Supplemental material

Microbiome-Based Clinical Pathogen Detection in Bronchoalveolar Lavage Fluid Using Illumina Short-Read and Nanopore Long-Read Sequencing

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Supplementary Table S1: Bacterial species identified within this study which were classified as potential pathogen. A reference for the classification as potential pathogen is given in the right column.

Potential Pathogen	Reference
Bordetella bronchiseptica	Gujju et al., 2021 [62]
Citrobacter koseri	Yao et al., 2021 [63]
Escherichia coli	Dalhoff et al., 2017 [64]; Ewig et al., 2021 [65]
Haemophilus influenzae	Dalhoff et al., 2017 [64]; Ewig et al., 2021 [65]
Listeria monocytogenes	Koufakis et al., 2015 [66]
Prevotella oris	Viswanath et al., 2022 [67]
Pseudomonas aeruginosa	Dalhoff et al., 2017 [64]; Ewig et al., 2021 [65]
Ralstonia pickettii	Ryan et al., 2011 [68]
Serratia marcescens	Dalhoff et al., 2017 [64]
Staphylococcus aureus	Dalhoff et al., 2017 [64]; Ewig et al., 2021 [65]
Stenotrophomonas sp. MYb57	-
Stenotrophomonas maltophilia	Dalhoff et al., 2017 [64]
Streptococcus agalactiae	Furuta et al., 2022 [69]
Streptococcus pneumoniae	Dalhoff et al., 2017 [64]; Ewig et al., 2021 [65]
Streptococcus pseudopneumoniae	Garriss et al., 2019 [70]
Tropheryma whipplei	Shi et al., 2024 [71]

Supplementary Table S2. Summary of identified bacteria in culture-based diagnostics and the top three detections with a relative abundance above 3% for NGS sequencing. ONT sequenced samples had the additional constraint of a minimum of 10 sequence reads. Pathogenic bacteria a denoted in bold.

Sample	Culture-based Routine Diagnostics (24h to 48h)	Illumina Short-Read Sequencing (32h)	Nanopore Long-Read Sequencing (8h)
P002	***C. koseri*** (plenty) *S. epidermidis* (mass)	*Corynebacterium* (3.1%)	***C. koseri*** (85.7%)
P003	None	None	None
P004	***S. aureus*** (plenty) *S. mitis* (sparse)	*Staphylococcus* (76.1%) *Streptococcus* (4.5%)	***S. aureus*** (85.0%)
P007	*E. faecium* (sparse) Coagulase-negative *Staphylococcus* (sparse)	*Veillonella* (12.1%)	None
P008	None	None	Excluded
P009	Pharyngeal flora (sparse)	*Streptococcus* (39.8%) *Veillonella* (3.3%)	None
P011	α-hemolytic *Streptococcus* (few)	*Gemella* (11.6%) *Streptococcus* (6.4%) *Rothia* (6.1%)	None
P013	***S. aureus*** (mass)	*Haemophilus* (4.5%)	***R. pickettii*** (7.4%) *L. curvatus* (6.9%) *S. hominis* (5.9%)
P014	***S. aureus*** (mass)	None	*P. myrsinacearum* (10.5%)
P105	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (few)	*Streptococcus* (21.6%) *Veillonella* (16.1%) *Prevotella* 7 (10.7%)	*V. atypica* (16.8%) *S. mitis* (16.5%) *S. salivarius* (12.1%)
P017	***S. pneumoniae*** (mass)	*Streptococcus* (99.9%)	***S. pneumoniae*** (100.0%)
P018	α-hemolytic *Streptococcus* (sparse)	*Streptococcus* (36.9%) *Rothia* (18.3%) *Enterococcus* (15.0%)	Excluded
P019	None	*Streptococcus* (13.6%) *Absconditabacteriales* (7.9%) *Alloprevotella* (7.4%)	Excluded
P021	None	*Veillonella* (7.6%) *Prevotella* 7 (4.9%) *Corynebacterium* (4.4%)	Excluded
P022	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty) ***P. aeruginosa*** (sparse)	*Veillonella* (15.8%) *Streptococcus* (10.1 %) *Prevotella* 7 (7.9%)	*C. concisus* (17.6%) *V. dispar* (13.9%) *S. parasanguinis* (10.1%)
P023	α-hemolytic *Streptococcus* (plenty) *R. mucilaginosa* (plenty)	*Streptococcus* (43.2%) *Gemella* (33.6%) *Rothia* (11.6%)	Excluded
P024	α-hemolytic *Streptococcus* (sparse) ***H. influenzae*** (mass)	*Haemophilus* (95.4%)	Excluded
P025	None	*Corynebacterium* (5.0%)	***S. aureus*** (93.0%)
P027	***S. aureus*** (mass)	*Staphylococcus* (53.3%) *Prevotellaceae* (38.0%) *Prevotella* 7 (7.3%)	Excluded
P028	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty)	*Selenomonas* (8.0%) *Alloprevotella* (7.6%)	Excluded

