

Table S1: Differentially expressed genes from RNA-seq analyses of the WT between 3 h and 6 h incubation in the *hrp*-inducing medium. Differentially expressed genes are grouped into functional categories according to the clusters of orthologous group (COG) database: FC, fold changes

A) Up-regulated genes from 3 h to 6 h (adjusted *P*-value < 0.05)

Locus tag	Gene description	log ₂ FC
Amino acid transport and metabolism		
EAMY_0208	<i>metE</i> , methionine synthase II	2.50
EAMY_0493	<i>ggt</i> , gamma-glutamyltransferase	2.44
EAMY_0141	<i>metF</i> , 5,10-methylenetetrahydrofolate reductase	1.92
EAMY_2715	<i>proX</i> , glycine betaine/choline-binding protein	1.62
EAMY_3342	<i>metA</i> , homoserine transsuccinylase	1.36
EAMY_1210	ABC-type spermidine/putrescine transport	1.34
EAMY_1072	<i>ophA</i> , ABC transporter substrate-binding protein	1.22
EAMY_1071	homocysteine S-methyltransferase family protein	1.16
EAMY_2728	<i>metN</i> , methionine ABC transporter ATP-binding protein	1.15
EAMY_2275	<i>aroQ</i> , chorismate mutase	1.15
EAMY_0876	<i>eif</i> , translation initiation factor EIF-2B	1.11
EAMY_0875	dioxygenase	1.10
EAMY_2714	<i>proW</i> , glycine betaine/choline-binding protein	1.06
EAMY_0874	<i>masA</i> , enolase-phosphatase	1.06
EAMY_0138	<i>metB</i> , cystathionine gamma-synthase	1.04
EAMY_1074	<i>ophC</i> , ABC transporter permease	1.03
EAMY_2713	<i>proV</i> , glycine betaine/choline-binding protein	1.01
Carbohydrate transport and metabolism		
EAMY_0497	<i>celB</i> , PTS system transporter subunit EIIC	3.59
EAMY_0498	<i>celA</i> , PTS system transporter subunit EIIB	3.54
EAMY_0495	<i>bglH</i> , beta-glucosidase	3.48
EAMY_0496	<i>celC</i> , PTS system transporter subunit EIIA	3.41
EAMY_0494	<i>bglA</i> , 6-phospho-beta-glucosidase	3.19
EAMY_0873	methylthioribulose-1-phosphate dehydratase	1.25
Cell motility		
EAMY_0532	<i>hrcN</i> , type III secretion system ATPase	1.72
Coenzyme transport and metabolism		
EAMY_1206	<i>bioB</i> , biotin synthetase	2.75
EAMY_1208	<i>bioC</i> , biotin synthesis protein	2.71
EAMY_1207	<i>bioF</i> , 8-amino-7-oxononanoate synthase	2.60
EAMY_1209	<i>bioD</i> , dethiobiotin synthetase	2.57
EAMY_0444	<i>mcyE</i> , Glutamate-1-semialdehyde aminotransferase	1.53
EAMY_0603	<i>metK</i> , S-adenosylmethionine synthetase	1.52

EAMY_0441	creatininase	1.21
EAMY_1205	<i>bioA</i> , DAPA aminotransferase	1.09
Defense mechanisms		
EAMY_2814	<i>ygbT</i> , CRISPR-associated protein Cas1	1.47
Inorganic ion transport and metabolism		
EAMY_1074	<i>ophC</i> , ABC transporter permease	1.03
Intracellular trafficking, secretion and vesicular transport		
EAMY_3019	type VI secretion system-associated protein	1.22
Lipid transport and metabolism		
EAMY_2827	<i>vraB</i> , 3-ketoacyl-CoA thiolase	1.55
EAMY_2828	<i>fadD</i> , acyl-CoA synthase	1.48
EAMY_2829	acyl-CoA thioester hydrolase	1.18
Nucleotide transport and metabolism		
EAMY_0442	dihydroorotate dehydrogenase	1.20
Post-translational modification, protein turnover and chaperones		
EAMY_0595	peroxiredoxin	2.26
EAMY_0594	<i>dsbD</i> , cytochrome c biogenesis protein	2.06
Secondary metabolites biosynthesis, transport and catabolism		
EAMY_2517	<i>entF</i> , non-ribosomal peptide synthetase	1.70
EAMY_2828	<i>fadD</i> , acyl-CoA synthase	1.48
EAMY_0447	<i>sypC</i> , gramicidin S synthetase II	1.37
EAMY_0448	<i>ppsD</i> , polyketide synthase	1.32
EAMY_0441	creatininase	1.21
Transcription		
EAMY_0593	<i>sigD</i> , RNA polymerase sigma factor	1.79
EAMY_0207	<i>metR</i> , transcriptional regulator	1.37
EAMY_0499	<i>ascG</i> , transcriptional regulator	1.14
EAMY_0536	<i>hrpL</i> , RNA polymerase sigma factor	1.04
Type III secretion system		
EAMY_0542	<i>hrpA</i> , Hrp pili protein	2.54
EAMY_0558	<i>dspF</i> , Hrp secreted pathogenicity-like protein	2.11
EAMY_0552	<i>hrpN</i> , harpin protein	2.11
EAMY_0527	<i>hrcS</i> , type III secretion protein	1.90
EAMY_0557	<i>dspE</i> , Hrp secreted pathogenicity-like protein	1.86
EAMY_0530	<i>hrpP</i> , type III secretion protein	1.83
EAMY_0551	<i>hrpV</i> , type III secretion protein	1.82
EAMY_0531	<i>hrpO</i> , type III secretion protein	1.78
EAMY_0529	<i>hrcQ</i> , type III secretion system apparatus protein	1.75
EAMY_0528	<i>hrcR</i> , type III secretion apparatus protein	1.75
EAMY_0555	<i>orfC</i> , HrpW-specific chaperone	1.75
EAMY_0532	<i>hrcN</i> , type III secretion system ATPase	1.72

