

Supplementary materials

Table S1. Clinical information (mean \pm SD or range) of the participants in this study.

	Healthy Subjects	Ulcerative Colitis Subjects
n (total)	11	10
n (females)	6	5
n (males)	5	5
Age (years)	20 - 44	18 - 42
BMI (18.5-24.9 Kg/ m²)	23.66 \pm 4.17	26.94 \pm 4.70
Glucose (70-110mg/gL)	77.63 \pm 5.86	109.00 \pm 52.05
Cholesterol (<200 mg/gL)	180.90 \pm 23.92	202.50 \pm 19.82
Triglycerides (<150 mg/gL)	76.54 \pm 21.40	118.75 \pm 56.75
HDL (>40 mg/gL)	61.54 \pm 12.63	52.50 \pm 3.50
LDL (<130 mg/gL)	104.18 \pm 24.34	127.00 \pm 33.00
Fecal calprotectin (<50 μg/g)	-	1827.94 \pm 2159.58
Partial Mayo score	-	4.22 \pm 1.61

BMI, Body Mass Index; HDL, High Density Lipoprotein; LDL, Low Density Lipoprotein. Partial Mayo score is calculated from "Stool frequency", "Rectal Bleeding" and Physician's global assessment". The range values considered normal for each value are shown in brackets.

Table S2. Comparison of the oral taxonomic profiles between UC participants of the study and a group of healthy donors.

Taxonomy	Mean \pm SD Healthy Volunteers	Mean \pm SD UC Patients	p-values
Phylum			
Actinobacteria	4.77 \pm 2.20	5.64 \pm 3.57	0.704
Bacteroidetes	33.88 \pm 5.46	31.46 \pm 10.18	0.704
Bacteroidetes	33.88 \pm 5.46	31.46 \pm 10.18	0.704
Epsilonbacteraeota	0.69 \pm 0.35	0.50 \pm 0.33	0.426

Firmicutes	44.89 ± 6.88	41.9 ± 5.56	0.511
Fusobacteria	5.29 ± 3.26	6.56 ± 3.68	0.468
Patescibacteria	3.75 ± 2.55	2.30 ± 1.69	0.314
Proteobacteria	6.24 ± 4.35	11.49 ± 7.47	0.072[#]
Spirochaetes	0.39 ± 0.80	0.09 ± 0.12	0.097[#]
Synergistetes	0.04 ± 0.08	0.01 ± 0.03	0.294
Tenericutes	0.05 ± 0.05	0.03 ± 0.05	0.287
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Family			
<i>Actinomycetaceae</i>	1.41 ± 0.71	1.30 ± 1.22	0.349
<i>Aerococcaceae</i>	0.05 ± 0.06	0.09 ± 0.15	0.802
<i>Atopobiaceae</i>	1.08 ± 0.56	0.67 ± 0.66	0.084[#]
<i>Bacteroidaceae</i>	0.03 ± 0.11	0.00 ± 0.00	1
<i>Bifidobacteriaceae</i>	0.03 ± 0.07	0.02 ± 0.04	0.310
<i>Burkholderiaceae</i>	0.08 ± 0.08	0.14 ± 0.12	0.481
<i>Campylobacteriaceae</i>	0.69 ± 0.35	0.50 ± 0.33	0.426
<i>Cardiobacteriaceae</i>	0.02 ± 0.02	0.05 ± 0.05	0.319
<i>Carnobacteriaceae</i>	1.27 ± 0.69	1.22 ± 0.55	0.972
<i>Corynebacteriaceae</i>	0.04 ± 0.03	0.33 ± 0.55	0.129
<i>Defluviitaleaceae</i>	0.02 ± 0.03	0.00 ± 0.00	0.014*
<i>Erysipelotrichaceae</i>	0.54 ± 0.23	0.50 ± 0.53	0.217
Family_XI	1.06 ± 0.42	1.90 ± 1.30	0.132
Family_XI	0.35 ± 0.24	0.23 ± 0.50	0.022*
Family_XIII	1.16 ± 0.89	0.35 ± 0.31	0.024*
<i>Flavobacteriaceae</i>	0.68 ± 0.45	1.35 ± 1.31	0.511
<i>Fusobacteriaceae</i>	2.48 ± 1.47	2.96 ± 2.49	0.972
<i>Lachnospiraceae</i>	3.38 ± 1.45	2.00 ± 1.33	0.061[#]
<i>Lactobacillaceae</i>	0.12 ± 0.33	0.37 ± 0.74	0.342

<i>Lentimicrobiaceae</i>	0.02 ± 0.02	0.02 ± 0.05	0.172
<i>Leptotrichiaceae</i>	2.81 ± 2.18	3.60 ± 2.58	0.511
<i>Micrococcaceae</i>	2.20 ± 1.65	3.30 ± 2.14	0.251
<i>Moraxellaceae</i>	0.04 ± 0.10	0.01 ± 0.02	0.508
<i>Mycoplasmataceae</i>	0.02 ± 0.02	0.03 ± 0.05	0.732
<i>Neisseriaceae</i>	2.19 ± 1.58	6.29 ± 5.14	0.019*
<i>Paludibacteraceae</i>	0.07 ± 0.12	0.04 ± 0.06	0.643
<i>Pasteurellaceae</i>	3.90 ± 2.83	5.00 ± 2.94	0.349
<i>Peptococcaceae</i>	0.16 ± 0.15	0.08 ± 0.16	0.064‡
<i>Peptostreptococcaceae</i>	2.54 ± 4.02	0.38 ± 0.46	0.044*
<i>Porphyromonadaceae</i>	5.92 ± 5.15	2.93 ± 2.83	0.223
<i>Prevotellaceae</i>	26.75 ± 8.24	26.76 ± 10.43	1
<i>Propionibacteriaceae</i>	0.00 ± 0.00	0.02 ± 0.04	0.147
<i>Rikenellaceae</i>	0.05 ± 0.12	0.00 ± 0.00	0.057‡
<i>Ruminococcaceae</i>	0.59 ± 0.42	0.24 ± 0.22	0.066‡
<i>Saccharimonadaceae</i>	2.84 ± 1.98	2.02 ± 1.77	0.426
<i>Spirochaetaceae</i>	0.39 ± 0.80	0.09 ± 0.12	0.096‡
<i>Streptococcaceae</i>	11.77 ± 4.98	12.29 ± 6.20	0.863
<i>Synergistaceae</i>	0.04 ± 0.08	0.01 ± 0.03	0.294
<i>Tannerellaceae</i>	0.16 ± 0.11	0.13 ± 0.10	0.698
<i>Veillonellaceae</i>	21.86 ± 7.26	22.24 ± 7.52	0.917
<i>Weeksellaceae</i>	0.16 ± 0.16	0.23 ± 0.15	0.173
Genus			
<i>Abiotrophia</i>	0.050 ± 0.055	0.090 ± 0.150	0.802
<i>Acholeplasma</i>	0.006 ± 0.016	0.000 ± 0.000	0.189
<i>Actinobacillus</i>	0.007 ± 0.021	0.029 ± 0.052	0.281
<i>Actinomyces</i>	1.397 ± 0.721	1.279 ± 1.202	0.387