		Prevotella (7.5%)	
P029	α-hemolytic *Streptococcus* (few)	*Streptococcus* (12.6%) *Porphyromonas* (3.6%)	*S. mitis* (10.3%) *H. parainfluenzae* (9.0%) *Selenomonas* sp. (8.8%)
P033	None	None	*L. sacchari* (37.5%)
P034	None	*Neisseria* (27.6%) *Haemophilus* (18.1%) *Streptococcus* (13.4%)	Excluded
P036	*Rothia* sp. (sparse)	*Rothia* (20.1%)	***H. influenzae*** (33.1%) *H. parainfluenzae* (19.8%) *N. macacae* (8.2.%)
P038	None	*Burkholderiales* (20.8%) *Parvimonas* (12.6%) *Neisseria* (5.7%)	Excluded
P039	*S. epidermidis* (sparse)	*Staphylococcus* (5.9%) *Prevotella 7* (3.4%)	None
P040	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty)	*Streptococcus* (10.3%) *Alloprevotella* (9.7%) *Prevotella* (9.6%)	Excluded
P041	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty)	*Prevotella 7* (9.1%) *Rothia* (8.9%) *Streptococcus* (8.5%)	None
P042	None	None	*Streptococcus* sp. (12.3%) *Selenomonas* sp. (10.0%) *Streptococcus* sp. (9.1%)
P043	***P. aeruginosa*** (few)	*Pseudomonas* (40.4%) *Enterobacteriaceae* (25.4%)	*S. mitis* (9.6%) *G. sanguinis* (9.3%) *V. atypica* (9.3%)
P044	***P. aeruginosa*** (plenty)	*Pseudomonas* (81.6%)	Excluded
P045	α-hemolytic *Streptococcus* (mass) *Rothia* sp. (few	*Prevotella 7* (26.9%) *Streptococcus* (12.9%) *Veillonella* (8.1%)	Excluded
P048	*E. faecium* (few)	*Enterococcus* (62.0%) *Rothia* (20.4%) *Lacticaseibacillus* (3.5%)	Excluded
P049	*E. faecium* (few)	*Enterococcus* (83.6%)	None
P050	None	*Porphyromonas* (15.4%) *Lactobacillales* (8.1%) *Actinomyces* (4.3%)	Not Determined
P051	α-hemolytic *Streptococcus* (few) *Rothia* sp. (sparse) Coagulase-negative *Staphylococcus* (sparse) *P. melaninogenica* (sparse)	*Veillonella* (26.1%) *Streptococcus* (23.9%) *Prevotella* 7 (8.6%)	*E. faecium* (90.0%)
P052	***S. aureus*** (few)	*Staphylococcus* (91.4%)	Excluded
P055	None	*Enterococcus* (4.6%) *Rothia* (4.1%)	None
P057	None	*Selenomonas* (4.6%) *Lactobacillales* (4.5%) *Intrasporangiaceae* (3.2%)	Excluded
P058	Coagulase-negative *Staphylococcus* (sparse)	*Staphylococcus* (76.9%) *Veillonella* (3.4%)	*S. epidermidis* (80.3%)

