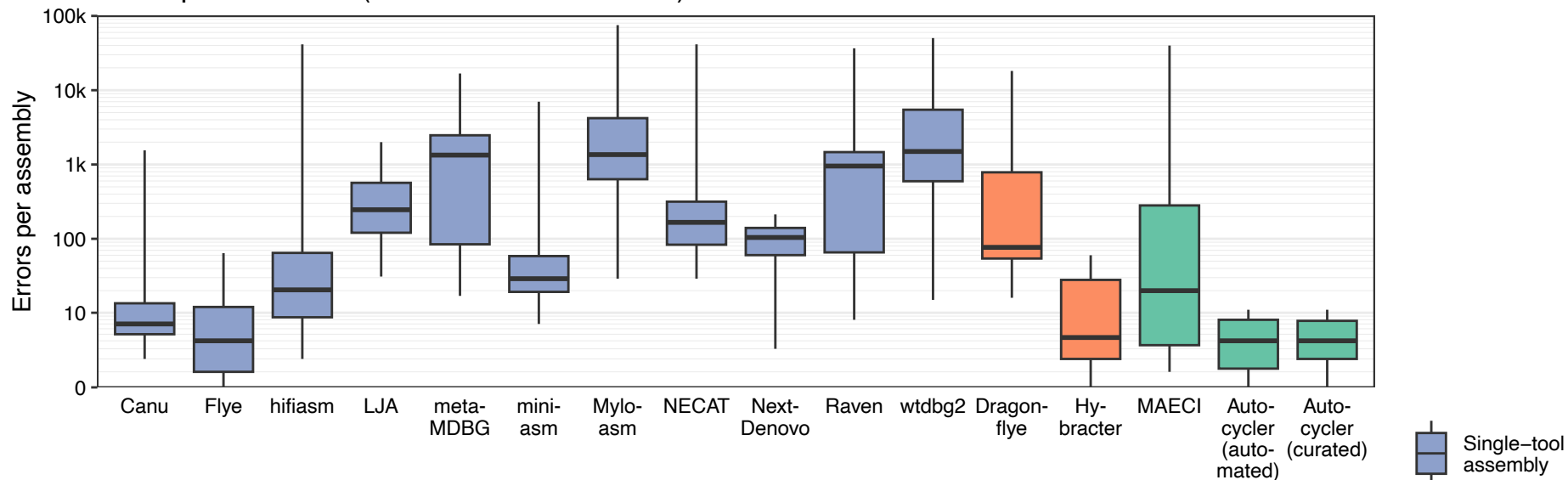


**A. Sequence errors (substitutions and indels)**



**B. Total errors (sequence errors + missing bases + extra bases)**

