



Comprehensive lung microbial gene and genome catalogs assist the mechanism survey of *Mesomycoplasma hyopneumoniae* strains causing pig lung lesions

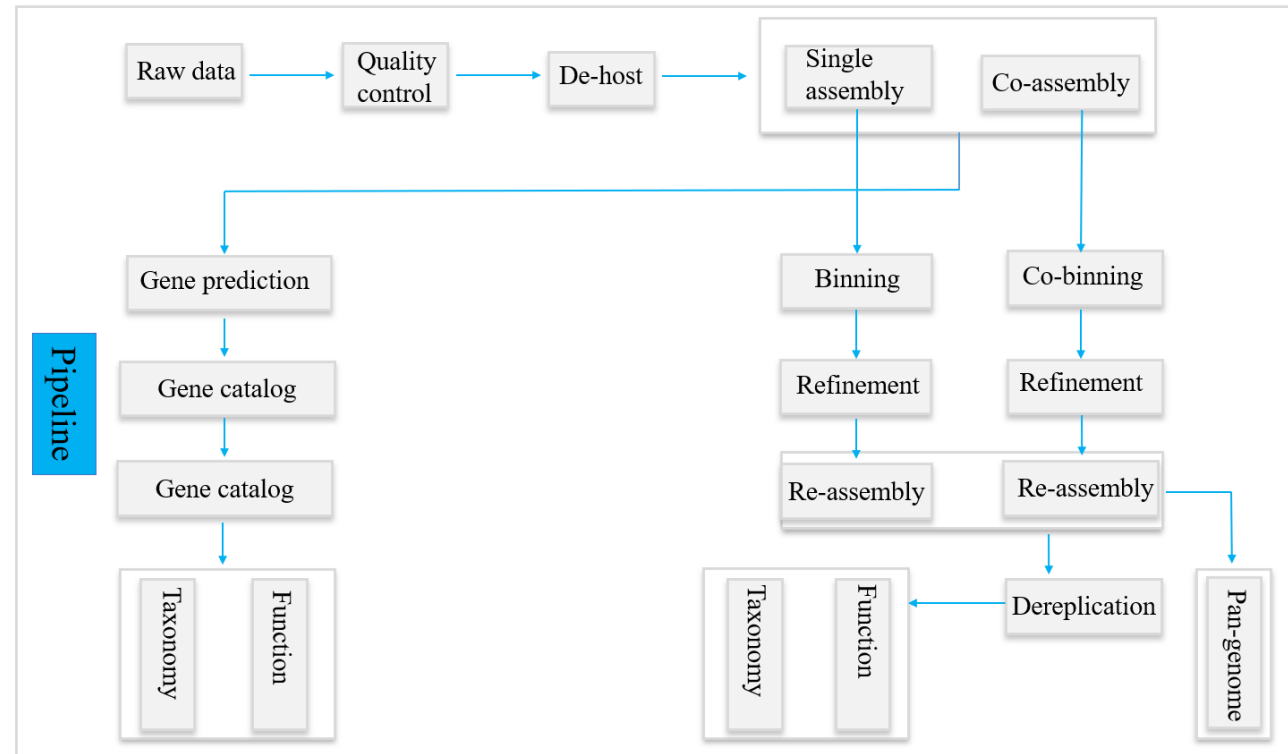
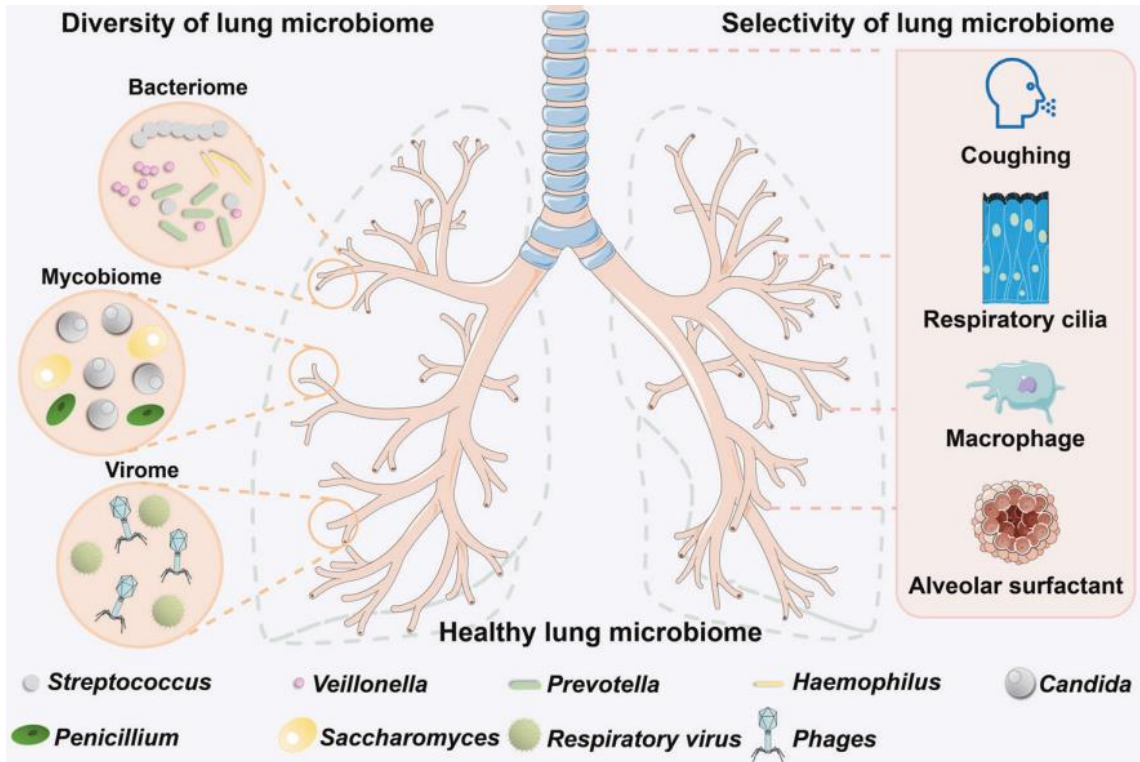
Jingquan Li[#], Fei Huang[#], Yunyan Zhou[#], Tao Huang, Xinkai Tong, Mingpeng Zhang, Jiaqi Chen, Zhou Zhang, Huipeng Du, Zifeng Liu, Meng Zhou, Yiwen Xiahou, Huashui Ai^{*}, Congying Chen^{*}, Lusheng Huang^{*}