P059	None	*Streptococcus* (9.8%) *Selenomonadaceae* (6.0%) *Chryseobacterium* (3.6%)	None
P060	*S. epidermidis* (mass)	*Rothia* (34.7%) *Streptococcus* (27.1%) *Enterococcus* (14.6%)	*S. mitis* (42.8%) *S. epidermidis* (21.4%) *E. faecium* (20.6%)
P065	None	*Brevibacterium* (6.0%) *Pseudomonas* (4.8%) *Actinomyces* (3.3%)	Excluded
P070	α-hemolytic *Streptococcus* (sparse)	*Streptococcus* (47.3%) *Rothia* (9.0 %) *Limosilactobacillus* (6.7%)	***S. pseudopneumoniae*** (35.6%) *Streptococcus* sp. (21.0%) ***S. agalactiae*** (18.4%)
P071	None	*Staphylococcus* (13.9%) *Enterococcus* (8.5%) *Corynebacterium* (6.6%)	Excluded
P072	***S. maltophilia*** (plenty)	*Stenotrophomonas* (95.4%)	***S. maltophilia*** (98.8%)
P073	None	*Staphylococcus* (6.9%)	Excluded
P074	α-hemolytic *Streptococcus* (sparse)	*Alloprevotella* (9.6%) *Actinomyces* (7.3%) *Gemella* (5.6%)	Not Determined
P075	α-hemolytic *Streptococcus* (sparse) Coagulase-negative *Staphylococcus* (sparse)	*Streptococcus* (19.1%) *Veillonella* (17.6%) *Prevotella* 7 (17.2%)	*V. atypica* (24.3%) *S. mitis* (17.1%) *L. gingivalis* (15.1%)
P076	α-hemolytic Streptococcus (few)	*Prevotella* (29.3%) *Mycoplasma* (13.6%) *Prevotellaceae* (13.0%)	*P. salivae* (21.6%) ***P. oris*** (19.2%) *P. stomatis* (7.2%)
P077	None	*Streptococcus* (8.1%) *Enterococcus* (5.9%) *Haemophilus* (3.4%)	Excluded
P079	α-hemolytic *Streptococcus* (sparse) *N. flava* (sparse) *V. parvula* (sparse) *S. parasanguinis* (sparse)	*Neisseria* (16.3%) *Haemophilus* (11.6%) *Veillonella* (10.3%)	*Streptococcus* sp. (15.4%) *N. perflava* (14.7%) *P. nanceiensis* (11.0 %)
P080	α-hemolytic *Streptococcus* (few) *R. mucilaginosa* (few)	*Streptococcus* (25.8%) *Veillonella* (16.5%) *Prevotella 7* (12.0%)	***S. pseudopneumoniae*** (22.8%) *S. mitis* (22.4%) *V. dispar* (10.4%)
P082	α-hemolytic *Streptococcus* (mass) Saproph. *Neisseria* (mass) ***E. coli*** (plenty)	*Prevotella 7* (24.4%) *Veillonella* (22.6%) *Streptococcus* (18.7%)	*Streptococcus* sp. (12.1%) *S. oralis* (12.1%) *V. dispar* (10.5%)
P083	α-hemolytic *Streptococcus* (few) Saproph. *Neisseria* (sparse) Coagulase-negative *Staphylococcus* (sparse)	*Prevotella 7* (17.3%) *Veillonella* (12.4%) *Actinomyces* (11.6%)	Not Determined
P085	None	*Staphylococcus* (7.4%) *Enterobacteriaceae* (6.4%)	*M. osloensis* (63,83%)
P086	None	*Streptococcus* (13.7%) *Pseudomonas* (5.3%)	None
P088	*S. epidermidis* (sparse) *A. odontolyticus* (sparse) *L. reuteri* (sparse)	*Lactobacillus* (12.4%) *Veillonella* (7.9%)	Excluded
P089	*S. mitis* (sparse)	*Rothia* (15.1%) *Veillonella* (11.4%)	None

