SUPPLEMENTAL MATERIAL

Refining the Application of Microbial Lipids as Tracers of *Staphylococcus aureus* Growth Rates in Cystic Fibrosis Sputum

Cajetan Neubauer [a,b], Ajay S. Kasi [c], Nora Grahl [d], Alex L. Sessions [b], Sebastian H. Kopf [e], Roberta Kato [c], Deborah A. Hogan [d], Dianne K. Newman [a,b,#]

[a] Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, California, USA

[b] Division of Geological and Planetary Sciences, California Institute of Technology, Pasadena, California, USA

[c] Children's Hospital Los Angeles, Pediatric Pulmonology, Los Angeles, California, USA

[d] Department of Microbiology and Immunology, Geisel School of Medicine at Dartmouth, Hanover, New Hampshire, USA

[e] Department of Geological Sciences, University of Colorado, Boulder, Colorado, USA

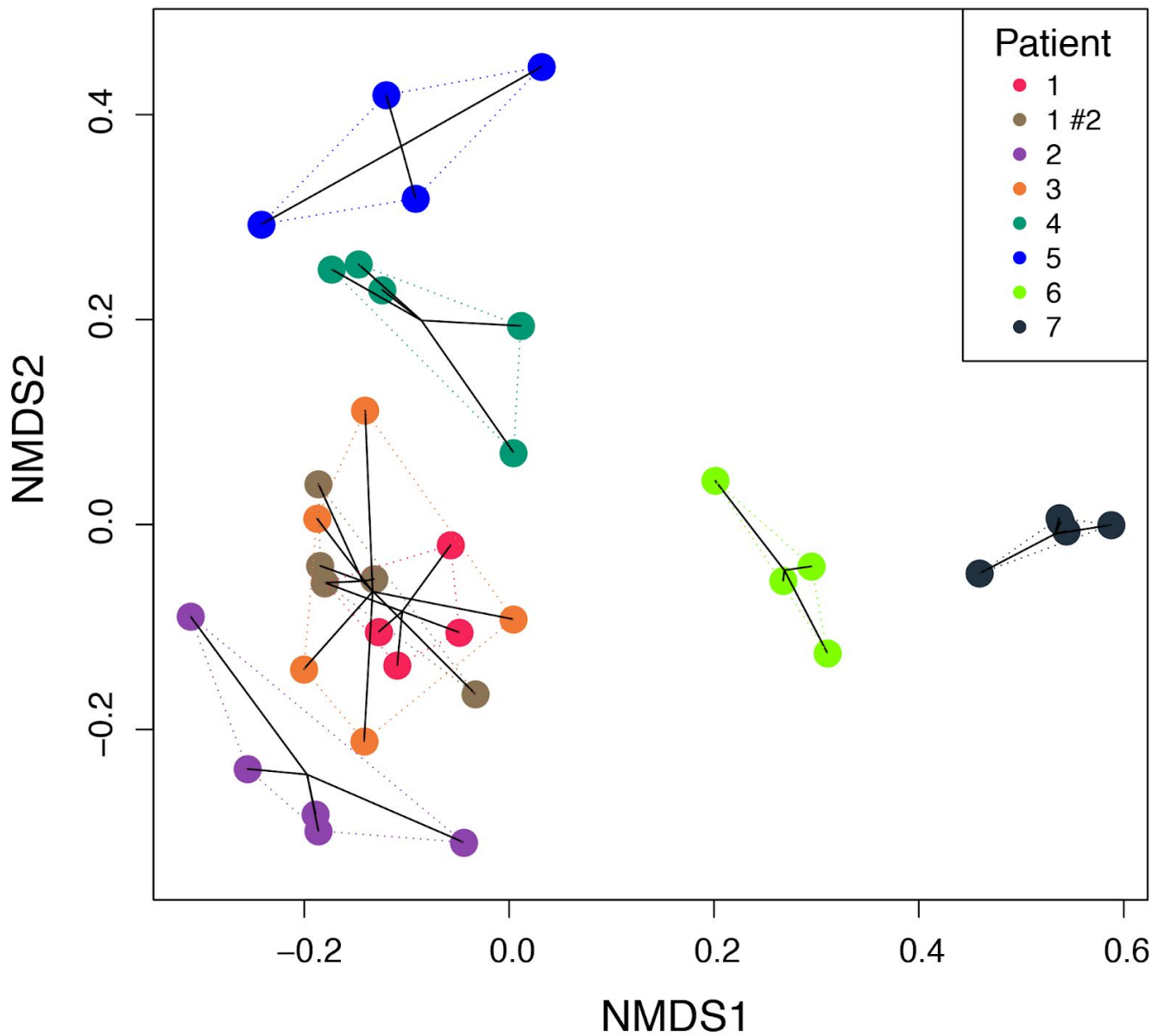**Contains: Fig. S1, Fig. S2, Table S1 and Table S2.**

