

Supplementary Materials:

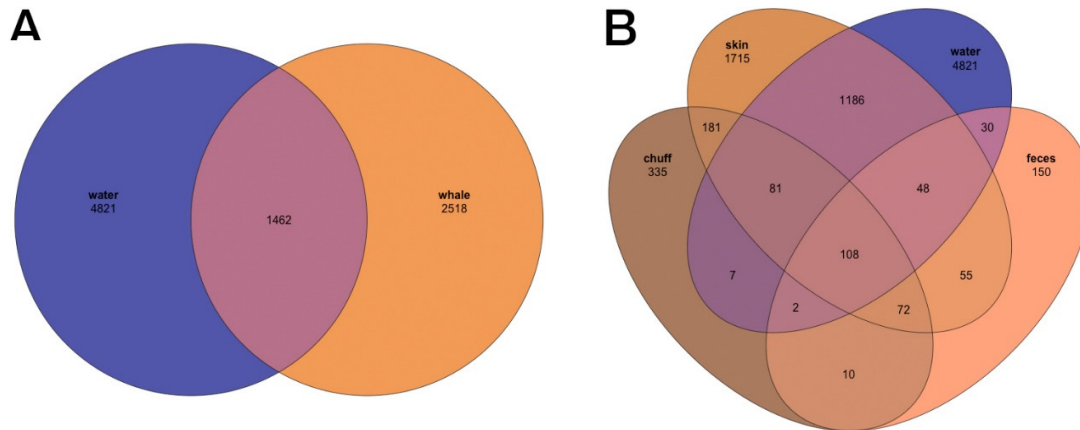


Figure S1. Venn diagram illustrating unique and shared ASVs by site and source.

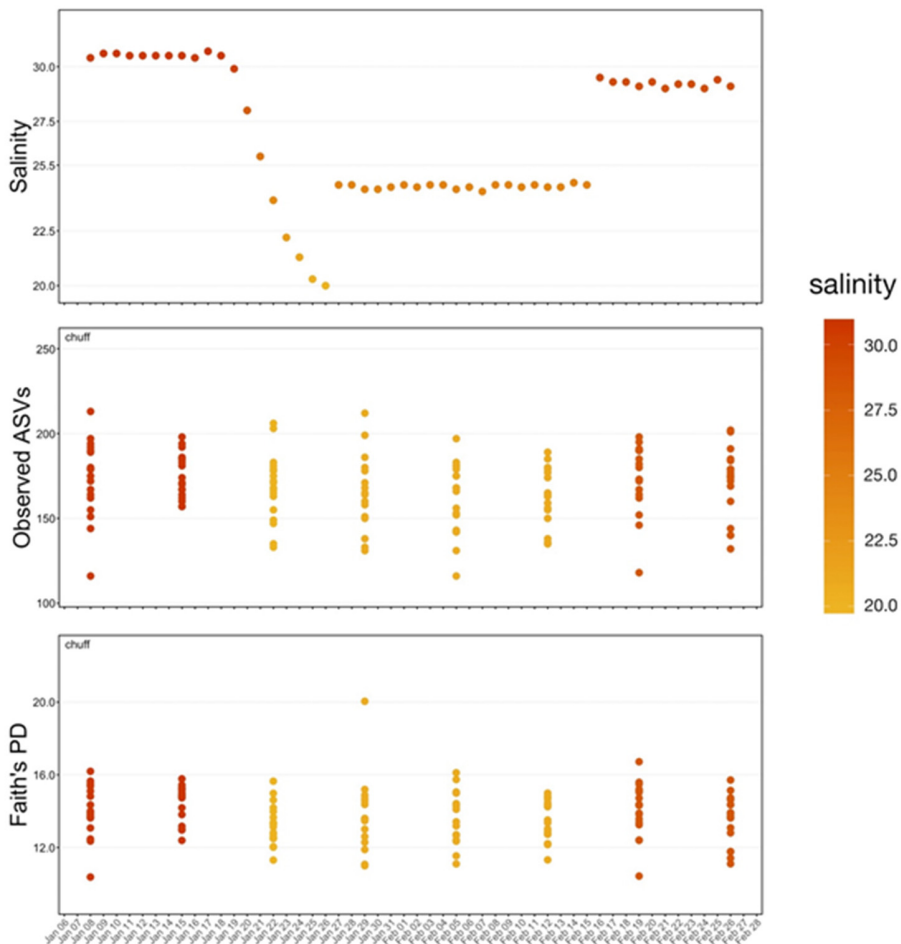


Figure S2. Scatterplot tracking changes on salinity (top), richness (Observed ASVs – middle), and diversity (Faith's PD – bottom) in fecal community diversity. Points are colored based on salinity values. There were no significant changes in diversity.

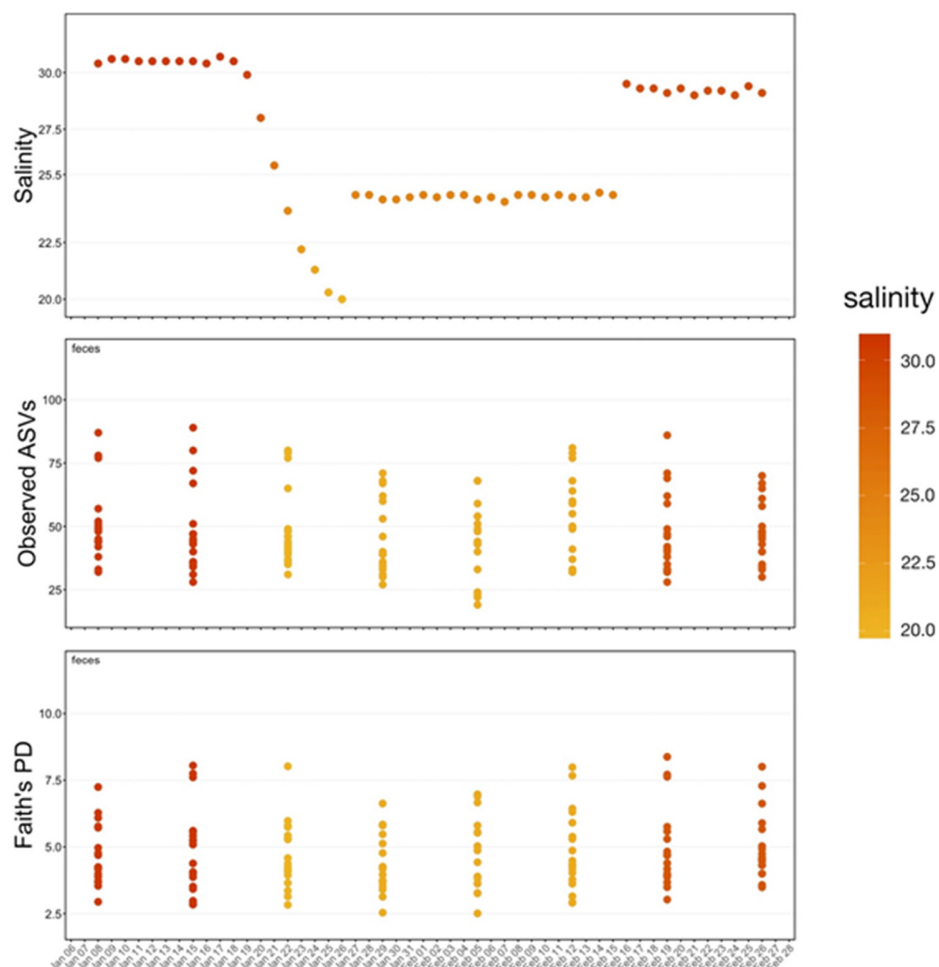


Figure S3. Scatterplot tracking changes on salinity (top), richness (Observed ASVs – middle), and diversity (Faith's PD – bottom) in chuff community diversity. Points are colored based on salinity values. There were no significant changes in diversity.