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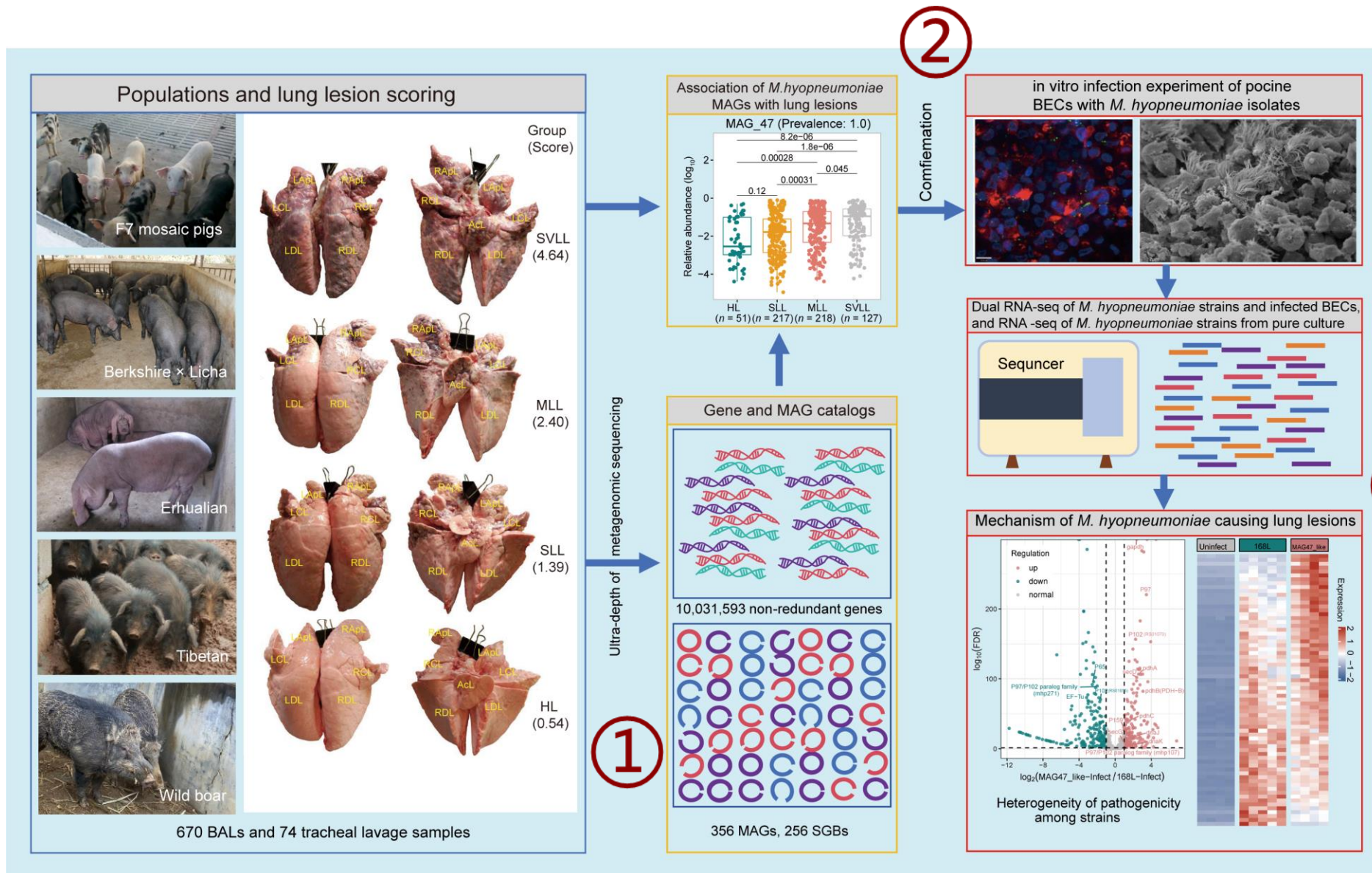
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Introduction



- ✓ Growing evidence has suggested that the lung microbiome has a significant impact on respiratory diseases.
- ✓ It is thus critical to reveal the community structure of the lung microbiome to explain its roles in maintaining lung health and in related disease.

