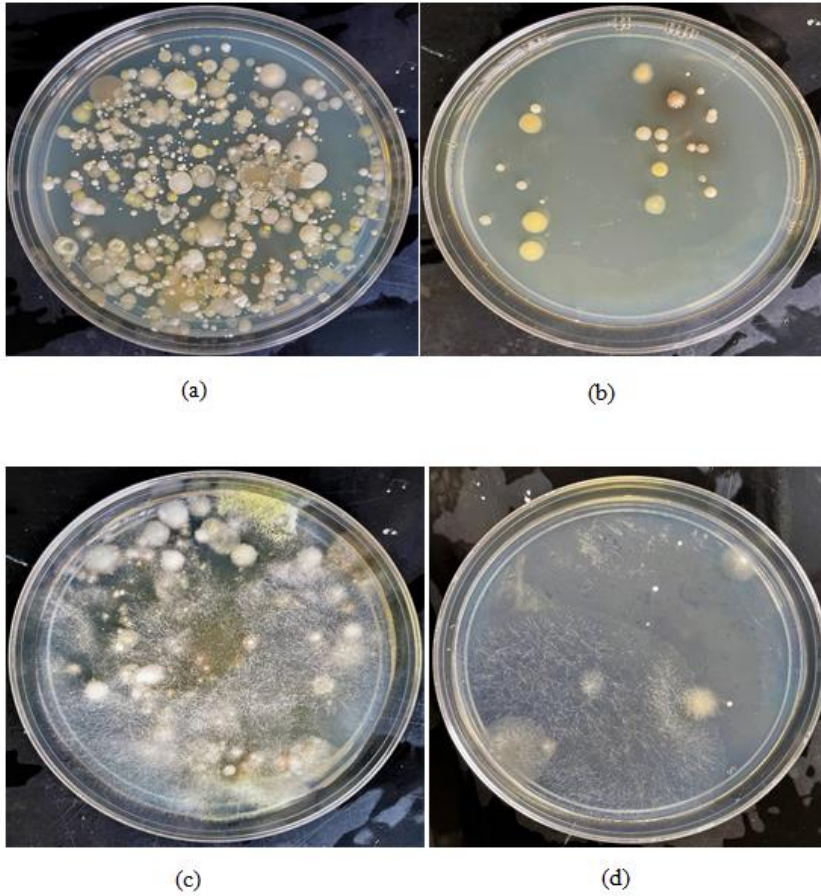


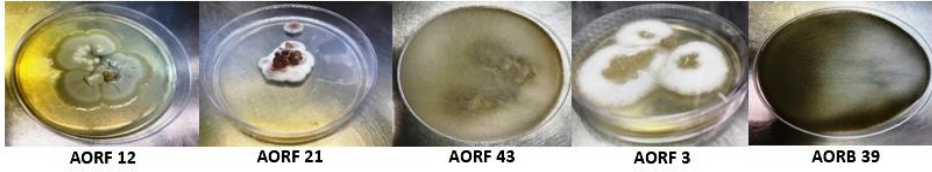
Supplementary Data



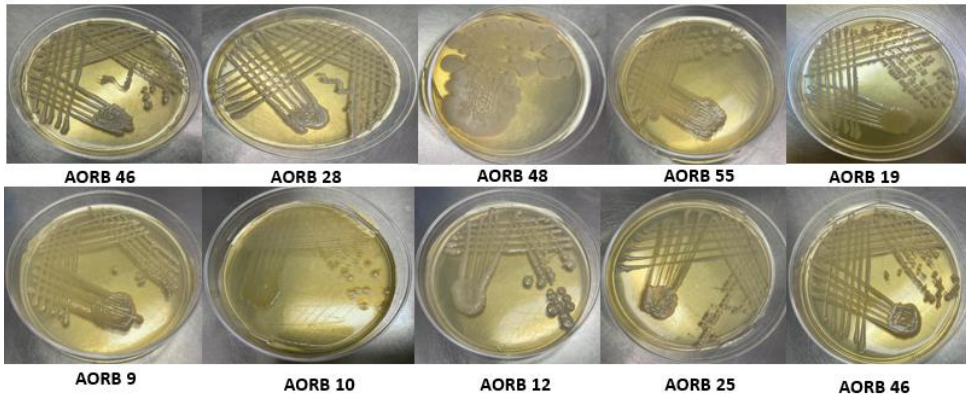
Supplementary Figure. 1 Secondary screening of microbial isolates (a) bacterial samples without serial dilution (b) bacterial samples after serial dilution (10^{-6}); and (c) fungal samples without serial dilution (d) fungal samples after serial dilution (10^{-6}).

