

Name	Sequence	Taxono my/ SINTAX	Taxono my/T- BAS	Bootstr ap	Maximu m Likeliho od	Tree Link
ASV1	ACTTCGG					http://TreeLink#10/ asv1
ASV2	ACATCGG					http://TreeLink#10/ asv2
erable Taxo	nomic Assig	nment:				

Links to asv1, asv2 in tree

Comparable

to RDP

classifier []

1) SINTAX using UNITE (fungi) and SILVA (bacteria) databases.

2) T-BAS using bootstrap backbone constraint and maximum likelihood evolutionary placement.