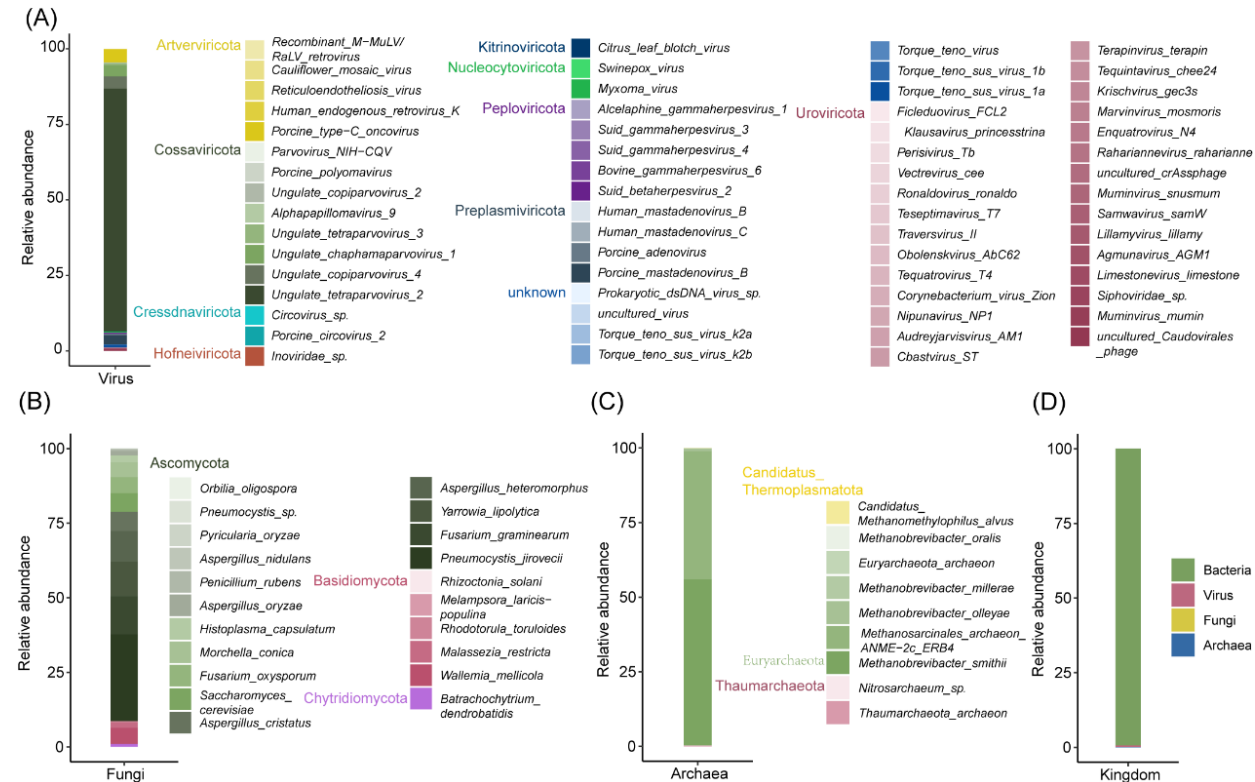
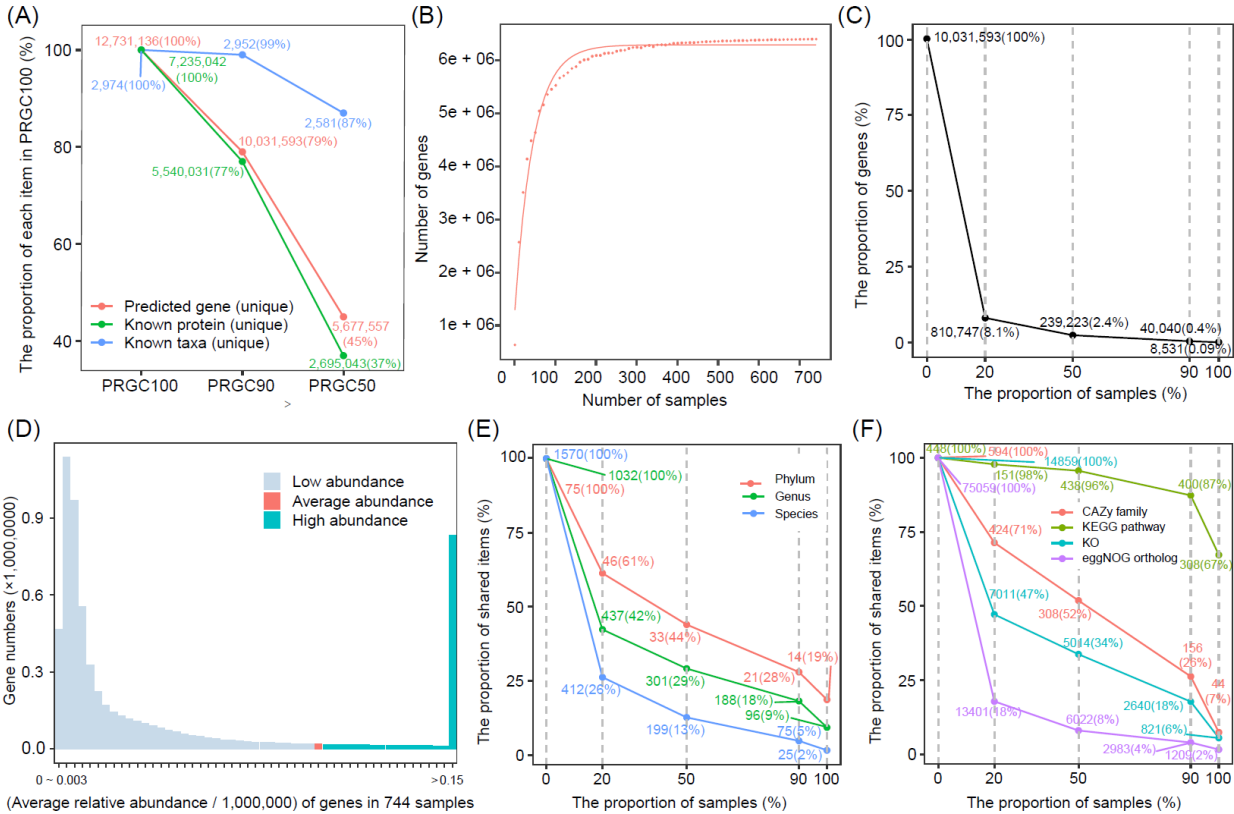
Highlights



