Tables and Figures

Table 1: Comparison of early-stage and late-stage pleural effusions of LTX recipients.

CHARACTERISTICS	EARLY STAGE	LATE STAGE	P
NUMBER OF PATIENTS	n=7	n=19	
AGE AT PE (YEARS), MEDIAN (IQR)	56.89 (53.87-61.23)	59.56 (54.94-61.64)	0.470$^{\#}$
SEX, N (%) FEMALE PATIENTS	1/7 (14.3%)	6/19 (31.6%)	0.629^{o}
SEX, N (%) MALE PATIENTS	6/7 (85.7%)	13/19 (68.4%)	
TIME TO PE (DAYS AFTER LTX), MEDIAN (IQR)	21 (20-24)	188 (131-513)	**0.0001$^{\#}$**
PREVIOUS THORACOCENTESIS, N (%)	1/7 (14%)	7/19 (37%)	0.269^{o}
TRANSPLANT TYPE			
SINGLE LTX, N (%)	-	1/19 (5.3%)	
DOUBLE LTX, N (%)	7/7 (100.0%)	18/19 (94.7%)	
ETIOLOGY OF PLEURAL EFFUSION			
POSTOPERATIVE, N (%)	7/7 (100.0%)	-	
UNCLEAR, N (%)	-	16 (84.2%)	
CHYLOTHORAX, N (%)	-	2 (10.5%)	
RENAL FAILURE, N (%)	-	1 (5.3%)	
CLASSIFICATION OF PLEURAL EFFUSION			
EXUDATE, N (%)	7/7 (100.0%)	15 (78.9%)	
TRANSUDATE, N (%)	-	4 (21.1%)	
UNDERLYING DISEASE FOR LTX PATIENTS			
ILD, N (%)	5/7 (71.4%)	13/19 (68.4%)	1.000^{o}
COPD, N (%)	0/7 (0%)	3/19 (15.8%)	0.540^{o}
CF / BRONCHIECTASIS, N (%)	1/7 (14.3%)	2/19 (10.5%)	1.000^{o}
RE-LTX FOR CLAD, N (%)	1/7 (14.3%)	1/19 (5.3%)	0.474^{o}
ANTIMICROBIAL PROPHYLAXIS / THERAPY			
AZITHROMYCIN, N (%)	0/7 (0%)	8/19 (42.1%)	0.062^{o}
PCP PROPHYLAXIS, N (%)	7/7 (100%)	17/19 (89.5%)	1.000^{o}
CMV PROPHYLAXIS, N (%)	3/7 (42.9%)	8/19 (42.1%)	1.000^{o}
FUNGAL PROPHYLAXIS, N (%)	7/7 (100%)	14/19 (73.7%)	0.278^{o}
IV OR PO ANTIBIOTICS AT DRAINAGE, N (%)	2/7 (28.6%)	2/19 (10.5%)	0.287^{o}

Table 1: Comparison of pleural effusions occurring early (n=7) (up to 60 days) vs. late (n=19) after lung transplantation. Statistics: $^{\#}$ unpaired Mann-Whitney test for non-parametric testing, ^{o} Chi-squared test for categorical data (Fisher exact test for 2 cells (>25%)).

Table 2: Comparison of late-stage pleural effusions of LTX recipients vs. pleural effusions of non-transplant patients

CHARACTERISTICS	LUNG TRANSPLANT	NON-TRANSPLANT	P
NUMBER OF PATIENTS	n=19	n=21	
AGE AT PE (YEARS), MEDIAN (IQR)	59.56 (54.94-61.64)	75.71 (65.79-82.43)	**0.0002[#]**
SEX, N (%) FEMALE PATIENTS	6/19 (31.6%)	7/21 (33.3%)	0.906[°]
SEX, N (%) MALE PATIENT	13/19 (68.4%)	14/21 (66.7%)	
TIME TO PE (DAYS AFTER LTX), MEDIAN (IQR)	184 (129.75-448.50)	-	
PREVIOUS THORACOCENTESIS, N (%)	7/19 (37%)	11/21 (52%)	0.324[°]
TRANSPLANT TYPE			
SINGLE LTX, N (%)	1/19 (5.3%)	-	
DOUBLE LTX, N (%)	18/19 (94.7%)	-	
ETIOLOGY OF PLEURAL EFFUSION			
UNCLEAR, N (%)	16 (84.2%)	1 (4.8%)	
CHYLOTHORAX, N (%)	2 (10.5%)	-	
RENAL FAILURE, N (%)	1 (5.3%)	2 (9.5%)	
HEART FAILURE, N (%)	-	8 (38.1%)	
(PARA-)MALIGNANT, N (%)	-	8 (38.1%)	
RHEUMATOID, N (%)	-	1 (4.8%)	
(PARA-)INFECTIOUS, N (%)	-	1 (4.8%)	
CLASSIFICATION OF PLEURAL EFFUSION			
EXUDATE, N (%)	15 (78.9%)	11 (52.4%)	
TRANSUDATE, N (%)	4 (21.1%)	10 (47.6%)	
UNDERLYING DISEASE FOR LTX PATIENTS			
ILD, N (%)	13/19 (68.4%)	-	
COPD, N (%)	3/19 (15.8%)	-	
CF / BRONCHIECTASIS, N (%)	2/19 (10.5%)	-	
RE-LTX FOR CLAD, N (%)	1/19 (5.3%)	-	
ANTIMICROBIAL PROPHYLAXIS / THERAPY			
AZITHROMYCIN, N (%)	8/19 (42.1%)	0/21 (0%)	0.001[°]
PCP PROPHYLAXIS, N (%)	17/19 (89.5%)	2/21 (9.5%)	<0.0001[°]
CMV PROPHYLAXIS, N (%)	8/19 (42.1%)	0/21 (0%)	0.001[°]
FUNGAL PROPHYLAXIS, N (%)	14/19 (73.7%)	0/21 (0%)	<0.0001[°]
IV OR PO ANTIBIOTICS AT DRAINAGE, N (%)	2/19 (10.5%)	7/21 (33.3%)	0.1328[°]