<i>Aggregatibacter</i>	0.085 ± 0.084	0.206 ± 0.294	0.971
<i>Alloprevotella</i>	3.003 ± 1.527	3.148 ± 2.102	0.918
<i>Alloscardovia</i>	0.001 ± 0.002	0.002 ± 0.007	0.729
<i>Alysiella</i>	0.008 ± 0.014	0.006 ± 0.012	0.814
<i>Anaeroglobus</i>	0.025 ± 0.029	0.014 ± 0.020	0.469
<i>Atopobium</i>	1.068 ± 0.563	0.673 ± 0.656	0.084[#]
<i>Bacteroides</i>	0.035 ± 0.109	0.000 ± 0.000	1
<i>Bergeriella</i>	0.001 ± 0.002	0.000 ± 0.000	0.391
<i>Bergeyella</i>	0.163 ± 0.159	0.225 ± 0.152	0.173
<i>Bifidobacterium</i>	0.016 ± 0.027	0.006 ± 0.014	0.257
<i>Bulleidia</i>	0.009 ± 0.017	0.000 ± 0.000	0.093[#]
<i>Butyrivibrio_2</i>	0.137 ± 0.107	0.183 ± 0.320	0.454
<i>Campylobacter</i>	0.686 ± 0.351	0.501 ± 0.327	0.426
<i>Candidatus_Saccharimonas</i>	0.321 ± 0.216	0.240 ± 0.236	0.503
<i>Capnocytophaga</i>	0.681 ± 0.449	1.351 ± 1.311	0.511
<i>Cardiobacterium</i>	0.020 ± 0.016	0.049 ± 0.053	0.318
<i>Catonella</i>	0.208 ± 0.138	0.190 ± 0.153	0.860
<i>Citrobacter</i>	0.001 ± 0.002	0.000 ± 0.000	0.391
<i>Comamonas</i>	0.001 ± 0.004	0.000 ± 0.000	0.391
<i>Corynebacterium</i>	0.040 ± 0.027	0.332 ± 0.547	0.128
<i>Cryptobacterium</i>	0.001 ± 0.002	0.002 ± 0.005	0.729
<i>Defluviitaleaceae_UCG-011</i>	0.022 ± 0.031	0.001 ± 0.004	0.014*
<i>Desulfobulbus</i>	0.001 ± 0.002	0.000 ± 0.000	0.391
<i>Dialister</i>	0.122 ± 0.128	0.108 ± 0.110	0.503
<i>Eggerthia</i>	0.004 ± 0.012	0.000 ± 0.000	0.391
<i>Eikenella</i>	0.020 ± 0.023	0.032 ± 0.034	0.424
<i>Erysipelotrichaceae_UCG-006</i>	0.001 ± 0.003	0.001 ± 0.003	0.945

<i>Ezakiella</i>	0.007 ± 0.014	0.000 ± 0.000	0.093[#]
Family_XIII_UCG-001	0.032 ± 0.039	0.008 ± 0.014	0.138
<i>Filifactor</i>	0.218 ± 0.428	0.014 ± 0.033	0.014**
<i>Fretibacterium</i>	0.034 ± 0.071	0.015 ± 0.030	0.294
<i>Fusobacterium</i>	2.475 ± 1.472	2.962 ± 2.493	0.972
<i>Gemella</i>	1.061 ± 0.424	1.903 ± 1.302	0.132
<i>Granulicatella</i>	1.266 ± 0.689	1.218 ± 0.554	0.972
<i>Haemophilus</i>	3.728 ± 2.775	4.658 ± 2.739	0.386
<i>Howardella</i>	0.001 ± 0.004	0.001 ± 0.002	1
<i>Johnsonella</i>	0.138 ± 0.175	0.059 ± 0.093	0.441
<i>Kingella</i>	0.050 ± 0.042	0.488 ± 1.184	0.417
<i>Lachnoanaerobaculum</i>	0.947 ± 0.599	0.333 ± 0.187	0.018*
<i>Lachnospiraceae_NK3A20_group</i>	0.002 ± 0.006	0.000 ± 0.000	0.391
<i>Lactobacillus</i>	0.118 ± 0.325	0.373 ± 0.739	0.342
<i>Lautropia</i>	0.071 ± 0.080	0.106 ± 0.118	0.831
<i>Leptotrichia</i>	2.784 ± 2.154	3.595 ± 2.582	0.511
<i>Megasphaera</i>	1.653 ± 1.565	1.065 ± 1.022	0.573
<i>Mobiluncus</i>	0.015 ± 0.023	0.008 ± 0.016	0.402
<i>Mogibacterium</i>	0.010 ± 0.014	0.002 ± 0.005	0.136
<i>Moraxella</i>	0.037 ± 0.103	0.007 ± 0.019	0.741
<i>Moryella</i>	0.007 ± 0.023	0.000 ± 0.000	0.391
<i>Mycoplasma</i>	0.018 ± 0.022	0.026 ± 0.047	0.732
<i>Neisseria</i>	2.013 ± 1.544	5.664 ± 5.148	0.034*
<i>Olsenella</i>	0.012 ± 0.039	0.000 ± 0.000	0.391
<i>Oribacterium</i>	1.250 ± 0.731	0.961 ± 0.685	0.511
<i>Parascardovia</i>	0.002 ± 0.005	0.000 ± 0.000	0.391
<i>Parvimonas</i>	0.338 ± 0.238	0.233 ± 0.498	0.022*

<i>Peptoanaerobacter</i>	0.003 ± 0.008	0.004 ± 0.006	0.895
<i>Peptococcus</i>	0.162 ± 0.149	0.075 ± 0.165	0.064*
<i>Peptoniphilus</i>	0.001 ± 0.002	0.000 ± 0.000	0.391
<i>Peptostreptococcus</i>	2.189 ± 3.849	0.341 ± 0.434	0.084*
<i>Phocaeicola</i>	0.015 ± 0.045	0.000 ± 0.000	0.189
<i>Porphyromonas</i>	5.921 ± 5.146	2.927 ± 2.826	0.223
<i>Prevotella</i>	4.179 ± 2.386	3.475 ± 2.266	0.756
<i>Prevotella_2</i>	0.240 ± 0.326	0.364 ± 0.360	0.672
<i>Prevotella_6</i>	1.196 ± 0.746	0.934 ± 0.862	0.314
<i>Prevotella_7</i>	18.104 ± 8.544	18.83 ± 9.337	0.917
<i>Pseudomonas</i>	0.000 ± 0.000	0.002 ± 0.003	0.147
<i>Pseudopropionibacterium</i>	0.000 ± 0.000	0.017 ± 0.043	0.147
<i>Pseudoramibacter</i>	0.005 ± 0.012	0.000 ± 0.000	0.189
<i>Pyramidobacter</i>	0.009 ± 0.029	0.000 ± 0.000	0.391
<i>Ralstonia</i>	0.008 ± 0.008	0.032 ± 0.063	0.633
<i>Rikenellaceae_RC9_gut_group</i>	0.047 ± 0.121	0.001 ± 0.002	0.057*
<i>Rothia</i>	2.203 ± 1.655	3.296 ± 2.135	0.251
<i>Ruminococcaceae_UCG-014</i>	0.585 ± 0.423	0.239 ± 0.220	0.066*
<i>Scardovia</i>	0.015 ± 0.042	0.009 ± 0.021	0.801
<i>Selenomonas</i>	0.193 ± 0.176	0.150 ± 0.152	0.479
<i>Selenomonas_3</i>	0.877 ± 0.844	0.674 ± 0.714	0.459
<i>Selenomonas_4</i>	0.028 ± 0.043	0.016 ± 0.020	0.797
<i>Shuttleworthia</i>	0.017 ± 0.025	0.008 ± 0.014	0.279
<i>Simonsiella</i>	0.003 ± 0.01	0.012 ± 0.027	0.524
<i>Solobacterium</i>	0.523 ± 0.241	0.500 ± 0.532	0.245
<i>Sphaerochaeta</i>	0.005 ± 0.016	0.000 ± 0.000	0.391
<i>Staphylococcus</i>	0.000 ± 0.000	0.005 ± 0.005	0.011*

<i>Stomatobaculum</i>	0.592 ± 0.374	0.242 ± 0.177	0.035*
<i>Streptobacillus</i>	0.008 ± 0.014	0.002 ± 0.006	0.281
<i>Streptococcus</i>	11.77 ± 4.984	12.291 ± 6.196	0.863
<i>Tannerella</i>	0.160 ± 0.115	0.132 ± 0.098	0.698
<i>Treponema_2</i>	0.389 ± 0.781	0.094 ± 0.116	0.096[#]
<i>Veillonella</i>	18.892 ± 7.413	20.180 ± 7.801	0.704

Table S3. Sequence of the differential ASVs detected between UC patients and healthy volunteers. Absolute number of reads detected per sample (number codes) in each group is also shown.