		Prevotellaceae (5.9%)	
P091	*S. mitis* (sparse) ***S. aureus*** (sparse) *R. mucilaginosa* (few)	*Rothia* (21.3%) *Streptococcus* (16.2%) *Prevotella 7* (16.1 %)	*Streptococcus* sp. (21.6%) *S. peroris* (17.8%) *V. atypica* (16.8%)
P092	None	*Prevotella 7* (15.6%) *Corynebacterium* (13.1%) *Rothia* (5.3%)	None
P093	α-hemolytic *Streptococcus* (mass) *N. flava* (mass) ***S. aureus*** (sparse) *P. melaninogenica* (plenty)	*Neisseria* (35.9%) *Streptococcus* (22.5%) *Haemophilus* (7.8%)	*N. flavescens* (32.3%) ***S. pneumoniae*** (27.3%) *H. haemolyticus* (7.3%)
P094	Pharyngeal flora (few)	*Micrococcales* (18.5%) *Prevotella 7* (16.2%) *Veillonella* (12.6%)	***T. whipplei*** (12.8%) *V. dispar* (12.1%) *V. atypica* (9.9%)
P095	***P. aeruginosa*** (mass)	*Pseudomonas* (77.1%) *Stenotrophomonas* (8.1%) *Neisseriaceae* (7.6%)	***P. aeruginosa*** (93.1%) ***S. maltophilia*** (4.5%)
P096	None	*Corynebacterium* (47.7%) *Enterococcus* (23.6%) *Neisseriaceae* (10.5%)	*E. faecium* (35.0%) *S. epidermidis* (18.5%) *C. tuberculostearicum* (8.3%)
P097	α-hemolytic *Streptococcus* (few) Coagulase-negative *Staphylococcus* (few) ***B. bronchiseptica*** (few)	*Micrococcales* (93.4%) *Bordetella* (4.4%)	***T. whipplei*** (92.7%) ***B. bronchiseptica*** (2.9%)
P098	None	*Enterococcus* (5.1%) *Acinetobacter* (3.5%) *Alphaproteobacteria* (3.3%)	None
P100	α-hemolytic *Streptococcus* (sparse) Saproph. *Neisseria* (sparse)	*Paracoccus* (26.0%) *Alloprevotella* (12.1%) *Neisseria* (9.6%)	*P. contaminans* (43.0%) *N. perflava* (16.7 %) *V. atypica* (4.4%)
P101	*E. faecium*	*Enterococcus* (5.6%) *Pediococcus* (3.1%)	*M. osloensis* (10.4%) *E. faecium* (7.8%)
P102	α-hemolytic *Streptococcus* (mass) ***S. aureus*** (few) *P. melaninogenica* (few)	*Rothia* (11.6%) *Fusobacterium* (11.1%) *Bacteroidales* (10.9%)	Not Determined
P103	None	*Veillonella* (16.6%) *Prevotella 7* (6.1%)	*V. dispar* (5.8%) *V. parvula* (5.3%) *M. osloensis* (4.6%)
P104	α-hemolytic *Streptococcus* (plenty)	*Prevotella 7* (19.2%) *Streptococcus* (14.9%) *Rothia* (14.0%)	*Streptococcus* sp. (18.0%) *S. mitis* (13.4%) *S. oralis* (9.5%)
P105	None	*Streptococcus* (3.2%) *Haemophilus* (3.0%)	*A. segnis* (10.7%) *S. oralis* (3.8%) *F. nucleatum* (3.1%)
P106	None	*Fusobacterium* (18.1%) *Limosilactobacillus* (9.2%) *Parvimonas* (8.1%)	*P. micra* (16.8%) *S. mitis* (7.0%) *C. rectus* (4.7%)
P107	***P. aeruginosa*** (plenty)	*Leptotrichia* (9.1%) *Veillonella* (6.1%) *Prevotellaceae* (5.0%)	*H. haemolyticus* (6.0%) *S. mitis* (4.2%) *Leptotrichia* sp. 212 (3.6%)
P108	None	None	*M. osloensis* (8.2%)
P109	None	*Veillonella* (12.4%) *Streptococcus* (8.7%)	*L. lactis* (48.5%) *S. saccharolyticus* (10.8 %)

