

SUPPLEMENTARY MATERIAL TO KLAFFL ET AL. 2013

Table S1. Oligonucleotides used in this study.

Function and oligonucleotide	Sequence (5' → 3') and properties ^a
Deletion of cg0196 and PCR analysis of the resulting mutant	
iolR_DF1_for	CCCAAGCTT <u>GAGG</u> TACTTGCCGAAAGATTG (<i>HindIII</i>)
iolR_DF1_rev	CTCGATTACTTGGCCGGAGGGCTACTTGGAAGTAGAGG
iolR_DF2_for	TCCGGCCAAGTAATCGAG
iolR_DF2_rev	CGGGATCCATCGCGTTGGCATTCTTC (<i>BamHI</i>)
K_DiolR_for	GCACGTTATGACCTGCAAACCTC
K_DiolR_rev	TACGGTCTGGCTATCTACATCC
Overexpression of cg0196 in <i>E. coli</i> BL21 (DE3)	
iolR_pET16b_for	GGAATTC <u>CATATG</u> ACCACCGAAGCTCCCATTTGG (<i>NdeI</i>)
iolR_pET16b_rev	CGGGATCCTTACCCTGCCACCAGAGTGGTTTC (<i>BamHI</i>)
DNA affinity chromatography and gel shift assays	
bt_anchor	GACCACGCGTATCGATGTCGAG
pck_btac_rev	GACCACGCGTATCGATGTCGAGTGCATCCAGTTCAGCAGTT
P_pck_1_for	TAGCGGAGTGCTTGGATTGTG
P_pck_1_rev	TGCGATCCAGTTCAGCAGTT
P_pck_2_rev	GAGAGCACCCGTTTAAATAGCC
P_pck_3_for	GGCTATTTAAACGGGTGCTCTC
P_pck_4_rev	CACATTCAGGGGACAACCTTCC
P_pck_5_for	GGAAAGTTGTCCCCTGGAATGTG
P_pck_6_rev	CTTTAGGTGAGACAACGGACAC
P_pck_7_for	GTGTCCGTTGTCTCACCTAAAG
P_pck_8_rev	GGCAACAAAACGCCAAGAACAGC
P_pck_9_for	GCTGTTCTTGGCGTTTTGTTGCC
P_pck_10_rev	CACTTAACATTCGGACAATAGG
P_pck_11_rev	CCCAGTTTTCCACCATTAACAC
P_pck_12_for	GTGTTAATGGTGGGAAAACCTG
P_pck_13_for	CCTATTGTCCGAATGTTAAGTG
P_iolRC_1_for	GCTGGCCAAAATGGGAGCTTC
P_iolRC_1_rev	TCGTGAGTGCTCGTCAAGTTAG
P_iolRC_2_rev	CATGAGCTTGTGGGTGGGC
P_iolRC_3_for	GCCCACCAACAAGCTCATG
P_iolRC_3_rev	AAGACCACCACCCGCAACTC
P_iolRC_4_for	GAGTTGCGGGTGGTGGTCTT
P_iolRC_4_rev	CAATAAAAGCCCTGGATGACACA
P_iolRC_5_for	TGTGTCATCCAGGGCTTTTATTG
P_iolRC_5_rev	GACCTGCAAACCTCTGCC
P_iolRC_6_for	GGGCAGAGTTTGCAGGTC
P_iolRC_6_rev	CTTGTCGACGAAAACCCCTCG
P_iolRC_7_for	CGAGGGGGTTTTCGTCGACAAG
P_iolRC_7_rev	CCCGAAAACGCGCAAAACCC

P_iolRC_8_for	GGGTTTTGCGCGTTTTTCGGG
P_iolRC_8_rev	CCTGACAAAGCAATACATTTCCG
P_iolRC_9_for	CGGAAATGTATTGCTTTGTCAGG
P_iolRC_9_rev	GACCCTCACGATCGCATGTC
P_iolRC_10_for	TCGTGAGGGTCGCCACATTC
P_iolT1_1_for	CCGCACCCTTATCCAGAAAC
P_iolT1_1_rev	GGCCTGAATGAAGGTACTAGCC
P_iolT1_2_rev	GGGTGTCTGCTTGGGTATGG
P_iolT1_3_for	CCATACCCAAGCAGACACCC
P_iolT1_4_rev	CTTTAATCGTGGCAGACACG
P_iolT1_5_for	CGTGTCTGCCACGATTAAAG
P_iolT1_6_for	ACATTGGTGATGTGAATCACTGCC

