Table S1. Characteristics of lung explant samples

procedure index*	recipiant Dx	sample site
1	CF	airway
2	CF	airway
3	ILD	airway
4	ILD	airway
5	IPF	airway
6	CF	airway
1	CF	mucous
3	ILD	mucous
6	CF	mucous
7	COPD	mucous
1	CF	lobe
2	CF	lobe
3	ILD	lobe
4	ILD	lobe
6	CF	lobe
4	ILD	donor trachea
4	ILD	mucous

CF-cystic fibrosis
ILD-interstitial lung disease
IPF-idiopathic pulmonary fibrosis
COPD-chronic obstructive pulmonary disease
* each sample with the same procedure index number was obtained in a single procedure from a single patient

Table S2. Phylum-level taxon occurrence by study subject (taxa with >10 total reads)

	CT1	CT2	CT3	CT4	CT5	CT6	CT7	CT8	CT9	CF1	CF2	CF3	CF4	CF5	CF6	CF7	CF8	CF9	CF10	CF11	CF12	CF13	CF14	CF15	CF16
Firmicutes	4292	503	731	3766	2123	6614	8787	7228	15044	2523	1037	23508	273	26161	1976	2784	1193	6433	1443	4320	698	8957	22988	6324	7231
Actinobacteria	312	48	51	519	251	1361	1354	668	2513	727	520	11388	2348	12886	1483	139	832	2731	775	1103	100	1817	1752	2560	4247
Proteobacteria	2044	116	385	1212	190	2217	2153	195	472	0	1173	4	132	7805	1010	3651	12	118	920	231	7022	507	125	2535	361
Bacteroidetes	1615	615	74	2333	489	1176	808	1015	4349	144	275	2341	63	880	244	294	90	234	68	137	309	371	696	357	90
no_assignment	470	84	29	213	923	214	100	42	62	65	137	705	32	642	284	200	55	124	35	35	26	31	86	159	78
Fusobacteria	46	244	95	609	166	787	545	262	478	4	4	21	0	143	2	57	0	39	32	0	23	0	18	47	1
TM7	92	22	16	34	44	214	114	24	532	17	7	134	0	5	5	9	0	1	14	15	7	4	0	6	14
SR1	0	77	4	2	38	32	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetes	0	2	0	46	4	4	2	48	0	0	0	0	0	3	0	0	0	1	0	0	0	0	4	1	0
Aquificae	76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanobacteria	23	0	4	0	0	10	0	5	0	8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Tenericutes	0	1	0	15	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0
Caldiserica	29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi	16	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteria	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planctomycetes	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crenarchaeota	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S3. Family-level taxon occurrence by study subject (taxa with >10 total reads)