Results

Characterization of the microbial gene catalog

Taxonomic compositions based on PRGC90

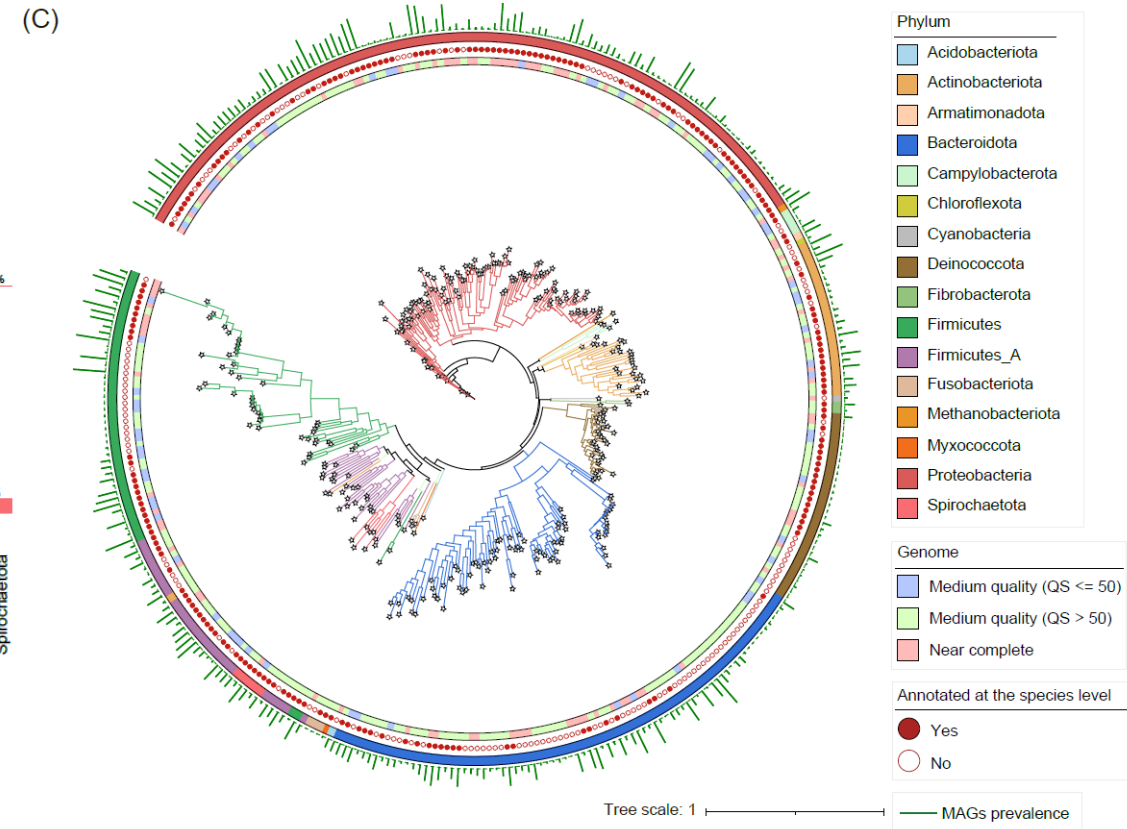
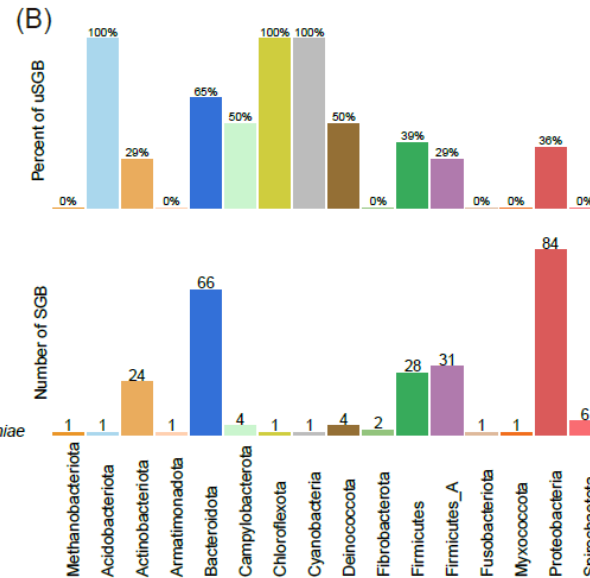
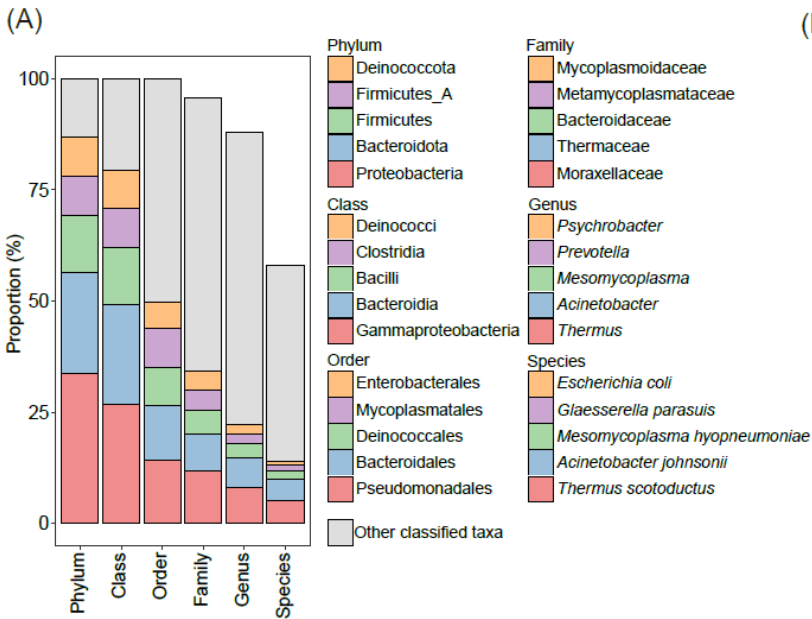


