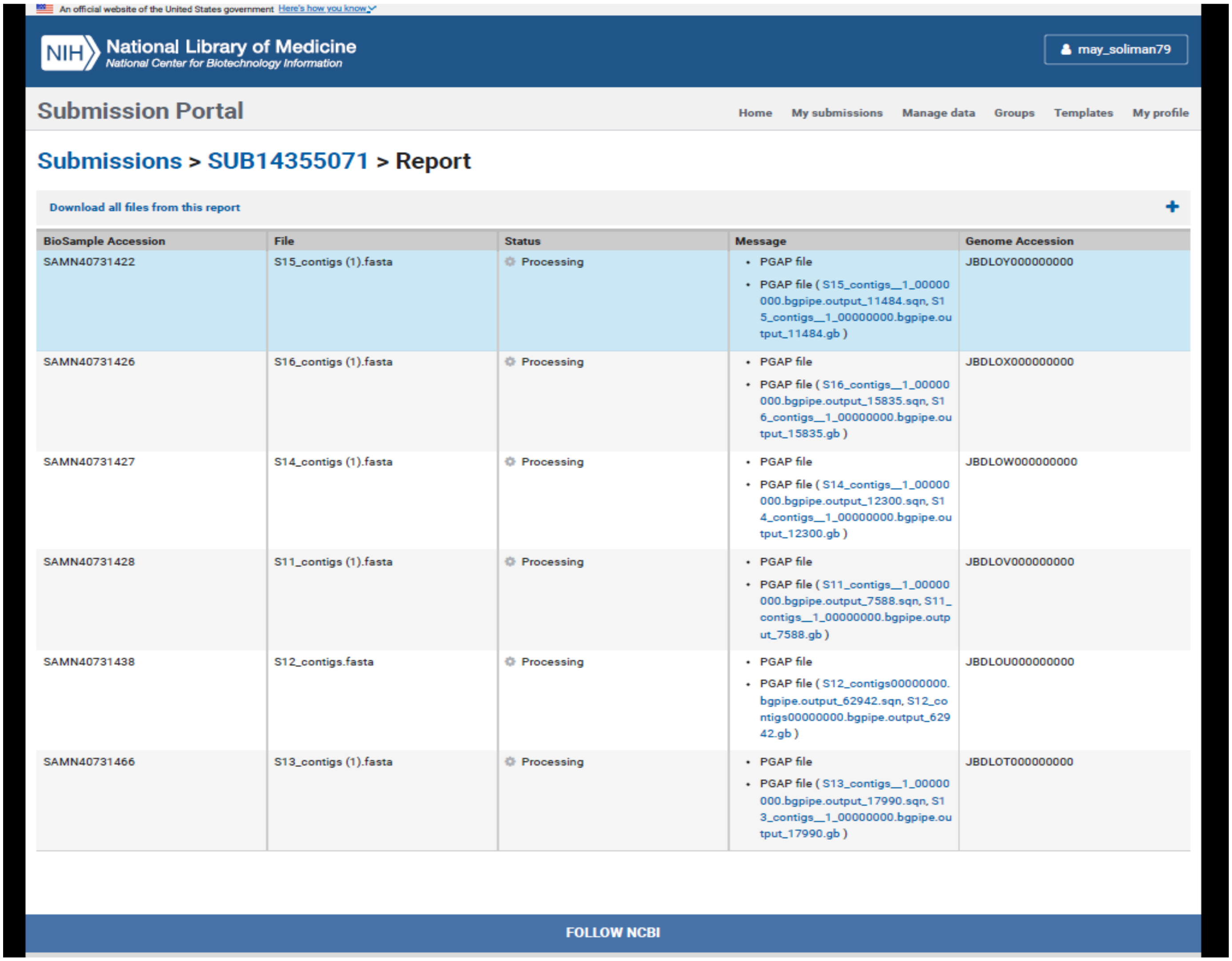
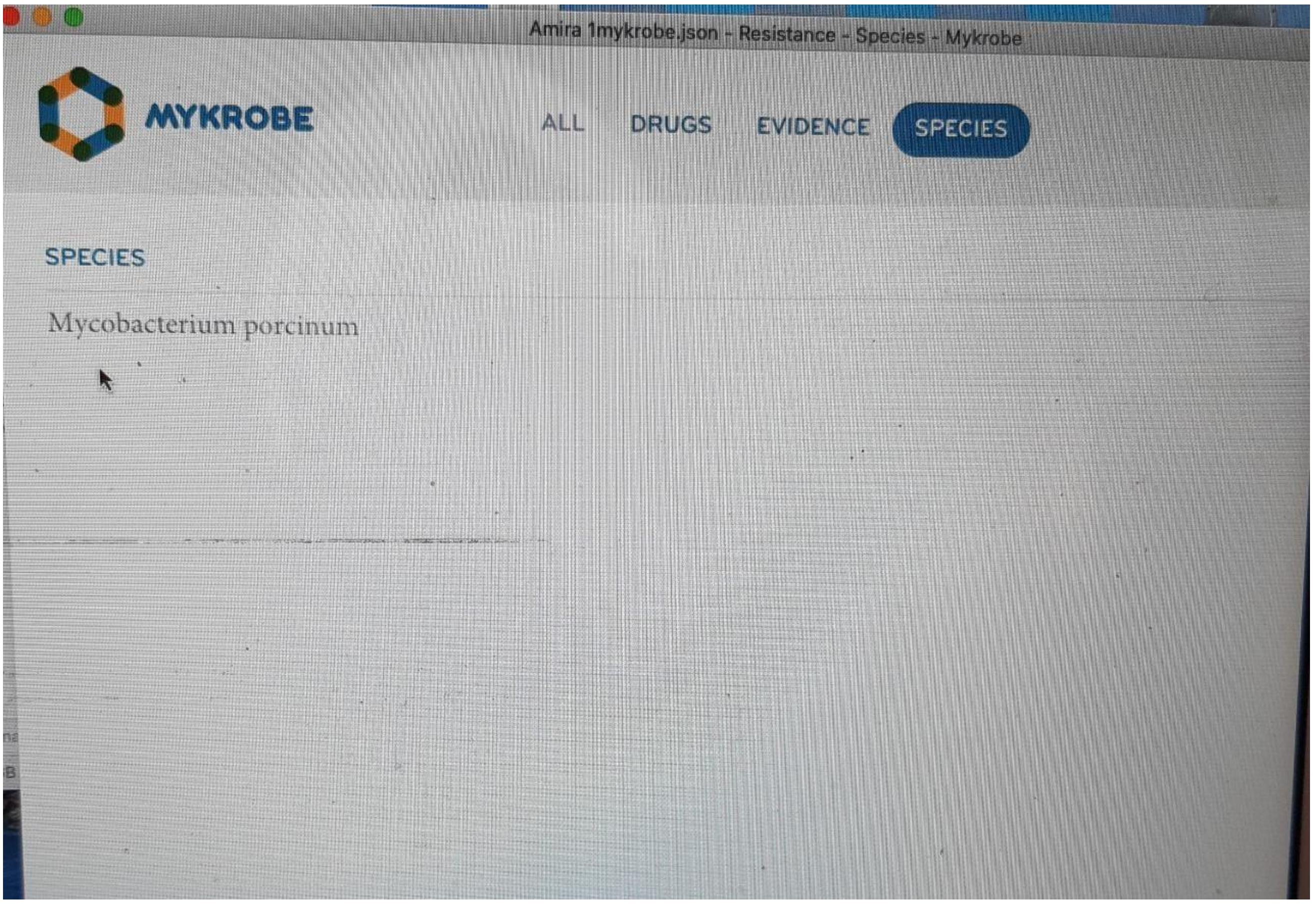
NCBI data of the sequenced NTM isolates

