Supplementary Online Content

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eTable. Read Count and Operational Taxonomic Unit (OTU) Assignment of Individual Skin Samples

eFigure 1. Microbial Distributions of All Samples at the Phylum and Genus Levels

eFigure 2. Dynamics of Bacterial Populations in the Presence and After Withdrawal of Antibiotic Treatment Stratified by Individual Patients

eReference

This supplementary material has been provided by the authors to give readers additional information about their work.

eTable. Read Count and Operational Taxonomic Unit (OTU) Assignment of Individual Skin Samples

Sample ID	Raw Reads	Reads Assigned to OTU	Unmapped Reads	% Unmapped Reads
03.AF.BL.L.cheek	96262	96215	47	0.05%
03.AF.BL.L.chin	77076	76982	94	0.12%
03.AF.BL.L.forehead	81311	81247	64	0.08%
03.AF.BL.R.cheek	72485	72412	73	0.10%
03.AF.BL.R.chin	75895	75750	145	0.19%
03.AF.BL.R.forehead	82590	82525	65	0.08%
03.AF.w12.L.cheek	75123	74892	231	0.31%
03.AF.w12.L.chin	76110	75960	150	0.20%
03.AF.w12.L.forehead	67789	67714	75	0.11%
03.AF.w12.R.cheek	78222	78021	201	0.26%
03.AF.w12.R.chin	86335	86233	102	0.12%
03.AF.w12.R.forehead	85326	85204	122	0.14%
03.AF.w4.L.cheek	70700	70607	93	0.13%
03.AF.w4.L.chin	81268	81144	124	0.15%
03.AF.w4.L.forehead	74708	74664	44	0.06%
03.AF.w4.R.cheek	83218	83090	128	0.15%
03.AF.w4.R.chin	121917	121790	127	0.10%
03.AF.w4.R.forehead	65309	65215	94	0.14%
03.AF.w5.L.cheek	111727	111629	98	0.09%
03.AF.w5.L.chin	95336	95253	83	0.09%
03.AF.w5.L.forehead	78137	78063	74	0.09%
03.AF.w5.R.cheek	83286	83204	82	0.10%
03.AF.w5.R.chin	68880	68819	61	0.09%
03.AF.w5.R.forehead	103422	103360	62	0.06%
04.AT.BL.L.chin	75129	74947	182	0.24%
04.AT.BL.L.forehead	84897	84661	236	0.28%
04.AT.BL.R.cheek	88073	87880	193	0.22%
04.AT.BL.R.chin	101387	101000	387	0.38%
04.AT.w12.L.cheek	85481	84985	496	0.58%
04.AT.w12.L.chin	66396	65843	553	0.83%
04.AT.w12.L.forehead	62489	62394	95	0.15%
04.AT.w12.R.cheek	77672	77310	362	0.47%
04.AT.w12.R.chin	63289	62471	818	1.29%
04.AT.w12.R.forehead	1735	0	1735	100%
04.AT.w4.L.cheek	91845	91709	136	0.15%
04.AT.w4.L.chin	63061	62900	161	0.26%
04.AT.w4.L.forehead	99058	98758	300	0.30%
04.AT.w4.R.cheek	90675	90507	168	0.19%
04.AT.w4.R.chin	65206	64932	274	0.42%
04.AT.w4.R.forehead	71199	70964	235	0.33%
04.AT.w5.L.cheek	68223	67924	299	0.44%
04.AT.w5.L.chin	85188	85034	154	0.18%