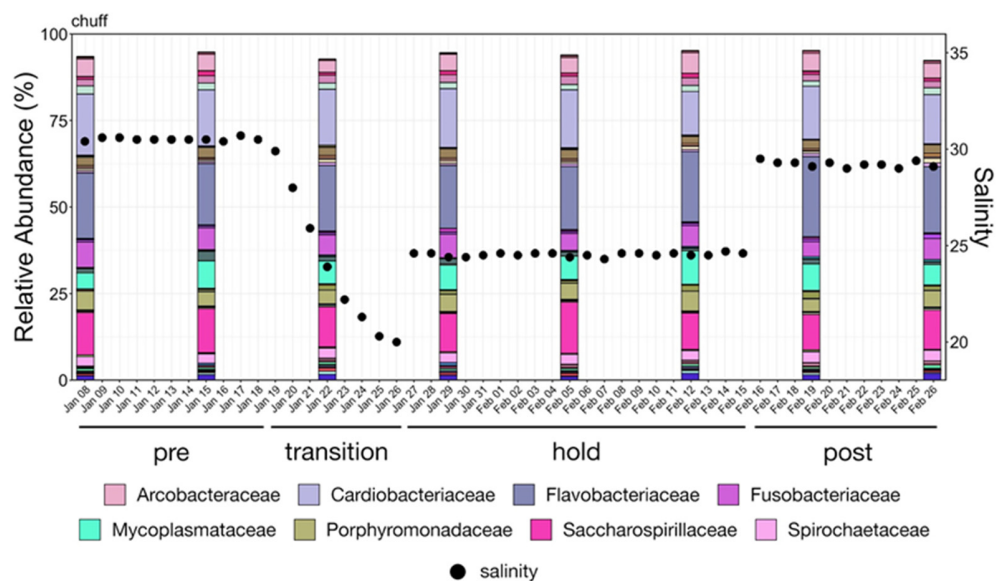


Figure S4. Barplot demonstrating the relative abundances of families within chuff samples throughout the water change. Salinities for each day are overlayed with black points. The 8 most abundant families across all samples are displayed in the legend.

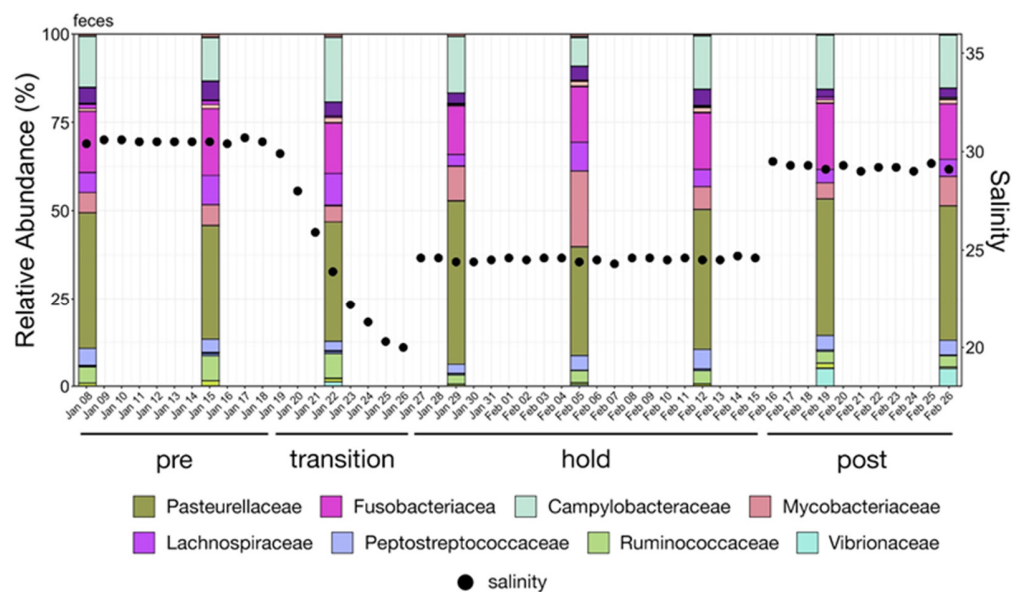


Figure S5. Barplot demonstrating the relative abundances of families within fecal samples throughout the water change. Salinities for each day are overlayed with black points. The 8 most abundant families across all samples are displayed in the legend.

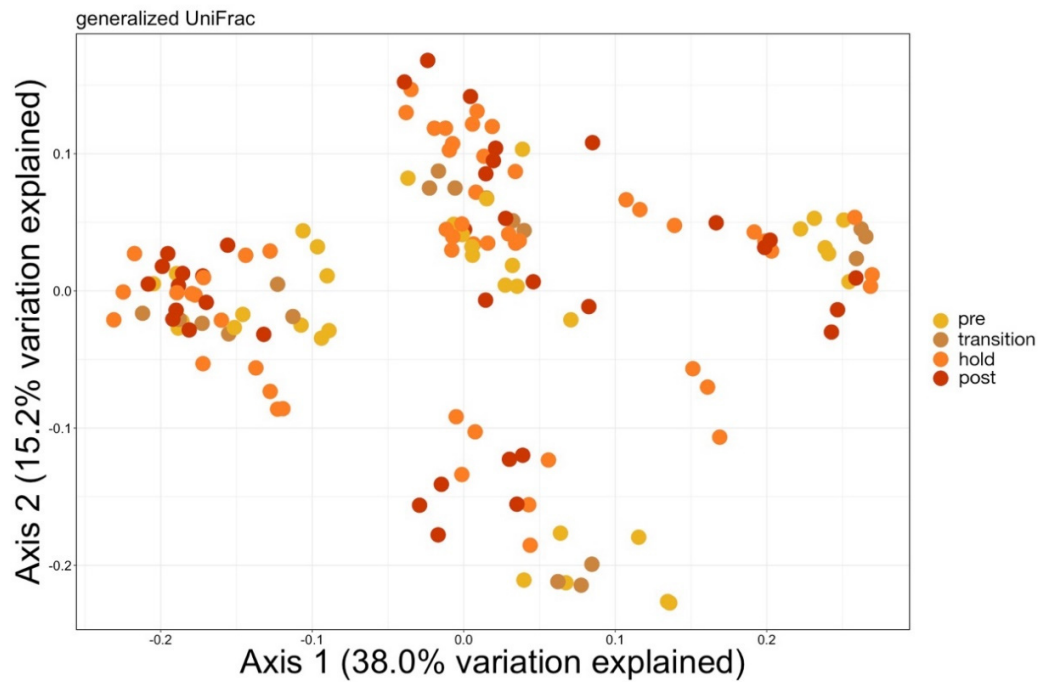


Figure S6. PCoA of the microbial communities from fecal samples throughout the water change. To aid visualization, samples are colored by phase opposed to salinity. There were no significant changes between phases.

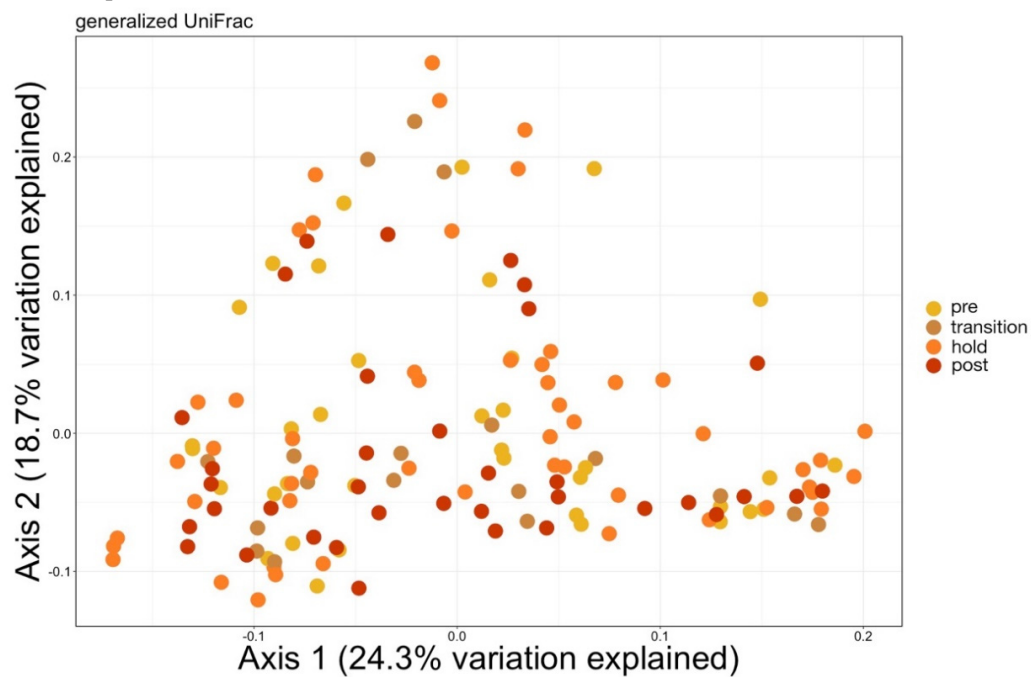


Figure S7. PCoA of the microbial communities from chuff samples throughout the water change. To aid visualization, samples are colored by phase opposed to salinity. There were no significant changes between phases.

