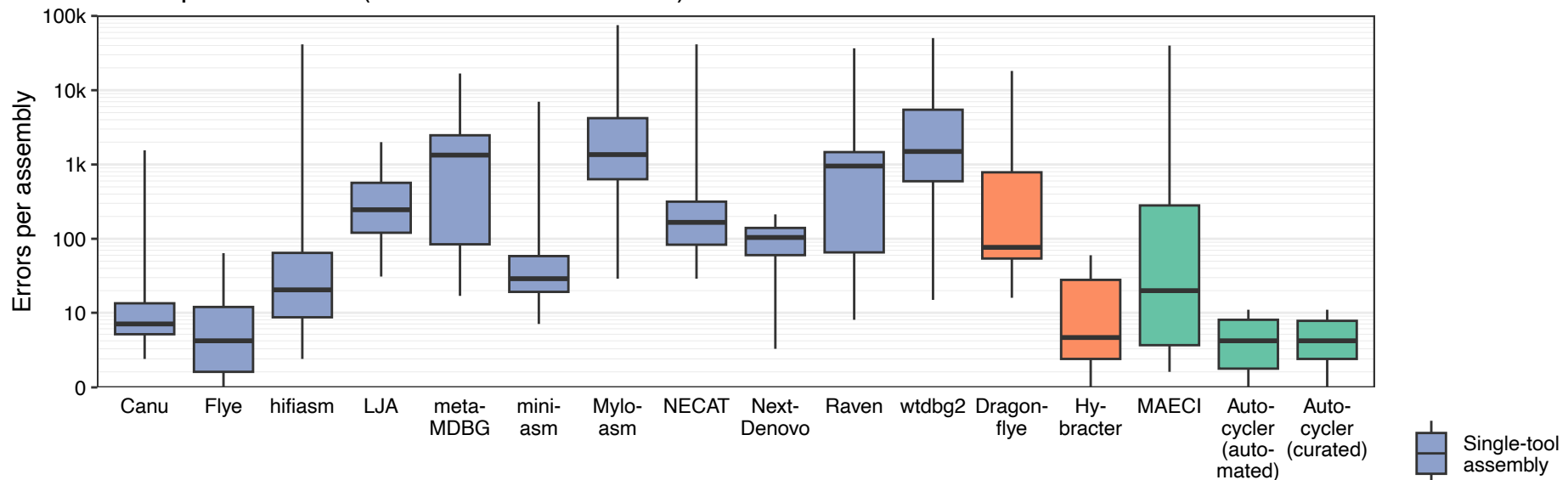


**A. Sequence errors (substitutions and indels)**



**B. Total errors (sequence errors + structural errors)**

