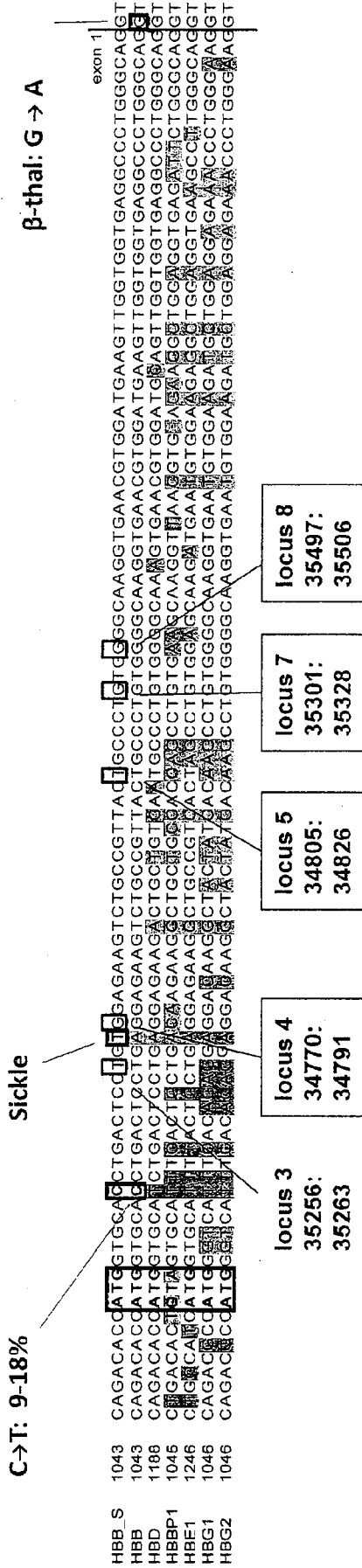


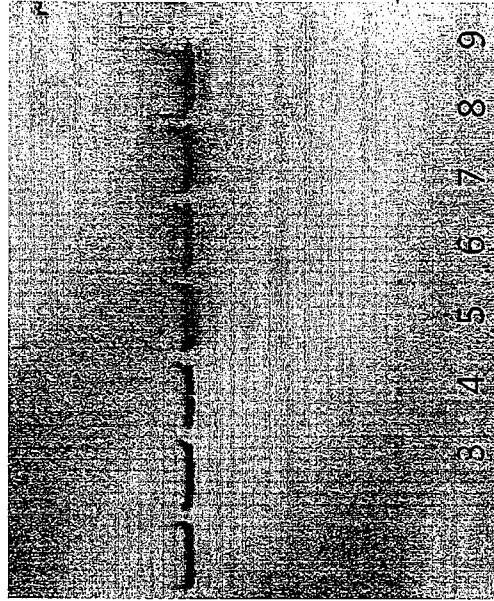


Locus	% indels, CD34 studies
	exp 1 exp 2
3	13.3 0.0
4	0.0 0.0
5	36.8 25.6
6	42.0 23.7
7	23.2 19.9

FIGURE 1

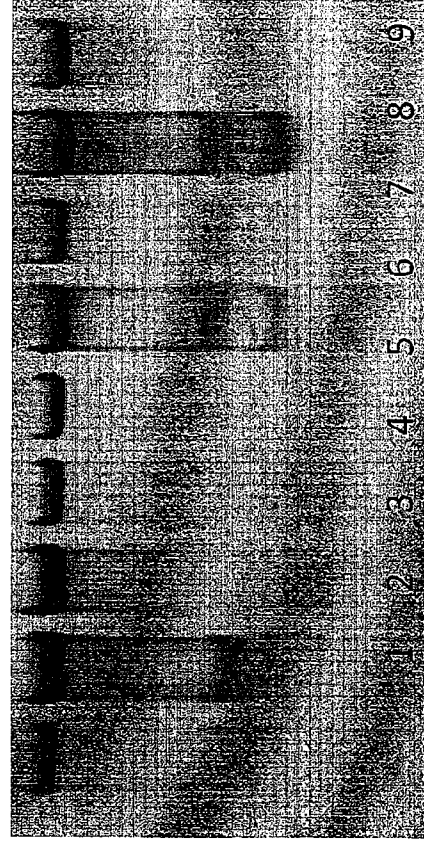
FIGURE 2

A. RFLP



		Cel1	RFLP
1	57/61	5.8	
2	68/01	12.0	
3	55/58	0.0	
4	55/58+F	0.0	
5	55/58+R	0.0	
6	11/33	16.5	
7	11/33+F	6.7	
8	11/33+R	24.6	
9	unt	0.0	

