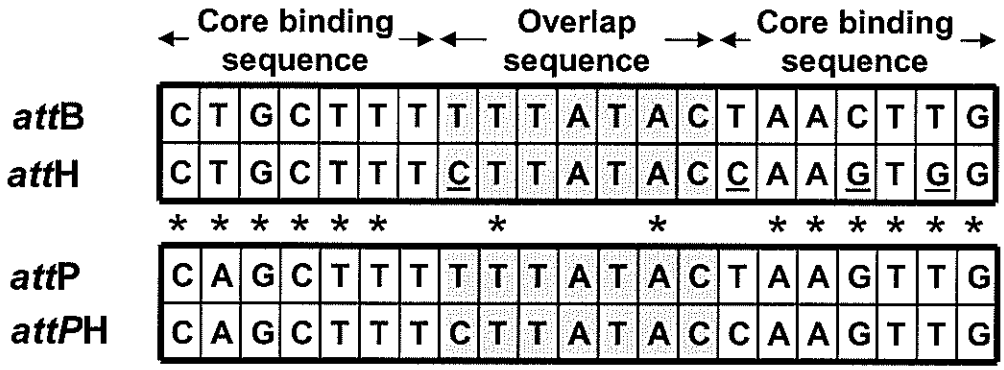

Core binding sequence
Overlap sequence
Core binding sequence
attB
attH
attP
attPH
C T G C T T T T T T A T A C T A A C T T G
C T G C T T T C T T A T A C C A A G T G G
C A G C T T T T T T A T A C T A A G T T G
C A G C T T T C T T A T A C C A A G T T G