Table S1. PERMANOVA and PERMDISP results from comparisons between microbial communities from water and those associated with different whale body sites (skin, chuff, and feces) based on generalized UniFrac values. Significant results are bolded (p-adj. < 0.05).

Test	Df	SS	Pseudo-F	R ²	p-adj.	PERMDISP (p-adj.)
water v. skin	1	12.242	182.269	0.397	0.0001	0.0001
water v. chuff	1	28.157	702.810	0.709	0.0001	0.1982
water v. feces	1	25.190	558.525	0.657	0.0001	0.0090
skin v. chuff	1	11.211	168.046	0.384	0.0001	0.0001
skin v. feces	1	13.052	181.505	0.400	0.0001	0.0001
chuff v. feces	1	20.244	458.771	0.618	0.0001	0.0007

Abbreviations: v., versus; Df, degrees of freedom; SS, sum of squares; p-adj., adjusted p-value

Table S2. Mean relative abundance and the standard error of the mean for the top 25 most abundant taxonomic phyla, families, and genera within water microbial communities from each of the four water change phases.

PRE			TRANSITION			HOLD			POST		
Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM
Proteobacteria	77.70	0.718	Proteobacteria	81.21	1.372	Proteobacteria	79.52	0.882	Proteobacteria	68.33	0.392
Bacteroidetes	5.98	0.388	Thaumarchaeota	5.86	0.246	Thaumarchaeota	7.47	0.364	Thaumarchaeota	11.34	0.245
Thaumarchaeota	4.94	0.191	Planctomycetes	4.62	0.335	Planctomycetes	4.29	0.247	Planctomycetes	7.15	0.140
Planctomycetes	4.88	0.208	Bacteroidetes	2.97	0.619	Bacteroidetes	3.19	0.191	Bacteroidetes	4.50	0.239
Actinobacteria	0.89	0.076	Actinobacteria	0.73	0.094	Actinobacteria	0.81	0.078	Patescibacteria	1.55	0.048
Verrucomicrobia	0.84	0.066	Chlamydiae	0.60	0.080	Verrucomicrobia	0.58	0.038	Actinobacteria	0.87	0.062
Chlamydiae	0.66	0.030	Patescibacteria	0.51	0.033	Patescibacteria	0.58	0.024	Cyanobacteria	0.78	0.025
Nitrospirae	0.60	0.044	Cyanobacteria	0.49	0.053	Nitrospirae	0.51	0.037	Nitrospirae	0.77	0.017
Acidobacteria	0.51	0.055	Firmicutes	0.49	0.043	Firmicutes	0.49	0.026	Verrucomicrobia	0.73	0.042
Cyanobacteria	0.45	0.015	Verrucomicrobia	0.41	0.097	Cyanobacteria	0.41	0.019	Dependentiae	0.67	0.054
Firmicutes	0.40	0.034	Nitrospirae	0.37	0.038	Acidobacteria	0.39	0.034	Firmicutes	0.62	0.031
Patescibacteria	0.39	0.018	Acidobacteria	0.36	0.041	Chlamydiae	0.37	0.031	Acidobacteria	0.51	0.026
Dependentiae	0.34	0.013	Fusobacteria	0.30	0.022	Fusobacteria	0.37	0.019	Fusobacteria	0.50	0.024
Nitrospinae	0.32	0.014	Dependentiae	0.28	0.024	Dependentiae	0.28	0.021	Chlamydiae	0.38	0.023
Fusobacteria	0.27	0.016	Nitrospinae	0.22	0.015	Nitrospinae	0.16	0.008	Nitrospinae	0.22	0.013
uncl. Bacteria	0.25	0.017	uncl. Bacteria	0.14	0.023	uncl. Bacteria	0.11	0.010	Omnitrophicaeota	0.18	0.011
Omnitrophicaeota	0.14	0.011	Chloroflexi	0.08	0.014	Omnitrophicaeota	0.08	0.008	uncl. Bacteria	0.17	0.010
Chloroflexi	0.12	0.010	Omnitrophicaeota	0.08	0.012	Chloroflexi	0.07	0.008	Lentisphaerae	0.16	0.011
Dadabacteria	0.07	0.012	Gemmatimonadetes	0.07	0.006	Lentisphaerae	0.07	0.008	Epsilonbacteraeota	0.14	0.011
Lentisphaerae	0.05	0.006	Nanoarchaeaeota	0.05	0.005	Epsilonbacteraeota	0.05	0.005	Dadabacteria	0.09	0.013
Gemmatimonadetes	0.04	0.003	Lentisphaerae	0.04	0.007	Nanoarchaeaeota	0.04	0.003	Chloroflexi	0.08	0.007
Nanoarchaeaeota	0.03	0.003	WPS-2	0.04	0.009	Dadabacteria	0.04	0.006	WPS-2	0.06	0.005
WPS-2	0.03	0.004	Epsilonbacteraeota	0.03	0.005	Gemmatimonadetes	0.03	0.003	Nanoarchaeaeota	0.05	0.004
Epsilonbacteraeota	0.02	0.003	Dadabacteria	0.03	0.014	WPS-2	0.03	0.003	Gemmatimonadetes	0.05	0.004
BRC1	0.02	0.004	BRC1	0.02	0.005	BRC1	0.02	0.003	Latescibacteria	0.01	0.002

PRE			TRANSITION			HOLD			POST		
Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM
Rhodobacteraceae	37.49	0.942	Rhodobacteraceae	31.76	1.706	Rhodobacteraceae	42.54	0.653	Rhodobacteraceae	35.25	0.561
Arenicellaceae	15.69	0.495	Cellvibrionaceae	24.74	1.011	Cellvibrionaceae	24.02	0.758	Cellvibrionaceae	14.79	0.358
Cellvibrionaceae	10.24	1.231	Arenicellaceae	13.31	0.884	Nitrosopumilaceae	7.47	0.364	Nitrosopumilaceae	11.34	0.245
Nitrosopumilaceae	4.94	0.191	Nitrosopumilaceae	5.86	0.246	Flavobacteriaceae	1.77	0.136	Flavobacteriaceae	2.99	0.175
Flavobacteriaceae	3.49	0.243	Flavobacteriaceae	1.61	0.387	Arenicellaceae	1.75	0.195	Pirellulaceae	2.26	0.067
Micavibrionaceae	1.24	0.062	Rubinisphaeraceae	1.45	0.123	Pirellulaceae	1.21	0.080	Micavibrionaceae	2.24	0.060
Saprospiraceae	1.18	0.136	Micavibrionaceae	1.33	0.094	Rubinisphaeraceae	1.06	0.094	Rubinisphaeraceae	1.74	0.054
γ -proteobacteria inc. sed.	1.11	0.048	Pirellulaceae	0.90	0.069	Haliaceae	1.04	0.052	Haliaceae	1.60	0.043
Rubinisphaeraceae	1.02	0.072	γ -proteobacteria inc. sed.	0.82	0.101	Micavibrionaceae	1.02	0.046	Phycisphaeraceae	1.16	0.024
Nitrosomonadaceae	0.93	0.064	Phycisphaeraceae	0.73	0.064	Phycisphaeraceae	0.74	0.040	Arenicellaceae	1.13	0.067
Spongiibacteraceae	0.91	0.068	Legionellaceae	0.65	0.046	Mycobacteriaceae	0.65	0.072	uncul. Gracilibacteria	0.92	0.042
Pirellulaceae	0.89	0.041	Mycobacteriaceae	0.57	0.080	Legionellaceae	0.63	0.055	Spongiibacteraceae	0.86	0.018
Phycisphaeraceae	0.89	0.032	Nitrosomonadaceae	0.54	0.063	Nitrosomonadaceae	0.58	0.032	Colwelliaceae	0.78	0.037

