Supplemental Methods:

Sex as a biological variable: Both male and female participants were involved in this study. Females enrolled at slightly higher levels and therefore comprised 52.5% of the participants.

Statistics: The proportion of participants with a given pathogen at each timepoint was analyzed by McNemar's exact test. Significant changes in pathogen abundance were determined using mixed-effects analysis comparing pre-ETI to post-ETI timepoints and one month on ETI to later post-ETI timepoints. Summary statistics including mean, standard deviation, and proportion were used to describe the baseline characteristics of the cohort. All statistics were performed in Graphpad PRISM.

Study approval: Institutional review board approval was granted at each individual participating site. The study was registered at ClinicalTrials.gov (NCT04038047).

Data availability: Data are available in the "Supporting data values" XLS file.

Supplemental Acknowledgements

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All enrolled participants (N = 236)* Age (years), mean (SD) 24.8 (10.9) Age (years) distribution, n (%) 12 to < 18	able ST. Demographics and Basenne Characteristics by visits attended.		
Age (years) distribution, n (%) 12 to < 18 85 (36.0%) Age (years) distribution, n (%) 12 to < 18 79 (33.5%) 30 or older 72 (30.5%) 30 or older 72 (30.5%) Sex, n (%) Male 112 (47.5%) Female 124 (52.5%) Race, n (%) White 220 (93.2%) Black or African American 4 (1.7%) Asian 0 (0%) American Indian or Alaska Native 0 (0%) Native Hawaiian or Other Pacific Islander 1 (0.4%) More than One Race 9 (3.8%) Unknown/Missing 2 (0.8%) Hispanic or Latino, n (%) Yes ppFEV, mean (SD) 80.4 (22.4) ppFEV, mean (SD) 80.4 (22.4) ppFEV distribution, n (%) < 65 63 (26.7%) 63 (26.7%) 65 to 90 83 (35.2%) > 90 90 (38.1%) Sweat Chloride (mmol/L), mean (SD) 87.5 (17.9) Height (cm) [18+ y.o.], mean (SD) 65.0 (13.7) BMI (kg/m2) [18+ y.o.], mean (SD) 23.2 (4.1) Genotype Group, n (%) F508del Heterozygous (MFF) 97 (41.1%)<	least one post-	Baseline and at least 3 post- ETI (n= 127)	
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Hispanic or Latino, n (%) Yes 17 (7.2%) No 219 (92.8%) ppFEV, mean (SD) 80.4 (22.4) ppFEV distribution, n (%) < 65	7 (4.0%)	5 (3.9%)	
No 219 (92.8%) ppFEV, mean (SD) 80.4 (22.4) ppFEV distribution, n (%) < 65	1 (0.6%)	1 (0.8%)	
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ppFEV distribution, n (%) < 65) 164 (92.7%)	118 (92.9%)	
65 to 90 83 (35.2%) > 90 90 (38.1%) Sweat Chloride (mmol/L), mean (SD) 87.5 (17.9) Height (cm) [18+ y.o.], mean (SD) 167.2 (9.4) Weight (kg) [18+ y.o.], mean (SD) 65.0 (13.7) BMI (kg/m2) [18+ y.o.], mean (SD) 23.2 (4.1) Genotype Group, n (%) F508del Homozygous F508del Heterozygous (MF) 97 (41.1%) F508del Heterozygous (G551D) 14 (5.9%) F508del Heterozygous (G551D) 12 (5.1%) Prior Modulator Use, n (%) None 119 (50.4%) Pathogens detected pre-ETI, n (%) None detected 7 (3.4%) Achromobacter spp. 12 (5.8%) 12 (5.8%)	78.41 (22.5)	78.6 (23.0%)	
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Weight (kg) [18+ y.o.], mean (SD) 65.0 (13.7) BMI (kg/m2) [18+ y.o.], mean (SD) 23.2 (4.1) Genotype Group, n (%) F508del Homozygous F508del Heterozygous (MF) 97 (41.1%) F508del Heterozygous (G551D) 14 (5.9%) F508del Heterozygous (other) 12 (5.1%) Prior Modulator Use, n (%) None Orkambi or Symdeko 104 (44.1%) Kalydeco 13 (5.5%) Pathogens detected pre-ETI, n (%) None detected Achromobacter spp. 12 (5.8%)	88.0 (18.1)	87.8 (18.7%)	
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Kalydeco 13 (5.5%) Pathogens detected pre-ETI, n (%) None detected 7 (3.4%) Achromobacter spp. 12 (5.8%)) 85 (48.0%)	58 (45.7%)	
Pathogens detected pre-ETI, n (%)None detected7 (3.4%)Achromobacter spp.12 (5.8%)) 81 (45.8%)	62 (48.8%)	
Achromobacter spp. 12 (5.8%)	11 (6.2%)	7 (5.5%)	
	6 (3.4%)	4 (3.1%)	
Burkholderia spp. 8 (3.9%)	12 (6.8%)	8 (6.3%)	
	8 (4.5%)	6 (4.7%)	
Pseudomonas aeruginosa 90 (43.7%)) 79 (44.6%)	57 (44.9%)	
Staphylococcus aureus 154 (74.8%)) 135 (76.3%)	95 (74.8%)	
Stenotrophomonas maltophilia 39 (18.9%)) 32 (18.1%)	26 (20.5%)	

