
Supporting Information for

Multi-stage assembled *Lactobacillus reuteri*-capsule patch for persistent anti-infection

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Results and discussion

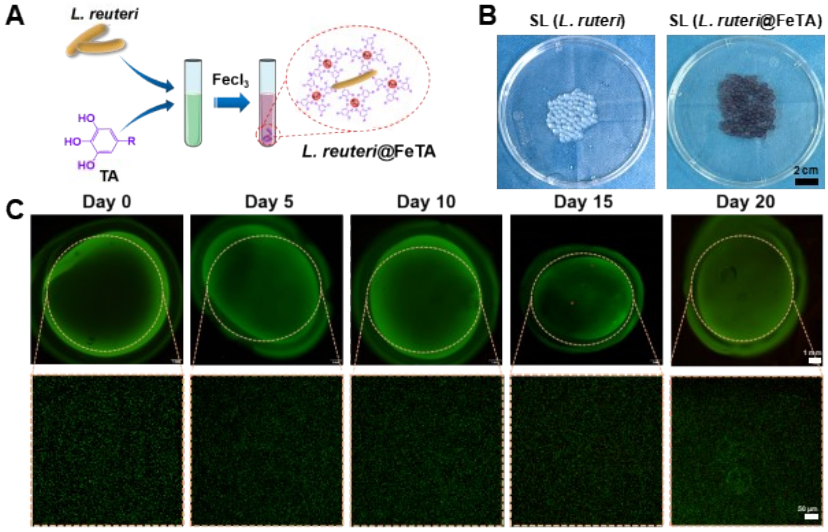

Fig. S1. (A) The synthesis schematic of *L. reuteri*@FeTA. (B) Representative images of SL capsule with *L. reuteri* and *L. reuteri*@FeTA, respectively. (C) CLSM images of *L. reuteri* living/dead strain in SL capsule.

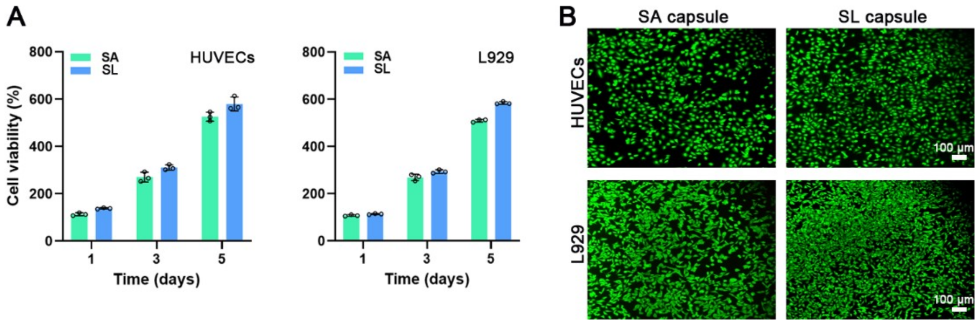

Fig. S2. The viability (A) and microscopic images (B) of Live/Dead stains HUVECs and L929 cells incubated by SA and SL capsule after 5 days.