uncl. γ -proteobacteria	0.87	0.059	uncl. Micavibrionales	0.53	0.034	uncl. γ -proteobacteria	0.54	0.028	Nitrospiraceae	0.77	0.017
Haliaceae	0.75	0.071	Haliaceae	0.49	0.060	Rubritaleaceae	0.53	0.035	uncl. γ -proteobacteria	0.71	0.029
Rubritaleaceae	0.70	0.066	uncl. γ -proteobacteria	0.48	0.061	Saprospiraceae	0.52	0.055	Nitrosomonadaceae	0.71	0.020
Mycobacteriaceae	0.63	0.060	Saprospiraceae	0.45	0.163	Colwelliaceae	0.52	0.038	Rubritaleaceae	0.65	0.041
Nitrospiraceae	0.60	0.044	Spongiibacteraceae	0.44	0.056	Nitrospiraceae	0.51	0.037	Mycobacteriaceae	0.63	0.059
Saccharospirillaceae	0.60	0.038	Colwelliaceae	0.43	0.037	Spongiibacteraceae	0.51	0.026	uncl. Micavibrionales	0.62	0.019
Shewanellaceae	0.44	0.023	Pasteurellaceae	0.42	0.055	γ -proteobacteria inc. sed.	0.43	0.022	Pasteurellaceae	0.51	0.049
uncl.	0.42	0.017	uncl. α -proteobacteria	0.41	0.028	Pasteurellaceae	0.36	0.022	uncl. MBAE14	0.48	0.031
Legionellaceae	0.41	0.025	Simkaniaceae	0.38	0.053	Fusobacteriaceae	0.31	0.017	Vermiphilaceae	0.44	0.056
uncl. γ -proteobacterium	0.39	0.041	Shewanellaceae	0.38	0.037	uncl.	0.31	0.012	Fusobacteriaceae	0.44	0.024
uncl. bacterium	0.39	0.026	Nitrospiraceae	0.37	0.038	Sphingomonadaceae	0.30	0.025	uncl. γ -proteobacteria	0.43	0.025
Simkaniaceae	0.38	0.018	Saccharospirillaceae	0.31	0.019	uncl. bacterium	0.28	0.013	Sphingomonadaceae	0.42	0.033
PRE			TRANSITION			HOLD			POST		
Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM
uncl. Rhodobacteraceae	37.17	0.948	uncl. Rhodobacteraceae	31.39	1.7361	uncl. Rhodobacteraceae	42.34	0.655	uncl. Rhodobacteraceae	35.02	0.566
Arenicella	15.44	0.510	uncl. Cellvibrionaceae	24.73	1.0098	uncl. Cellvibrionaceae	24.00	0.758	uncl. Cellvibrionaceae	14.76	0.358
uncl. Cellvibrionaceae	10.23	1.231	Arenicella	13.29	0.8839	Candidatus Nitrosopumilus	7.45	0.364	Candidatus Nitrosopumilus	11.31	0.244
Candidatus Nitrosopumilus	4.92	0.190	Candidatus Nitrosopumilus	5.84	0.2451	Arenicella	1.69	0.199	uncl. Micavibrionaceae	2.24	0.060
uncl. Micavibrionaceae	1.24	0.062	uncl. Rubinisphaeraceae	1.38	0.1229	uncl. Micavibrionaceae	1.02	0.046	uncl. Rubinisphaeraceae	1.57	0.051
Tenacibaculum	0.97	0.044	uncl. Micavibrionaceae	1.33	0.0940	uncl. Rubinisphaeraceae	0.94	0.086	Parahalia	1.12	0.022
Nitrosomonas	0.93	0.064	γ -proteobacteria inc. sed.	0.68	0.0786	Parahalia	0.68	0.035	Arenicella	1.02	0.067
uncl. Rubinisphaeraceae	0.91	0.066	uncl. Legionellaceae	0.59	0.0419	Mycobacterium	0.65	0.072	Tenacibaculum	0.94	0.026
uncl. γ -proteobacteria	0.87	0.059	Mycobacterium	0.57	0.0797	uncl. Legionellaceae	0.60	0.055	uncl. Gracilibacteria	0.92	0.042
uncl. Flavobacteriaceae	0.85	0.080	Tenacibaculum	0.57	0.0624	Nitrosomonas	0.58	0.032	uncl. Flavobacteriaceae	0.86	0.093
γ -proteobacteria inc. sed.	0.72	0.036	Nitrosomonas	0.54	0.0634	Tenacibaculum	0.55	0.038	Blastopirellula	0.79	0.023
BD1-7 clade	0.71	0.046	uncl. γ -proteobacteria	0.48	0.0607	uncl. Flavobacteriaceae	0.55	0.049	Colwellia	0.78	0.037
Mycobacterium	0.63	0.060	uncl. Micavibrionales	0.45	0.0299	uncl. γ -proteobacteria	0.54	0.028	Nitrospira	0.77	0.017
Nitrospira	0.60	0.044	Colwellia	0.42	0.0363	Colwellia	0.52	0.038	uncl. γ -proteobacteria	0.71	0.029
Lewinella	0.60	0.071	uncl. Alphaproteobacteria	0.41	0.0281	Nitrospira	0.51	0.037	Nitrosomonas	0.71	0.020
Oleispira	0.57	0.035	Actinobacillus	0.41	0.0540	Blastopirellula	0.49	0.027	Mycobacterium	0.63	0.059
Formosa	0.50	0.040	uncl. Flavobacteriaceae	0.39	0.1244	Haloferula	0.36	0.028	Bythopirellula	0.63	0.021
uncl. Saprospiraceae	0.44	0.052	BD1-7 clade	0.39	0.0472	Actinobacillus	0.35	0.022	BD1-7 clade	0.61	0.014
Haloferula	0.43	0.048	Blastopirellula	0.38	0.0275	BD1-7 clade	0.34	0.013	Pir4 lineage	0.58	0.021
uncl. MBAE14	0.39	0.041	uncl. Simkaniaceae	0.37	0.0511	Lewinella	0.31	0.046	Actinobacillus	0.49	0.050
uncl. bacterium	0.39	0.026	Nitrospira	0.37	0.0378	Bythopirellula	0.31	0.025	uncl. MBAE14	0.48	0.031
Phycisphaera	0.38	0.018	Shewanella	0.35	0.0312	Fusobacterium	0.31	0.017	SM1A02	0.44	0.013
uncl.	0.37	0.017	Phycisphaera	0.31	0.0313	uncl. bacterium	0.28	0.013	uncultured bacterium	0.44	0.056
uncl. planctomycete	0.37	0.028	Coxiella	0.30	0.0212	SM1A02	0.27	0.018	Fusobacterium	0.44	0.024
Blastopirellula	0.36	0.019	Oleispira	0.29	0.0165	Pir4 lineage	0.27	0.021	uncultured bacterium	0.43	0.016

Abbreviations: uncl., unclassified; uncul., uncultured.

Table S3. Mean relative abundance and the standard error of the mean for the top 25 most abundant taxonomic phyla, families, and genera within skin microbial communities from each of the four water change phases.

PRE			TRANSITION			HOLD			POST		
Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM

Proteobacteria	76.89	2.187	Proteobacteria	78.86	3.285	Proteobacteria	74.00	2.084	Proteobacteria	70.82	3.181
Bacteroidetes	18.53	2.224	Bacteroidetes	17.32	3.069	Bacteroidetes	18.14	1.884	Bacteroidetes	20.03	2.828
Verrucomicrobia	0.78	0.161	Fusobacteria	1.09	0.419	Fusobacteria	1.77	0.489	Epsilonbacteraeota	2.01	1.280
Planctomycetes	0.68	0.097	Planctomycetes	0.49	0.129	Epsilonbacteraeota	1.17	0.331	Actinobacteria	1.26	0.307
Firmicutes	0.60	0.272	Firmicutes	0.33	0.120	Actinobacteria	1.07	0.260	Fusobacteria	1.21	0.431
Fusobacteria	0.46	0.181	Thaumarchaeota	0.33	0.099	Firmicutes	1.02	0.440	Firmicutes	0.88	0.234
Actinobacteria	0.42	0.091	Actinobacteria	0.31	0.121	Planctomycetes	0.68	0.100	Patescibacteria	0.69	0.107
Epsilonbacteraeota	0.32	0.164	Tenericutes	0.30	0.176	Tenericutes	0.53	0.281	Verrucomicrobia	0.54	0.092
Thaumarchaeota	0.28	0.049	Epsilonbacteraeota	0.25	0.144	Verrucomicrobia	0.40	0.082	Dependentiae	0.51	0.136
unassigned Bacteria	0.26	0.061	Chloroflexi	0.16	0.067	Patescibacteria	0.30	0.072	Planctomycetes	0.36	0.068
Patescibacteria	0.19	0.055	Patescibacteria	0.14	0.056	Thaumarchaeota	0.27	0.041	unassigned Bacteria	0.31	0.110
Chloroflexi	0.15	0.039	Nitrospirae	0.08	0.076	Cyanobacteria	0.12	0.052	WPS-2	0.31	0.178
Dependentiae	0.08	0.015	unassigned Bacteria	0.08	0.026	Spirochaetes	0.10	0.039	Thaumarchaeota	0.30	0.065
Tenericutes	0.07	0.032	Spirochaetes	0.07	0.041	unassigned Bacteria	0.10	0.016	Tenericutes	0.25	0.075
Acidobacteria	0.07	0.026	Chlamydiae	0.06	0.043	Acidobacteria	0.07	0.025	Spirochaetes	0.22	0.070
Cyanobacteria	0.07	0.017	Verrucomicrobia	0.05	0.017	Euryarchaeota	0.07	0.062	Cyanobacteria	0.14	0.037
Nitrospirae	0.04	0.011	Dependentiae	0.04	0.021	Dependentiae	0.05	0.014	Acidobacteria	0.04	0.016
WPS-2	0.04	0.013	Omnitrophicaeota	0.02	0.015	Nitrospirae	0.05	0.014	Chloroflexi	0.03	0.014
Chlamydiae	0.02	0.005	Acidobacteria	0.01	0.005	Chloroflexi	0.04	0.009	Chlamydiae	0.03	0.008
Spirochaetes	0.01	0.007	WPS-2	0.01	0.003	Chlamydiae	0.02	0.006	Nanoarchaeaeota	0.01	0.011
Omnitrophicaeota	0.01	0.005	Lentisphaerae	<0.01	0.003	Lentisphaerae	0.01	0.005	Nitrospirae	0.01	0.006
Fibrobacteres	0.01	0.007	Cyanobacteria	<0.01	0.002	Omnitrophicaeota	0.01	0.003	Omnitrophicaeota	0.01	0.006
Nanoarchaeaeota	0.01	0.005	Deinococcus-Thermus	<0.01	0.002	Gemmatimonadetes	0.01	0.003	BRC1	0.01	0.005
Lentisphaerae	0.01	0.004	Euryarchaeota	<0.01	0.002	Dadabacteria	<0.01	0.002	Lentisphaerae	<0.01	0.004
Elusimicrobia	<0.01	0.003	Nanoarchaeaeota	<0.01	0.001	Nanoarchaeaeota	<0.01	0.003	PAUC34f	<0.01	0.004