Complementary oligonucleotides for gel shift assays

P_iolT1_O1+	ATGGAAAACCATAACCCAAGCAGACACCCCC
P_iolT1_O1-	GGGGGTGTCTGCTTGGGTATGGTTTTCCAT
P_iolT1_O2+	CAAGCAGACACCCCCACCCCTAAGTATTAC
P_iolT1_O2-	GTAATACTTAGGGGTGGGGTGTCTGCTTG
P_iolT1_O3+	ACCCCTAAGTATTACCAATTACTCAAAAGT
P_iolT1_O3-	ACTTTTTGAGTAATTGGTAATACTTAGGGGT
P_iolT1_O4+	CAATTACTCAAAAGTATTCAAAAAAGTTT
P_iolT1_O4-	AACTTTTTTTTGAATACTTTTGAGTAATTG
P_iolT1_O5+	ATTCAAAAAAGTTTGTTATGTACGATTGA
P_iolT1_O5-	TCAATCGTACATAACAACTTTTTTTGAAT
P_iolT1_O6+	GTTATGTACGATTGACGGGACATATCGTGT
P_iolT1_O6-	ACACGATATGTCCCGTCAATCGTACATAAC
P_iolT1_O7+	CGGGACATATCGTGTCTGCCACGATTAAAG
P_iolT1_O7-	CTTTAATCGTGGCAGACACGATATGTCCCG
P_iolRC_O1+	GTTGCCCACCCAACAAGCTCATGTAAATGT
P_iolRC_O1-	ACATTTACATGAGCTTGTTGGGTGGGCAAC
P_iolRC_O2+	AGCTCATGTAAATGTGTTAGGACATTTGAA
P_iolRC_O2-	TTCAAATGTCCTAACACATTTACATGAGCT
P_iolRC_O3+	GTTAGGACATTTGAACAATGTAAGTACTGAGTT
P_iolRC_O3-	AACTCAGTTACATTGTTCAAATGTCCTAAC
P_iolRC_O4+	CAATGTAAGTACTGAGTTGCGGGTGGTGGTCTT
P_iolRC_O4-	AAGACCACCACCCGCAACTCAGTTACATTG
P_iolRC_O5+	TATTGATCTGACATTATCACTTGCATTAGG
P_iolRC_O5-	CCTAATGCAAGTGATAATGTCAGATCAATA
P_iolRC_O6+	ATCACTTGCAATTAGGGAATGAGTAGCGAAA
P_iolRC_O6-	TTTCGCTACTCATTCCCTAATGCAAGTGAT
P_iolRC_O7+	GAATGAGTAGCGAAACTTAGTGAAAAGGGC
P_iolRC_O7-	GCCCTTTTCACTAAGTTTCGCTACTCATT
P_iolRC_O8+	CTTAGTGAAAAGGGCAGAGTTTGCAGGTCA
P_iolRC_O8-	TGACCTGCAAACTCTGCCCTTTTCACTAAG
P_iolRC_O9+	AGAGTTTGCAGGTCATAACGTGCAACTTTG
P_iolRC_O9-	CAAAGTTGCACGTTATGACCTGCAAACTCT
P_iolRC_O10+	TAACGTGCAACTTTGTAAACCCCGCACCTT