	CT1	CT2	CT3	CT4	CT5	CT6	CT7	CT8	CT9	CF1	CF2	CF3	CF4	CF5	CF6	CF7	CF8	CF9	CF10	CF11	CF12	CF13	CF14	CF15	CF16
Streptococcaceae	2203	122	383	2461	1541	3976	7115	5267	9127	1588	817	16865	186	13222	1489	2532	693	6202	994	3485	596	4387	5045	3915	4712
Micrococcaceae	86	11	40	280	169	792	695	477	1386	671	431	11197	1561	11999	541	94	491	2649	449	729	95	1640	1388	2259	3931
Staphylococcaceae	120	14	29	159	136	404	265	799	460	562	4	1590	12	9659	32	7	111	67	80	183	22	3503	16808	911	657
Pseudomonadaceae	0	0	0	2	0	0	0	0	0	0	1158	2	130	382	998	3643	12	105	760	1	7015	500	117	887	356
Prevotellaceae	1558	328	46	1535	209	626	586	881	4008	104	273	1000	63	577	212	199	26	78	50	12	141	213	551	113	74
no_assignment	633	295	111	530	1129	730	339	84	594	187	161	2013	54	1635	355	259	151	185	111	229	93	184	385	584	471
Veillonellaceae	1633	200	142	571	160	896	853	405	3458	118	167	662	51	465	245	13	115	78	93	0	14	121	47	51	0
Pasteurellaceae	137	36	102	297	22	596	1596	97	365	0	0	0	0	4732	0	0	0	0	59	210	0	0	1	368	0
Carnobacteriaceae	6	6	22	47	18	134	42	15	62	125	2	2385	0	1728	37	126	201	0	153	350	5	591	106	1015	1016
Neisseriaceae	102	63	274	180	163	1550	509	82	40	0	0	0	0	2640	0	0	0	11	93	7	1	0	3	1216	2
Actinomycetaceae	115	23	9	177	70	517	459	97	845	5	56	29	286	494	271	6	244	17	285	359	2	61	237	271	220
Lachnospiraceae	168	115	55	163	120	565	230	131	1255	3	33	197	0	134	56	17	2	37	44	0	27	42	167	49	2
Porphyromonadaceae	0	40	14	570	101	241	77	107	10	0	2	1254	0	148	0	84	44	72	6	0	104	137	87	165	7
Leptotrichiaceae	45	91	51	26	40	469	421	76	430	0	1	19	0	124	0	4	0	33	28	0	0	0	0	22	0
Fusobacteriaceae	1	153	44	583	126	318	124	186	48	4	3	2	0	19	2	53	0	6	4	0	23	0	18	25	1
Xanthomonadaceae	1530	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	1	0	5	0	0	0
TM7_genera_incertae_sedis	93	23	16	34	44	214	114	24	532	17	7	135	0	5	5	9	0	1	14	15	7	4	0	6	14
Bifidobacteriaceae	0	0	0	2	0	0	0	35	0	2	13	3	393	23	538	39	79	19	6	8	0	2	63	2	72
Erysipelotrichaceae	71	9	5	57	16	78	34	22	124	5	8	548	12	7	9	13	4	22	1	0	13	65	32	8	13
Lactobacillaceae	12	0	1	0	0	0	0	375	2	1	2	0	11	1	68	0	0	9	1	226	0	6	364	0	86
Coriobacteriaceae	0	13	1	28	6	23	138	39	220	0	9	5	86	38	99	0	4	3	10	2	1	103	49	2	0
Moraxellaceae	5	0	0	698	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Incertae Sedis XIII	13	9	2	8	9	52	50	7	252	0	0	0	0	4	6	6	0	2	14	0	2	58	125	7	0
Flavobacteriaceae	14	21	9	14	25	97	49	21	25	40	0	52	0	47	15	3	2	62	1	9	3	6	3	25	9
Aerococcaceae	0	0	2	2	0	17	0	17	0	0	0	0	0	132	0	0	0	0	0	0	4	0	0	1	365
Peptostreptococcaceae	0	2	0	89	10	50	25	90	3	0	0	98	0	6	0	7	0	0	2	0	14	27	0	14	0
Corynebacteriaceae	51	0	0	9	0	7	39	16	21	44	0	0	0	224	0	0	0	2	14	0	0	1	3	4	0
Campylobacteraceae	128	14	6	19	5	55	38	10	63	0	1	0	0	10	0	0	0	0	0	0	0	0	0	0	0
Incertae Sedis XI	0	2	1	49	18	60	14	39	7	0	2	0	0	6	0	6	0	5	1	0	0	14	46	5	1
Eubacteriaceae	0	8	0	17	17	35	14	10	68	0	0	0	0	0	0	0	0	0	7	0	0	12	12	2	0
SR1_genera_incertae_sedis	0	79	4	2	39	33	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spirochaetaceae	0	2	0	46	4	4	2	48	0	0	0	0	0	3	0	0	0	1	0	0	0	0	4	1	0
Propionibacteriaceae	43	0	1	3	2	8	0	1	4	0	0	1	1	2	13	0	0	0	0	1	2	1	1	1	0
Thermaceae	68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Comamonadaceae	58	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	1	0
Caulobacteraceae	0	3	0	0	0	7	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	52	0
Hydrogenothermaceae	51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chloroplast	10	0	4	0	0	10	0	5	0	8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Mycoplasmataceae	0	1	0	15	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0
Caldisericaceae	29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aquificaceae	25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Enterococcaceae	0	0	1	0	0	11	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	1	8
Cellulomonadaceae	0	0	0	0	0	0	0	0	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Burkholderiaceae	10	0	1	0	0	0	0	0	2	0	0	0	0	1	2	0	0	0	1	0	0	0	0	0	2
Anaerolineaceae	16	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peptococcaceae	0	0	1	0	2	8	3	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Alcaligenaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0	0	0
Cardiobacteriaceae	4	0	0	0	0	0	0	3	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Planctomycetaceae	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S4. Amplifiable microbial rDNA abundance in subject samples assessed by qPCR

