Table S3. Functional categories with significant increase or decrease expression in the fatty acid model.

Functional category	**Genes in functional category**	**Number of genes with significant expression**					
Increase expression LC-FA	**FC (%FC)**	**FE**			**FS**		
		Total FC	(%Total)	(%Total/% FC)	Total FC	(%Total)	(%Total/%FC)
virulence, detoxification, adaptation	238 (5.91)	7	(6.03)	1.02	9	(8.65)	**1.46**
Lipid metabolism	272 (6.77)	7	(6.03)	0.89	5	(4.81)	0.71
information pathways	242 (6.03)	13	(11.21)	**1.86**	7	(6.73)	1.12
cell wall and cell processes	773 (19.22)	10	(8.62)	*0.45*	21	(20.19)	1.05
insertion seqs and phages	147 (3.66)	1	(0.86)	*0.23*	1	(0.96)	*0.26*
PE/PPE	168 (4.18)	0	(0.00)	*0.00*	9	(8.65)	**2.07**
intermediary metabolism and respiration	936 (23.31)	38	(32.76)	**1.41**	20	(19.23)	0.82
regulatory proteins	198 (4.93)	6	(5.17)	1.05	4	(3.85)	0.78
unknown +conserved hypotheticals	1048 (25.95)	33	(28.44)	1.09	28	(26.92)	1.04
TOTAL genes	4022 (100)	116	(100)	1.00	104	(100)	1.00

Decrease expression LC-FA	**FC (%FC)**	**FE**			**FS**		
		Total FC	(%Total)	(%Total/%FC)	Total FC	(%Total)	(%Total/%FC)
virulence, detoxification, adaptation	238 (5.91)	12	(10.81)	**1.83**	15	(9.38)	**1.59**
Lipid metabolism	272 (6.77)	7	(6.31)	0.93	7	(4.38)	0.65
information pathways	242 (6.03)	9	(8.11)	1.34	15	(9.38)	**1.55**
cell wall and cell processes	773 (19.22)	25	(22.52)	1.17	18	(11.11)	*0.58*
insertion seqs and phages	147 (3.66)	1	(0.90)	*0.25*	7	(4.38)	1.18
PE/PPE	168 (4.18)	6	(5.40)	1.29	7	(4.38)	1.05
intermediary metabolism and respiration	936 (23.31)	16	(14.14)	0.61	36	(22.5)	0.97
regulatory proteins	198 (4.93)	4	(3.60)	0.73	17	(10.63)	**2.16**
unknown +conserved hypotheticals	1048 (25.95)	30	(27.02)	1.04	40	(25)	0.96
TOTAL genes	4022 (100)	111	(100)	1.00	160	(100)	1.00

Genes were organized based on functional categories (FC) according to Tuberculist (http://tuberculist.epfl.ch/).
%FC, percentage of genes in each functional category related to the total number of genes; Total FC, number of genes in a functional category with significant increased or decreased expression in each phase of growth; %Total, percentage of genes in a functional category related to the total number of genes with significant increased or decreased expression in each phase of growth; %Total/%FC, ratio of percentage of genes with increased or decreased expression in each functional categories and phase of growth. Ratio values over-represented showed in **bold** and under-represented showed in *italics*.