ASV	Code	Sequence	Total number of reads detected per sample (codes) in UC group										Total number of reads detected per sample (codes) in Control group										
			11	11	12	12	12	12	12	13	13	13	56	58	60	65	67	69	73	75	77	82	85
Assign	ed		6	8	0	2	4	6	8	0	2	4											
ASV4		GCAGCAGTGGGAATCTCCGCAATGGACGA																					
		AAGTCTGACGGAGCAACGCCGCGTGAGTGAT																					
		GACGGCCTCGGGTTGTAAAGCTCTGTTAATC																					
		GGGACGAAAGGCCTTCTTGCATAAGTGAGA																					
		AGGATTGACGGTACCGGAATAGAAAGCCACG																					
		GCTAACTACGTGCCAGCAGCCGCGTAATACG	0	16	85	46	8	65	0	0	0	0	64	0	0	0	0	0	0	0	0	0	0
		TAGGTGGCAAGCGTTGTCGGATTATTGGGC																					
		GTAAAGCGCGCAGCGGGATCAGTCAGTCT																					
		GTCTAAAAGTCGGGGCTAACCCCGTGATG																					
		GGATGGAAACTGCTGATCTAGAGTATCGGAGA																					

	AGCGACTTCTGGACGAAACTGACGCTGAG																							
	GCGCGAAAGCCAGGGGAGCGAACGGGATTAG																							
	ATAC																							
	GCAGCAGTGGGAATCTTCCGCAATGGACGA																							
	AACTCTGACGGAGCAACGCCGCGTGAGTGAT																							
	GACGGCCTCAGGTGTAAAGCTCTGTTAATC																							
	GGGACGAAAGGCCTCTGCGAACAGTTAGA																							
	AGGATTGACGGTACCGAATAGAAAGCCACG																							
	GCTAACTACGTGCCAGCAGCCGCGTAATACG																							
	TAGGTGGCAAGCGTTGTCCGGAATTATTGGGC																							
ASV14	GTAAAGCGCCGCAGGGGATCAGTTAGTCTG	0	49 5	89 6	10 6	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	TCTTAAAAGTCGGGCTAACCCGTGATGG																							
	GATGGAAACTGCTGATCTAGAGTATCGGAGAG																							
	GAAAGTGAATTCTAGTGTAGCGGTGAAATG																							
	CGTAGATATTAGGAAGAACACCAGTGGCAA																							
	GGCGACTTCTGGACGAAACTGACGCTGAGG																							
	CGCGAAAGCCAGGGAGCGAACGGGATTAGA																							
	TAC																							
	GCAGCAGTGGGAATATTGGACAATGGACCA																							
	AGAGTCTGATCCAGCAATTCTGTGTGCACGAT																							
	GAAGTTTCGGAATGTAAAGTGCTTCAGTTG																							
ASV39	GGAAGAAAAAAATGACGGTACCAACAGAAG																							
	AAGTACGGCTAAATACGTGCCAGCAGCCG	0	38 6	0	11 9	19 4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	GGTAATACGTATGTCACAAGCGTTATCCGGAT																							
	TTATTGGCGTAAAGCGCGTAGGTGGTTAT																							
	GTAAGTCTGATGTAAAATGCAGGGCTCAACT																							
	CTGTATTGCGTTGAAACTGTGTAAGAGT																							

		ACTGGAGAGGTAAGCGGAACATACAAGTAG																	
		AGGTGAAATTCTGAGATATTGTAGGAATGCC																	
		GATGGGAAAGCCAGCTTACTGGACAGATACT																	
		GACGCTAACAGCGAAGCGTGGTAGCAAA																	
		CAGGATTAGATAAC																	
		GCAGCAGTGAGGAATATTGGTCAATGGACGA																	
		AAGTCTGAACCAGCCAAGTAGCGTGCAGGAT																	
		GACGGCCCTCCGGTTGTAACACTGCTTITAGTT																	
		GGGAATAAAAAAAGGGACGTGTCCCTTATTGT																	
		ATGTACCTTCAGAAAAAGGACCGGCTAATTCC																	
		GTGCCAGCAGCCGCGTAATACCGAAGGTCC																	
ASV21	9	AGGC GTT AT CCGG ATT TATTGGGTTAAAGGG	28	0	0	0	0	0	0	13	3	0	9	0	0	0	0	0	0
		AGCGTAGCGGATTGTTAAGTCAGCGGTTAAA																	
		GGGTGTGGCTCAACCATGCATTGCCGTGAAA																	
		CTGGCGATCTGAGTGCAGACAGGGATGCCGG																	
		AATT CGTGGGTAGCGGTGAAATGCTTAGATA																	
		TCACGAAGAACTCCGATCGCGAAGGCAGGTG																	
		TCCGGGCTGCAACTGACGCTGAGGGCTCGAAAG																	
		TGTGGGTATCAAACAGGATTAGATAAC																	
		GCTGCAGTGGGAATATTGCGCAATGGGGC																	
		AACCCTGACCGCAGCCATGCCGCGTGAATGAA																	
		GAAGGCCTCGGGTTGTAAGTTCTTCGGTA																	
ASV75	4	GCGAGGAAGGCATTAGTTAACAGACTAGGT	0	0	0	0	0	0	0	0	0	0	0	14	44	14	87	41	32
		GATTGACGTAACTACAGAAGAAGCACCGGCT												0	8	6	0	5	12
		AACTCCGTGCCAGCAGCCGCGTAATACCGA															0	0	17
		GGGTGCGAGCGTTAACCGAAATACTGGCGT															5	10	85
		AAAGGGCACCGCAGGCCGTGACTTAAGTGAGG															0	0	17

	TGTGAAAGCCCCGGGCTAACCTGGGAATTGC ATTCATACTGGGTCGCTAGAGTACTTAGGG AGGGTAGAATTCCACGTGTAGCGGTGAAATG CGTAGAGATGTGGAGGAATACCGAAGGCGAA GGCAGCCCCTGGGAATGTACTGACGCTCATG TGCGAAAGCGTGGGAGCAAACAGGATTAGA TAC GCTGCAGTGAGGAATCTTCCACAATGGCGAA AGCCTGATGGAGCAACGCCGCGTGAAGGATG AAGGCCTCGGGTTGTAACCTCTTTATGAGT GAAGAATATGACGGTAACTCATGAATAAGCA CCGGCTAACTACGTGCCAGCAGCCGCGTCAT ACGTAGGGTGCAAGCATTATCCGGAGTGAUTG		
ASV75 6	GGCGTAAAGAGTTGCGTAGGC GGTTAACGAG TGAATAGT GAAACCTGGTGGCTAACCATACA GACTATTATTCAAAC TGTAAACTCGAGAATG GTAGAGGTAACTGGAATTCTAGTGTAGGAGT GAAATCCGTAGATATTAGAAGGAACACCGAT GGCGTAGGCAGGTTACTGGGCCATTCTGACG CTAAGGCACGAAAGCGTGGGAGCGAACCGG ATTAGATAC GCAGCAGTGGGAATATTG CACAATGGCGC AAGCCTGATGCAGCGACGCCGCGT GAGGGAT	0 0 0 0 0 0 0 0 0 0 0 0 29 10 12 26 68 50 90 13 10 96 9 2 1 9 9 6 6 81 4	
ASV75 8	GACGGCCTCGGGTTGTAACCTCTGTTAGCA GGGAAGAAGAGAGATTGACGGTACCTGCAGA GAAAGCGCCGGCTAACTACGTGCCAGCAGCC GCGGTAATACGTAGGGCGCGAGCGTTGTCCGG	0 39 0 0 0 0 43 0 0 0 44 0 65 0 29 71 0 66 90 50 45 8 4 1 6 1 4 2 9	

	AATTATTGGCGTAAAGAGCTGTAGGCCGTT TGTGCGTCTGCTGTGAAAGGCCGGGCTTAA CTCCGTGTATTGCAGTGGTACGGCAGACTA GAGTGCAGTAGGGAGACTGGAATTCTGGTG TAGCGGTGGAATGCGCAGATATCAGGAGGAA CACCGATGGCGAAGGCAGGTCTCTGGCTGTA ACTGACGCTGAGAAGCGAAAGCATGGGGAGC AACAGGATTAGATA GCTGCAGTGGGAATCTTCCGCAATGGACGAA AGTCTGACGGAGCAACGCCGCGTGAGTGATG ACGCCCTCGGGTTGTAAGCTCTGTTAACG GGACGAAAGGTCTCTGCGAATAGTTAGAGG AATTGACGGTACCGGAATAGAAAGCCACGGC TAACTACGTGCCAGCAGCCGCGTAATACGTA GGTGGCAAGCGTTGTCCGATTATTGGCGT AAAGCGCGCGAGGCGGATCAGTCAGTCGTC 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 59 87 77 77 71 0 68 18 5 9 8 53	
ASV76 2	TTAAAAGTTGGGGCTAACCCCGTGTGGGA TGGAAACTGCTGATCTAGAGTATCGGAGAGGA AAGTGGAAATTCTTAGTGTAGCGGTGAAATGCG TAGATATTAGGAAGAACACCAGTGGCGAAGG CGACTTCTGGACGAAAAGTGACGCTGAGGCG CGAAAGCCAGGGAGCGAACGGGATTAGATA C	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 18 67 14 34 37 55 76 32 0 0 32 0 6 2
ASV76 3	GCTGCAGTGAGGAATATTGGTCAATGGCGAG AGCCTGAACCAGCCAAGTCGCCTGAAGGATG ACTGTCTATGGATTGTAAACTTCTTTATACG GGAATAACAAGAGGCCACGTGTGGCTCCCTGC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 23 0 0 18 67 14 34 37 55 76 32 0 0 32 0 6 2