PRE			TRANSITION			HOLD			POST		
Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM
Rhodobacteraceae	26.84	2.923	Rhodobacteraceae	28.96	6.620	Rhodobacteraceae	32.55	3.337	Rhodobacteraceae	23.43	3.430
Flavobacteriaceae	15.84	2.241	Saccharospirillaceae	17.11	5.716	Flavobacteriaceae	14.43	1.730	Flavobacteriaceae	16.33	2.797
Saccharospirillaceae	15.40	3.795	Moraxellaceae	16.72	4.990	Saccharospirillaceae	6.82	1.741	Moraxellaceae	11.10	3.403
Moraxellaceae	6.34	1.331	Flavobacteriaceae	15.45	3.060	Moraxellaceae	6.65	1.593	Pasteurellaceae	6.14	1.778
Arenicellaceae	5.99	0.998	Cardiobacteriaceae	5.16	2.017	Pasteurellaceae	5.25	1.170	Sphingomonadaceae	4.83	1.108
Cardiobacteriaceae	3.82	1.148	Burkholderiaceae	3.28	1.339	Cardiobacteriaceae	3.25	0.706	Cardiobacteriaceae	2.93	0.711
Pasteurellaceae	2.87	1.170	Pasteurellaceae	2.47	0.851	Burkholderiaceae	2.83	0.373	uncl. γ -proteobacteria	2.08	0.941
Spongiibacteraceae	2.32	0.548	Leptotrichiaceae	0.94	0.375	Saprospiraceae	2.29	0.424	Alteromonadaceae	1.94	0.446
uncl. MBAE14	1.94	0.486	Haliaceae	0.65	0.183	Arenicellaceae	2.06	0.489	Burkholderiaceae	1.93	0.319
Sphingomonadaceae	1.31	0.318	Alteromonadaceae	0.52	0.105	Sphingomonadaceae	1.67	0.365	Campylobacteraceae	1.75	1.231
Saprospiraceae	1.30	0.245	Saprospiraceae	0.48	0.143	Haliaceae	1.61	0.253	Saccharospirillaceae	1.74	0.466
Alteromonadaceae	1.27	0.239	Colwelliaceae	0.46	0.198	Fusobacteriaceae	1.21	0.422	Arenicellaceae	1.70	0.354
uncl. γ -proteobacteria	1.14	0.334	Cellvibrionaceae	0.43	0.167	Spongiibacteraceae	1.20	0.148	uncl. MBAE14	1.57	0.329
Weeksellaceae	0.83	0.364	Porphyromonadaceae	0.39	0.271	Colwelliaceae	1.14	0.651	Hyphomonadaceae	1.30	0.333
Rhizobiaceae	0.72	0.310	Sphingomonadaceae	0.35	0.143	Cellvibrionaceae	0.96	0.176	Saprospiraceae	1.23	0.344
Burkholderiaceae	0.71	0.255	Arenicellaceae	0.34	0.061	Alteromonadaceae	0.95	0.296	Weeksellaceae	1.18	0.435
Shewanellaceae	0.70	0.277	Spongiibacteraceae	0.33	0.067	Campylobacteraceae	0.81	0.264	Spongiibacteraceae	1.16	0.197
Pseudoalteromonadaceae	0.65	0.182	Nitrosopumilaceae	0.33	0.099	Hyphomonadaceae	0.80	0.217	Shewanellaceae	0.82	0.548
Cellvibrionaceae	0.62	0.110	Mycoplasmataceae	0.30	0.176	uncl. γ -proteobacteria	0.75	0.197	Rhizobiaceae	0.70	0.221
Micavibrionaceae	0.44	0.148	Blattabacteriaceae	0.26	0.232	Thiotrichaceae	0.72	0.217	Colwelliaceae	0.68	0.301
Haliaceae	0.43	0.073	Shewanellaceae	0.24	0.087	Mycobacteriaceae	0.70	0.229	Fusobacteriaceae	0.68	0.334
Rubritaleaceae	0.39	0.060	Crocinitomicaceae	0.24	0.162	γ -proteobacteria inc. sed.	0.65	0.156	Haliaceae	0.65	0.185
Puniceicoccaceae	0.37	0.109	Vibrionaceae	0.19	0.067	uncl. MBAE14	0.57	0.184	Xanthomonadaceae	0.58	0.337
Hyphomonadaceae	0.34	0.064	Weeksellaceae	0.18	0.092	Leptotrichiaceae	0.56	0.182	Cellvibrionaceae	0.56	0.115
Lachnospiraceae	0.33	0.180	Thiotrichaceae	0.17	0.072	Mycoplasmataceae	0.49	0.264	Leptotrichiaceae	0.54	0.166

PRE			TRANSITION			HOLD			POST		
Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM
uncl. Rhodobacteraceae	25.92	2.939	uncl. Rhodobacteraceae	28.44	6.597	uncl. Rhodobacteraceae	31.35	3.347	uncl. Rhodobacteraceae	21.93	3.391
Oleispira	15.18	3.816	Psychrobacter	16.68	4.991	Tenacibaculum	7.68	1.252	Psychrobacter	10.46	3.365
Tenacibaculum	9.44	1.740	Oleispira	16.33	5.799	Psychrobacter	6.55	1.591	Tenacibaculum	9.47	2.315
Psychrobacter	5.92	1.244	Tenacibaculum	14.18	3.034	Oleispira	5.99	1.740	Actinobacillus	4.74	1.685
HTCC5015	4.60	0.990	uncultured	5.09	2.013	Actinobacillus	4.29	1.039	uncl. Flavobacteriaceae	3.98	1.169