Figure 1

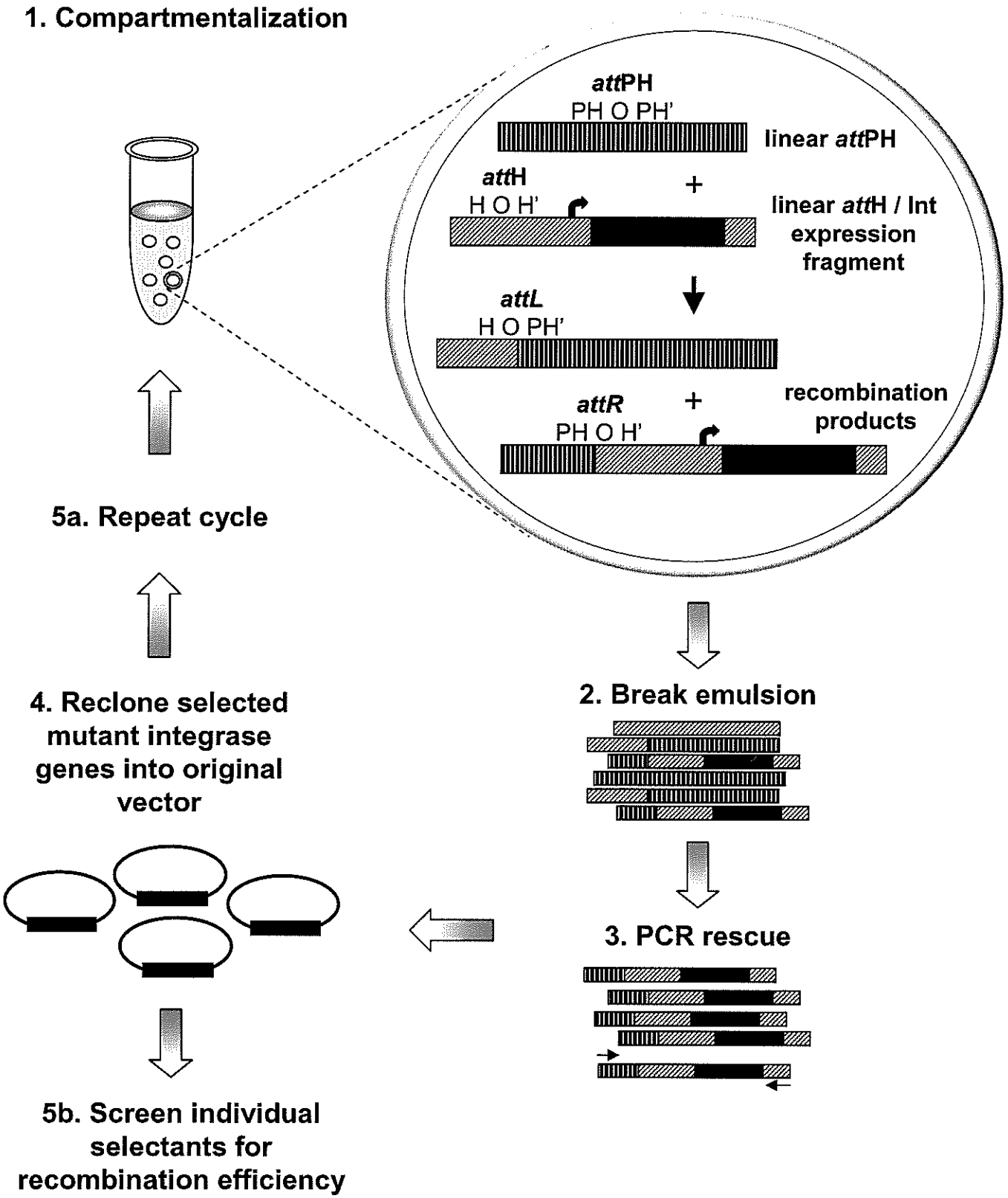

1. Compartmentalization
attPH
PH O PH'
linear attPH
attH
H O H'
+
linear attH / Int expression fragment
attL
H O PH'
attR
PH O H'
+
recombination products
5a. Repeat cycle
2. Break emulsion
3. PCR rescue
4. Reclone selected mutant integrase genes into original vector
5b. Screen individual selectants for recombination efficiency