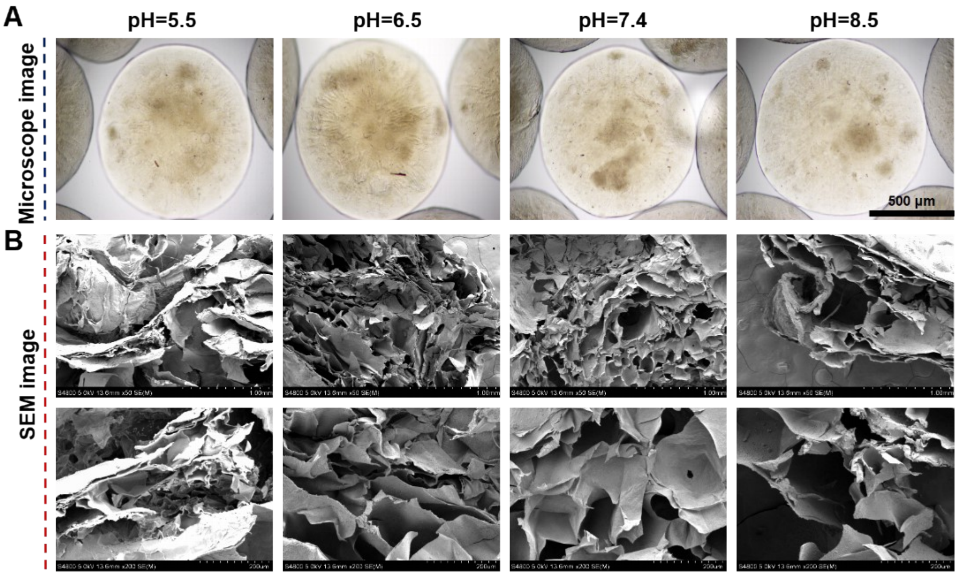

Fig. S3. (A) Representative images of SL capsule in different pH value at microscopy. (B) Representative SEM images of SL capsule in different pH value.

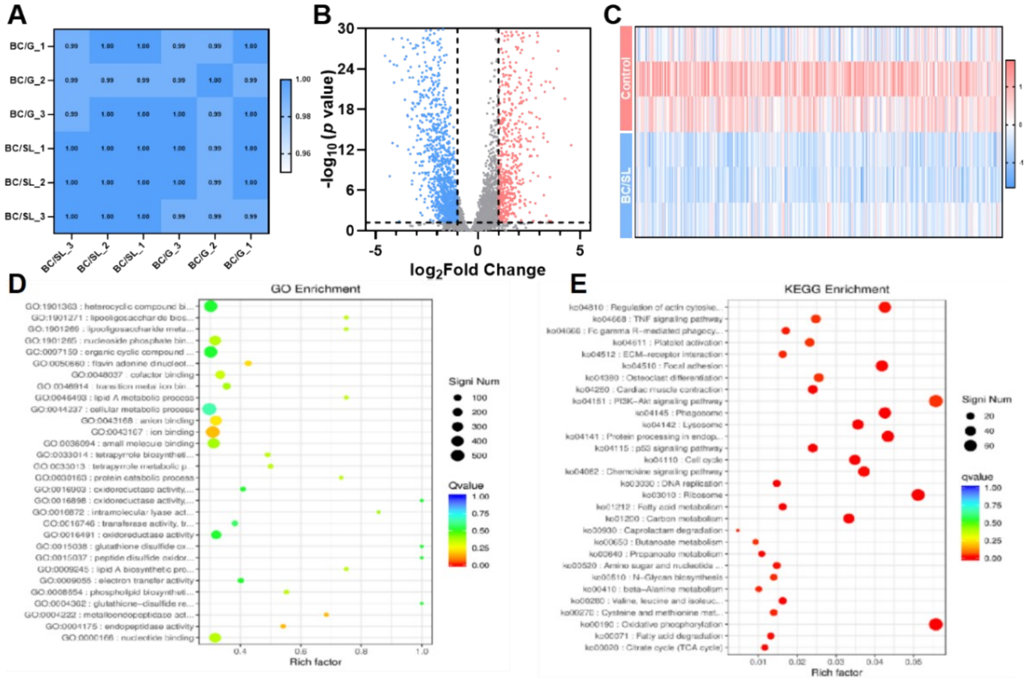

Fig. S4. Transcriptomic analysis in bacteria (*P. aeruginosa*) of BC/SL vs. control. (A) Heatmap of Pearson correlation. (B) Volcano plot of differentially expressed genes. (C) Heatmap analysis of differentially expressed genes. The enrichment of (D) GO terms and (E) KEGG pathways.

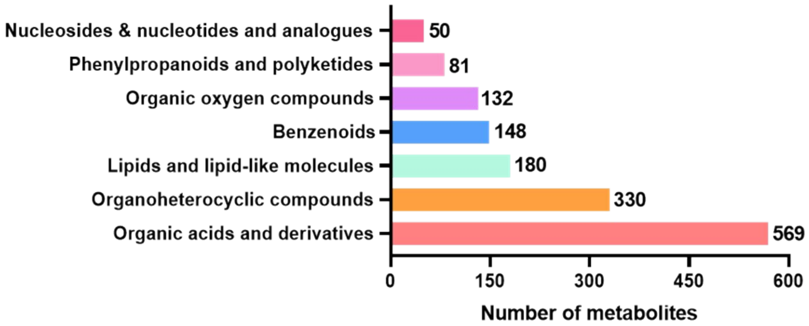

Fig. S5. The metabolite analysis of BC/SL.

