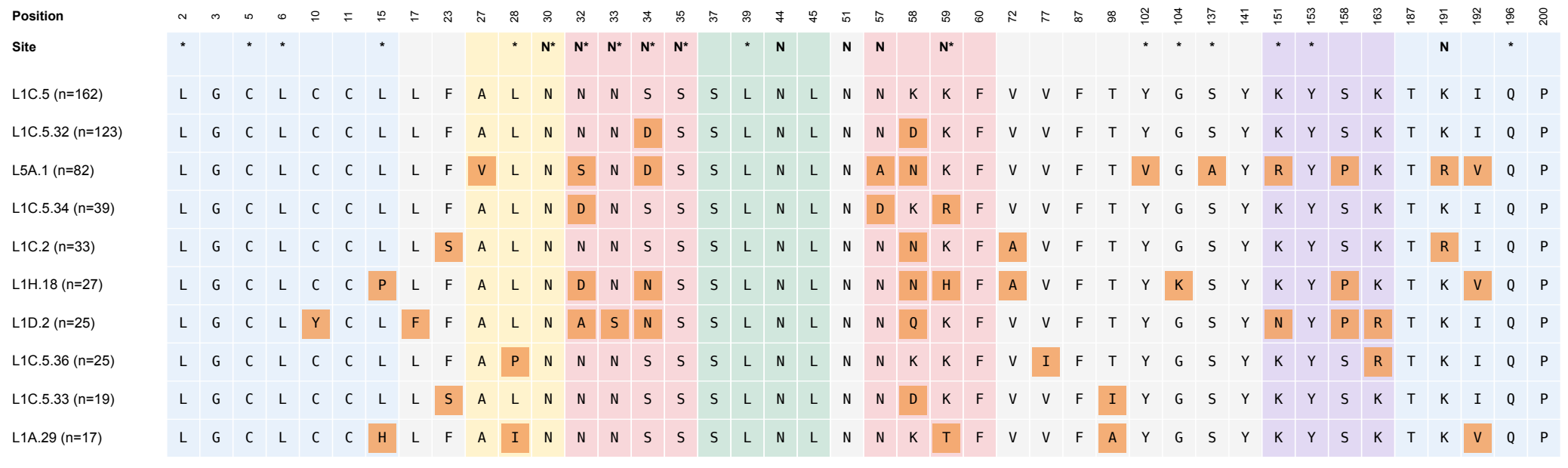

Position
2 3 5 6 10 11 15 17 23 27 28 30 32 33 34 35 37 39 44 45 51 57 58 59 60 72 77 87 98 102 104 137 141 151 153 158 163 187 191 192 196 200
Site
* * * N* N* N* N* * N N* * * N
L1C.5 (n=162) L G C L C C L L F A L N N N S S S L N L N N K K F V V F T Y G S Y K Y S K T K I Q P
L1C.5.32 (n=123) L G C L C C L L F A L N N N D S S L N L N N D K F V V F T Y G S Y K Y S K T K I Q P
L5A.1 (n=82) L G C L C C L L F V L N S N D S S L N L N A N K F V V F T V G A Y R Y P K T R V Q P
L1C.5.34 (n=39) L G C L C C L L F A L N D N S S S L N L N D K R F V V F T Y G S Y K Y S K T K I Q P
L1C.2 (n=33) L G C L C C L L S A L N N N S S S L N L N N N K F A V F T Y G S Y K Y S K T R I Q P
L1H.18 (n=27) L G C L C C P L F A L N D N N S S L N L N N N H F A V F T Y K S Y K Y P K T K V Q P
L1D.2 (n=25) L G C L Y C L F F A L N A S N S S L N L N N Q K F V V F T Y G S Y N Y P R T K I Q P
L1C.5.36 (n=25) L G C L C C L L F A P N N N S S S L N L N N K K F V I F T Y G S Y K Y S R T K I Q P
L1C.5.33 (n=19) L G C L C C L L S A L N N N S S S L N L N N D K F V V F I Y G S Y K Y S K T K I Q P
L1A.29 (n=17) L G C L C C H L F A I N N N S S S L N L N N K T F V V F A Y G S Y K Y S K T K V Q P
Orange cells differ from the L1C.5 consensus. N = predicted N-glycosylation motif start; * = positive-selection site discussed in the manuscript.
B cell epitope
Decoy epitope
HVR-1/HVR-2
Neutralizing epitope
T cell epitope
Other discussed site