Isolates	Submission ID	BioProject	BioSample	Accession	Organism
1	SUB14355071	PRJNA1095647	SAMN40731422	JBDLOY000000000	*M. fortuitum*
2	SUB14355071	PRJNA1095647	SAMN40731426	JBDLOX000000000	*M. fortuitum*
3	SUB14355071	PRJNA1095647	SAMN40731466	JBDLOT000000000	*M. abscessus*
4	SUB14355071	PRJNA1095647	SAMN40731428	JBDLOV000000000	*M. porcinum*
5	SUB14355071	PRJNA1095647	SAMN40731438	JBDLOU000000000	*M. porcinum*
6	SUB14355071	PRJNA1095647	SAMN40731427	JBDLOW000000000	*M. abscessus*



Submissions > SUB14355071 > Report

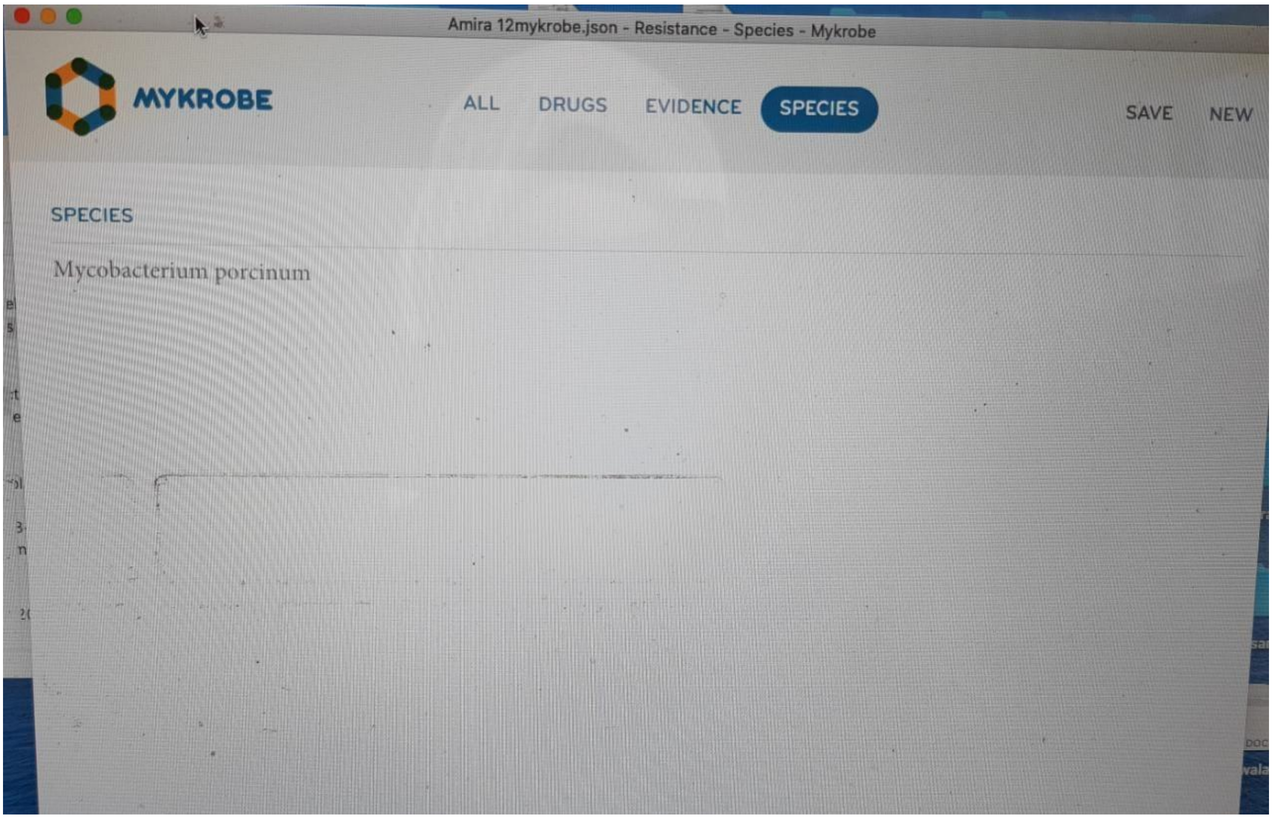
BioSample Accession	File	Status	Message	Genome Accession
SAMN40731422	S15_contigs (1).fasta	Processing	• PGAP file • PGAP file (S15_contigs__1_00000000.bgpipe.output_11484.sqn, S15_contigs__1_00000000.bgpipe.output_11484.gb)	JBDLOY000000000
SAMN40731426	S16_contigs (1).fasta	Processing	• PGAP file • PGAP file (S16_contigs__1_00000000.bgpipe.output_15835.sqn, S16_contigs__1_00000000.bgpipe.output_15835.gb)	JBDLOX000000000
SAMN40731427	S14_contigs (1).fasta	Processing	• PGAP file • PGAP file (S14_contigs__1_00000000.bgpipe.output_12300.sqn, S14_contigs__1_00000000.bgpipe.output_12300.gb)	JBDLOW000000000
SAMN40731428	S11_contigs (1).fasta	Processing	• PGAP file • PGAP file (S11_contigs__1_00000000.bgpipe.output_7588.sqn, S11_contigs__1_00000000.bgpipe.output_7588.gb)	JBDLOV000000000
SAMN40731438	S12_contigs.fasta	Processing	• PGAP file • PGAP file (S12_contigs00000000.bgpipe.output_62942.sqn, S12_contigs00000000.bgpipe.output_62942.gb)	JBDLOU000000000
SAMN40731466	S13_contigs (1).fasta	Processing	• PGAP file • PGAP file (S13_contigs__1_00000000.bgpipe.output_17990.sqn, S13_contigs__1_00000000.bgpipe.output_17990.gb)	JBDLOT000000000



