Table SI. Inter-patient variability for microbial diversity, relative abundance of *Staphylococcus* spp. and *S. aureus* concentration per time-point for lesional and non-lesional skin

	Day	Number of samples	Microbial diversity (Shannon diversity index) Mean ± SD (CoV)	Relative abundance of *Staphylococcus* spp. (%) Mean ± SD (CoV)	*S. aureus* concentration based on culture (Log10 CFU/ml) Mean ± SD (CoV)	*S. aureus* concentration based on qPCR (Log10) copies/1000 16S rRNA gene copies) Mean ± SD (CoV)
Lesional skin						
Initial sample set	0	19	3.8±1.7 (45.9)	54.0±31.8 (58.9)	2.9±2.7 (94.1)	1.1±0.9 (88.4)
	7	20	4.1±1.9 (45.5)	54.2±29.5 (54.4)	3.9±2.9 (74.1)	1.4±0.9 (66.2)
	14	18	3.7±1.6 (44.1)	61.9±29.0 (46.9)	4.3±1.9 (45.3)	1.5±0.9 (58.1)
	21	17	4.0±1.8 (45.9)	55.2±31.6 (57.3)	3.2±2.4 (76.0)	1.3±1.0 (72.3)
	28	20	4.3±1.5 (35.6)	50.4±31.5 (62.5)	3.2±2.6 (80.8)	1.3±0.9 (68.1)
	35	17	4.5±1.8 (40.9)	50.6±30.0 (59.3)	3.7±2.3 (61.6)	1.3±0.9 (64.9)
	42	17	4.9±1.7 (35.5)	42.2±27.5 (65.2)	2.8±2.6 (90.6)	1.0±0.9 (89.8)
Second sample set	0	9	3.3±1.9 (58.2)	74.2±20.0 (27.0)	Not applicable	1.3±0.9 (64.5)
	7	12	3.4±2.1 (61.2)	67.9±30.9 (45.5)	Not applicable	1.4±0.9 (61.3)
	14	12	4.3±2.0 (46.1)	56.6±30.6 (54.0)	Not applicable	1.2±0.8 (68.8)
	21	11	3.9±2.3 (58.3)	67.3±27.2 (40.4)	Not applicable	1.3±0.8 (62.2)
	28	10	3.0±1.7 (55.7)	76.2±22.3 (29.3)	Not applicable	1.3±0.7 (52.4)
	35	10	3.4±1.7 (49.3)	76.0±21.5 (28.3)	Not applicable	1.5±0.7 (45.7)
	42	12	3.4±1.8 (51.9)	73.7±22.0 (29.9)	Not applicable	1.4±0.6 (46.7)
Non-lesional skin						
Initial sample set	0	16	5.1±1.0 (20.5)	23.1±19.3 (83.7)	0.8±1.3 (156.9)	0.7±0.8 (117.9)
	7	17	5.2±0.8 (16.3)	21.8±17.2 (78.6)	0.8±1.5 (193.6)	0.7±0.8 (108.4)
	14	17	5.4±0.9 (16.3)	20.5±13.8 (67.3)	1.1±1.4 (125.7)	0.7±0.8 (114.6)
	21	17	5.3±1.0 (19.2)	19.4±16.1 (83.2)	0.8±1.3 (161.4)	0.6±0.8 (124.9)
	28	20	5.1±1.0 (19.3)	20.8±17.5 (84.1)	0.6±1.2 (206.8)	0.7±0.8 (126.7)
	35	17	5.5±1.1 (20.1)	20.9±13.3 (63.7)	0.7±1.3 (192.6)	0.7±0.9 (116.8)
	42	18	5.3±1.5 (28.0)	21.9±21.6 (98.7)	0.5±1.0 (196.0)	0.7±0.8 (120.6)

SD: standard deviation; CFU: colony-forming units; CoV: coefficient of variation.