Table 2: Comparison of late-stage pleural effusions in LTX recipients (n=19) vs. pleural effusions in non-transplant patients (n=21). Statistics: [#] unpaired Mann-Whitney test for non-parametric testing, [°] Chi-squared test for categorical data (Fisher exact test for >2 cells (25%)).

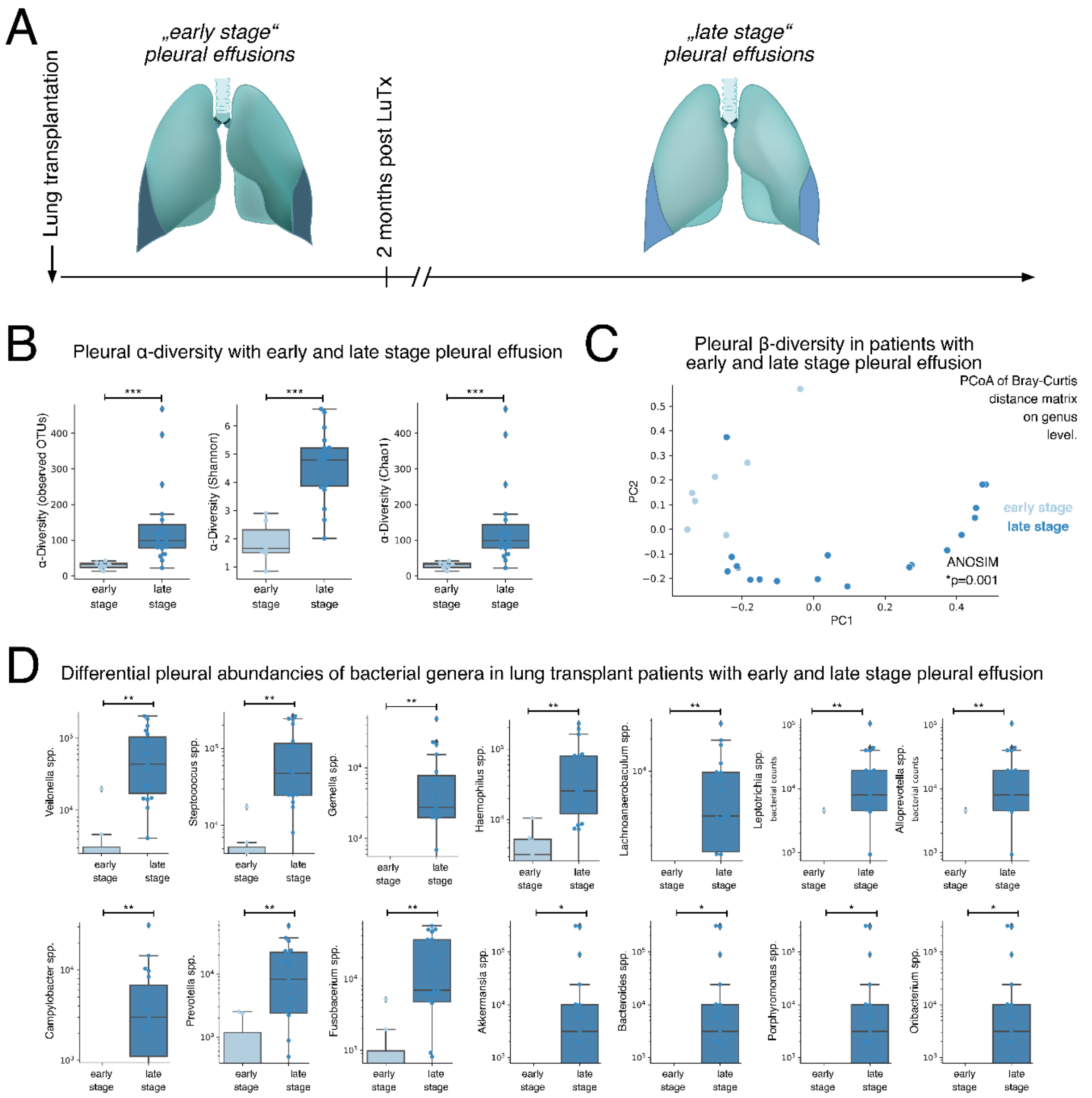

Figure 1: Pleural microbiome differences between early- and late-stage pleural effusions after lung transplantation. (A) Illustration of early-stage pleural effusions occuring less than 60 days after lung transplantation and late-stage pleural effusion seen later-on. **(B)** Differences between early-stage (n=7) and late-stage (n=19) pleural effusions regarding their α-diversity quantified by three different non-phylogenetic α diversity indices on OTU level. **(C)** Differences between early- and late-stage pleural effusions regarding their β diversity using a non-phylogenetic Bray-Curtis distance matrix and Principal Coordinate Analysis (PCoA) on genus level. **(D)** Differential abundancies of bacterial genera between early- and late-stage pleural effusions post lung transplantation.