	ATGTACCGTATGAATAAGCATCGGCTAACTCC GTGCCAGCAGCCGCGGTAAATACGGAGGATGC GAGCGTTATCCGGATTATTGGGTTAAAGGG TGCCTAGGC GGCTGTTAAGTCAGCGGTGAAA TCTAGGAGCTTAACCTCTAAATTGCCATTGATA CTGGCGGGCTTGAGTAGATGAGGTAGGC AATGCGTGGTGTAGCGGTGGAATGCATAGATA TCACCGAGAACTCCGATTGCGAAGGCAGCTTA CTAAGGTACAAC TGACGCTGAAGCACGAAAG CGTGGGTATCAAACAGGGATTAGATA GCTGCAGTGGGAATCTTCCGCAATGGACGAA AGTCTGACGGAGCAACGCCGCGTGAGTGATG ACGGCCTC GGTTGTAAGCTCTGTTAAC GGACGAATGGTTCTTGCGAATAGTGCGAGG ATTTGACGGTACCGGAATAGAAAGCCACGGCT AAACTACGTGCCAGCAGCCGCGGTAAATACGTA GGTGGCAAGCGTTGTC CGGAATTATTGGCGT AAAGCGCGCCAGGCGGATTGGTCAGTCTGTC	0 0 0 0 0 0 0 0 0 0	57 70 49 16 18 29 40 25 47 19 95 3 1 9 3 6 0 0 4 7
ASV76 5	TTAAAAGT CGGGGCTTAACCCCGT GATGGGA TGGAAACTGCCAATCTAGAGTATCGGAGAGG AAAGTGGATT CCTAGTGTAGCGGTGAAATGC GTAGATATTAGGAAGAACACCAGTGGCGAAG GCGACTTTCTGGACGAAA ACTGACGCTGAGGC GCGAAAGCCAGGGAGCGAACCGGGATTAGAT AC		
ASV77 3	GCTGCAGTGAGGAATATTGGTCAATGGCGAG AGCCTGAACCAGCCAAGTAGCGTGAGGATG	0 0 0 0 0 0 0 0 0 0	42 64 74 0 0 85 36 0 27 97 0 9 4 5 0 0 85 9 0 9

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ASV77		8	
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ASV78 1	GGCGTTATCCGGATTATTGGGTTAAAGGGA	0	0	0	0	0	0	0	0	0	0	13	28	39	27	0	0	7	15	14	0	25
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ASV78 7	GCGGTAATACGTAGGGCGCGAGCGTTGTCCGG	33	0	15	94	28	87	13	20	0	11	0	0	0	91	0	19	0	22	13	21	0
	AATTATTGGCGTAAAGAGCTTGTAGGCGTT	5	19	0	1	2	98	1			1	0	0	0	9	0	0	0	0	6	9	0
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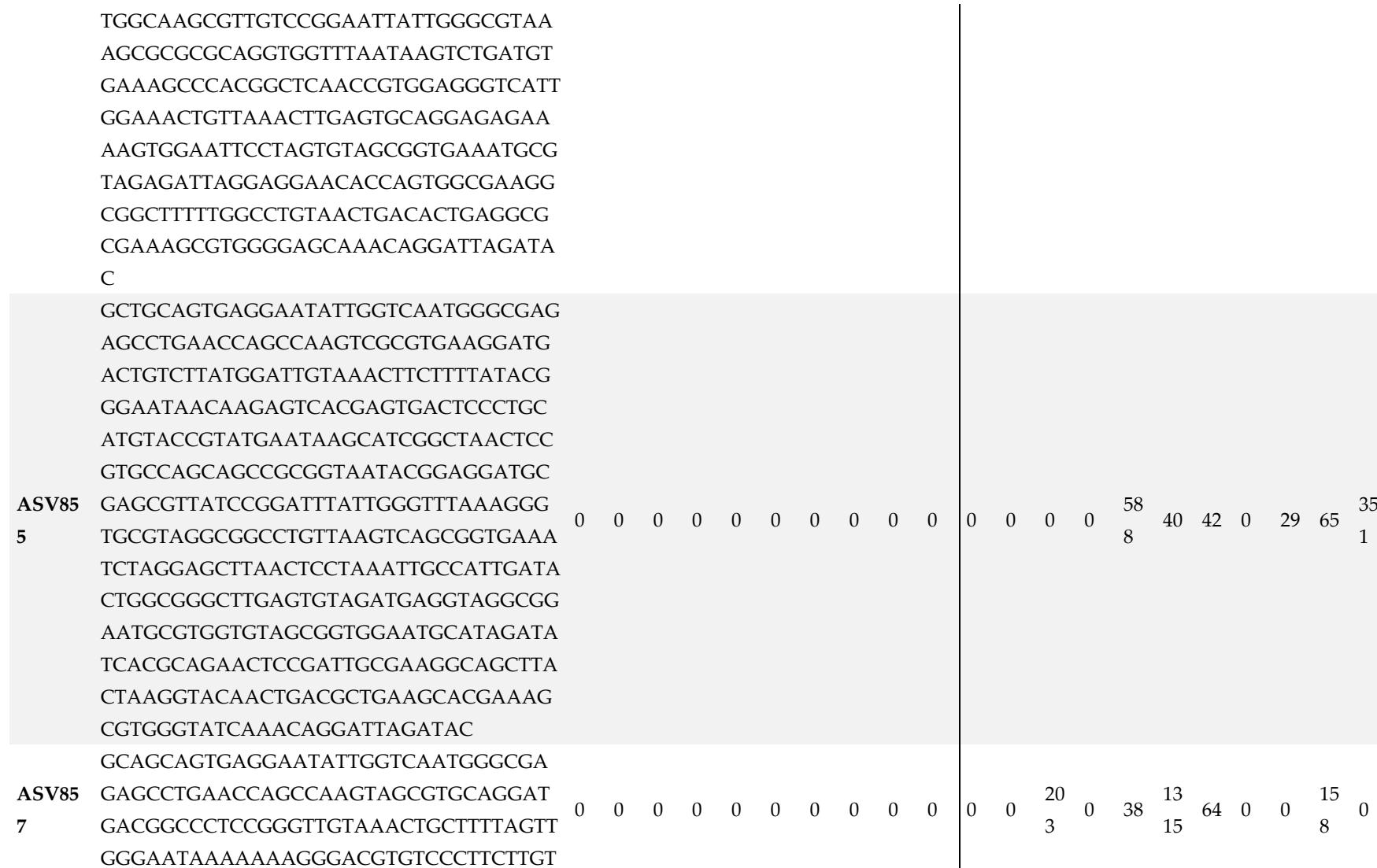
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ASV79	2	AGCGTTATCCGGATTATTGGGTTAAAGGGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	42	51	21	92	0	32	30		
		CGTAGGCGGCCTGTTAAGTCAGCGGTGAAAT															2	1	3	7					
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		GCTGCAGTGGGAATATTGCACAAATGGCGA																							
		AAGCCTGATGCGACAGCGCGTGAAAGAT																							
		GAAGGTCTTGGATCGTAAAGTTCTGTTGAG																							
		GGGAAGATAATGACGGTACCGTGTGAGGAAG																							
ASV79	5	CCCCGGCTAACTACGTGCCAGCAGCGCGGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	39	14	92	10	79	0	34	68	
		ATACGTAGGGGGCTAGCGTTATCCGGATTAC															8	0	0	0	8	0	9	2	
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		GTCGGTGGTAAAGGCTACGGCTAACCGTAG																							
		TAAGCCGCCAAACTGGAGGACTTGAGTGC																							
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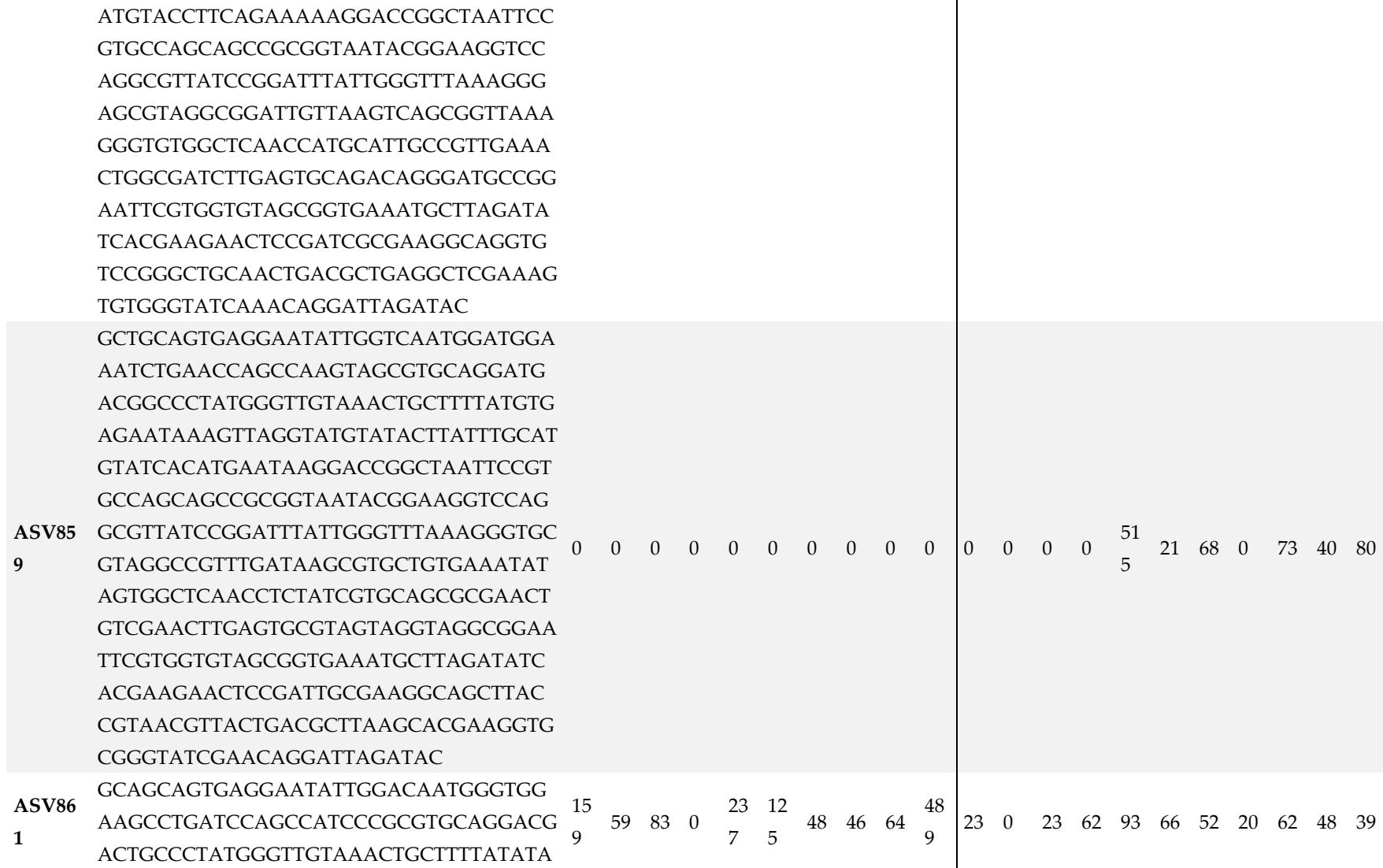
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ASV80	GCTGCAGTGAGGAATATTGGTCAATGGCGAG AGCCTGAACCAGCCAAGTAGCGTCAGGATG ACGGCCCTATGGGTGAAACTGCTTTATGTG GGGATAAAAGTGAGCTACGTGAGTTATTGCA GGTACCATGAATAAGGACCGGCTAACCG TGCCAGCAGCCGCGGTAAACCGAACGGTCCA GGCGTTATCCGGATTATTGGGTTAAAGGGA GCGTAGGCCGTGGATTAAGCGTGTGTGAAAT GTAGACGCTCACGTCTGAATTGCAGCGCGAA	0 0 0 0 0 0 0 0 0 0	92 42 19 55 78 0 16 0 17 88 75 4 3 2 4