16S rDNA QPCR	assay	Dx: sample	avg cp/mL	SEM cp/mL	n
ind. sputum	515F/1391R	CT: sputum	17,369,520	12,278,000	9
ind. sputum	515F/1391R	CF: sputum	21,950,320	5,333,440	16
lung explant	515F/907R	CF: airway	39,995,368	23,091,336	3
lung explant	515F/907R	CF: mucus	145,484,398	102,873,004	2
lung explant	515F/907R	CF: lower lobes	22,975,629	13,264,986	3
lung explant	515F/907R	DC: airway	8,543,071	4,932,344	3
lung explant	515F/907R	DC: mucus	6,411,453	3,701,654	3
lung explant	515F/907R	DC: lower lobes	43,117,254	30,488,503	2

rDNA: ribosomal DNA
qPCR: quantitative polymerase chain reaction
Dx: diagnoisis
SEM: standard error of the mean

Table S5. List of microbial families represented as matching in “presence” or “absence” status in comparisons between sputum cohorts and explant cohort

family name / RDP ID	coverage of CT sputum by explant	coverage of CF sputum by explant
Acetobacteraceae	status match	status match
Actinomyces	status match	status match
Actinomycetaceae	status match	status match
Aerococcaceae	status match	status mismatch
Aeromonadaceae	status match	status match
Alcaligenaceae	status match	status match
Alicyclobacillaceae	status match	status match
Anaerolineaceae	status match	status match
Anaerosphaera	status match	status match
Aquificaceae	status match	status match
Atopobium	status match	status match
Bacillaceae	status match	status match
Bacteroidales_incertae_sedis	status match	status match
Bavariicoccus	status match	status match
Beijerinckiaceae	status match	status match
Bifidobacteriaceae	status match	status mismatch
Bradyrhizobiaceae	status match	status match
Brevibacteriaceae	status match	status match
Burkholderiaceae	status match	status match
Burkholderiales_incertae_sedis	status match	status match
Caldisericaceae	status match	status match
Calditerrivibrio	status match	status match
Campylobacteraceae	status mismatch	status match
Cardiobacteriaceae	status match	status match
Carnobacteriaceae	status match	status match
Catonella	status match	status match
Caulobacteraceae	status match	status match
Cellulomonadaceae	status match	status match
Chitinophagaceae	status match	status match
Chloroplast	status mismatch	status mismatch
Chloroplast	status match	status match
Chromatiaceae	status match	status match
Clostridiaceae	status match	status match
Comamonadaceae	status match	status match
Coriobacteriaceae	status mismatch	status mismatch
Corynebacteriaceae	status match	status match
Cryomorphaceae	status mismatch	status mismatch
Cyclobacteriaceae	status match	status match
Cystobacteraceae	status match	status match
Cytophagaceae	status match	status match
Deferribacteraceae	status match	status match
Deinococcaceae	status match	status match
Dermacoccaceae	status match	status match
Desulfovibrionaceae	status match	status match
Dictyoglomaceae	status match	status match
Dietziaceae	status match	status match
Enterobacteriaceae	status match	status match
Enterococcaceae	status match	status match
Erysipelotrichaceae	status mismatch	status mismatch
Eubacteriaceae	status mismatch	status match
Eubacterium	status match	status match
Family I	status match	status match

Family VI	status match	status match
Family_II	status match	status match
Filifactor	status match	status match
Flavobacteriaceae	status match	status match
Fusobacteriaceae	status match	status match
Fusobacterium	status mismatch	status match
Gemella	status match	status match
Gemmatimonas	status match	status match
Gp1	status match	status match
Gp2	status match	status match
Gp3	status match	status match
Helicobacteraceae	status match	status match
Hydrogenophilaceae	status match	status match
Hydrogenothermaceae	status match	status match
Hyphomicrobiaceae	status match	status match
Iamiaceae	status match	status match
Incertae Sedis XI	status mismatch	status match
Incertae Sedis XIII	status mismatch	status mismatch
Incertae Sedis XIV	status match	status match
Incertae_Sedis_XI	status match	status match
Ktedonobacteraceae	status match	status match
Lachnospiraceae	status mismatch	status mismatch
Lactobacillaceae	status match	status match
Lactobacillaceae	status mismatch	status mismatch
Leptotrichia	status match	status match
Leptotrichiaceae	status match	status match
Listeriaceae	status match	status match
Methylobacteriaceae	status mismatch	status mismatch
Microbacteriaceae	status match	status match
Micrococcaceae	status match	status match
Micromonosporaceae	status match	status match
Moraxella	status match	status match
Moraxellaceae	status mismatch	status match
Mycobacteriaceae	status match	status match
Mycoplasma	status match	status match
Mycoplasmataceae	status match	status match
Neisseriaceae	status match	status match
Nitrospiraceae	status match	status match
Nocardiaceae	status match	status match
OP10_genera_incertae_sedis	status match	status match
Oribacterium	status match	status match
Oxalobacteraceae	status match	status match
Pasteurellaceae	status mismatch	status mismatch
Peptococcaceae	status match	status match
Peptostreptococcaceae	status match	status match
Phyllobacteriaceae	status match	status match
Planctomycetaceae	status match	status match
Polyangiaceae	status match	status match
Porphyromonadaceae	status match	status match
Prevotella	status match	status match
Prevotellaceae	status match	status match
Propionibacteriaceae	status match	status match
Pseudomonadaceae	status match	status mismatch
Rhodobacteraceae	status match	status match
Rhodocyclaceae	status match	status match
Rhodospirillaceae	status match	status match
Rothia	status match	status match
Ruminococcaceae	status match	status match