P_iolRC_O10-	AAGGTGCGGGGTTAACAAAGTTGCACGTTA
P_iolRC_O11+	CGGAAATGTATTGCTTTGTCAGGACAATGTG
P_iolRC_O11-	CACATTGTCTTGACAAAGCAATACATTTCCG
P_iolRC_O12+	CTTTGTCAGGACAATGTGTTATTGTGCATGA
P_iolRC_O12-	TCATGACAATAACACATTGTCCTGACAAAG
P_iolRC_O13+	TTATTGTGCATGACATGCGATCGTGAGGGTC
P_iolRC_O13-	GACCCTCACGATCGCATGTCATGACAATAA
IolR_BS_P_iolC_M1+	TATGTAGTTGTCAGGACAATGTGTTA
IolR_BS_P_iolC_M1-	TAACACATTGTCCTGACAACACTACATA
IolR_BS_P_iolC_M2+	TATTGCTGGTGCAGGACAATGTGTTA
IolR_BS_P_iolC_M2-	TAACACATTGTCCTGCACCAGCAATA
IolR_BS_P_iolC_M3+	TATTGCTTTGTACTTACAATGTGTTA
IolR_BS_P_iolC_M3-	TAACACATTGTAAGTACAAAGCAATA
IolR_BS_P_iolC_M4+	TATTGCTTTGTCAGGCACCTGTGTTA
IolR_BS_P_iolC_M4-	TAACACAGGTGCCTGACAAAGCAATA
IolR_BS_P_iolC_M5+	TATTGCTTTGTCAGGACAAGTGTTA
IolR_BS_P_iolC_M5-	TAAACACTTGCCTGACAAAGCAATA
IolR_BS_P_pck_O1+	TCCGAATGTTAAGTGTTAATGGT
IolR_BS_P_pck_O1-	ACCATTAACACTTAACATTCGGA
IolR_BS_P_pck_M1+	TCCGAATGTTAAGACAAAATGGT
IolR_BS_P_pck_M1-	ACCATTTTGTCTTAACATTCGGA
IolR_BS_P_pck_M2+	TCCGACGTGTAAGTGTTAATGGT
IolR_BS_P_pck_M2-	ACCATTAACACTTACACGTCGGA
IolR_BS_P_pck_M3+	TCCGAATGTTAAGGTGGAATGGT
IolR_BS_P_pck_M3-	ACCATTCCACCTTAACATTCGGA
IolR_BS_P_pck_M4+	TCCGACGTGTAAGGTGGAATGGT
IolR_BS_P_pck_M4-	ACCATTCCACCTTACACGTCGGA

^a Recognition sites for restriction endonucleases are underlined, restriction endonucleases are indicated in parentheses. Complementary sequences for nested PCR or for generating overlap-extension PCR products are printed in italics.

Table S2. Transcriptional start sites of *iolR*, *iolC*, and *iolT1*

Gene	Sequence ^a
cg0196 (<i>iolR</i>)	cactaagtttcgc <u>TactCA</u> ttccctaagT <u>GaTA</u> atgTcagatc AA
cg0197 (<i>iolC</i>)	taatnttcggaaatgta <u>TtgC</u> ttgtcaggacaatgT <u>GtTAT</u> tgTcatgac A
cg0223 (<i>iolT1</i>)	tcaaaagTattCAaaaaaagtttgttatgTAcgATtgacggg A tcaaaagtattcaaaaaaagtttgttatgtacgaTTGACgggacatatcgtgtcTGccAcgATtaaagac A

^aTranscriptional start sites (TSS, bold) were identified by RNAseq as described in the Methods. The -35 and -10 regions are underlined and conserved bases are indicated by capitals. Two TSS were identified for the genes *iolR* and *iolT1*, with higher amounts of transcript starting from the TSS proximal to the start codon.

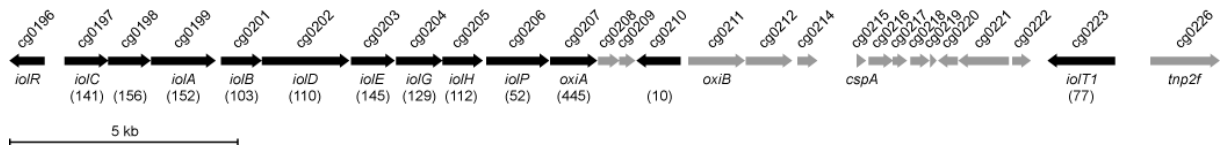


FIG. S1. Map of the *C. glutamicum* genome region (position 167,835 to 194,468 of NC_006958) encoding functions relevant for *myo*-inositol catabolism. Genes exhibiting a ≥ 10 -fold increased mRNA level in the $\Delta iolR$ mutant compared to the wild-type are shown in black and the ratio for each gene is given in parentheses.