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ASV81 4	GTGTAAAGGGTGCCTAGGCAGGGAAAATAAGT CAGTATGTGAAATCCCTCGGCTCAACTGAGGA	14 8	0 16 72 0 80 30 0 0 0 0 0 92 0 35 20 26 35 51 20 22 9 92 3 7 6
	ACTGCAACTGAAACTATTTCTGAGTGTGA AGGGAAAGTGGAATTCTAGTGTAGCGGTG AAATGCGTAGAGATTAGGAGGAACACCAAGTG GCGAAGGCGACTTCTGGCAACAACTGACGC TGAGGCACGAAAGTGTGGGGAGCAAACAGGA TTAGATAC		
	GCTGCAGTGAGGAATATTGGTCAATGGCGCG AGCCTGAACCAGCCAAGTAGCGTGCAGGATG ACGGCCCTATGGGTGTAACACTGCTTTGTATG		
ASV81 6	GGGATAAAAGTCATCACGTGTATTGTTGCA GGTACCATACGAATAAGGACCGGCTAATCCG TGCCAGCAGCCCGGTAAATACGGAAGGTCCG GGCGTTATCCGGATTATTGGGTTAAAGGGA GCGTAGGCCGGAGATTAAGTGTGTTGTGAAAT	0 0 0 0 0 0 0 0 0 0 0 51 23 18 0 41 23 0 0 10 0 26 0 8 5 0 0 3	

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ASV82 1	TGGGTGTAAAGGGAGCGTAGACGGAATGGCA AGTCTGAAGTGAAATACCGGGCTAACCTGG GAACTGCTTGGAAAATGTTCTAGAGTGT GGAGAGGTAAGTGAATTCCCTGGTGTAGCGGT GAAATGCGTAGATATCAGGAAGAACACCGGA GGCGAAGGCCGGCTACTGGACAATAACTGAC GTTGAGGCTCGAAAGCGTGGGATCAAACAG GATTAGATAC GCTGCAGTGGGAATATTGCACAATGGCGC AACCTGATGCAGCAACGCCGCGTGAAGGAT	0 0	0 0 79 82 54 52 84 75 0 15 39 2 7
ASV83 4	GAAGGCCTCGGGTTGAAACTCTGTCCTAG GGGAAGAAACAATGACATTACCCCTGGAGG AACCCCCGGCTAACTACGTGCCAGCAGCCGC GGTAATACTAGGGGGCGAGCGTTATCCGGA ATTATTGGCGTAAAGAGTGCCTAGGTGGCAC	0 0	0 0 12 76 0 17 33 10 0 11 30 3 1 1 3 0 5 4

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ASV84	2	GC GTT ATCCGGATT TATTGGGTTAAAGGGTGC	0	0	0	0	0	0	0	0	0	0	0	0	60
		GTAGGCCGTTGATAAGCGTGCTGTGAAATAT										0	0	0	2
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ASV85	2	AAGGATTCGGTTCGTAAGCTCTGTTAGG	0	0	0	0	0	0	0	0	0	11	0	44	41
		GAAGAATGATTGTATACTATACAGTA										0	1	61	15
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ASV86	GGCGTAAAGTGTCCGTAGTCTGAATTGAAAG	0	0	0	0	0	0	0	0	0	0	0	26	36
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ASV87	GGCGTAAAGGACCGTAGGCGGATTATCAA GTCTCTGTGAAATCCTATGGCTAACCATAGA ACTGCTTGGAAACTGATAATCTAGAGTGAGG GAGAGGCAGATGGAATTGGTGGTAGGGGT AAAATCCGTAGAGATCACCAAGGAATACCCATT GCGAAGGCGATCTGCTGGAACTCAACTGACGC TAATGCGTAAAGCGTGGGAGCAAACAGGA TTAGATAC	0 0 0 0 0 0 0 0 0 0	0 89 74 37 38 61 37 0 92 61	11 4
8				

