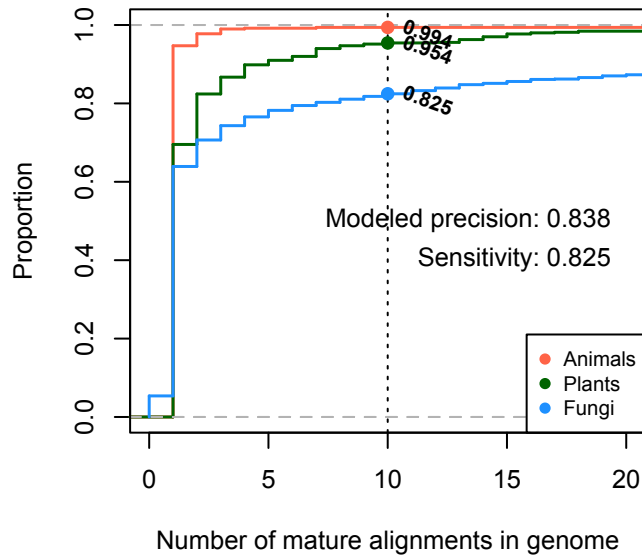


A. Locus finding precision by alignment



B. Fold accuracy in known mi/milRNAs