Figure 2A

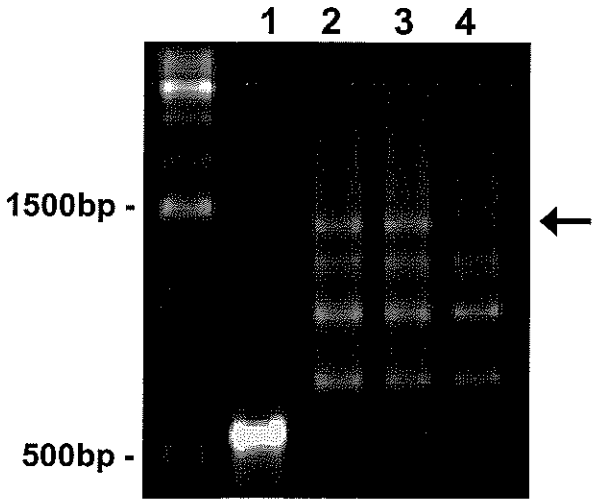


Figure 2B

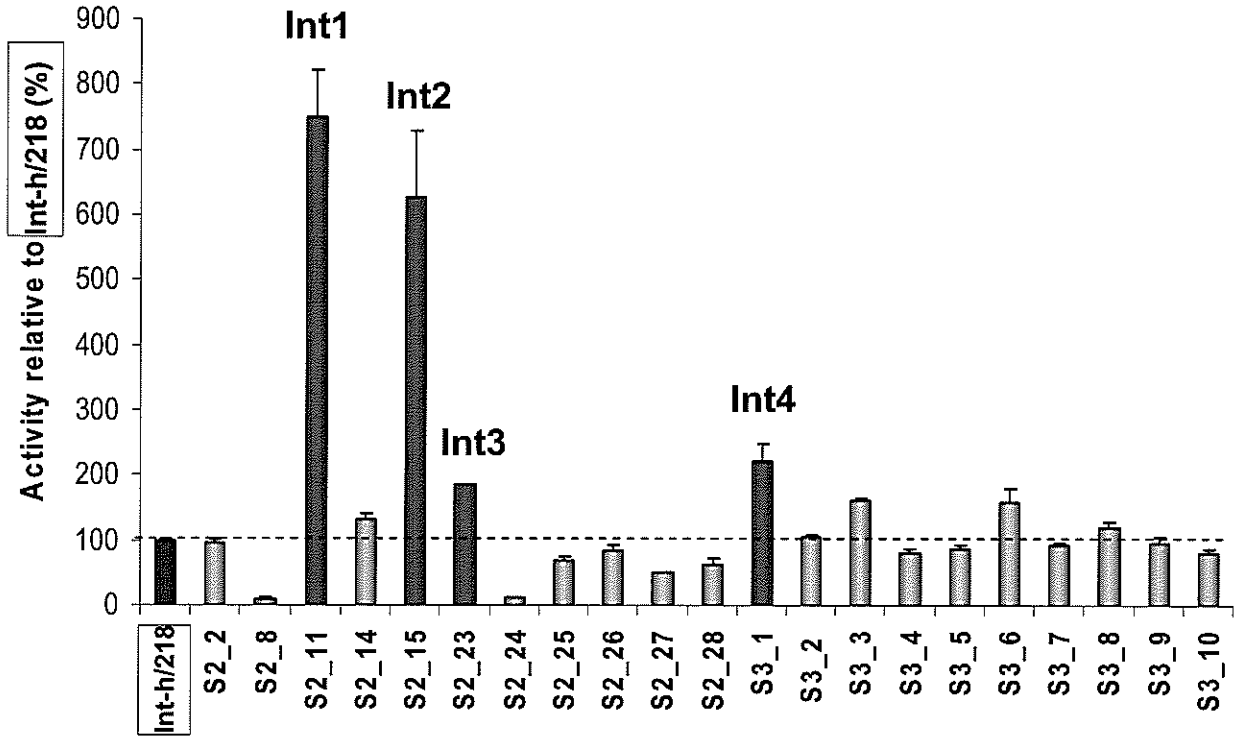


Figure 3A

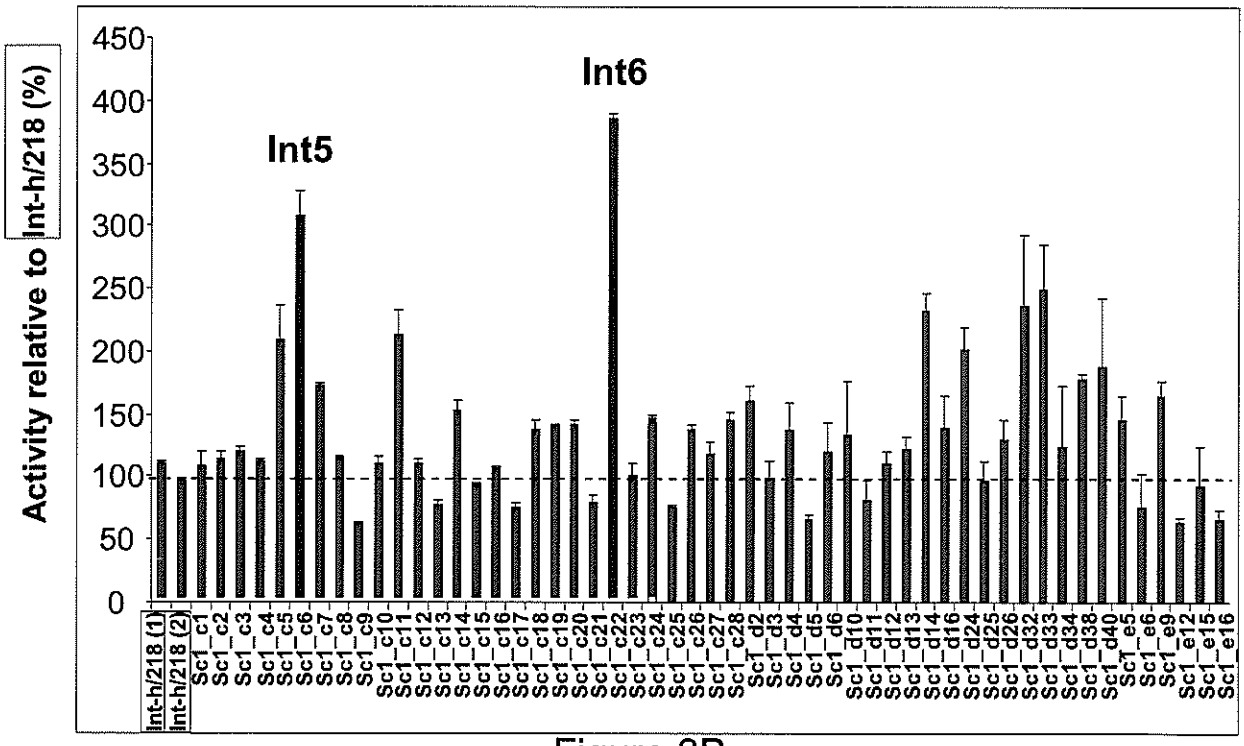