Amira 1mykrobe.json - Resistance - Species - Mykrobe

SPECIES

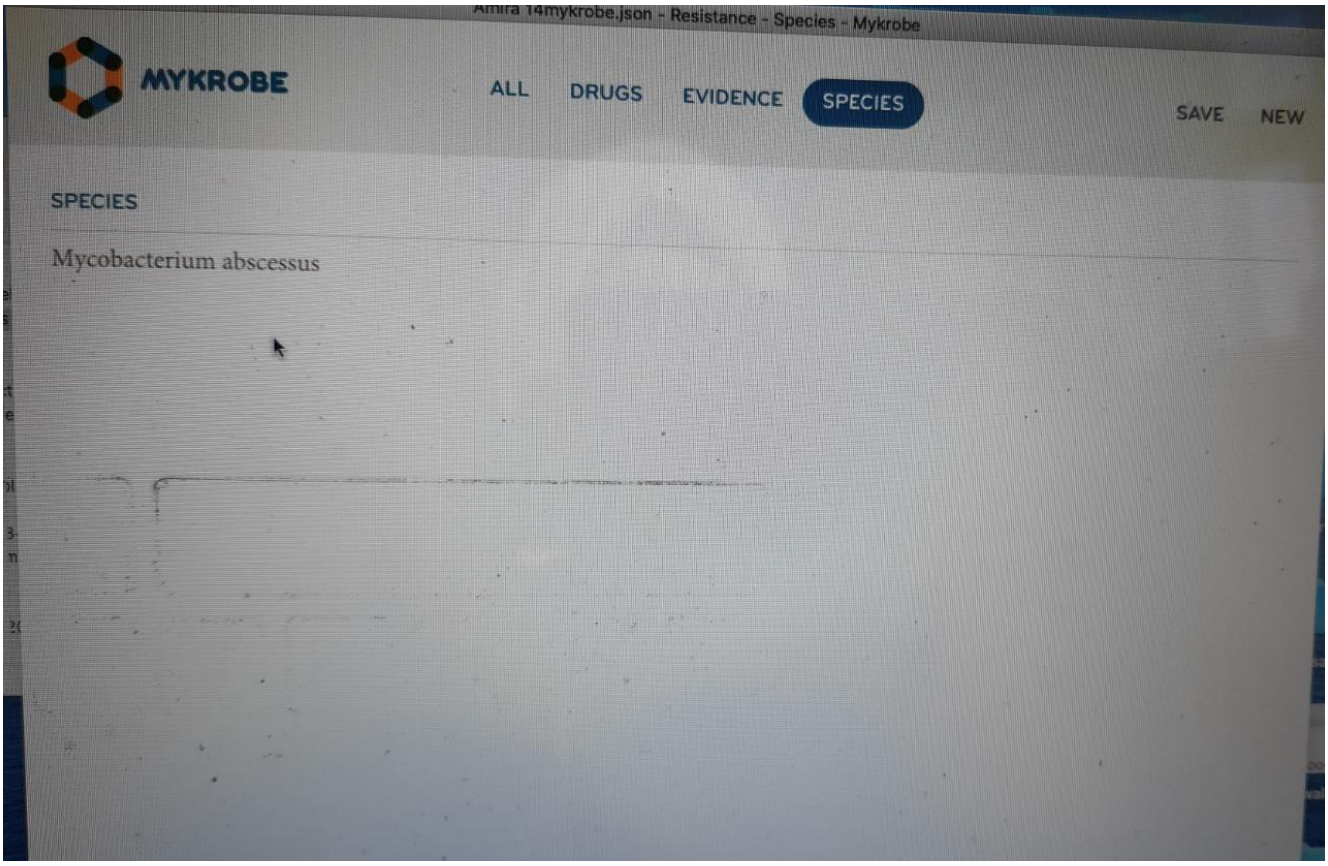