Shewanellaceae	status match	status match
Solobacterium	status match	status match
Sphingobacteriaceae	status match	status match
Sphingomonadaceae	status match	status match
Spirochaetaceae	status mismatch	status match
SR1_genera_incertae_sedis	status mismatch	status match
Staphylococcaceae	status match	status match
Streptococcaceae	status match	status match
Subdivision3_genera_incertae_sedis	status match	status match
Syntrophobacteraceae	status match	status match
Thermaceae	status match	status match
Thermodesulfobacteriaceae	status match	status match
Thermodesulforhabdus	status match	status match
TM7_genera_incertae_sedis	status mismatch	status mismatch
Treponema	status match	status match
unclassified 0.1.2.9.1.1	status match	status match
unclassified 0.1.5.1.1.1	status mismatch	status mismatch
unclassified 0.2.14.1.1.7	status match	status match
unclassified 0.2.14.1.2.11	status match	status match
unclassified 0.2.14.1.3.1	status mismatch	status mismatch
unclassified 0.2.14.2.2.18	status match	status match
unclassified 0.2.14.2.5.1	status match	status match
unclassified 0.2.14.5.1.1	status mismatch	status mismatch
unclassified 0.2.2.1.10.1	status match	status match
unclassified 0.2.2.1.3.45	status match	status match
unclassified 0.2.20.1.11.3	status match	status match
unclassified 0.2.20.1.12.1	status mismatch	status mismatch
unclassified 0.2.20.1.6.15	status mismatch	status mismatch
unclassified 0.2.20.2.2.6	status match	status match
unclassified 0.2.20.2.8.1	status match	status match
unclassified 0.2.20.3.10.1	status match	status match
unclassified 0.2.20.3.8.8	status match	status match
unclassified 0.2.20.5.17.1	status match	status match
unclassified 0.2.20.6.1.1	status mismatch	status mismatch
unclassified 0.2.29.1.1.15	status mismatch	status mismatch
unclassified 0.2.36.1.1.1	status mismatch	status mismatch
unclassified 0.2.4.2.1.7	status match	status match
unclassified 0.2.4.3.1.8	status match	status match
unclassified 0.2.4.4.1.3	status match	status match
unclassified 0.2.4.5.1.1	status mismatch	status mismatch
unclassified 0.3.1.1.1.1	status mismatch	status mismatch
Veillonellaceae	status match	status match
Verrucomicrobiaceae	status match	status match
Xanthomonadaceae	status match	status match

Fig. S1. Plots of phylum abundances by cohort for the 12 phyla analyzed in Fig. 2

