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Two separate modules of the conserved regulatory RNA AbcR1 address multiple target mRNAs in and outside of the translation initiation region

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Supplementary Table S1: List of all putative AbcR1 targets.

Protein spots with fold changes >2 or <0.5 are listed. Spots listed with numbers were not excised or subjected to mass spectrometry.

protein name/label	locus tag	product	ΔAbcR1/WT
Atu4577	*atu4577*	ABC transporter substrate binding protein	66,90
PykA	*atu3762*	pyruvate kinase	36,86
RbsB	*atu3821*	ABC transporter substrate-binding protein (ribose)	25,64
Atu0857	*atu0857*	oxidoreductase	13,45
Atu2188	*atu2188*	oxidoreductase	9,42
MalE	*atu2601*	ABC transporter, substrate binding protein (maltose)	8,05
Pgi	*atu0404*	glucose-6-phosphate isomerase	6,64
Atu4046	*atu4046*	ABC transporter substrate-binding protein (glycine betaine)	6,22
MurE	*atu2099*	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6- diaminopimelate ligase	5,87
Atu1879	*atu1879*	ABC transporter, substrate binding protein (amino acid)	4,50
Atu0157	*atu0157*	ABC transporter, substrate binding protein	3,87
Atu4678	*atu4678*	ABC transporter substrate-binding protein (amino acid)	3,85
Atu2422	*atu2422*	ABC transporter, substrate binding protein (amino acid GABA)	3,66
FrcB	*atu0063*	ABC transporter, substrate binding protein (sugar)	2,13
DppA	*atu4113*	ABC transporter substrate-binding protein (dipeptide)	2,07
39	-	-	3,95
40	-	-	2,76
41	-	-	8,18
42	-	-	3,04
43	-	-	4,75
44	-	-	3,22
45	-	-	4,43
46	-	-	4,34
47	-	-	3,51
48	-	-	3,84
Atu3259	*atu3259*	dehydrogenase	0,20
RplI	*atu1088*	50S ribosomal protein L9	0,18
AtpH	*atu2625*	ATP Synthase delta chain	0,16
MurB	*atu2092*	UDP-N-acetylenolpyruvoylglucosamine reductase	0,08
RplY	*atu2227*	50S ribosomal protein L25	0,05
1	-	-	0,12
2	-	-	0,24

protein name/label	locus tag	product	ΔAbcR1/WT
3	-	-	1,67
4	-	-	0,25
5	-	-	0,08
6	-	-	0,38
7	-	-	0,16
8	-	-	0,08
9	-	-	0,31
10	-	-	0,38
11	-	-	0,37
12	-	-	0,40
13	-	-	0,08
14	-	-	0,15
15	-	-	0,21
16	-	-	0,29
17	-	-	0,33
18	-	-	0,95
19	-	-	0,13
20	-	-	0,92
21	-	-	0,16
22	-	-	0,07
23	-	-	0,18
24	-	-	0,13
25	-	-	0,22
26	-	-	0,10
27	-	-	0,05
28	-	-	0,00
29	-	-	0,04
30	-	-	0,04
31	-	-	0,02
32	-	-	0,02
33	-	-	0,03
34	-	-	0,05
35	-	-	0,07
36	-	-	0,04
37	-	-	0,03
38	-	-	0,07

Supplementary Table S2: Features of putative Hfq targets.

Protein spots with fold changes >2 or <0.5 are listed. Spots listed with numbers were not excised or subjected to mass spectrometry. # indicates protein spots used for quantitation if proteins were identified in multiple spots.

