Supplementary materials

Text S1.Sequencing data information

Genomic DNA was extracted from the samples using a DNA extraction kit (MagPure Soil DNA LQ Kit (Magan)). The concentration of DNA was verified with Nano Drop 2000 (Thermo Fisher Scientific, USA) and agarose gel. The quality of amplicons was visualized using gel electrophoresis, purified with AMPure XP beads (Agencourt), and amplified for another round of PCR. After being purified with the AMPure XP beads once more, the final amplicon was quantified using the Qubit dsDNA assay kit. Equal amounts of purified amplicon were pooled for subsequent sequencing.

The raw sequencing data was in FASTQ format. Illumina MiSeq (Illumina, USA) sequencing generates raw double-ended sequences, which are referred to as raw data. The raw data processing flow chart can be seen in Figure S1. The flow chart for processing raw data can be seen in Figure S1. The paired-end reads were then preprocessed using Cutadapt software (version 4.4, Sweden) to detect and remove the adapter. After trimming, the paired-end reads were filtering low quality sequences, denoised, merged, and the chimera reads were detected and removed using DADA2 with the default parameters of QIIME2 (2020.11). Finally, the software generated the representative reads and the ASV abundance table. The representative read of each ASV was selected using the QIIME2 package. All representative reads were annotated and blasted against the Silva database Version 138 (or unite) (16S/18S/ITS rDNA) using q2-feature-classifier with the default parameters.

A total of 19 samples were analyzed. The raw read data ranged from 78,044 to 81,872. After undergoing quality control, the clean tag data ranged from 65,256 to 76,158. The valid tags (the final data used for analysis) were obtained by removing chimeras from the clean tags, and their data distribution ranged from 63,247 to 74,396. The number of ASVs in each sample ranged from 63 to 790.

The statistical analysis of project samples was performed. ANOVA algorithm showed that the number of different ASVs was 10, the number of different genera was 4, and the number of different phyla was 3. Kruskal Wallis algorithm: The number of different ASVs is 12, the number of different genera is 7, and the number of different phyla is 3.

Table S1 chemical element in the PMs

Chemical element	Mass （mg/kg）	Methods
Na	0.796±0.065	AAS,ICP-AES,INAA,XRF
Mg	1.40±0. 06	ICP-AES,ICP-MS,XRF
Al	5.04±0. 10	ICP-AES,ICP-MS,INAA,XRF
K	1.37±0. 06	AAS,ICP-AES,XRF
Ga	6.69±0. 24	ICP-AES,ICP-MS,INAA,XRF
Ti	0.292±0. 033	ICP-AES,ICP-MS,INAA,PIXE,XRF
Fe	2.92±0. 17	ICP-AES,ICP-MS,INAA,XRF
Zn	0.114±0. 010	ICP-AES,ICP-MS,INAA,PIXE,XRF
V	73.2±7. 0	ICP-AES,ICP-MS,INAA
Mn	686±42	ICP-AES,ICP-MS,INAA,PIXE,XRF
Ni	63.8±3. 4	AAS,ICP-AES,ICP-MS
Cu	104±12	ICP-AES,ICP-MS,PIXE,XRF
As	90.2±10. 7	HG-AAS,HG-ICP-AES,ICP-AES, ICP-MS,INAA,XRF
Sr	469±16	ICP-AES,ICP-MS,XRF
Cd	5.60±0. 43	ICP-AES,ICP-MS
Ba	874±65	ICP-AES,ICP-MS,INAA
Pb	403±32	ICP-AES,ICP-MS,XRF
U	4.33±0. 26	ICP-MS,INAA

Table S2. Results of the correlation between inflammatory cytokines and microorganisms (Spearman correlation coefficient |r| and p-value). If $|r| > 0.5$ and $p < 0.05$, it indicates a significant correlation.* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