04.AT.w5.L.forehead	73545	73325	220	0.30%
04.AT.w5.R.cheek	102016	101928	88	0.09%
04.AT.w5.R.chin	81101	80929	172	0.21%
04.AT.w5.R.forehead	60613	60299	314	0.52%
05.CB.BL.L.cheek	78901	77744	1157	1.47%
05.CB.BL.L.chin	108591	107572	1019	0.94%
05.CB.BL.L.forehead	70669	69974	695	0.98%
05.CB.BL.R.cheek	78023	77134	889	1.14%
05.CB.BL.R.chin	77728	76899	829	1.07%
05.CB.BL.R.forehead	70992	69802	1190	1.68%
05.CB.w12.L.cheek	63146	63094	52	0.08%
05.CB.w12.L.chin	52152	52093	59	0.11%
05.CB.w12.L.forehead	49456	49418	38	0.08%
05.CB.w12.R.cheek	9822	9771	51	0.52%
05.CB.w12.R.chin	29464	29428	36	0.12%
05.CB.w12.R.forehead	56029	55990	39	0.07%
05.CB.w4.L.cheek	81875	80779	1096	1.34%
05.CB.w4.L.chin	56037	55997	40	0.07%
05.CB.w4.L.forehead	55446	54923	523	0.94%
05.CB.w4.R.cheek	63921	63064	857	1.34%
05.CB.w4.R.chin	64598	64553	45	0.07%
05.CB.w4.R.forehead	90283	89437	846	0.94%
05.CB.w5.L.cheek	58948	58867	81	0.14%
05.CB.w5.L.chin	57515	57473	42	0.07%
05.CB.w5.L.forehead	56128	56046	82	0.15%
05.CB.w5.R.cheek	51543	51476	67	0.13%
05.CB.w5.R.chin	66759	66691	68	0.10%
05.CB.w5.R.forehead	52145	52100	45	0.09%
07.AS.BL.L.cheek	9375	9351	24	0.26%
07.AS.BL.L.chin	23970	23945	25	0.10%
07.AS.BL.L.forehead	42353	42288	65	0.15%
07.AS.BL.R.cheek	41296	41261	35	0.08%
07.AS.BL.R.chin	47098	47053	45	0.10%
07.AS.BL.R.forehead	38525	38450	75	0.19%
07.AS.w4.L.cheek	34490	34444	46	0.13%
07.AS.w4.L.chin	39924	39898	26	0.07%
07.AS.w4.L.forehead	18658	18641	17	0.09%
07.AS.w4.R.cheek	21	0	21	100%
07.AS.w4.R.chin	34254	34229	25	0.07%
07.AS.w4.R.forehead	18599	18582	17	0.09%
07.AS.w5.L.cheek	8755	8746	9	0.10%
07.AS.w5.L.chin	211	0	211	100%
07.AS.w5.L.forehead	44126	44078	48	0.11%
07.AS.w5.R.cheek	20910	20885	25	0.12%
07.AS.w5.R.chin	23	0	23	100%
07.AS.w5.R.forehead	25899	25878	21	0.08%