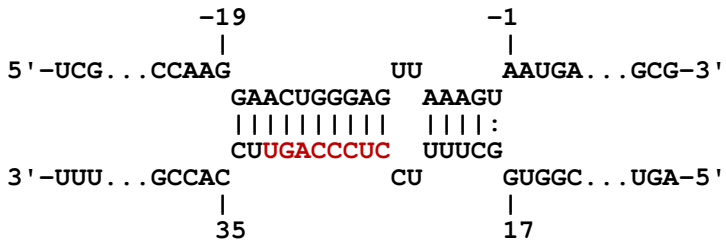
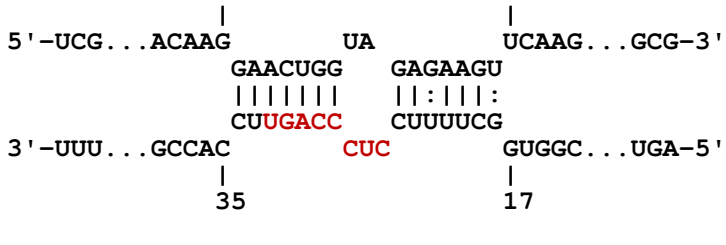
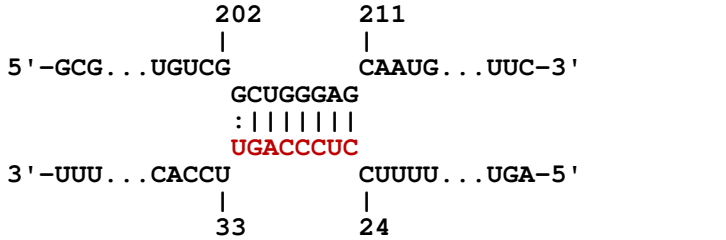
protein name/label	locus tag	product	Δ*hfq*/WT
PcaC	*atu0858*	putative carboxymuconolactone decarboxylase	65,8077198
Atu0157	*atu0157*	ABC transporter substrate binding protein	60,67809868
Atu2604	*atu2604*	Oxidoreductase	55,78796992
Atu5531	*atu5531*	ABC transporter substrate binding protein	20,71308017
Atu4695	*atu4695*	ABC transporter substrate binding protein (oligopeptide)	13,63688394
Atu4577	*atu4577*	ABC transporter substrate binding protein	12,54303892
Atu4695	*atu4695*	ABC transporter substrate binding protein (oligopeptide)	11,61771707
MalE	*atu2601*	ABC transporter substrate binding protein (maltose)	7,169555597
AmaB	*atu2385*	N-carbamoyl-beta-alanine amidohydrolase	6,708581645
HutU	*atu3931*	Urocanase	5,678129298
#Atu0857	*atu0857*	Oxidoreductase	5,490012597
Atu4046	*atu4046*	ABC transporter substrate binding protein (glycin betaine)	4,962024378
Atu1879	*atu1879*	ABC transporter substrate binding protein (amino acid)	4,885786984
Atu0398	*atu0398*	conserved hypothetical protein	3,637844472
ArcA	*atu4007*	Arginase	3,24507874
Atu4740	*atu4740*	zinc-binding dehydrogenase	3,018451845
Atu4431	*atu4431*	ABC transporter substrate binding protein (oligopeptide)	2,962362067
Atu4676	*atu4676*	putative malate dehydrogenase	2,811725562
Atu2422	*atu2422*	ABC transporter substrate binding protein (GABA)	2,658909087
Atu2022	*atu2022*	NADP-dependent alcohol dehydrogenase	2,626096189
Atu0263	*atu0263*	Oxidoreductase	2,591932351
DppA	*atu4113*	ABC transporter substrate binding protein (dipeptide)	2,4564486
1	-	-	6,240642688
2	-	-	5,397093128
3	-	-	6,936007796
4	-	-	2,591932351
5	-	-	3,637844472
6	-	-	12,16845878
7	-	-	2,551982148
8	-	-	2,962362067
9	-	-	2,658909087

protein name/label	locus tag	product	Δ*hfq*/WT
10	-	-	2,811725562
11	-	-	2,4564486
12	-	-	2,338221815
13	-	-	2,401355932
14	-	-	2,120774982
#FrcB	*atu0063*	ABC transporter substrate binding protein (fructose)	0,430774702
ChvE	*atu2348*	Sugar binding protein	0,386364062
Atu1157	*atu1157*	conserved hypothetical protein	0,364868372
Atu1122	*atu1122*	nucleoside diphosphate kinase	0,327254871
AldA	*atu2224*	Aldehyde dehydrogenase	0,244421652
AglE	*atu0591*	ABC transporter substrate binding protein (alpha-glucoside)	0,211557861
15	-	-	0,134451393
16	-	-	0,159718144
17	-	-	0,073125579
18	-	-	0,058893108
19	-	-	0,05986198
20	-	-	0,030749161
21	-	-	0,136306268
22	-	-	0,052205518
23	-	-	0,026924695
24	-	-	0,059873559
25	-	-	0,194242804
26	-	-	0,149815916

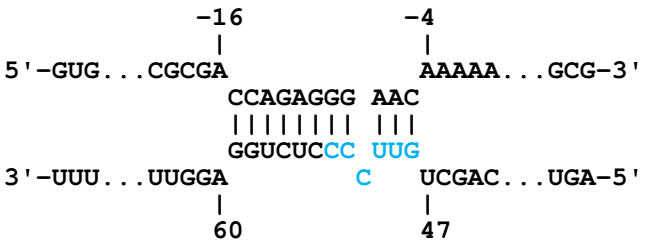
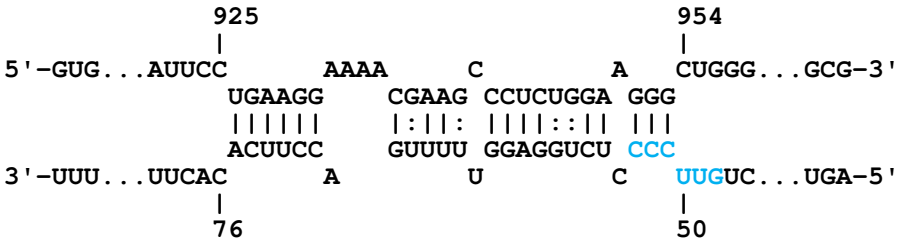
Supplementary Table S3: List of IntaRNA hybrids for AbcR1 in *A. tumefaciens* as predicted by the CopraRNA program.