Mycobacterium porcinum



Amira 12mykrobe.json - Resistance - Species - Mykrobe

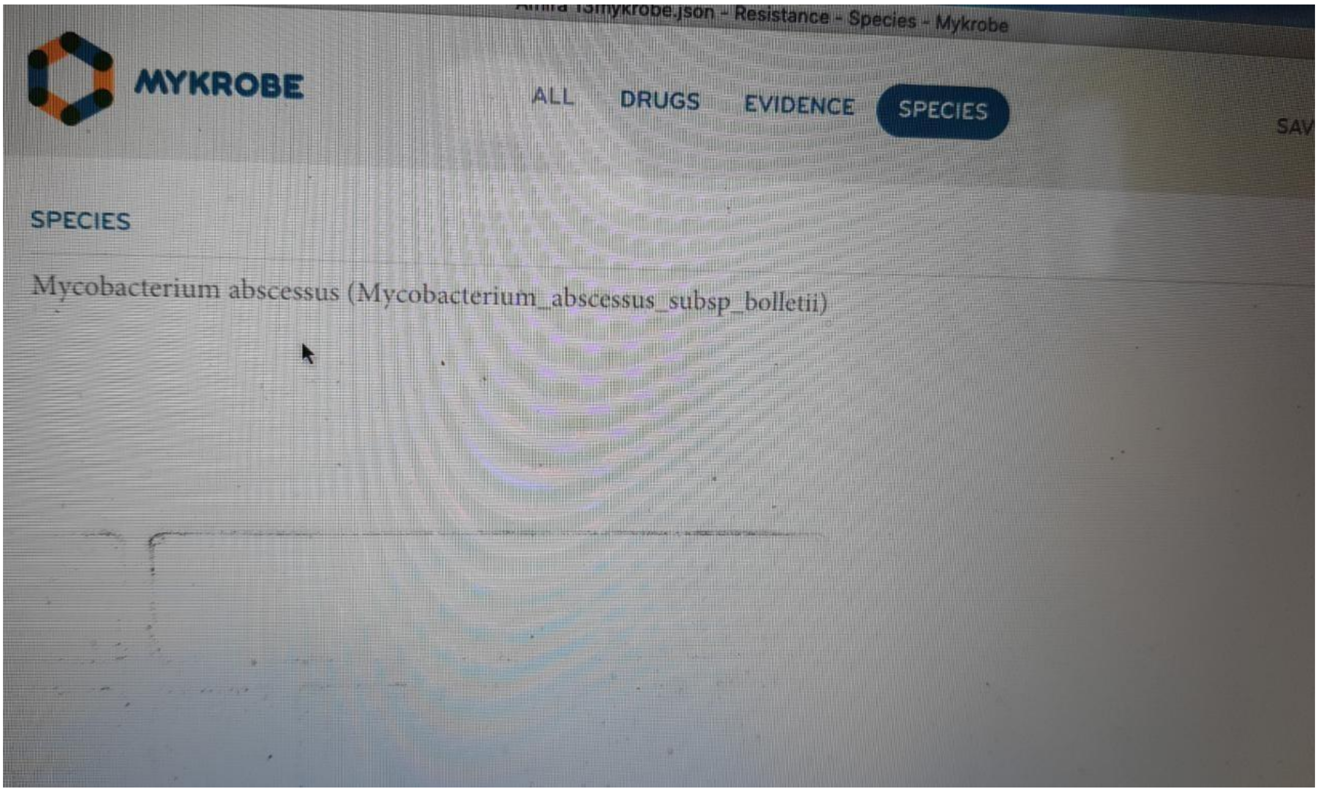