B. CEL-I



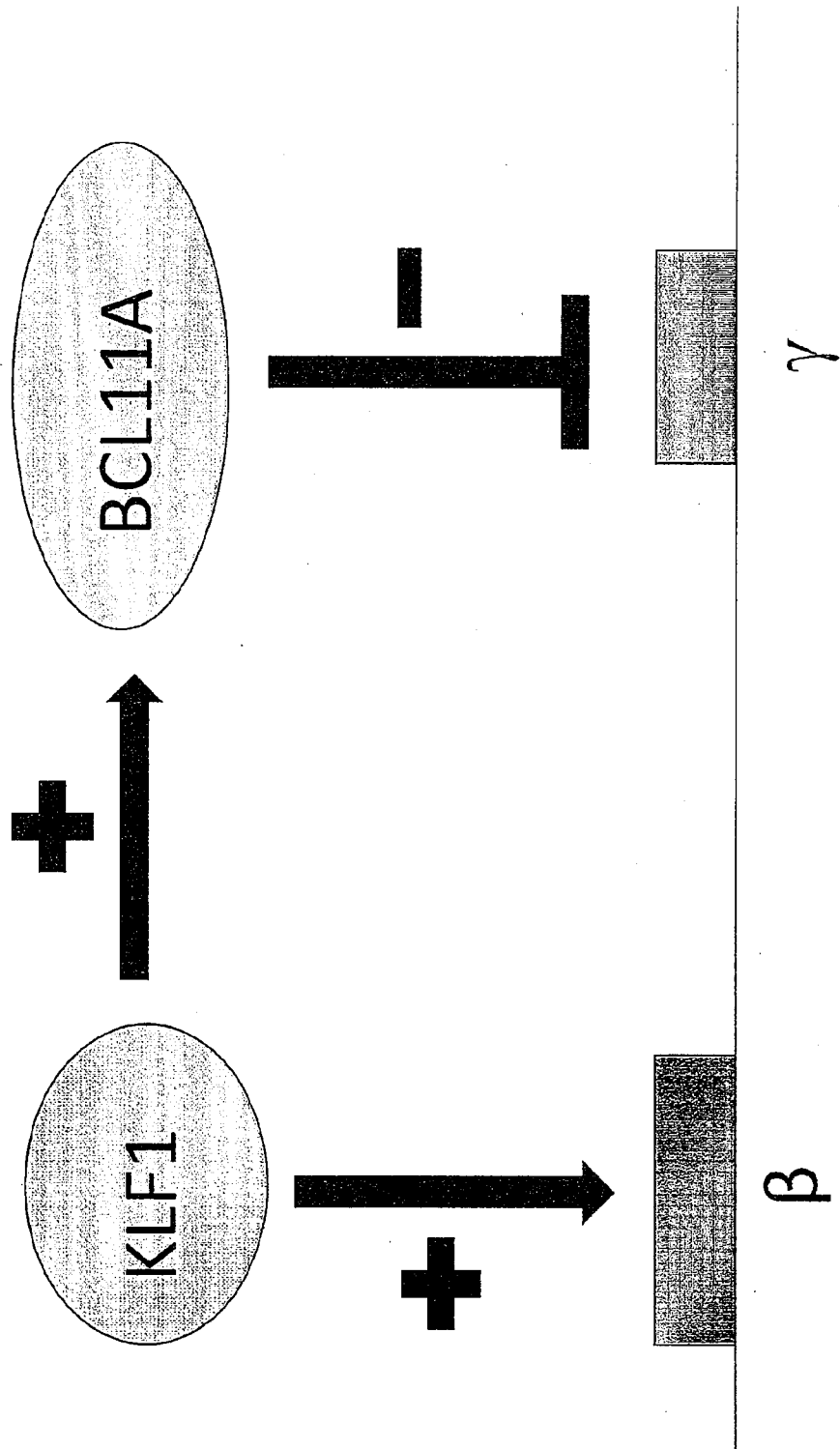
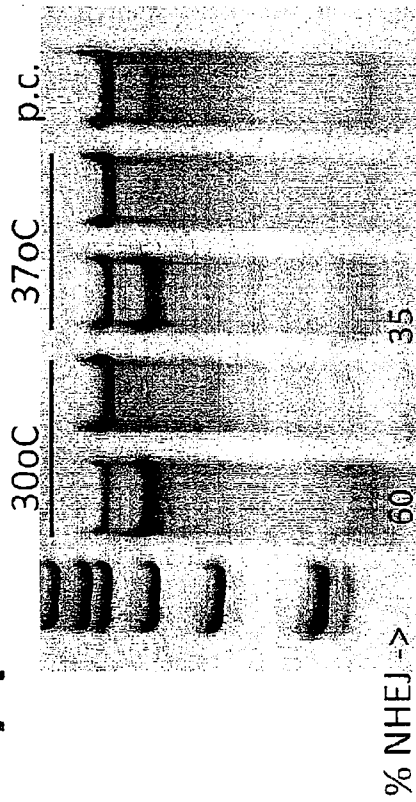