- A comprehensive pig lower respiratory tract gene catalog (PRGC) containing 10,031,593 genes
- Based on this catalog, we revealed taxonomic and functional composition of the pig lower respiratory tract microbiome

Results

Taxonomic composition of 356 MAGs

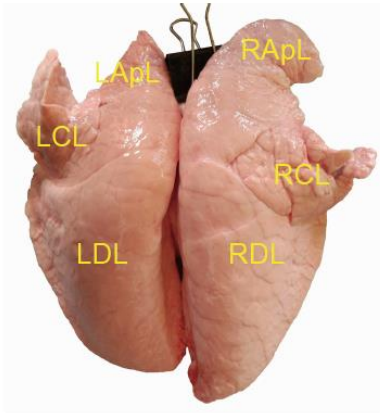
Phylogenetic tree of 356 MAGs



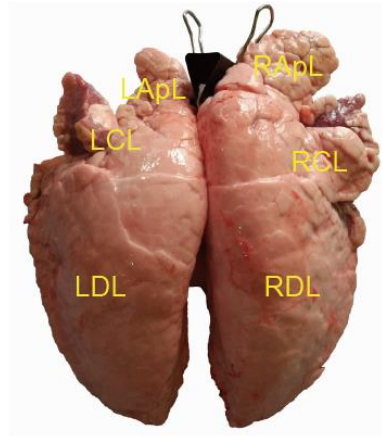
- ✓ 1965 MAGs were recovered from the pig lower respiratory tract microbiome.
- ✓ 1965 MAGs were clustered into 356 non-redundant MAGs and 256 species-level genome bins (SGBs).
- ✓ 41.8% were defined as unknown SGBs (uSGBs).