		Rothia (7.1%)	*R. inusitata* (6.6%)
P110	***S. maltophilia*** (sparse)	*Stenotrophomonas* (37.5%) *Corynebacterium* (23.3%) *Streptococcus* (20.4%)	***Stenotrophomonas* sp. *MYb57*** (56.5%) *S. mitis* (34.3%)
P111	None	*Porphyromonas* (42.6%) *Veillonella* (11.5%) *Alloprevotella* (8.5%)	*P. stomatis* (23.3%) *V. atypica* (15.2%) *P. pasteri* (10.1%)
P112	*R. mucilaginosa* (plenty) α-hemolytic *Streptococcus* (sparse)	*Streptococcus* (20.1%) *Veillonella* (19.8%) *Rothia* (13.2%)	*Streptococcus* sp. (43.9%) *V. dispar* (27.7%) *C. concisus* (8.1%)
P113	None	*Streptococcus* (17.6%) *Prevotella 7* (8.9%) *Veillonella* (7.8%)	*Streptococcus* sp. (13.1%) *S. oralis* (9.8%) *G. elegans* (9.1%)
P114	None	*Streptococcus* (24.9%) *Fusobacterium* (17.5%) *Gemella* (13.2%)	*S. anginosus* (34.1%) *G. morbillorum* (18.0%) *P. micra* (13.4%)
P115	***E. coli*** (plenty) *S. salivarius* (plenty) *P. melaninogenica* (few)	*Veillonella* (15.1%) *Prevotella 7* (12.4%) *Streptococcus* (8.9%)	*S. oralis* (12.5%) *V. atypica* (12.0%) *V. dispar* (12.0%)
P116	*E. faecalis* (sparse)	*Streptococcus* (19.9%) *Veillonella* (6.2%) *Haemophilus* (3.2%)	***L. monocytogenes*** (11.0%) *T. bourrellyi* (6.9%)
P117	None	*Corynebacterium* (6.6%)	*B. deliciosa* (5.6%)
P118	None	None	*B. subtilis* (6.8%) *O. sancta* (3.8%)
P119	α-hemolytic *Streptococcus* (sparse)	*Streptococcus* (12.5%) *Rothia* (8.8%) *Haemophilus* (8.2%)	*H. parainfluenzae* (30.8%) *S. infantis* (4.7%) *S. sanguinis* (4.4%)
P120	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty) *R. mucilaginosa* (plenty)	*Prevotella 7* (27.9%) *Staphylococcus* (26.2%) *Rothia* (16.9%)	*S. epidermidis* (37.7%) *S. mitis* (16.9%) *S. oralis* (16.3%)
P123	Coagulase-negative *Staphylococcus* (few)	*Prevotella* 7 (10.6 %) *Saccharimonadaceae* (10.6 %) *Veillonella* (8.9%)	*Streptococcus* sp. (11.7%) *M. micronuciformis* (8.8%) *S. salivarius* (8.3%)
P124	Coagulase-negative *Staphylococcus* (plenty) *E. faecalis* (few)	*Staphylococcus* (38.2%) *Enterococcus* (22.7%) *Corynebacterium* (8.6%)	*S. epidermidis* (46.8%) *E. faecalis* (29.4%) ***L. monocytogenes*** (3.3%)
P125	None	*Streptococcus* (37.1%) *Rothia* (14.2%) *Veillonella* (9.3%)	*S. mitis* (38.0%) *H. parainfluenzae* (28.4%) *V. atypica* (6.2%)
P126	α-hemolytic *Streptococcus* (mass) ***S. aureus*** (mass) ***S. marcescens*** (plenty) *H. parahaemolyticus* (mass)	*Haemophilus* (20.6%) *Prevotella 7* (15.6%) *Streptococcus* (12.7%)	*H. parahaemolyticus* (46.3%) *S. mitis* (6.7%) *H. parainfluenzae* (5.3%)
P127	α-hemolytic *Streptococcus* (sparse)	*Prevotella 7* (17.7%) *Veillonella* (7.9%) *Staphylococcus* (6.5%)	*Streptococcus* sp. (22.3%) *V. dispar* (11.5%) *V. atypica* (10.0%)
P128	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty) Coagulase-negative *Staphylococcus* (sparse)	*Streptococcus* (24.1%) *Rothia* (19.5%) *Prevotella* 7 (8.8%)	*S. mitis* (36.8%) *S. infantis* (11.3%) *S. oralis* (10.0%)

