

* = hAng-2 amino acids that were shown to interact with Tie-2 by crystal structure analysis.

▲ = Amino acids that differ between hAng-2 and hAng-1 and that correspond to Tie-2-interacting amino acid residues.

Figure 1

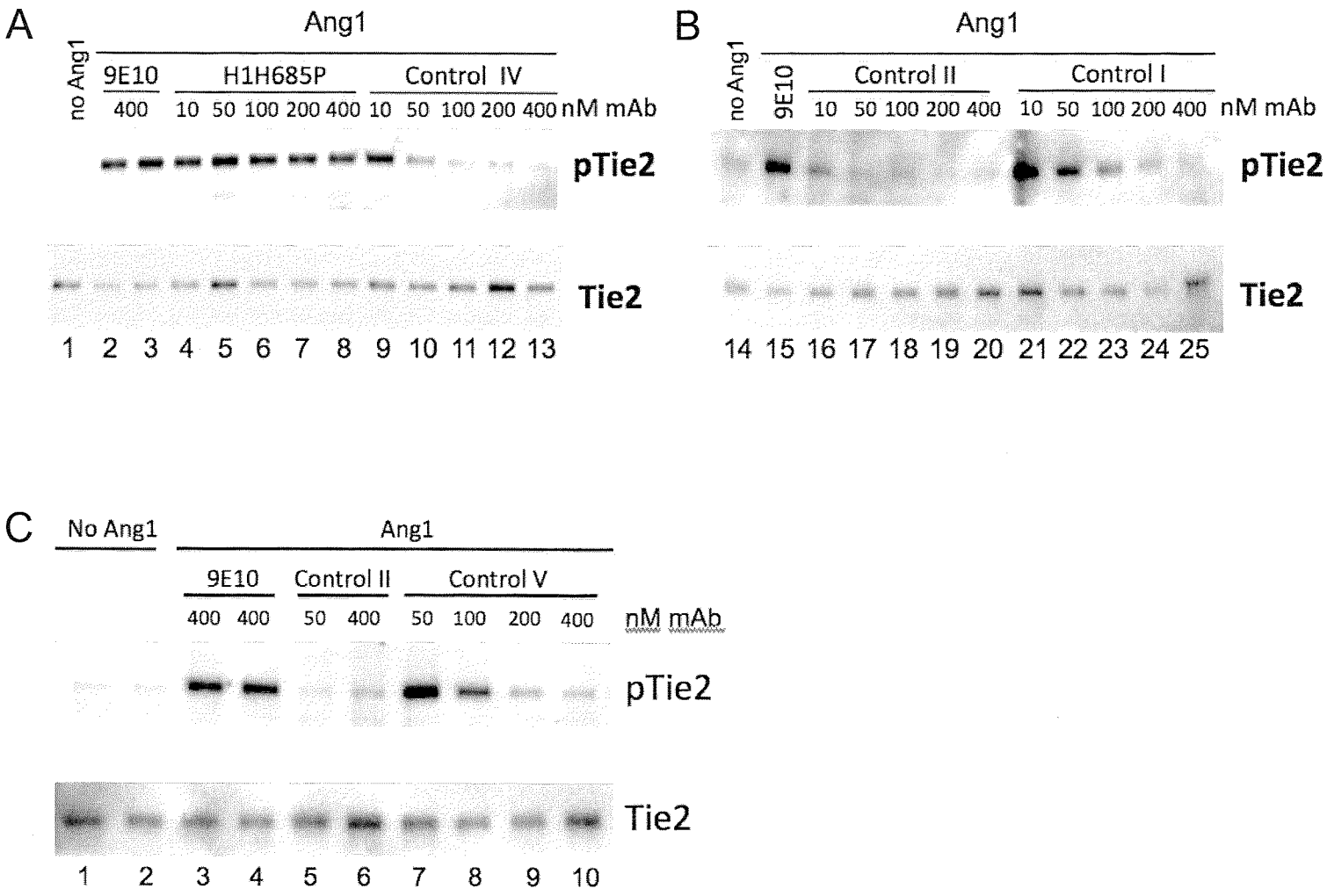

A
Ang1
no Ang1
9E10
H1H685P
Control IV
400
10 50 100 200 400 10 50 100 200 400 nM mAb
pTie2
Tie2
1 2 3 4 5 6 7 8 9 10 11 12 13
B
Ang1
no Ang1
9E10
Control II
Control I
10 50 100 200 400 10 50 100 200 400 nM mAb
pTie2
Tie2
14 15 16 17 18 19 20 21 22 23 24 25
C
No Ang1
Ang1
9E10
Control II
Control V
400 400 50 400 50 100 200 400 nM mAb
pTie2
Tie2
1 2 3 4 5 6 7 8 9 10

Figure 2

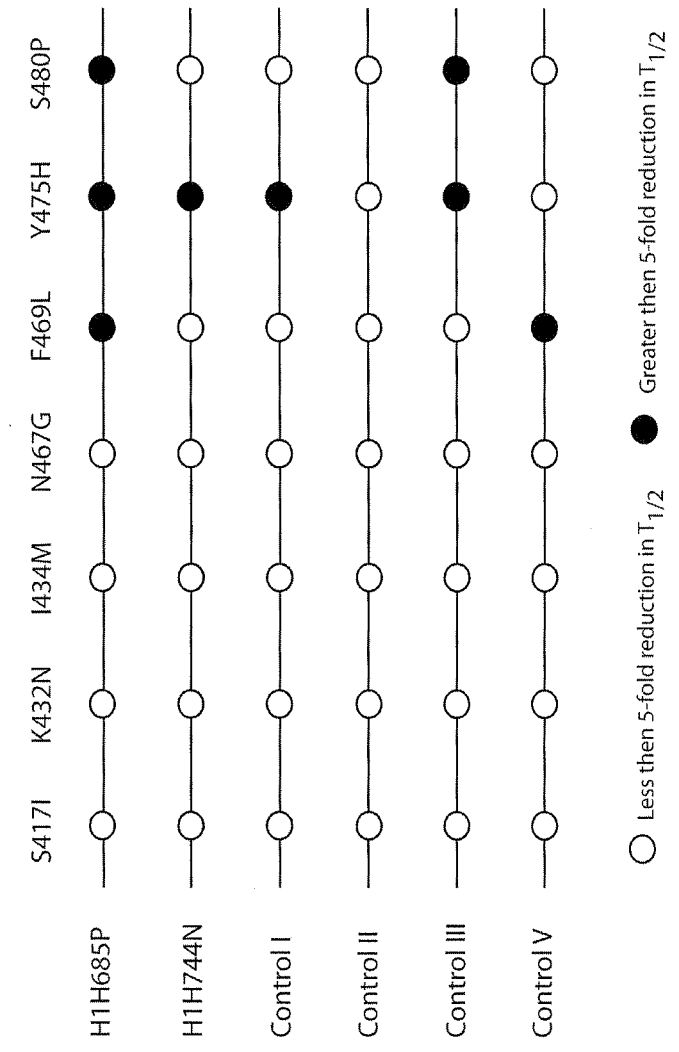

S417I
K432N
I434M
N467G
F469L
Y475H
S480P
H1H685P
H1H744N
Control I
Control II
Control III
Control V
Less then 5-fold reduction in T1/2
Greater then 5-fold reduction in T1/2

Figure 3