Table SII. Intra-patient variability per patient for: (a) lesional and (b) non-lesional skin by indicating low coefficient of variation (CoV) of ≤25% for microbial diversity, relative abundance of *Staphylococcus* spp. or *S. aureus* concentration (*green shading*) and a high CoV of >25% (*orange shading*)

Patient group	Day	Number of samples	Microbial diversity (Shannon diversity index) Mean ± SD (CoV)	Relative abundance of *Staphylococcus* spp. (%) Mean ± SD (CoV)	*S. aureus* concentration based on culture (Log10 CFU/ml) Mean ± SD (CoV)	*S. aureus* concentration based on qPCR (Log10 copies/1000 16S rRNA gene copies) Mean ± SD (CoV)
Lesional skin						
Initial sample set						
I	1	6	2.5±0.7 (29.2)	85.6±8.7 (10.2)	5.3±0.7 (13.8)	1.9±0.3 (15.8)
	2	7	2.9±0.9 (32.6)	79.8±9.4 (11.8)	4.3±2.2 (51.5)	1.8±0.9 (48.9)
	3	5	3.4±1.1 (32.3)	78.9±9.6 (12.2)	4.9±0.6 (12.1)	2.2±0.3 (11.3)
	4	7	3.3±0.7 (21.1)	74.7±12.8 (17.2)	4.4±2.1 (47.3)	2.2±0.3 (12.4)
	5	7	3.1±0.5 (14.4)	56.6±11.5 (20.3)	1.0±1.7 (173.4)	1.0±0.6 (57.4)
	6	7	2.9±1.4 (49.3)	80.0±18.0 (22.5)	4.7±2.3 (49.0)	1.4±0.9 (64.1)
	7	5	4.0±0.8 (20.8)	60.8±15.1 (24.8)	3.0±1.9 (63.9)	1.5±0.3 (20.4)
II	8	7	3.0±1.2 (40.4)	68.0±19.8 (29.1)	5.7±1.6 (28.3)	1.6±0.8 (49.2)
	9	7	3.4±1.4 (40.4)	64.5±21.8 (33.9)	4.1±2.1 (51.7)	2.0±0.7 (33.8)
	10	4	2.6±1.8 (70.7)	75.3±27.2 (36.2)	4.9±2.4 (48.6)	1.8±0.9 (50.8)
	11	7	4.3±1.5 (35.4)	55.8±21.0 (37.7)	5.6±1.5 (27.1)	1.7±0.8 (48.1)
	12	7	4.7±1.3 (28.7)	50.3±22.3 (44.1)	4.2±1.7 (40.2)	4.1±0.6 (42.3)
	13	7	5.1±1.5 (29.2)	28.2±14.9 (51.6)	4.3±1.0 (23.8)	1.4±0.6 (43.0)
	14	6	3.7±1.7 (44.9)	49.8±34.8 (69.8)	2.1±1.7 (80.3)	1.0±0.9 (88.0)
	15	6	3.2±3.0 (92.2)	59.0±43.8 (74.2)	3.5±3.8 (109.7)	1.7±1.1 (65.4)
III	16	6	5.5±0.4 (7.1)	14.7±5.4 (36.5)	All negative	All negative
	17	7	6.3±0.5 (7.9)	11.4±3.8 (33.0)	All negative	One sample positive
	18	6	6.1±0.6 (9.5)	13.8±8.8 (63.4)	4.1±2.7 (65.8)	0.4±0.4 (103.9)
	19	7	5.8±0.6 (9.7)	15.0±7.7 (51.1)	All negative	One sample positive
	20	7	6.4±0.8 (11.9)	25.6±11.4 (44.6)	3.1±1.6 (50.5)	1.0±0.3 (30.2)
Second sample set						
I	1	5	1.2±0.3 (26.3)	98.5±1.3 (1.3)	Not applicable	1.6±0.4 (22.5)