Figure 3B

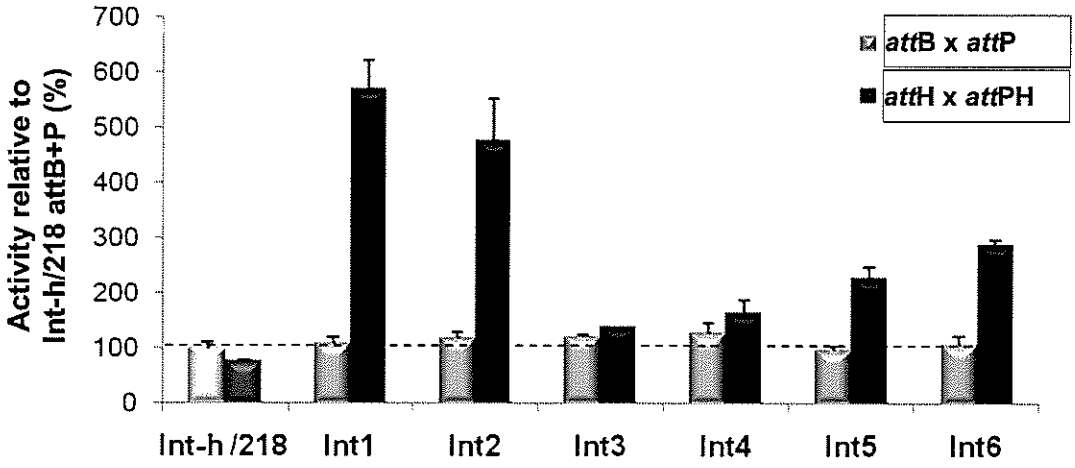


Figure 4A

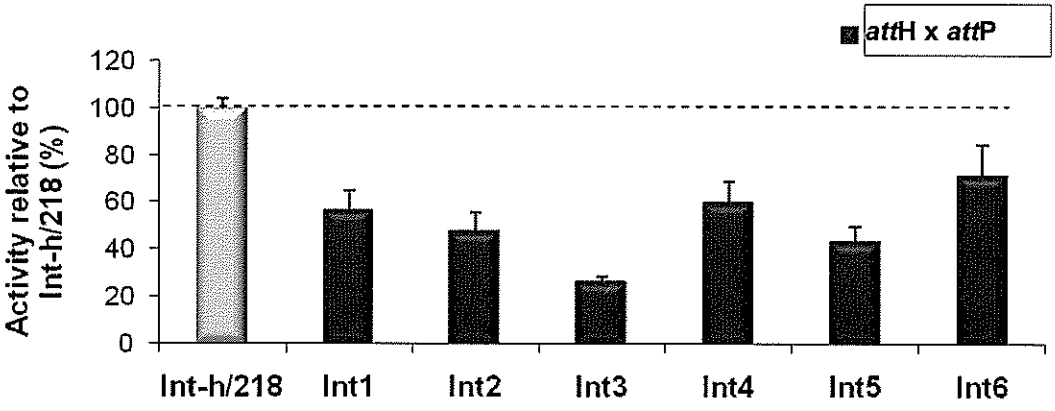


Figure 4B

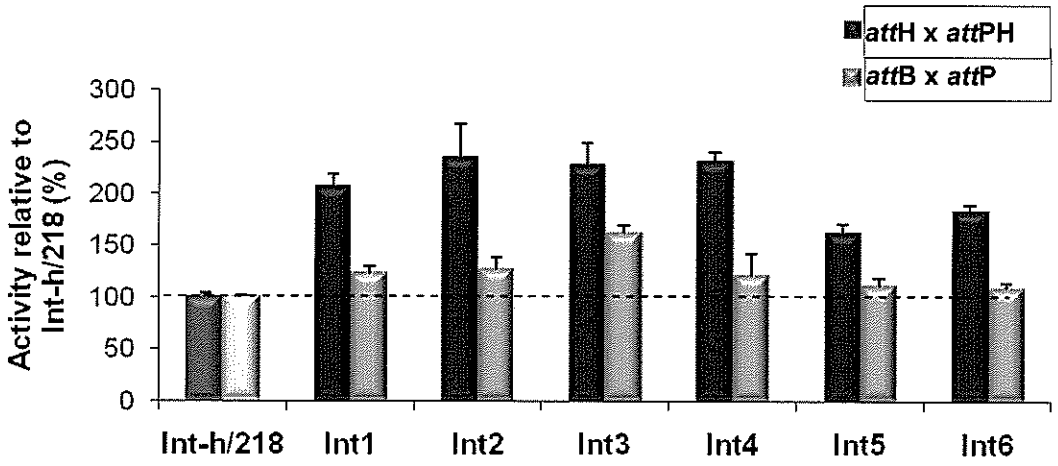