Statistics: For comparison of α diversity Mann-Whitney-U test was used. For comparison of β diversity Analysis of Similarities (ANOSIM) was used. For comparison of differential abundancies repeated Mann-Whitney-U test with multiple testing adjustment using the Benjamini-Hochberg procedure was used. $*p<0.05$, $**p<0.01$, $***p<0.001$.

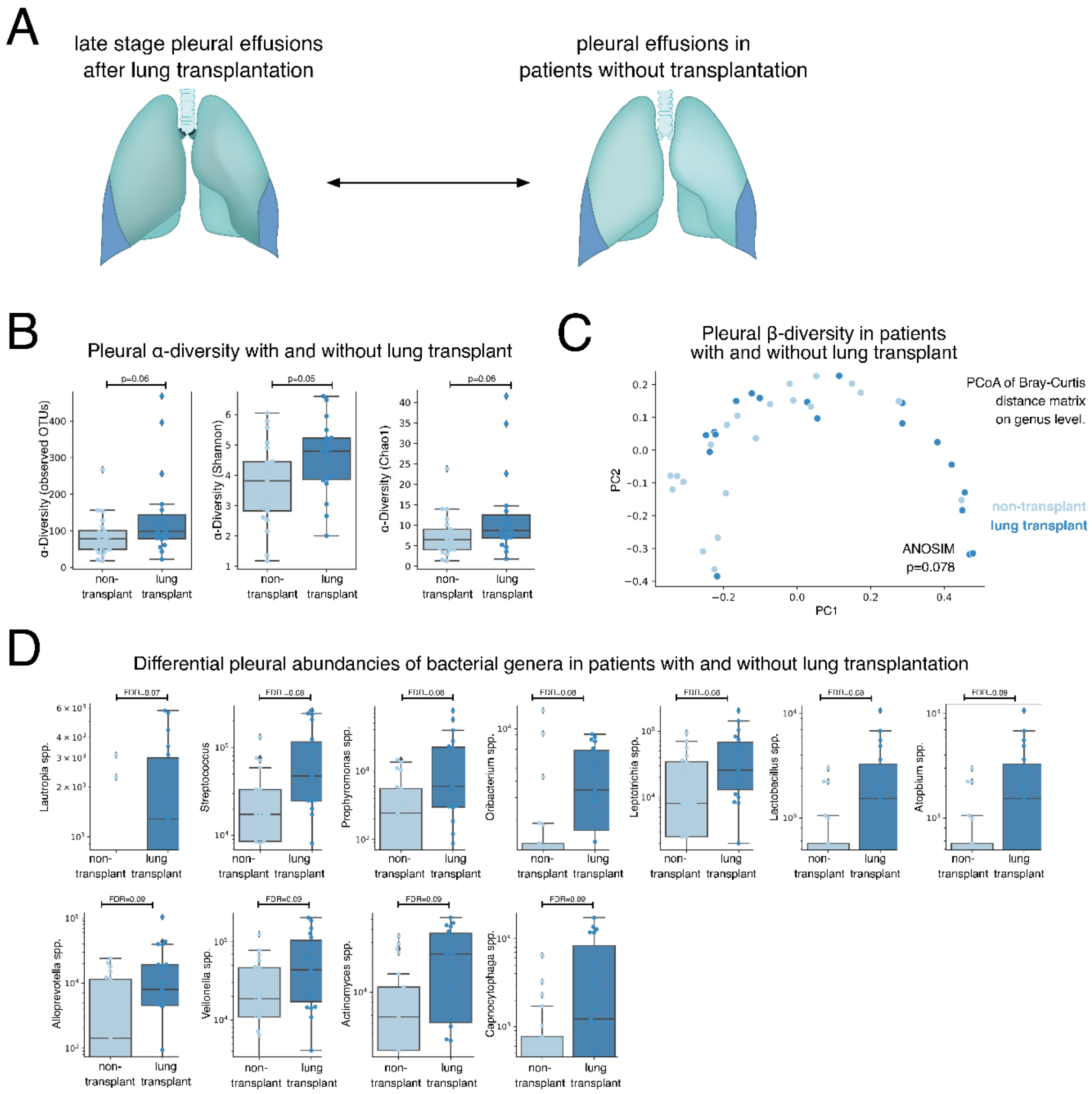

Figure 2: Pleural microbiome differences between LTX recipients and non-transplant patients. (A) Comparison of the pleural effusion microbiome of lung transplant recipients with late-stage pleural effusion microbiome (n=19) with non-transplant patients (n=21). **(B)** Differences between lung transplant pleural effusions with pleural effusions from non-transplant patients regarding their α diversity quantified by three different non-phylogenetic α diversity indices on OTU level. **(C)** Differences between lung transplant and non-transplant pleural effusions regarding their β diversity using a non-phylogenetic Bray-Curtis distance matrix and Principal Coordinate Analysis (PCoA) on genus level. **(D)** Differential abundancies of bacterial genera between pleural effusions of lung transplant patients with pleural effusions on non-transplant patients.

<u>Statistics:</u> For comparison of α diversity Mann-Whitney-U test was used. For comparison of β-diversity Analysis of Similarities (ANOSIM) was used. For comparison of differential abundancies repeated Mann-Whitney-U test with multiple testing adjustment using the Benjamini-Hochberg procedure was used. *p<0.05, ** p<0.01, ***p<0.001.