Inflammatory Cytokines			IgG	IgE	IL-4	IL-13	TNF-α	IFN-γ
Phylum	*Desulfobacterota*	|r|	**0.5222**	**0.7109**	0.1568	0.2014	0.2406	0.1513
		p	**0.0218**	**0.0006**	0.5216	0.4083	0.3211	0.5364
	Acidobacteriota	|r|	**0.5234**	**0.5566**	0.3261	0.0117	0.0059	0.0195
		p	**0.0215**	**0.0133**	0.1730	0.9620	0.9810	0.9368
	Fusobacteriota	|r|	0.2382	0.2594	0.0170	0.2360	**0.5316**	0.3232
		p	0.3262	0.2835	0.9449	0.3306	**0.0192**	0.1771
	Firmicutes	|r|	0.2614	**0.4842**	0.3614	0.0158	0.1614	0.0982
		p	0.2785	**0.0374**	0.1289	0.9512	0.5077	0.6887
	Deferribacterota	|r|	0.3521	**0.4739**	0.2007	0.2172	0.2435	0.2731
		p	0.1393	**0.0404**	0.4099	0.3718	0.3151	0.2579
Genus	*Pseudoxanthomonas*	|r|	**0.5057**	**0.7057**	0.1894	0.1586	0.0167	0.0370
		p	**0.0272**	**0.0007**	0.4373	0.5167	0.9458	0.8804
	Desulfovibrio	|r|	**0.5387**	**0.6862**	0.3468	0.1550	0.1279	0.2041
		p	**0.0173**	**0.0012**	0.1458	0.5265	0.6018	0.4018
	Enterococcus	|r|	**0.4632**	**0.6807**	0.2596	0.0070	0.0509	0.0526
		p	**0.0475**	**0.0018**	0.2818	0.9799	0.8372	0.8316
	Parabacteroides	|r|	0.0475	0.0018	**0.2818**	**0.9799**	0.8372	**0.8316**
		p	0.9512	0.3024	**0.0189**	**0.0119**	0.1035	**0.0086**
	Fusobacterium	|r|	0.3463	0.3915	0.0747	0.3338	**0.5794**	0.3644
		p	0.1464	0.0974	0.7612	0.1625	**0.0093**	0.1251
	Alloprevotella	|r|	0.1807	0.1999	0.2722	**0.5635**	0.3657	**0.5337**
		p	0.4590	0.4120	0.2596	**0.0120**	0.1236	**0.0186**
	Clade_Ia	|r|	**0.5542**	**0.5507**	0.3427	0.2740	0.4079	0.3886
		p	**0.0138**	**0.0146**	0.1509	0.2563	0.0830	0.1002
	Prevotellaceae NK3B31 group	|r|	0.0669	0.2574	0.0537	0.3750	**0.5341**	**0.4915**
		p	0.7856	0.2873	0.8271	0.1137	**0.0185**	**0.0326**
	Prevotella	|r|	0.2842	0.3860	**0.5263**	0.3632	0.1211	0.3211
		p	0.2374	0.1035	**0.0222**	0.1270	0.6207	0.1800
	Photobacterium	|r|	0.2722	0.4229	**0.5172**	0.3498	0.1463	0.3278
		p	0.2595	0.0712	**0.0234**	0.1421	0.5502	0.1707
	Methylophaga	|r|	**0.5141**	0.3468	0.1377	0.3468	0.2140	0.3689
		p	**0.0243**	0.1458	0.5739	0.1458	0.3790	0.1201
	Bifidobacterium	|r|	**0.5037**	**0.4951**	0.3766	0.1119	0.1641	0.1698
		p	**0.0279**	**0.0311**	0.1120	0.6483	0.5020	0.4871
	Coprococcus	|r|	**0.4958**	0.4295	0.0276	0.1008	0.1478	0.1450
		p	**0.0309**	0.0665	0.9106	0.6813	0.5461	0.5537
	Lachnospiraceae NK4A136 group	|r|	0.1211	0.2273	0.2018	0.3765	**0.4906**	0.4291
		p	0.6214	0.3494	0.4073	0.1121	**0.0330**	0.0667
	Chryseobacterium	|r|	0.1133	0.1152	0.2168	**0.4863**	0.3515	0.4453
		p	0.6443	0.6386	0.3727	**0.0348**	0.1400	0.0561
	Rodentibacter	|r|	0.3357	**0.4640**	0.2369	0.2205	0.2567	0.2896
		p	0.1600	**0.0454**	0.3287	0.3644	0.2888	0.2291

	[Ruminococcus] gnavus group	**|r|**	**0.5331**	0.3225	0.1415	0.1382	0.0099	0.0395
		p	**0.0188**	0.1781	0.5634	0.5726	0.9680	0.8725
	Faecalibacterium	**|r|**	0.0836	0.1377	0.4476	0.4034	**0.5411**	0.3862
		p	0.7336	0.5739	0.0546	0.0868	**0.0167**	0.1025
	Mucispirillum	**|r|**	0.3521	**0.4739**	0.2007	0.2172	0.2435	0.2731
		p	0.1393	**0.0404**	0.4099	0.3718	0.3151	0.2579
	Methyloversatilis	**|r|**	**0.7376**	**0.9068**	0.3166	0.1403	0.0612	0.0126
		p	**0.0003**	**0.0000**	0.1866	0.5666	0.8035	0.9592