Figure 4C

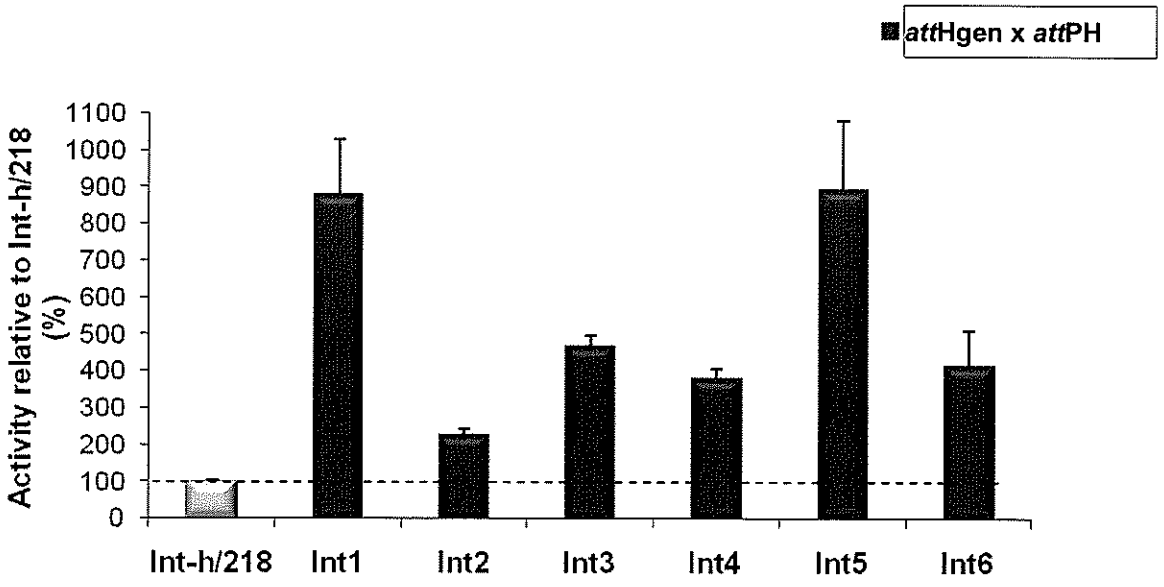


Figure 4D

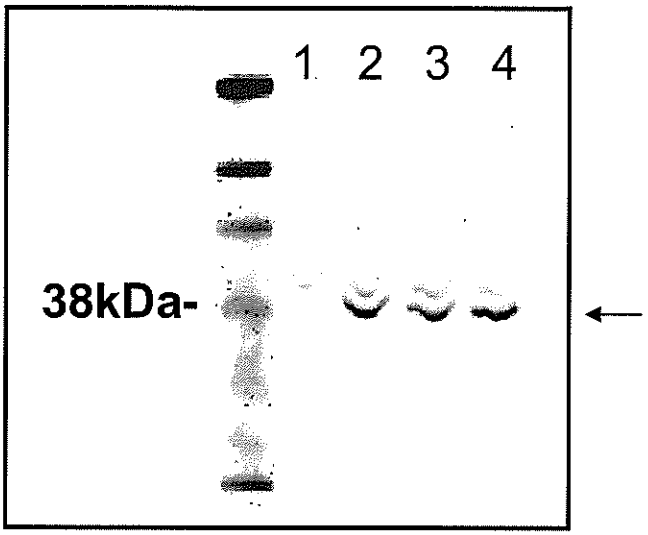


Figure 5A

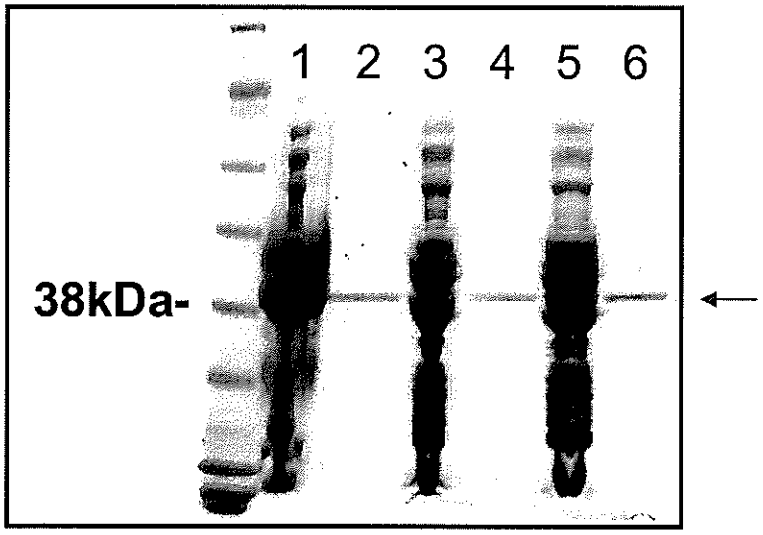


