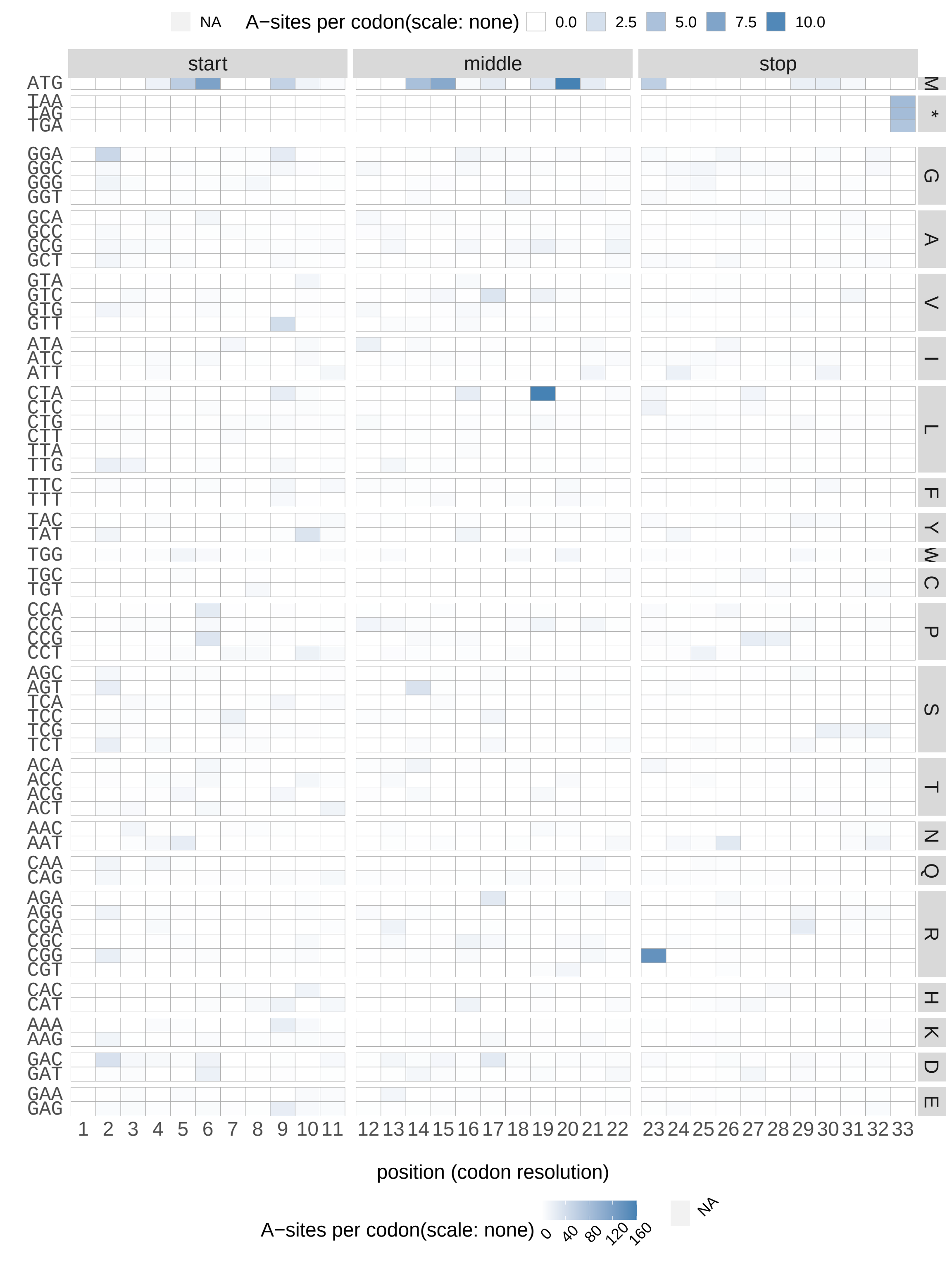
NA
A−sites per codon(scale: none)
0.0
2.5
5.0
7.5
10.0
start
middle
stop
ATG
TAA
TAG
TGA
GGA
GGC
GGG
GGT
GCA
GCC
GCG
GCT
GTA
GTC
GTG
GTT
ATA
ATC
ATT
CTA
CTC
CTG
CTT
TTA
TTG
TTC
TTT
TAC
TAT
TGG
TGC
TGT
CCA
CCC
CCG
CCT
AGC
AGT
TCA
TCC
TCG
TCT
ACA
ACC
ACG
ACT
AAC
AAT
CAA
CAG
AGA
AGG
CGA
CGC
CGG
CGT
CAC
CAT
AAA
AAG
GAC
GAT
GAA
GAG
M
*
G
A
V
I
L
F
Y
W
C
P
S
T
N
Q
R
H
K
D
E
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
position (codon resolution)
A−sites per codon(scale: none)
0
40
80
120
160
NA