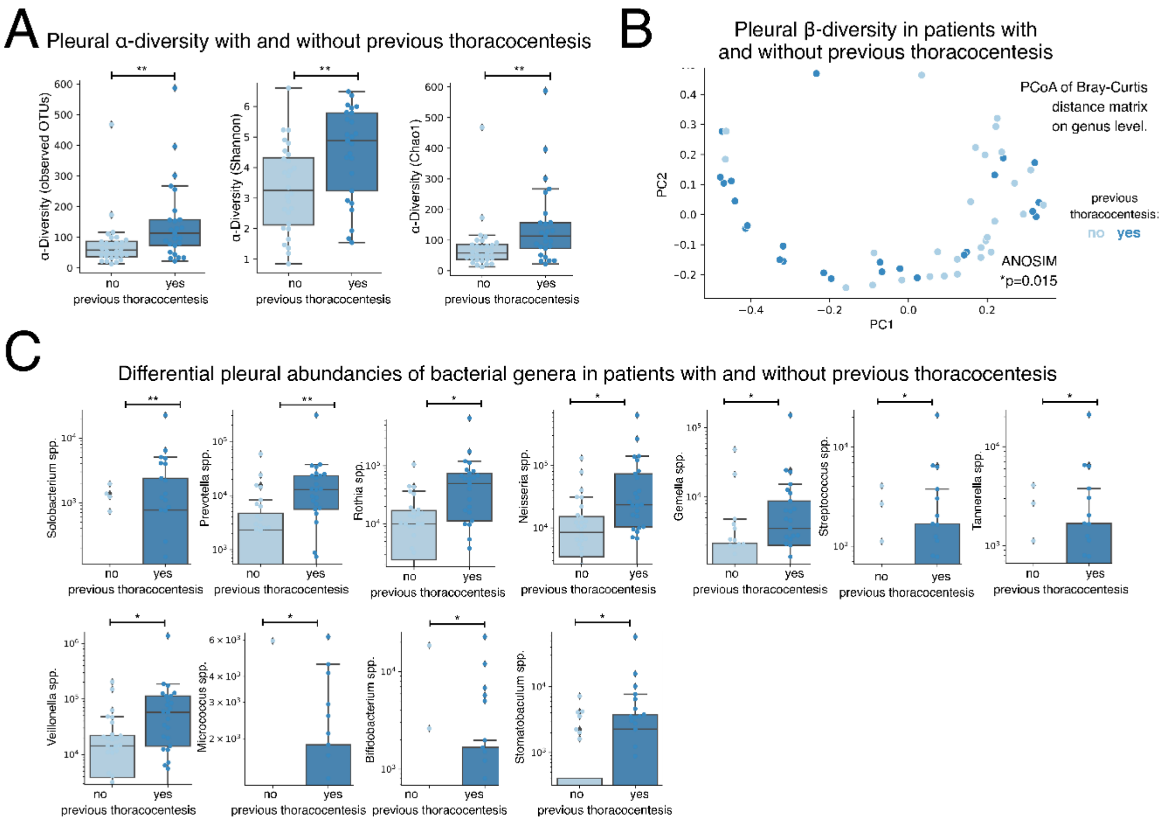

Figure 3: Previous thoracenteses influence the pleural microbiome in pleural effusions. (A) Differences between pleural effusions with (n=24) and without previous thoracentesis (n=28) regarding their α diversity quantified by three different non-phylogenetic α-diversity indices on OTU level. **(B)** Differences between pleural effusions with and without previous thoracentesis regarding their β diversity using a non-phylogenetic Bray-Curtis distance matrix and Principal Coordinate Analysis (PCoA) on genus level. **(C)** Differential abundancies of bacterial genera between pleural effusions with and without previous thoracentesis.

Statistics: For comparison of α diversity Mann-Whitney-U test was used. For comparison of β-diversity Analysis of Similarities (ANOSIM) was used. For comparison of differential abundancies repeated Mann-Whitney-U test with multiple testing adjustment using the Benjamini-Hochberg procedure was used. *p<0.05, ** p<0.01, ***p<0.001.