uncl. Flavobacteriaceae	4.30	1.816	Phocoenobacter	1.94	0.838	uncl. Cardiobacteriaceae	3.22	0.700	uncl. Cardiobacteriaceae	2.86	0.699
uncl. Cardiobacteriaceae	3.80	1.148	Pusillimonas	1.41	0.626	uncl. Flavobacteriaceae	2.93	0.583	uncl. Sphingomonadaceae	2.53	0.842
Actinobacillus	2.32	1.125	Cupriavidus	1.37	0.846	HTCC5015	1.72	0.463	uncl. γ-proteobacteria	2.08	0.941
uncult. γ-proteobacteria	1.94	0.486	Oceanivirga	0.93	0.376	Cupriavidus	1.70	0.249	Campylobacter	1.75	1.231
BD1-7 clade	1.89	0.389	uncl. Saccharospirillaceae	0.78	0.684	Lewinella	1.44	0.336	uncl. MBAE14	1.57	0.329
Arenicella	1.39	0.370	Parahalia	0.55	0.167	Parahalia	1.32	0.246	uncl. Alteromonadaceae	1.53	0.428
uncl. Alteromonadaceae	1.21	0.236	uncl. Alteromonadaceae	0.51	0.104	Fusobacterium	1.21	0.422	HTCC5015	1.44	0.335
uncl. Gammaproteobacteria	1.14	0.334	Actinobacillus	0.50	0.093	Colwellia	1.13	0.651	Phocoenobacter	1.36	0.714
Ornithobacterium	0.73	0.306	uncl. Burkholderiaceae	0.49	0.300	uncl. Cellvibrionaceae	0.96	0.176	Erythrobacter	1.12	0.295
uncl. Rhizobiaceae	0.71	0.311	Colwellia	0.45	0.190	Phocoenobacter	0.93	0.619	Cupriavidus	1.09	0.142
Lewinella	0.69	0.147	uncl. Cellvibrionaceae	0.42	0.167	uncl. Alteromonadaceae	0.92	0.296	BD1-7 clade	0.98	0.177
Psychrobium	0.67	0.277	Porphyromonas	0.39	0.271	Campylobacter	0.81	0.264	Oleispira	0.89	0.421
Pseudoalteromonas	0.65	0.182	uncl. Saprospiraceae	0.35	0.114	uncl. Saccharospirillaceae	0.77	0.258	Psychrobium	0.81	0.548
uncl. Cellvibrionaceae	0.61	0.111	uncl. Flavobacteriaceae	0.33	0.094	uncl. γ-proteobacteria	0.75	0.197	Lewinella	0.78	0.289
Erythrobacter	0.60	0.299	Cand. Nitrosopumilus	0.33	0.099	Aequorivita	0.72	0.673	uncl. Saccharospirillaceae	0.78	0.269
Phocoenobacter	0.54	0.160	Mycoplasma	0.30	0.176	Cocleimonas	0.72	0.217	uncl. Hyphomonadaceae	0.70	0.195
uncl. Saprospiraceae	0.52	0.145	uncl. Sphingomonadaceae	0.26	0.108	Mycobacterium	0.70	0.229	Fusobacterium	0.68	0.334
Mesonina	0.50	0.229	uncl. Blattabacteriaceae	0.26	0.232	uncl. Saprospiraceae	0.68	0.147	Ornithobacterium	0.67	0.279
uncl. Micavibrionaceae	0.44	0.148	BD1-7 clade	0.25	0.063	Marinicella	0.63	0.156	Paracoccus	0.67	0.206
Paracoccus	0.43	0.122	Arenicella	0.25	0.061	uncl. Burkholderiaceae	0.61	0.089	Colwellia	0.67	0.301

Abbreviations: uncl., unclassified; uncul., uncultured.; Cand., Candidatus

Table S4. Mean relative abundance and the standard error of the mean for every taxonomic phyla, and the top 25 most abundant families, and genera within chuff microbial communities from each of the four water change phases.

PRE			TRANSITION			HOLD			POST		
Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM
Proteobacteria	37.37	2.129	Proteobacteria	38.10	2.954	Proteobacteria	35.81	1.927	Proteobacteria	33.29	1.626
Bacteroidetes	29.29	1.140	Bacteroidetes	29.56	1.864	Bacteroidetes	30.40	1.445	Bacteroidetes	32.47	1.500
Tenericutes	6.66	1.024	Tenericutes	6.92	0.727	Tenericutes	8.26	0.895	Firmicutes	7.62	0.610
Fusobacteria	6.97	0.732	Firmicutes	6.63	0.595	Epsilonbacteraeota	6.76	0.436	Tenericutes	7.16	0.868
Epsilonbacteraeota	7.04	0.450	Fusobacteria	6.07	1.112	Fusobacteria	6.35	0.633	Epsilonbacteraeota	6.41	0.431
Firmicutes	4.77	0.370	Epsilonbacteraeota	5.12	0.577	Firmicutes	5.38	0.317	Fusobacteria	5.59	0.555
Patescibacteria	3.85	0.235	Patescibacteria	3.72	0.297	Patescibacteria	2.95	0.165	Patescibacteria	3.24	0.249
Spirochaetes	2.76	0.198	Spirochaetes	3.00	0.128	Spirochaetes	2.88	0.262	Spirochaetes	3.21	0.350
Actinobacteria	0.91	0.154	Actinobacteria	0.65	0.124	Actinobacteria	0.85	0.111	Actinobacteria	0.89	0.089
uncl. Bacteria	0.37	0.113	uncl. Bacteria	0.21	0.110	uncl. Bacteria	0.35	0.133	uncl. Bacteria	0.13	0.038
Thaumarchaeota	0.01	0.003	Thaumarchaeota	0.01	0.004	Thaumarchaeota	<0.01	0.002	Planctomycetes	<0.01	0.001
Hydrogenedentes	<0.01	0.001				Planctomycetes	<0.01	0.001	Dependentiae	<0.01	0.001
FBP	<0.01	0.001				Cyanobacteria	<0.01	0.001			
Planctomycetes	<0.01	<0.001				Lentisphaerae	<0.01	<0.001			
Nitrospirae	<0.01	<0.001									
Dependentiae	<0.01	<0.001									
Nitrospinae	<0.01	<0.001									

PRE			TRANSITION			HOLD			POST		
Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM
Flavobacteriaceae	18.30	1.049	Flavobacteriaceae	18.94	1.581	Flavobacteriaceae	18.91	1.123	Flavobacteriaceae	21.11	1.559
Cardiobacteriaceae	16.93	0.870	Cardiobacteriaceae	16.19	0.986	Cardiobacteriaceae	15.35	0.810	Cardiobacteriaceae	14.74	0.727
Saccharospirillaceae	12.46	0.879	Saccharospirillaceae	11.59	1.314	Saccharospirillaceae	12.17	0.911	Saccharospirillaceae	10.79	0.614

Leptotrichiaceae	6.81	0.728	Mycoplasmataceae	6.55	0.750	Mycoplasmataceae	7.85	0.892	Mycoplasmataceae	6.75	0.864
Mycoplasmataceae	6.27	1.027	Leptotrichiaceae	5.78	1.140	Leptotrichiaceae	5.87	0.630	Leptotrichiaceae	5.18	0.558
Arcobacteraceae	4.90	0.330	Porphyromonadaceae	3.93	0.741	Porphyromonadaceae	5.17	0.536	Arcobacteraceae	4.66	0.367
Porphyromonadaceae	4.77	0.510	Arcobacteraceae	3.36	0.302	Arcobacteraceae	5.06	0.416	Porphyromonadaceae	4.24	0.492
Spirochaetaceae	2.73	0.196	Spirochaetaceae	2.91	0.126	Spirochaetaceae	2.82	0.262	Spirochaetaceae	3.15	0.351
Crocinitomicaceae	2.64	0.376	γ -proteobacteria inc. sed	2.65	0.813	Crocinitomicaceae	2.41	0.420	Crocinitomicaceae	2.51	0.457
uncul. Gracilibacteria	2.23	0.117	Crocinitomicaceae	2.39	0.596	Burkholderiaceae	2.29	0.321	Clostridiales Fam. XI	2.01	0.248
Campylobacteraceae	2.14	0.177	Burkholderiaceae	2.29	0.563	uncul. Gracilibacteria	1.73	0.087	Clostridiales Fam. XII	1.95	0.241
Moraxellaceae	2.00	0.689	uncul. Gracilibacteria	2.07	0.210	Campylobacteraceae	1.70	0.154	Burkholderiaceae	1.89	0.306
Burkholderiaceae	2.00	0.379	Clostridiales Fam. XI	1.85	0.239	γ -proteobacteria inc. sed	1.60	0.294	uncul. Gracilibacteria	1.85	0.166
uncul. Absconditabacteriales	1.58	0.143	Campylobacteraceae	1.77	0.380	Weeksellaceae	1.50	0.153	Weeksellaceae	1.76	0.224
Weeksellaceae	1.46	0.198	Weeksellaceae	1.68	0.396	Clostridiales Fam. XI	1.46	0.180	Campylobacteraceae	1.75	0.163
γ -proteobacteria inc. sed	1.37	0.219	Clostridiales Fam. XII	1.66	0.184	Clostridiales Fam. XII	1.26	0.079	Pasteurellaceae	1.64	0.591
Blattabacteriaceae	1.11	0.284	Pasteurellaceae	1.54	0.673	Pasteurellaceae	1.17	0.279	uncul. Absconditabacteriales	1.32	0.108
Clostridiales Fam. XI	1.10	0.134	uncul. Absconditabacteriales	1.54	0.125	Moraxellaceae	1.15	0.165	γ -proteobacteria inc. sed	1.27	0.276
Clostridiales Fam. XII	1.07	0.071	Moraxellaceae	1.19	0.291	uncul. Absconditabacteriales	1.13	0.094	Moraxellaceae	1.07	0.185
Lachnospiraceae	0.64	0.047	Vibrionaceae	0.95	0.548	Blattabacteriaceae	1.09	0.199	Lachnospiraceae	0.99	0.126
uncul. Clostridiales	0.63	0.081	Blattabacteriaceae	0.78	0.189	uncul. Clostridiales	0.65	0.074	Blattabacteriaceae	0.85	0.171
Pasteurellaceae	0.47	0.102	uncul. Clostridiales	0.73	0.100	Lachnospiraceae	0.63	0.049	uncul. Clostridiales	0.77	0.117
Actinomycetaceae	0.46	0.092	Lachnospiraceae	0.65	0.093	Defluviitaleaceae	0.50	0.038	Defluviitaleaceae	0.71	0.053
Defluviitaleaceae	0.45	0.044	Defluviitaleaceae	0.64	0.114	uncul. β -proteobacteriales	0.50	0.066	uncul. Bacteroidales	0.67	0.182
Sedimenticolaceae	0.40	0.071	uncul. γ -proteobacteria	0.48	0.125	Fusobacteriaceae	0.48	0.197	Actinomycetaceae	0.66	0.076

