

Supplementary Data

Figure S1

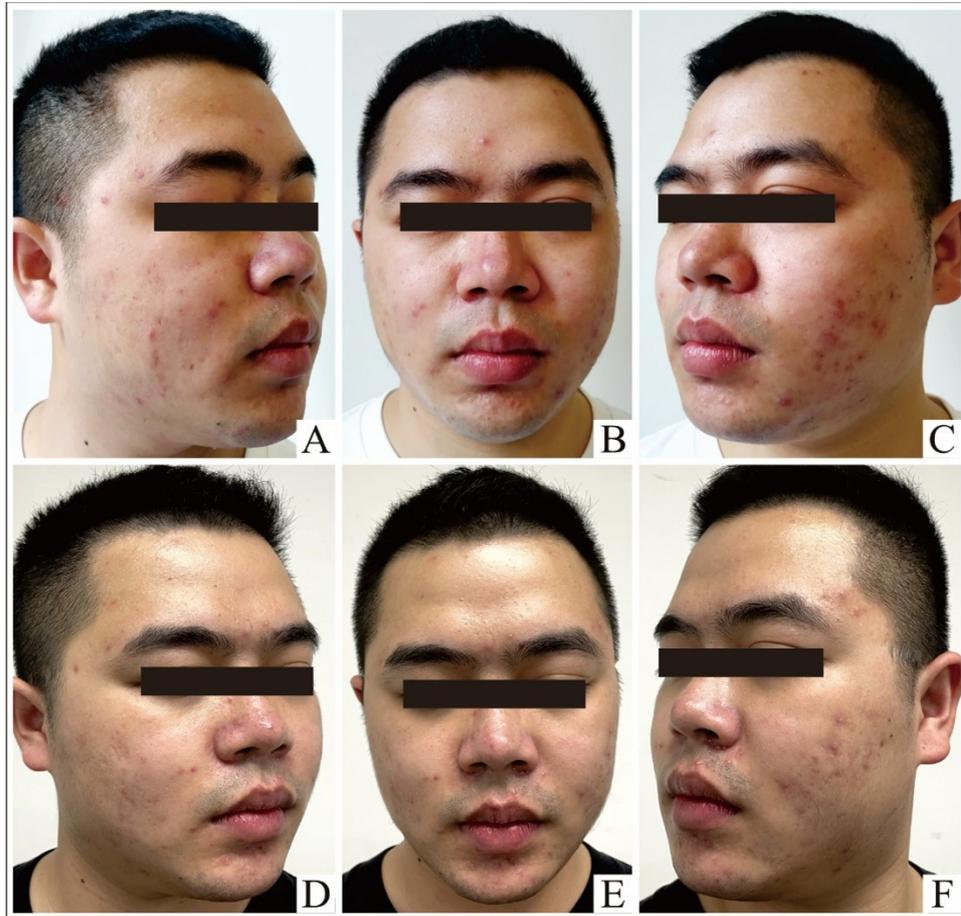


Figure S1 Acne vulgaris patient A, B, and C is before treatment, and D, E, and F is after eight weeks of 2% SSA treatment.

