

S5 Table. Genes and 5’-/3’-UTRs displaying decreased expression 4 hours after induction of EcpR1 overproduction (P-value ≤ 0.05 and M ≥ 0.7 or ≤ -0.7).

Gene ID	Name	Description	M value	Region
<i>Cellular processes and signaling (6)</i>				
SMc00888		Putative 2-component receiver domain protein	-0.99	CDS
SMc00887		Diguanylate cyclase/phosphodiesterase	-0.90	CDS
SMc03090	<i>chew3</i>	Putative chemotaxis protein	-0.87	5'UTR
SMc00023		Putative DSBA oxidoreductase	-0.74	CDS
SMc02868		Putative multidrug efflux system	-0.73	5'UTR
SMc00059	<i>divJ</i>	Histidine protein kinase (cell division)	-0.71	CDS
<i>Metabolism (11)</i>				
SMc01020		Putative oxidoreductase	-3.48	CDS
SMB20338		Putative transporter	-2.16	CDS
SMB20484	<i>supA</i>	Putative ABC transporter periplasmic sugar-binding	-1.65	5'UTR
SMB21168		Putative inner membrane transport protein	-1.52	CDS
SMA1163		Cation transport P-type ATPase	-0.95	CDS
SMc02677	<i>proC</i>	Probable pyrroline-5-carboxylate reductase	-0.87	CDS
SMc01971	<i>puuC</i>	Putative gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase	-0.80	5'UTR
SMA0855	<i>nodP1</i>	ATP-sulfurylase small subunit	-0.75	5'UTR
SMB21192	<i>cbbA2</i>	Putative fructose-bisphosphate aldolase	-0.71	3'UTR
SMc04386	<i>aatB</i>	Aspartate aminotransferase B	-0.70	3'UTR
<i>Information storage and processing (9)</i>				
SMc01336	<i>rne</i>	Ribonuclease E	-1.78	5'UTR
SMc02851		Transcriptional regulator, MarR family	-1.36	CDS
SMB20665		Partial transposase of insertion ISRM17 protein	-1.13	CDS
SMc00021	<i>ccrM</i>	Cell cycle-regulated adenine DNA methyltransferase	-1.13	3'UTR
SMc00289	<i>cspA5</i>	Putative cold shock transcription regulator	-0.89	5'UTR
SMc03958	<i>tolQ</i>	Putative transport transmembrane protein	-0.82	5'UTR
SMc01714		Hypothetical transmembrane protein	-0.77	CDS
SMc00108		Putative acetyltransferase	-0.76	5'UTR
SMc03874		Hypothetical protein	-0.75	5'UTR
<i>Cell motility (8)</i>				
SMc03038	<i>flaB</i>	Flagellin B protein	-2.51	CDS
SMc03037	<i>flaA</i>	Flagellin A protein	-2.32	CDS
SMc03049	<i>flgL</i>	Putative flagellar hook-associated protein	-1.92	CDS
SMc04114	<i>pilA1</i>	Putative pilin subunit protein	-1.36	CDS
SMc03051	<i>flbT</i>	Putative flagellin synthesis repressor protein	-1.19	CDS
SMc03052	<i>flbD</i>	Putative basal-body rod modification protein	-1.09	CDS
SMc03039	<i>flaD</i>	Flagellin D protein	-0.90	CDS
SMc03050	<i>flaF</i>	Putative flagellin synthesis regulator	-0.87	CDS
<i>Poorly characterized (18)</i>				
SMc03107		Conserved hypothetical protein	-2.83	CDS
SMB20848		Conserved hypothetical membrane protein	-2.34	CDS
SMc00239		Conserved hypothetical transmembrane protein	-2.30	CDS
SMc01001		Hypothetical transmembrane protein	-2.04	5'UTR
SMcORF4		Hypothetical protein	-1.94	5'UTR
SMB21211		Putative membrane protein	-1.41	5'UTR
SMc03746		Hypothetical protein	-1.28	CDS
SMA0661		Conserved hypothetical protein	-0.98	5'UTR
SMA0667		Conserved hypothetical protein	-0.93	5'UTR
SMc02392		Hypothetical protein	-0.87	5'UTR
SMc03161		Glucose-fructose oxidoreductase	-0.83	5'UTR
<u>SMc02139</u>	<u><i>gcrA</i></u>	<u>Cell cycle regulator</u>	<u>-0.76</u>	<u>5'UTR</u>
SMc00507		Hypothetical protein	-0.76	CDS
SMA0907		Conserved hypothetical protein	-0.75	5'UTR
SMc03832		Conserved hypothetical signal peptide protein	-0.72	CDS
SMc04010		Conserved hypothetical protein	-0.71	5'UTR
SMB22001	<i>msbA2</i>	Surface saccharide ABC transporter ATP-binding	-0.70	3'UTR
SMc03013		Conserved hypothetical protein	-0.70	CDS

The M value represents the log₂ ratio of transcript levels.

Cell cycle related candidates are indicated in bold and experimentally confirmed targets are underlined.