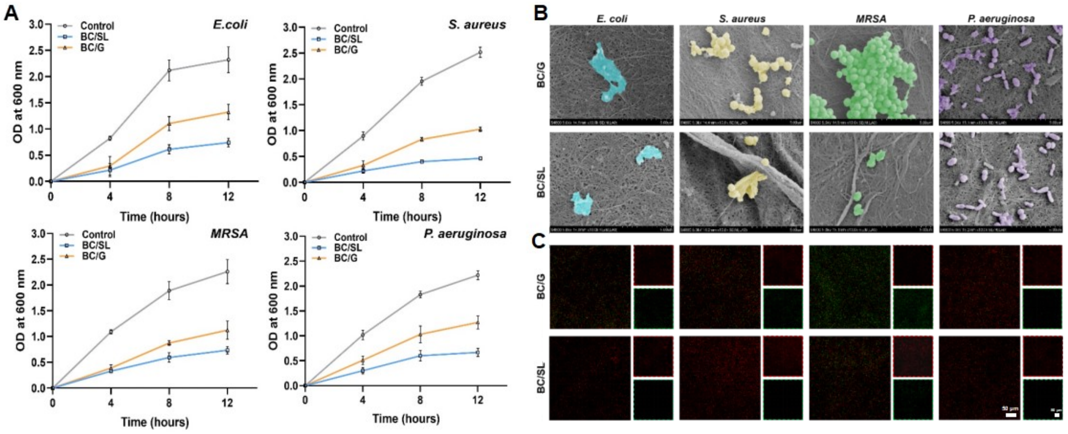

Fig. S6. The growth curve of bacteria (A), representative SEM images (B), and CLSM images (C) of bacteria living/dead strain under sample influence, at 1st cycle of bacterial supplementation.

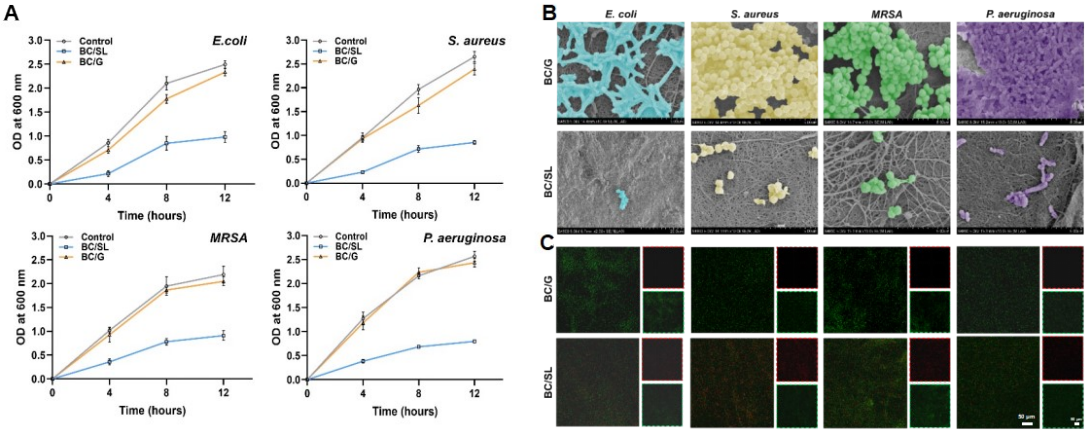

Fig. S7. The growth curve of bacteria (A), representative SEM images (B), and CLSM images (C) of bacteria living/dead strain under sample influence, at 2nd cycle of bacterial supplementation.