Commented [WU1]: Reviewer 2, Comment 4: Please provide detail procedures for the isolation step, including photos of secondary screening to show how to see these pure colonies.

Author's reply: Detailed procedure for the isolation step has been described in section 2.4, page 6 and photos of secondary screening showing single colonies are added as Supplementary Figure 1.

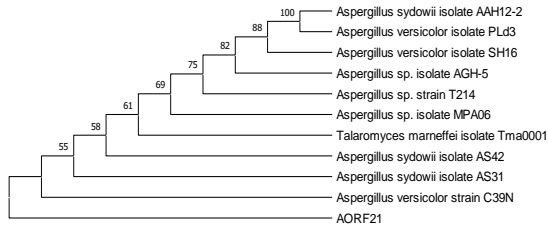


Supplementary Figure. 3 Pure cultures of bacterial isolates selected from secondary screening

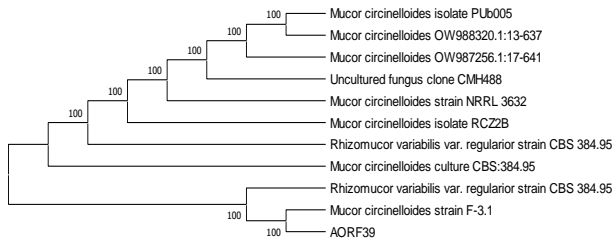


Supplementary Figure. 2 Pure cultures of fungal isolates selected from secondary screening

