

Supplementary Data

Figure S1

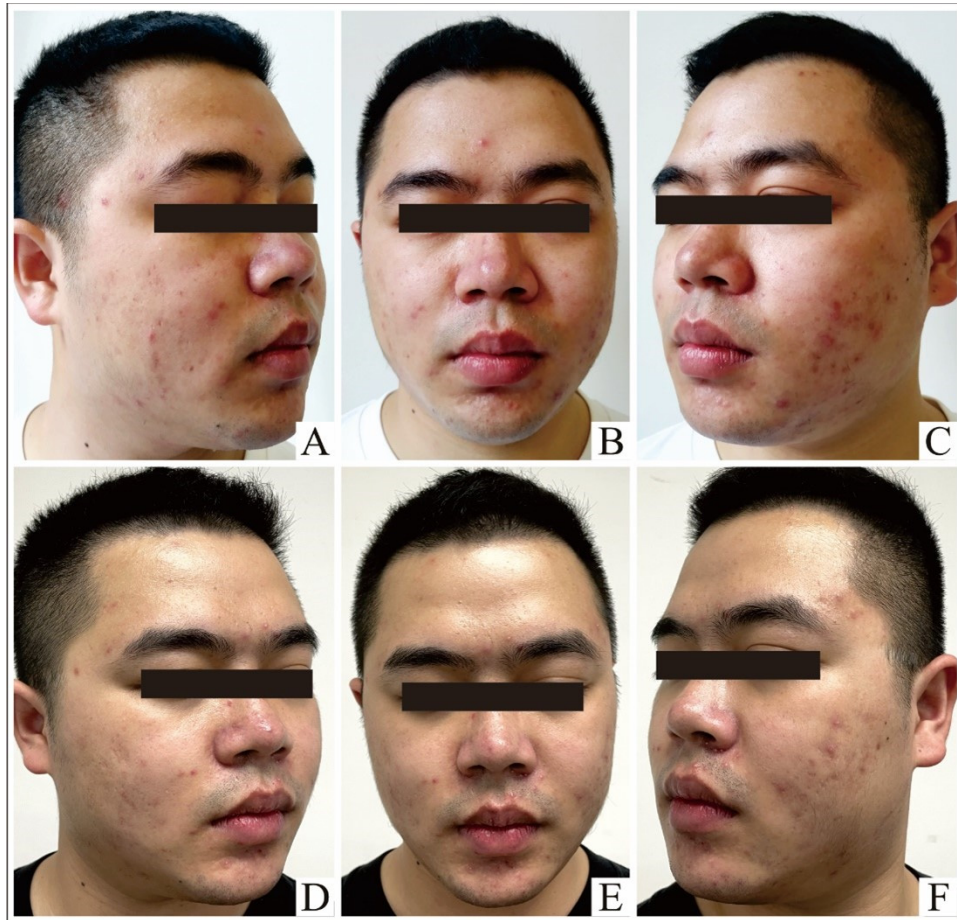


Figure S1 Acne vulgaris patient A, B, and C is before treatment, and D, E, and F is after eight weeks of 2% SSA treatment.

Figure S2:

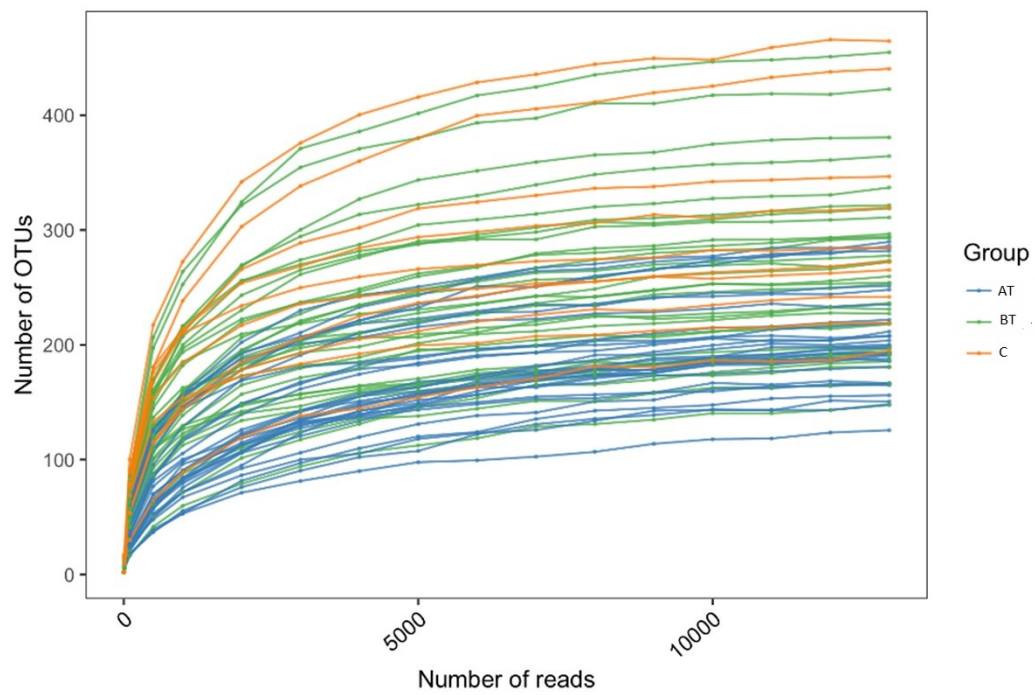


Figure S2 Dilution curve of each sample, BT for before-treated acne samples, AT for after treatment with 2%SSA, and C for control