	2	6	2.0±0.8 (38.3)	93.7±5.8 (6.2)	Not applicable	1.5±0.3 (22.4)
	3	7	1.6±1.1 (64.4)	89.8±11.5 (12.8)	Not applicable	1.5±0.6 (41.3)
	4	7	2.2±1.0 (47.7)	82.6±11.2 (13.6)	Not applicable	1.7±0.6 (34.3)
	5	5	3.0±0.9 (30.1)	76.0±12.3 (16.2)	Not applicable	1.6±0.3 (17.8)
	6	7	3.7±1.1 (30.3)	72.8±16.1 (22.2)	Not applicable	2.0±0.2 (11.2)
	7	7	3.8±1.9 (49.8)	76.7±17.7 (23.1)	Not applicable	1.9±0.2 (10.4)
II	8	7	3.2±1.7 (51.8)	72.8±30.0 (41.2)	Not applicable	1.5±0.5 (33.3)
	9	7	5.3±1.5 (28.2)	52.8±22.3 (42.3)	Not applicable	1.2±0.4 (29.9)
III	10	6	5.8±1.1 (19.0)	44.8±17.6 (39.3)	Not applicable	0.2±0.4 (161.3)
	11	7	5.7±1.1 (19.9)	37.9±15.3 (40.3)	Not applicable	0.4±0.3 (74.9)
	12	5	4.8±1.0 (19.9)	41.5±19.5 (46.9)	Not applicable	1.4±0.4 (29.2)
Non-lesional skin						
Initial sample set						
I	1	7	4.6±0.7 (16.0)	52.8±9.8 (18.6)	2.0±1.5 (72.6)	2.1±0.2 (11.8)
	2	7	6.1±0.4 (5.9)	11.2±4.2 (37.7)	0.3±0.8 (264.6)	0.3±0.4 (124.9)
	3	7	5.2±0.5 (9.8)	38.7±6.8 (17.5)	1.0±1.2 (125.5)	1.4±0.3 (23.8)
	4	6	4.7±0.6 (12.2)	24.1±14.6 (60.5)	0.4±1.1 (244.9)	0.9±1.0 (112.9)
	5	7	2.9±0.6 (19.5)	15.2±4.5 (29.4)	All negative	0.4±0.4 (89.0)
	6	7	5.4±0.4 (7.9)	29.2±8.9 (30.5)	0.4±1.1 (264.6)	0.1±0.5 (557.6)
	7	5	5.3±0.6 (11.3)	15.4±5.8 (37.4)	All negative	0.3±0.3 (114.6)
II	8	7	4.0±1.2 (29.3)	20.1±30.8 (153.3)	1.3±1.6 (129.7)	0.7±1.0 (147.1)
	9	3	5.3±0.4 (8.3)	20.1±5.6 (27.7)	1.7±1.4 (86.6)	1.5±0.5 (30.4)
	10	6	4.7±0.9 (20.0)	37.1±19.2 (51.7)	2.2±1.9 (83.8)	1.3±0.5 (36.3)
	11	7	5.4±0.8 (14.1)	37.5±14.3 (38.1)	2.7±1.2 (45.0)	1.7±0.3 (19.2)
	12	7	5.7±0.7 (12.5)	16.2±6.6 (40.5)	0.4±1.0 (264.6)	0.6±0.4 (60.3)
	13	7	6.5±0.6 (8.7)	11.4±4.1 (36.2)	1.4±1.3 (93.6)	0.8±0.3 (35.1)
	14	2	6.1±0.8 (12.8)	18.8±5.5 (29.2)	All negative	0.5±0.7 (141.4)
	15	6	5.5±0.5 (9.7)	29.0±13.6 (46.8)	All negative	1.2±0.7 (63.3)
III	16	5	4.7±0.8 (17.7)	5.7±2.4 (42.0)	All negative	All negative
	17	7	6.5±0.2 (3.5)	10.0±1.0 (10.1)	All negative	All negative
	18	6	5.9±0.4 (7.5)	4.6±2.1 (45.8)	0.7±1.2 (156.2)	0.1±0.3 (255.6)
	19	7	5.3±0.6 (10.6)	6.0±2.8 (46.0)	All negative	All negative
	20	6	6.0±0.3 (4.2)	12.1±2.9 (24.4)	All negative	0.0±0.4 (1517.5)

SD: standard deviation; CoV: coefficient of variation.

