## Appendix 1 Methods

Study participants of patients whose bronchoalveolar lavage fluid (BALF) samples were used for microbiome analysis

To explore associations of BALF microbiome and pneumonia severity in diabetic patients, the BALF samples from 177 patients which consisted of 137 patients without diabetes mellitus (DM) and 40 patients with DM, were sequenced using metagenomic next-generation sequencing(mNGS). The reasons for bronchoscopy include: 1) septic shock requiring the use of vasoactive drugs, respiratory failure requiring invasive mechanical ventilation, multiple organ dysfunction and other life-threatening conditions in the early stage of pneumonia; 2) patients with persistent exacerbation of infection symptoms or rapid radiographic progression after 48-72 hours of standard empirical anti-infective therapy; 3) patients with negative results of traditional pathogen detection methods requiring further identification of pathogens, and 4) identification of patients with non-infectious diseases (e.g., pulmonary involvement of connective tissue disease, pulmonary lymphoma, etc.) Demographics and clinical characteristics of 177 patients were showed in Table S1.
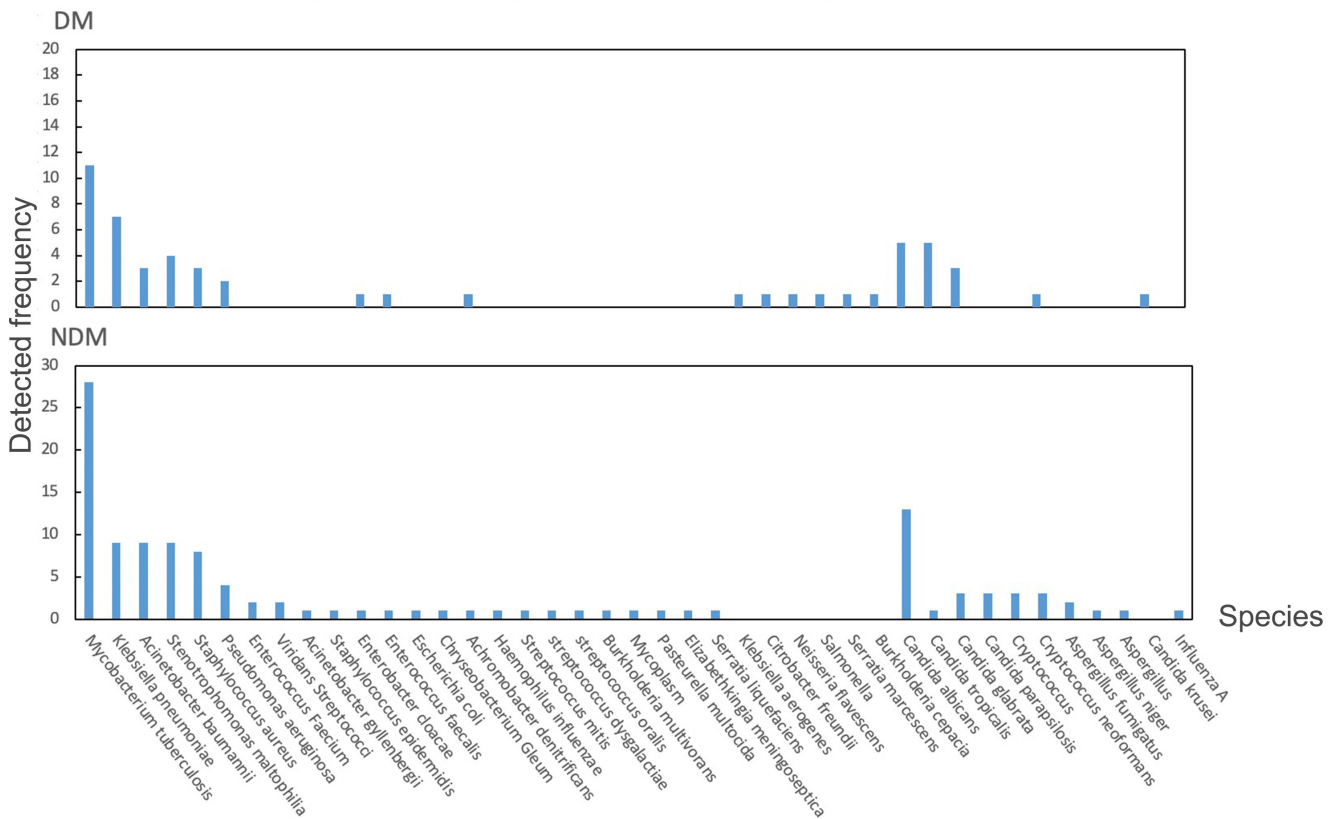
Figure S1 Pathogens detected in pneumonia applying metagenome next-generation sequencing technology in DM group and NDM group. DM, diabetes mellitus; NDM, non-diabetes mellitus.
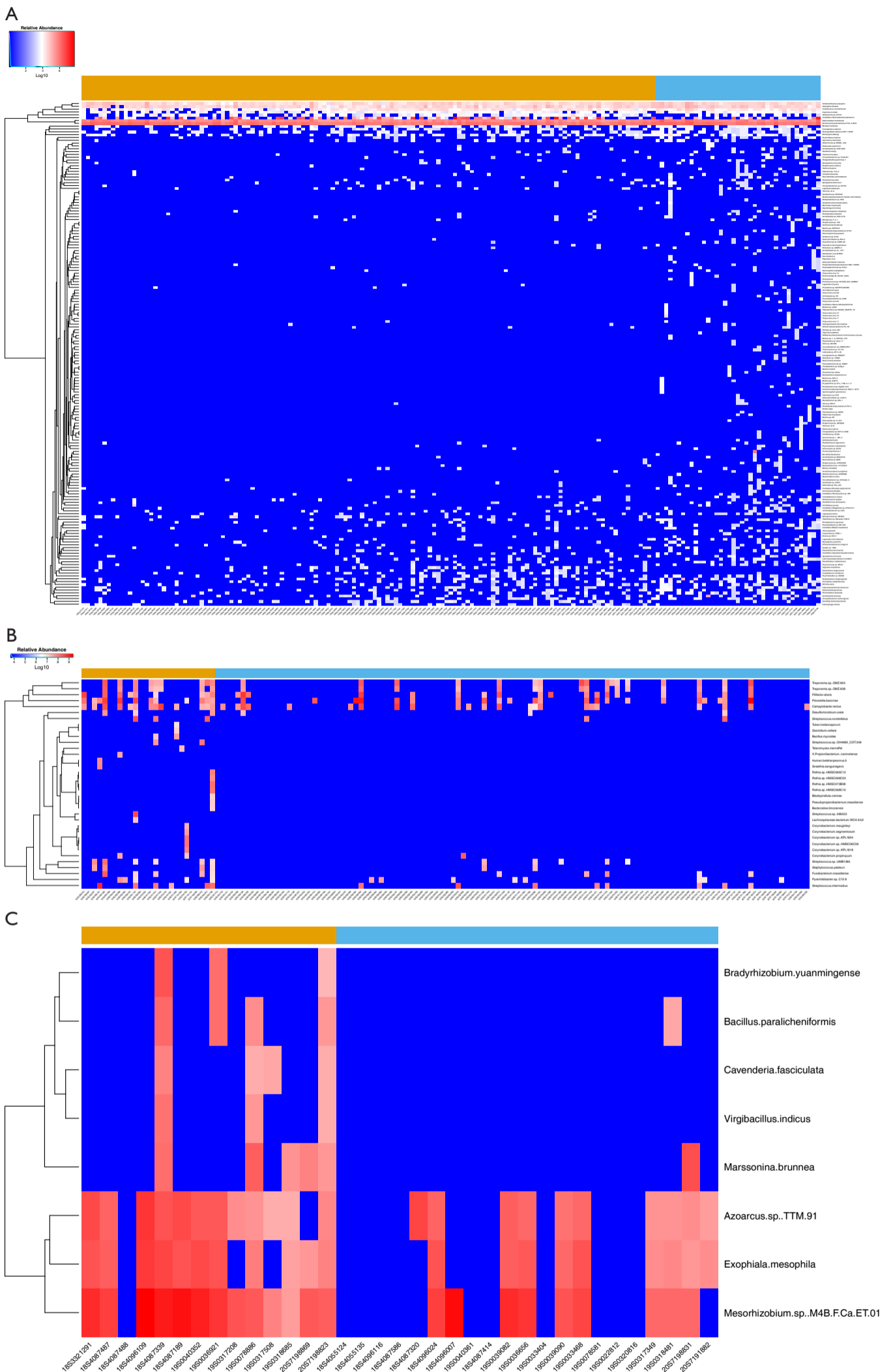
Figure S2 Microecological analysis heatmap of diabetes complicated with pneumonia. (A) Relative abundance between DM group and NDM group. (B) Relative abundance of mild pneumonia between DM group and NDM group. (C) Relative abundance of severe pneumonia between DM group and NDM group. DM, diabetes mellitus; NDM, non-diabetes mellitus.

