Supplemental figures

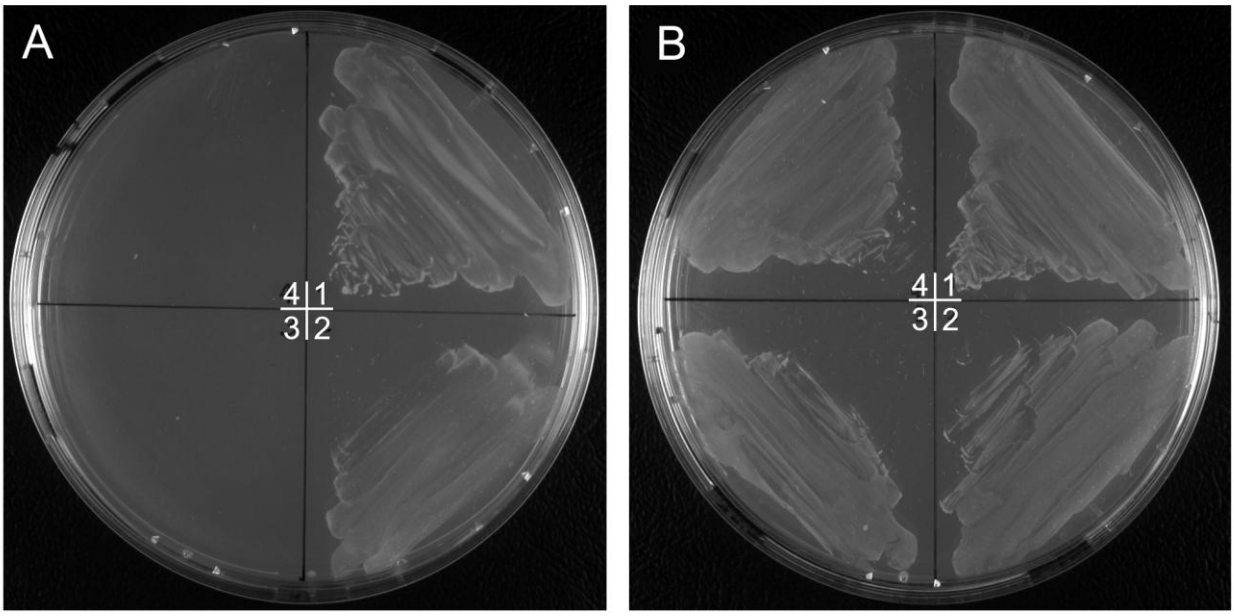

Fig. S1. Cultivation of *C. glutamicum* strains on minimal medium (MM) with 5 mM PAA (A) or 5 mM glucose as carbon source (B). MM agar plates with glucose were incubated for 24 h at 30 ℃, while plates with PAA were incubated for 48 h at the same temperature. The growth of AS 1.542 and ATCC 13032/pEC-K18*mob*2::*paa* was also observed in MM broth, and same results were observed. Labels: 1, *C. glutamicum* AS 1.542; 2, *C. glutamicum* ATCC 13032/pEC-K18*mob*2::*paa*; 3, *C. glutamicum* ATCC 13032/pEC-K18*mob*2; 4, *C. glutamicum* ATCC 13032.