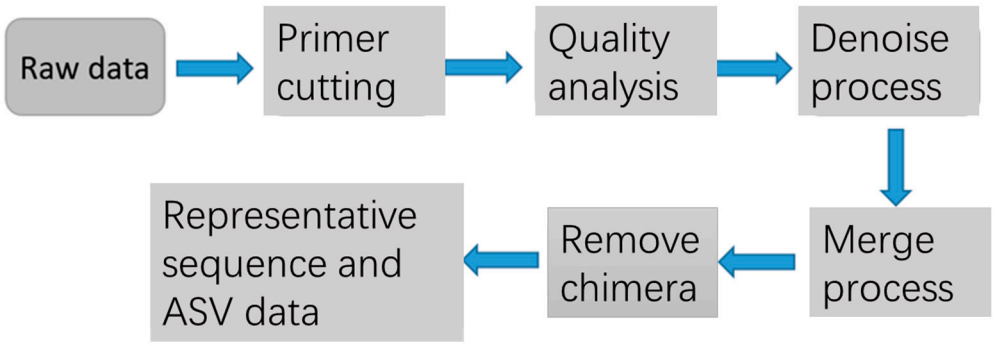

Figure S1. Data Processing Flow Chart. Illumina MiSeq. Using the cutadapt software, remove the primers from the raw data sequence. Using DADA2, the paired-end raw data from the previous step is analyzed with Qiime2 default parameters for quality control, including quality filtering, noise reduction, splicing, and chimera detection. This analysis aims to obtain the representative sequence and ASV abundance table.