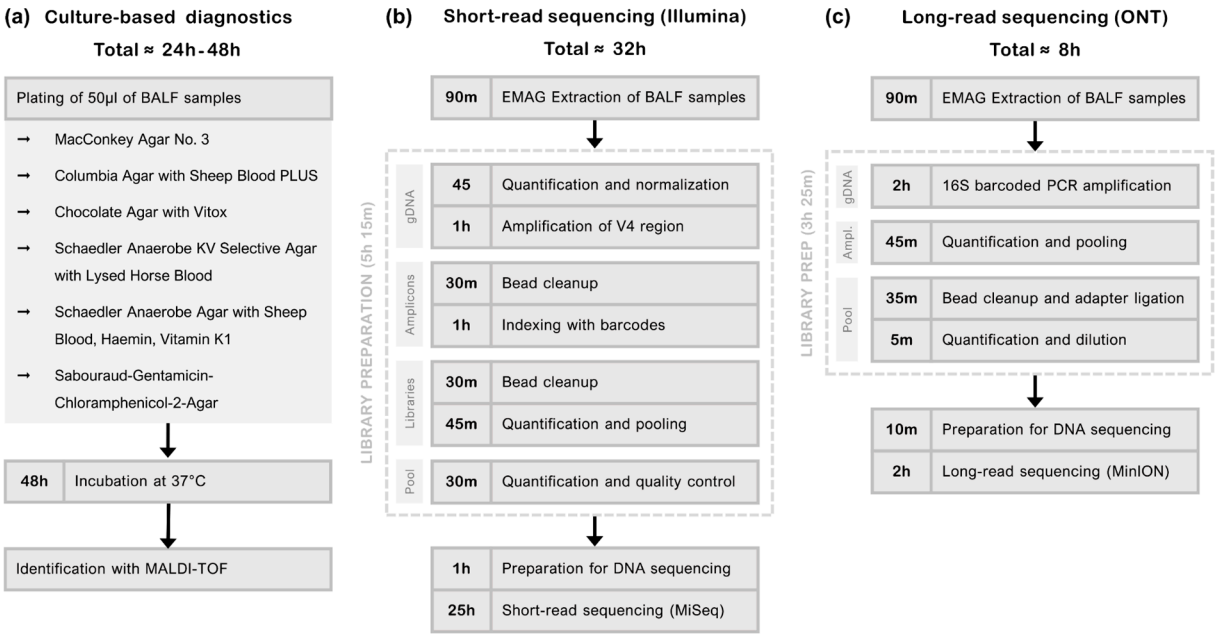
P130	None	*Streptococcus* (4.2%) *Prevotella 7* (3.9%) *Pirellulaceae* (3.9%)	None
P131	None	*Acetobacteraceae* (5.6%) *Brachybacterium* (4.0%) *Staphylococcus* (3.8%)	None
P133	***S. maltophilia*** (mass) α-hemolytic *Streptococcus* (plenty)	*Stenotrophomonas* (58.0%) *Prevotella 7* (14.2.%) *Streptococcus* (10.0%)	***S. maltophilia*** (91.9%)
P134	None	None	None
P135	None	*Rothia* (6.9%) *Haemophilus* (6.1%) *Streptococcus* (4.9%)	None
P137	None	*Veillonella* (37.2%) *Prevotella* (7.9%) *Neisseriaceae* (7.2%)	*V. parvula* (48.0%) *V. rogosae* (11.0%) *N. elongata* (4.6%)
P138	α-hemolytic *Streptococcus* (plenty) Saproph. *Neisseria* (plenty)	*Micrococcales* (27.0%) *Veillonella* (15.9%) *Prevotella* 7 (13.4%)	*V. atypica* (22.8%) ***T. whipplei*** (14.9%) *M. micronuciformis* (12.9%)
P140	***C. koseri*** (plenty)	*Veillonella* (23.2%)	***C. koseri*** (87.1%) *V. dispar* (4.3%)
P141	α-hemolytic *Streptococcus* (few) Saproph. *Neisseria* (few)	*Veillonella* (16.9 %) *Prevotella 7* (12.9%) *Streptococcus* (11.9%)	*V. atypica* (17.0%) *S. salivarius* (12.7%) *V. dispar* (12.1%)
P142	None	*Staphylococcus* (4.9%) *Pseudomonas* (3.4%)	*T. erythraeum* (32,02%)
P143	***S. aureus*** (mass)	*Streptococcus* (22.9%) *Staphylococcus* (16.1%) *Prevotella 7* (14.1%)	***S. pneumoniae*** (57.2%) ***S. aureus*** (9.2%) *S. mitis* (3.0%)
P144	***S. aureus*** (few) α-hemolytic *Streptococcus* (few) *P. melaninogenica* (few) *L. salivarius* (sparse)	*Streptococcus* (34.4%) *Rothia* (24.4%) *Prevotella* 7 (9.2%)	*S. mitis* (55.3%) ***S. pseudopneumoniae*** (16.9%) *G. haemolysans* (6.6%)

Supplementary Table S3. Overview of the number of BALF samples classified by their composition for Illumina short-read and ONT long-read sequencing.

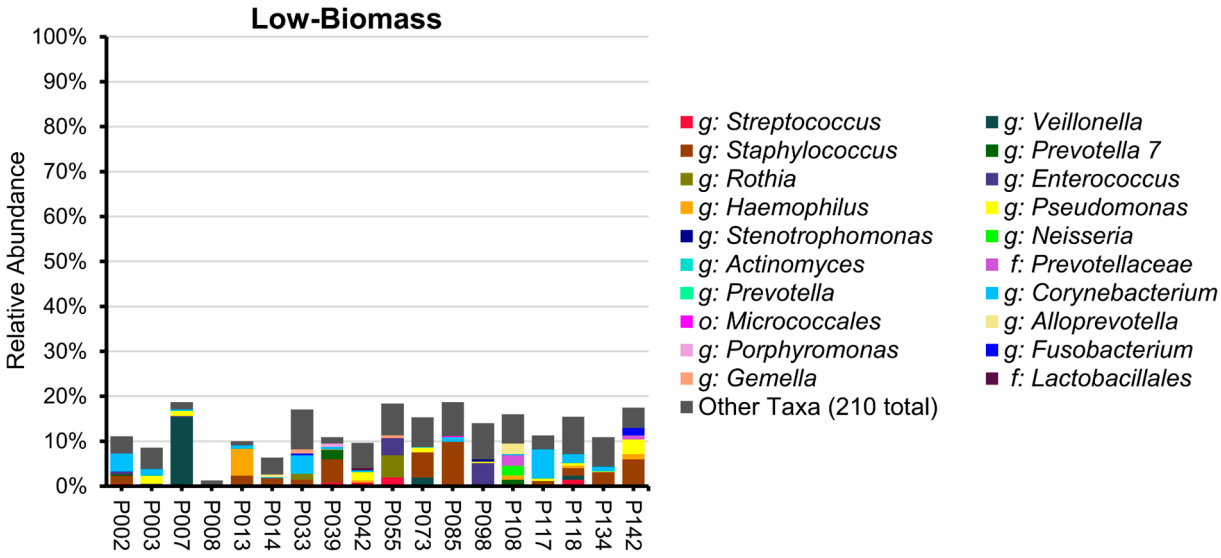
	Negative Culture		**Commensals in Culture**		**Potential Pathogens in Culture**	
	Illumina	**ONT**	**Illumina**	**ONT**	**Illumina**	**ONT**
Monomicrobial	0	4	3	8	10	13
Polymicrobial	6	9	17	14	7	5
Multimicrobia	20	9	19	7	6	2
Low-Biomass	13	6	2	3	3	1