eFigure 1. Microbial Distributions of All Samples at the Phylum and Genus Levels
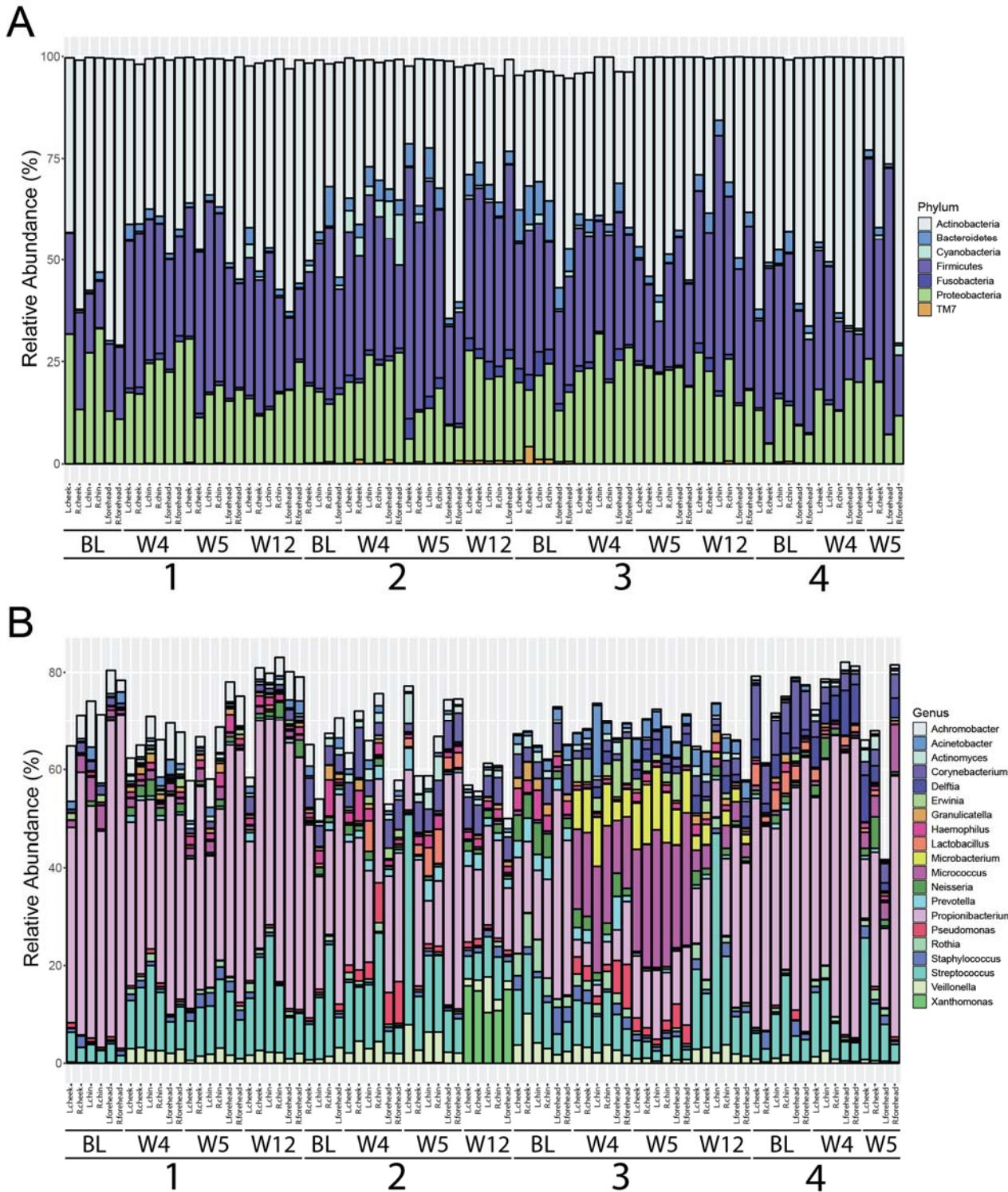
eFigure 1. Taxonomy bar plots comparing microbial distributions of skin samples from all 4 patients at the **A.** Phylum level showing all phyla with relative abundance greater than 0.1% across all samples and **B.** Genus level showing top 30 genera across all samples. BL indicates baseline; W4, week 4; W5, week 5; W12; week 12. Taxonomy bar plots created with phyloseq[1] package in R.