Table S1 Correlation analysis between clinical parameters of patients in DM group and NDM group and severe pneumonia

Group	Clinical characteristics	Rho
NDM	Mechanical ventilation	0.726988
DM	Mechanical ventilation	0.735131
	Lymphocyte count	−0.643752
	Albumin	−0.613042
	Eosinophil count	−0.602504
	Calcium	−0.611149
	D-dimer	0.649085
	CRP	0.687266
	CD3$^+$ T cell	−0.770858
	CD4$^+$ T cell	−0.799530
	CD8$^+$ T cell	−0.618590
	C3	−0.645375
	TNF	0.657536
	Urine protein	0.670476
	LDH	0.617324
	Myoglobin	0.605297
	PCT	0.786436

This table only shows results (|Rho| >0.6) applying the Spearman correlation. Rho >0 indicates positive correlation, Rho <0 indicates negative correlation. DM, diabetes mellitus; NDM, non-diabetes mellitus; CRP, C-reactive protein; C3, complement3; TNF, tumor necrosis factor; LDH, lactate dehydrogenase; PCT, procalcitonin; Rho, Spearman's rank correlation coefficient.

Table S2 Demographics and clinical characteristics of patients in DM group and NDM group whose BALF samples were used for microbiome analysis

Characteristics	DM (n=40)	NDM (n=137)	P value
Socio-demographic details			
Age (years)	63.75±11.65	52.99±16.42	<0.001*
≥60	70.48±6.19	68.98±6.85	0.185
Male sex	29 (72.50)	74 (54.01)	0.037*
Smoking	15 (37.50)	36 (26.28)	0.168
BMI, kg/m^2	22.14±3.57	23.40±3.73	0.003*
Severe cases	14 (35.00)	21 (15.33)	0.006*
Admission to ICU	5 (12.50)	4 (2.92)	0.044*
Mechanical ventilation	5 (12.50)	4 (2.92)	0.044*
Comorbidity			
Hypertension	23 (57.50)	25 (18.25)	<0.001*
Asthma	0 (0.00)	4 (2.92)	0.576
COPD	0 (0.00)	3 (2.19)	>0.99
Coronary heart disease	5 (12.50)	5 (3.65)	0.081
Cerebral infarction	4 (10.00)	5 (3.65)	0.230

Data are presented as mean ± SD or n (%) by applying Fisher's exact test or Wilcoxon rank sum test. Continuous variables were analyzed using Student's *t*-test or Mann-Whitney U test as appropriate. *, statistical significance (P<0.05). DM, diabetes mellitus; NDM, non-diabetes mellitus; BALF, bronchoalveolar lavage fluid; BMI, body mass index; ICU, intensive care unit; COPD, chronic obstructive pulmonary disease; SD, standard deviation.

Differential microorganisms between MP and SP
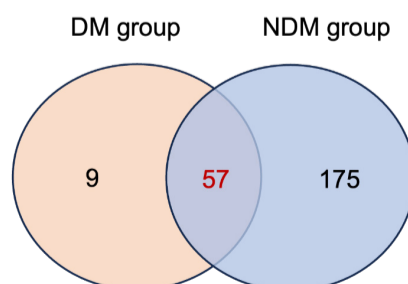
Figure S3 Venn diagram of differential microorganisms between MP and SP in DM and NDM groups. MP, mild pneumonia; SP, severe pneumonia; DM, diabetes mellitus; NDM, non-diabetes mellitus.

