

**Table S3. Relationships between *B. subtilis* and *C. glutamicum* strains, plasmids and primers used in this work**

Strain	Plasmid	Primer	Sequence (5'→3') <sup>a</sup>	Template
TC35	pBSB_P <sub>pftAB</sub>	P <sub>pftAB</sub> _FW	<u>CCGCGGGCTTTCCCAGCCTCTTGATTATTTAACC</u> AA	BSB168
		P <sub>pftAB</sub> _RV	GTTCCTCCTTCCCACCCTCATTATAAATAAGAA	BSB168
TC58	pGEMT_lytST	LytT_FW	GATAAAGGAAGCGCAATTGC	BSB168
		LytT_RV	CAATGGAACAGGCAGTTTTTA	BSB168
	pGEMT_lytST::cm	Cm_lytT_FW	TCCCCCGGGGATTCACCGACAAACAACAGATAAAA	pDG1661
		Cm_lytT_RV	CCATCGATGGTATAAAAACCTTCTTCAACTAACGGG	pDG1661
TC63	pDG1661_P <sub>pftB</sub>	P <sub>pftB</sub> _FW	CGGGATCCCGTTTGGTACCCTCATTATAAATAAGAA	BSB168
		P <sub>pftB</sub> _RV	CCCAAGCTTGGGGCTTTGTTCGTGAATACTGAATATA	BSB168
TC60, TC61 & TC62	pGEMT_pftAB	insert_pftAB_FW	CCCCACCCAGAATACAAAGA	BSB168
		insert_pftAB_RV	GGATGAACTGGCTTACTTGC	BSB168
	pGEMT_pftA	pGEMT_pftA_FW	TCCCCCGGGGAAATCATATTTGAAACCAGCATAAT	pGEMT_pftAB
		pGEMT_pftA_RV	GCTCTAGAGCACAAAAACAGTGCAAAGCCCGCAGAA	pGEMT_pftAB
	pGEMT_pftB	pGEMT_pftB_FW	TCCCCCGGGGGAACCATGGCAACAACAAGGAGTGA	pGEMT_pftAB
		pGEMT_pftB_RV	GCTCTAGAGCTAAAGGATTGGCTCTTGGAACATCCG	pGEMT_pftAB
	pGEMT_pftAB::cm	cm_FW	TCCCCCGGGGATCTTTATTCTTCAACTAAAGCACCCATTAG	pDG1661
		cm_RV	GCTCTAGAGCGTAGAGGATCTGGAGCTGTA	pDG1661
	pGEMT_pftA::cm_P <sub>pftAB</sub>	cm_P <sub>pftAB</sub> _FW	GCTCTAGAGCGGATCCCGTTTGGTACCCTCATTATA	pDG1661_P <sub>pftA</sub>
		cm_P <sub>pftAB</sub> _RV	TCCCCCGGGGGAATAAAAACCTTCTTCAACTAACGG	pDG1661_P <sub>pftA</sub>
TC73	pMUTIN4_lytST	lytST_FW	CGGGATCCATATTTTTTCTCCGCCTGTAAGCAAGTT	BSB168
		lytST_RV	CGAGCTCGTTATAAAGCGCTTACAAGATAACATGCC	BSB168

TC74, TC75 & TC76	pDR111_ <i>pftAB</i>	<i>pftAB_FW</i>	<u>TCACGCGTCGACAGGAGGACTACTATGAGTGCTAAAAAAGTGTAC</u>	BSB168
		<i>pftB_RV</i>	<u>TCCTAGCTAGCTTATCCTCCGATCAGCTGCACGAACAC</u>	BSB168
TC153, TC154	pDR111_ <i>pftAB</i>	618 FW	AAGGAAAAAAGCGGCCGCCAAACTTAAGAGTGTGTT	pic618
		618 RV	CTGGTGAAAAGAAAAACCACCTGGCGCCCAATACG	pic618
	pDG1664_P <sub>hs</sub> <i>pftAB</i>	P <sub>hs</sub> <i>pftAB</i> FW	AAATACGGGCAGACATGGCCTGCCCGGTTATTATTA	pDR111_ <i>pftAB</i>
		P <sub>hs</sub> <i>pftAB</i> RV	AAGGAAAAAAGCGGCCCGGATTAATTAATTCAGAACGCTCGGTTG	pDR111_ <i>pftAB</i>
TC125, TC126 & TC149	pBSB_P <sub><i>pftAB-lyt1</i></sub> , pBSB_P <sub><i>pftAB-lyt2</i></sub> & pBSB_P <sub><i>pftAB-lyt1.2</i></sub>	<i>lyt1_FW</i>	<u>CGGGATCCAT</u> TCTGCAACTCAGACCCGCTATACG	pBSB_P <sub><i>pftAB</i></sub>
		<i>lyt1,2_FW</i>	<u>CGGGATCCAGACCCGCTATACGGCATGTTATCT</u>	pBSB_P <sub><i>pftAB</i></sub>
		<i>lyt2_RV</i>	<u>GCGGATCCCCGAAATGGCTGAAATGCAA</u>	pBSB_P <sub><i>pftAB</i></sub>
		<i>lyt1,2_RV</i>	<u>GCGGATCCCCGAAAAGCCGCCCATCAAATATGG</u>	pBSB_P <sub><i>pftAB</i></sub>
TC122, TC124	pPftA_SPA	<i>pftA-LIC1</i>	<u>GGGTTCCCTGGCGCGAGCCGGGTTTTTAACACAAGC</u>	BSB168
		<i>pftA-LIC2</i>	<u>TTGGGCTGGCGCGAGCATGGTGAACGAGTTCGTTATTG</u>	BSB168
	pPftB_SPA	<i>pftB-LIC1</i>	<u>GGGTTCCCTGGCGCGAGCGGCTCTATCTGCTCTGTACG</u>	BSB168
		<i>pftB-LIC2</i>	<u>TTGGGCTGGCGCGAGCTCCTCCGATCAGCTGCACG</u>	BSB168
TC199	pSG-SPA-NTER	OOD141	<u>GGGCTCGAGATGAGTGCTAAAAAAGTGTACGGG</u>	BSB168
		OOD142	<u>GGGGCGGCCGCTTAATGGTGATGGTGATGGTGTCTCCTCCGATCAGC</u> TGCACG	BSB168
TC202, TC203	pXMJ_ <i>pftAB</i>	<i>pftAB_Cg_fw</i>	<u>TCACGCGTCGACAGGAGGACTACTATGAGTGCTAAAAAAGTGTAC</u>	BSB168
		<i>pftAB_Cg_rev</i>	<u>TCCCCCGGGGTTATCCTCCGATCAGCTGCACGAACAC</u>	BSB168

<sup>a</sup> Restriction sites and additional LIC and His<sub>6</sub> sequences are underlined