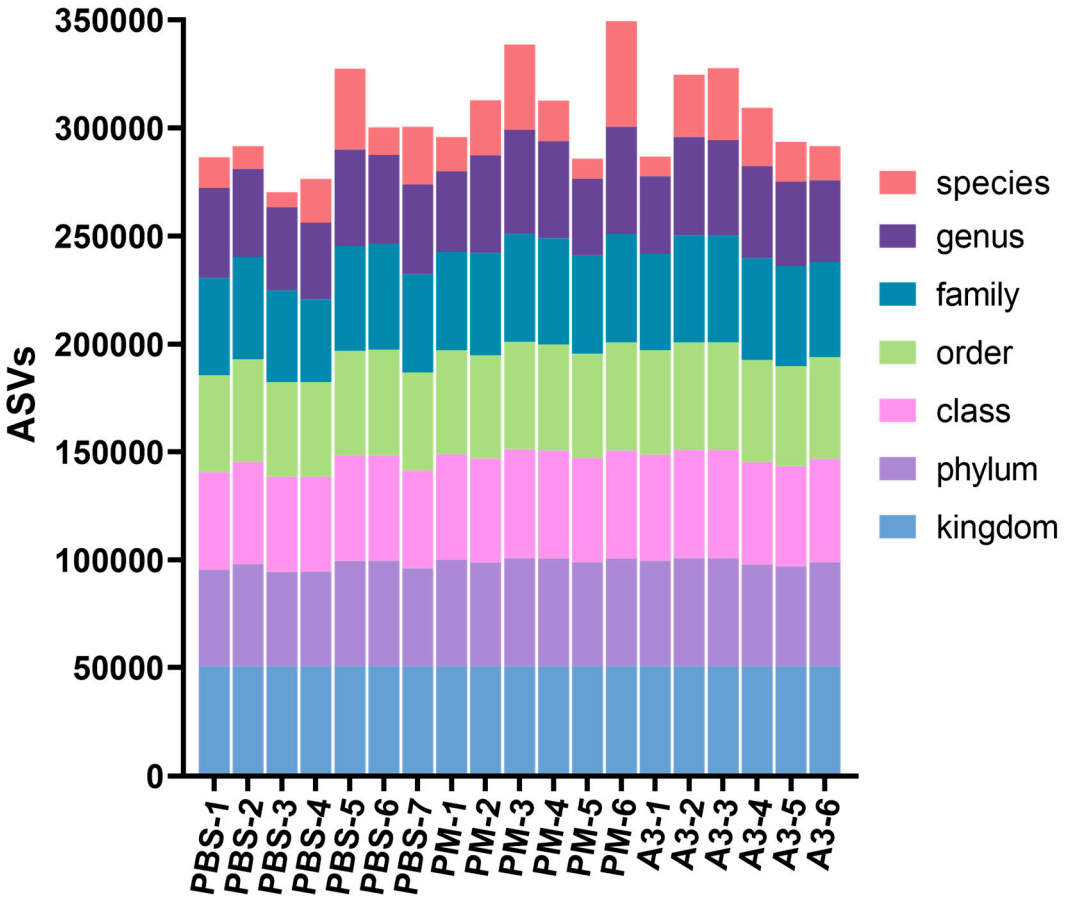

Figure S2. ASV level barplot of each sample

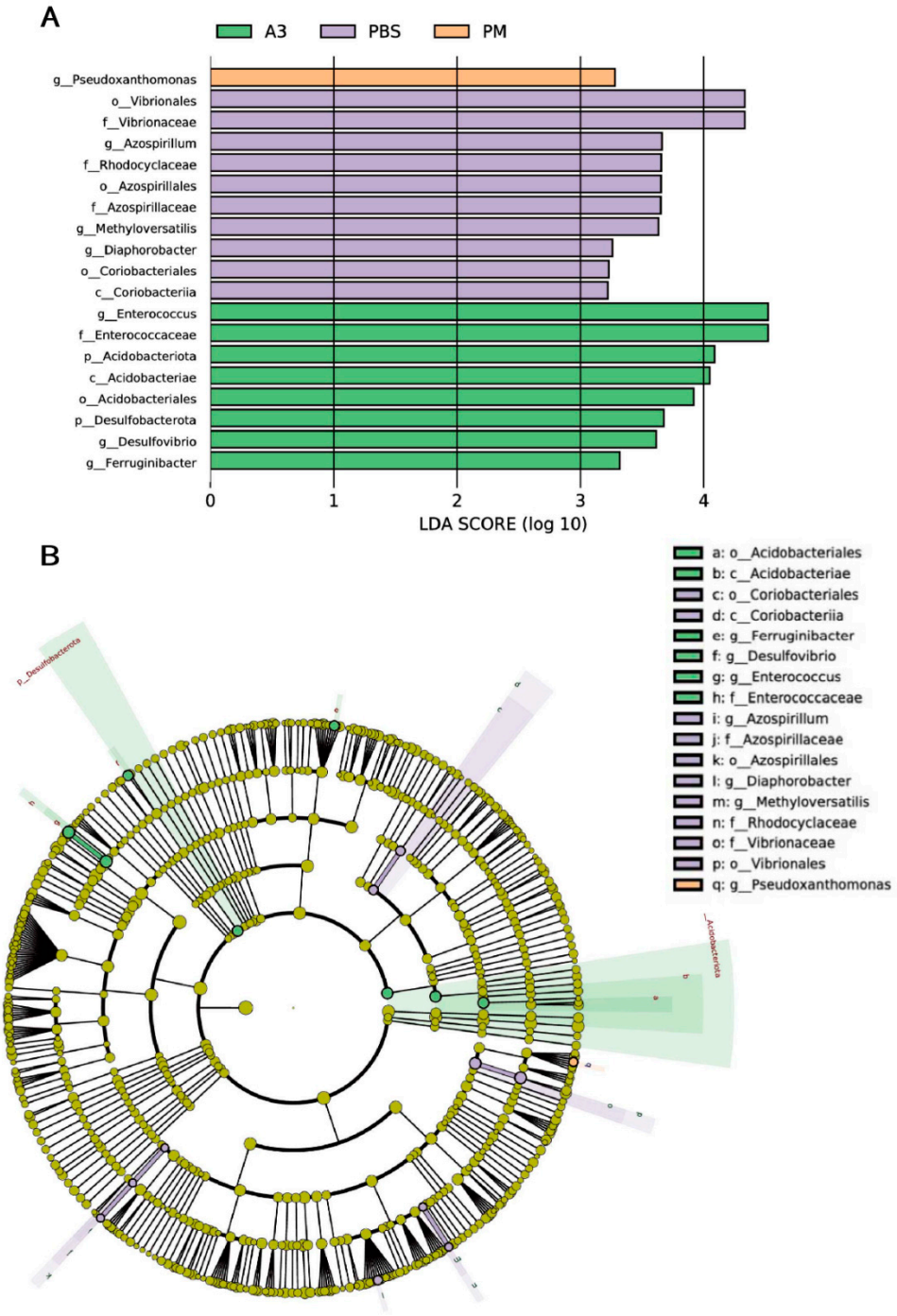

Figure S3. Enrichment of microbial taxa in lung tissue of mice in different groups. (A) The species score map of the mouse microbiome in different groups was utilized to distinguish between the groups by color. The bars of various colors represented species with relatively high abundance in their corresponding color group; (B) example of annotated branch of differentially enriched species, Different groups are distinguished by color, and nodes represent species in the corresponding color group that differ significantly in abundance relative to other taxa. The diameter of nodes is proportional to relative abundance. Nodes in each layer represent phyla, class, order, family, and genus from inside out. PBS, PBS control; PM, PMs exposure; A3, Pla a3 protein exposure.

