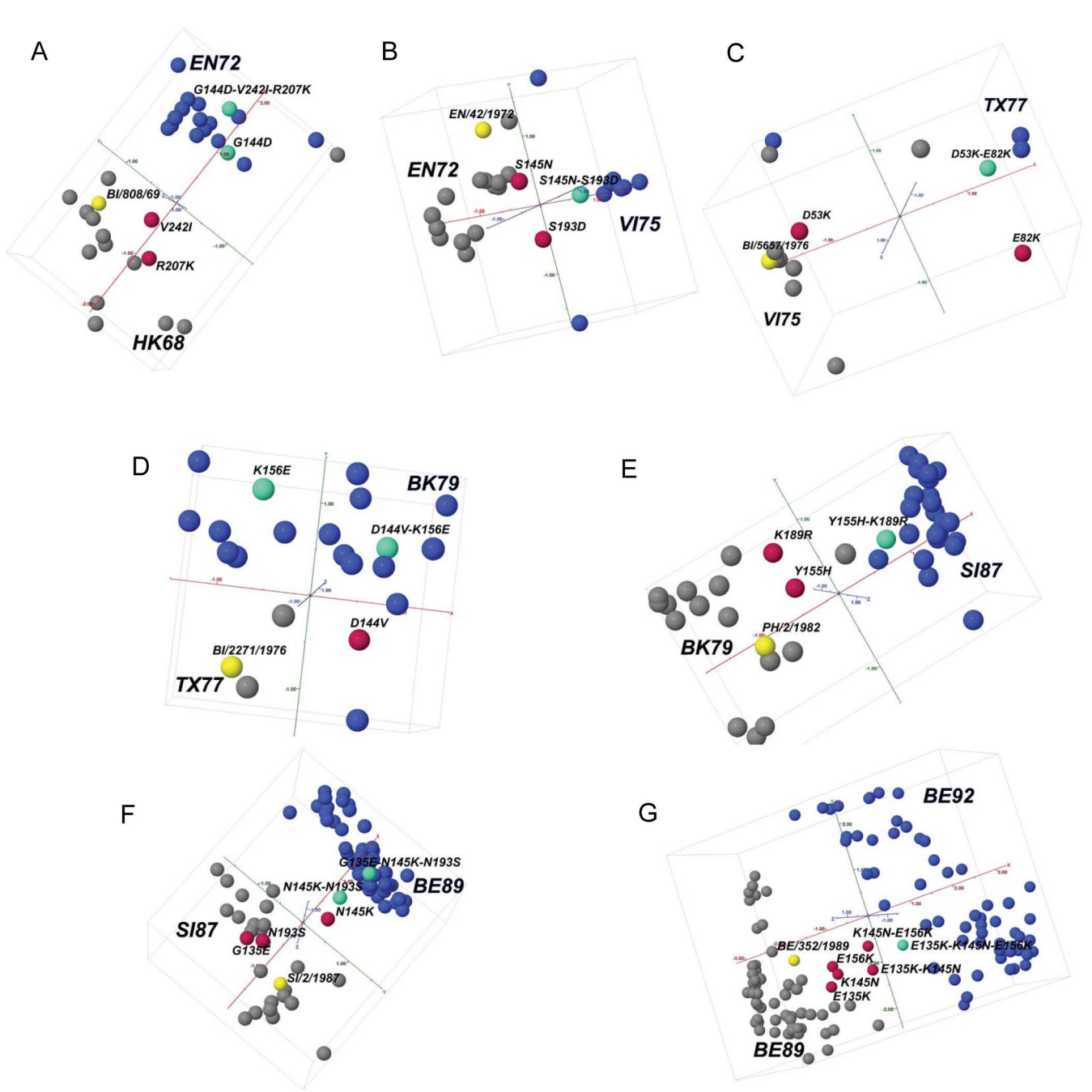
FIG. W5. Maps showing the effects of predicted residues in antibody-binding sites in driving designated antigenic drifts *(A-G)*. Each colored ball on the map represents a virus: gray balls denote the viruses in the previous cluster of an antigenic drift event; blue balls denote the viruses in the drifted cluster; and the yellow ball represents the wild-type strain from which we generated simulated drift variants by mutating key residues in its HA sequence. Each mutant is marked with its mutation type on the wild-type strain. For example, N145K denotes the viruses obtained by mutating the amino acid asparagine (N) to lysine (K) in position 145 of the wild-type strain, and G135K-N145K represents a double mutation derived similarly. The mutations not driving antigenic drift are marked in red, and those driving antigenic drift are marked in light blue. One unit on the map corresponds to a 2-fold change in HI titer


A
EN72
G144D-V242I-R207K
G144D
BI/808/69
V242I
R207K
HK68
B
EN/42/1972
EN72
S145N
S145N-S193D
S193D
VI75
C
TX77
D53K-E82K
D53K
BI/5657/1976
E82K
VI75
D
K156E
BK79
D144V-K156E
D144V
BI/2271/1976
TX77
E
Y155H-K189R
K189R
Y155H
SI87
PH/2/1982
BK79
F
G135E-N145K-N193S
N145K-N193S
BE89
N145K
SI87
N193S
G135E
SI/2/1987
G
BE92
K145N-E156K
BE/352/1989
E135K-K145N-E156K
E156K
E135K-K145N
K145N
E135K
BE89