FIG S1 – Microbial community analysis of CF sputum by nonmetric multidimensional scaling (NMDS; Stress=0.11) analysis of the NanoString data. Black lines connect each sample to the centroid of the Patient ID. The outline of all samples from a single Patient ID is indicated by dotted lines. Weighted species abundances (percentage value^0.25) were used to calculate Bray-Curtis dissimilarity. Patient ID contributed 82% to the observed variance in the dataset (PERMANOVA; $p < 0.001$).
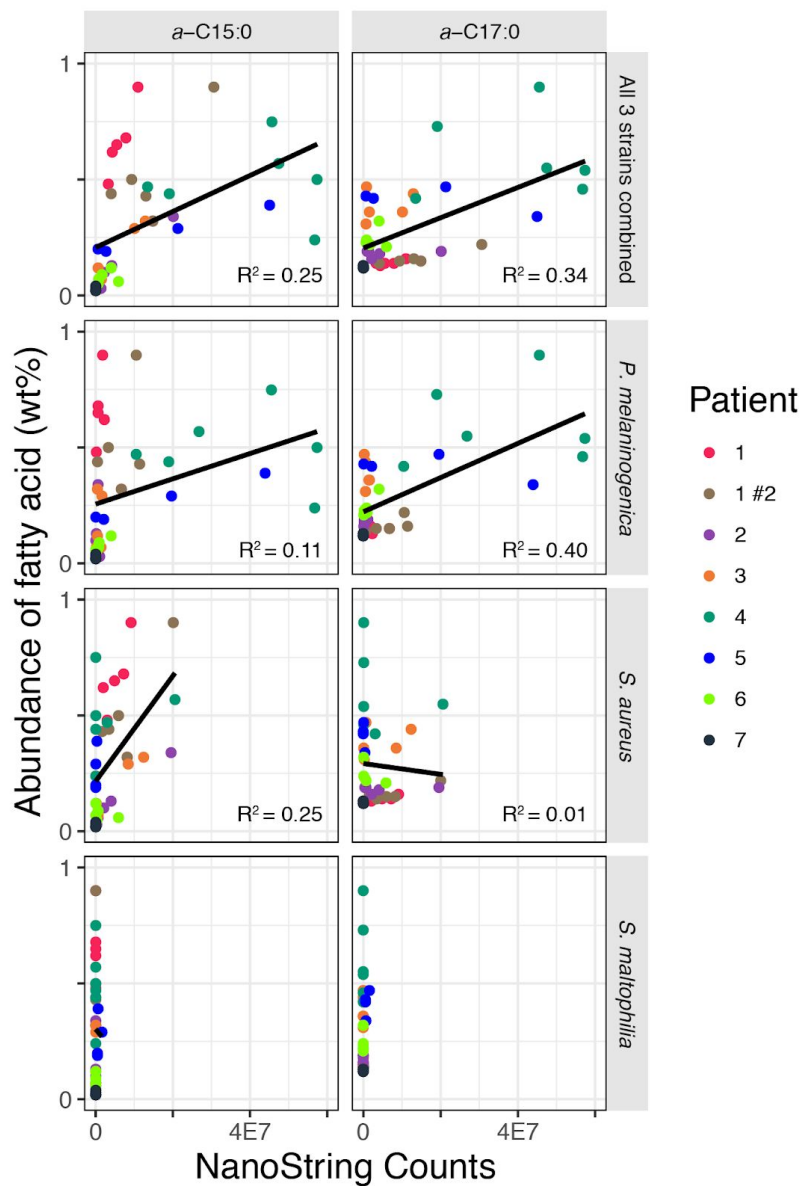
FIG S2 – The amount of *anteiso* fatty acids detected in CF sputum has a moderately positive correlation with microbial producers of *anteiso* fatty acids. Abundance of *anteiso* fatty acids relative to NanoString ribosomal RNA counts. Panels for *S. aureus*, *S. maltophilia* and *P. melaninogenica*, as well as the combined counts of all three strains, are shown for all samples of the longitudinal dataset.

