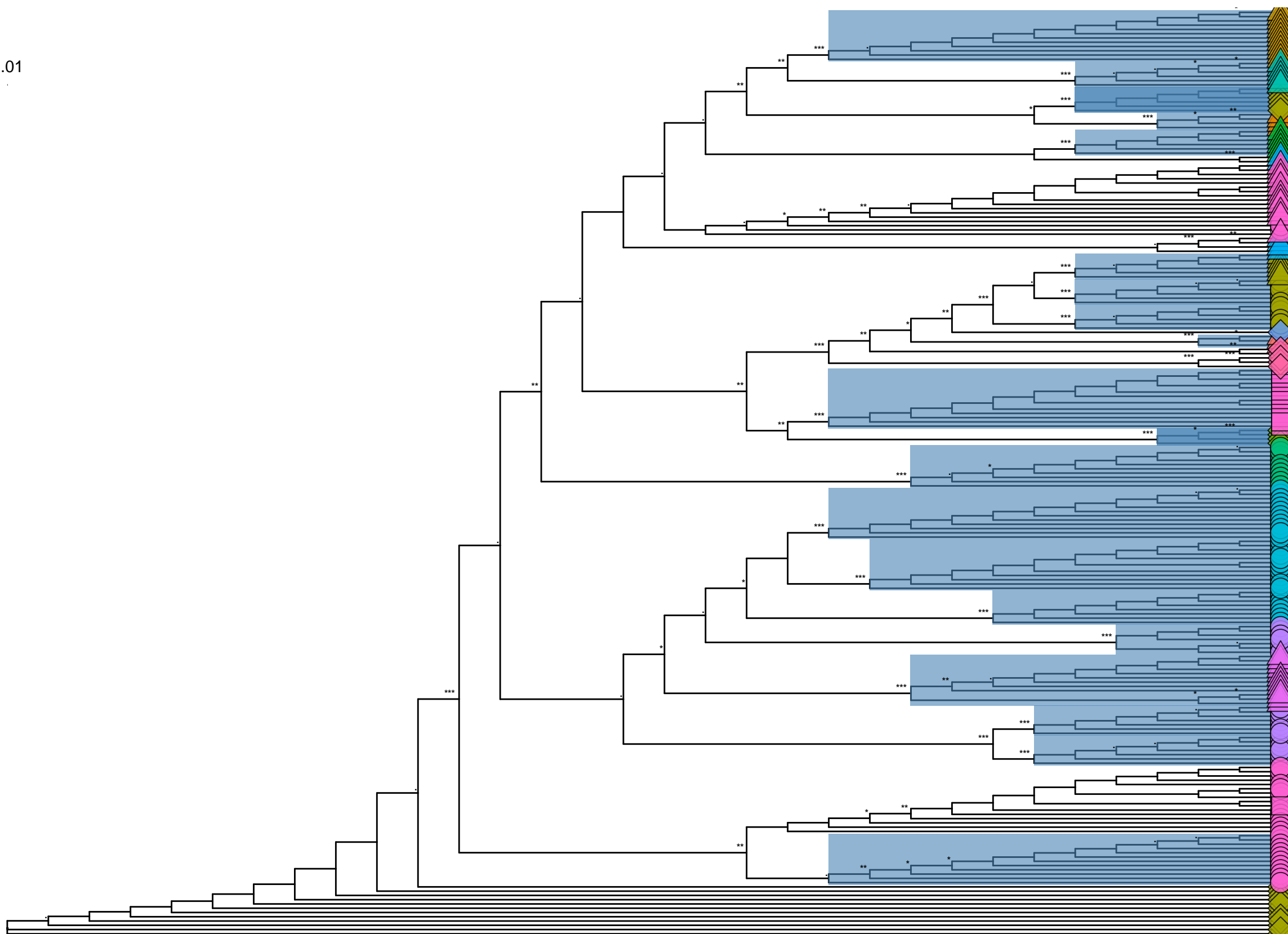


# Maximum likelihood phylotranscriptomic tree








0.01



## Study

- Vidal–Dupiol2014
- Yuan2017
- Zhou2017
- Brener–Raffali2018
- Delgadillo–Nuno2018
- Tang2018
- Wecker2018
- Zhou2018

# Species

-  Poquita–Du2019  
 Zhou2019  
 Buitrago–Lopez2020  
 Chuang–Mitarai2020  
 Li2020  
 ConnellyEAPSI  
 Grupstra2022