EAMY_0547	<i>hrpF</i> , type III secretion protein	1.71
EAMY_0526	<i>hrcT</i> , type III secretion apparatus protein	1.71
EAMY_0550	<i>hrpT</i> , type III secretion lipoprotein	1.71
EAMY_0548	<i>hrpG</i> , type III secretion protein	1.71
EAMY_0544	<i>hrcJ</i> , type III secretion inner-membrane protein	1.70
EAMY_0545	<i>hrpD</i> , type III secretion protein	1.69
EAMY_0549	<i>hrcC</i> , type III secretion system outer membrane pore	1.68
EAMY_0556	<i>hrpW</i> , harpin protein	1.68
EAMY_0525	<i>hrcU</i> , type III secretion protein	1.68
EAMY_0533	<i>hrpQ</i> , type III secretion system protein	1.67
EAMY_0543	<i>hrpB</i> , type III secretion system protein	1.67
EAMY_0546	<i>hrpE</i> , type III secretion apparatus protein	1.65
EAMY_0554	<i>orfB</i> , avirulence protein	1.64
EAMY_0535	<i>hrpJ</i> , type III secretion system protein	1.63
EAMY_0553	<i>orfA</i> , Tir chaperone family protein	1.61
EAMY_0534	<i>hrcV</i> , type III secretion inner-membrane protein	1.60
EAMY_0520	<i>hsvA</i> , Hrp-associated systemic virulence protein	1.60
EAMY_0521	<i>hsvB</i> , Hrp-associated systemic virulence protein	1.40
EAMY_0519	<i>hrpK</i> , pathogenicity locus protein	1.38
EAMY_0653	<i>eop2</i> , type III effector	1.36
EAMY_0536	<i>hrpL</i> , RNA polymerase sigma factor	1.04
EAMY_0522	<i>hsvC</i> , Hrp-associated systemic virulence protein	1.02
Uncharacterized/functional unknown proteins		
EAMY_0524	hypothetical protein	1.68
EAMY_0446	hypothetical protein	1.52
EAMY_2816	<i>ygcl</i> , Cse1-family CRISPR-associated protein	1.51
EAMY_0443	<i>ygbF</i> , CRISPR-associated protein Cas2	1.51
EAMY_2817	<i>ygck</i> , Cse2-family CRISPR-associated protein	1.50
EAMY_3111	<i>ygcH</i> , Cse3-family CRISPR-associated protein	1.40
EAMY_0445	<i>mcYE</i> , beta-ketoacyl synthase	1.40
EAMY_2815	hypothetical protein	1.39
EAMY_2818	<i>ygcJ</i> , Cse4-family CRISPR-associated protein	1.37
EAMY_2813	hypothetical protein	1.33
EAMY_2819	<i>ygcI</i> , CRISPR-associated protein Cas5	1.30
EAMY_0523	<i>irp</i> , polyketide synthase	1.30
EAMY_0206	biphenyl 2,3-dioxygenase	1.26

B) Down-regulated genes from 3 h to 6 h (adjusted *P*-value < 0.05)

Locus tag	Gene description	log ₂ FC
Amino acid transport and metabolism		

EAMY_1631	<i>astB</i> , succinylarginine dihydrolase	-1.27
EAMY_1628	<i>astC</i> , succinylornithine transaminase	-1.22
EAMY_1629	<i>astA</i> , arginine <i>N</i> -succinyltransferase	-1.18
EAMY_2799	<i>medA</i> , methionine gamma-lyase	-1.13
EAMY_2196	<i>adhB</i> , alcohol dehydrogenase	-1.03
Carbohydrate transport and metabolism		
EAMY_3043	<i>ydfJ</i> , major facilitator superfamily permease	-1.28
Energy production and conversion		
EAMY_1630	<i>astD</i> , NAD-dependent aldehyde dehydrogenase	-1.32
EAMY_3089	<i>fadH</i> , NADH:flavin oxidoreductase	-1.03
General function prediction only		
EAMY_2196	<i>adhB</i> , alcohol dehydrogenase	-1.03
Intracellular trafficking, secretion and vesicular transport		
EAMY_2969	heme/hemopexin utilization protein B	-1.03
Lipid transport and metabolism		
EAMY_0878	<i>yafH</i> , Acyl-CoA dehydrogenase	-1.35
EAMY_0223	<i>fadB</i> , fatty acid oxidation complex subunit alpha	-1.14
EAMY_0222	<i>fadA</i> , acetyl-CoA acetyltransferase	-1.08
Uncharacterized/functional unknown proteins		
EAMY_2970	nuclear pore complex protein	-1.09