Supplementary data to the manuscript:

"Maltose uptake by the novel ABC-transport system MusEFGK₂I causes increased expression of *ptsG* in *Corynebacterium glutamicum*"

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The supplementary data comprise one table (Table S1) and four figures (FIG. S1, FIG. S2, FIG. S3, FIG. S4).

TABLE S1. Oligonucleotides used in this study.

Name	Sequence (5'-3')	Purpose, restriction site		
DelMus_1	GG <u>GGATCC</u> AACCGCGAACTGCT	Deletion of mus genes, BamHI		
DelMus_2	CTTATAAATTTGGAGTGTGAAGGTTATTGCGTG CGAACGATCCGTAGTGTGAG	Deletion of <i>mus</i> genes		
DelMus_3	CACGCAATAACCTTCACACTCCAAATTTATAAGACGACTACCTGCTGCCATAC	Deletion of <i>mus</i> gens		
DelMus_4	GG <u>GGATCC</u> TGCCTTGGCAATGA	Deletion of mus genes, BamHI		
ΔMusConF	TAGATGGCGCACAGTGACTC	Verification of <i>mus</i> deletion		
ΔMusConR	TAACTACCGCAACACCGATG	Verification of <i>mus</i> deletion		
DelPtsG_1	<u>GTCGAC</u> GGGCATAATTCTGACAGTGTG	Deletion of <i>ptsG</i> , SalI		
DelPtsG_2	CTTATAAATTTGGAGTGTGAAGGTTATTGCGTG GGACGCCAAGAACTGATGGG	Deletion of <i>ptsG</i>		
DelPtsG_3	CACGCAATAACCTTCACACTCCAAATTTATAAGCCGCTGACTTCATTCGATCC	Deletion of <i>ptsG</i>		
DelPtsG_4	<u>GGATCC</u> TAAGGACGCCATGTCAAACC	Deletion of <i>ptsG</i> , BamHI		
ΔPtsGConF	TCGTACGGTGTGGTTAAG	Verification of <i>ptsG</i> deletion		
ΔPtsGConR	AGTATGCACCGCGTAATC	Verification of <i>ptsG</i> deletion		
MusFor	TCTAGA TGGCGCACAGTGACTCACTT	Cloning of pXMJ19-musEFGK and pXMJ19-musEFGKI, XbaI		
MusRev	ACCGGTCGAGTATGCGATTCATGGT	Cloning of pXMJ19-musEFGK, AgeI		
MusLoRev	GG <u>GGATCC</u> ATGACGTGGATACCACTACC	Cloning of pXMJ19-musEFGKI and pXMJ19-cg2701, BamHI		
MusI-For	GG <u>GGATCC</u> TTCTCCACGCAGAGGCACAT	Cloning of pXMJ19-cg2701 and pXMJ19-cg2701-strep, BamHI		
MusI-Rev	GAGCTCTCAATTTTTCGAACTGCGGGTGGCTCCAGCTGCCACCGCTACCGCCTGCAAAGGGGGCTATCGG	Cloning of pXMJ19-cg2701-Strep, SacI		
Cg2703_for	GCTTCTTGGAGGCCACATTG	RT-PCR, cg2703 RNA Probe, inactivation of cg2703		
Cg2703_rev	GGGCCCTAATACGACTCACTATAGGGTATCGCGGTTACCGTTGGAG	RT-PCR, cg2703 RNA Probe, inactivation of cg2703		

Cg2708_for	ACTGAAGATCGCCGGCAAGT	RT-PCR, cg2708 RNA Probe, inactivation of cg2708			
Cg2708_rev	GGGCCCTAATACGACTCACTATAGGGATTATCCTCCGGCGTCATGG	RT-PCR, cg2708 RNA Probe, inactivation of cg2708			
Cg2707_for	CCTATTCCGCCTATCTCGTC RT-PCR, cg2707 RNA Probe, inactivation of				
Cg2707_rev	GGGCCCTAATACGACTCACTATAGGGGGGGGGGATAGTCGGTTCGTATT	RT-PCR, cg2707 RNA Probe, inactivation of cg2707			
Cg2701_for	TTCGCTGACCTAGTCATCGT	RT-PCR, cg2701 RNA Probe, inactivation of cg2701			
Cg2701_rev	GGGCCCTAATACGACTCACTATAGGGACTGCGAGGAAGAACAGGTA	RT-PCR, cg2701 RNA Probe, inactivation of cg2701			
PrmusF-for	TCTAGAATGACAACTGGGCTGCTGAG	musF-Pr probe, cloning of pET2-PmusF, XbaI			
PrmusF-TS-for	TCTAGA TCTCCTCACCGCCTTCC	Cloning of pET2-PmusF-TS, XbaI			
PrmusF-rev	GGATCCTTATGGCGTTGGTGATAGTGGTG	musF-Pr probe, cloning of pET2-PmusF and pET2-PmusF-TS,			
ramBp3b_forw	ACGCGTCGACGATGTGGCCCCGACCACGCCG	<i>ramB</i> p3b probe			
ramBp3b_rev	ACTGAGGTGTTGCAAACTTGTTGATTTTCGCT	<i>ramB</i> p3b probe			
RACE-cg2704-SP1	AAGTTGGTACCGCGGAGT	5'-RACE. cDNA synthesis			
RACE-cg2704-SP2	AGGCGAAATGTTGACTG	5'-RACE, nested primer			
Oligonucleotide dT	GACCACGCGTATVGATGTCGACTTTTTTTTTTTTTTTTTT	5'-RACE, amplification of dA-tailed cDNA			

anchor primer ^a Restriction sites in the oligonucleotides are underlined, V represents an A, C, or G, linker sequences for cross over PCR are shown in bold, T7-promoter sequences for *in vitro* transcription are shown in italics, the sequences encoding the strep-tag and the linker in the oligonucleotide MusI-rev are shown in red and green, respectively.