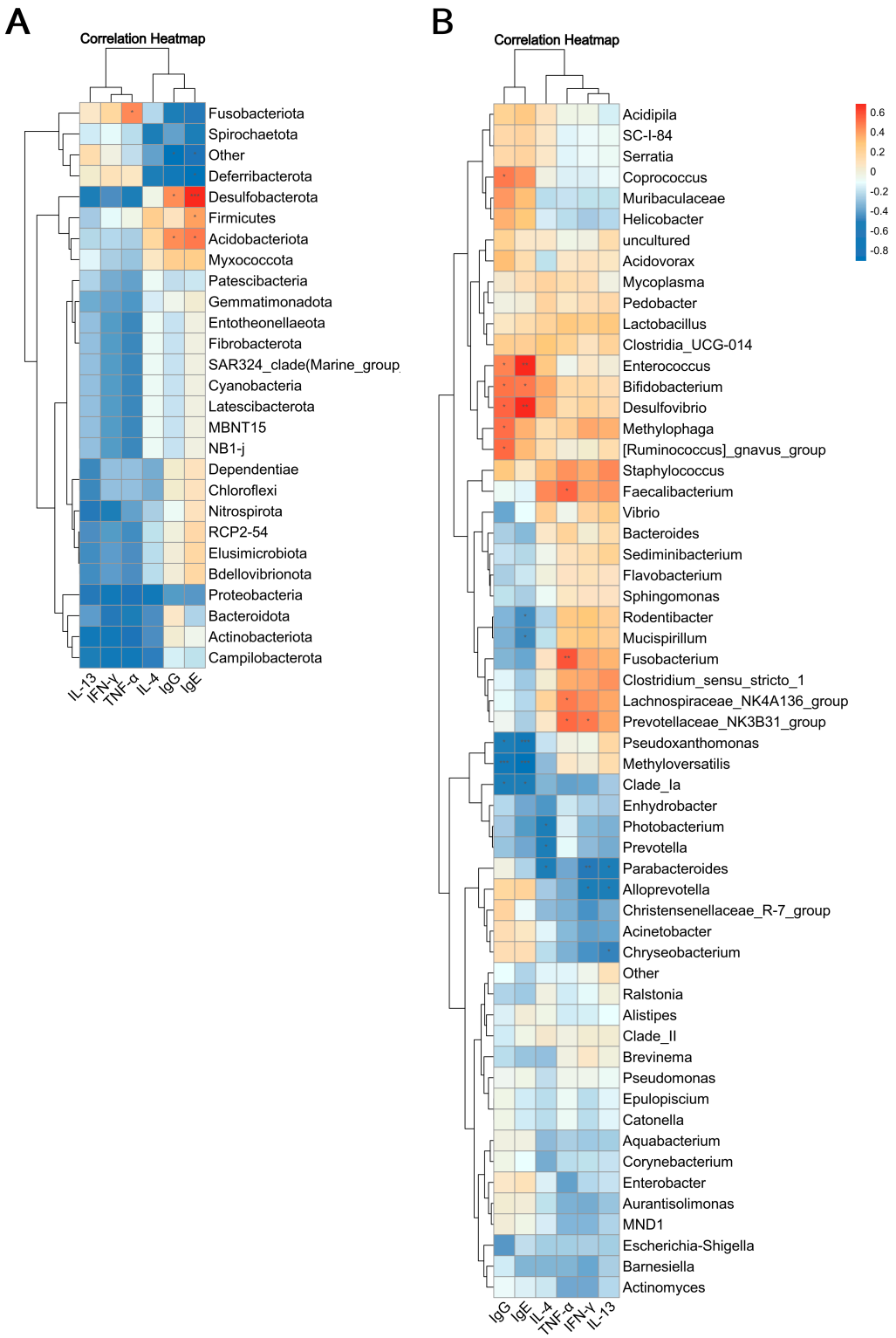

Figure S4. Correlationship between lung injury markers and varieties of microbial in lung tissue after the mice exposed to PMs and Pla a3 protein. The heatmap shows the correlation analysis at the phylum (A) and genus (B) levels. Red indicates a positive correlation, blue indicates a negative correlation, and the intensity of the color indicates the strength of the correlation. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.