**Figure S2:**

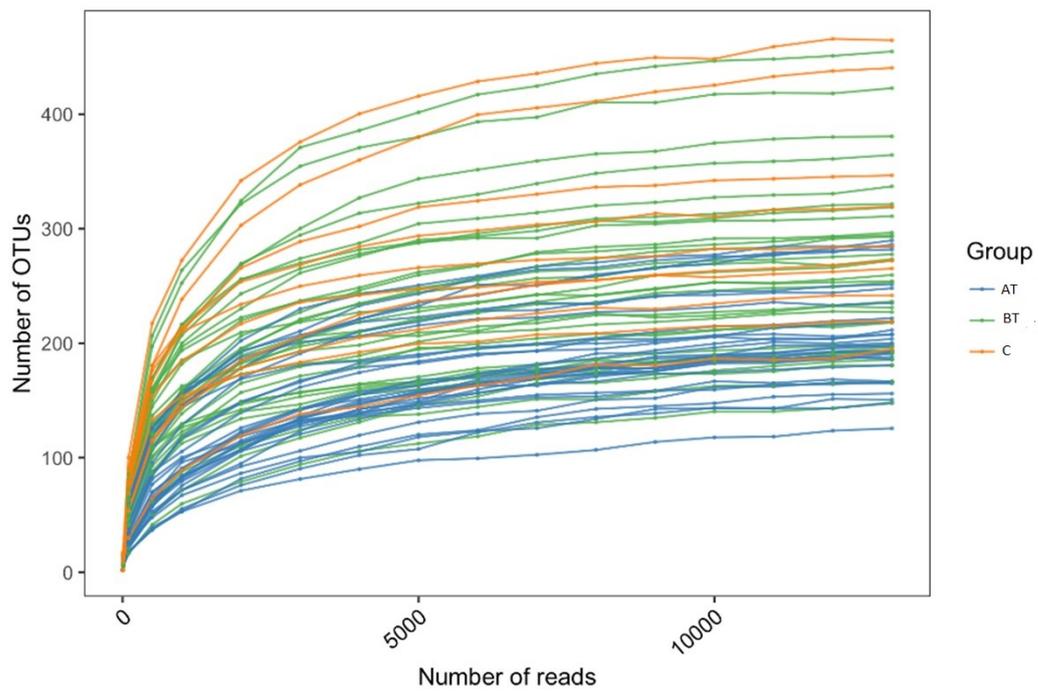


Figure S2 Dilution curve of each sample, BT for before-treated acne samples, AT for after treatment with 2%SSA, and C for control

**Figure S3**

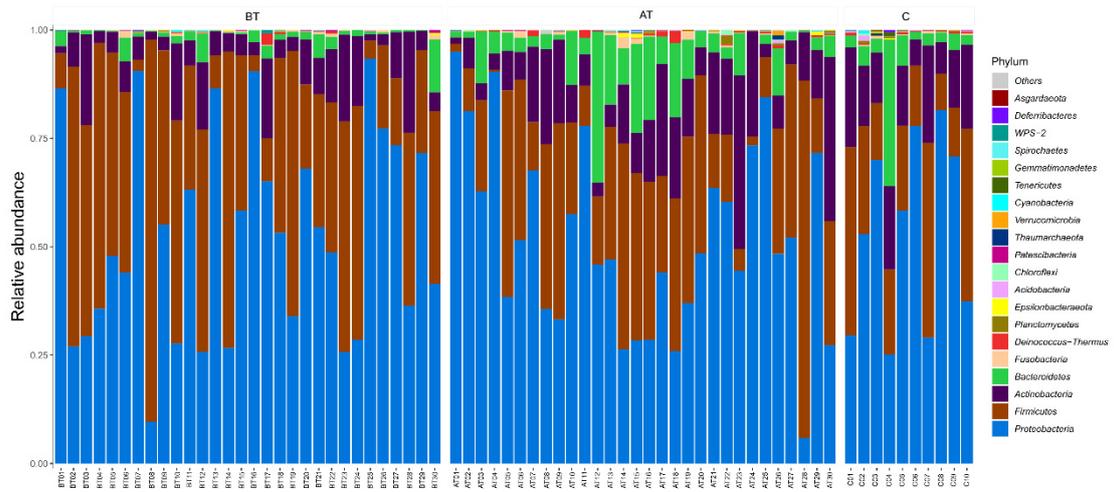


Figure S3 Relative abundance of facial microbiota at phylum level among the pre-treated (BT) (n= 30), treated (AT) (n=30), and (C) (n=10) acne groups, Barplot presenting mean relative abundance in terms of percentage for each sample.