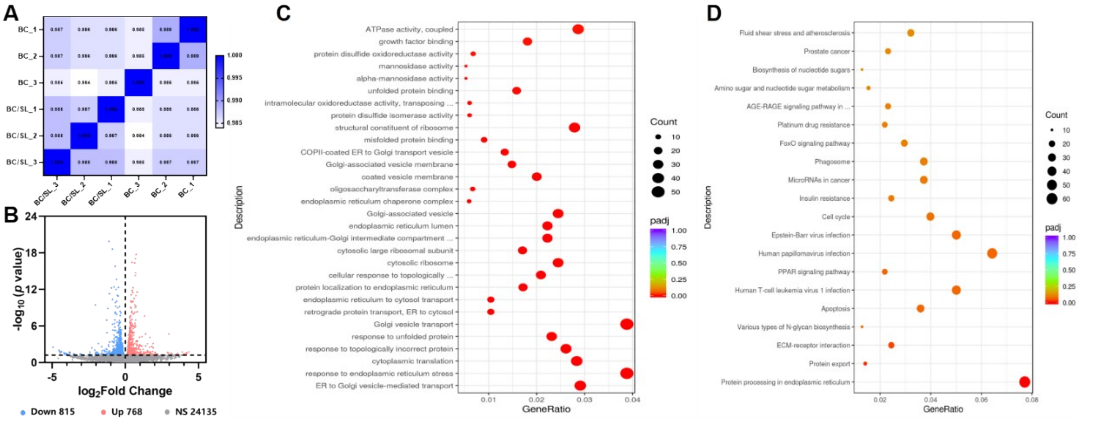

Fig. S8. Transcriptomic analysis in cell (L929) of BC/SL vs. BC/G. (A) Heatmap of Pearson correlation. (B) Volcano plot of differentially expressed genes. (C) Heatmap analysis of differentially expressed genes. The enrichment of (D) GO terms and (E) KEGG pathways.

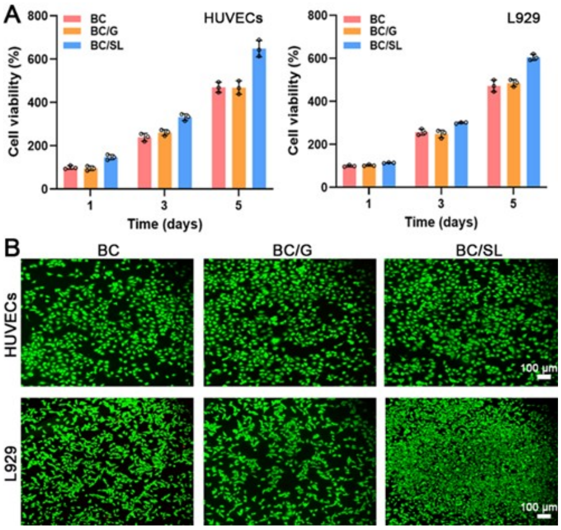

Fig. S9. The viability (A) and microscopic images (B) of Live/Dead stains HUVECs and L929 cells incubated by BC, BC/G, and BC/SL after 5 days.

