Supplementary information

Supplementary Table 1. Bacteria and plasmids

Strain name	Relevant characteristics	Source of
		reference
V329	Expresses Bap. Biofilm positive.	1
V329_His	6xHis tag cloned at the end of B region of Bap	This study
V329_SpyTag	SpyTag cloned at the end of B region of Bap	This study
V329 Mefp3	Mefp3 gene cloned at the end of B region of Bap	This study
V329 MT1	MT1 gene cloned at the end of B region of Bap	This study
V329 SnapTag	SnapTag gene cloned at the end of B region of Bap	This study
V329 mCherry	mCherry gene cloned at the end of B region of Bap	This study
BL21 (DE3)	$F^- ompT hsdS_B(r_B^-, m_B^-)$ gal dcm lon λ (DE3 [lac]	Novagen
	lacUV5-T7 gene1 ind1 sam7 nin5])	
BL21(DE3)+pET46-	BL21 carrying pET46 for overexpression of Bap_B	This study
ek/LIC:bap B:SpyTag	protein fused to SpyTag protein	
BL21(DE3)+pET46-	BL21 carrying pET46 for overexpression of GFP	This study
ek/LIC:	protein fused to SpyCatcher protein	
<i>gfp</i> :SpyCatcher		
BL21(DE3)+pET46-	BL21 carrying pET46 for overexpression of	This study
ek/LIC:SpyCatcher	SpyCatcher protein	
BL21(DE3)+pET46-	BL21 carrying pET46 for overexpression of GFP	This study
ek/LIC:gfp	protein	
E. faecalis 23	esp-, non-biofilm forming	2
V329 <i>∆bap</i>	V329 with deletion in <i>bap</i> gene	3
Plasmid name	Description	Source of
		reference
pJET1.2/blunt	Cloning vector	Termo Scientific
pET46-ek/LIC	Expression vector	Novagen
pSNAP-tag®(T7)-2	Expression vector encoding the SNAP-tag protein	New England
		Biolabs
pUAI108-GFPCatcher	Expression vector encoding <i>gfp-spycatcher</i> sequence	This study
·· MAL · 2 MT1	under the expression of <i>Ptac</i> promoter	A 1
pMAL-c2x-M11	Plasmid used to amplify the metallothionein (MTT)	Adegene
PHRR	Plasmid used to amplify the <i>mcherry</i>	-
pE146-	pE146 for induction of Bap_B protein fused to	This study
ek/LIC: <i>bap</i> B:SpyTag	Spylag protein	
pE146-ek/LIC:	pE146 for induction of GFP protein fused to	This study
gfp:SpyCatcher	SpyCatcher protein	T
pE146-ek/LIC:	pE146 for induction of SpyCatcher protein	This study
SpyCatcher	ETAC 6 is lesting CCEP and in	This states
pE140-ek/LIC:g/p	$E_{\rm resc} = \frac{1}{2} \sum_{i=1}^{N} \sum_{j=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{i=1}$	
рмар	<i>E. coll - S. aureus</i> snuttle vector with a	5
	thermosensitive origin of replication for Gram-	
-MAD (mMAD for integrating (while to give the characteristic	This stades
pMAD:0XHIS	MAD for integrating 6xHis tag in the chromosome	This study
pwiAD:Spy1ag	chromosome	i nis study
pMAD:Mefn3	pMAD for integrating Mefp3 tag in the chromosome	This study
pMAD:MT1	pMAD for integrating MT1 tag in the chromosome	This study
pMAD:SnanTag	pMAD for integrating SnanTag tag in the	This study
L	chromosome	1110 00000
pMAD:mCherry	pMAD for integrating mCherry tag in the	This study
	chromosome	