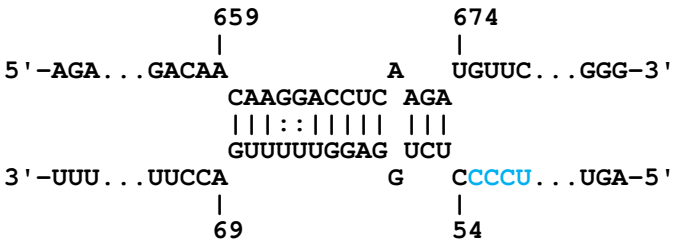
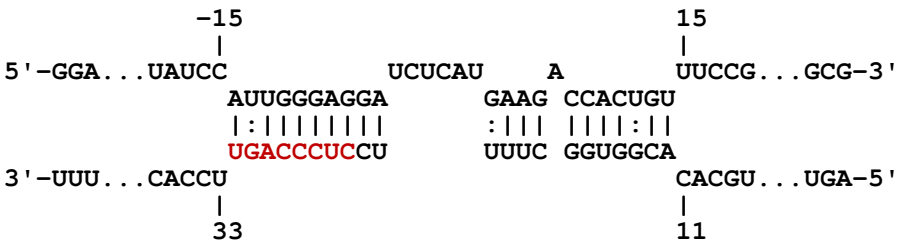
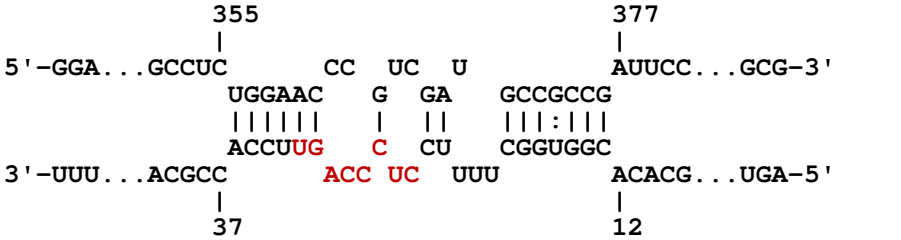
The list contains the results of the best optimal and suboptimal IntaRNA predictions for AbcR1 and its verified target mRNAs. The respective locus tags of target mRNAs are given in column 1. The following columns show the start of the interaction in the target mRNA sequence, end of the interaction in the target sequence, start of the interaction in the sRNA input sequence, end of interaction in the sRNA sequence, energy of predicted IntaRNA duplexes and visualizations of predicted IntaRNA duplexes. Numbering of mRNA nucleotides is given relative to the start codon. Responsible nucleotides of AbcR1 module 1 and module 2 are marked in red and blue, respectively.

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu3114	510	519	22	31	-13,3954	509 520 | | 5'-GUG...CAGAC UUCGC...UUC-3' CUGGGAGGAA |||||||||| GACCCUCCUU 3'-UUU...ACCUU UUCGG...UGA-5' | | 32 21
atu3114	-14	-1	16	29	-12,4938	-15 1 | | 5'-GUG...CAAUA UU AUGCC...UUC-3' GGGAGGAG GCCA |||||||: |||| CCCUCCUU CGGU 3'-UUU...CUUGA UU GGCAC...UGA-5' | | 30 15

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu2422	-18	-2	18	34	-17,2419	
atu2422	844	859	18	34	-9,63245	
atu2601 (*malE*)	203	210	25	32	-9,72186	

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu2601 (malE)	214	231	14	30	-8,08281	213 232 | | 5'-GCG...AGCAA CC C ACGCU...UUC-3' UG AGGA AAGGCCACC || |||| ||:|||||| AC UCCU UUUCGGUGG 3'-UUU...CCUUG CC CACAC...UGA-5' | | 31 13
atu4259	1450	1480	45	73	-9,46243	1449 1481 | | 5'-GAA...UGCAU A UCAU A CGGUC...CUU-3' GAGG CAGAAACC UCC GA GGAACAGC :||| ||:||||| ||| || ||||||| UUCC GUUUUUGG AGG CU CCUUGUCG 3'-UUU...CACAC A U CC ACUAC...UGA-5' | | 74 44
atu4259	103	109	48	54	-8,02975	102 110 | | 5'-GAA...AUUCU CGCAG...CUU-3' GGGGAAC ||||||| CCCCUUG 3'-UUU...GGUCU UCGAC...UGA-5' | | 55 47