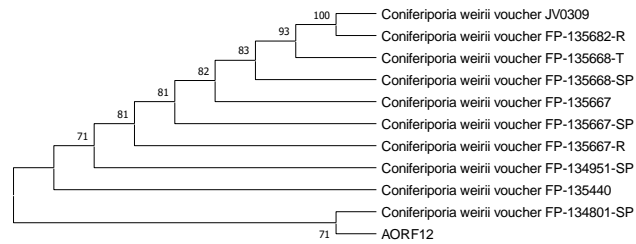
a) AORF21



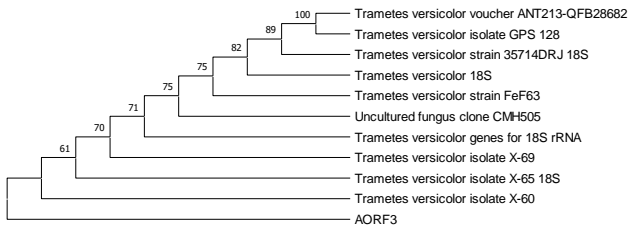
b) AORF39



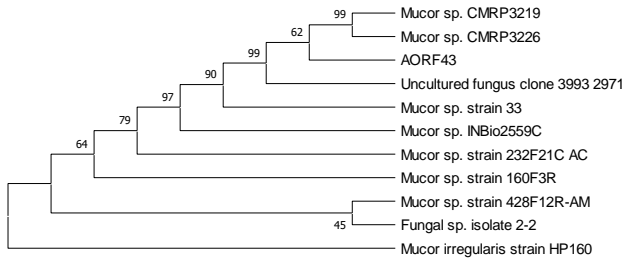
c) AORF12



d) AORF3

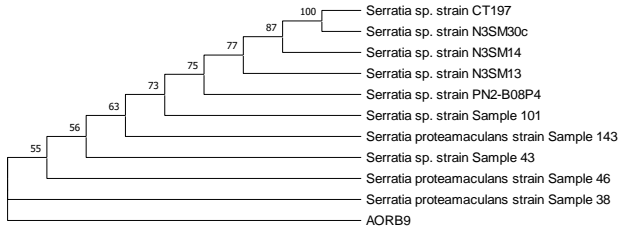


e) AORF43

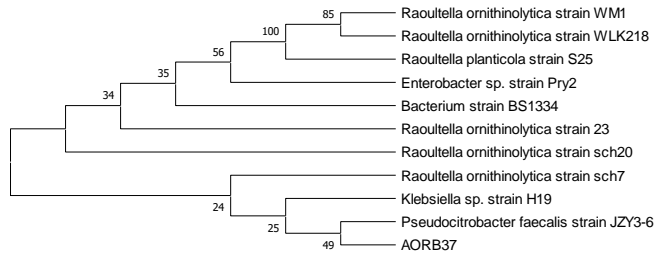


Supplementary Figure. 4 (a) to (e): Phylogenetic tree of five selected lignin degrading fungal strains based on neighbor joining criteria using MEGA-X. The percentage of replicate trees associated taxa are clustered together using the bootstrap test (1000 replicates) are shown next to the branches.