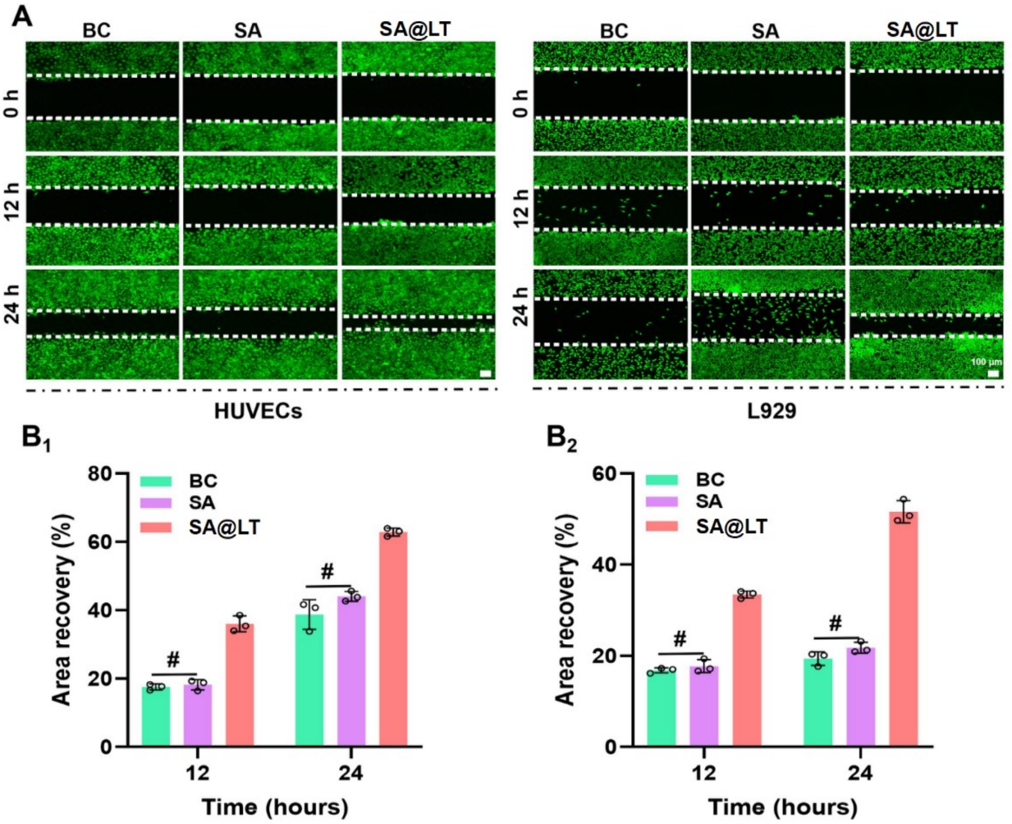

Fig. S10. The migration of L929 cells and HUVECs in a scratch assay (A) with statistics of the area recovery rate (B) incubated by BC, BC/G, and BC/SL.

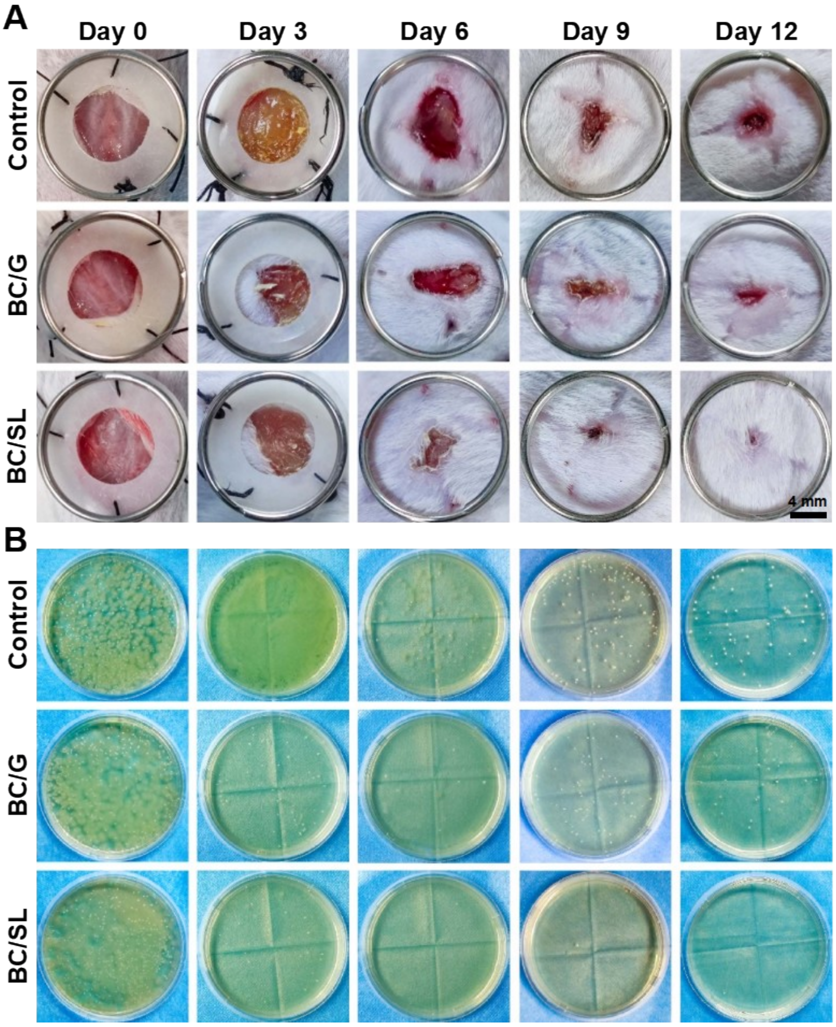

Fig. S11. Representative image of wounds (A) and survival bacteria clones (B) at a predetermined time. The wound site without additional bacteria.