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu4046	-15	-5	48	59	-9,06033	
atu4046	926	953	51	75	-5,93626	
atu6027 (*nocT*)	693	700	48	55	-9,50552	

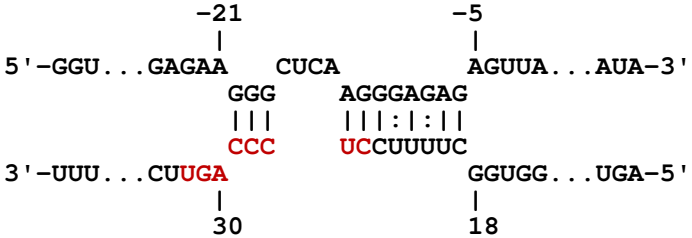
locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu6027 (nocT)	660	673	55	68	-5,77928	
atu0063 (*frcB*)	-14	14	12	32	-12,1984	
atu0063 (frcB)	356	376	13	36	-6,92872	

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu0857	594	614	13	35	-10,0282	593 615 | | 5'-CCC...GCCGC AU C GGCCA...CGG-3' GGAACUG G AGAGCUACCG ||||||| | |:|||:|||| CCUUGAC C UUUCGGUGGC 3'-UUU...CGCCA CCUC U ACACG...UGA-5' | | 36 12
atu0857	82	97	39	54	-7,16622	81 98 | | 5'-CCC...GCGCC CGA UUGGC...CGG-3' GGGG AGCUGGUGC |||| |||||:||| CCCC UCGACUACG 3'-UUU...GGUCU UUG CCACC...UGA-5' | | 55 38
atu1879	220	227	26	33	-6,40746	219 228 | | 5'-ACU...CCAAU CGGCA...CAG-3' GACUGGGA :||||||| UUGACCCU 3'-UUU...CCACC CCUUU...UGA-5' | | 34 25

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu1879	299	310	52	63	-5,10324	298 311 | | 5'-ACU...GGAAC A UCGAU...CAG-3' GCCUCCAGA GG :|||||||| || UGGAGGUCU CC 3'-UUU...GUUUU C CUUGU...UGA-5' | | 64 51
atu4113 (*dppA*)	-32	-3	14	35	-13,9444	-33 -2 | | 5'-GCC...CCGCA UAGAAAAA AG A AGAUG...CGU-3' GGAACU G GGAAAGG CCACC |||||| | |||||:| ||||| CCUUGA C CCUUUUC GGUGG 3'-UUU...CGCCA C CU CACAC...UGA-5' | | 36 13
atu4113 *(dppA)*	828	837	59	68	-5,42523	827 838 | | 5'-GCC...GCCGA AAGCU...CGU-3' CAAGAACCUC |||:|||||| GUUUUUGGAG 3'-UUU...UUCCA GUCUC...UGA-5' | | 69 58

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu4431	927	946	55	74	-7,23038	926 947 | | 5'-GAA...AACCA AA GA AGCCG...GCU-3' GAAG CGAGAACCU AGA |||| |:|:||||| ||| CUUC GUUUUUGGA UCU 3'-UUU...UCACA CA GG CCCCU...UGA-5' | | 75 54
atu4431	166	181	13	34	-6,57593	165 182 | | 5'-GAA...CAUUC UCC AAGUC...GCU-3' GAACUG GCCGCCG |||||| |||:||| CUUGAC CGGUGGC 3'-UUU...GCCAC CCUCCUUUU ACACG...UGA-5' | | 35 12
atu4678	-15	-9	47	53	-9,51503	-16 -8 | | 5'-AUA...UUGAU AAUCA...AUC-3' GGGAGCA ||||:|| CCCUUGU 3'-UUU...GUCUC CGACU...UGA-5' | | 54 46

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu4678	558	571	57	71	-4,07341	557 572 | | 5'-AUA...GCCAC UCC CCGUU...AUC-3' GGUC ACCUCCA |||| ||||||| CCAG UGGAGGU 3'-UUU...CACUU UUUU CUCCC...UGA-5' | | 72 56
atu5192 (attC)	385	402	15	35	-7,05469	384 403 | | 5'-GCG...AAACC U UC AAUA-3' GGA CU AG AAAGCCAC ||| || || |||||||| CCU GA UC UUUCGGUG 3'-UUU...CGCCA U CCC CU GCACA...UGA-5' | | 36 14
atu5192 (*attC*)	282	290	109	117	-4,6405	281 291 | | 5'-GCG...CGCAU GAGAC...AUA-3' GAGAAGAGA :|:||:||| UUUUUUUCU 3'- CCCGG...UGA-5' | | 117 108

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu2348 (chvE)	908	933	48	77	-6,99008	
atu2348 (chvE)	-20	-6	19	29	-6,53859	
atu2625 (atpH)	-8	23	48	80	-13,7642	

locus tag	target start	target end	AbcR1 start	AbcR1 end	energy	interaction
atu2625 (atpH)	36	43	18	25	-5,51037	35 44 | | 5'-UGG...GUAGC AUGCG...CGU-3' GGAAAGGU |||||:|: CCUUUUCG 3'-UUU...ACCCU GUGGC...UGA-5' | | 26 17

Supplementary Table S4: Oligonucleotides used in this study.