Table SIII. Characteristics of the 3 groups of patients with different microbiological phenotypes

Clinical trial	Initial sample set			Second sample set		
	Group I (n = 7)	Group II (n = 8)	Group III (n = 5)	Group I (n = 7)	Group II (n = 2)	Group III (n = 3)
Sex, n (%)						
Female	4 (57)	4 (50)	4 (80%)	6 (86)	1 (50)	1 (33)
Male	3 (43)	4 (50)	1 (20%)	1 (14)	1 (50)	2 (67)
Age, years, mean±SD	25.7±5.4	22.9±4.4	21.2±1.5	26.7±14.3	20.5±2.1	22.7±1.2
Fitzpatrick skin type, n (%)						
I	1 (14)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
II	2 (29)	6 (75)	4 (80)	4 (57)	1 (50)	0 (0)
III	1 (14)	1 (12)	1 (20)	1 (14)	0 (0)	2 (67)
IV	1 (14)	1 (12)	0 (0)	1 (14)	0 (0)	1 (33)
V	2 (29)	0 (0)	0 (0)	0 (0)	1 (50)	0 (0)
VI	0 (0)	0 (0)	0 (0)	1 (14)	0 (0)	0 (0)
Target area for sample collection, n (%)						
Antecubital fossa	6 (86)	7 (88)	3 (60)	7 (100)	2 (100)	3 (100)
Dorsal neck	1 (14)	0 (0)	1 (20)	0 (0)	0 (0)	0 (0)
Front side of shoulder/upper arm	0 (0)	1 (12)	0 (0)	0 (0)	0 (0)	0 (0)
Back/below scapula	0 (0)	0 (0)	1 (20)	0 (0)	0 (0)	0 (0)
Season of participation, n (%)						
Spring	3 (43)	5 (63)	3 (60)	0 (0)	0 (0)	0 (0)
Summer	1 (14)	1 (12)	0 (0)	4 (57)	2 (100)	2 (67)
Autumn	3 (43)	2 (25)	2 (40)	3 (43)	0 (0)	1 (33)
Winter	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Clinical AD score, mean±SD oSCORAD*	20.0±6.2	20.2±2.1	13.4±4.2	21.4±4.7	18.5±1.0	12.5±0.9
Microbial diversity, mean±SD Shannon diversity index**	3.2±0.5	3.8±0.9	6.0±0.4	2.5±1.0	4.3±1.4	5.4±0.5
Relative abundance of *Staphylococcus* spp., mean±SD %***	73.8±10.8	56.4±14.3	16.1±5.5	84.3±9.9	62.8±14.2	41.4±3.5
S. aureus concentration, mean±SD log10 CFU/ml****	3.9±1.5	4.3±1.2	1.4±2.0	Not applicable	Not applicable	Not applicable
S. aureus concentration, mean±SD log10 nuc gene copies/1000 16S rRNA gene copies*****	1.7±0.4	1.6±0.3	0.3±0.4	1.7±0.2	1.4±0.3	0.5±0.8
Total load of bacterial DNA, mean±SD 16S rRNA gene copies/ml	5.7±0.5	5.5±0.4	5.4±0.4	7.0±0.3	7.0±0.1	6.6±0.5
Total load of human DNA, mean±SD RNaseP gene copies/ml******	3.6±0.4	3.4±0.4	2.9±0.5	4.2±0.4	4.2±0.1	4.2±0.2

All statistical analyses were performed with the 1-way ANOVA test: *$p = 0.032$ and $p = 0.028$ for the initial and second sample set, respectively; **$p < 0.001$ and $p = 0.006$ for the initial and second sample set, respectively; ***$p < 0.001$ for both sample sets; ****$p < 0.001$ for the initial sample set; ****$p < 0.001$ and $p = 0.010$ for the initial and second sample set, respectively; ******$p = 0.026$ for the initial sample set.
AD: atopic dermatitis; oSCORAD: objective-SCORing Atopic Dermatitis; CFU: colony-forming units.