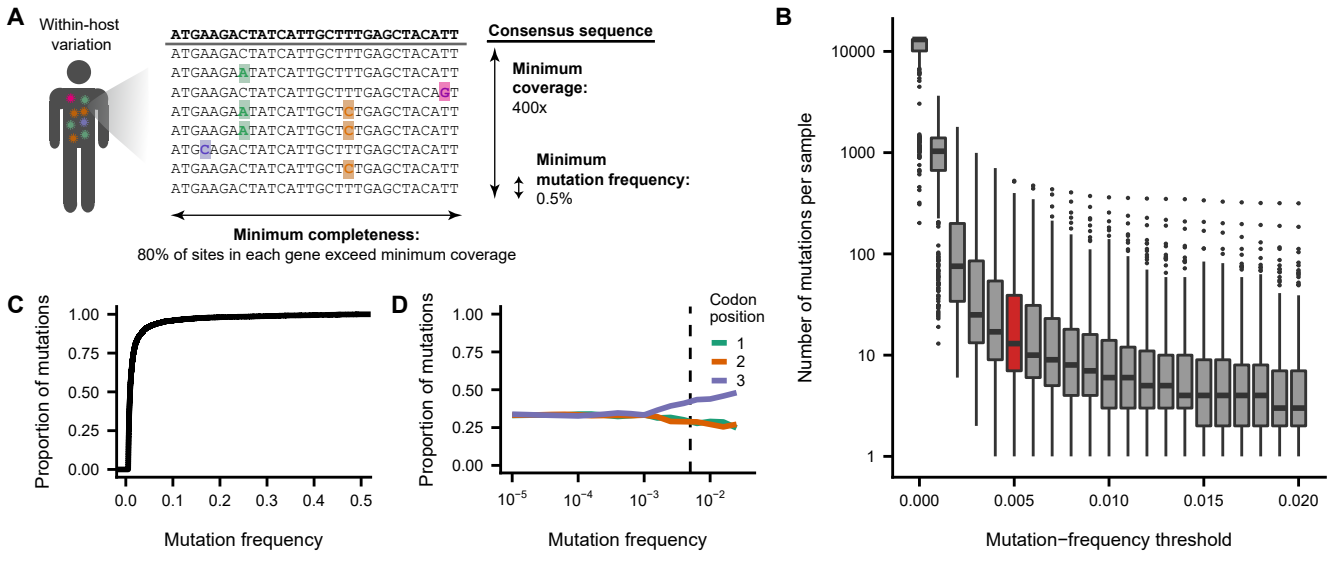
A
Within-host variation
ATGAAGACTATCATTGCTTTGAGCTACATT
ATGAAGACTATCATTGCTTTGAGCTACATT
ATGAAGAATATCATTGCTTTGAGCTACATT
ATGAAGACTATCATTGCTTTGAGCTACAGT
ATGAAGAATATCATTGCTCTGAGCTACATT
ATGAAGAATATCATTGCTCTGAGCTACATT
ATGCAGACTATCATTGCTTTGAGCTACATT
ATGAAGACTATCATTGCTCTGAGCTACATT
ATGAAGACTATCATTGCTTTGAGCTACATT
Consensus sequence
Minimum coverage: 400x
Minimum mutation frequency: 0.5%
Minimum completeness:
80% of sites in each gene exceed minimum coverage
B
Number of mutations per sample
10000
1000
100
10
1
0.000
0.005
0.010
0.015
0.020
Mutation−frequency threshold
C
Proportion of mutations
1.00
0.75
0.50
0.25
0.00
0.0
0.1
0.2
0.3
0.4
0.5
Mutation frequency
D
Proportion of mutations
1.00
0.75
0.50
0.25
0.00
10^{-5}
10^{-4}
10^{-3}
10^{-2}
Mutation frequency
Codon position
1
2
3