T7 promoter sequences for generation of in vitro transcripts are written in bold letters. Restriction sites are underlined. Exchanged nucleotides used for site-directed mutageneses are shaded in grey.

Oligonucleotide	Purpose	Sequence (5' to 3')
RNAprobe_*atu2422*fw	Northern analysis; RNA-probe for *atu2422* [1]	CGGCGTGAAATTCGTTGTC
RNAprobe_*atu2422*rv	Northern analysis; RNA-probe for *atu2422* [1]	**GAAATTAATACGACTCACTATAGG**GTCACGCCGGCAGCATTG
RNAprobe_*atu1879*fw	Northern analysis; RNA-probe for *atu1879* [1]	CCAATGACTGGGACGGCA
RNAprobe_*atu1879*rv	Northern analysis; RNA-probe for *atu1879* [1]	**GAAATTAATACGACTCACTATAGGG**TGGCGATGTCGAGCTTATAT
RNAprobe_*frcB*_fw	Northern analysis; RNA-probe for *frcB*	CATCGTTCCGGCCGTACAG
RNAprobe_*frcB*_rv	Northern analysis; RNA-probe for *frcB*	**GAAATTAATACGACTCACTATAGGG**TTGTCGTCTTCATCGCCGATC
RNAprobe_*malE*_fw	Northern analysis; RNA-probe for *malE* [2]	CGGTTCCACCGCCCTTGG
RNAprobe_*malE*_rv	Northern analysis; RNA-probe for *malE* [2]	**GAAATTAATACGACTCACTATAGGG**CGCGAACTGCTTCAGCGTGC
RNAprobe_*atu4678*fw	Northern analysis; RNA-probe for *atu4678* [2]	CGTCGATGTCGGCGTTGCGTCG
RNAprobe_*atu4678*rv	Northern analysis; RNA-probe for *atu4678* [2]	**GAAATTAATACGACTCACTATAGGG**CGTCGATCTGACCCTGGC TAAG
RNAprobe_*dppA*_fw	Northern analysis; RNA-probe for *dppA2* [2]	CGCCGGAAGGCTTCGATCC
RNAprobe_*dppA*_rv	Northern analysis; RNA-probe for *dppA2* [2]	**GAAATTAATACGACTCACTATAGGG**CCACGGGTTCTTGGTATC ACCC
RNAprobe_*atu0857*fw	Northern analysis; RNA-probe for *atu0857*	GCCGAGGCGGGACGCAAG
RNAprobe_*atu0857*rv	Northern analysis; RNA-probe for *atu0857*	**GAAATTAATACGACTCACTATAGGG**GCAGGTCACGGTTTTCCT GACG
RNAprobe_*atu4577*fw	Northern analysis; RNA-probe for *atu4577*	CTGGGTTCCCTTTACCGCAGT
RNAprobe_*atu4577*rv	Northern analysis; RNA-probe for *atu4577*	**GAAATTAATACGACTCACTATAGGG**ATGCCGACCGCCTGCTCG
RNAprobe_*atu4046*fw	Northern analysis; RNA-probe for *atu4046*	TCCATGGCCGAAAAAGGCC
RNAprobe_*atu4046*rv	Northern analysis; RNA-probe for *atu4046*	**GAAATTAATACGACTCACTATAGGG**GCTGTGCGGTGACAAC
RNAprobe_*atpH*_fw	Northern analysis; RNA-probe for *atpH*	GCACTTCTCGACGAAAGCGAC
RNAprobe_*atpH*_rv	Northern analysis; RNA-probe for *atpH*	**GAAATTAATACGACTCACTATAGGG**GGTAACGCTCTTCAGCGCC
RNAprobe_*atu4431*fw	Northern analysis; RNA-probe for *atu4431* [2]	CCTGAAGACCGGTTATGCCGG
RNAprobe_*atu4431*rv	Northern analysis; RNA-probe for *atu4431* [2]	**GAAATTAATACGACTCACTATAGGGG**TTCTCGTTCTTCTGGTTG AGGC
RNAprobe_*atu4259*fw	Northern analysis; RNA-probe for *atu4259* [2]	CCCAATGACAGCTTGACGGTCG
RNAprobe_*atu4259*rv	Northern analysis; RNA-probe for *atu4259* [2]	**GAAATTAATACGACTCACTATAGGG**CCATGGAAAGGGCCTGGC
RNAprobe_*chvE*_fw	Northern analysis; RNA-probe for *chvE*	GTCCTCGTGATCGCGTCGATC