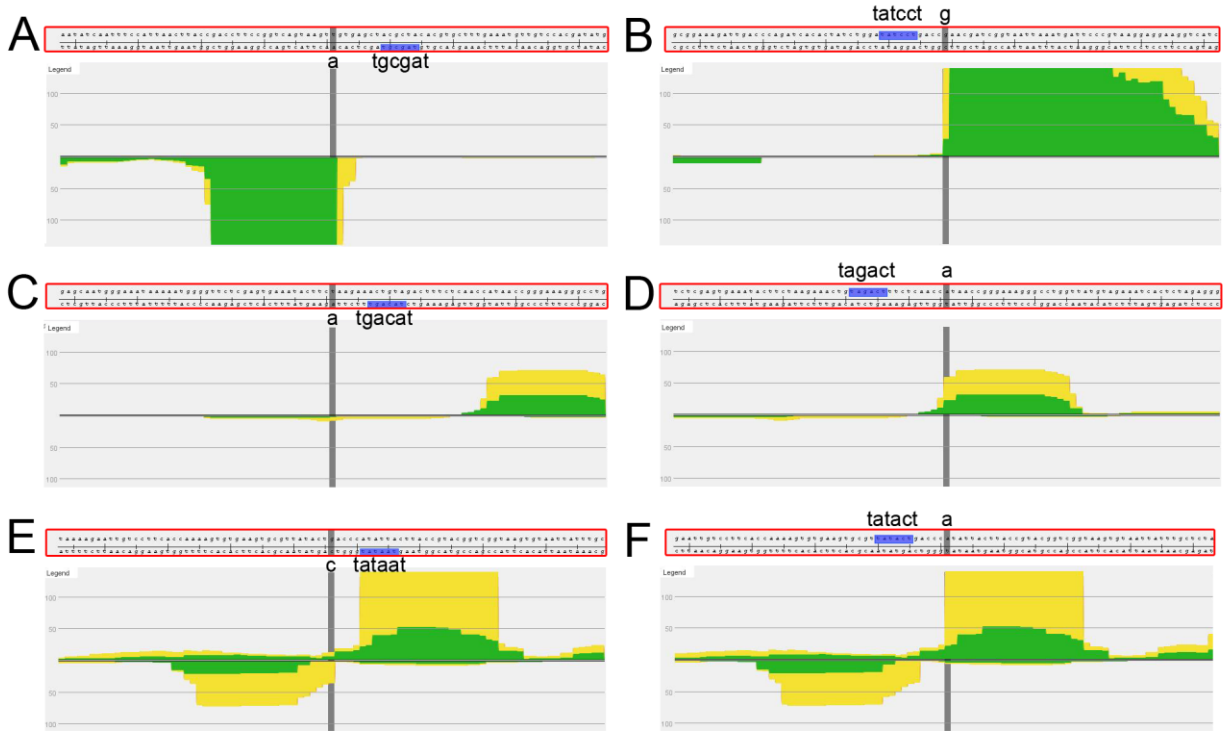

Fig. S2. Identification of probable transcription start sites (TSS) and promoter regions in the *paa* gene cluster of the strain AS 1.542. Letters A to F refer to region that spans the probable TSS and promoter of *paaK* (A), *paaA* (B), *paaR* (C), *paaI* (D), *paaY* (E), and *paaZ* (F) genes, and their sequence is shown in the red box. The TSS is indicated by gray background and the -10 region by blue background. The sequences of TSS and -10 regions are indicated outside the red box. Values for perfect and best matching reads (see Table 2, manuscript) are indicated by green and yellow color, respectively.

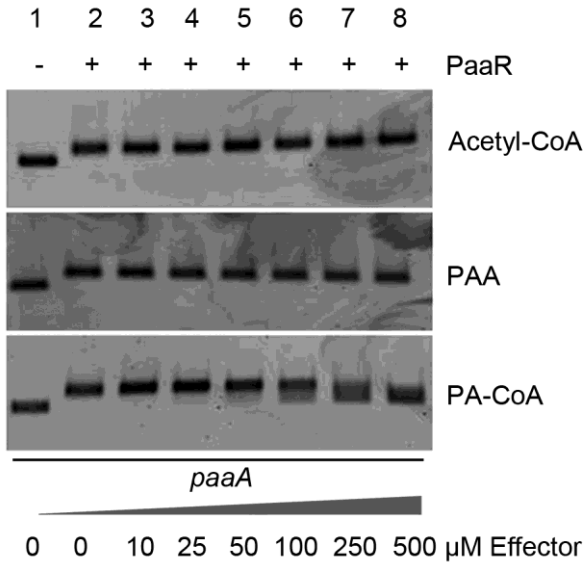

Fig. S3. Effect of Acetyl-CoA, PAA and PA-CoA on PaaR binding to the Cy3-labeled DNA probe for *paaA*. Whether 5 pmol PaaR protein was added to the reaction mixture is indicated by – and + above the gel picture. Acetyl-CoA, PAA and PA-CoA were added to the reaction mixture in the indicated concentration gradient.