eFigure 2. Dynamics of Bacterial Populations in the Presence and After Withdrawal of Antibiotic Treatment Stratified by Individual Patients
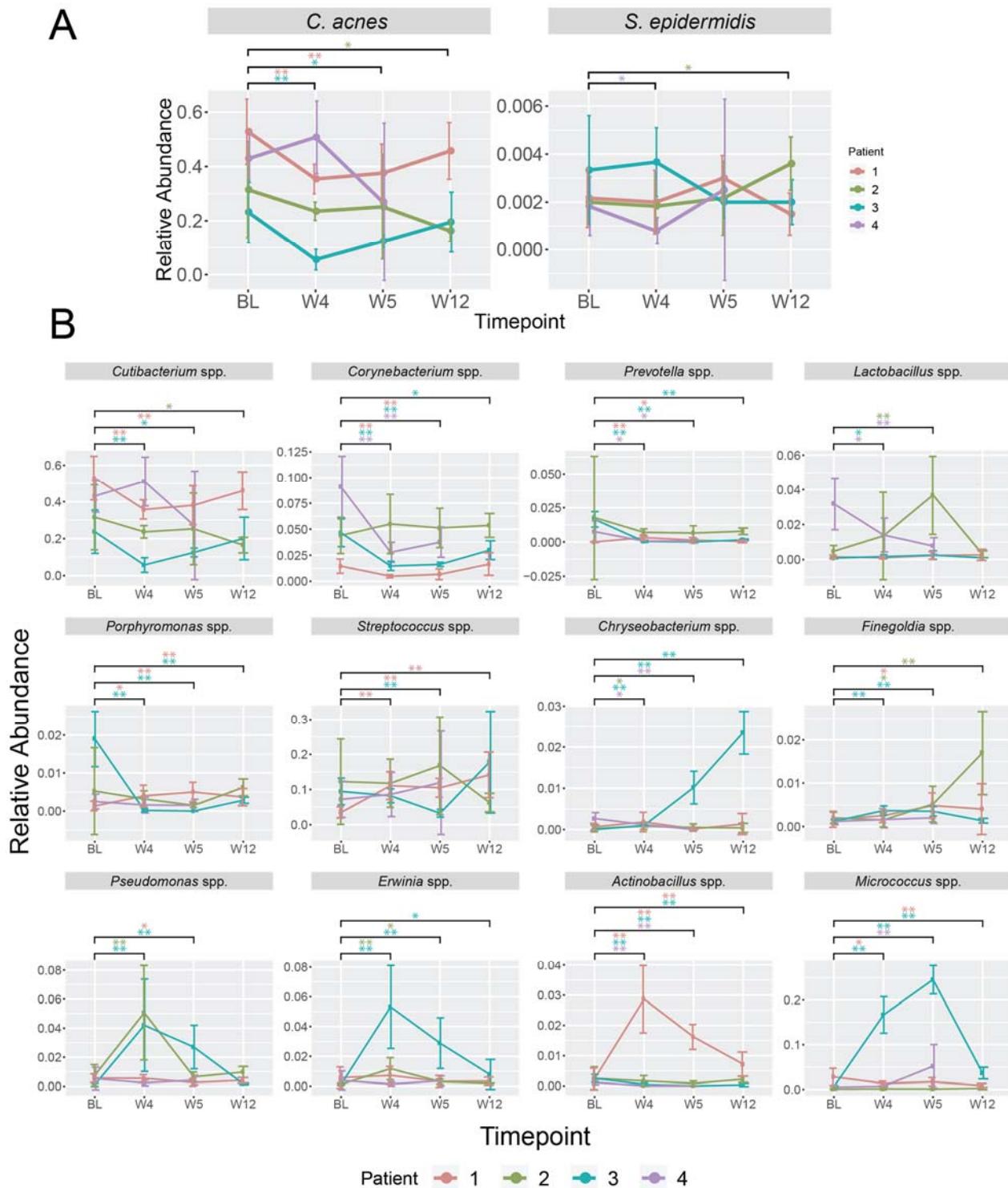
eFigure 2. A. Relative abundance of *Cutibacterium acnes* and *Staphylococcus epidermidis* at various times during and after antibiotic treatment in individual patients. **B.** Relative abundance of selected bacterial genera at various times during and after antibiotic treatment in individual patients. Error bars indicate 95% CIs. *P* values calculated using *t* tests with 1000 Monte Carlo permutations and 5% false-discovery rate adjustment. *$P < .05$, **$P < .01$. BL indicates baseline; W4, week 4; W5, week 5; W12; week 12.

eReference

1. McMurdie PJ, Holmes S. phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS One.* 2013;8(4):e61217.