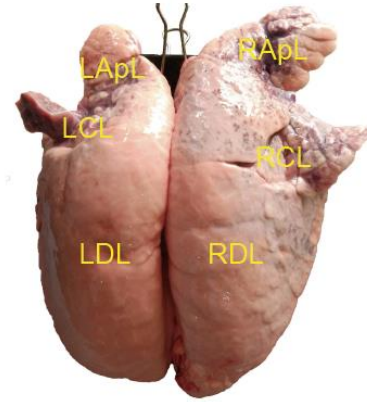
Results



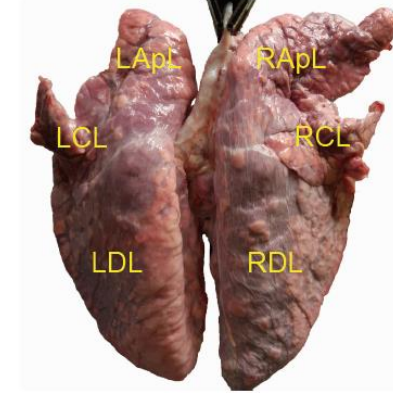
Score 0.54
Group HL



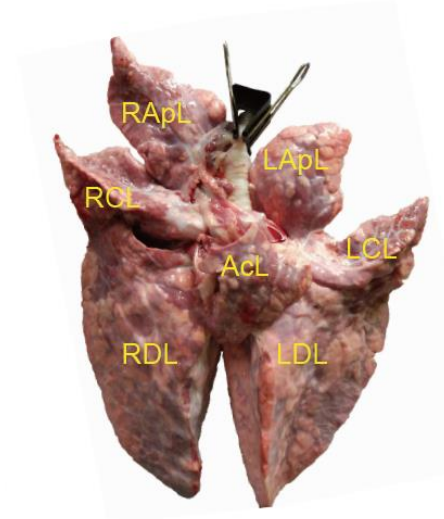
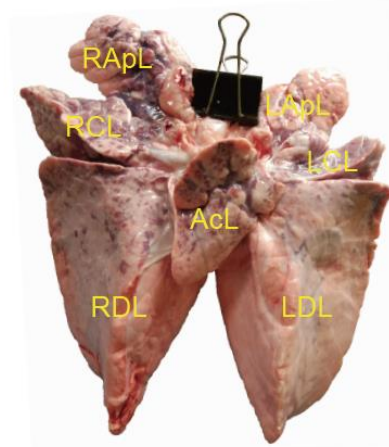
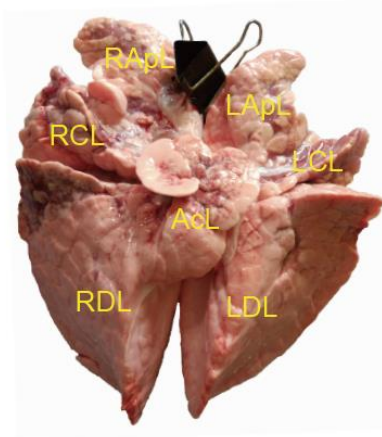
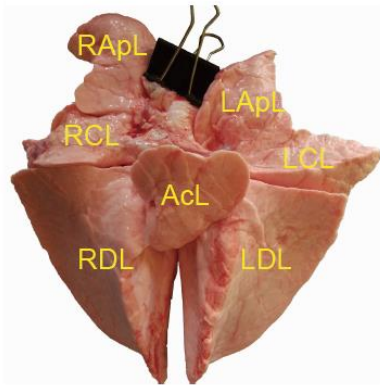
Score 1.39
Group SLL



Score 2.40
Group MLL



Score 4.64
Group SVLL

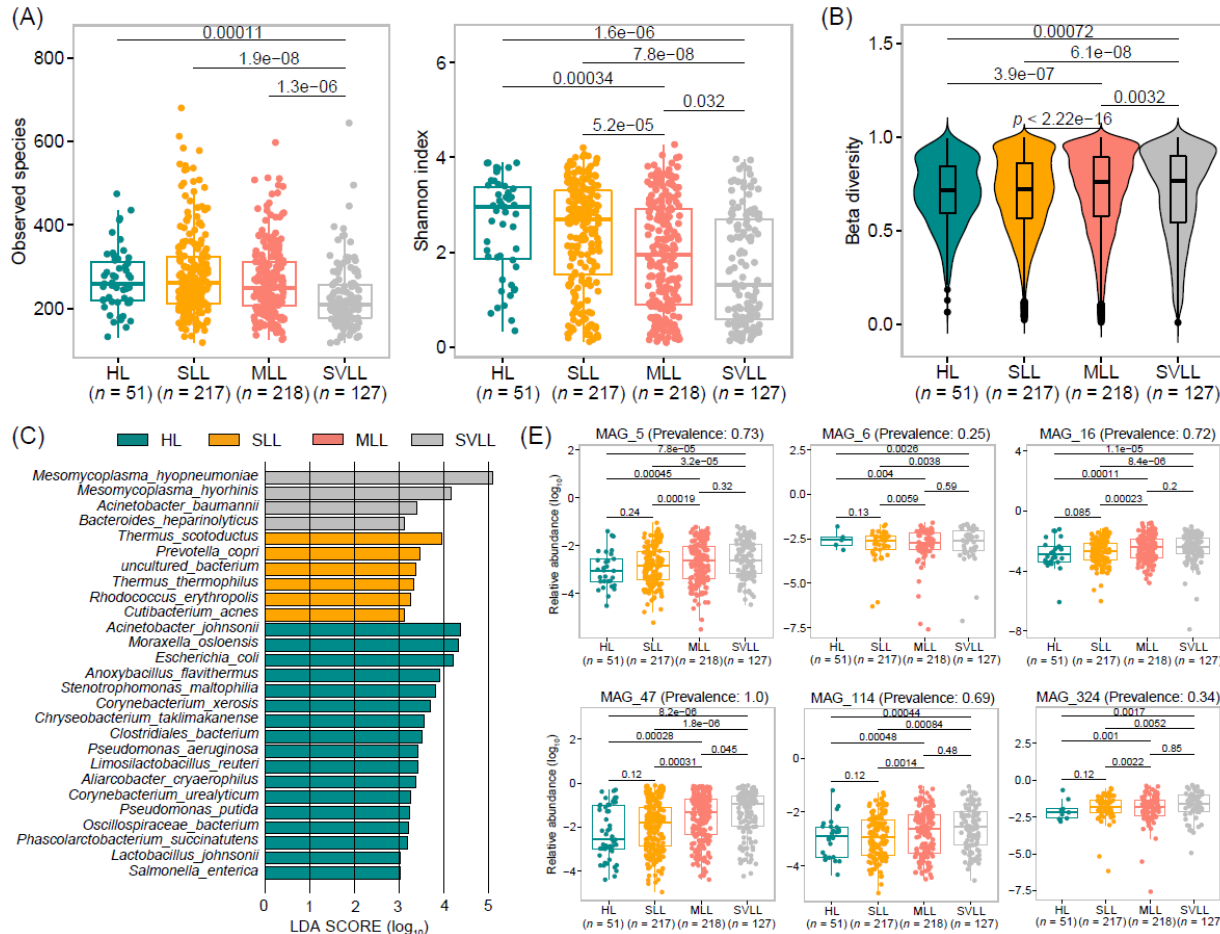


613 F₇ pigs in the mosaic population were well phenotyped and divided into four groups according to their lung lesion scores

