TABLE S1 Primers for RACE and cloning

primer name	primer sequence	use in this study	reference
sinI-5'-RACE1	ATCGGTGACCGTGACGATATGG	5'-RACE of SMc00168	50
sinI-5'-RACE2	ATGGTGACCTGGTTCGATGC	5'-RACE of of SMc00168	50
PsinI-H-fwd	CCTAAAGCTTCAACGATTCTCGGCATATCC	Construction of pLK64	50
PsinI-X-rev	TCCTTCTAGAACCGTTTCCGTTCACTATCCT	Construction of pLK64	50
PsinI-X-revII	GGCTCTAGACATTTTTTCGCTCCATGCGT	Construction of pLK60	This study
sinI-noTGA+ATG-X-rev	GATTCTAGACATGGCGGCGCGTGCCGTTTCAAGC	Construction of pLK61	This study
PsinR-H-fwd	TGCCAAGCTTCGCATATTCTGTCGCCGT	Construction of pLK65	50
PsinR-X-rev	CAAATCTAGACATGCCGTAACACCGAAAC	Construction of pLK65	50
PcspA3-H-fwd	TGCCAAGCTTGAAGACGCAATACCTCGTCA	Construction of pLK002	24
PcspA3-X-rev	CAAATCTAGACTCGGCCATGCGTCAGGT	Construction of pLK002	24
PcspA3-219-rev	ACAGTAAGAGTGATGGGTTT	Fusion primer for construction of pLKpLKrec01	This study
PcspA3_msinI-fwd	AAACCCATCACTCTTACTGTATCGCGTAATCACGCATGG	Fusion primer for construction of pLKpLKrec01	This study
PsinI-29-rev	GTAGCGATGCTGTCAGGCT	Fusion primer for construction of pLKpLK rec02	This study
PsinI_mcspA3-fwd	AGCCTGACAGCATCGCTACGTTCGGGCAATCTGCGA	Fusion primer for construction of pLKpLKrec02	This study
rne-NdeI-fwd	CGCACATATGGCAGAGAAAATGCTTATC	Construction of pBSrne and pWBrne	This study
rne-XbaI-rev	TGCTCTAGATTAGAAGAAACCGCGGCG	Construction of pBSrne and pWBrne	This study
rneT5stop-H-rev	CATAAGCTTTCAATCTTCGTCGGACTCCT	Construction of pWBrne675 and pK1123-2024	This study
rne-B-1123-fwd	ATCGGATCCCTCTACAACAAGGACATCAGCGA	Construction of pK1123-2024	This study
rne-E-79-fwd	GAAGAATTCGATTTCGAATCGG	Construction of pK79-926	This study
rne-B-926-rev	ATCGGATCCGCGATCTCCTTCAGACGCTT	Construction of pK79-926	This study

TABLE S2 Primer pairs for qRT-PCR analysis

target gene	forward strand	reverse strand	primer pair efficiency or reference
SMc00170; *sinR*	CTGGATATCGTGGAATATGG	GGGTCGATCCTGTAAAGC	1.951
SMc00168, *sinI*, amplification of bp 4-251	TCAGGATAGTGAACGGAAA	GTATCGTCCAGCATATTCG	1.933
SMc00168, *sinI*, amplification of bp 232-434	AATATGCTGGACGATACGTT	GTGACGATATGGCTGATG	1.856
SMc01336, *rne*, upstream of mini-Tn5	ACATCATCATCAACCAGACC	AGGCAATCCTTTAGCTTCTT	1.924
SMc01336, *rne*, downstream of mini-Tn5	CGAGAGTGTCGATGAAGAAG	CCCTTTTTGGGTTTTGTC	1.908
SMc01317, *rpoB*	ATCCTCGACACCTTCTACAC	GATAGTTGCCGTAGAGATCG	1.987
SMc03224, *16S*	TCTACGGAATAACGCAGG	GTGTCTCAGTCCCAATGT	ref. 55

Culture Nr.	Strain	IPTG	Position \ time (min)	+1	+20	+24	+114	+117	+133	+219	+239	+243	+262	+268	+284	+295	+297	+306	+313	+330	+326	+332	+337	+338	+357	+359
1	2011	-	-	9		6									1											8
2	2011	+	60	12		5															1					6
3	2011 (pWBrne)	-	-	4	2	2			2				2							2						
4	2011 (pWBrne)	+	20			1				1																
	2011 (pWBrne)	+	40			2		2										1							1	1
	2011 (pWBrne)	+	60				1						1			1										1
5	2011 (pWBrne)	-	-	6		2								1												
6	2011 (pWBrne)	+	20			3																				
	2011 (pWBrne)	+	40																2							
	2011 (pWBrne)	+	60																			1	2	1		
7	*rne::Tn5* (pWBrne)	-	-	15																						
8	*rne::Tn5* (pWBrne)	+	20	3																						
	rne::Tn5 (pWBrne)	+	40	3		2					1															
	rne::Tn5 (pWBrne)	+	60	3		1																				
9	*rne::Tn5* (pWBrne)	-	-	9																						
10	*rne::Tn5* (pWBrne)	+	20	3																						
	rne::Tn5 (pWBrne)	+	40	3		3																				
	rne::Tn5 (pWBrne)	+	60									2					2									

Table S3. The results of all 5'-RACE experiments in detail. For the determination of 5'-ends of RNA by 5'-RACE *S. meliloti* cells were grown in TY medium to an OD_{600} of 1.0. Ectopic expression of *rne* was induced by addition of 1 mM IPTG. Cells were harvested 20 min, 40 min, and 60 min after induction. No IPTG was added to the control cultures. RNA was isolated and 5'-RACE analysis of *sinI* was performed. Given is the number of the clones corresponding to a certain position in the *sinI* transcript (+1 is the transcriptional start site, +24 is the putative RNase E cleavage site between the Shine-Dalgarno sequence and the start codon). Results are listed separately for each independent culture. For cultures with IPTG, the results are shown in a time resolution manner.