SPECIES

Mycobacterium porcinum



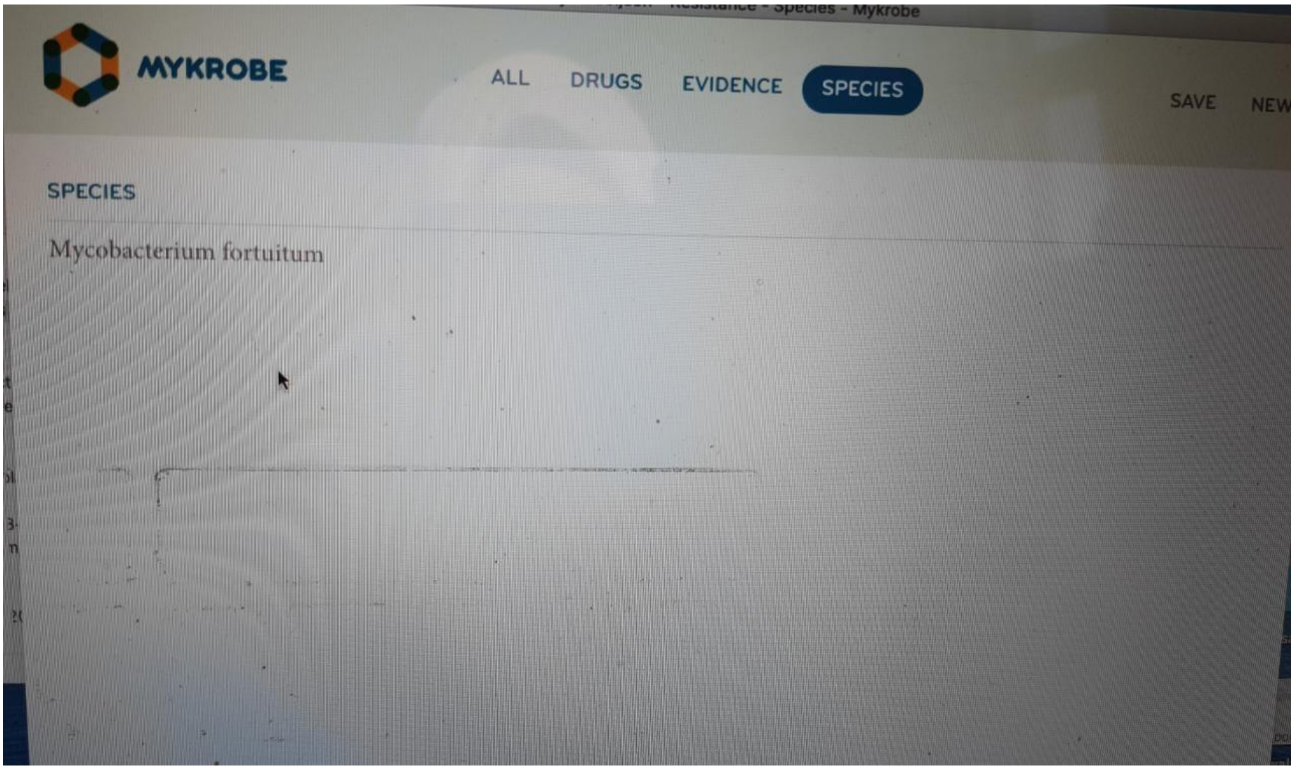
SPECIES

Mycobacterium abscessus