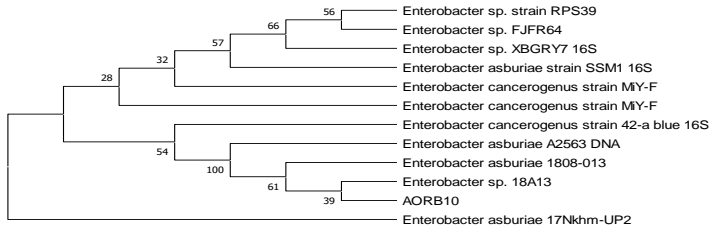
a) AORB9



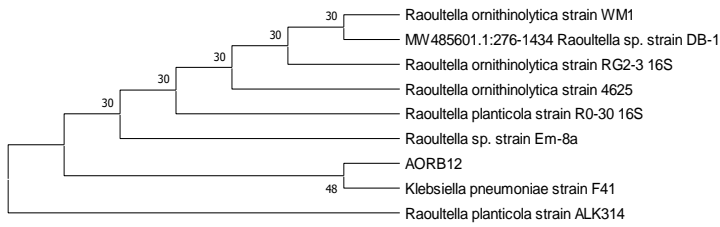
b) AORB37



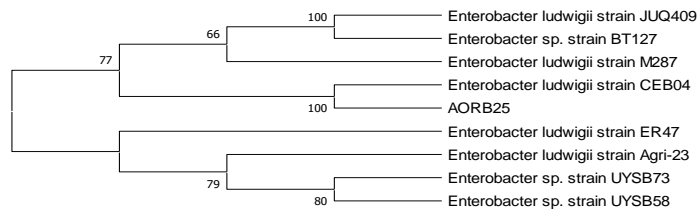
c) AORB10



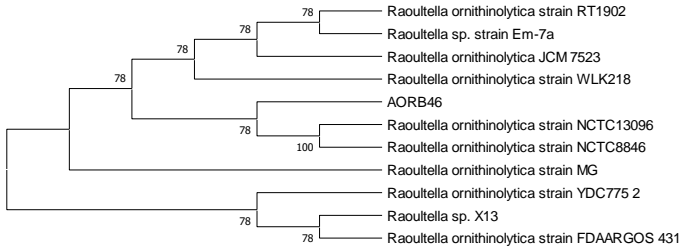
d) AORB12



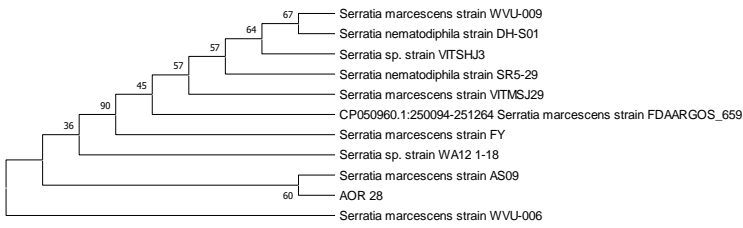
e) AORB25



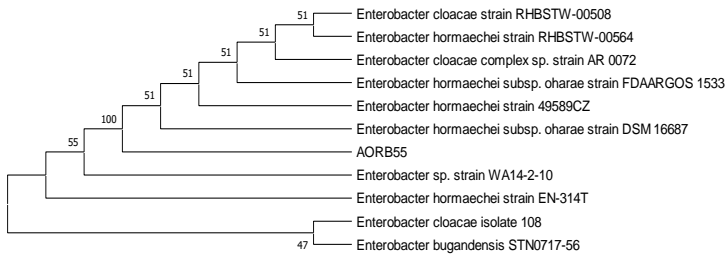
f) AORB46



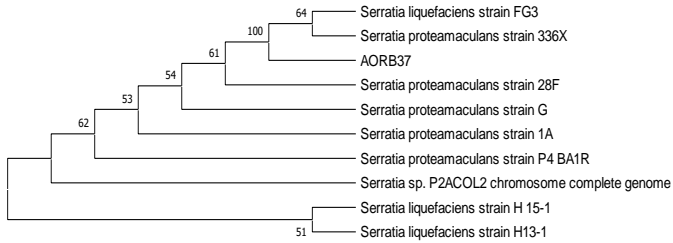
g) AORB28



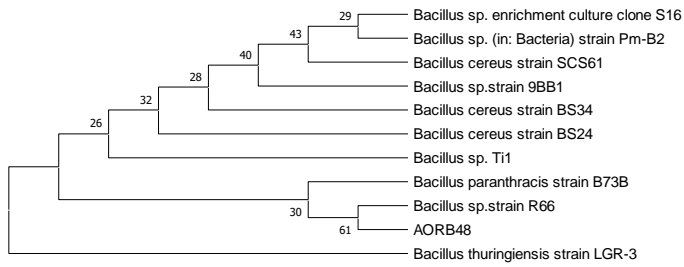
h) AORB55



i) AORB19



j) AORB48



Supplementary Figure. 5 (a) to (j): Phylogenetic tree of ten selected lignin degrading bacterial strains based on neighbor joining criteria using MEGA-X. The percentage of replicate trees associated taxa are clustered together using the bootstrap test (1000 replicates) are shown next to the branches.

Supplementary Table 1. Species and isolate information of five selected fungal strains based on laccase enzyme production

Sample No	Similarity %	Strain	Division	Accession No.
AORF12	99%	<i>Conifera poria weirii</i> JV0309	Basidiomycota	KR350568.1
AORF21	100%	<i>Aspergillus sydowii</i> 49G11	Ascomycota	MT594361.1
AORF39	96%	<i>Mucor circinellodes</i> Pub005	Zygomycota	MT279285.1
AORF43	97%	<i>Mucor</i> sp. CMRP 3219	Zygomycota	MH424492.1
AORF3	98%	<i>Trametes versicolor</i> ANT213 QFB286	Basidiomycota	MN992530.1

Commented [WU2]: Reviewer 1, Comment 2:Table 2 and Table 3 should be removed to supplementary materials.

Author's reply: Removed the tables and placed them on the revised supplementary file in page 9

Supplementary Table 2. Species and isolate information of ten selected bacterial strains based on laccase enzyme production

Sample No	Similarity %	Strain	Class	Gram nature	Accession No.
AORB9	99%	<i>Serratia</i> sp. CT197	Gammaproteobacteria	Gram negative	MT561436.1
AORB10	98%	<i>Enterobacter</i> sp. XBGRY7	Gammaproteobacteria	Gram negative	KJ1849721.1
AORB12	98%	<i>Raoultella ornitholytica</i> 4625	Gammaproteobacteria	Gram negative	MT545114.1
AORB25	99%	<i>Enterobacter ludwigii</i> JUQ409	Gammaproteobacteria	Gram negative	MN826154.1
AORB 28	98%	<i>Serratia marcescens</i> AS09	Gammaproteobacteria	Gram negative	MT598027.1
AORB37	91%	<i>Raoultella ornitholytica</i> Sch7	Gammaproteobacteria	Gram negative	JX294891.1
AORB48	95%	<i>Bacillus</i> sp. Ti1	Bacilli	Gram positive	MZ707571.1
AORB55	94%	<i>Enterobacter hormaechei</i> EN 314T	Gammaproteobacteria	Gram negative	MT539386.1
AORB19	99%	<i>Serratia proteamaculans</i> 336X	Gammaproteobacteria	Gram negative	MT598027.1
AORB46	99%	<i>Raoultella ornitholytica</i> RT 1902	Gammaproteobacteria	Gram negative	MT568560.1

Commented [WU3]: Reviewer 1, Comment 2:Table 2 and Table 3 should be removed to supplementary materials.

Author's reply: Removed the tables and placed them on the revised supplementary file in page 9

