

Supplementary Material

YerA41, a *Yersinia ruckeri* bacteriophage: determination of a non-sequencable DNA bacteriophage genome via RNA-sequencing.

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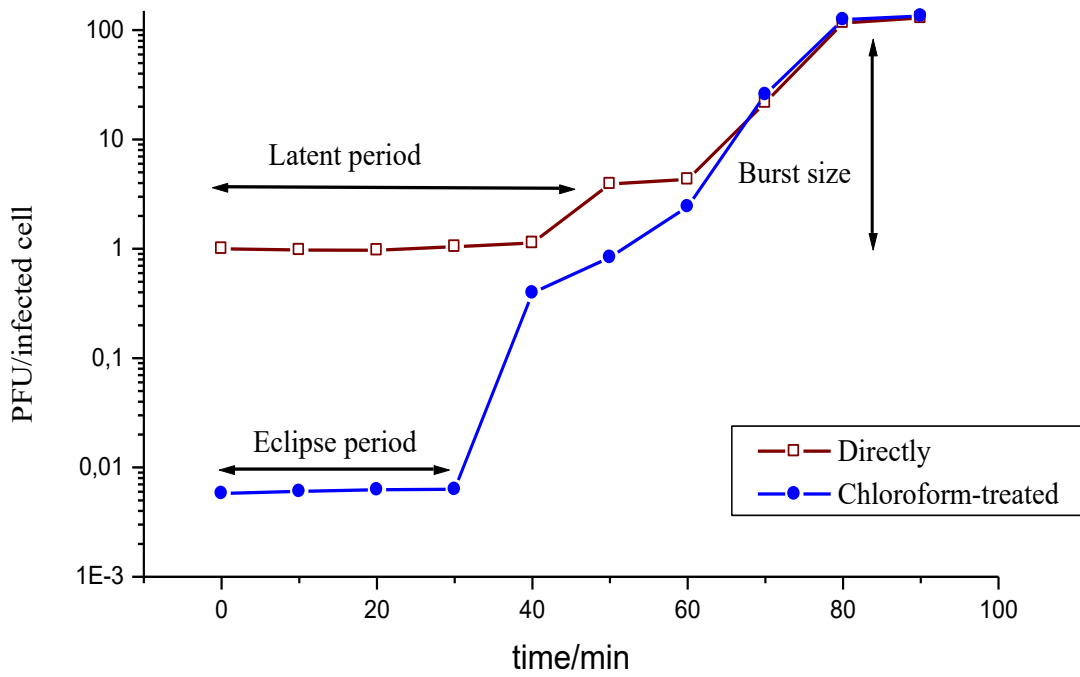


Figure S1. One-step growth curve of bacteriophage YerA41. Shown are PFU per infected cell in chloroform-treated and -untreated cultures at different time points. Each data point represents a mean of two experiments. The number of plaque forming units (PFU) in the immediately diluted 0 min time point samples was set to 1 to represent the number of infected cells in the experiment, and the PFU of all the other samples were normalized against that number. The burst size was then directly obtained from the normalized value after the rise period

Table S1. Bacterial strains used in this study (YRLBSC, Yersinia Research Laboratory Bacterial Strain Collection).

Species	Strain	O-serotype	Description	Reference(s)/Source
<i>Shigella flexneri</i>	784/83	-		YRLBSC
<i>Salmonella typhimurium</i>	ATCC13311	-		YRLBSC
<i>Providencia rettgeri</i>	121/84	-	patient isolate	YRLBSC
<i>Yersinia bercovieri</i>	3016/84	58,16	patient isolate	[1]
<i>Yersinia bercovieri</i>	127/84	-	patient isolate	YRLBSC
<i>Yersinia enterocolitica</i>	1539	-		YRLBSC
	gk132	1	patient isolate	YRLBSC
	JDE029	1		[2]
	JDE766	1,2,3		[2]
	15126/78	3		YRLBSC
	YeO3-R1	3	spontaneous rough mutant of YeO3-c	[3]
	3102/80	10	patient isolate	[4]
	3788/80	10		YRLBSC
	gc1209-79	13	patient isolate	[5]
	gc9312-78	13,18	patient isolate	[5]
	2446/84	13,7	patient isolate	YRLBSC
	421/84	13,7	patient isolate	YRLBSC
	ST5074	13a, 13b		YRLBSC
	ST5081	13a,13b		YRLBSC
	15712/83	14	patient isolate	YRLBSC
	RBC36M3	15		[6]
	IP614	15		YRLBSC
	gk2943	2	patient isolate	[7]
	gk1142	2		[7]
	gc874-77	20		[5]
	gc1223-75	20		[5]
	RBE736	21		[6]
	WI-81-50	21		[8]
	431/84	25		YRLBSC
	8425/83-φR1-37-R	25,26	φR1-37 resistant spontaneous mutant of strain 8425/83	YRLBSC
	18425/83	25,26,44	patient isolate	YRLBSC
	63/84	26,44	patient isolate	YRLBSC
	5186/84	28,50		YRLBSC
	6471/76	3	pYV ⁺ patient isolate	[4]
	gc2139-72	34		[5]
	7104/83	35,36	patient isolate	YRLBSC
	248/84	35,52	patient isolate	YRLBSC
	gc3973-76	4	patient isolate	[5]
	RBE701	4,32		[6]
	JDE701	4,32	patient isolate	[8]
	346/84	41(27), 43	patient isolate	YRLBSC
	19942/83	41(27),42 K1	patient isolate	YRLBSC
	647/83	41(27),43		YRLBSC
	626/84	41(27)42	patient isolate	YRLBSC
	9613/83	41(27)K1	patient isolate	YRLBSC
	264/85	41,43	patient isolate	YRLBSC
	477/78	5		YRLBSC
	892/82	5		YRLBSC
	14779/83	5		YRLBSC
	gk7500	5,27		[7]
	MPDE654	5,27		[9]
	3229	50		[4]
	3229-φR1-37-R	50	φR1-37 resistant spontaneous mutant of strain 3229	YRLBSC
	590/80	6	patient isolate	[4]
	341/84	6	patient isolate	YRLBSC