Supplementary Table S4. OTUs removed as contamination because of their association with the negative controls used during Illumina short-read sequencing.

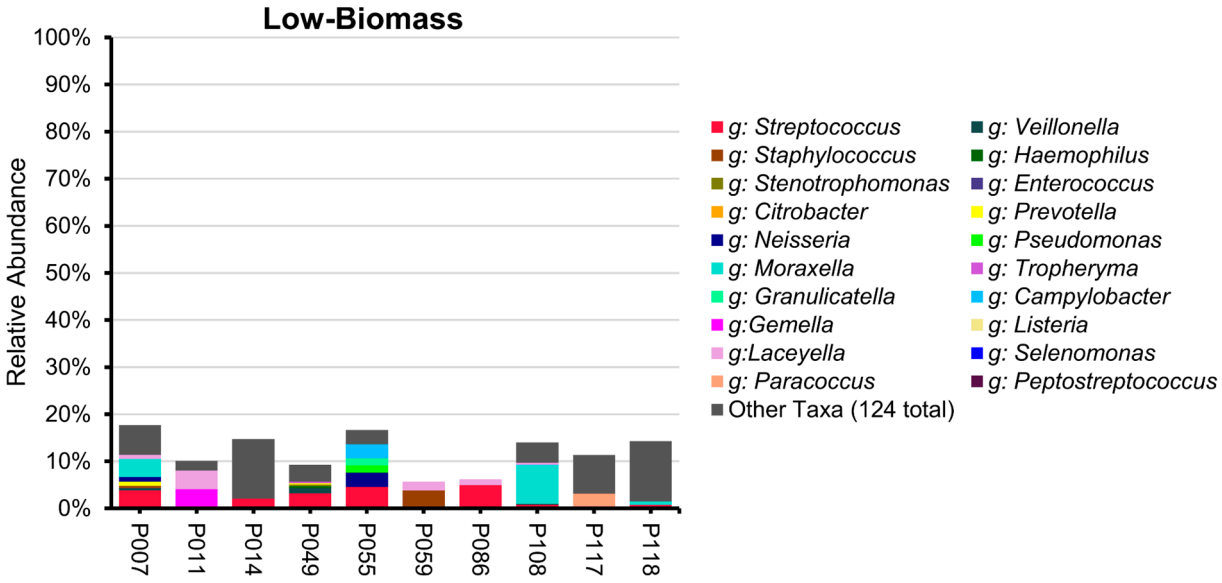
OTU ID	Genus
OTU0001	*Escherichia-Shigella*
OTU0007	*Pseudomonas*
OTU0008	*Pseudomonas*
OTU0010	*Enhydrobacter*
OTU0012	*Cutibacterium*
OTU0019	*Rhodobacteraceae* unclassified
OTU0042	*Micrococcus*
OTU0053	*Corynebacterium*
OTU0054	*Micrococcales* unclassified
OTU0069	*Methylobacterium-Methylorubrum*
OTU0077	*Brevundimonas*
OTU0079	*Corynebacteriales* unclassified
OTU0093	*Acinetobacter*
OTU0097	*Xanthobacteraceae* unclassified
OTU0098	*Kocuria*
OTU0107	*Cupriavidus*
OTU0108	*Methylobacterium-Methylorubrum*
OTU0109	*Lactococcus*
OTU0122	*Comamonadaceae* unclassified
OTU0125	*Pontibacter*
OTU0143	*Propionibacteriaceae* unclassified
OTU0200	*Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*
OTU0209	*Chryseobacterium*
OTU0210	*Sphingomonas*
OTU0212	*Chryseobacterium*
OTU0213	*Acidibacter*
OTU0254	*Burkholderia-Caballeronia-Paraburkholderia*
OTU0271	*Yersiniaceae* unclassified
OTU0290	*Sphingomonas*
OTU0463	*Bacteroides*
OTU0481	*Ruminococcus*
OTU0533	*Lachnospiraceae* unclassified