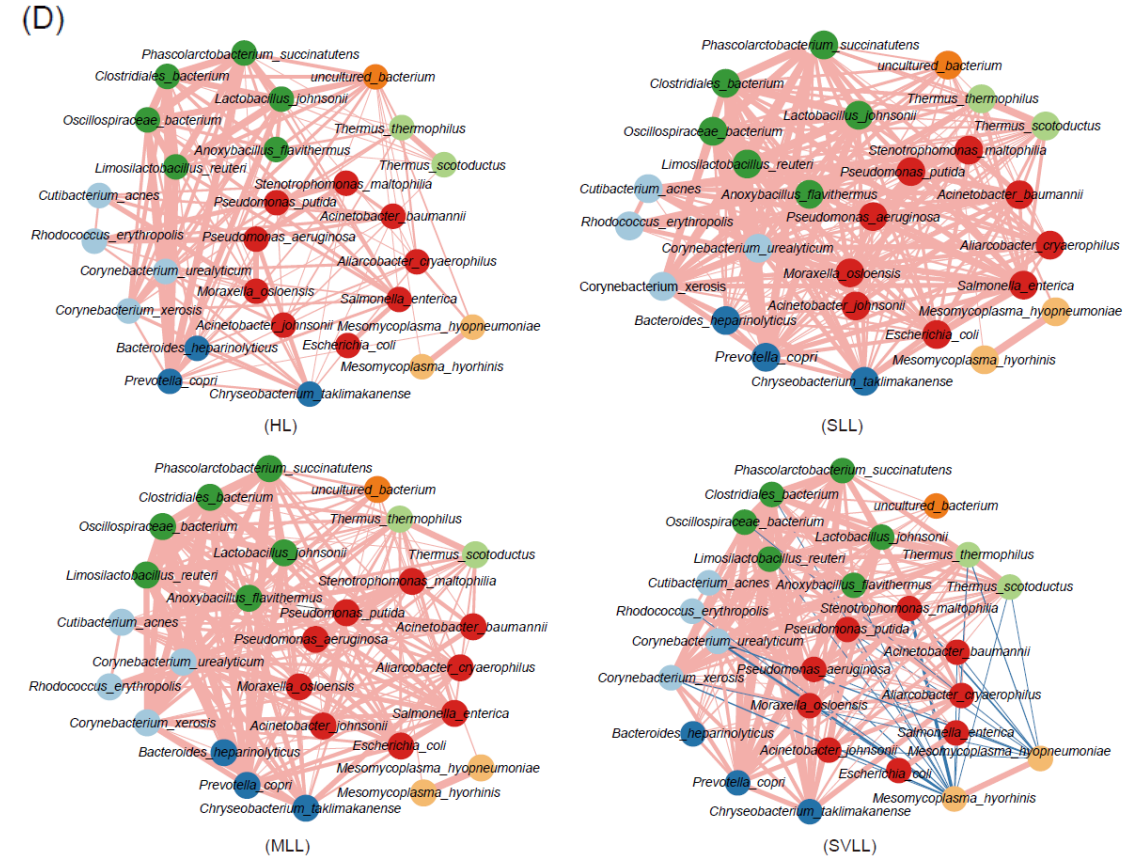


Results

Association of microbial taxa with lung lesions



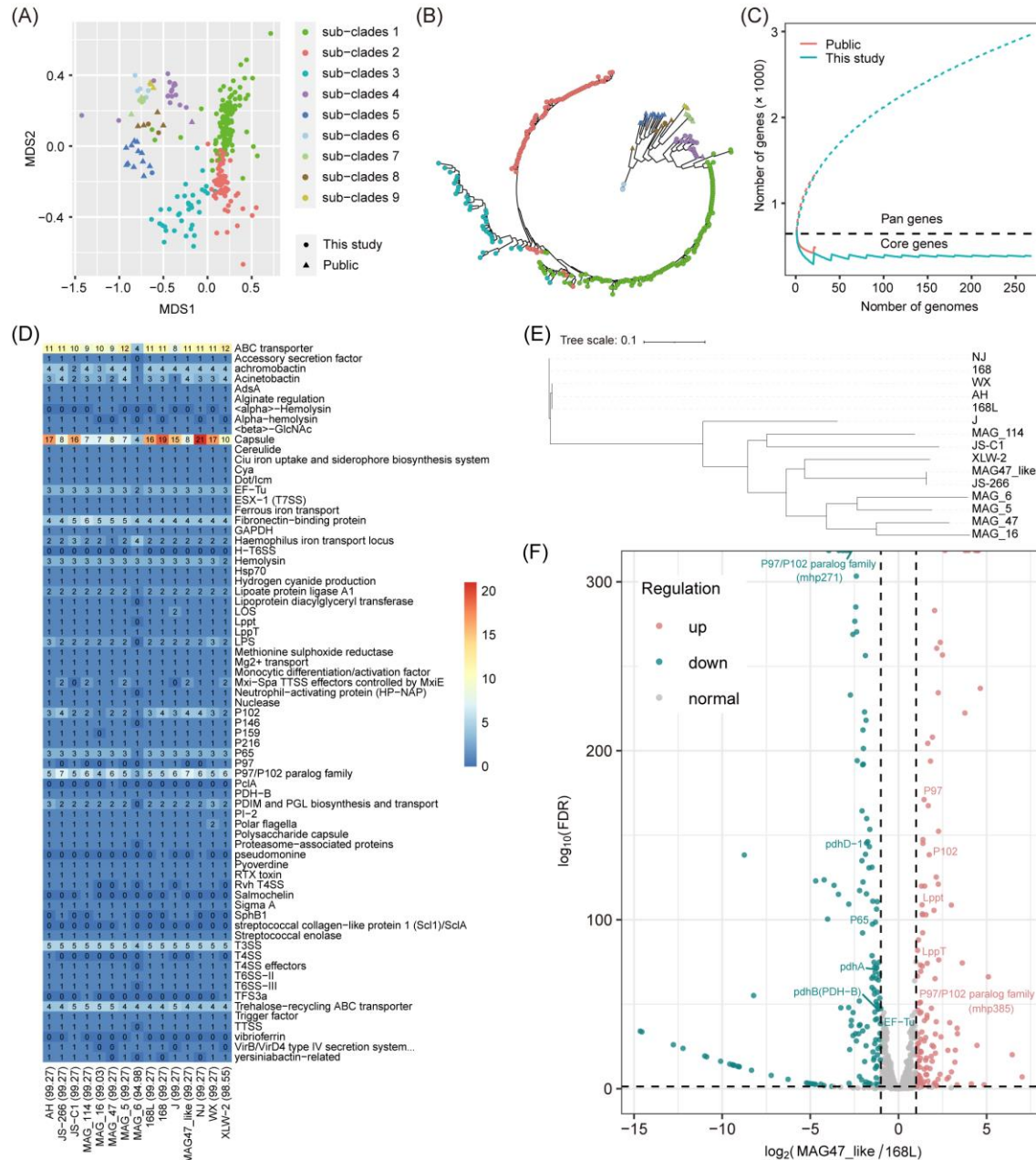
Co-abundance network of lung lesion-associated taxa



Identifying bacterial strains associated with lung lesions and its interaction network

Results

Pangenomes and the distribution of virulence factors in *M. hyopneumoniae* strains



MAGs constructed in this study expanded the genetic diversity of *M. hyopneumoniae* genomes greatly.

Differential gene expressions between MAG47_like and 168L strains.

✓ The MAG47_like strain with high pathogenicity had higher expression levels of virulence factor genes, especially, the genes encoding adhesins and adhesion-related proteins.



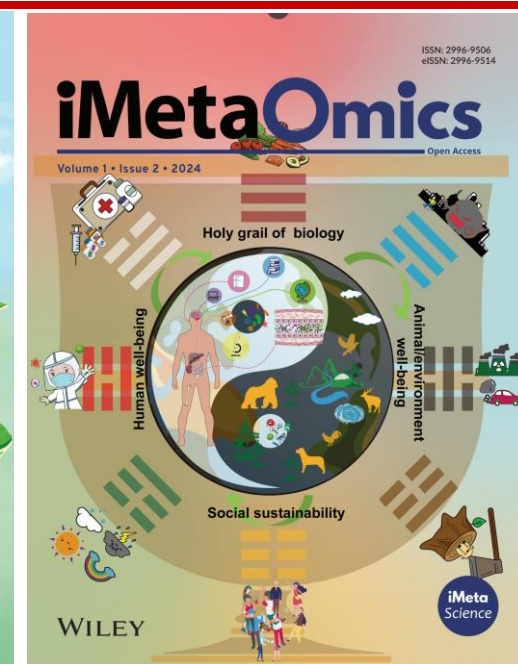
