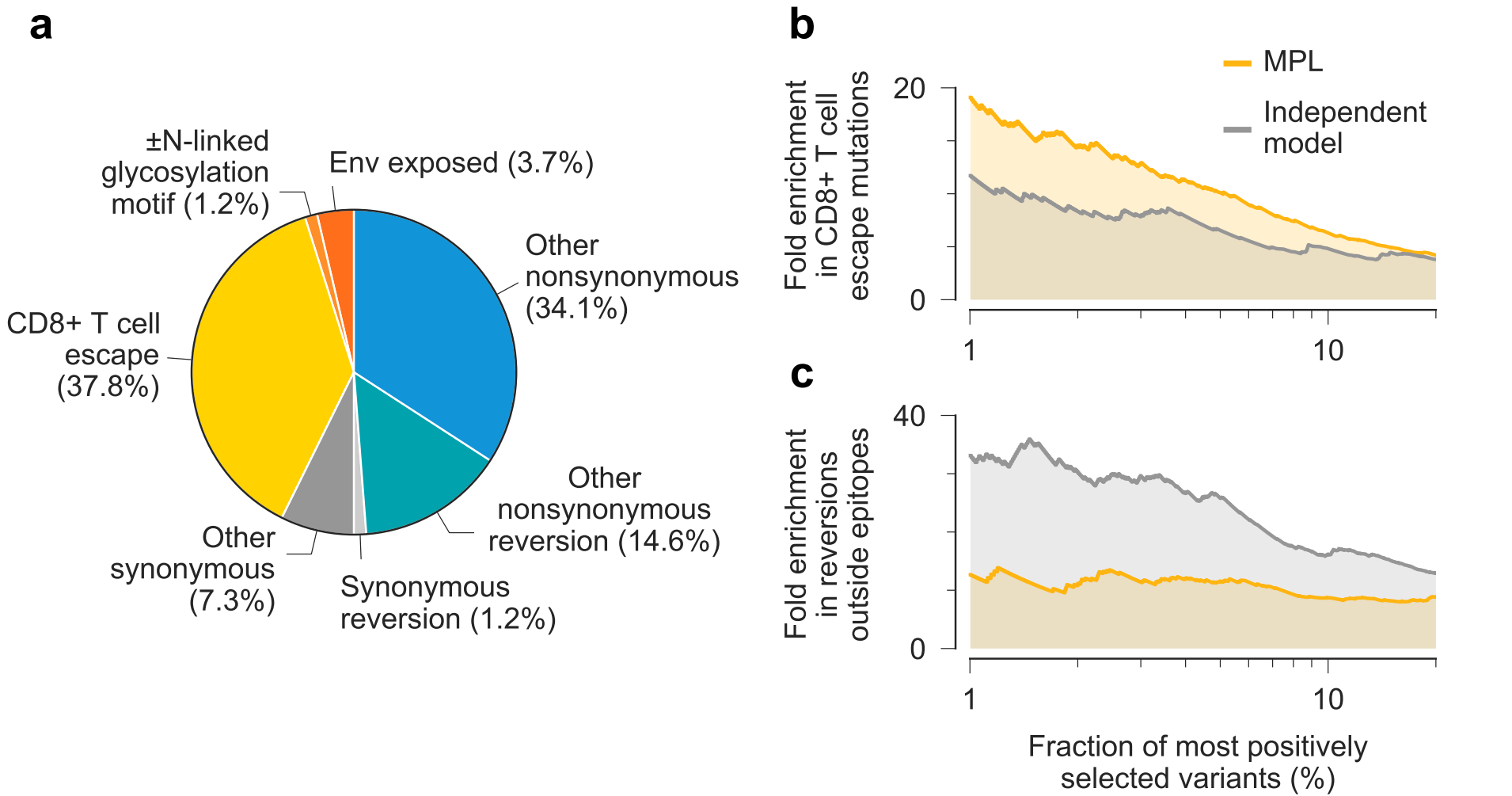
a
±N-linked glycosylation motif (1.2%)
Env exposed (3.7%)
Other nonsynonymous (34.1%)
CD8+ T cell escape (37.8%)
Other nonsynonymous reversion (14.6%)
Other synonymous (7.3%)
Synonymous reversion (1.2%)
b
MPL
Independent model
Fold enrichment in CD8+ T cell escape mutations
20
0
1
10
c
Fold enrichment in reversions outside epitopes
40
0
1
10
Fraction of most positively selected variants (%)