Supplemental Table S1. Bacteria strains, plasmids and primers used in this study

Strain, plasmid or primer	Relevant features or sequences[a]	Source, reference or note
***C. glutamicum* strains**		
Strain AS 1.542	Wild type strain AS 1.542	(1)
AS 1.542/*paaR*$^{\Delta HTH}$	Strain AS 1.542 with deletion of the HTH domain of *paaR* gene	this study
ATCC 13032	Type strain	(2)
ATCC 13032/ pEC-K18*mob*2::*paa*	ATCC 13032 carrying pEC-K18*mob*2::*paa*	this study
***E. coli* strains**		
ER2566	NEB IMPACT Kit	NEB
ER2566/pTXB1::*paaR*	PaaR protein expression strain carrying pTXB1::*paaR*	this study
Plasmids		
pK18*mobsacB*	cloning vector for allelic exchange, Km^R	(5)
pK18*mobsacB*::*paaR*$^{\Delta HTH}$	pK18*mobsacB* carrying *paaR* gene with deletion of its HTH domain, Km^R	this study
pTXB1	NEB IMPACT Kit, Amp^R	NEB
pTXB1::*paaR*	pTXB1 derivative for expression of PaaR protein, Amp^R	this study
pEC-K18*mob2*	*C. glutamicum* cloning vector, Km^R	(3)
pEC-K18*mob2*::*paa*	pEC-K18*mob2* carrying the whole cluster of *paa* genes, Km^R	this study
pETCRP	pET-28a derivative containing the *glxR* gene from *C. glutamicum*, Km^R	(4)
Primers[b]		
725_DL_HTH_A	AGGTCTCGAATTCTCCGGTCAGTAAGTTGTGAG (Eco31I)	To generate pK18*mobsacB*::*paaR*$^{\Delta HTH}$
725_DL_HTH_B	GGATCCATTGCCGTTCTGTG	
725_DL_HTH_C	CACAGAACGGCAATGGATCCCTTGGGAAATGCTCGTTGGA	
725_DL_HTH_D	AGGTCTCGGATCCGCTCCCCTGGTGGAATTACA (Eco31I)	
paa_ga1	TCACTCATTAGGCACCCCAGGGGGCTTGGTTTTAGAGGAAG	
paa_ga2	AAACGTGGCAAATAGGCAGGAACCCCATACGAATCGCATC	
paa_vector_ga1	CTTCCTCTAAAACCAAGCCCCCTGGGGTGCCTAATGAGTGA	To generate pEC-K18*mob*2::*paa*
paa_vector_ga2	GATGCGATTCGTATGGGGTTCCTGCCTATTTGCCACGTTT	
723_RT_F	CGTAGCCAATGACGAAGGTT	For RT-qPCR analysis of *paa* cluster genes
723_RT_R	CAGCACTCCAAGCTGGTTAT	
724_RT_F	GTCAGTGGGGTGATGACAAG	
724_RT_R	CTCCGAACCATGGAGTGAAG	
725_RT_F	TAATTCTGCGGTGGTGTCTG	
725_RT_R	TTCGACTTCGTGGCAACTCT	
727_RT_F	TCGTTGAAGGCCATGGGTAT	
727_RT_R	CGGCGCAATGAAATGGATCT	
728_RT_F	GCCTGAGGCTAACTGGATTT	
728_RT_R	GTGCGAGCTGGGTAATTGAA	
729_RT_F	CTCAAACCGCGGATTATCCC	
729_RT_R	GTAGGTTGCATGGCGGTAAG	
730_RT_F	CCTTGGCTGGTGGATATCTC	
730_RT_R	AGATGACGGGCAATAGTCTG	
731_RT_F	TTGCTCGACTCTGGGACATT	
731_RT_R	AAAGCCTTCACGCTTTAGGG	
732_RT_F	GCCAGTACGTTGCTCTACGA	
732_RT_R	GAGGCTGGTGACGTGAATCT	
733_RT_F	GCTCGGGACGAAACATCAAA	
733_RT_R	ATCAAGGGTTGCGCCTAAGT	
734_RT_F	TTCGCCCTGATGATCTAGCA	
734_RT_R	GATTCCACCATCGCAGTAGC	
735_RT_F	TGCCTCTGGTGCAGATATCG	
735_RT_R	GCTTCTGGCTGACCAAACTT	
736_RT_F	GCGGTTCCTGAGTCTTTTGA	
736_RT_R	TGGGTAGCCACCACAATTTC	
737_RT_F	GCCTGCGTCATCATGAAGAA	
737_RT_R	GATGGCAACCGACAGTCTTT	
738_RT_F	CTCCCCAACACCAATGTGAT	
738_RT_R	TGCTTCTGCGGTGATGTAAC	
740_RT_F	GCGCACCCCAAGACTTTAAC	
740_RT_R	TCCCTGCAACTCCCCTATAC	
725E_int1	GGTGGTCATATGATGACTCCAACGAGCATTTC (NdeI)	To generate