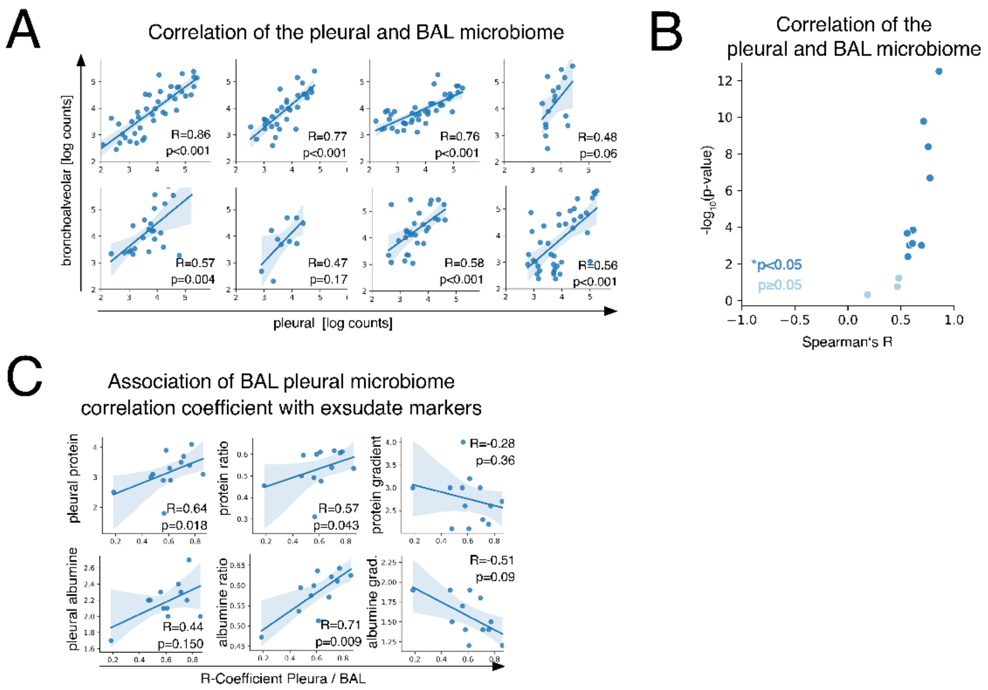

Figure 4: Correlation of the microbiome of pleural effusions and associated bronchoalveolar lavages (n=14). (A) Representative regression plot of pleural and bronchoalveolar lavage (BAL) microbial DNA abundancy on genus level. **(B)** Vulcano plot of the Spearman's correlation coefficient and type II error. **(C)** Correlation of the Spearman's rank correlation coefficient between pleural and BAL microbiome and different exudate markers.

Statistics: For all correlations the Spearman's rank correlation coefficient was used.

Supplementary Tables and Figures

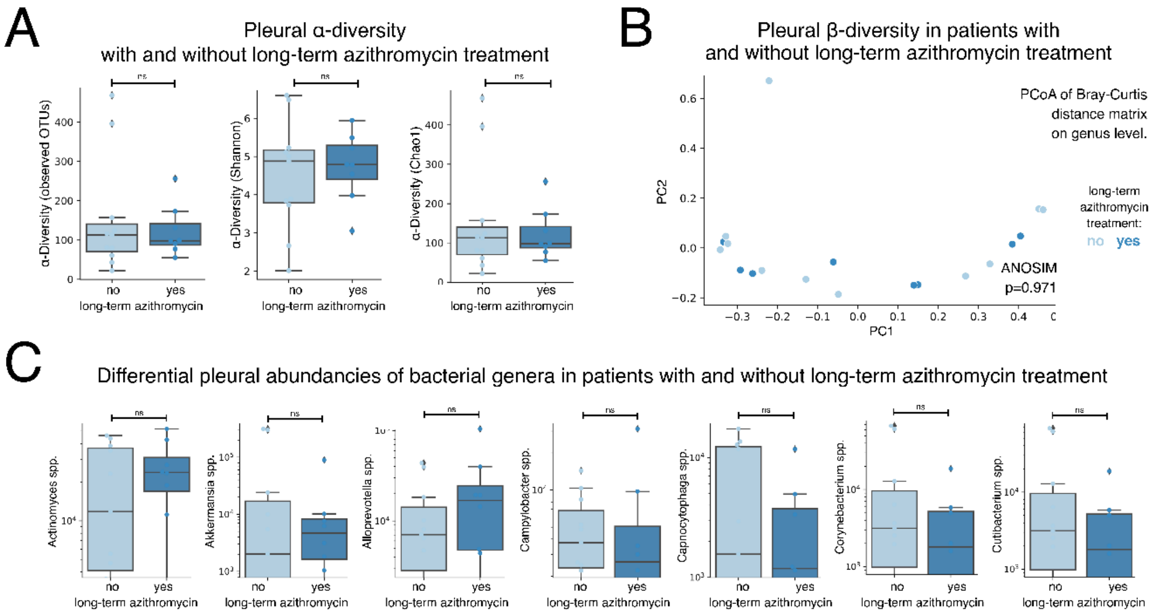

Figure S1: Long term azithromycin therapy does not influence the pleural microbiome in pleural effusions of LTX recipients. (A) Differences between pleural effusions with (n=8) and without long-term azithromycin treatment (n=11) regarding their α diversity quantified by three different non-phylogenetic α-diversity indices on OTU level. **(B)** Differences between pleural effusions with and without long-term azithromycin treatment regarding their β diversity using a non-phylogenetic Bray-Curtis distance matrix and Principal Coordinate Analysis (PCoA) on genus level. **(C)** Differential abundancies of bacterial genera between pleural effusions with and without long-term azithromycin therapy.

Statistics: For comparison of α diversity Mann-Whitney-U test was used. For comparison of β diversity Analysis of Similarities (ANOSIM) was used. For comparison of differential abundancies repeated Mann-Whitney-U test with multiple testing adjustment using the Benjamini-Hochberg procedure was used.

Table S1: Laboratory findings of early-stage and late-stage pleural effusions in LTX recipients.