Figure 5B

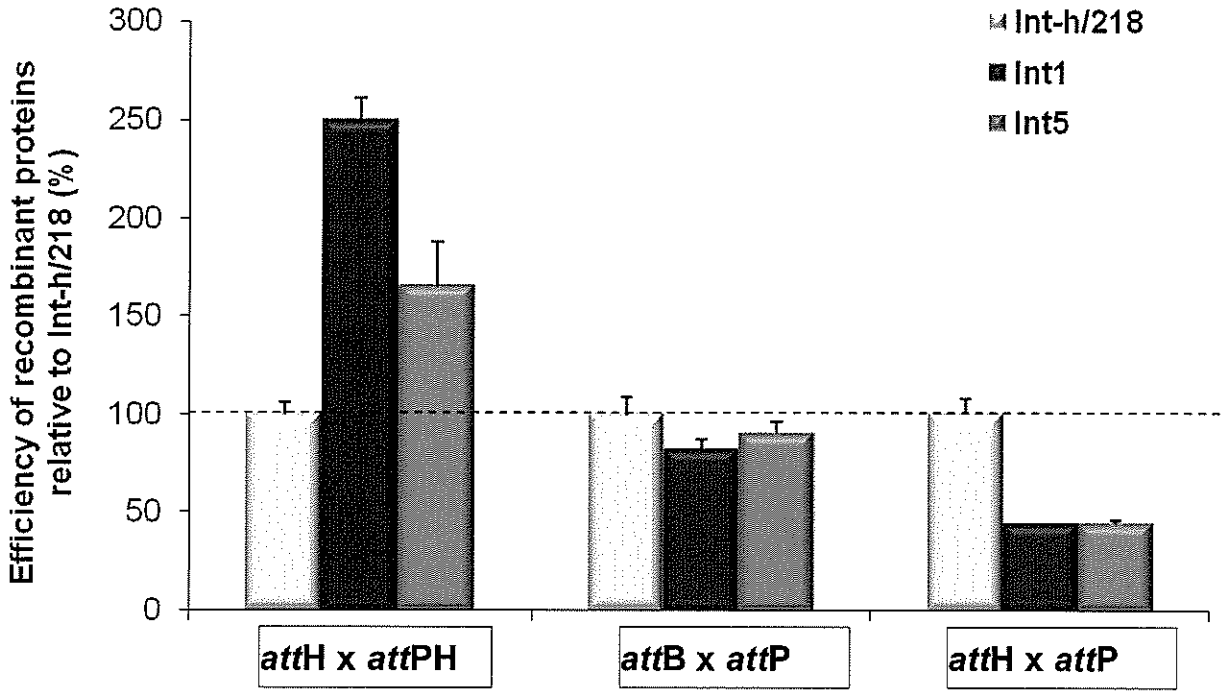


Figure 6A

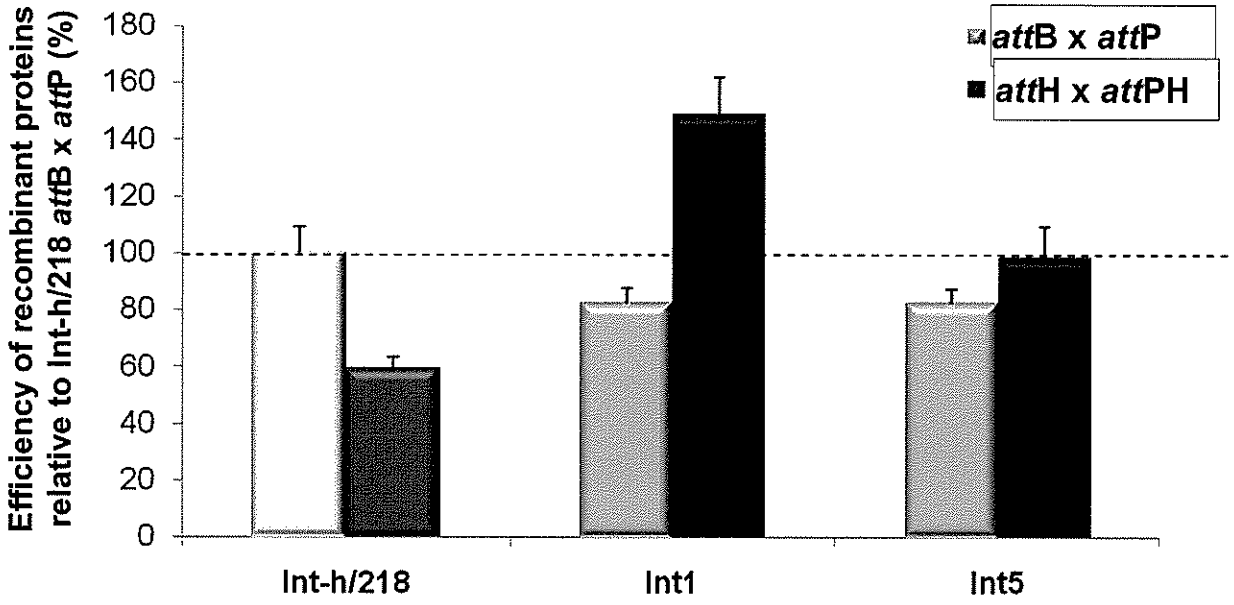


Figure 6B

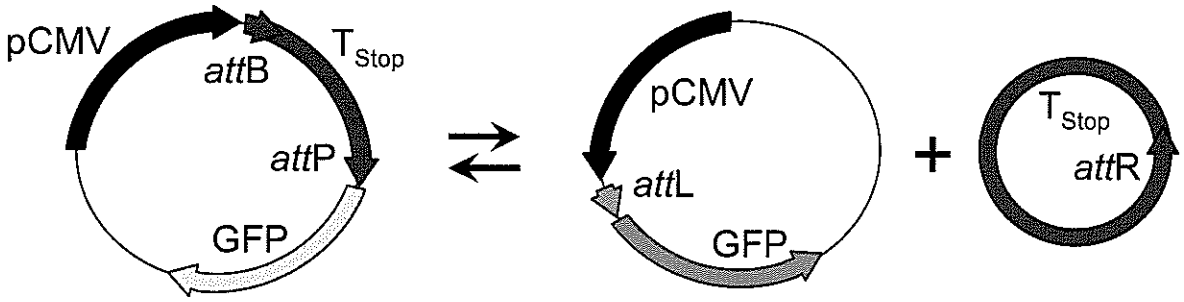