725E_int2	GGTGGTTGCTCTTCCGCAAGTGCTGGGTGTGGCTGTTT (SapI)	pTXB1::*paaR*
724_upstream_F[b]	GGTCCATTGTGGGTGGAAGA	
724_upstream_R	CCACACCCAGCACTTAGACT	
725_upstream_F	CCGGTGGCGGGAAGCGCTTG	
725_upstream_R[b]	CCAGGTCAGACTCAATTTGT	
728_upstream_F	TTCGGGGAATGTCTCGAACT	
728_upstream_R[b]	GCTGTATCTGCGTTTGTGTC	To generate Cy3 labeled upstream DNA probes of *paaK*, *paaR/I*, *paaA*, *paaY/Z* and *hemH*
738_upstream_F	CAGTTCGCCGAGCTGAATAG	
738_upstream_R[b]	CCCACTGTCCCTGAAGGTAG	
hemH_EMSA_1	CGTGGTACGCCTCATTTAGT	
hemH_EMSA_2[b]	CATCCGATGTGCGTTCATTC	
724_oligo_F	TTTCCATTAACTTACCGACCTTCCGGTCAGTAAGTTGTGA	
724_oligo_R	TCACAACTTACTGACCGGAAGGTCGGTAAGTTAATGGAAA	
725_oligo_F	TTTCTCAACCATAACCGGGAAAGGGCCTGGTTATGTAGAA	
725_oligo_R	TTCTACATAACCAGGCCCTTTCCCGGTTATGGTTGAGAAA	
728_oligo_F	TCTGGATATCCTGACCGAACGATCGGTAATTAAATGATTC	To generate competition DNA fragments of *paaK*, *paaR/I*, *paaA*, *paaY/Z* and *argC* for PaaR EMSA
728_oligo_R	GAATCATTTAATTACCGATCGTTCGGTCAGGATATCCAGA	
738_oligo_F	ACCCATATTACTTACCGTACGGTCGGTAAGTGTAATTATT	
738_oligo_R	AATAATTACACTTACCGACCGTACGGTAAGTAATATGGGT	
argC_EMSA1	CAAAAATTTATGCATGAATAATTTGCATGATCATGCATAA	
argC_EMSA2	TTATGCATGATCATGCAAATTATTCATGCATAAATTTTTG	
724_oligo_GlxR_F[b]	TTTCAAAGCACGTGTAGCGTAGCTCACAACTTACTGACCG	To generate Cy3 labeled DNA fragments of *paaK*, *paaA* and *paaY/Z* for GlxR EMSA
724_oligo_GlxR_R	CGGTCAGTAAGTTGTGAGCTACGCTACACGTGCTTTGAAA	
728_oligo_GlxR_F[b]	GATCGCGGAAAGATTGACCCAGATCACACTATCTGGATAT	
728_oligo_GlxR_R	ATATCCAGATAGTGTGATCTGGGTCAATCTTTCCGCGATC	
738_oligo_GlxR_F[b]	CTTCACCAAAAGTGTGAAGTGCGTTATACTGACCCATATT	
738_oligo_GlxR_R	AATATGGGTCAGTATAACGCACTTCACACTTTTGGTGAAG	

[a] Restriction enzyme cut sites are underlined.
[b] These primers are labeled with Cy3 fluorescence.

References for supplemental Table S1

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