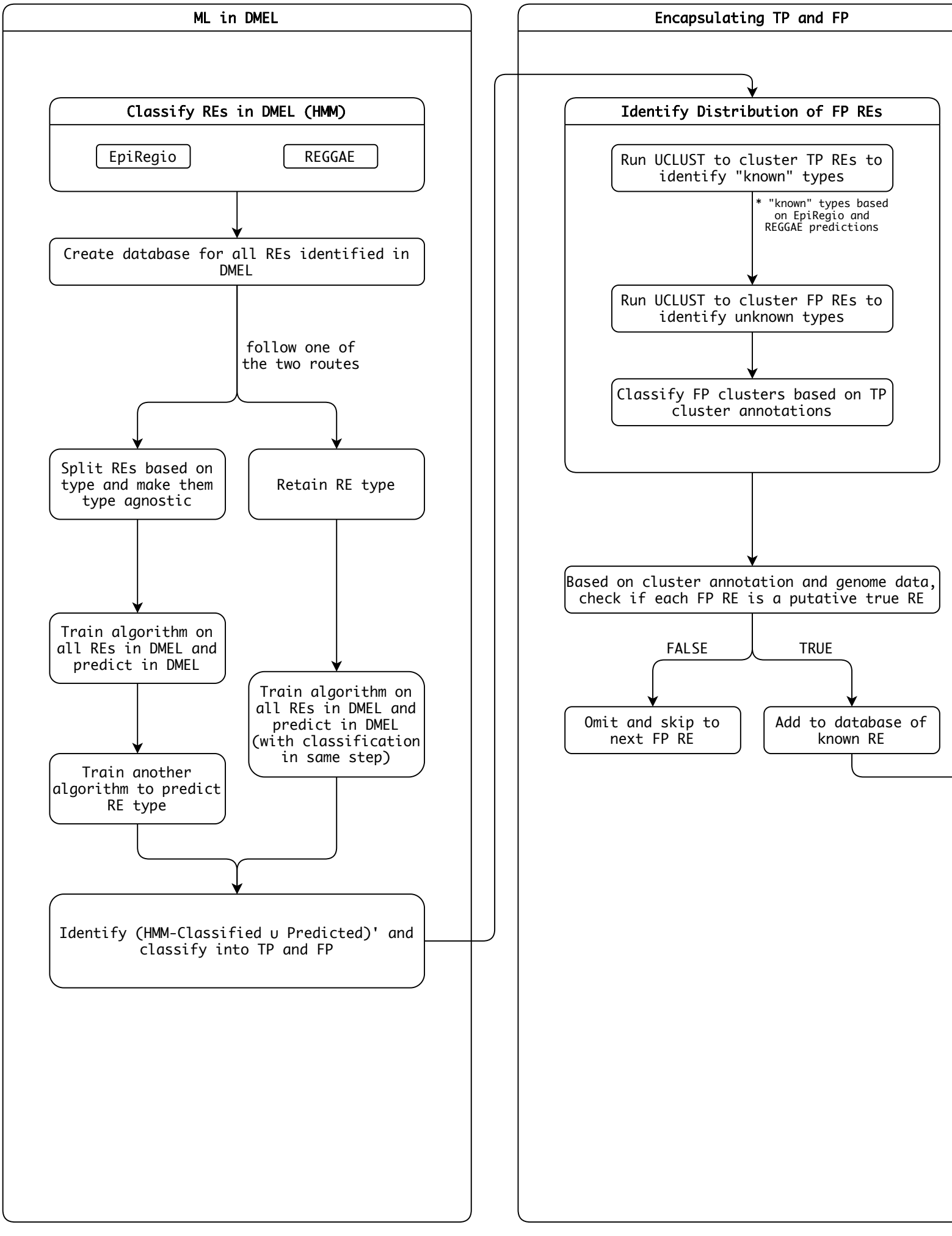
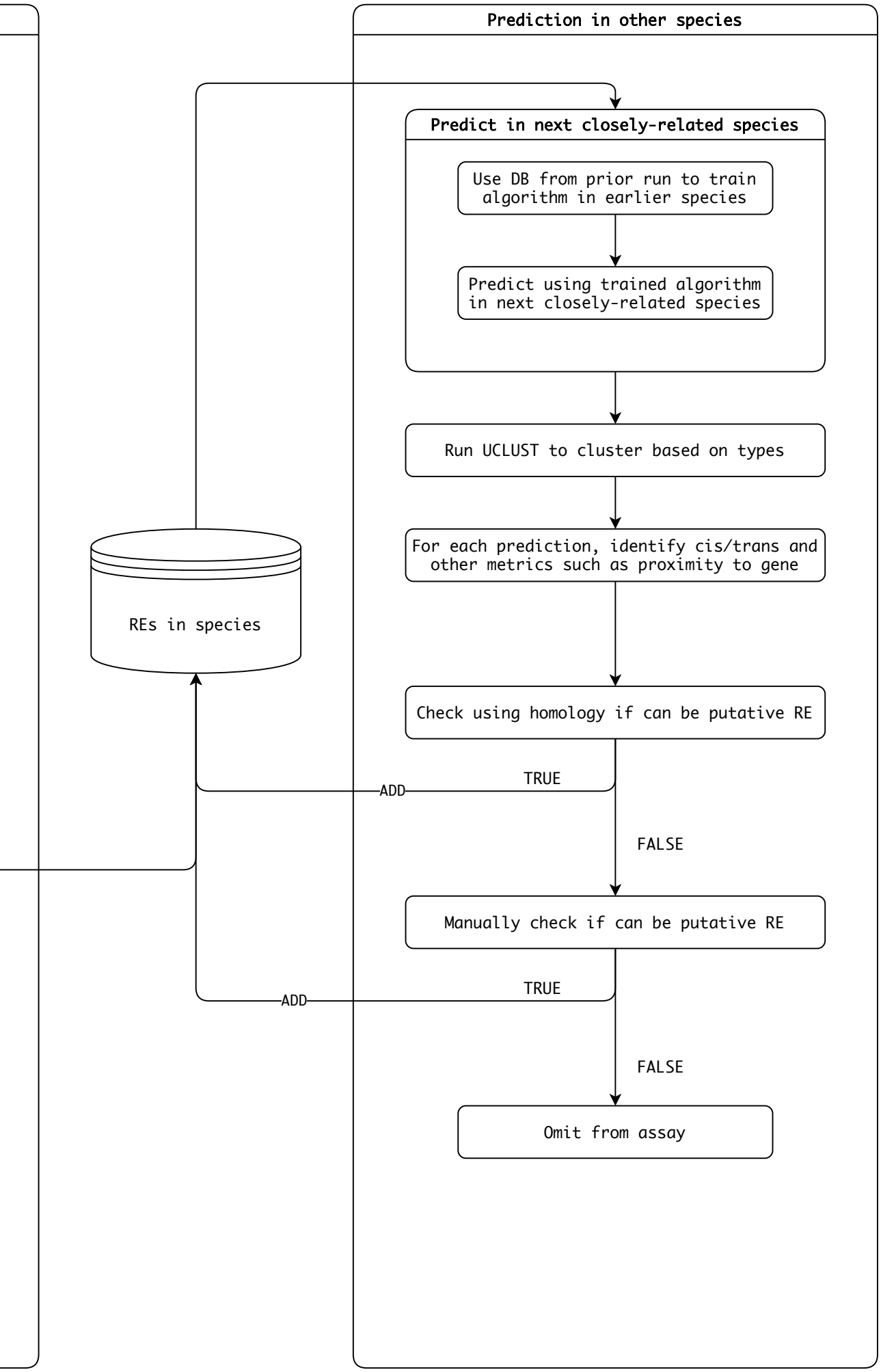

ML in DMEL
Classify REs in DMEL (HMM)
EpiRegio
REGGAE
Create database for all REs identified in DMEL
follow one of the two routes
Split REs based on type and make them type agnostic
Retain RE type
Train algorithm on all REs in DMEL and predict in DMEL
Train another algorithm to predict RE type
Train algorithm on all REs in DMEL and predict in DMEL (with classification in same step)
Identify (HMM-Classified ∪ Predicted)' and classify into TP and FP
Encapsulating TP and FP
Identify Distribution of FP REs
Run UCLUST to cluster TP REs to identify "known" types
* "known" types based on EpiRegio and REGGAE predictions
Run UCLUST to cluster FP REs to identify unknown types
Classify FP clusters based on TP cluster annotations
Based on cluster annotation and genome data, check if each FP RE is a putative true RE
FALSE
TRUE
Omit and skip to next FP RE
Add to database of known RE


Prediction in other species
Predict in next closely-related species
Use DB from prior run to train algorithm in earlier species
Predict using trained algorithm in next closely-related species
Run UCLUST to cluster based on types
For each prediction, identify cis/trans and other metrics such as proximity to gene
Check using homology if can be putative RE
TRUE
ADD
FALSE
Manually check if can be putative RE
TRUE
ADD
FALSE
Omit from assay
REs in species