Figure 7

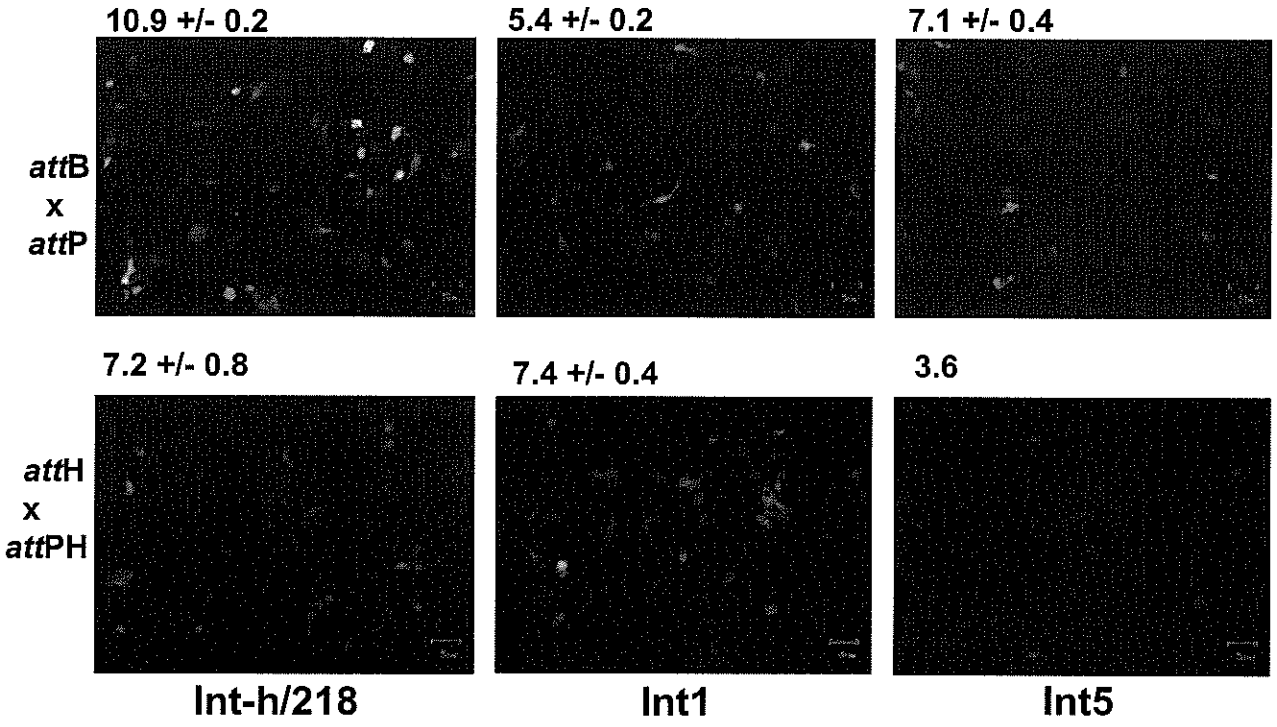

10.9 +/- 0.2
5.4 +/- 0.2
7.1 +/- 0.4
attB
x
attP
7.2 +/- 0.8
7.4 +/- 0.4
3.6
attH
x
attPH
Int-h/218
Int1
Int5