Species	Strain	O-serotype	Description	Reference(s)/Source
	189/80	6,30	patient isolate	[4]
	6737/80	6,30	patient isolate	[4]
	1309/80	6,31		[4]
	438/80	6,31		YRLBSC
	22848/79	7,8		YRLBSC
	605	7,8	patient isolate	YRLBSC
	1308/83	7,8		YRLBSC
	5898/83	7,8		YRLBSC
	17869/83	7,8		YRLBSC
	623/83	7,8	patient isolate	YRLBSC
	21368/83	7,8	patient isolate	YRLBSC
	21943/83	7,8	patient isolate	YRLBSC
	TAMTU	8		YRLBSC
	p310	8	patient isolate	YRLBSC
	MCH314	8	patient isolate	YRLBSC
	CDCA2635	8		[10]
	8081	8		[11]
	277/74	9	patient isolate	YRLBSC
	Ruokola/71	9	patient isolate	[4]
	4367/83	K1 nt		YRLBSC
	5653/80	na		YRLBSC
	8533/84	na	patient isolate	YRLBSC
	10/84	nt	patient isolate	YRLBSC
	gc2138-72	nt	patient isolate	[5]
	659/83	nt K1	patient isolate	YRLBSC
	15240/84	nt	patient isolate	YRLBSC
<i>Yersinia frederikseni</i>	146/85	-		YRLBSC
	12733/85	-		YRLBSC
	22714/85	-		YRLBSC
	3400/83	16		YRLBSC
	3317/84	35	patient isolate	YRLBSC
	38/83	48		YRLBSC
	BR166/97	-		YRLBSC
<i>Yersinia intermedia</i>	9/85	16,21		YRLBSC
	821/84	52,54	patient isolate	YRLBSC
<i>Yersinia kristensenii</i>	404/81	-		YRLBSC
	3688/85	-	patient isolate	YRLBSC
	119/84	12,25	patient isolate	[4]
	404/81	16	patient isolate	YRLBSC
	317/82	16		YRLBSC
<i>Yersinia mollareti</i>	92/84	59(20,36,7)		[1]
<i>Yersinia pestis</i>	EV76			YRLBSC
	KIM D27			YRLBSC
<i>Yersinia pseudo-tuberculosis</i>	2812/79	1		YRLBSC
	6088	10		[12]
	R80	11		[12]
	MW86	12		[12]
	N916	13		[12]
	CN3	14		[12]
	93422	15		[12]
	Pa3606	1b		[12]
	Kuratani	1c		[12]
	lab strain	2		YRLBSC
	p28	2		YRLBSC
	lab strain	2a		YRLBSC
	208	2a		[12]
	1779	2b		[13]
	274	2c		[12]
	324/80	3		YRLBSC
	Marsu	3		YRLBSC
	51	4a		[12]
	Pa3422	4b		[12]

Species	Strain	O-serotype	Description	Reference(s)/Source
	204	5a		[12]
	197	5b		[12]
	DD110	6		[12]
	257	7		[12]
	151	8		[12]
<i>Yersinia similis</i>	MW48	9		YRLBSC
	R626R	9		YRLBSC
	R708Ly	9		YRLBSC
	R708	9		[12]
<i>Yersinia ruckeri</i>	OMBL3			YRLBSC
	RS41		host for phage YerA41	[14]

Table S2. List of predicted protein coding genes identified in YerA41 sequence scaffolds. The phage particle associated proteins (PPAP) were identified using LC-MS/MS analysis.

geneID	Scaffold	protein length [aa]	expected function	phase of expression	PPAP
001	1	196	hypothetical protein	late	
002	1	104	hypothetical protein	late	x
003	1	101	hypothetical protein	late	x
004	1	175	hypothetical protein	late	x
005	1	157	hypothetical protein	late	x
006	1	132	hypothetical protein	late	x
007	1	622	Putative DNA packaging terminase	late	x
008	1	136	hypothetical protein	late	x
009	1	113	hypothetical protein	late	x
010	1	516	hypothetical protein	late	x
011	1	289	hypothetical protein	late	x
012	1	271	Putative prohead core protein protease	late	x
013	1	401	hypothetical protein	late	x
014	1	471	Putative capsid protein	late	x
015	1	285	hypothetical protein	late	
016	1	299	Putative sugar binding protein	late	x
017	1	113	hypothetical protein	late	x
018	1	309	hypothetical protein	late	
019	1	171	Putative RNA polymerase sigma factor	late	x
020	1	188	hypothetical protein	late	
021	1	199	hypothetical protein	late	
022	1	247	hypothetical protein	late	x
023	1	61	hypothetical protein	late	
024	1	860	Putative phage tail sheath protein	late	x
025	1	179	Putative tail protein	late	
026	1	176	hypothetical protein	late	
027	1	251	hypothetical protein	early	
028	1	1043	Putative tail family	late	x
029	1	221	hypothetical protein	late	
030	1	107	hypothetical protein	late	
031	1	367	Putative tail protein	late	
032	1	123	Putative tail protein	late	
033	1	723	hypothetical protein	late	