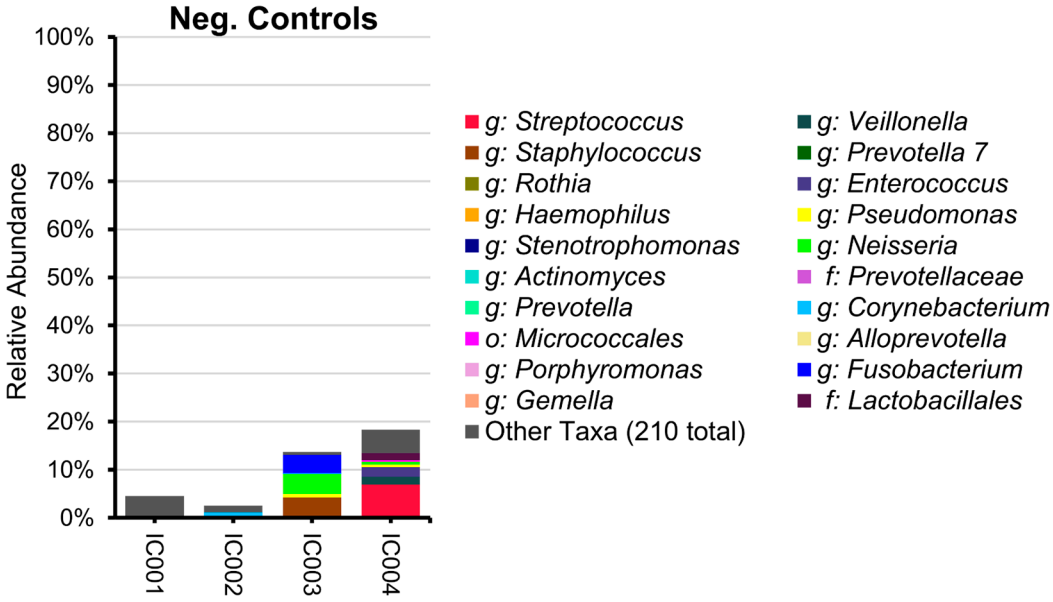
Supplementary Figure S1. Overview of the workflows and time estimated for completion of (a) culture-based diagnostics, (b) Illumina sequencing and (c) ONT sequencing.



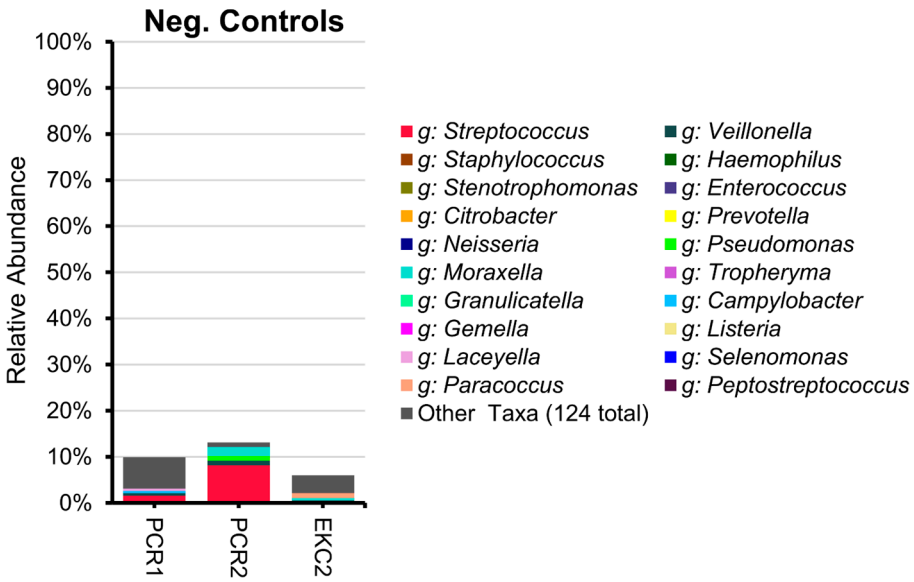
Supplementary Figure S2. Illumina short-read sequenced BALF samples classified as low-biomass.



Supplementary Figure S3. ONT long-read sequenced BALF samples classified as low-biomass.



Supplementary Figure S4. Remaining negative controls for Illumina short-read sequencing after removal of detected contaminations (Supplementary Table S3).



Supplementary Figure S5. Remaining negative controls for ONT long-read sequencing after removal of contaminations by *Delftia acidovorans*, *Escherichia coli*, *Paracoccus angustae* and *Paracoccus marinus*.