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Construction	Primer name	Sequence 5'-3'
Bap-Snap	Bap_SNAP_A_EcoRI	5'-GAATTCGAAACTGTAGGCGTTAGAGT
	Bap_SNAP_B	5'-GGTGGTGCGCTTCATTTCGCAGTCTTTGTCCATATTTACAGTTGCTGTACCAAC
	Bap_SNAP_C	5'-GAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTTTCAGATGGTACATTCTCAGTG
	Bap_SNAP_D_BamHI	5'-GGATCCTGTATTTACTTCATCTAATGTTGG
	SNAPtag_A	5'-TTGGTACAGCAACTGTAAATATGGACAAAGATTGCGAAATGA
	SNAPtag_A	5'ACACTGAGAATGTACCATCTGATCCCAGACCCGGTTTACCCAG
Bap-HIS	BapB_B_HIS_rev2	5'-GTGGTGATGGTGATGATGATTTACAGTTGCTGTACCAACTGTTGTACCCT
	BapB_C_HIS_fw	5'-CATCATCACCATCACCACTCAGATGGTACATTCTCAG
Bap-Spy	Bap_Spy_B	5'-CTTCGTCGGCTTGTAGGCGTCCACCATCACGATGTGGGCATTTACAGTTGCTGTACCAAC
	Bap_Spy_C	5'-GCCCACATCGTGATGGTGGACGCCTACAAGCCGACGAAGTCAGATGGTACATTCTCAGT
	Spy_tag_fw	5'-GGGCCAGCCGGTACCGCCCACATCGTGATGGTGGACGCCTACAAGCCGACGAAG
	Spy_tag_rv	5'-GGGCCAGCCGGTACCCTTCGTCGGCTTGTAGGCGTCCACCATCACGATGTGGGC
Bap-Mef3	Bap-Mefp3-B	5'-CGGGCCATAGTAATCCGCATTTACAGTTGCTGTACCAAC
	Bap-Mefp3-C	5'-AGACGCGGCAAATACTGGTTCAGATGGTACATTCTCAGTG
	Mefp3-Fw	5'-GCGGATTACTATGGCCC
	Mefp3-Rv	5'-CCAGTATTTGCCGCGT
Bap-mCherry	Bap-mCherry-B	5'-TCTTCTTCACCTTTACTAGTATTTACAGTTGCTGTACCAAC
	Bap-mCherry-C	5'-GGTATGGATGAATTATACAAAGATGGTACATTCTCAGTGTCA
	mCherry-pHRR-Fw	5'-ACTAGTAAAGGTGAAGAAGATA
	mCherry-pHRR-Rv	5'-TTTGTATAATTCATCCATACCAC
Bap-MT1	Bap_Oro_B	5'-GGAGCAGTTGGGGTCCATATTTACAGTTGCTGTACCAAC
	Bap_Oro_C	5'-GTGCACGTGCTGTGCCTCAGATGGTACATTCTCAGT
	Oro_A	5'-TACAGCAACTGTAAATATGGACCCCAACTGCTCC
	Oro_B	5'-ACACTGAGAATGTACCATCTGAGGCACAGCACGTGCAC
rBapB_Spy	Bap-LIC-Fw	5'-GACGACGACAAGATGCAAAAATCTTTAGGTTACACAGATAATTATAC
	Bon LIC By	5'GAGGAGAAGCCCGGTTCTTCGTCGGCTTGTAGGCGTCCACCATCACGATGTGGGCGCCAGAACCACCG
	Вар-ЕІС-Кі	TGCCATTTACAGTTGCTGTACCAACTGTTGTAC
Catcher-Gfp	GFP_Ek_LIC_Fw	5'-GACGACGACAAGATGAGTAAAGGAGAAGAACTTTTC
	Catcher_EK-LIC_Rv	5'-GAGGAGAAGCCCGGTTAAATATGAGCGTCACCTTTAG
Gfp	GFP_Ek_LIC_Fw	5'GACGACGACAAGATGAGTAAAGGAGAAGAACTTTTC
	<u>GFP_Ek_LIC_Rv</u>	5'GAGGAGAAGCCCGGTTATTTGTATAGTTCATCCATGCC

1 Supplementary Table 2. Oligonucleotides and plasmids used in this study



Supplementary Figure 1: Negative control for SNAP fluorescence. a) S. aureus expressing the Bap without SNAP-tag was grown in LB and LB-glu until stationary phase (OD600=5). Cells were labelled with SNAP-surface 488 substrate and Hoechst. The fluorescence of SNAP-surface 488 and Hoechst, the combination of both signals (merge panels) and the differential interference contrast (DIC) images are shown. Scale bar of panels represents 5 µm. b) The fluorescence intensity was determined using the Intensity profile plugin of the Icy-software. Graphs correspond to the mean of the intensity profiles of cross-sections cells (n=20). Gray shadow corresponds to the standard deviation of the mean.

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