034	1	243	Putative tail-associated lysozyme	late	
035	1	95	Putative tail-associated lysozyme	late	
036	1	122	hypothetical protein	late	
037	1	551	Putative baseplate wedge	late	x
038	1	538	hypothetical protein	late	
039	1	165	hypothetical protein	late	
040	1	135	Putative capsid protein	late	
041	1	104	Putative virion structural protein	late	
042	1	361	Putative baseplate wedge protein	late	x
043	1	386	Putative tail fiber protein	late	x
044	1	207	Phage tail fiber assembly protein	late	x
045	1	246	Putative tail fiber protein	late	x
046	1	108	hypothetical protein	late	
047	1	95	hypothetical protein	late	
048	1	113	hypothetical conserved protein	early	
049	1	177	Putative endolysin	late	x
050	1	153	hypothetical protein	late	
051	1	97	hypothetical protein	late	
052	1	169	hypothetical protein	late	x
053	2	230	hypothetical protein	early	
054	2	556	Putative DNA directed RNA polymerase, subunit	early	x
055	2	518	Putative DNA-directed RNA polymerase, subunit	early	x
056	2	924	Putative DNA-directed RNA polymerase	early	x
057	2	78	hypothetical protein	early	
058	2	335	hypothetical protein	middle	x
059	2	167	hypothetical protein	middle	
060	2	222	Putative 5'-deoxynucleotidase	middle	
061	2	1306	Putative DNA polymerase	middle	x
062	2	279	hypothetical protein	middle	
063	2	232	hypothetical protein	middle	
064	2	370	Putative UDP-GlcNAc 2-epimerase	middle	
065	2	257	Putative oxidoreductase	middle	
066	2	230	Putative SDR family oxidoreductase	middle	
067	2	231	Putative polysaccharide deacetylase	middle	
068	2	455	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)	middle	
069	2	393	hypothetical protein	middle	x
070	2	272	Putative glycerophosphodiester phosphodiesterase	middle	
071	2	217	hypothetical protein	middle	x
072	2	50	hypothetical protein	middle	
073	2	106	hypothetical protein	early	
074	2	165	hypothetical protein	middle	x
075	2	154	hypothetical protein	early	
076	2	178	hypothetical conserved protein	middle	x
077	2	156	hypothetical protein	middle	x
078	2	186	Putative lytic transglycosylase	early	x
079	2	97	hypothetical protein	middle	
080	2	106	hypothetical conserved protein	early	
081	2	166	hypothetical protein	early	
082	3	205	hypothetical protein	middle	
083	3	124	hypothetical protein	early	
084	3	177	hypothetical protein	middle	
085	3	60	hypothetical protein	middle	

086	3	304	hypothetical protein	middle	
087	3	116	hypothetical protein	early	
088	3	101	hypothetical protein	middle	
089	3	69	hypothetical protein	middle	
090	3	124	hypothetical protein	middle	
091	3	134	hypothetical protein	middle	
092	3	142	hypothetical conserved protein	middle	
093	3	153	hypothetical protein	middle	
094	3	69	hypothetical protein	middle	
095	3	82	hypothetical protein	middle	
096	3	123	hypothetical protein	early	
097	3	257	Putative DNA polymerase III, subunit	early	
098	3	62	hypothetical protein	middle	
099	3	204	hypothetical protein	middle	
100	3	179	hypothetical conserved protein	middle	
101	3	215	hypothetical protein	middle	
102	3	104	hypothetical protein	middle	
103	3	91	hypothetical conserved protein	middle	
104	3	124	hypothetical protein	middle	
105	3	115	hypothetical protein	middle	x
106	3	92	hypothetical protein	middle	
107	3	143	hypothetical protein	middle	
108	3	87	hypothetical protein	middle	
109	3	363	Ribonucleotide reductase	middle	
110	3	757	ribonucleoside-diphosphate reductase subunit alpha	middle	x
111	3	177	hypothetical conserved protein	middle	x
112	3	473	Putative ribosomal protein modification protein	middle	x
113	3	80	hypothetical protein	middle	
114	3	215	Putative dCTP deaminase	middle	
115	3	124	hypothetical protein	middle	
116	3	124	Putative RNA 2'-phosphotransferase	early	
117	3	216	hypothetical protein	early	
118	3	106	hypothetical protein	early	
119	3	273	hypothetical protein	early	
120	3	126	hypothetical protein	early	
121	3	58	hypothetical protein	early	
122	3	191	hypothetical protein	early	
123	3	62	hypothetical protein	early	
124	3	203	hypothetical protein	middle	
125	3	102	hypothetical protein	early	x
126	3	254	Putative endonuclease-like protein	early	
127	3	385	Putative thymidylate synthetase	middle	
128	3	102	hypothetical protein	middle	
129	3	155	hypothetical protein	middle	x
130	4	76	hypothetical protein	early	
131	4	127	hypothetical protein	early	
132	4	241	hypothetical protein	early	x
133	4	74	Putative transglycosylase	middle	
134	4	193	hypothetical protein	early	
135	4	677	Putative DNA topoisomerase	early	x
136	4	440	Putative DNA topoisomerase	middle	x
137	4	241	Putative DNA polymerase III, subunit	middle	x
138	4	84	hypothetical protein	middle	

139	4	69	hypothetical protein	middle	x
140	4	305	Putative structural protein	middle	
141	4	265	Putative dUTP diphosphatase	middle	x
142	4	95	hypothetical protein	middle	
143	4	484	Putative ATP-dependent DNA helicase	middle	x
144	4	54	hypothetical protein	middle	
145	4	359	Putative replicative helicase	middle	
146	4	73	hypothetical protein	middle	
147	4	201	hypothetical protein	middle	
148	4	377	hypothetical protein	middle	x
149	4	322	Putative exodeoxyribonuclease	middle	x
150	5	119	hypothetical protein	early	
151	5	80	hypothetical protein	middle	
152	5	130	hypothetical protein	middle	x
153	5	130	hypothetical protein	middle	
154	5	224	hypothetical protein	middle	x
155	5	171	hypothetical protein	middle	
156	5	106	hypothetical protein	middle	
157	5	142	hypothetical protein	middle	
158	5	80	hypothetical protein	middle	
159	5	155	hypothetical protein	middle	
160	5	190	hypothetical protein	middle	
161	5	251	Putative tail fiber protein	early	
162	5	540	Putative DNA directed RNA polymerase, subunit / Putative DNA helicase	early	
163	5	76	hypothetical protein	middle	
164	5	59	hypothetical protein	middle	
165	5	41	hypothetical protein	middle	
166	5	67	hypothetical conserved protein	middle	
167	5	210	Putative endonuclease	middle	x
168	5	94	hypothetical protein	middle	
169	5	141	hypothetical conserved protein	middle	
170	5	125	hypothetical protein	middle	
171	5	102	hypothetical protein	middle	
172	5	91	hypothetical conserved protein	middle	
173	5	34	hypothetical protein	middle	
174	5	120	Putative phage baseplate assembly protein	middle	
175	5	52	hypothetical protein	middle	
176	5	40	hypothetical protein	late	
177	5	82	hypothetical protein	middle	
178	6	203	hypothetical protein	early	
179	6	283	Putative exonuclease	middle	
180	6	1012	Putative exonuclease	middle	x
181	6	58	hypothetical protein	middle	x
182	6	173	hypothetical protein	middle	x
183	6	184	hypothetical conserved protein	middle	
184	6	138	hypothetical protein	middle	
185	6	201	hypothetical conserved protein	middle	x
186	6	68	hypothetical protein	early	
187	6	107	hypothetical protein	early	
188	6	94	hypothetical protein	early	
189	7	233	Putative endonuclease-like protein	early	
190	7	675	DNA topoisomerase	early	x