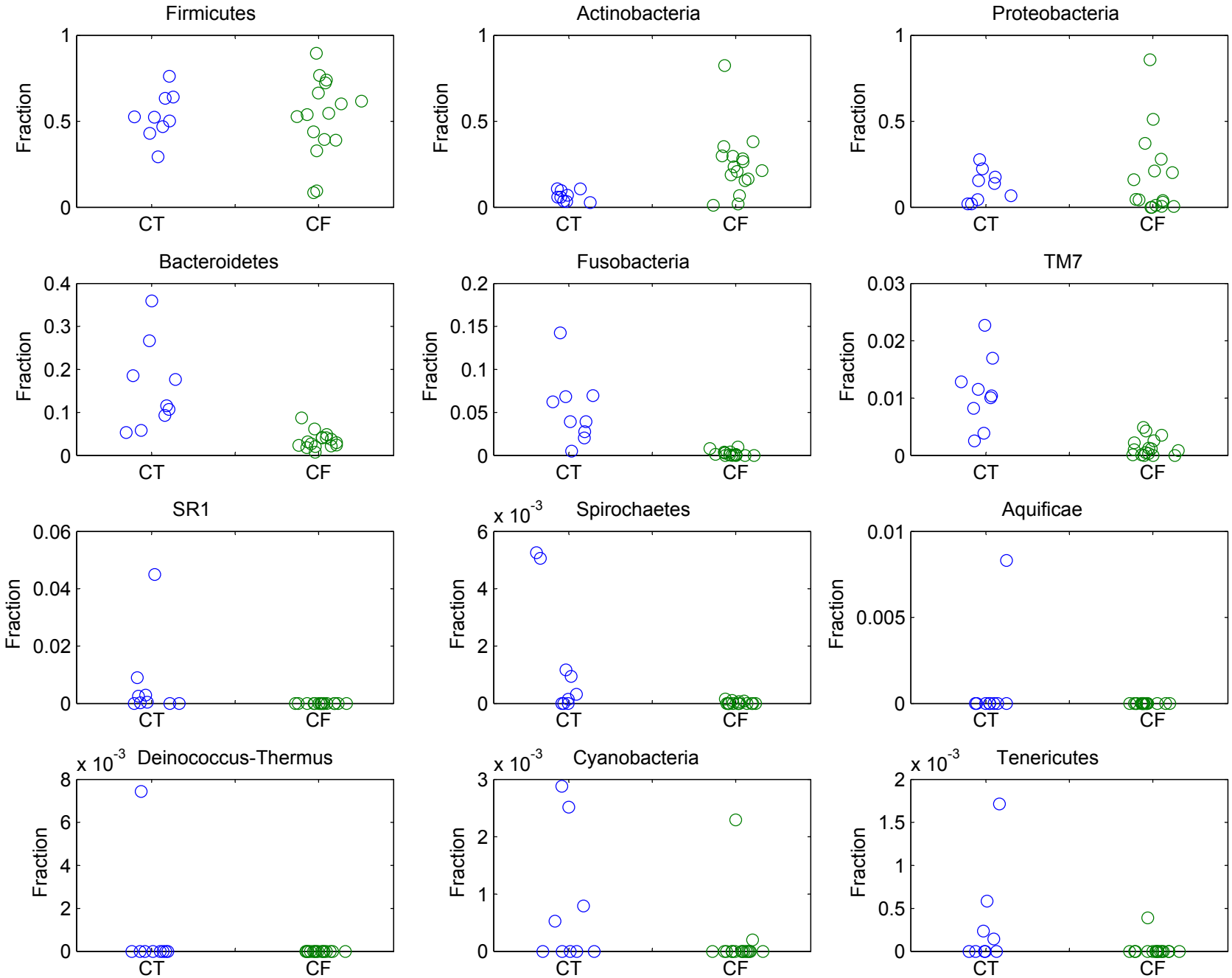


Fig. S2. Plots of family abundances by cohort for the 41 phyla analyzed in Fig. 2