CHARACTERISTICS	EARLY STAGE	LATE STAGE	P
	n=7	n=19	
SERUM CHEMISTRY			
TOTAL PROTEIN (G/DL), MEAN (SD)	5.2 (4.6-5.8)	5.8 (5.6-6.1)	**0.030**[#]
ALBUMIN (G/DL), MEAN (SD)	3.1 (2.9-3.2)	3.7 (3.2-3.9)	**0.012**[#]
LDH (U/L), MEDIAN (IQR)	238 (205-254)	285 (241-392)	0.053[#]
CRP (MG/DL), MEDIAN (IQR)	4.3 (0.8-6.3)	0.5 (0.2-2.3)	0.060[#]
KREATININ (MG/DL), MEAN (SD)	0.9 (0.7-1.2)	1.5 (1.3-1.9)	**0.002**[#]
NT-PROBNP (PG/ML), MEDIAN (IQR)	489 (45-970)	1938 (932-4541)	**0.013**[#]
PLEURAL FLUID CHEMISTRY			
PROTEIN (G/DL), MEAN (SD)	2.7 (2.2-3.0)	3.1 (2.8-3.7)	0.132[#]
ALBUMIN (G/DL), MEDIAN (IQR)	1.7 (1.0-2.0)	2.2 (2.0-2.4)	**0.005**[#]
LDH (U/L), MEDIAN (IQR)	473 (206-906)	152 (134-194)	**0.005**[#]
LDH (U/L) > 500 U/L, N (%)	*3 (42.9%)*	*0*	
LDH (U/L) > 1000 U/L, N (%)	*1 (14.3%)*	*0*	
TRIGLYCERIDES (MG/DL), MEDIAN (IQR)	24 (13-57)	17 (14-26)	0.397[#]
TRIGLYCERIDES (MG/DL) > 110 MG/DL, N (%)	*0*	*2*	
CHOLESTERIN (MG/DL), MEDIAN (IQR)	66 (51-71)	60 (47-69)	0.647[#]
HEMOGLOBIN (MG/DL), MEDIAN (IQR)	0.15 (0.05-3.10)	0.04 (0.02-0.25)	0.166[#]
PH, MEDIAN (IQR)	7.42 (7.30-7.45)	7.37 (7.35-7.43)	0.859[#]
LACTATE (MMOL/L), MEDIAN (IQR)	2.4 (2.1-4.3)	2.6 (1.9-3.8)	0.709[#]
GLUCOSE (MG/DL), MEAN (SD)	109 (51-149)	127 (93-144)	0.456[#]
PLEURAL FLUID CELL COUNTS			
TOTAL CELL COUNT (CELLS/µL), MEDIAN (IQR)	1592 (325-3577)	503 (258-1110)	0.312[#]
POLYMORPHONUCLEAR (%), MEDIAN (IQR)	63 (9-74)	4 (3-20)	**0.004**[#]
NEUTROPHIL GRAN. (%), MEDIAN (IQR)	12 (4-74)	3 (0-14)	0.067[#]
EOSINOPHIL GRAN. (%), MEDIAN (IQR)	0 (0-2)	0 (0-0)	0.117[#]
MONOCYTES (%), MEDIAN (IQR)	6 (2-13)	7 (4-13)	0.214[#]
MACROPHAGES (%), MEDIAN (IQR)	0 (0-0)	9 (0-41)	**0.048**[#]
LYMPHOCYTES (%), MEDIAN (IQR)	21 (5-70)	81 (54-86)	**0.043**[#]
MICROBIOLOGY			
POS. BACTERIAL CULTURE, N (AVAILABLE N)	0 (7)	1 (19)	
POS. TBC MICROSCOPY, N (AVAILABLE N)	0 (4)	0 (17)	
POS. TBC PCR, N (AVAILABLE N)	0 (4)	0 (17)	
POS. TBC CULTURE, N (AVAILABLE N)	0 (4)	0 (17)	
POS. NTM PCR, N (AVAILABLE N)	-	0 (18)	

Table S1: Comparison of pleural effusions occurring early (n=7) (up to 60 days) vs. late (n=19) after lung transplantation. Statistics: [#] unpaired Mann-Whitney test for non-parametric testing, [o] Chi-squared test for categorical data (Fisher exact test for >2 cells (25%)).

Table S2: Laboratory findings of pleural effusions in LTX recipients and non-transplant patients.

CHARACTERISTICS	LUNG TRANSPLANT	NON-TRANSPLANT	P
	n=19	n=21	
SERUM CHEMISTRY			
TOTAL PROTEIN (G/DL), MEAN (SD)	5.8 (5.6-6.1)	5.9 (5.6-6.6)	0.497[#]
ALBUMIN (G/DL), MEAN (SD)	3.7 (3.2-3.9)	3.7 (3.1-4.0)	0.966[#]
LDH (U/L), MEDIAN (IQR)	285 (241-392)	252 (189-494)	0.542[#]
CRP (MG/DL), MEDIAN (IQR)	0.5 (0.2-2.3)	3.5 (0.8-12)	**0.008**[#]
KREATININ (MG/DL), MEAN (SD)	1.5 (1.3-1.9)	1.4 (0.8-2.3)	0.322[#]
NT-PROBNP (PG/ML), MEDIAN (IQR)	1938 (932-4541)	3590 (1266-5915)	0.506[#]
PLEURAL FLUID CHEMISTRY			
PROTEIN (G/DL), MEAN (SD)	3.1 (2.8-3.7)	3.1 (2.2-4.1)	0.644[#]
ALBUMIN (G/DL), MEAN (SD)	2.2 (2.0-2.4)	1.7 (1.5-2.4)	0.371[#]
LDH (U/L), MEDIAN (IQR)	152 (134-194)	168 (107-445)	0.616[#]
LDH (U/L) > 500 U/L, N (%)	*0*	*4 (19%)*	
LDH (U/L) > 1000 U/L, N (%)	*0*	*2 (9.5%)*	
TRIGLYCERIDES (MG/DL), MEDIAN (IQR)	17 (14-26)	19 (11-29)	1.000[#]
TRIGLYCERIDES (MG/DL) > 110 MG/DL, N (%)	*2*	*0*	
CHOLESTERIN (MG/DL), MEDIAN (IQR)	60 (47-69)	44 (32-66)	0.155[#]
HEMOGLOBIN (MG/DL), MEDIAN (IQR)	0.04 (0.02-0.25)	0.02 (0.01-0.05)	0.327[#]
PH, MEDIAN (IQR)	7.37 (7.35-7.43)	7.44 (7.35-7.46)	0.055[#]
LACTATE (MMOL/L), MEDIAN (IQR)	2.6 (1.9-3.8)	1.7 (1.2-2.6)	0.091[#]
GLUCOSE (MG/DL), MEAN (SD)	127 (93-144)	113 (91-123)	0.279[#]
PLEURAL FLUID CELL COUNTS			
TOTAL CELL COUNT (CELLS/µL), MEDIAN (IQR)	503 (258-1110)	747 (348-2267)	0.119[#]
POLYMORPHONUCLEAR (%), MEDIAN (IQR)	4 (3-20)	10 (3-13)	0.462[#]
NEUTROPHIL GRAN. (%), MEDIAN (IQR)	3 (0-14)	9 (1-17)	0.146[#]
EOSINOPHIL GRAN. (%), MEDIAN (IQR)	0 (0-0)	0 (0-0)	0.965[#]
MONOCYTES (%), MEDIAN (IQR)	7 (4-13)	10 (4-26)	0.162[#]
MACROPHAGES (%), MEDIAN (IQR)	9 (0-41)	4 (2-10)	**0.049**[#]
LYMPHOCYTES (%), MEDIAN (IQR)	81 (54-86)	52 (12-66)	**0.018**[#]