Table S3 The fifty-seven differential microorganisms between mild pneumonia and severe pneumonia detected both in the DM and NDM groups

Number	Microbes
1	*Alloprevotella.rava*
2	*Alloprevotella.tannerae*
3	*Prevotella.baroniae*
4	*Actinomyces.graevenitzii*
5	*Veillonella.dispar*
6	*Prevotella.intermedia*
7	*Prevotella.sp..A2879*
8	*Streptococcus.sanguinis*
9	*Veillonella.atypica*
10	*Prevotella.sp..oral.taxon.306*
11	*Prevotella.nanceiensis*
12	*Campylobacter.showae*
13	*Prevotella.pallens*
14	*Prevotella.jejuni*
15	*Porphyromonas.endodontalis*
16	*Prevotella.sp..ICM33*
17	*Aggregatibacter.segnis*
18	*Leptotrichia.sp..oral.taxon.215*
19	*Prevotella.scopos*
20	*Prevotella.oris*
21	*Streptococcus.mitis*
22	*Prevotella.melaninogenica*
23	*Veillonella.sp..S13053.19*
24	*Veillonella.rogosae*
25	*Veillonella.parvula*
26	*Prevotella.salivae*
27	*Tannerella.forsythia*
28	*Haemophilus.parainfluenzae*
29	*Neisseria.sicca*
30	*Kingella.denitrificans*
31	*Neisseria.elongata*
32	*Porphyromonas.gingivalis*
33	*Prevotella.histicola*
34	*Treponema.denticola*
35	*Neisseria.sp..HMSC068C04*
36	*Haemophilus.parahaemolyticus*
37	*Porphyromonas.sp..oral.taxon.279*
38	*Neisseria.mucosa*
39	*Prevotella.veroralis*
40	*Gemella.sanguinis*
41	*Streptococcus.infantis*
42	*Neisseria.subflava*
43	*Prevotella.shahii*
44	*Prevotella.sp..oral.taxon.473*
45	*Fusobacterium.periodonticum*
46	*Veillonella.tobetsuensis*
47	*Tannerella.sp..oral.taxon.HOT.286*
48	*Prevotella.sp..oral.taxon.313*
49	*Prevotella.aurantiaca*
50	*Fusobacterium.pseudoperiodonticum*
51	*Prevotella.pleuritidis*
52	*Campylobacter.rectus*
53	*Veillonella.sp..oral.taxon.158*
54	*Neisseria.flavescens*
55	*Porphyromonas.sp..KLE.1280*
56	*Prevotella.sp..C561*
57	*Fusobacterium.nucleatum*

The results are presented by applying Wilcoxon rank sum test. DM, diabetes mellitus; NDM, non-diabetes mellitus.

Table S4 Spearman's rank correlation analysis between microbes and clinical features

Microbes	Clinical features	|Rho| >0.6
Porphyromonas endodontalis	Urine protein	−0.678309949
Lactobacillus mudanjiangensis	complement C3	0.682852315
Prevotella intermedia	Complement C3	0.654661164
Porphyromonas endodontalis	Complement C3	0.785181851
Virgibacillus profundi	Complement C3	0.731494203
Clostridioides difficile	Complement C3	0.670408241
Prevotella oris	Complement C3	0.620496364
Bacillus fortis	Complement C3	0.620205314
Prevotella salivae	Complement C3	0.617072964
Waddlia chondrophila	Complement C3	0.717100589
Salmonella sp. zj-f94	Complement C3	0.720440516
Agrococcus jejuensis	Complement C3	0.707911116
Pseudomonas sp. 2995-1	Complement C3	0.620235195
Shigella sonnei	Complement C3	0.657793514
Campylobacter rectus	Complement C3	0.642789647
Paenibacillus odorifer	TNF	0.639009650
Phycomyces blakesleeanus	TNF	0.639009650
Botrytis cinerea	TNF	0.602494813
Pseudomonas viridiflava	TNF	0.633333333
Enterococcus faecium	TNF	0.650000000
Exserohilum turcicum	TNF	0.707474970
Bordetella bronchiseptica	TNF	0.639009650
Neisseria gonorrhoeae	TNF	0.639009650
Capronia epimyces	TNF	0.616666667
Trypanosoma brucei	TNF	0.707474970
Virgibacillus indicus	TNF	0.707474970
Cavenderia fasciculata	TNF	0.782216559
Pseudoalteromonas elyakovii	TNF	0.821822461
Paeniglutamicibacter antarcticus	TNF	0.707474970
Staphylococcus aureus	TNF	0.616666667
Trypanosoma cruzi	TNF	0.821822461

This table only shows results (|Rho| >0.6) applying the Spearman correlation. Rho, Spearman's rank correlation coefficient; TNF, tumor necrosis factor.