Table S1. Demographics and Baseline Characteristics by visits attended.

* Data on all enrolled participants previously published in (1)

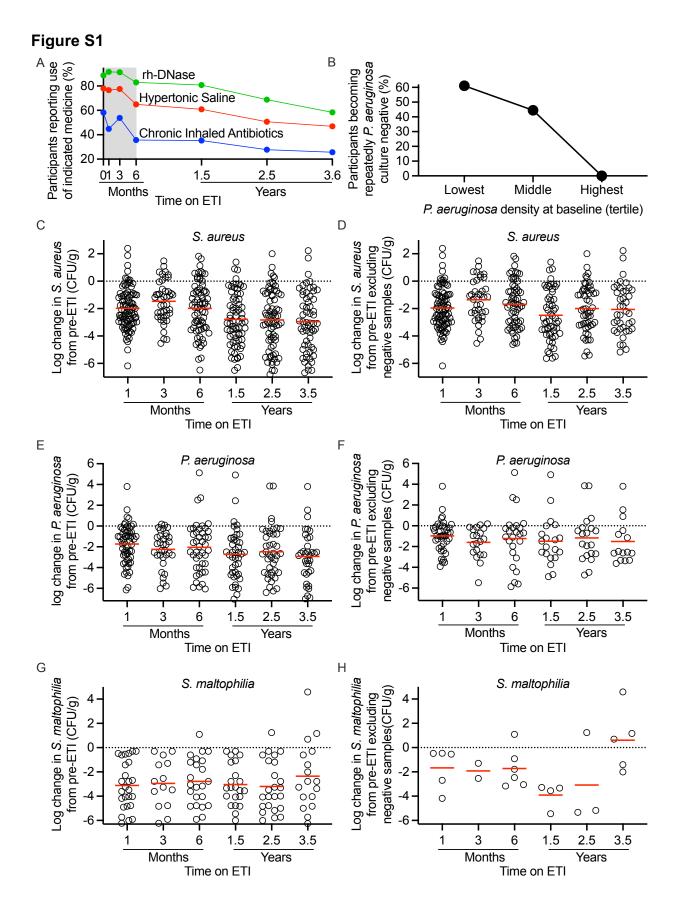
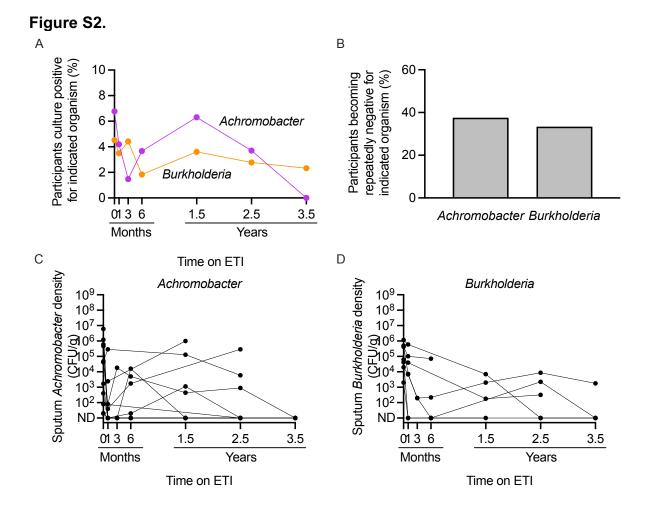