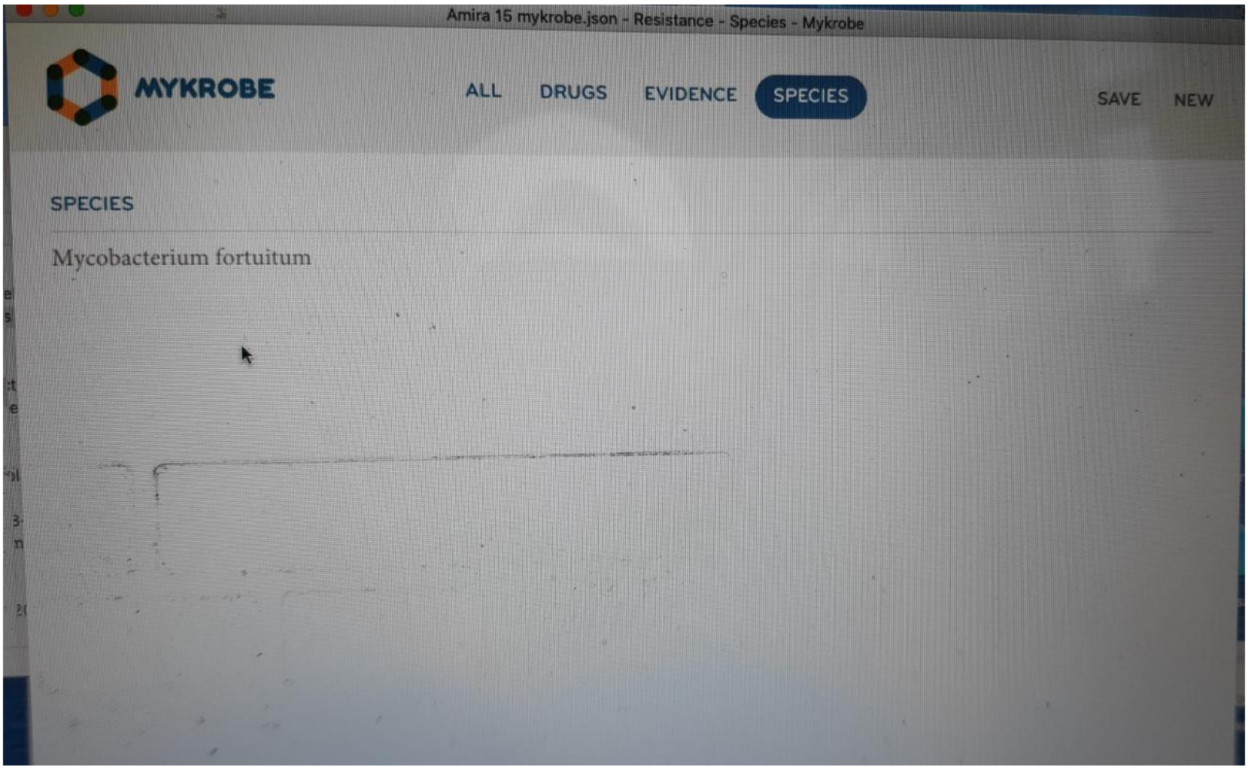
SPECIES

Mycobacterium abscessus (Mycobacterium_abscessus_subsp_bolletii)