Figure 8

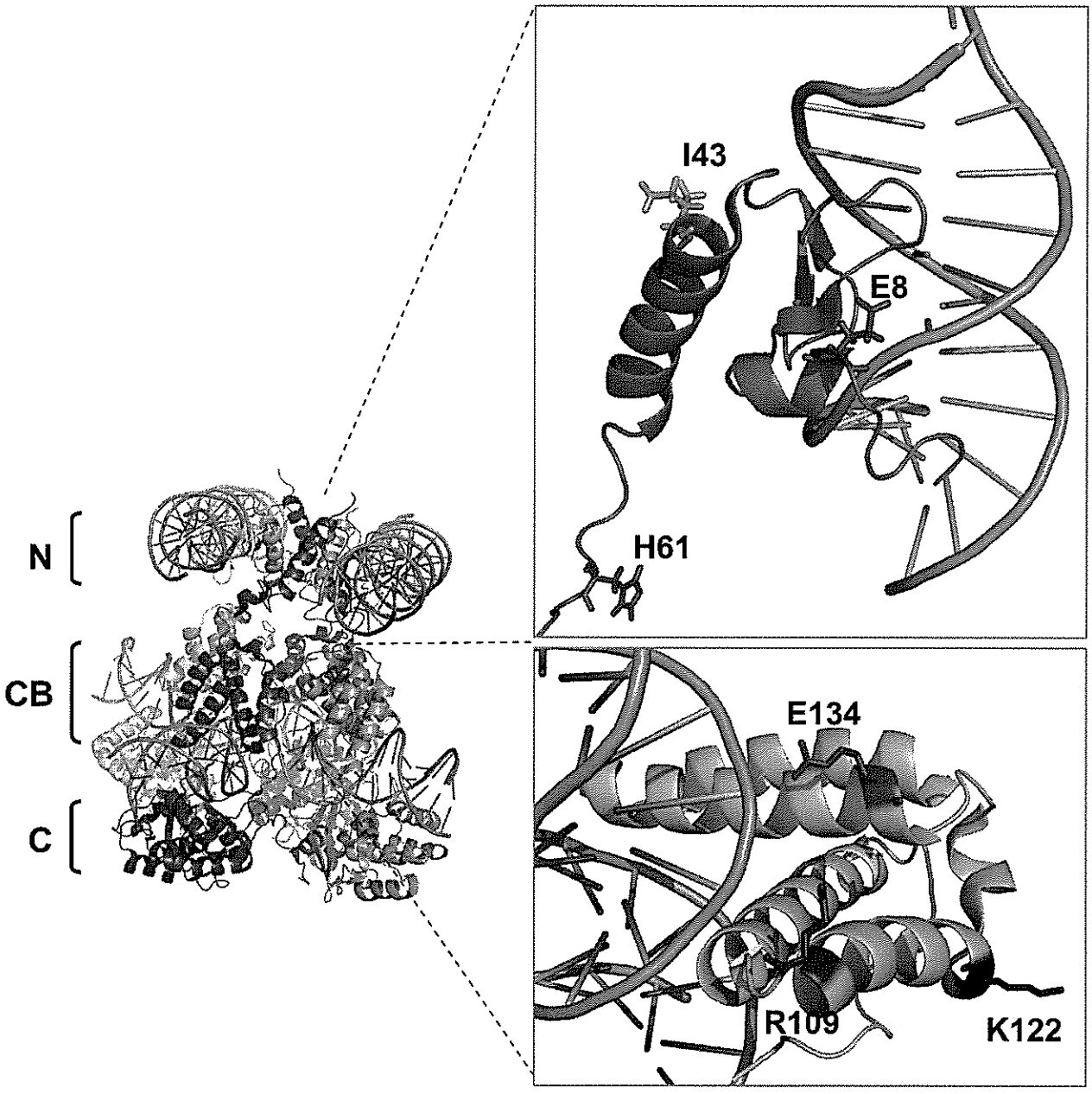


Figure 9

Name	Total mutations	Mutations										
Int1	2		I43F	H61R								
Int2	6				R109G		E134G	A154V	A182T	G252L	I253L	
Int3	2					K122R						C262R
Int4	2	E8K		H61R								
Int5	1		I43F									
Int6	2			H61R		K122R						

Table 1

Figure 10

pLIR (attB + attP)



Figure 11A

pGFP3.1 (attH + attPH)

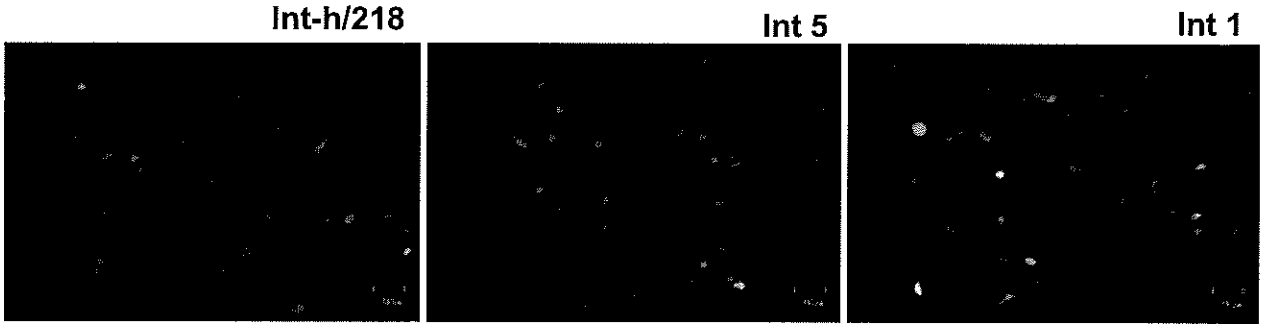


Figure 11B