PRE			TRANSITION			HOLD			POST		
Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM
uncul. Cardiobacteriaceae	15.87	0.826	uncul. Cardiobacteriaceae	15.10	0.916	uncul. Cardiobacteriaceae	14.41	0.746	uncul. Cardiobacteriaceae	13.98	0.709
uncul. Saccharospirillaceae	12.41	0.878	uncul. Saccharospirillaceae	11.58	1.315	uncul. Saccharospirillaceae	12.16	0.911	Tenacibaculum	11.67	0.549
Tenacibaculum	11.09	0.411	Tenacibaculum	11.27	0.645	Tenacibaculum	10.67	0.468	uncul. Saccharospirillaceae	10.78	0.614
Oceanivirga	6.80	0.728	Mycoplasma	6.55	0.749	Mycoplasma	7.84	0.892	uncul. Flavobacteriaceae	7.52	1.120
Mycoplasma	6.26	1.026	uncul. Flavobacteriaceae	5.84	1.097	uncul. Flavobacteriaceae	6.49	0.666	Mycoplasma	6.74	0.861
uncul. Flavobacteriaceae	5.11	0.653	Oceanivirga	5.78	1.140	Oceanivirga	5.87	0.630	Oceanivirga	5.18	0.558
Arcobacter	4.90	0.330	Porphyromonas	3.93	0.741	Porphyromonas	5.17	0.536	Arcobacter	4.66	0.367
Porphyromonas	4.77	0.510	Arcobacter	3.36	0.302	Arcobacter	5.06	0.416	Porphyromonas	4.24	0.492
Fluviicola	2.64	0.376	Marinicella	2.64	0.813	Fluviicola	2.41	0.420	Fluviicola	2.51	0.457
uncul. Gracilibacteria	2.23	0.117	Fluviicola	2.39	0.595	Sediminispirochaeta	2.28	0.266	Sediminispirochaeta	2.49	0.313
Campylobacter	2.14	0.177	Sediminispirochaeta	2.09	0.138	uncul. Gracilibacteria	1.73	0.087	Fusibacter	1.90	0.236
Gangjinia	2.00	0.214	uncul. bacterium	2.07	0.210	uncul. Burkholderiaceae	1.71	0.317	uncul. Gracilibacteria	1.85	0.166
Sediminispirochaeta	1.89	0.202	Campylobacter	1.77	0.380	Campylobacter	1.70	0.154	Helcococcus	1.77	0.250
Psychrobacter	1.82	0.554	Gangjinia	1.73	0.541	Marinicella	1.60	0.294	Gangjinia	1.77	0.300
uncul. Absconditabacteriales	1.58	0.143	Fusibacter	1.62	0.175	Gangjinia	1.60	0.268	Campylobacter	1.75	0.163
Marinicella	1.37	0.220	Helcococcus	1.60	0.254	Helcococcus	1.30	0.179	uncul. Burkholderiaceae	1.33	0.287
uncul. Burkholderiaceae	1.28	0.381	uncul. Absconditabacteriales	1.54	0.125	Fusibacter	1.23	0.077	uncul. Absconditabacteriales	1.32	0.108
uncul. Blattabacteriaceae	1.11	0.284	uncul. Burkholderiaceae	1.49	0.598	uncul. Absconditabacteriales	1.13	0.094	Marinicella	1.27	0.276
Fusibacter	1.04	0.068	Actinobacillus	1.26	0.661	Psychrobacter	1.10	0.162	Actinobacillus	1.19	0.581
Ornithobacterium	1.02	0.100	Psychrobacter	1.16	0.280	Ornithobacterium	1.09	0.142	Ornithobacterium	1.13	0.195

Helcococcus	0.97	0.123	Vibrio	0.95	0.548	uncl. Blautabacteriaceae	1.09	0.199	Psychrobacter	0.97	0.162
Treponema 2	0.84	0.097	Suttonella	0.91	0.201	Actinobacillus	0.80	0.266	uncl. Lachnospiraceae	0.94	0.125
Suttonella	0.82	0.115	uncl. Weeksellaceae	0.89	0.325	Suttonella	0.77	0.104	uncl. Blautabacteriaceae	0.85	0.171
uncl. Clostridiales	0.63	0.081	Treponema	0.82	0.100	uncl. Clostridiales	0.65	0.074	uncl. Clostridiales	0.77	0.117
uncl. Lachnospiraceae	0.62	0.047	Ornithobacterium	0.79	0.111	uncl. Lachnospiraceae	0.60	0.050	UCG-011	0.71	0.053

Abbreviations: uncl., unclassified; uncul., uncultured.; Cand., Candidatus

Table S5. Mean relative abundance and the standard error of the mean for every taxonomic phyla, and the top 25 most abundant families, and genera within fecal microbial communities from each of the four water change phases.

PRE			TRANSITION			HOLD			POST		
Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM	Phylum	Mean	SEM
Proteobacteria	38.65	2.875	Proteobacteria	37.32	4.436	Proteobacteria	40.70	2.375	Proteobacteria	45.62	3.343
Firmicutes	22.92	1.881	Firmicutes	23.77	3.293	Firmicutes	17.57	1.896	Fusobacteria	17.18	2.593
Fusobacteria	18.08	2.602	Epsilonbacteraeota	18.25	5.189	Fusobacteria	15.17	1.782	Epsilonbacteraeota	15.09	2.837
Epsilonbacteraeota	13.30	2.438	Fusobacteria	14.40	3.352	Epsilonbacteraeota	13.03	2.218	Firmicutes	15.02	1.661
Actinobacteria	5.76	1.147	Actinobacteria	4.63	0.842	Actinobacteria	12.49	2.578	Actinobacteria	6.35	1.654
Bacteroidetes	1.24	0.458	Bacteroidetes	1.59	0.744	Bacteroidetes	0.93	0.196	Bacteroidetes	0.67	0.173
Tenericutes	0.06	0.020	Tenericutes	0.04	0.014	Tenericutes	0.10	0.026	uncl. Bacteria	0.04	0.037
Thaumarchaeota	0.00	0.001	Planctomycetes	0.00	0.004	Patescibacteria	0.01	0.004	Tenericutes	0.04	0.016
Patescibacteria	0.00	0.001	Patescibacteria	0.00	0.001	Spirochaetes	0.00	0.001	Spirochaetes	0.00	0.002
uncl. Bacteria	0.00	0.001	Spirochaetes	0.00	0.001	uncl. Bacteria	0.00	0.001	Patescibacteria	0.00	0.001
Spirochaetes	0.00	0.001				Planctomycetes	0.00	0.000	Thaumarchaeota	0.00	0.000
Planctomycetes	0.00	0.001									
Nitrospirae	0.00	0.000									