Figure S3

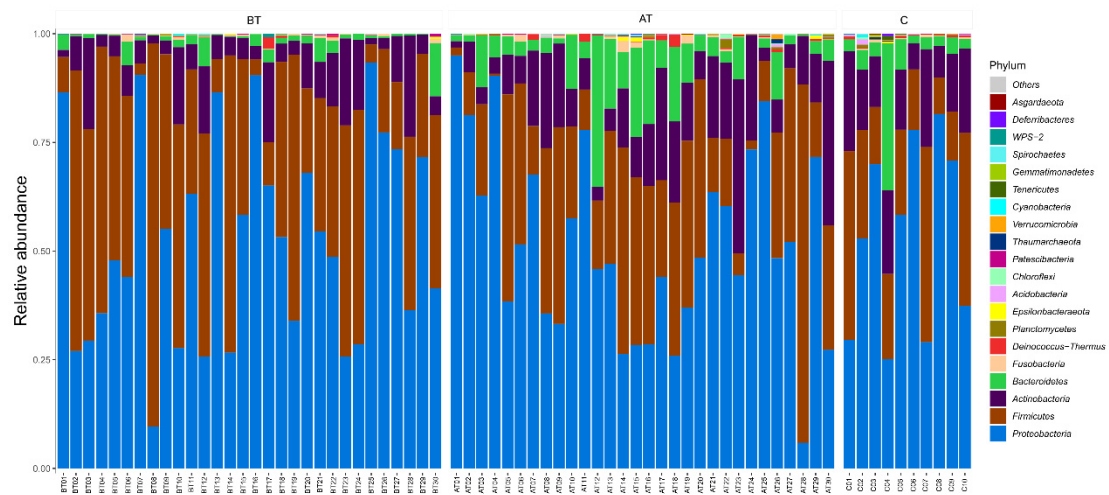


Figure S3 Relative abundance of facial microbiota at phylum level among the pre-treated (BT) (n= 30), treated (AT) (n=30), and (C) (n=10) acne groups, Barplot presenting mean relative abundance in terms of percentage for each sample.

Figure S4

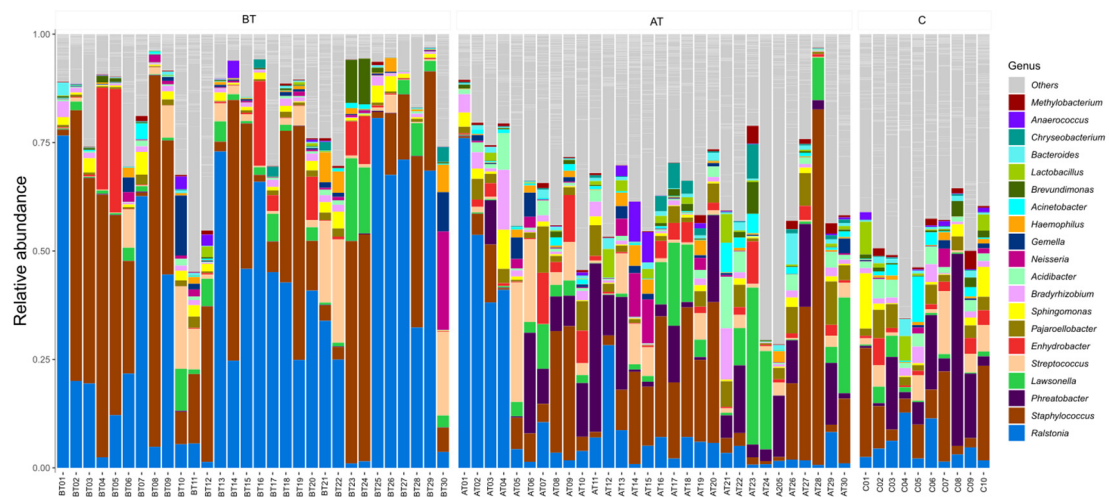


Figure S4 Relative abundance of facial microbiota at genus level among the pre-treated (BT) (n=30), treated (AT) (n=30), and control (C) (n=10) groups. A: Barplot presenting relative abundance in terms of percentage for each sample.

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

Groups	Chao1	Shannon	Simpson	Faith's PD
BT Group	123.7122 \pm 30.6102	1.9807 \pm 0.7235	0.6654 \pm 0.1718	10.2221 \pm 2.3806
AT Group	179.2085 \pm 64.9888	3.0285 \pm 0.7674	0.8406 \pm 0.1501	13.4247 \pm 3.5314
C Group	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.

Bacterial composition	Standard* (%)	Analysis** (%)
<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.