RNAprobe_*chvE*_rv	Northern analysis; RNA-probe for *chvE*	**GAAATTAATACGACTCACTATAGGG**CCGCTGTCGATGTAAGGCTTC
runoff_*malE*_1_fw	plasmid generation for *malE*_1 runoff transcription	**GAAATTAATACGACTCACTATAGGG**AGTTGATGCACACGGTGGC
runoff_*malE*_1_rv	plasmid generation for *malE*_1 runoff transcription	AAAAGATATCTGATCTCCTTGTCGGCGGC
runoff_*malE*_2_fw	plasmid generation for *malE*_2 runoff transcription	**GAAATTAATACGACTCACTATAGGG**GCTGGATCTATTGCGGCGA CAAG
runoff_*malE*_2_rv	plasmid generation for *malE*_2 runoff transcription	AAAAGATATCTGCCGGCGGCTGCAAGCG
runoff_*atu1879*_fw	plasmid generation for *atu1879* runoff transcription	AAAA**GAAATTAATACGACTCACTATAGGG**CGACATCGACATCGCC AAGG
runoff_*atu1879*_rv	plasmid generation for *atu1879* runoff transcription	AAAAGATATCGGAGGCGTTCCGGCGTG
runoff_*frcB*_fw	plasmid generation for *frcB* runoff transcription	AAAA**GAAATTAATACGACTCACTATAGGG**CGGGTAACCGTCAC GGTG
runoff_*frcB*_rv	plasmid generation for *frcB* runoff transcription	AAAAGATATCCGGTTTTGGTAATCAGGCAAACC
runoff_*atu4678*_fw	plasmid generation for *atu4678* runoff transcription	**GAAATTAATACGACTCACTATAGGG**ATAGTGATCGCGCCTTCAACG
runoff_*atu4678*_rv	plasmid generation for *atu4678* runoff transcription	AAAAGATATCGCGTGCCGGACGAAATGATG
runoff_*atu0857*_fw	plasmid generation for *atu0857* runoff transcription	AAAA**GAAATTAATACGACTCACTATAGGG**CCCGCAACGGTCG CTTCC
runoff_*atu0857*_rv	plasmid generation for *atu0857* runoff transcription	AAAAGATATCCCGATCCCGCTCGATGCAC
runoff_*dppA2*_fw	plasmid generation for *dppA2* runoff transcription	AAAA**GAAATTAATACGACTCACTATAGGG**CAACGGGGCCGCAG GAAC
runoff_*dppA2*_rv	plasmid generation for *dppA2* runoff transcription	AAAAGATATCCTTTGCCATGGCTGGCATGG
runoff_*chvE*_fw	plasmid generation for *chvE* runoff transcription	AA**GAAATTAATACGACTCACTATAGGG**CTCCACCATCTTCAAGGAC
runoff_*chvE*_rv	plasmid generation for *chvE* runoff transcription	AAAAGATATCCACTGCAACCGGCTTCAG
runoff_*atpH*_fw	plasmid generation for *atpH* runoff transcription	AAAA**GAAATTAATACGACTCACTATAGGG**TGGAGCCCCATCGCT GATG
runoff_*atpH*_rv	plasmid generation for *atpH* runoff transcription	AAAAGATATCCCTGAACCGCTTCGACCG
runoff_*atu3114*_fw	plasmid generation for *atu3114* runoff transcription	AA**GAAATTAATACGACTCACTATAGGG**CCAGCGCTGTCTTCTTTGA CAAGG
runoff_*atu3114*_rv	plasmid generation for *atu3114* runoff transcription	AAAAGATATCGCTCGCATCGGCCGTGGC
runoff_C2A_fw	plasmid generation for AbcR1 runoff transcription [1]	**GAAATTAATACGACTCACTATAGGG**AGTTGATGCACACGGTGGC
runoff_C2A_rv	plasmid generation for AbcR1 runoff transcription [1]	GATATCAAAAAAAGAGGGCCGCCGG
QC_AbcR1_3xA_fw	plasmid generation for AbcR1Mut1 runoff transcription	GATGCACACGGTGGCTTTTCCAAACAGTTCCACCGCATCAGCTG
QC_AbcR1_3xA_rv	plasmid generation for AbcR1Mut1 runoff transcription	CAGCTGATGCGGTGGAACTGTTTGGAAAAGCCACCGTGTGCATC
QC_AbcR1_4xA_fw	plasmid generation for AbcR1Mut2 runoff transcription	AGTTCCACCGCATCAGCTGTAAAACTCTGGAGGTTTTTGACCTT
QC_AbcR1_4xA_rv	plasmid generation for AbcR1Mut2 runoff transcription	AAGGTCAAAAACCTCCAGAGTTTTACAGCTGATGCGGTGGAACT
QC_AbcR1_3x/4A_fw	plasmid generation for AbcR1Mut1+2 runoff transcription	CGGTGGCTTTTCCAAACAGTTCCACCGCATCAGCTGTAAAACTC TGGAG
QC_AbcR1_3x/4A_rv	plasmid generation for AbcR1Mut1+2 runoff transcription	CTCCAGAGTTTTACAGCTGATGCGGTGGAACTGTTTGGAAAAGC CACCG
runoff_*atu2422*_rv	*atu2422* mapping of binding sites [1]	AAAAGATATCAACGCGACCATGGCGGTC

