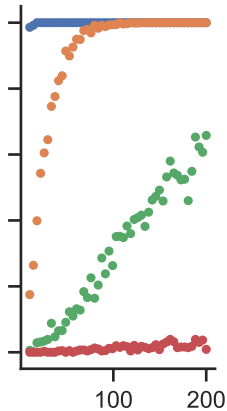
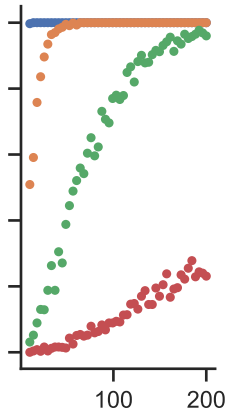
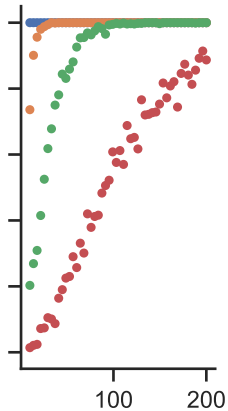
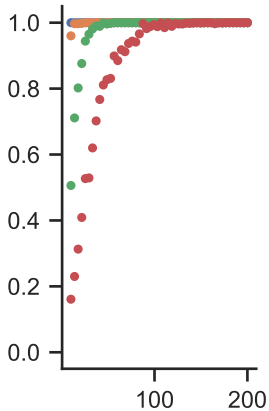


Fraction of mutations for
which fitness is estimated



Sequencing depth