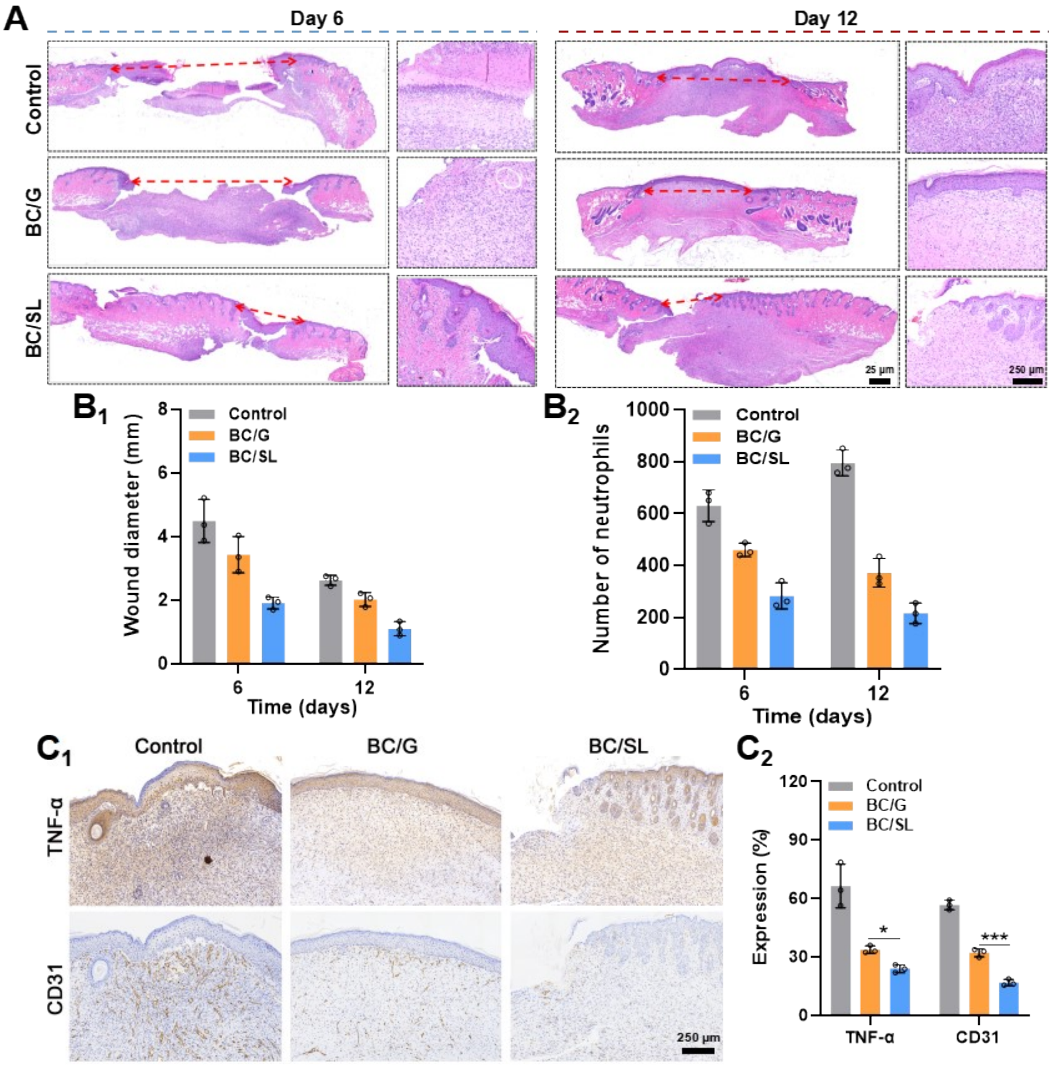

Fig. S12. (A) Images of H&E stained wound tissue 6 days and 12 days. (B1) The statistics of wound diameter, (B2) number of new hair follicles. The immunohistochemistry of TNF-α and CD-31 in wound tissue at 12 days with the expression statistics. The wound site without additional bacteria.