Table S2: Comparison of late-stage effusions of LTX recipients (n=19) vs pleural effusions of non-transplant patients (n=21). Statistics: [#] unpaired Mann-Whitney test for non-parametric testing, [o] Chi-squared test for categorical data (Fisher exact test for >2 cells (25%)).

Table S3: Most abundant bacterial genera in pleural effusions after lung transplantation (n=26).

BACTERIA GENUS	MEDIAN READS
STREPTOCOCCUS	25015
VEILLONELLA	20673
PREVOTELLA_7	18487
ROTHIA	17156
LEPTOTRICHIA	16259
HAEMOPHILUS	15706
NEISSERIA	12198
ACTINOMYCES	10925
STAPHYLOCOCCUS	6405
FUSOBACTERIUM	5618
ALLOPREVOTELLA	4805
CORYNEBACTERIUM	4717
PORPHYROMONAS	4085
PREVOTELLA	2756
LACHNOANAEROBACULUM	2683

Table S4: Differential pleural abundancies of bacterial genera in early- (n=7) and late-stage (n=19) pleural effusions of LTX recipients.

BACTERIA GENUS	SAMPLES WITH DETECTED GENUS	COUNTS EARLY STAGE [IQR]	COUNTS LATE STAGE [IQR]	FDR
VEILLONELLA	19/26	0 - 3.1x10^{3}	1.7x10^{4} - 1.0x10^{5}	0.0043
GEMELLA	7/26	0-0	2.0x10^{3} - 7.7x10^{3}	0.0043
HAEMOPHILUS	21/26	0-5.3x10^{3}	1.2x10^{4} - 8.0x10^{4}	0.0043
LACHNOANAEROBACULUM	9/26	0-0	1.7x10^{3} - 9.7x10^{3}	0.0043
STREPTOCOCCUS	20/26	0-5.2x10^{3}	2.5x10^{4} – 1.2x10^{5}	0.0043
LEPTOTRICHIA	20/26	0-4.7x10^{3}	1.3x10^{4} – 6.8x10^{4}	0.0043
ALLOPREVOTELLA	12/26	0-0	4.6x10^{3} - 1.9x10^{4}	0.0073
CAMPYLOBACTER	6/26	0-0	1.1x10^{3} – 6.8x10^{3}	0.0076
PREVOTELLA	11/26	0-1.2x10^{3}	1.2x10^{3} – 2.4x10^{3}	0.0076
FUSOBACTERIUM	14/26	0-9.8x10^{2}	4.8x10^{3} – 3.6x10^{4}	0.0076
ORIBACTERIUM	8/26	0-0	1.7x10^{3} - 6.9x10^{3}	0.0093
PORPHYROMONAS	13/26	0-1.4x10^{3}	3.0x10^{3} – 2.2x10^{4}	0.0096
AKKERMANSIA	9/26	0-0	0 – 1.0x10^{4}	0.0171
FACALIBACTERIUM	6/26	0-0	0 – 6.7x10^{3}	0.0155
ACTINOMYCES	16/26	0-5.3x10^{3}	5.1x10^{3} - 3.7 x10^{4}	0.0171
STAPHYLOCCUS	14/26	0-3.2x10^{3}	4.1x10^{3} – 1.7x10^{4}	0.0182
NEISSERIA	20/26	0-9.9x10^{3}	9.0x10^{3} – 7.6x10^{4}	0.0182
SELENOMONAS	9/26	0-0	0 – 9.7x10^{3}	0.0199
LACTOBACILLUS	6/26	0-0	0 – 8.0x10^{3}	0.0223
PREVOTELLA_7	22/26	2.7x10^{3} - 1.4x10^{3}	1.2 x10^{4} – 7.4 x10^{4}	0.0287

Table S5: Most abundant bacterial genera in pleural effusions of non-transplant patients (n=21).

BACTERIA GENUS	MEDIAN READS
VEILLONELLA	18793
STREPTOCOCCUS	17322
PREVOTELLA_7	14252
HAEMOPHILUS	13592
NEISSERIA	12763
ROTHIA	10268
LEPTOTRICHIA	8048
STAPHYLOCOCCUS	7809
PREVOTELLA	5887
ACTINOMYCES	5810
CORYNEBACTERIUM	4494
FUSOBACTERIUM	3186
MEGASPHAERA	2858
PORPHYROMONAS	2441
GEMELLA	2071

Table S6: Differential pleural abundancies of bacterial genera in late-stage effusions of patients after lung transplantation (n=19) and pleural effusions of patients without transplantation (n=21).