runoff_*malE2*_rv	*malE2* mapping of binding sites	AAAAGATATCTGCCGGCGGCTGCAAGCG
runoff_*atu3114*_rv	*atu3114* mapping of binding sites	AAAAGATATCGCTCGCATCGGCCGTGGC

[1] oligonucleotides were previously generated by Wilms *et al.*, 2011

[2] oligonucleotides were previously generated by Wilms *et al.*, 2012

Supplementary Table S5: Strains and plasmids used in this study.

Strain or plasmid		Relevant Characteristics	Reference or source
Strains			
Escherichia coli			
DH5α		Cloning host	(Hanahan, 1983)
JM83		Cloning host	(Hanahan, 1983)
Agrobacterium tumefaciens			
C58		wild-type	C. Baron, Montreal, Canada
C58 ΔC2A		Derivate of the wild-type with deletion of the AbcR1 gene	(Wilms *et al.*, 2011)
C58 Δ*hfq*		Derivate of the wild-type with deletion of the *hfq* gene	(Wilms *et al.*, 2012)
Plasmids			
pUC18		Amp^r; cloning vector	(Norrander *et al.*, 1983)
pBBSyn		Km^r; complementation vector	(Giacomini *et al.*, 1994)
runoff_C2A	(pBO1608)	Amp^r; pUC18 derivate carrying AbcR1 with additional T7-promotor	(Wilms *et al.*, 2011)
runoff_AbcR1QC1	(pBO2085)	pBO1608 carrying site-directed mutagenesis of AbcR1 nucleotides 26-28 TCC-AAA	This study
runoff_AbcR1QC2	(pBO2091)	pBO1608 carrying site-directed mutagenesis of AbcR1 nucleotides 50-53 TCCC-AAAA	This study
runoff_AbcR1QC1+2	(pBO2084)	pBO2085 carrying site-directed mutagenesis of AbcR1 nucleotides 50-53 TCCC-AAAA	This study
runoff_*atu2422*	(pBO1649)	Amp^r; pUC18 derivate carrying *atu2422* (50 nt +/- AUG) with additional T7-promotor	(Wilms *et al.*, 2011)
runoff_*atu1879*	(pBO2088)	Amp^r; pUC18 derivate carrying *atu1879* (+158/+301 AUG) with additional T7-promotor	This study
runoff_*frcB*	(pBO2092)	Amp^r; pUC18 derivate carrying *frcB* (-48/+103 AUG) with additional T7-promotor	This study
runoff_*malE*_1	(pBO2057)	Amp^r; pUC18 derivate carrying *malE* (-50/+100 AUG) with additional T7-promotor	This study
runoff_*malE*_2	(pBO2096)	Amp^r; pUC18 derivate carrying *malE* (+100/+250 AUG) with additional T7-promotor	This study
runoff_*atu4678*	(pBO2058)	Amp^r; pUC18 derivate carrying *atu4678* (-50/+100 AUG) with additional T7-promotor	This study
runoff_*dppA2*	(pBO2087)	Amp^r; pUC18 derivate carrying *dppA2* (-45/+72 AUG) with additional T7-promotor	This study
runoff_*atu0857*	(pBO2090)	Amp^r; pUC18 derivate carrying *atu0857* (-50/+47 AUG) with additional T7-promotor	This study
runoff_*atu3114*	(pBO2086)	Amp^r; pUC18 derivate carrying *atu3114* (+437/+588 AUG) with additional T7-promotor	This study
runoff_*chvE*	(pBO2094)	Amp^r; pUC18 derivate carrying *chvE* (-85/+68 AUG) with additional T7-promotor	This study
runoff_*atpH*	(pBO2089)	Amp^r; pUC18 derivate carrying *atpH* (-50/+97 AUG) with additional T7-promotor	This study
runoff_*atpH*QC	(pBO2095)	pBO2089 carrying site-directed mutagenesis of *atpH* nucleotides 11-15 CCTCC-TTTTT	This study

