

Additional file 3. Table S3. RT-qPCR validation of nine differentially expressed genes according to microarray data. Linear regression fit analysis was applied and correlation coefficient used for validate the data ($y = 0.973x + 0.107$; $R^2 = 0.97$)

Locus Tag	Locus	Description	Expression ratios ^{a, b}	
			Microarray ^c	RT-qPCR ^d
<i>lp_2945</i>	<i>lpdC</i>	nonoxidative aromatic acid decarboxylase, subunit C	8.09	8.58
<i>lp_0271</i>	<i>lpdB</i>	nonoxidative aromatic acid decarboxylase, subunit B	4.72	4.33
<i>lp_2940</i>	-	cell surface protein precursor, LPXTG-motif cell wall anchor	3.84	4.38
<i>lp_2956</i>	<i>tanLp1</i>	tannase (tannin acylhydrolase)	3.37	2.22
<i>lp_1424</i>	-	NADPH-dependent FMN reductase family protein	1.78	1.64
<i>lp_0349</i>	<i>amtB</i>	ammonium transport protein	-2.81	-2.84
<i>lp_0129</i>	<i>hsp1</i>	small heat shock protein	0.35	0.19
<i>lp_0789</i>	<i>gapB</i>	glyceraldehyde 3-phosphate dehydrogenase	-0.28	-0.27
<i>lp_1036</i>	<i>rplB</i>	50S ribosomal protein L2	-1.02	-0.67
<i>lp_2799</i>		amino acid transport protein	-0.21	-0.17
<i>lp_2057</i>	<i>ldhD</i>	D-lactate dehydrogenase	-1.15	0.01

^a Genes ratios >1.5 fold changes (either increase or decrease) were statistically significant ($p < 0.05$); except for *ldhD* gene (regarded as a constitutive gene)

^b values close to zero indicate no change respect to reference genes (*ldhD*, *16SARNr*, *gyrA*, *dnaG*)

^c $\log_2$ ratio(M), where ratio(M) = fold change

^d $\log_2$ ratios of average fold change