1   **Supporting Figure Legends**

2   **Figure S1. Competition assay of *E. faecalis* harboring plasmid vector.** The overnight

3   cultures of *E. faecalis* OG1S and *E. faecalis* OG1S harboring pAM401 (open bar) or

4   pHT1100 (closed bar) were mixed equally with a 100-dilution in fresh THB broth,

5   followed by co-cultivation at 37°C. At the indicated time point, the percentage of

6   plasmid-harboring cells in the entire population was determined by the ratio of cfu on

7   THB with chloramphenicol (plasmid-harboring cells) against that of THB without

8   antibiotics (sample of the entire population including cells with and without plasmid).

9

10   **Figure S2. Diversity of BacL$_1$ and BacL$_2$ homologues.** Phylogenic tree of BacL$_1$ (A)

11   and BacL$_2$ (B) homologues of *E. faecalis* strains was constructed using JTT model by

12   MEGA7 based on the amino acid sequences alignment generated by ClustalW ver.2.0.

13   The tree with the highest log likelihood is shown. The percentages of trees in which the

14   associated taxa clustered together are shown next to the branches. Initial tree(s) for the

15   heuristic search were obtained automatically by applying Neighbor-Join and BioNJ

16   algorithms to a matrix of pairwise distances estimated using a JTT model, and then

17   selecting the topology with superior log likelihood value. The tree is drawn to scale,

18   with branch lengths measured in the number of substitutions per site. The analysis

19   involved 148 or 153 amino acid sequences for BacL$_1$ or BacL$_2$, respectively. All

20   positions containing gaps and missing data were eliminated. Names of the source strain

21   and plasmid were represented and colored by Bac41-type (clade) as shown in Fig. 2.

22   Type (clade) I, orange; type (clade) IIa, yellow; type (clade) IIb, pink; type (clade) III,

23   blue.

24

25   **Figure S3. Amino acid sequence alignment of BacA homologues.** Amino acid

26   sequences of various clades BacA were aligned. The regions predicted as peptidoglycan

27 binding (PGB) domain and glycosyl hydrolase 25 (GH25) domain are highlighted by

28 grey boxes. Immunity determinant region suggested in this study is highlighted by red

29 box. The region that shows low similarity between clades IIa- and IIb-BacA is

30 highlighted by orange box. Predicted transmembrane (TM) domain was highlighted by

31 yellow. Names of the source strain and plasmid are represented.

32

33 **Figure S4. Diversity of BacI1 and BacI2 homologues.** Phylogenic tree of BacI1 (A)

34 and BacI2 (B) homologues of *E. faecalis* strains was constructed using JTT model by

35 MEGA6 based on the amino acid sequences alignment generated by ClustalW ver.2.0.

36 The tree with the highest log likelihood is shown. The percentages of trees in which the

37 associated taxa clustered together are shown next to the branches. Initial tree(s) for the

38 heuristic search were obtained automatically by applying Neighbor-Join and BioNJ

39 algorithms to a matrix of pairwise distances estimated using a JTT model, and then

40 selecting the topology with superior log likelihood value. The tree is drawn to scale,

41 with branch lengths measured in the number of substitutions per site. The analysis

42 involved 125 or 159 amino acid sequences for BacI1 or BacI2, respectively. All

43 positions containing gaps and missing data were eliminated. Names of the source strain

44 and plasmid were represented and colored by Bac41-type (clade) as shown in Fig. 2A.

45 Type (clade) I, orange; type (clade) IIa, yellow; type (clade) IIb, pink; type (clade) IIc,

46 cyan.

47

48 **Figure S5. Amino acid sequence alignment of BacI1 and BacI2 homologues.** Amino

49 acid sequences of various clades BacI1 (A) or BacI2 (B) were aligned. Predicted

50 transmembrane (TM) domains are highlighted by yellow. Inside or outside regions

51 predicted by TMHHM server are also indicated. Names of the source strain and plasmid

52 were represented.