191	7	119	hypothetical protein	middle	
192	7	118	hypothetical protein	middle	
193	7	481	Putative helicase	early	x
194	8	98	hypothetical protein	early	
195	8	298	Putative DNA polymerase	early	
196	8	73	hypothetical conserved protein	early	
197	8	639	hypothetical protein	early	x
198	8	70	hypothetical protein	early	
199	9	637	Putative DNA ligase	early	x
200	9	65	hypothetical protein	-	
201	9	82	hypothetical protein	-	

Table S3. Transcriptional response in YerA41 infected *Y. ruckeri* cells. The lists of genes differentially expressed at 15, 30 and 60 min p.i. LogFC; log-ratio of a transcript's expression values in two different conditions. FDR; False Discovery Rate.

15 min vs 0

Gene	Function of the gene product	logFC	FDR
CSF007_0230	Promiscuous sugar phosphatase YidA%2C haloacid dehalogenase-like phosphatase family	0.86	0.000484
CSF007_0240	Outer membrane lipoprotein YidQ	-1.116	7.97×10^{-8}
CSF007_0245	16 kDa heat shock protein A	-1.37	0.000331
CSF007_0250	16 kDa heat shock protein B	-1.62	5.50×10^{-7}
CSF007_0605	Aerobic C4-dicarboxylate transporter for fumarate%2C L-malate%2C D-malate%2C succinate	-1.23	1.07×10^{-9}
CSF007_0665	Glutathione reductase	2.88	3.43×10^{-31}
CSF007_0675	Oligopeptidase A	-1.03	0.000428
CSF007_0690	Universal stress protein A	-1.20	1.55×10^{-7}
CSF007_0800	hypothetical protein	-1.12	1.77×10^{-5}
CSF007_0860	High-affinity gluconate transporter GntT	-1.38	4.39×10^{-9}
CSF007_0865	Gluconokinase	-2.12	9.37×10^{-17}
CSF007_0935	Transcriptional activator of maltose regulon%2C MalT	-1.49	7.07×10^{-14}
CSF007_0940	Maltodextrin phosphorylase	-1.31	6.96×10^{-5}
CSF007_0980	Ferrous iron-sensing transcriptional regulator FeoC	-1.20	2.28×10^{-7}
CSF007_0985	Ferrous iron transport protein B	-1.50	6.78×10^{-11}
CSF007_0990	Ferrous iron transport protein A	-1.75	6.88×10^{-8}
CSF007_10065	Ferritin-like protein 2	1.36	1.89×10^{-7}
CSF007_1015	hypothetical protein	-0.74	0.000568
CSF007_10170	Putative membrane protein	0.99	6.75×10^{-5}
CSF007_10235	Ribosomal RNA large subunit methyltransferase A	0.84	1.69×10^{-5}
CSF007_10335	Lipid A export ATP-binding/permease protein MsbA	-0.95	3.88×10^{-5}
CSF007_10695	hypothetical protein	1.26	3.55×10^{-6}
CSF007_11010	Lysine decarboxylase%2C inducible	1.29	9.23×10^{-7}
CSF007_11035	Transcriptional repressor of PutA and PutP / Proline dehydrogenase (Proline oxidase) / Delta-1-pyrroline-5-carboxylate dehydrogenase	-1.12	9.24×10^{-6}
CSF007_11450	tRNA-Ser	-1.87	1.17×10^{-5}
CSF007_11455	hypothetical protein	-2.12	8.23×10^{-28}
CSF007_1170	Transcriptional regulator YPDSF_0092%2C LacI family	-1.06	1.61×10^{-5}
CSF007_11760	Putrescine importer	1.43	1.44×10^{-7}
CSF007_11775	Ferrichrome transport ATP-binding protein FhuC	-1.57	3.04×10^{-10}
CSF007_11780	Iron(III) dicitrate transport system permease protein FecD	-1.60	1.44×10^{-7}