FIG. S1. Maltose uptake of *C. glutamicum* WT, different concentrations (0.5 - 30 μ M) of [¹⁴C]-maltose were tested. Data represent mean values of three independent measurements from 2 independent cultivations and were fitted according to the Michaelis-Menten equation.



FIG. S2. Genomic locus of the intergenic region of the *C. glutamicum musE* and *musF* genes. Coding regions are shaded in grey and shown in italics, the *musE* Stop codon and the *musF* ATG start codon are underlined. The *musF* transcriptional start site (TS_{musF}) is shaded in black, -10 region is shown in bold. Overlapping putative RamA binding sites are shown in half boxes.

	RamA1 RamA2
1	<pre>gctaa agctctattcccgtccccctcgccacactccttccaatagcggag 'musE</pre>
51	ggcggggggggggggtgggggtgggggtggggcccgcgtcgcgagcttgtgc
101	gcgagcagttattccaCATCCTcagcctcCtccccaccgccttccccg -10 TS _{musF}
151	ctgggaaacgtgtggcaccacctgaaattaaggtttcaccacc <mark>ATGcaag</mark> musF'

FIG. S3. Alignment of *C. glutamicum* MusI with the hypothetical proteins from *B. longum* NCC2705, *S. agalactiae* 2603 and *S. pneumonia* TIGR4, each contains 5 transmembrane regions, the DUF 624 motif (residues 30 to 101 in the amino acid sequence of SP_1677) and is encoded adjacent to an genes for an ABC transport system. Amino acids identical in three sequences are shaded in black and similar amino acids are shaded in grey.

		10) 20) 30) 40	50	60
Must [C. alutamicum]	1		RTLGPESKDY	AALSLFADIN	 T VNNT T VTTC	FEVENGEMST.	RTAHAVTGOM
BL0145 [B. longum]	1	M	NWLAPDSKEM	RAWSNLVDGV	WINITMLVTS	IPLITICAAL	TAGHDACRRS
SP 1677 [S. pneumoniae]	1	MAOKGVSLIK	AAFDTDNFLM	RESEKVLDIV	TANLLEVVSC	LPIVTICVAK	ISLYETMFEV
SAG0038 [S. agalactiae]	1	-MKKANOLIA	AIFDVNNP	OGCNVVFDLA	LINILEMITC	LPLVTICAAK	ISLYRTLWOK
		-		-			
		70) 80) 90	100) 110	120
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MusI [C. glutamicum]	53	VREEGSRRGS	AFVRGLLTRP	GVNTAWWIIS	AVAALAAYE	FAIIAKADLG	SMGLILRAAL
BL0145 [B. longum]	52	IEGEGKGVTA	NYFKSFKANF	IKATLI	WMPFLVAL	IALVWSWIVL	QITPULIIKF
SP_1677 [S. pneumoniae]	61	KKSRRVPVFK	IMLRSFRQNL	KLGLQUGUME	IGIVFLTLSD	LYLFWGQTAL	PFQLUKAICL
SAG0038 [S. agalactiae]	60	LEGDQTNLLI	LMIKHLKKEW	FQGMLIGUVE	SILVVIIFD	LTILHYQIGF	IVSEKITCY
		13() 14() 15() 160) 170	180
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MusI [C. glutamicum]	113	ISGLIVLGSV	SVWEFHLDAP	GLGFRORITO	AMMKAVGHLP	RUULAIUP	GIVLVIYPVF
BL0145 [B. longum]	106	ALTILWLIGF	EWVFALOARF	ENTVAGTLKN	AFIFGISHIA	MIVAIVIVDA	VFVTLIVASW
SP 1677 [S. pneumoniae]	121	GILIFLTIVM	LASYPIAARY	DLSWKEILQK	GLMLASFNFP	WFFLMLAIUV	LIVMVLYLSA
SAG0038 [S. agalactiae]	120	AFLLLTVMTS	IYLFPMAARY	EMSLLDTVKK	SFIMACLNLK	WIGVIMFLII	MTWFIMVQSS
		190	200) 210	220)	
		<u>.</u> <u>.</u>	· · · · · <u>·</u> · · · · ·				
MusI [C. glutamicum]	171	FPAQWCGYLF	FLAVIGPALA	VYLAELVLQW	PELNSQTPDS	PFA	
BL0145 [B. longum]	166	FYMPGCLFLL	VILGYGTMLM	LHIPVTERVE	KPYLID		
SP_1677 [S. pneumoniae]	181	FSLLLEGSVF	LLFGF <mark>G</mark> LLVF	IQTGLMEKIF	AKYQ		
	100			TREET TEL OTION	3 TEATROODIE	<u> </u>	

FIG. S4. Genomic organisation of gene clusters from *C. glutamicum* ATCC13032, *B. longum* NCC2705, *S. agalactiae* 2603 and *S. pneumonia* TIGR4 encoding ABC-transporters. Genes encoding *musI*-like proteins are shown in red, genes for permeases in yellow, substrate binding proteins in green, and ATPase in blue. Genes encoding additional (hypothetical) proteins are coloured in grey.

