0593	*entC*	0.01	19.5	isochorismate hydroxymutase 2, enterochelin biosynthesis	Iron transport
b0473	*htpG*	0.02	19.2	chaperone Hsp90, heat shock protein C 62.5	Heat Shock
b2155	*cirA*	0.02	18.7	outer membrane receptor for iron-regulated colicin I receptor; porin; requires tonB gene product	Iron transport
b4511	*ybdZ*	0.01	18.1	conserved protein	
b0594	*entE*	0.01	17.9	2,3-dihydroxybenzoate-AMP ligase	Iron transport
b2150	*mglB*	0.01	16.5	galactose-binding transport protein; receptor for galactose taxis	
b4367	*fhuF*	0.02	16.2	orf, hypothetical protein	Iron transport
b2659	*csiD*	0.01	15.5	orf, hypothetical protein	

Supplementary Table 2b

The top 10 genes out of 696 significantly up-regulated (p<0.05, fold change>2) genes at 60 min after isooctane treatment

B.No	Gene	*p* value	Fold Change 60min/0min	Gene description	Stress Response
b1493	*gadB*	0.03	50.7	glutamate decarboxylase isozyme	Acid stress
b3517	*gadA*	0.03	44.8	glutamate decarboxylase isozyme	Acid stress
b1492	*gadC*	0.03	31.1	acid sensitivity protein, putative transporter	Acid stress
b1616	*uidB*	0.04	18.1	glucuronide permease	
b4365	*yjjQ*	0.04	16.1	putative regulator	
b1264	*trpE*	0.03	15.2	anthranilate synthase component I	
b2851	*ygeG*	0.03	13.3	orf, hypothetical protein	
b3512	*gadE*	0.03	11.6	orf, hypothetical protein	Acid stress
b4067	*actP*	0.04	10.9	putative transport protein	
b3506	*slp*	0.03	10.7	outer membrane protein induced after carbon starvation	