CSF007_11785	Putative periplasmic substrate-binding transport protein PTS system%2C fructose-specific IIB component-PTS system%2C	-1.95	3.45×10^{-15}
CSF007_11810	fructose-specific IIC component Fructose-specific phosphocarrier protein HPr-PTS system%2C fructose-	1.95	1.10×10^{-11}
CSF007_11820	specific IIA component	1.30	3.62×10^{-5}
CSF007_11865	Mannonate dehydratase	-1.46	8.78×10^{-10}
CSF007_11875	D-mannonate oxidoreductase	-1.87	3.62×10^{-13}
CSF007_1205	hypothetical protein	-0.75	0.000372
CSF007_1210	Cyclic AMP receptor protein	-1.32	5.98×10^{-8}
CSF007_12280	Uncharacterized protein YfaZ precursor	0.98	9.55×10^{-6}
CSF007_12285	Catalase	4.10	3.26×10^{-59}
CSF007_12375	NADH-ubiquinone oxidoreductase chain E NADH-ubiquinone oxidoreductase chain C-NADH-ubiquinone	-0.86	0.00015
CSF007_12380	oxidoreductase chain D	-1.01	5.05×10^{-5}
CSF007_12385	NADH-ubiquinone oxidoreductase chain B	-0.85	0.000486
CSF007_12390	NADH ubiquinone oxidoreductase chain A	-0.90	7.72×10^{-5}
CSF007_12450	Ascorbate-specific PTS system%2C EIIA component	-3.07	6.74×10^{-23}
CSF007_12455	Putative sugar phosphotransferase component II B	-3.21	1.62×10^{-22}
CSF007_12460	membrane protein Histidine ABC transporter%2C histidine-binding periplasmic protein	-2.21	3.34×10^{-18}
CSF007_12505	precursor HisJ	-1.23	0.000314
CSF007_12510	hypothetical protein	-1.37	1.65×10^{-5}
CSF007_12625	3-oxoacyl-[acyl-carrier-protein] synthase%2C KASI	-0.89	0.000999
CSF007_12645	Putative membrane protein YfcA	0.80	0.00062
CSF007_12680	3-ketoacyl-CoA thiolase	-1.24	1.82×10^{-7}
CSF007_12840	Nucleoside permease NupC	-0.94	1.43×10^{-5}
CSF007_12845	tRNA-Lys	1.17	0.000997
CSF007_12920	hypothetical protein	0.88	0.00014
CSF007_12965	Sialic acid transporter (permease) NanT	-1.92	2.90×10^{-12}
CSF007_12985	N-acetylmannosamine-6-phosphate 2-epimerase	-0.95	0.000242
CSF007_13080	NADP-dependent malic enzyme	-1.12	9.98×10^{-8}
CSF007_1330	tRNA 5-methylaminomethyl-2-thiouridine synthase TusB	0.86	0.000399
CSF007_13380	hypothetical protein	-1.16	1.44×10^{-6}
CSF007_13405	Inosine-5-monophosphate dehydrogenase	0.91	0.000343
CSF007_13705	Sigma factor RpoE regulatory protein RseC	1.25	2.39×10^{-6}
CSF007_13710	Sigma factor RpoE negative regulatory protein RseB precursor	1.01	6.13×10^{-6}
CSF007_13720	RNA polymerase sigma factor RpoE	0.98	0.000806
CSF007_13750	Pyruvate formate-lyase	1.13	5.01×10^{-5}
CSF007_13880	Phosphosugar isomerase/binding protein	-1.01	2.19×10^{-6}
CSF007_13885	D-ribulokinase	-0.94	6.94×10^{-7}
CSF007_13895	Ribose ABC transport system%2C permease protein RbsC Ribose/xylose/arabinose/galactoside ABC-type transport system ATP-	-1.48	1.29×10^{-12}
CSF007_13900	binding protein	-2.08	2.79×10^{-28}
CSF007_13905	hypothetical protein Ribose/xylose/arabinose/galactoside ABC-type transport system	-3.28	2.14×10^{-13}
CSF007_13910	periplasmic sugar binding protein	-2.48	1.26×10^{-19}
CSF007_13970	Acid shock protein 2 precursor	-1.40	4.10×10^{-7}
CSF007_14045	hypothetical tRNA/rRNA methyltransferase yfiF	0.88	0.00058
CSF007_14050	hypothetical protein	3.31	1.55×10^{-34}
CSF007_14055	Thioredoxin 2	4.53	2.39×10^{-54}
CSF007_14060	hypothetical protein	3.64	2.92×10^{-48}
CSF007_14065	Protein acetyltransferase Hypothetical protein YqcC clustered with tRNA pseudouridine	2.30	5.60×10^{-23}
CSF007_14315	synthase C	0.82	7.39×10^{-5}

CSF007_14500	Galactose operon repressor%2C GalR-LacI family of transcriptional regulators	-0.92	1.31×10^{-6}
CSF007_14700	Predicted hemolysin III like membrane protein	-0.80	0.000572
CSF007_14715	Glycine cleavage system H protein	-0.81	0.000445
CSF007_14720	Aminomethyltransferase (glycine cleavage system T protein)	-1.11	3.59×10^{-9}
CSF007_14815	hypothetical protein	2.02	5.84×10^{-7}
CSF007_14820	hypothetical protein	3.31	1.76×10^{-11}
CSF007_15070	hypothetical protein	-0.92	1.30×10^{-6}
CSF007_15200	Amide synthase component of siderophore synthetase	2.78	6.43×10^{-21}
CSF007_15205	2%2C3-dihydro-2%2C3-dihydroxybenzoate dehydrogenase of siderophore biosynthesis	2.16	1.07×10^{-14}
CSF007_15210	Isochorismatase of siderophore biosynthesis	2.07	2.68×10^{-13}
CSF007_15255	Enterobactin synthetase component F%2C serine activating enzyme	1.52	6.32×10^{-9}
CSF007_15260	Polymyxin synthetase PmxB	1.82	9.44×10^{-19}
CSF007_15265	Enterobactin esterase	1.30	1.40×10^{-7}
CSF007_15270	Ferrichrome-iron receptor	1.10	5.01×10^{-5}
CSF007_15345	Biopolymer transport protein ExbD/ToIR	-1.10	0.000176
CSF007_15665	23S rRNA (guanine-N-2-)-methyltransferase rlmG	0.84	0.000204
CSF007_15715	hypothetical protein	-2.64	2.61×10^{-10}
CSF007_15720	Hexuronate transporter	-2.38	7.15×10^{-28}
CSF007_15765	Inner membrane protein YqjF	0.95	5.66×10^{-6}
CSF007_1600	Acetyl-coenzyme A synthetase	-0.93	1.66×10^{-6}
CSF007_16000	hypothetical protein	-1.42	2.65×10^{-6}
CSF007_16005	Trehalose-6-phosphate hydrolase	-2.46	3.37×10^{-14}
CSF007_16010	PTS system%2C trehalose-specific IIB component-PTS system%2C trehalose-specific IIC component	-3.39	3.53×10^{-41}
CSF007_16315	Maltose operon periplasmic protein MalM	-1.51	6.85×10^{-6}
CSF007_16325	Maltose/maltodextrin transport ATP-binding protein MalK	-1.81	6.80×10^{-6}
CSF007_16340	Maltose/maltodextrin ABC transporter%2C substrate binding periplasmic protein MalE	-1.68	5.91×10^{-8}
CSF007_16355	PsiE protein	1.32	6.05×10^{-10}
CSF007_16360	Glucose-6-phosphate isomerase	2.24	6.00×10^{-22}
CSF007_16530	Isocitrate lyase	-0.69	0.000926
CSF007_17470	Soluble pyridine nucleotide transhydrogenase	-1.14	1.89×10^{-6}
CSF007_17480	Peroxiredoxin family protein/glutaredoxin	6.95	4.94×10^{-128}
CSF007_17485	Dihydrolipoamide dehydrogenase	7.07	1.97×10^{-146}
CSF007_17495	hypothetical protein	2.06	1.51×10^{-26}
CSF007_17500	hypothetical protein	1.79	5.04×10^{-20}
CSF007_1760	Aspartate ammonia-lyase	-1.01	6.88×10^{-5}
CSF007_17650	Glycerol uptake facilitator protein	-2.39	1.55×10^{-28}
CSF007_17655	Glycerol kinase	-2.56	1.20×10^{-19}
CSF007_17695	6-phosphofructokinase	1.21	1.03×10^{-6}
CSF007_17975	Glutamine synthetase type I	-1.09	0.00014
CSF007_17985	Nitrogen regulation protein NR(I)	-0.76	0.000579
CSF007_18075	Ribose ABC transport system%2C periplasmic ribose-binding protein RbsB	-1.41	1.96×10^{-11}
CSF007_18080	Ribose ABC transport system%2C permease protein RbsC	-0.72	0.000851
CSF007_18085	Ribose ABC transport system%2C ATP-binding protein RbsA	-1.51	7.72×10^{-10}
CSF007_18090	Ribose ABC transport system%2C high affinity permease RbsD	-1.66	1.10×10^{-11}
CSF007_1900	tRNA-Gly	0.81	7.70×10^{-5}
CSF007_3355	Aconitate hydratase 2	-1.69	3.40×10^{-12}
CSF007_5505	hypothetical protein	-0.78	1.77×10^{-5}
CSF007_5525	Glutamate Aspartate periplasmic binding protein precursor GltI	-1.56	7.31×10^{-11}
CSF007_5790	Citrate synthase (si)	-3.23	8.51×10^{-22}