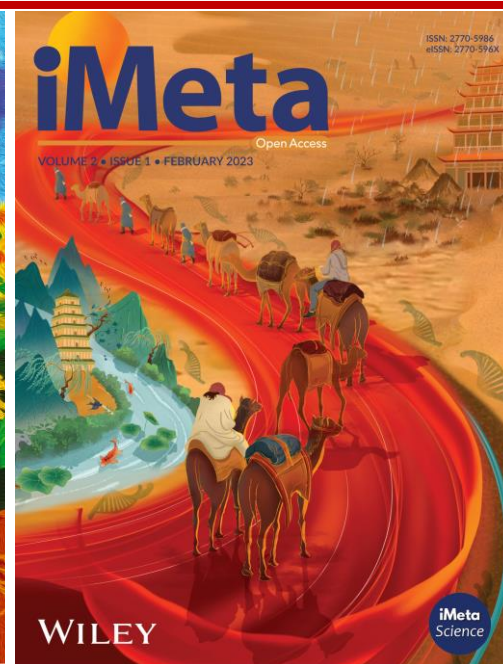
Summary

- ❑ We constructed a gene catalog that contained an unprecedented number of 10,031,593 microbial genes and recovered 356 MAGs from the swine lower respiratory tract microbiome.
- ❑ Using these catalogs, we found the heterogeneity in the microbial composition of the swine lower respiratory tract microbiome among individuals.
- ❑ The pan-genome of *Mesomycoplasma hyopneumoniae* strains was analyzed to explore the distribution of virulence factors in different strains. And the mechanism of their different pathogenic abilities among strains was elucidated.
- ❑ We confirmed the effect of *M. hyopneumoniae* adhesion on the lung lesions, and its molecular mechanism was clarified.

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