**Figure S4**

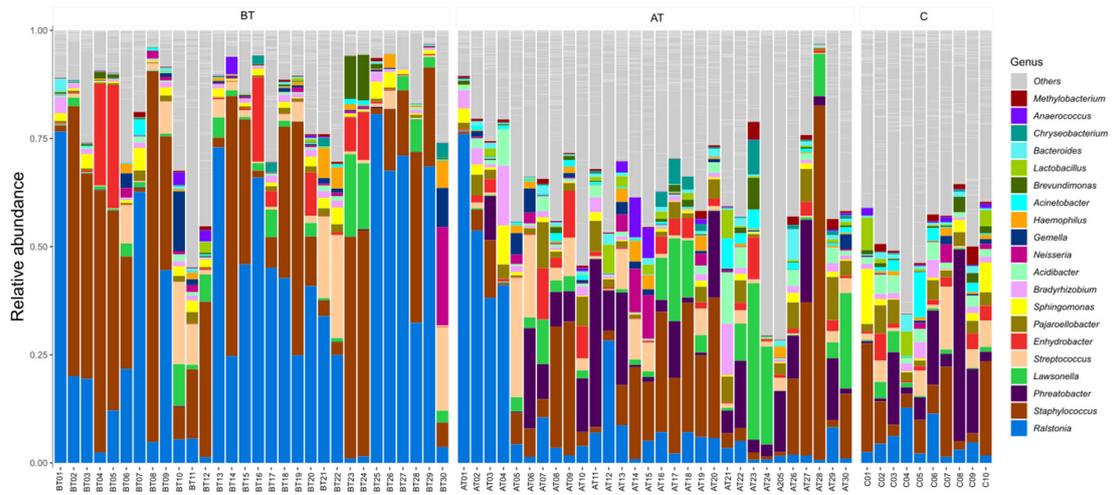


Figure S4 Relative abundance of facial microbiota at genus level among the pre-treated (BT) (n=30), treated (AT) (n=30), and control (C) (n=10) groups. A: Barplot presenting relative abundance in terms of percentage for each sample.

Table S1: Changes in bacterial  $\alpha$ -diversity of the pre-treated (BT), post-treatment (AT), and (C) groups in response to 2% SSA treatment.

| <b>Groups</b>   | <b>Chao1</b>           | <b>Shannon</b>      | <b>Simpson</b>      | <b>Faith's PD</b>    |
|-----------------|------------------------|---------------------|---------------------|----------------------|
| <b>BT Group</b> | 123.7122 $\pm$ 30.6102 | 1.9807 $\pm$ 0.7235 | 0.6654 $\pm$ 0.1718 | 10.2221 $\pm$ 2.3806 |
| <b>AT Group</b> | 179.2085 $\pm$ 64.9888 | 3.0285 $\pm$ 0.7674 | 0.8406 $\pm$ 0.1501 | 13.4247 $\pm$ 3.5314 |
| <b>C Group</b>  | 216.5951 $\pm$ 76.4681 | 3.7105 $\pm$ 0.5069 | 0.9289 $\pm$ 0.0530 | 15.3615 $\pm$ 2.6681 |

Footnotes; BT: Before treatment; AT: After treatment; C group: Control (Healthy)

Table S2: Bacterial composition of the ZymoBIOMICSTM Microbial Community DNA Standard expressed as 16S rRNA gene percentages.

| <b>Bacterial composition</b>   | <b>Standard* (%)</b> | <b>Analysis** (%)</b> |
|--------------------------------|----------------------|-----------------------|
| <i>Bacillus subtilis</i>       | 17.4                 | 19.75                 |
| <i>Staphylococcus aureus</i>   | 15.5                 | 14.95                 |
| <i>Lactobacillus fermentum</i> | 18.4                 | 16.65                 |
| <i>Listeria monocytogenes</i>  | 14.1                 | 13.35                 |
| <i>Escherichia coli</i>        | 10.1                 | 9.2                   |
| <i>Salmonella enterica</i>     | 10.4                 | 9.55                  |
| <i>Enterococcus faecalis</i>   | 9.9                  | 8.95                  |
| <i>Pseudomonas aeruginosa</i>  | 4.2                  | 4.55                  |

Footnote

\*Community composition of the standard

\*\*community composition after the actual analysis and testing of the standard.