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ASV89 3	GCTGCAGTGGGAATATTGACAATGGGG AACCTGATGCAGCGACGCCGCGTGAGTGA GAAGTATTCGGTATGTAAAGCTCTATCAGCA GGGAAGATAATGACAGTACCTGACTAAGAAG CCCCGGCTAACTACGTGCCAGCAGCCGGTA ATACGTAGGGGCAAGCGTTATCCGGATTAC TGGGTGTAAAGGGAGCGTAGACCGAATGGCA AGTCTGAAGTGAACCCGGGCTAACCTG GGGACTGCTTGGAAACTGTTGTTAGAGTGT TGGAGAGGTAAGTGGAAATTCTGGTAGCGG TGAAATGCGTAGATATCAGGAAGAACACCGG AGCGAAGCGGCTTACTGGACAATAACTGA	0 0 0 0 0 0 0 0 0 0	0 0 30 0 11 13 0 51 0 58 18 1 1

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ASV89	AGCGAGCGCAGGCCGTCAATTAAAGTCTGATGT	0	0	0	0	0	0	0	0	0	0	0	0	6	56	0	0	0	0	14
4	GAAAGCCCCCGGCTAACCGGGGAGGGTCAT																			7
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ASV89	CCCCGGCTAAATACGTGCCAGCAGCCCGGTA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0
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ASV90 5		0 0 0 0 0 0 0 0 0 0 0 37 0 0 74 92 13 9 0 0 95 99

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ASV90 6	TATTGGGCATAAAGGGCATCTAGGCGGCC CAAGTCAGGGGTGAAAACCTGCGGCTAAC GCAGGCCTGCCCTTGAAACTGATAGGCTGGAG TACCGGAGAGGTGGACGGAACTGCACGAGTA GAGGTGAAATTCTGTAGATATGTGCAGGAATGC CGATGATGAAGATAGTTCACTGGACGGTAAC GACGCTGAAGTGC GAAAGCCGGGGAGCGAA CAGGATTAGATACT	0 0 0 0 0 0 0 0 0 0	0 0 0 0 12 10 21 0 0 20 11 8 4 4 0 0 7	
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ASV96 4	AGCGTTATCCGGATTATTGGGTTAAAGGG ACCGTAGGCTGGAGATTAAGTGTGTTGTGAAA TGTAGACGCTCAACGCTCTGAATTGCAGGCCAT ACTGGTTCCCTGAGTACGCACAACGTTGGCG GAATTCGTCGTGTAGCGGTGAAATGCTTAGAT ATGACGAAGAACTCCGATTGCGAAGGCAGCT GACGGGAGCGCAACTGACGCTTAAGCTCGAA GGTGCGGGTATCAAACAGGATTAGATAC GCTGCAGTGGGAATTGCACAATGGGGGA AACCTGATGCAGCGACGCCGCGTGAGTGAA	0 0 0 0 0 0 0 0 0 0 0 12 0 0 0 38 0 0 26 0 38
ASV96 7	GAAGTATTCCGGTATGTAAGCTCTATCAGCA GGGAAGAAAATGACGGTACCTGAGTAAGAAG CCCCGGCTAACTACGTGCCAGCAGCCGCGGT ATACGTAGGGGCAAGCGTTATCCGGATTAC	0 0 0 0 0 0 0 0 0 0 0 23 54 79 0 0 0 0 79 0 0

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	GCTGCAGTGGGGATATTGCACAATGGAGGA AACTCTGATGCAGCGACGCCGCGTGAGTGAA GAAGTATTCCGGTATGTAAAGCTCTATCAGCA GGGAAGATGATGACGGTACCTGACTAAGAAG CCCCGGCTAACTACGTGCCAGCAGCCGCGGTA ATACGTAGGGGCAAGCGTTATCCGGATTAC	
ASV97 9	TGGGTGAAAGGGAGCGCAGGGCGTTGGCA AGTGAGAGTGGAAAGCAGGGGCTAACCCCC CTGACTGCTCCAAA ACTGTAAACTTGAGTA TGGGAGAGGCAGGCCGAATTCTAGTGTAGC GGTGAATGCTTAGATATTAGGAAGAACACC GGTGGCGAAGGC GGCTGCTGGACCAAAACT GACGCTGAGGCTCGAAGCGTGGTAGCAAAC CAGGATTAGATAAC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 39 0 43 0 0 79 10 5
ASV10 01	GCTGCAGTGGGAATATTGCACAATGGGGGA AACCTGATGCAGCGACGCCGCGTGAGTGAA GAAGTATTCCGGTATGTAAAGCTCTATCAGCA GGGAAGATAATGACAGTACCTGACTAAGAAG CCCCGGCTAACTACGTGCCAGCAGCCGCGGTA	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 33 0 53 32 39

	ATACGTAGGGGGCAAGCGTTATCCGGATTAC TGGGTGTAAAGGGAGCGTAGACGGAGTGGCA AGTCTGAAGTGAAAACCCTGGGCTTAACCTGG GGACTGCTTGGAAACTGTTAATCTAGAGTGTGTT GGAGAGGTAAGTGAATTCCCTGGTGTAGCGGT GAAATGCGTAGATATCAGGAAGAACACCGGA GGCGAAGGCCGCTTACTGGACAATAACTGAC GTTGAGGCTCGAAAGCGTGGGATCAAACAG GATTAGATAC		
	GCAGCAGTGGGAATATTGGACAATGGGGGG AACCTGATCCAGCGACGCCGCGTGAGTGA GAAGTATTCCGTATGAAAGCTCTATCAGCA GGGAAGAAAATGACGGTACCTGACTAAGAAG CCCCGGCTAACTACGTGCCAGCAGCCGGTA ATACGTAGGGGGCAAGCGTTATCCGGATTAC		
ASV10 10	TGGGTGTAAAGGGAGCGCAGACGGCTGGCA AGTCTGAAGTGAAAGCCGGGGCTTAACCCCG GGACTGCTTGGAAACTGTAAGCTAGAGTGT CGGAGAGGTAAGTGAATTCCCAGTGTAGCG GTGAAATGCGTAGATATTGGGAGGAACACCG GTGGCGAAGGCCGCTTACTGGACGATAACTG ACGTGAGGCTCGAAGCGTGGGAGCAAAAC AGGATTAGATAC	0 0 43 0 0 0 23 0 0 0 0 0 21 39 17 14 65 43 0 34 24	
ASV10 15	GCAGCAGCTAAGAATATTCCGCAATGGACGG AACTGACGGAGCGACGCCGCGTGATGAA GAAGGCTGAAAAGTTGAAATCCCTTTGTTG ATGAAGAATAAGGGTGAGAGGGAAATGCTCAT	0 0 0 0 0 0 0 0 0 0 0 0 0 0 46 52 11 0 0 89 17	

	CTGATGACGGTAATCGACGAATAAGCCCCGG CTAATTACGTGCCAGCAGCCGCGGTAAACACGT AAGGGCGAGCGTTGTCGAATTATTGGCG TAAAGGCATGTAGGCCGTTGTAAGCCTGG TGTGAAATCCTGGGCTTAACCCCAGAACATGC ATTGGGTACTGCACGACTTGAATTACGGAAGG GAAACTGGAATTCCAAGTGTAGGGGTGGAATC TGTAGATATTGGAAGAACACCGGTGGCGAAG GCGGGTTCTGGCCGATAATTGACGCTGAGAT GCGAAAGTGTGGGATCGAACAGGATTAGAT AC		
	GCAGCAGTGGGGATATTGCACAATGGGGGG AACCTGATGCAGCAACGCCGCGTGAGTGATG AAGGCCCTAGGTCGTAAGCTCTGCGTATG GGAAGAAACAAATGACTGTACCATAAGAA AGCCCCGGCTAACTACGTGCCAGCAGCCCG GTAATACGTAGGGGCAAGCGTTATCCGAAT		
ASV10 50	TACTGGCGTAAAGGGTGCCTAGGCGGCTAAT TAAGTCGAGGTAAAAGGCAGTAGCTCAACTA TTGTTGGGCCTGAAACTAATTAGCTTGAGTAT AGGAGAGGAAAGTGGATTCCCGTGTAGCG GTGAAATGCGTAGATATCGGGAGGAATACCG GTGGCGAAGGCAGTTCTGGACTATAACTGA CGCTGAGGCACGAAAGCGTGGGTAGCAAACA GGATTAGATAC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 17 4 0 31 49 5	
ASV11 01	GCTGCAGTGAGGAATATTGGACAATGGTCGGA AGACTGATCCAGCCATGCCGCGTGCAGGAAG	0 0 0 0 0 0 0 0 0 0 0 0 26 40 0 0 0 83 28	