PRE			TRANSITION			HOLD			POST		
Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM	Family	Mean	SEM
Pasteurellaceae	35.55	3.388	Pasteurellaceae	34.06	4.480	Pasteurellaceae	39.21	2.480	Pasteurellaceae	38.68	3.563
Fusobacteriaceae	18.06	2.599	Campylobacteraceae	18.24	5.189	Fusobacteriaceae	15.15	1.783	Fusobacteriaceae	17.17	2.593
Campylobacteraceae	13.28	2.438	Fusobacteriaceae	14.27	3.367	Campylobacteraceae	13.01	2.218	Campylobacteraceae	15.08	2.837
Lachnospiraceae	6.96	1.081	Lachnospiraceae	8.94	1.948	Mycobacteriaceae	12.45	2.578	Mycobacteriaceae	6.35	1.654
Ruminococcaceae	5.82	0.815	Ruminococcaceae	6.97	1.807	Lachnospiraceae	5.41	0.878	Vibrionaceae	5.08	1.676
Mycobacteriaceae	5.73	1.149	Mycobacteriaceae	4.61	0.844	Peptostreptococcaceae	4.04	0.674	Lachnospiraceae	4.30	0.548
Clostridiaceae 1	4.82	0.608	Clostridiaceae 1	3.82	0.782	Clostridiaceae 1	3.75	0.400	Peptostreptococcaceae	4.09	0.700
Peptostreptococcaceae	4.28	0.508	Peptostreptococcaceae	2.59	0.300	Ruminococcaceae	3.26	0.439	Ruminococcaceae	3.21	0.757
Succinivibrionaceae	1.11	0.376	Erysipelotrichaceae	1.41	0.392	Erysipelotrichaceae	0.98	0.164	Clostridiaceae 1	2.32	0.252
Enterobacteriaceae	1.07	0.393	Vibrionaceae	1.28	0.833	Succinivibrionaceae	0.51	0.172	Erysipelotrichaceae	1.05	0.139
Erysipelotrichaceae	1.00	0.260	Succinivibrionaceae	0.96	0.335	Bacteroidaceae	0.50	0.113	Succinivibrionaceae	0.86	0.388
Bacteroidaceae	0.60	0.170	Rikenellaceae	0.67	0.367	Enterobacteriaceae	0.28	0.046	Enterobacteriaceae	0.46	0.118
Rikenellaceae	0.45	0.224	Bacteroidaceae	0.57	0.283	Rikenellaceae	0.27	0.107	Rikenellaceae	0.27	0.109
Desulfovibrionaceae	0.26	0.098	Enterobacteriaceae	0.38	0.135	Vibrionaceae	0.23	0.095	Bacteroidaceae	0.26	0.064
Burkholderiaceae	0.18	0.075	Burkholderiaceae	0.34	0.119	Burkholderiaceae	0.17	0.062	Desulfovibrionaceae	0.22	0.098
Prevotellaceae	0.14	0.068	Prevotellaceae	0.20	0.107	Cardiobacteriaceae	0.11	0.021	Cardiobacteriaceae	0.12	0.024
Vibrionaceae	0.13	0.055	Cardiobacteriaceae	0.13	0.034	Flavobacteriaceae	0.11	0.043	Flavobacteriaceae	0.09	0.038
Cellvibrionaceae	0.12	0.013	Leptotrichiaceae	0.13	0.077	Desulfovibrionaceae	0.09	0.030	Saccharosporillaceae	0.07	0.012
Rhodobacteraceae	0.09	0.012	Flavobacteriaceae	0.11	0.061	uncl. RF39	0.07	0.025	Burkholderiaceae	0.05	0.015
Mycoplasmataceae	0.04	0.019	Saccharosporillaceae	0.06	0.019	Saccharosporillaceae	0.06	0.013	uncl. Bacteria	0.04	0.037
Arenicellaceae	0.04	0.007	Desulfovibrionaceae	0.06	0.027	Lactobacillaceae	0.06	0.018	Moraxellaceae	0.03	0.013
Atopobiaceae	0.03	0.014	uncl. RF39	0.03	0.014	vadinBB60	0.03	0.016	Mycoplasmataceae	0.03	0.016
Cardiobacteriaceae	0.03	0.009	Lactobacillaceae	0.02	0.017	Mycoplasmataceae	0.03	0.009	Rhodobacteraceae	0.02	0.008
Moraxellaceae	0.02	0.019	Crocinitomicaceae	0.02	0.016	Porphyromonadaceae	0.03	0.010	uncl. γ-proteobacteria	0.02	0.018
Flavobacteriaceae	0.02	0.008	Arenicellaceae	0.01	0.009	Rubrobacteriaceae	0.02	0.023	Prevotellaceae	0.02	0.010

PRE			TRANSITION			HOLD			POST		
Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM	Genus	Mean	SEM
Actinobacillus	35.54	3.388	Actinobacillus	34.01	4.469	Actinobacillus	39.21	2.480	Actinobacillus	38.68	3.563
Fusobacterium	18.06	2.599	Campylobacter	18.24	5.189	Fusobacterium	15.15	1.783	Fusobacterium	16.99	2.595
Campylobacter	13.28	2.438	Fusobacterium	14.26	3.368	Campylobacter	13.01	2.218	Campylobacter	15.08	2.837
Mycobacterium	5.73	1.149	Mycobacterium	4.61	0.844	Mycobacterium	12.45	2.578	Mycobacterium	6.35	1.654

Clostridium sensu stricto 1	3.68	0.509	Blautia	2.97	1.382	Clostridium sensu stricto 1	2.46	0.311	Photobacterium	5.08	1.676
Peptoclostridium	2.40	0.442	Clostridium sensu stricto 1	2.15	0.308	Lachnoclostridium	1.96	0.322	Clostridium sensu stricto 1	1.58	0.205
Epulopiscium	2.39	1.010	Hydrogenoanaerobacterium	1.99	1.020	Peptoclostridium	1.43	0.391	Lachnoclostridium	1.41	0.329
Lachnoclostridium	1.71	0.348	Lachnoclostridium	1.93	0.721	Clostridium sensu stricto 13	1.30	0.240	Peptoclostridium	1.26	0.423
Ruminiclostridium 9	1.63	0.434	Clostridium sensu stricto 13	1.67	0.578	Tyzzereella 3	1.24	0.469	Ruminiclostridium 9	1.14	0.548
Clostridium sensu stricto 13	1.15	0.187	Photobacterium	1.28	0.833	Ruminiclostridium 9	1.21	0.307	Paeniclostridium	1.02	0.382
Anaerobiospirillum	1.11	0.376	Epulopiscium	1.27	0.639	Epulopiscium	0.97	0.300	Romboutsia	1.01	0.414
UCG-005	1.04	0.394	Ruminiclostridium 9	1.12	0.353	Romboutsia	0.97	0.316	Tyzzereella 3	0.89	0.261
Hydrogenoanaerobacterium	0.98	0.331	Peptoclostridium	1.00	0.269	Paeniclostridium	0.65	0.186	Anaerobiospirillum	0.86	0.388
Proteus	0.91	0.387	Tyzzereella 3	0.98	0.321	Hydrogenoanaerobacterium	0.57	0.133	Epulopiscium	0.79	0.329
Blautia	0.81	0.211	UCG-005	0.97	0.387	Paraclostridium	0.52	0.176	Clostridium sensu stricto 13	0.74	0.145
GCA-900066225	0.80	0.180	Anaerobiospirillum uncl.	0.96	0.335	Anaerobiospirillum	0.51	0.172	UCG-005	0.69	0.282
fissicatena group	0.76	0.237	Ruminococcaceae	0.92	0.389	Bacteroides	0.50	0.113	Blautia	0.67	0.215
Tyzzereella 3	0.61	0.142	fissicatena group	0.68	0.266	Turicibacter	0.46	0.135	Turicibacter	0.61	0.128
Bacteroides	0.60	0.170	Alistipes	0.67	0.367	Blautia	0.43	0.139	Paraclostridium	0.36	0.160
Paraclostridium	0.55	0.251	Oscillospira	0.65	0.227	fissicatena group	0.43	0.102	GCA-900066225	0.33	0.090
Tyzzereella	0.47	0.134	uncl. Lachnospiraceae	0.60	0.207	UCG-005	0.37	0.126	Hydrogenoanaerobacterium	0.32	0.088
Romboutsia	0.46	0.138	Bacteroides	0.57	0.283	Erysipelatoclostridium	0.33	0.111	fissicatena group	0.30	0.081
Alistipes	0.45	0.224	Romboutsia	0.54	0.180	Tyzzereella	0.30	0.041	Proteus	0.27	0.118
uncl. Ruminococcaceae	0.45	0.133	Tyzzereella	0.50	0.178	Alistipes	0.27	0.107	Alistipes	0.27	0.109
Fournierella	0.44	0.191	Turicibacter	0.47	0.219	GCA-900066225	0.27	0.051	Bacteroides	0.26	0.064

Abbreviations: uncl., unclassified; uncul., uncultured.; Cand., Candidatus