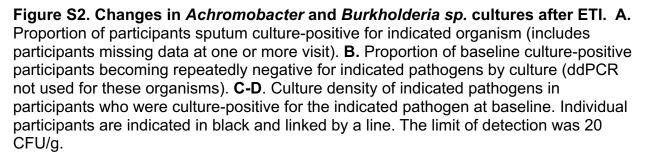
Figure S1. Pathogen response to ETI

A. Proportion of participants reporting use of indicated medication at each visit. At enrollment, participants were asked to maintain prescribed treatments through the first 6 months of the study (grey shaded area).

B. Proportion of participants becoming repeatedly culture-negative is highest among participants with the lowest baseline Pa density. Baseline Pa density was calculated by tertial; lowest tertial had baseline Pa sputum density less than 1×10^5 CFU/g and highest density tertial had baseline Pa sputum greater than 1.1×10^7 CFU/g. Plot shows percentage of participants in each tertial that became repeatedly-culture negative. Repeatedly culture negative was defined as participants for whom at least the last three sputum samples provided (post-ETI) were culture negative. To be included in this analysis participants had to be Pa positive pre-ETI and provided at least three sputum samples post-ETI. Importantly, Pa densities of samples in the lowest baseline Pa density tertile group generally far exceeded the limit of detection. Thirteen of 18 of the samples in this group had baseline Pa densities 100-fold higher than the limit of detection. Thus, it is unlikely conversion to repeatedly culture-negative status in the lowest tertile group was due to false-negative results that can sometime occur near detection limits.

C-G. By-participant average pathogen responses to ETI. Change in CFU/g in participants who were baseline culture-positive for indicated pathogens, including (B, D, F) and not including (C, E, G) culture-negative samples. To calculate log changes, log-transformed pre-ETI CFU/g values were subtracted from the post-ETI CFU/g values for each participant. Individual participants are indicated in black, averages in red. The limit of detection was 20 CFU/g.





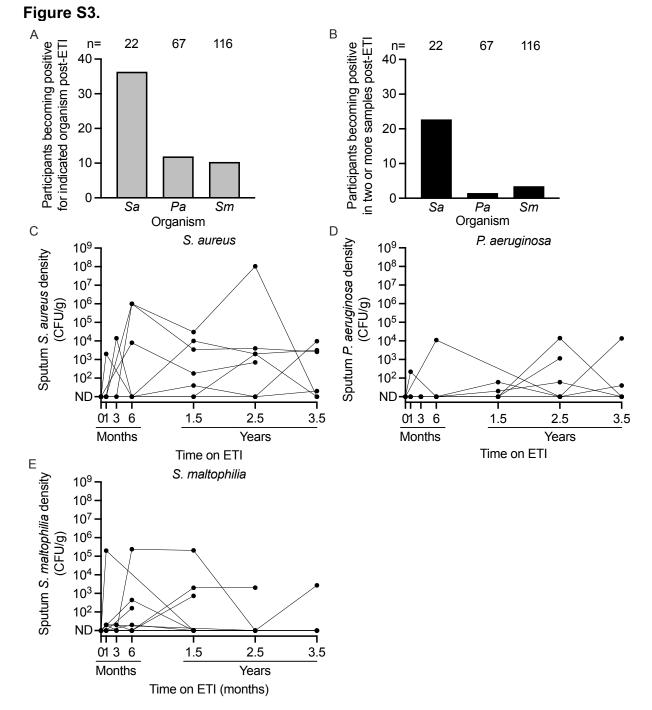


Figure S3. Participants with "new" positive cultures. Participants include in this analysis were considered negative pre-ETI if they were culture negative at the baseline visit <u>and</u> culture negative by registry report for the two-years preceding the study **A&B.** The percent of participants negative pre-ETI who had any positive cultures for indicated organisms (**A**) or at least two positive cultures (**B**) post-ETI. Participants shown in **B** are included in **A**. The number of pathogen negative participants pre-ETI is indicated above the graph. **C-E.** Culture density of indicated pathogens in these "new infections.