Figure S1

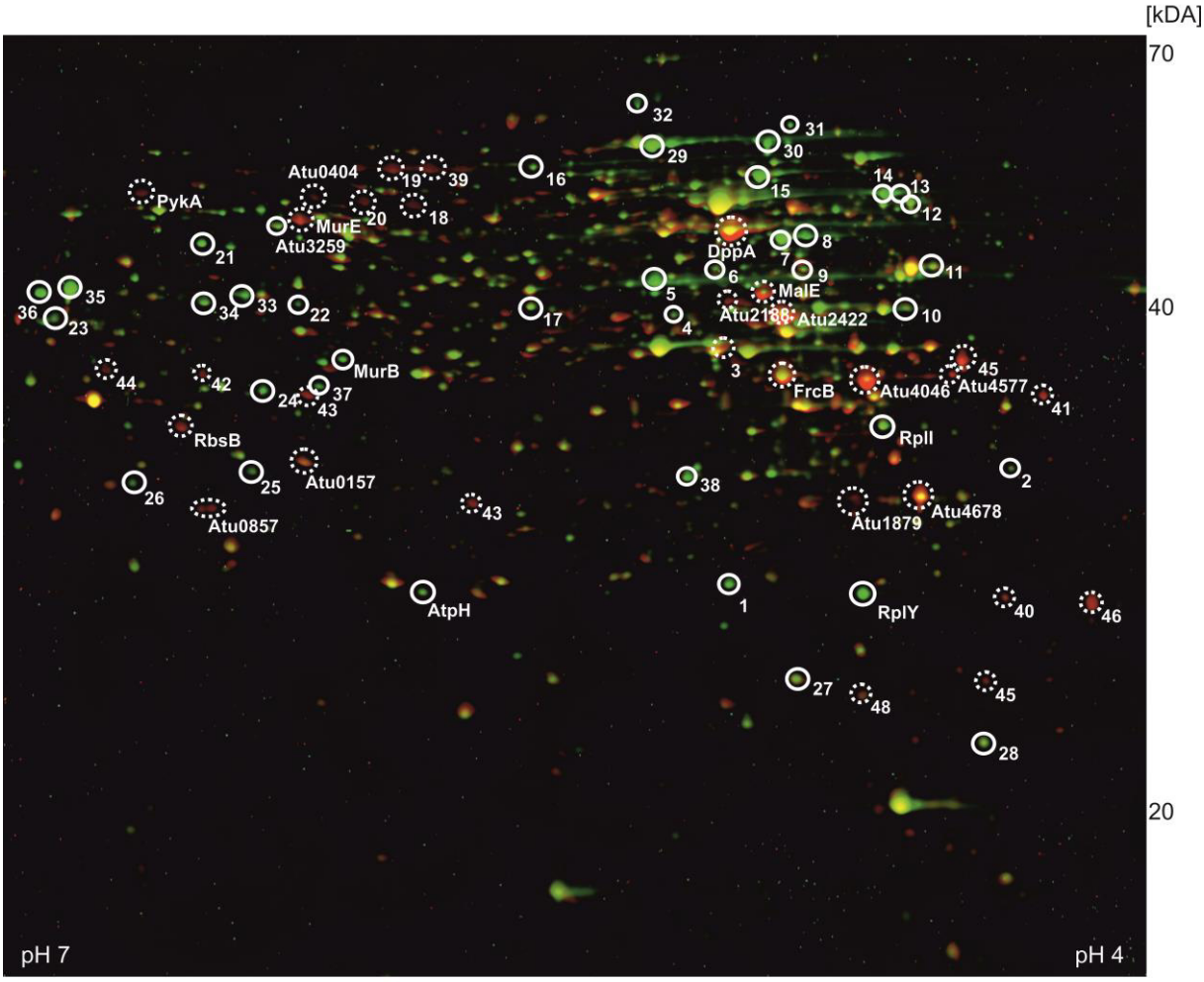


Fig. S1. Identification of AbcR1 targets by 2D-PAGE.

Total protein samples from stationary growth phase (OD600: 1.5) of the A. tumefaciens wild-type (WT) and the AbcR1 deletion mutant (ΔAbcR1) were subjected to two-dimensional PAGE. Proteins overrepresented in WT or in ΔAbcR1 preparations are shown in green or red, respectively. Proteins present in equal amounts in both preparations appear in yellow. 5 (green spots) and 15 (red spots) proteins significantly accumulated equally in three replicates of WT (closed white circles) or in ΔAbcR1 (dotted white circles) and were analyzed via MALDI-TOF. Altered proteins that were not identified by MALDI-TOF are marked with numbers.