A length 25 sequences without two-base encoding

% of sequences correctly aligned

Number of base substitutions

length 25 sequences without two-base encoding

B length 25 sequences with two-base encoding

% of sequences correctly aligned

Number of base substitutions

length 25 sequences with two-base encoding

C length 50 sequences without two-base encoding

% of sequences correctly aligned

Number of base substitutions

length 50 sequences without two-base encoding

D length 50 sequences with two-base encoding

% of sequences correctly aligned

Number of base substitutions

length 50 sequences with two-base encoding