BACTERIA GENUS	SAMPLES WITH DETECTED GENUS	COUNTS NON-TRANSPLANT [IQR]	COUNTS LUNG TRANSPLANT [IQR]	FDR
LEPTOTRICHIA	32	$2.5x10^3$-$3.4x10^3$	$1.3x10^4$-$6.8x10^4$	0.0563
PORPHYROMONAS	18	0-$5.5x10^3$	$3.0x10^3$-$2.2x10^4$	0.0563
ORIBACTERIUM	10	0-1.3 $x10^3$	$1.7x10^3$-$6.9x10^3$	0.0563
STREPTOCOCCUS	36	$8.5x10^3$-$3.3x10^4$	$2.5x10^4$-$1.2x10^5$	0.0563
LACTOBACILLUS	8	0-0	0-$8.0x10^3$	0.0563
ACTINOMYCES	25	$2.8x10^3$-$1.1x10^4$	$5.1x10^3$-$3.7x10^4$	0.0700
ALLOPREVOTELLA	19	0-$1.1x10^4$	$4.6x10^3$-$1.9x10^4$	0.0700
VEILLONELLA	36	$1.1x10^4$-$4.7x10^4$	$1.7x10^4$-$1.0x10^5$	0.0700
HAEMOPHILUS	35	$5.9x10^3$-$2.0x10^4$	$1.2x10^4$-$8.0x10^4$	0.0744
FUSOBACTERIUM	21	0-$7.8x10^3$	$4.8x10^3$-$3.6x10^4$	0.0744
LACHNOANAEROBACULUM	13	0-$4.5x10^3$	$1.7x10^3$-$9.7x10^3$	0.0785
ROTHIA	33	$6.4x10^3$-$2.0x10^4$	$1.4x10^4$-$6.4x10^4$	0.0917
AKKERMANSIA	14	0-$3.8x10^3$	0-$1.0x10^4$	0.1337
PREVOTELLA_7	33	$9.2x10^3$-$4.4x10^4$	$1.2x10^4$-$7.4x10^4$	0.1457
GEMELLA	9	0-$3.5x10^3$	$2.0x10^3$-$7.7x10^3$	0.1457
CUTIBACTERIUM	11	0-$3.7x10^3$	0-$6.1x10^3$	0.1925
NEISSERIA	35	$6.8x10^3$-$2.6x10^4$	$9.0x10^3$-$7.6x10^4$	0.1925
PREVOTELLA	23	0-$9.7x10^3$	$2.4x10^3$-$2.2x10^4$	0.1925
SELENOMONAS	15	0-$5.7x10^3$	0-$9.7x10^3$	0.1925
CORYNEBACTERIUM	18	$1.5x10^2$-$7.8x10^3$	$4.0x10^3$-$1.0x10^4$	0.2062

Table S7: Differential pleural abundancies of bacterial genera in patients with (n=24) and without (n=28) previous thoracocentesis.

BACTERIA GENUS	SAMPLES WITH DETECTED GENUS	COUNTS WITHOUT PREVIOUS THORACOCENTESIS [IQR]	COUNTS WITH PREVIOUS THORACOCENTESIS [IQR]	FDR
PREVOTELLA	25	0-4.7x10^3	5.3x10^3-2.3x10^4	0.0105
ROTHIA	40	2.4x10^3-1.7x10^4	1.1x10^4-7.1x10^4	0.0121
GEMELLA	11	0-2.1x10^3	1.8x10^3-7.2x10^3	0.0121
NEISSERIA	42	3.4x10^3-1.5x10^4	1.0x10^4-7.6x10^4	0.0121
STREPTOCOCCUS	43	5.6x10^3-2.5x10^4	1.7x104-1.1x10^5	0.0145
VEILLONELLA	42	3.9x10^3 -2.2x10^4	1.4x10^4-1.0x10^5	0.0203
CORYNEBACTERIUM	23	0-6.2x10^3	3.9x10^3-1.5x10^4	0.0484
FUSOBACTERIUM	24	0-6.9x10^3	2.6x10^3-3.7x10^4	0.0484
HAEMOPHILUS	42	4.6x10^3-1.9x10^4	9.7x10^3-7.9x10^4	0.0484
PREVOTELLA_7	40	4.1x10^3 -2.2x10^4	9.9x10^3-7.0x10^4	0.0558
PORPHYROMONAS	21	0-5.2x10^3	1.7x10^3-1.6x10^4	0.0679
ACTINOMYCES	30	0-1.1x10^4	3.8x10^3-3.5x10^4	0.0679
LEPTOTRICHIA	38	2.5x10^3-1.9x10^4	7.0x10^3-7.7x10^4	0.0698
ALLOPREVOTELLA	21	0-6.8x10^3	4.1x10^2-2.0x10^4	0.0708
CUTIBACTERIUM	15	0-2.9x10^3	0-1.2x10^4	0.0759
SELENOMONAS	17	0-3.4x10^3	0-9.7x10^3	0.0759
LACHNOANEROBACULUM	16	0-3.7x10^3	0-8.9x10^3	0.0861
MEGASPHAERA	15	0-3.4x10^3	0-9.0x10^3	0.1578
ORIBACTERIUM	12	0-2.6x10^3	0-5.9x10^3	0.2257
STAPHYLOCOCCUS	30	1.9x10^3-1.6x10^4	4.3x10^3-1.7x10^4	0.2363