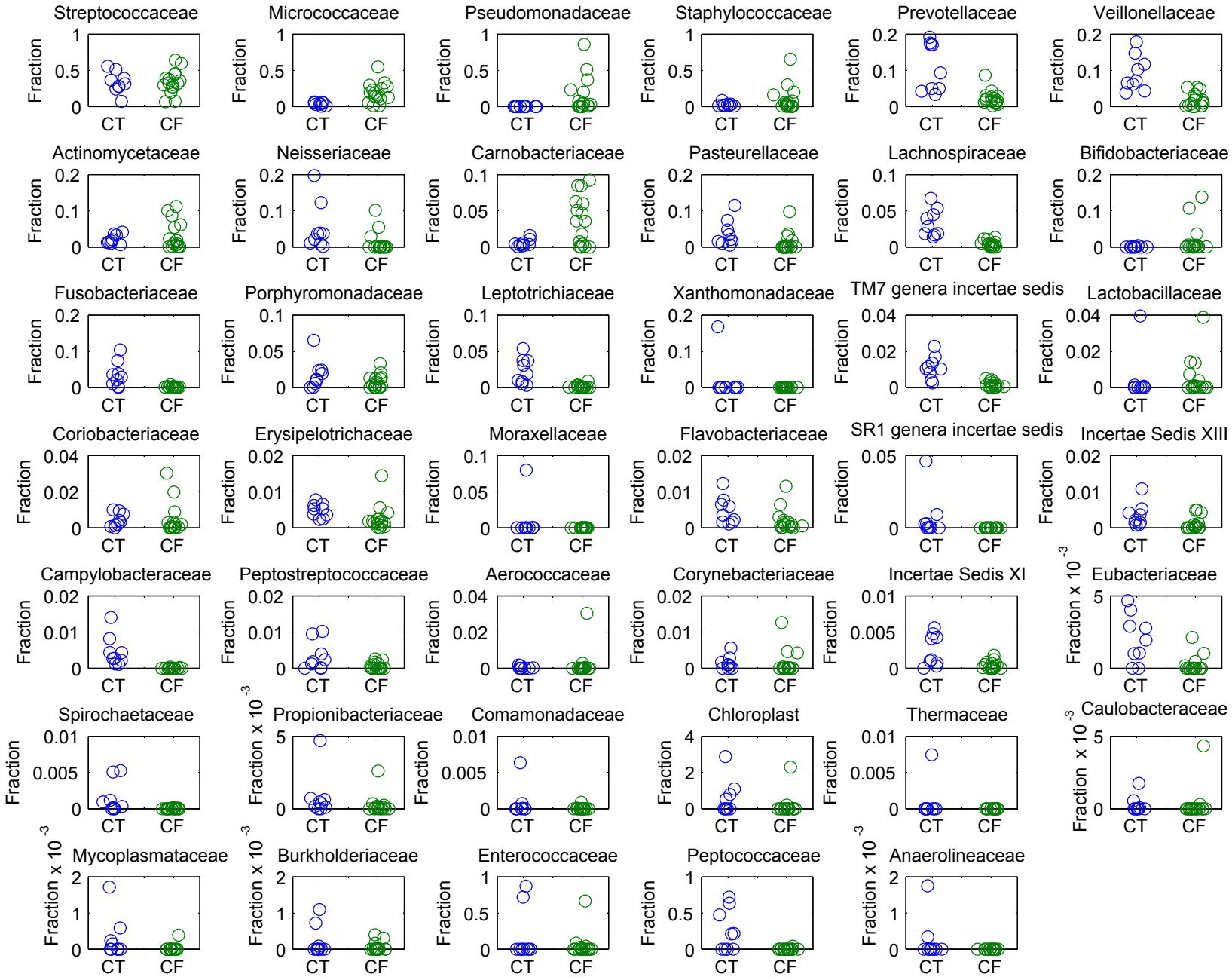


Fig. S3. Histogram of correlation coefficients among the clinical variables making up the index of inflammatory markers

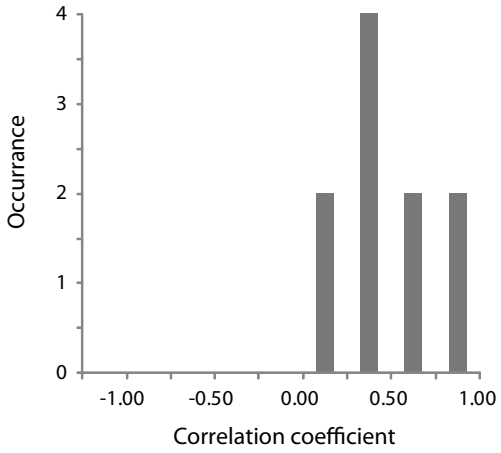
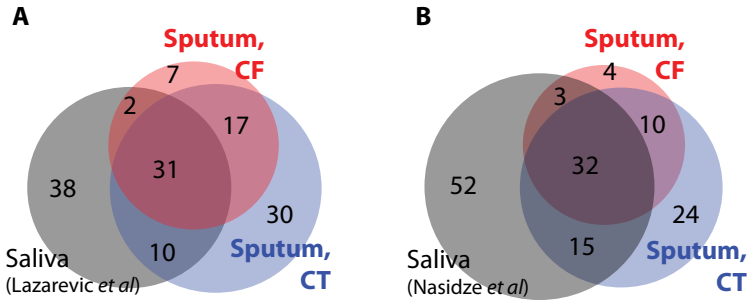


Fig. S4. Taxon occurrence in the sputum of the control and CF cohorts in comparison with saliva



number of unique and shared genera detected