SPECIES

Mycobacterium fortuitum

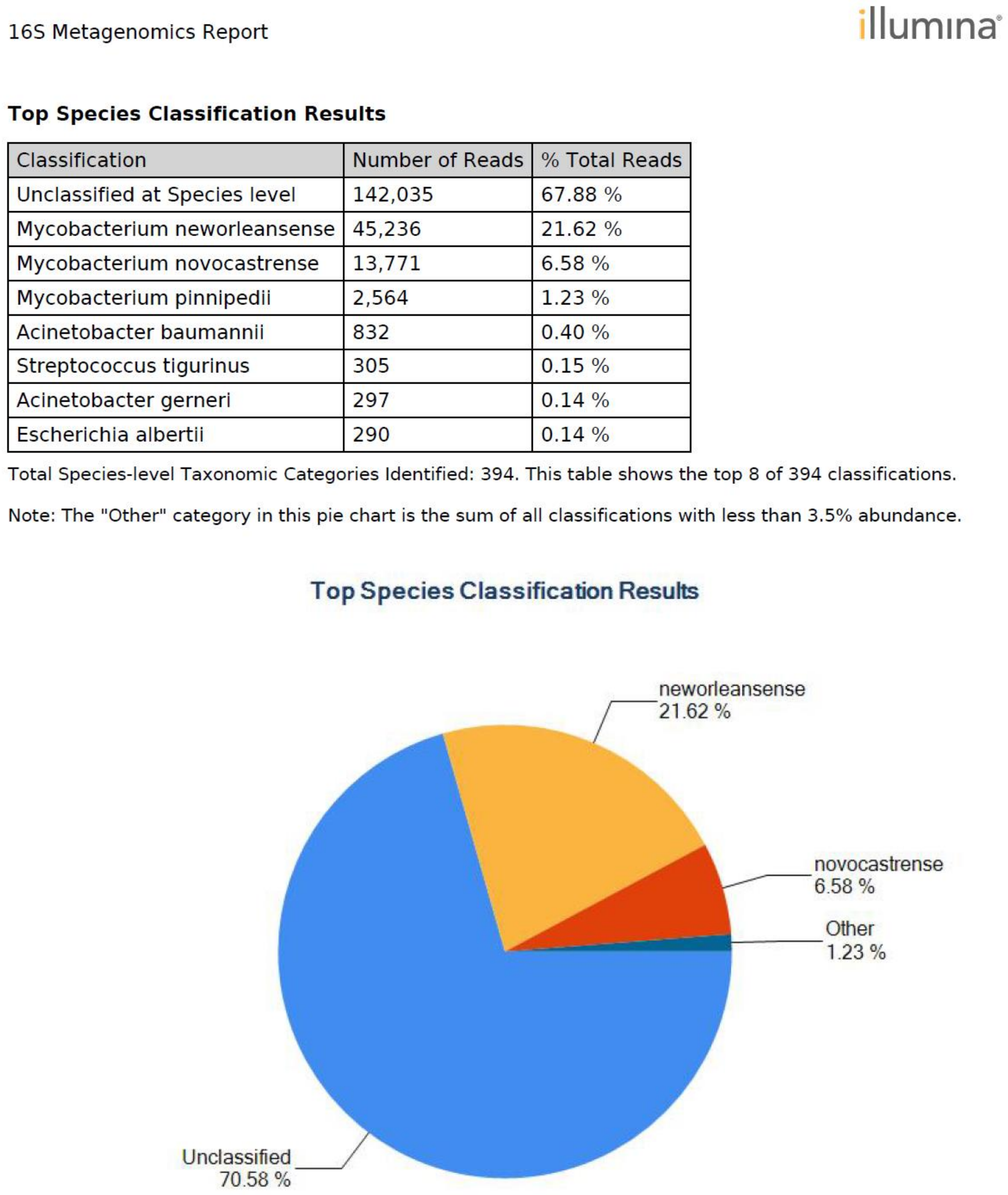


Amira 15 mykrobe.json - Resistance - Species - Mykrobe

SPECIES

Mycobacterium fortuitum

16S metagenomics report of NTM isolate identifies as *M. neworleansense*



16S Metagenomics Report

Top Species Classification Results

Classification	Number of Reads	% Total Reads
Unclassified at Species level	142,035	67.88 %
Mycobacterium neworleansense	45,236	21.62 %
Mycobacterium novocastrense	13,771	6.58 %
Mycobacterium pinnipedii	2,564	1.23 %
Acinetobacter baumannii	832	0.40 %
Streptococcus tigurinus	305	0.15 %
Acinetobacter gerneri	297	0.14 %
Escherichia albertii	290	0.14 %

Total Species-level Taxonomic Categories Identified: 394. This table shows the top 8 of 394 classifications.

Note: The "Other" category in this pie chart is the sum of all classifications with less than 3.5% abundance.

Top Species Classification Results