	ACGGCCTATGGGTTGAAACTGCTTGCAGG GGAAGAATAAGGAGTACGTGACTTGATGAC GGTACTCTGCGAATAAGCATCGCTAACCCG TGCCAGCAGCCGCGGTAAATACGGAGGATGCG AGCGTTATCCGAATCATTGGTTAAAGGGT CCGTAGGCGGGCTAATAAGTCAGAGGTGAAA GCGCTCAGCTCAACTGAGCAACTGCCTTGAA ACTGTTAGTCTGAATGGTGTGAAGTAGTTGG AATGTGTAGTGTAGCGGTGAAATGCTTAGATA TTACACAGAACACCGATAGCGAAGGCATATT ACTAACAAATTAAATTGACGCTGATGGACGAAAG CGTGGGGAGCGAACAGGATTAGATAC GCTGCAGTAGGAAATTGCGCAATGGGGGA AACCTGACGCAGCAACGCCGCGTGGAGGAT GACACTTTCCGGAGCGTAAACTCCTTGTAG GGAAGAATAATGACGGTACCTAACGAATAAG CACCGGCTAACTCCGTGCCAGCAGCCGCGTA ATACGGAGGGTGCAGCGTTACTCGGAATCAC		
ASV11 53	TGGCGTAAAGGACCGTAGGCGGATTATCA AGTCTCTGTGAAATCTAGTGGCTTAACCACTA AACTGCTTGGAAACTGATAATCTAGAGTAAG GGAGAGGCAGATGGAATTCTTGGTGTAGGGT AAAATCCGTAGAGATCAAGAAGAATACTTATT GCGAAGGCGATCTGCTAGAACTTAACTGACGC TAATGCGTAAAGCGTGGGAGCAAACAGGA TTAGATAC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 17 0 0 47 0 5 0 32	
			1

	GCTGCAGTGAGGAATATTGGACAATGGTCGGA AGACTGATCCAGCCATGCCCGTGCAGGATGA AGGTCTATGGATTGAACTGCTTTGTAAGG GAAGAATAAGGAGTACGTGTACTTGATGACG GTACCTTACGAATAAGCATCGGCTAACTCCGT GCCAGCAGCCCGGTAATACGGAGGATGCGA																								
ASV11 58	CGCTTATCCGGAATCATGGGTTAAAGGGTC CGTAGGCGGCTGATAAGTCAGAGGTGAAAG CGCTTAGCTCAACTAACGAACTGCCCTTGAAA CTGTCAGTCTGAATGATTGTGAAGTAGTTGG AATGTGTAGTGTAGCGGTGAAATGCTTAGATA TTACACAGAACACCGATAGCGAAGGCATATT ACTAACAAATTATTGACGCTGATGGACGAAAG CGTGGGGAGCGAACAGGATTAGATAC GCTGCAGTGGGAATCTCCGCAATGGCGCA AGCCTGACGGAGCAACGCCCGTGAAG AAGGTCTTCGGATCGTAAAGCTCTGTTGACGG GGACGAACGTGCGGGGTGCGAATAGCGCTTG TAATGACGGTACCTGTCGAGGAAGGCCACGGCT AACTACGTGCCAGCAGCCCGGTAAACGTA GGTGGCGAGCGTTGTCGGAAATCATGGCGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	36	0	0	14	0	15 5	20		
ASV11 61	AAAGGGAGCCAGGCCGGCGGTAAAGCTTA CTTAAAAGTGCAGGGCTCAACCCCGTATGGG AGAGAAACTATCGGTCTTGAGTACAGGAGAG GAAAGCGGAATTCCCAGTGTAGCGGTGAAAT GCGTAGATATTGGAAAGAACACCAACTGGCGA AGGCGGTTCTGGACTGCAACTGACGCTGAG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23	34	0	68	0	38	0	0	0

	GCTCGAAAGCCAGGGAGCGAACGGGATTAG																				
	ATAC																				
	GCAGCAGTAGGGAATCTCGCAATGGGGGG																				
	AACCCTGACCGAGCAACGCCGCGTGAGTCAA																				
	GAAGGTTTCGGATCGTAAGCTCTGTTCAA																				
	GAGAAGAACGGGTGTGAGAGTGGAAAGTTCA																				
	CACTGTGACGGTATCTTACCAAGAAAGGGACGG																				
	CTAACTACGTGCCAGCAGCCGGTAATACGT																				
	AGTCCCAGCGTTGCCGGATTATTGGCG																				
	TAAAGCGAGCGCAGGCAGTTAGATAAGTCTG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	42	0	1	3	7	
ASV13 29	AAGTTAAAGGCTGTGGCTTAACCATACTACGC																	35	2	0	0
	TTTGGAAACTGTTAACCTGAGTGCAGAAGGG																				
	GAGAGTGAATTCCATGTGTAGCGGTGAAATG																				
	CGTAGATATGGAGGAACACCCGGTGGCGAA																				
	AGCGGCTCTGGTCTGTAACTGACGCTGAGG																				
	CTCGAAAGCGTGGGAGCAAACAGGATTAGA																				
	TAC																				
	GCAGCAGTGAGGAATATTGGTCAATGGCGA																				
	GAGCCTGAACCAGCCAAGTAGCGTGCAGGAT																				
	GACGGCCCTCCGGGTGAAACTGCTTTAGTT																				
	GGGAATAAAAAAAGGACTTGTCCCTTCTGT																				
ASV13 63	ATGTACCTTCAGAAAAAGGACCGGCTAATTCC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14	4	0	1
	GTGCCAGCAGCCGCGTAATACCGAAGGTCC																	0	0	0	0
	AGGCATTATCCGGATTATTGGGTTAAAGGG																				
	AGCGTAGGCGGATTGTTAAGTCAGCGGTTAAA																				
	GGGTGTGGCTAACCATACATTGCCGTTGAAA																				
	CTGGCGATCTGAGTGCAGACAGGGATGCCGG																				

	AATTCTGGTGTAGCGGTGAAATGCTTAGATA TCACGAAGAACACTCCGATCGCGAAGGCAGGTG TCCGGGCTGCAACTGACGCTGAGGCTCGAAAG TGTGGGTATCAAACAGGATTAGATAC ASV14 05	GCAGCAGCTAAGAACATTCCGCAATGGCGC AAGCCTGACGGAGCGACGCCCGCTGAATGAA GAAGGCCGAAAGGTTGAAATTCTTTAAGT TTGAAGAACAAACCAGTATAGGAAATGATACTG AGATGACGGTAAAATTGAATAAGCCCCGGCT AATTACGTGCCAGCAGCGCGTAACACGTA AGGGCGAGCGTTGTCGAATTATTGGCGT AAAGGGTATGCAGGCGTTAGATAAGCCGG 0 7 0 0 10 0 40 13
	AC GCAGCAGTAGGAAATCTCGCAATGGACGA AACTCTGACCGAGCAACGCCCGCTGAGTGAA GAAGGTTTCCGATCGTAAAGCTCTGTTGAA ASV14 14	GAAGAACAGGGTGTGAGAGTGGAAAGTCA 0 0 0 0 0 0 0 0 0 0 1 2 23 37 0 0 0 2 0 0 CACTGTGACGGTATCTTACCAAGAAAGGGACGG CTAACTACGTGCCAGCAGCGCGCTAATACGT AGGTCCCAGCGTTGCCGGATTATTGGCG TAAAGCGAGCGCAGCGGTTAGATAAGCTG