CSF007_5795	Succinate dehydrogenase cytochrome b-556 subunit	-2.64	4.76×10^{-26}
CSF007_5800	Succinate dehydrogenase hydrophobic membrane anchor protein	-2.49	4.39×10^{-19}
CSF007_5805	Succinate dehydrogenase flavoprotein subunit	-2.65	2.01×10^{-22}
CSF007_5810	Succinate dehydrogenase iron-sulfur protein	-2.47	1.33×10^{-16}
CSF007_5815	2-oxoglutarate dehydrogenase E1 component	-1.80	2.19×10^{-13}
CSF007_5820	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex	-1.41	7.97×10^{-8}
CSF007_5825	Succinyl-CoA ligase [ADP-forming] beta chain	-1.60	7.19×10^{-8}
CSF007_5830	Succinyl-CoA ligase [ADP-forming] alpha chain	-1.63	1.56×10^{-9}
CSF007_5840	Cytochrome d ubiquinol oxidase subunit I	1.21	1.89×10^{-6}
CSF007_5845	Cytochrome d ubiquinol oxidase subunit II	1.14	1.98×10^{-6}
CSF007_5895	tRNA-Lys	1.27	0.000561
CSF007_5900	tRNA-Lys	0.96	5.80×10^{-7}
CSF007_5905	tRNA-Lys	1.00	5.13×10^{-8}
CSF007_5965	Galactose-1-phosphate uridylyltransferase	-1.33	7.03×10^{-8}
CSF007_5970	UDP-N-acetylglucosamine 4-epimerase-UDP-glucose 4-epimerase	-1.48	2.09×10^{-10}
CSF007_6300	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase	4.39	4.13×10^{-66}
CSF007_6370	Possible MFS Superfamily transporter precursor	1.04	4.09×10^{-5}
CSF007_6390	hypothetical protein	-1.65	4.00×10^{-5}
CSF007_6395	Galactose/methyl galactoside ABC transport system%2C D-galactose-binding periplasmic protein MglB	-2.08	2.72×10^{-14}
CSF007_6400	Galactose/methyl galactoside ABC transport system%2C ATP-binding protein MglA	-1.13	1.92×10^{-7}
CSF007_6500	6-phosphogluconate dehydrogenase%2C decarboxylating	1.82	1.02×10^{-13}
CSF007_6595	L-serine dehydratase%2C beta subunit-L-serine dehydratase%2C alpha subunit	-1.06	0.000227
CSF007_6600	Serine transporter	-1.30	3.63×10^{-7}
CSF007_6685	Glutaredoxin 1	3.96	8.92×10^{-56}
CSF007_6760	Arginine ABC transporter%2C periplasmic arginine-binding protein ArtI	0.95	8.89×10^{-7}
CSF007_6765	Arginine ABC transporter%2C ATP-binding protein ArtP	1.05	9.24×10^{-6}
CSF007_6870	Thioredoxin reductase	2.23	3.39×10^{-20}
CSF007_9025	Alkyl sulfatase	-0.93	2.94×10^{-6}
CSF007_9035	hypothetical protein	-1.05	9.23×10^{-7}
CSF007_9550	Putative transport protein	-1.80	4.34×10^{-12}
CSF007_9585	tRNA-Val	1.15	3.88×10^{-5}
CSF007_9590	Pyruvate kinase	1.95	7.27×10^{-15}
CSF007_9605	Sulfur acceptor protein SufE for iron-sulfur cluster assembly	0.94	0.000484
CSF007_9610	Cysteine desulfurase%2C SufS subfamily	0.97	4.77×10^{-5}
CSF007_9630	Iron binding protein SufA for iron-sulfur cluster assembly	0.71	0.000742
CSF007_9650	Phosphoenolpyruvate synthase	-1.82	6.56×10^{-15}
CSF007_9670	hypothetical protein	-2.85	1.01×10^{-17}
CSF007_9675	TonB-dependent hemin%2C ferrichrome receptor	-1.55	9.46×10^{-16}
CSF007_9680	Hemin transport protein HmuS	-1.06	1.77×10^{-5}
CSF007_9870	hypothetical protein	-1.83	7.14×10^{-6}