TABLE S1 Study participant demographic information

Patient	1	1 #2	2	3	4	5	6	7	8	9	10
Age (yr)	9	9	19	12	14	17	14	17	17	22	17
Gender	F	F	M	M	M	M	M	F	F	F	M
Days Hospitalized	12	14	14	13	10	10	10	19	NA	14	NA
FEV1% (admission)	31	32	59	63	NA	77	43	25	NA	69	NA
FEV1% (discharge)	40	34	71	75	120	83	80	30	NA	80	NA
FEV1% (baseline)	34	34	70	80	118	86	74	36	50	75	25
BMI (percentile)	55	55	2	19	73	85	40	15	8	$21kg/m^2$	12

TABLE S2 Additional information about study participants

Patient	CFTR mutations	Days in hospital	Samples collected during hospitalization	Sputum sample at baseline health	CF sputum culture*
1	F508del, G408S	12	6	Y	MSSA, PA
1 (#2)	F508del, G408S	14	6	Y	MSSA, PA
2	3849+10kbC>T, 2183delAA>G	14	4	Y	MSSA, *Achromobacter xylosoxidans*
3	F508del, unknown	13	5	N	MSSA
4	F508del, N1303K	10	6	N	MSSA, mucoid PA
5	F508del, F508del	10	3	N	MSSA, PA
6	F508del, F508del	10	4	Y	MRSA, mucoid PA
7	F508del, 296+2T>A	19	6	N	MSSA, mucoid PA
8	F508del, I507del	0	0	Y	PA
9	F508del, 3171delC	14	1	N	MSSA, mucoid PA
10	G542X, G542X	0	0	Y	Achromobacter

*MSSA = Methicillin sensitive *Staphylococcus aureus*, PA = *Pseudomonas aeruginosa*

TABLE S2 (continued) Additional information about study participants

Patient	Non-tuberculous mycobacteria*	Antibiotics used	Chronic antibiotics	Baseline FEV1%	FEV1% Admission	FEV1% Discharge
1	N	Cefepime, Tobramycin	Azithromycin, Inhaled Tobramycin	34	31	40
1 (#2)	N	Cefepime, Tobramycin	Azithromycin, Inhaled Tobramycin	34	32	34
2	N	Piperacillin-Tazobactam, Inhaled Colistin	Azithromycin, Inhaled Tobramycin	70	59	71
3	N	Oxacillin, Cefepime, Tobramycin	Inhaled Tobramycin	80	63	75
4	*Mycobacterium abscessus*	Piperacillin-Tazobactam, Tobramycin	Inhaled Tobramycin	118	N/A	120
5	*Mycobacterium abscessus*	Piperacillin-Tazobactam, Tobramycin	None	86	77	83
6	N	Ceftazidime, Tobramycin, Vancomycin	Azithromycin, Inhaled Tobramycin, Inhaled Aztreonam	74	43	80
7	*Mycobacterium avium*	Amikacin, Meropenem, Ciprofloxacin	Inhaled Aztreonam, Inhaled Tobramycin	36	25	30
8	*Mycobacterium abscessus*	N/A	Azithromycin, Inhaled Amikacin	50	N/A	N/A
9	N	Cefepime, Tobramycin	Azithromycin, Inhaled Tobramycin, Inhaled Aztreonam	75	69	80
10	N	N/A	Inhaled Aztreonam, Inhaled Colistin	25	N/A	N/A

* N: not detected in culture

N/A indicates instances where no data was available