Supplementary Information

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| **SI Table 1. Bacterial strains** | | |
| **Strain**s **or plasmid**s | **Genotype or characteristics** | **Source or reference** |
| **Strains** |  |  |
| *E. coli* DH5α | F-ϕ80*lacZΔM15Δ(lacZYA-argF)*U169 *recA1 endA1 hsd*R17(rK−, mK+) *phoA supE44 λ-thi-1 gyr*A96 *rel*A1 | Invitrogen, Carlsbad, CA |
| ***B. subtilis*** |  |  |
| *B. subtilis* 1A751 | *his nprR2 nprE18 DaprA3 DeglS102 DbglT bglSRV* | (Wolf et al. 1995) |
| BS(pWB) | 1A751 containing pWB; Kmr | This work |
| BS(pWB-AIO6BS) | 1A751 containing pWB-AIO6BS; Kmr | This work |
| BS*∆tepA* | 1A751∆*tepA::zeo* | This work |
| BS*∆ymfH* | 1A751∆*ymfH::zeo* | This work |
| BS*∆yrrN* | 1A751∆*yrrN::zeo* | This work |
| BS*∆ywpE* | 1A751∆*ywpE::zeo* | This work |

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| **SI Table 2. Plasmids** | | |
| **Plasmids** | **Genotype and/or relevant characteristic(s)** | **Source** |
| pWB | Kmr, deleted sacB signal of the vector pWB980 | This work |
| pWB-AIO6BS | Kmr, AIO6BS, pWB | This work |
| pT-tepA | Kmr, the gene *tepA* and its flanking sequence, | This work |
| pT-ymfH | Kmr, the gene *ymfH* and its flanking sequence, | This work |
| pT-yrrN | Kmr, the gene *yrrN* and its flanking sequence, | This work |
| pT-ywpE | Kmr, the gene *ywpE* and its flanking sequence, | This work |
| p*∆tepA* | Zeor, *tepA* deletion vector | This work |
| p*∆ymfH* | Zeor, *ymfH* deletion vector | This work |
| p*∆yrrN* | Zeor, *yrrN* deletion vector | This work |
| p*∆ywpE* | Zeor, *ywpE* deletion vector | This work |
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**SI Table 3. Primers**

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| **Primer name** | **Sequence 5′-3′** |
| zeocin-F  zeocin-R | GGTCTGATCGATCTCTGCAGTCGCG  ATTTGTCCTACTCAGGAGAGCGTTC |
| tepA-TF  tepA-TR | CAACCTGCTTAAACCAAAATATTTGA  GCTGCACGTGAGAAAGCAGCAATATG |
| ymfH-TF  ymfH-TR | GACGTGGACAGTAACCAGGTACAATC TTTCAGCCGGGGTAAATTGATTCATC |
| yrrN-TF  yrrN-TR | GTATGAACAAATAAATGACTATATAG CAGCAGCCTCCGCGGTTGGAATCCCG |
| ywpE-TF  ywpE-TR | CCGGGCCTTTTCAATATCCAAATGAG  GCCCCAACATTGCAGGATTTTTTCCT |
| ymfH-T-zeo-F  ymfH -T-zeo-R | GAACGCTCTCCTGAGTAGGACAAATCTGACTGTCTGCAAGGTTGTTCCT  CGCGACTGCAGAGATCGATCAGACCGCTGTTCATATTCGATTGGTTTGATC |
| ywpE-T-zeo-F  ywpE-T-zeo-R | GAACGCTCTCCTGAGTAGGACAAATCCGAAGGGCGCCTCGTTGTGAAAG  CGCGACTGCAGAGATCGATCAGACCCCCGGCGCATTGTTGCCGCCCC |
| tepA -JD-up | CAGCCGGAAGCCAAGGTGAACCATTAGCTG |
| ymfH -JD-up | CAAACGCCGCTTCTCGAGAAAGGGCTCCAG |
| yrrN-JD-up | AGGGCTGACGCCAGGGCCGATTGCCAATGC |
| ywpE-JD-up | GAGACAGAGGTGCCTGCATCCGGAGTGCTG |
| zeocin-JD-down | TTCGTGGACACGACCTCCGACCACTCGGCG |
| tepA-JD-F | catcgtatggaaaacacagaagaag |
| tepA-JD-R | cgtccttcttctttccttgcttcat |
| ymfH-JD-F | ccaatcgaatatgaacagcttcagg |
| ymfH-JD-R | aggaacaaccttgcagacagtcag |
| yrrN-JD-F | aaccgtttccttgaagaagaatccgg |
| yrrN-JD-R | aaccagagctcttagtgacgccga |
| ywpE-JD-F | tgtatggccaaaagaatcaaccaattc |
| ywpE-JD-R | gccgggatcaaaaaatgggtgagg |

Reference in S1

Wolf M, Geczi A, Simon O, Borriss R (1995) Genes encoding xylan and beta-glucan hydrolysing enzymes in *Bacillus subtilis*: characterization, mapping and construction of strains deficient in lichenase, cellulase and xylanase. Microbiology 141 ( Pt 2):281-90