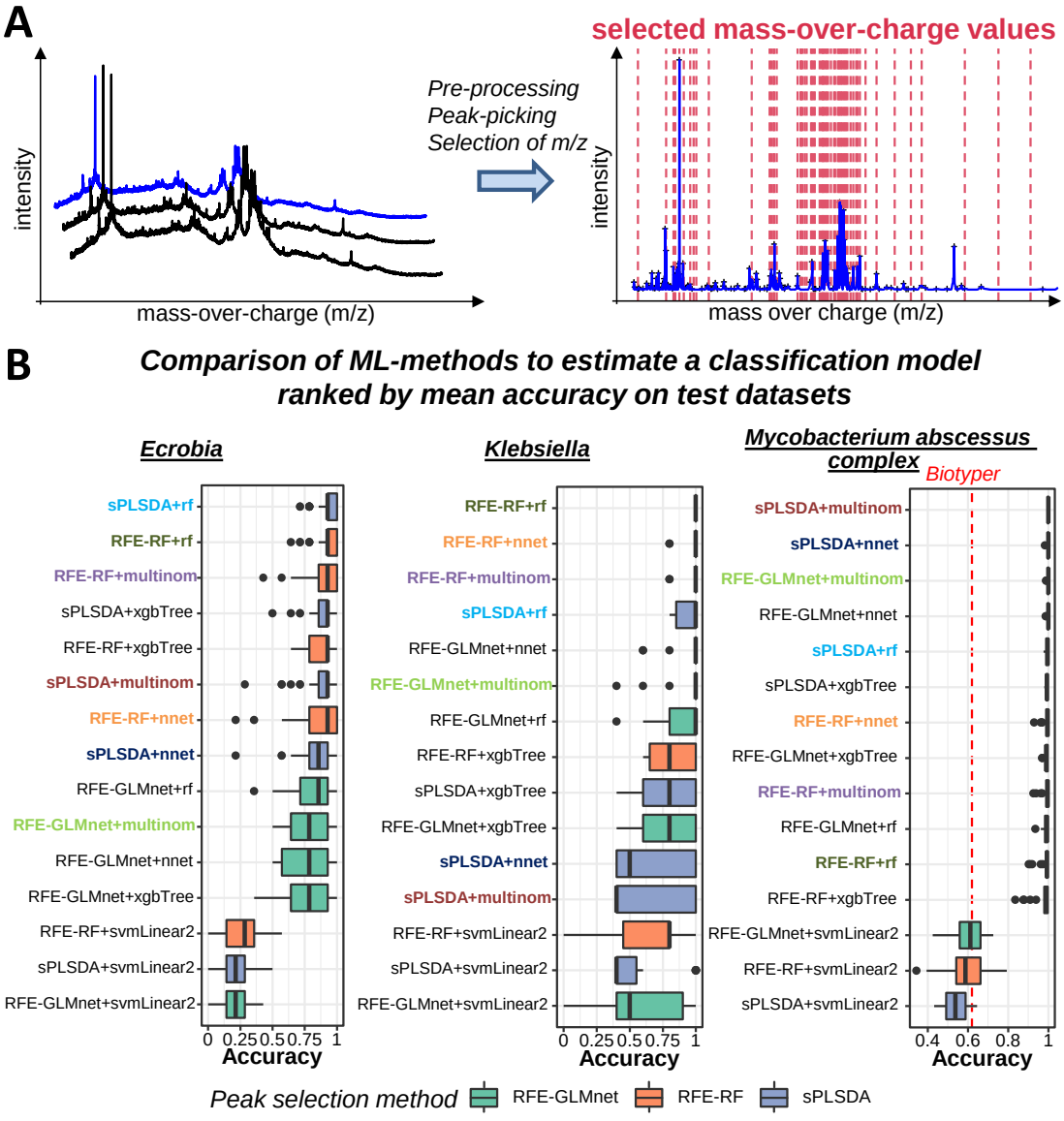

A: MSclassifR proposes pipelines to preprocess mass spectra and find discriminant mass-over-charge values. **B**: Accuracies obtained on test sets for the 3 datasets (Wilke et al., 2020), (Lasch, Stämmler and Schneider, 2016), (Godmer, Aubry, *et al.*, 2021). Top 3 methods are highlighted with different colors. Red dashed line named "Biotyper" is the accuracy level (61%) using Bruker® database (Library Mycobacteria v5.0) coupled to the MALDI Biotyper®.