RNAseq read depth, trimming, and alignment rates Study Vidal-Dupiol2014 read proportions read counts Yuan2017 Zhou2017 100%-Brener-Raffali2018 1.2e + 08Delgadillo-Nuno2018 Tang2018 75% Wecker2018 Lead count 8.0e+07 4.0e+07 Zhou2018 proportion Poquita-Du2019 Zhou2019 50% Buitrago-Lopez2020 Chuang-Mitarai2020 Li2020 **ConnellyEAPSI** 25% Grupstra2022 **Species** 0%-0.0e + 00acuta damicornis sp8 verrucosa pipeline step pipeline step