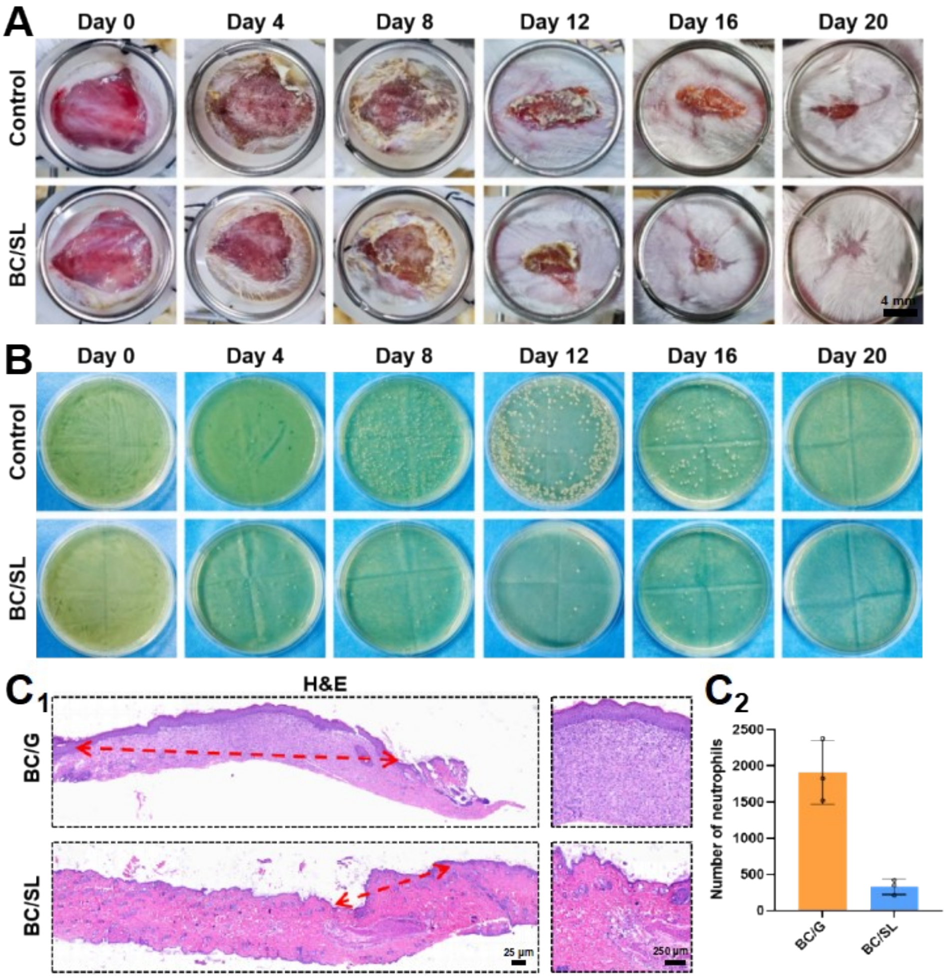

Fig. S13. Representative image of wounds (A) and survival bacteria clones (B) at a predetermined time. (C) Images of H&E stained wound tissue at days. The wound site was infected by *P. aeruginosa* in large area.

Tab. S1. Primer sequence used in q-PCR analysis (human).

Gene name	**Forward primer**	**Reverse primer**
GAPDH	TTCCACCCATGGCAAATTCC	GACTCCACGACGTACTCAGC
COL8A	TGACACCTGAGGTCAAGCAC	ATCTTGCACCAGGCTAGCAG
HMOX1	TTGATGGGGTGAAACCTCCG	TGTCTGCCGTTGTAGAGCAG
CCN1	CTTTTCAACCCTCTGCACGC	AGGACGCACTTCACAGATCC
CCN4	CTCTAACGTCAATGCCCGGT	CCTGCGAGAGTGAAGTTCGT
SOD2	GTGGGAGTCCAAGGTTCAGG	TAGTAAGCGTGCTCCCACAC
FGFR	ACCAAACCAAACCCTGTAGC	CCTCCAATTCGGTGGTCAGG
KLF	CCGTCCTATGCCGCTACAAT	TCGCAGAAGTGGATACGTCG
CSF2	TCAAAGAAGCCCTGAACCTCC	GGTGAAATTGCCCCGTAGAC