30 min vs 0

Gene ID	Function of the gene product	logFC	FDR
CSF007_0245	16 kDa heat shock protein A	-1.80	6.55×10^{-6}
CSF007_0605	Aerobic C4-dicarboxylate transporter for fumarate%2C L-malate%2C D-malate%2C succinate	-1.09	0.000456
CSF007_0675	Oligopeptidase A	-1.29	0.000435

CSF007_0690	Universal stress protein A	-1.56	5.98×10^{-6}
CSF007_0865	Gluconokinase	-1.80	7.28×10^{-6}
CSF007_0915	Aerobic glycerol-3-phosphate dehydrogenase	1.28	5.16×10^{-6}
CSF007_0935	Transcriptional activator of maltose regulon%2C MalT	-1.48	8.42×10^{-7}
CSF007_10015	putative lipoprotein	1.14	0.000789
CSF007_10150	PTS system%2C mannose-specific IIA component / PTS system%2C mannose-specific IIB component	-2.00	2.32×10^{-6}
CSF007_10155	PTS system%2C mannose-specific IIC component	-1.86	2.38×10^{-10}
CSF007_10160	PTS system%2C mannose-specific IID component	-1.58	5.83×10^{-5}
CSF007_10265	Lipid A acylation protein PagP%2C palmitoyltransferase	1.12	0.000305
CSF007_10385	Cold shock protein CspG	2.52	7.97×10^{-5}
CSF007_11035	Transcriptional repressor of PutA and PutP / Proline dehydrogenase (Proline oxidase) / Delta-1-pyrroline-5-carboxylate dehydrogenase	-2.14	5.30×10^{-14}
CSF007_11425	Beta-galactosidase	-1.18	4.19×10^{-5}
CSF007_11455	hypothetical protein	-1.57	4.48×10^{-5}
CSF007_1165	Putative membrane receptor protein	-1.42	2.99×10^{-7}
CSF007_11760	Putrescine importer	1.71	4.96×10^{-5}
CSF007_11865	Mannonate dehydratase	-2.13	6.04×10^{-12}
CSF007_11875	D-mannonate oxidoreductase	-2.57	4.08×10^{-14}
CSF007_1210	Cyclic AMP receptor protein	-1.42	1.30×10^{-5}
CSF007_12285	Catalase	1.54	9.40×10^{-9}
CSF007_12340	NADH-ubiquinone oxidoreductase chain L	-1.12	0.000547
CSF007_12345	NADH-ubiquinone oxidoreductase chain K	-1.38	9.35×10^{-5}
CSF007_12350	NADH-ubiquinone oxidoreductase chain J	-1.29	7.97×10^{-5}
CSF007_12355	NADH-ubiquinone oxidoreductase chain I	-1.22	0.00014
CSF007_12360	NADH-ubiquinone oxidoreductase chain H	-1.07	0.000101
CSF007_12365	NADH-ubiquinone oxidoreductase chain G	-1.17	0.000143
CSF007_12450	Ascorbate-specific PTS system%2C EIIA component	-3.17	6.76×10^{-10}
CSF007_12455	Putative sugar phosphotransferase component II B	-3.52	1.76×10^{-9}
CSF007_12460	membrane protein	-2.35	7.75×10^{-9}
CSF007_12810	Glucokinase	-2.03	3.32×10^{-5}
CSF007_12920	hypothetical protein	1.11	0.000155
CSF007_12965	Sialic acid transporter (permease) NanT	-2.72	4.08×10^{-14}
CSF007_13080	NADP-dependent malic enzyme	-1.68	2.82×10^{-9}
CSF007_13300	Putative heat shock protein YegD	1.37	4.65×10^{-5}
CSF007_13400	GMP synthase [glutamine-hydrolyzing]	1.29	5.70×10^{-5}
CSF007_13405	Inosine-5-monophosphate dehydrogenase	1.19	0.000169
CSF007_13880	Phosphosugar isomerase/binding protein	-1.98	6.52×10^{-9}
CSF007_13885	D-ribulokinase	-2.04	9.33×10^{-14}
CSF007_13895	Ribose ABC transport system%2C permease protein RbsC	-2.07	7.16×10^{-12}
CSF007_13900	Ribose/xylose/arabinose/galactoside ABC-type transport system ATP-binding protein	-2.06	7.97×10^{-5}
CSF007_13905	hypothetical protein	-5.24	6.87×10^{-10}
CSF007_13910	Ribose/xylose/arabinose/galactoside ABC-type transport system periplasmic sugar binding protein	-3.70	1.55×10^{-33}
CSF007_14710	Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein)	-1.40	2.51×10^{-6}
CSF007_14715	Glycine cleavage system H protein	-1.88	3.38×10^{-7}
CSF007_14720	Aminomethyltransferase (glycine cleavage system T protein)	-1.68	7.18×10^{-10}
CSF007_15470	3%2C4-dihydroxy-2-butanone 4-phosphate synthase	2.00	9.22×10^{-14}
CSF007_15695	Inner membrane protein ygjV	-1.22	0.00046
CSF007_15700	Altronate dehydratase	-1.53	1.13×10^{-5}
CSF007_15705	Altronate oxidoreductase	-1.56	2.24×10^{-6}
CSF007_15710	Uronate isomerase	-1.55	1.79×10^{-5}