	AAGTAAAGGCTGTGGCTAACCATAGTACGC TTGGAAACTGTTAACCTGAGTGCAGAAGGG GAGAGTGAATTCCATGTGTAGCGGTGAAATG CGTAGATATGGAGGAACACCGGTGGCAA AGCGGCTCTGGTCTGTAACTGACGCTGAGG CTCGAAAGCGTGGGAGCAAACAGGATTAGA TAC		
	GCAGCAGTGGGGATATTGCACAATGGAGGA AACTCTGATGCAGCGACGCCGCGTGAGTGA GAAGTATTCGGTATGTAAGCTCTACAGCA GGGAAGAAAGACTCGAAAGAGAGATGACGGT ACCTGACTAAGAAGCTCCGGCTAAATACGTGC CAGCAGCCGCGTAATACGTATGGAGCAAGC		
ASV14 73	GTTATCCGATTACTGGGTGAAAGGGAGCG CAGACGGTTATGCAAGTCTGAAGTGAAAAAC CACGGCTCAACTGTGGTCTTGCTTGGAAACT GTGTAACTAGAGTGTCCGAAGGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATCGTAGATAT TAGGAAGAACACCGGAGGCCAAGGCGCTTA CTGGACGATAACTGACGTTGAGGCTCGAAGGC GTGGGTAGCAAACAGGATTAGATAC GCTGCAGTAGGAAATCTTCACAATGGCGAA AGCCTGATGGAGCAACGCCGCGTCAGGATG	0 0 0 0 0 0 0 0 0 0 0 0 0 6 69 0 0 0 0 3 0 13	
ASV15 69	AAGGCCTCGGGTTGTAAGTGTCTTATAAG CGAGAAATATGATGGTAACCTATGAATAAGG ATCGGCTAACTACGTGCCAGCAGCCGCGGTCA TACGTAGGATCCGAGCATTATCCGGAGTGA	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 18 0 8 0 0 20 37	

	GGGTGTAAGAGTTGCGTAGGTGGCATAGTAA																			
	GTAGATAGTGAAATCTGGTGGCTAACCATTC																			
	AGACTATTATCTAAACTGCTAAGCTCGAGACC																			
	GTTAGGGTAACTGGAATTCTAGTGTAGGAG																			
	TGAAATCCGTAGATATTAGAAGGAACACCGAT																			
	AGCGTAGGCAGGTTACTGGGACGGTTCTGACA																			
	CTAAGGCACGAAAGCGTAGGGAGCAAACGGG																			
	ATTAGATAC																			
	GCAGCAGTGGGAATATTGGCAATGGGAGG																			
	AATCCTGACCCAGCGACGCCGCGTGAACGAA																			
	GACGGCCTTCGGGTTGAAAGTCTTTATGTG																			
	GGAAGAAGGAAGTGACGGTACCATGAATA																			
	AGCCCCGGCTAACTACGTGCCAGCAGCCCG																			
	GTAATACGTAGGGGGAGCGTTGTCCCGAAT																			
ASV16	TAATGGCGTAAAGGGCACGCAGGCTGTGCTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	5	39	0	0
00	CAAGTCAGCTGTAAAAGGATGCGGCTTAACCG																		25	0
	TGTTATGCAGTTGAGACTGAGGTGCTGGAGTA																			0
	CCGGAGAGGCAAGTGGAATTCCCAGTGTAGC																			0
	GGTGAAATGCGTAGATATTGGGAAGAACATC																			0
	GGTGGCGAAGGCGACTTGCTGGACGGTAAC																			0
	ACGCTGAGGTGCGAAAGCCAGGGTAGCGAAC																			0
	GGGATTAGATAC																			0

**p*-value<0.05; #*p*-value<0.1.

Table S4. Description of the sequencing run and processing

Sample Code	Group	Input reads	Quality- filtered reads	Denoised reads Forward	Denoised reads Reverse	Paired- end merged reads	Non- chimeric reads	Final reads
56	Control	79908	62444	61829	62032	60519	54601	54601
58	Control	102243	78502	77419	77831	75389	71334	71334
60	Control	99651	71118	69912	70317	67779	64016	64016
65	Control	124833	91466	90088	90755	87173	82955	82955
67	Control	115307	84464	82861	83501	79513	76139	76139
69	Control	92486	67008	65412	66120	62136	59336	59336
73	Control	105805	80748	79740	80065	77069	70409	70409
75	Control	108758	81360	80240	80733	78720	76665	76665
77	Control	91382	67852	66682	67191	64834	63685	63685
82	Control	97737	72821	72294	72476	71252	68432	68432
85	Control	89930	65055	63228	64049	60371	57376	57376
116	UC	149803	116075	114284	114992	110618	101948	101948
118	UC	141359	111029	109818	110277	106798	93466	93466
120	UC	136138	96031	94148	94952	90306	82309	82309
122	UC	109042	84824	84002	84063	82794	78065	78065
124	UC	103869	75887	75533	75616	74393	70769	70769
126	UC	118484	87416	86804	87006	85449	83263	83263
128	UC	152860	115980	113633	114896	109248	99097	99097
130	UC	136590	104676	103532	103926	100432	93799	93799
132	UC	131378	93634	92659	93269	91037	80523	80523
134	UC	116715	86682	85498	86083	82568	75494	75494

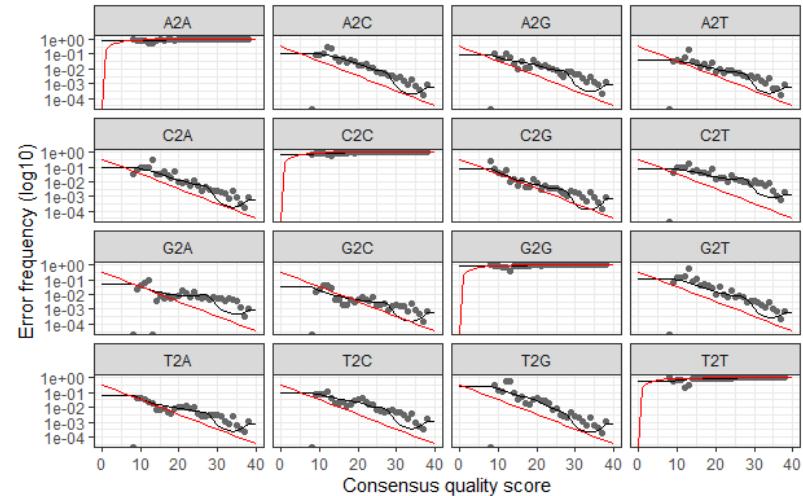


Figure S1. Plot showing error rates for each possible transition ($A \rightarrow C$, $A \rightarrow G$, ...) (Points are the observed error rates for each consensus quality score). The black line shows the estimated error rates after convergence of the machine-learning algorithm. The red line shows the error rates expected under the nominal definition of the Q-score. Here the estimated error rates (black line) are a good fit to the observed rates (points), and the error rates drop with increased quality as expected.

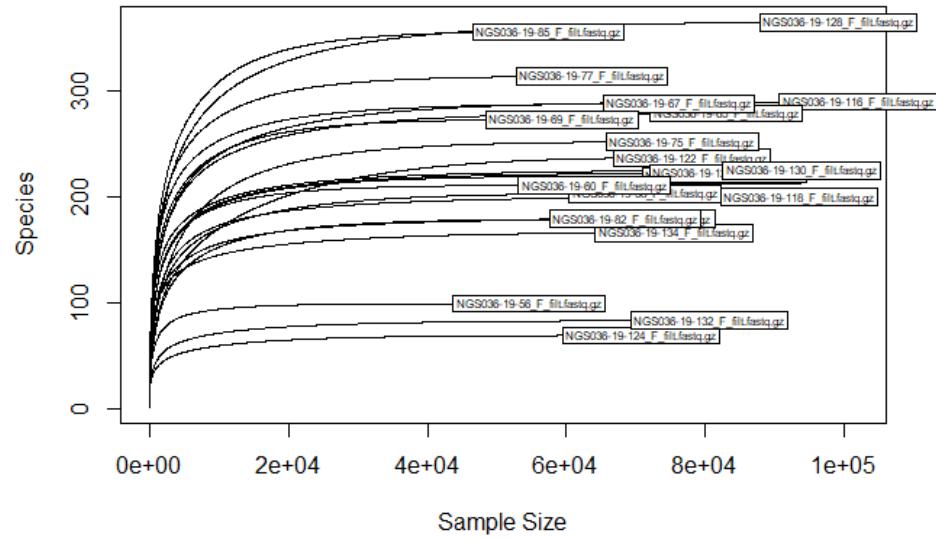


Figure S2. Rarefaction curves per sample that show the sequencing depth of the study.