CSF007_15715	hypothetical protein	-3.74	1.21×10^{-17}
CSF007_15720	Hexuronate transporter	-2.40	1.25×10^{-10}
CSF007_15880	Outer membrane stress sensor protease DegQ%2C serine protease	-1.41	7.04×10^{-5}
CSF007_16000	hypothetical protein	-1.99	6.12×10^{-6}
CSF007_16005	Trehalose-6-phosphate hydrolase PTS system%2C trehalose-specific IIB component-PTS system%2C	-3.86	3.31×10^{-24}
CSF007_16010	trehalose-specific IIC component	-3.85	1.29×10^{-27}
CSF007_16175	tRNA dihydrouridine synthase B	1.38	6.73×10^{-6}
CSF007_16180	DNA-binding protein Fis	1.28	0.00037
CSF007_16315	Maltose operon periplasmic protein MalM Maltoporin (maltose/maltodextrin high-affinity receptor%2C phage	-2.03	0.000431
CSF007_16320	lambda receptor protein)	-2.12	0.000568
CSF007_16325	Maltose/maltodextrin transport ATP-binding protein MalK Maltose/maltodextrin ABC transporter%2C substrate binding	-2.93	3.65×10^{-8}
CSF007_16340	periplasmic protein MalE	-2.03	1.45×10^{-6}
CSF007_17480	Peroxiredoxin family protein/glutaredoxin	1.12	7.36×10^{-5}
CSF007_17485	Dihydrolipoamide dehydrogenase	1.28	2.16×10^{-7}
CSF007_1760	Aspartate ammonia-lyase	-1.98	3.86×10^{-12}
CSF007_17650	Glycerol uptake facilitator protein	-2.08	5.48×10^{-11}
CSF007_17655	Glycerol kinase	-3.31	2.81×10^{-15}
CSF007_1770	Heat shock protein 60 family co-chaperone GroES	-1.22	0.000862
CSF007_17975	Glutamine synthetase type I	1.92	4.07×10^{-5}
CSF007_17980	Nitrogen regulation protein NtrB Ribose ABC transport system%2C periplasmic ribose-binding protein	1.44	1.74×10^{-7}
CSF007_18075	RbsB	-1.57	8.42×10^{-7}
CSF007_18085	Ribose ABC transport system%2C ATP-binding protein RbsA	-1.85	2.56×10^{-6}
CSF007_18090	Ribose ABC transport system%2C high affinity permease RbsD	-2.16	4.82×10^{-8}
CSF007_3355	Aconitate hydratase 2	-1.66	1.56×10^{-6}
CSF007_5505	hypothetical protein	-1.18	1.44×10^{-5}
CSF007_5790	Citrate synthase (si)	-3.11	8.36×10^{-10}
CSF007_5795	Succinate dehydrogenase cytochrome b-556 subunit	-2.04	9.68×10^{-13}
CSF007_5800	Succinate dehydrogenase hydrophobic membrane anchor protein	-2.64	1.15×10^{-10}
CSF007_5805	Succinate dehydrogenase flavoprotein subunit	-3.18	3.94×10^{-18}
CSF007_5810	Succinate dehydrogenase iron-sulfur protein	-3.06	6.67×10^{-15}
CSF007_5815	2-oxoglutarate dehydrogenase E1 component Dihydrolipoamide succinyltransferase component (E2) of 2-	-2.96	3.74×10^{-18}
CSF007_5820	oxoglutarate dehydrogenase complex	-2.87	1.10×10^{-12}
CSF007_5825	Succinyl-CoA ligase [ADP-forming] beta chain	-2.86	5.80×10^{-10}
CSF007_5830	Succinyl-CoA ligase [ADP-forming] alpha chain	-3.01	4.78×10^{-14}
CSF007_5840	Cytochrome d ubiquinol oxidase subunit I	1.49	0.000107
CSF007_5845	Cytochrome d ubiquinol oxidase subunit II	1.48	2.78×10^{-5}
CSF007_6145	ATP-dependent RNA helicase RhlE Non-specific DNA-binding protein Dps / Iron-binding ferritin-like	1.44	0.000103
CSF007_6300	antioxidant protein / Ferroxidase Galactose/methyl galactoside ABC transport system%2C D-galactose-	1.90	5.48×10^{-11}
CSF007_6395	binding periplasmic protein MglB Galactose/methyl galactoside ABC transport system%2C ATP-binding	-2.79	1.40×10^{-17}
CSF007_6400	protein MglA	-1.72	6.99×10^{-9}
CSF007_9025	Alkyl sulfatase	-1.32	1.03×10^{-5}
CSF007_9550	Putative transport protein	-1.51	2.19×10^{-6}
CSF007_9590	Pyruvate kinase	2.11	9.00×10^{-13}
CSF007_9650	Phosphoenolpyruvate synthase	-2.54	1.16×10^{-9}
CSF007_9675	TonB-dependent hemin%2C ferrichrome receptor	-1.13	0.000184
CSF007_9680	Hemin transport protein HmuS	-1.38	0.000972

60 min vs 0

Gene ID	Function of the gene product	logFC	FDR
CSF007_0245	16 kDa heat shock protein A	1.28	0.000686
CSF007_0915	Aerobic glycerol-3-phosphate dehydrogenase PTS system%2C fructose-specific IIB component-PTS system%2C	1.66	3.28×10^{-9}
CSF007_11810	fructose-specific IIC component	4.34	2.17×10^{-20}
CSF007_11815	1-phosphofructokinase Fructose-specific phosphocarrier protein HPr-PTS system%2C fructose-	3.35	5.91×10^{-9}
CSF007_11820	specific IIA component	4.38	4.38×10^{-13}
CSF007_11825	Putative Mut family protein	1.32	2.73×10^{-8}
CSF007_13975	Glutaredoxin-like protein NrdH	2.84	5.11×10^{-12}
CSF007_13980	Ribonucleotide reduction protein NrdI	3.24	4.52×10^{-19}
CSF007_13985	Ribonucleotide reductase of class Ib (aerobic)%2C alpha subunit	2.89	2.17×10^{-20}
CSF007_13990	Ribonucleotide reductase of class Ib (aerobic)%2C beta subunit 2%2C3-dihydro-2%2C3-dihydroxybenzoate dehydrogenase of	2.59	1.36×10^{-16}
CSF007_15205	siderophore biosynthesis	1.03	0.000604
CSF007_15220	Isochorismate synthase of siderophore biosynthesis	1.10	0.000399
CSF007_17655	Glycerol kinase	1.56	3.18×10^{-5}
CSF007_9650	Phosphoenolpyruvate synthase	-1.98	1.77×10^{-13}
CSF007_9890	Manganese ABC transporter%2C periplasmic-binding protein SitA	0.99	0.000138

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