Figure 3

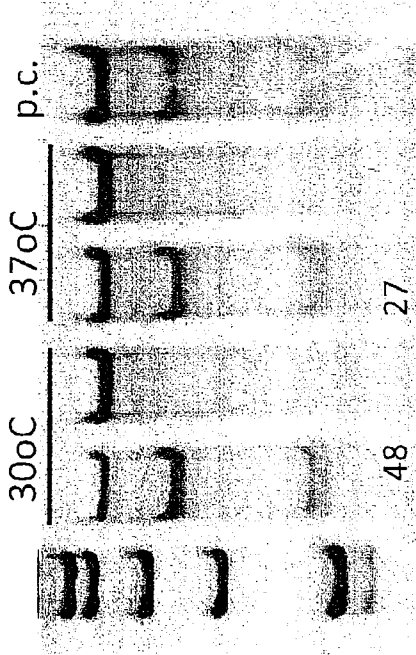
A

Bcl11A #2 29527/28



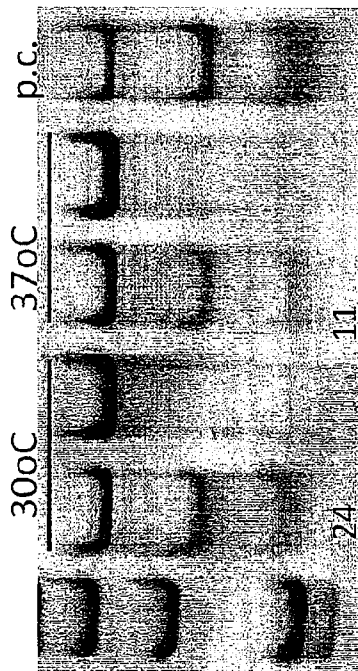
HPRT 29250/51

B



KLF1 33237/38

C



KLF1

D

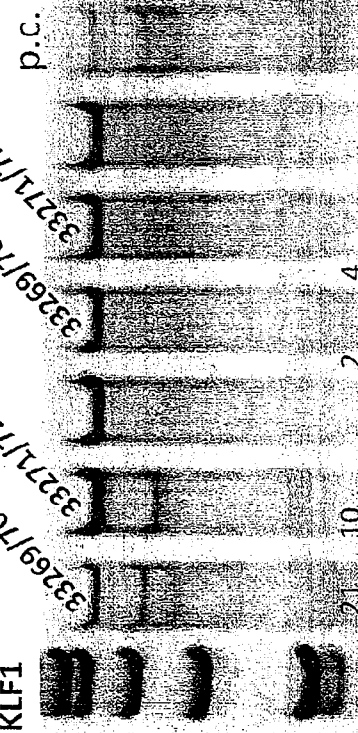


Figure 4

E

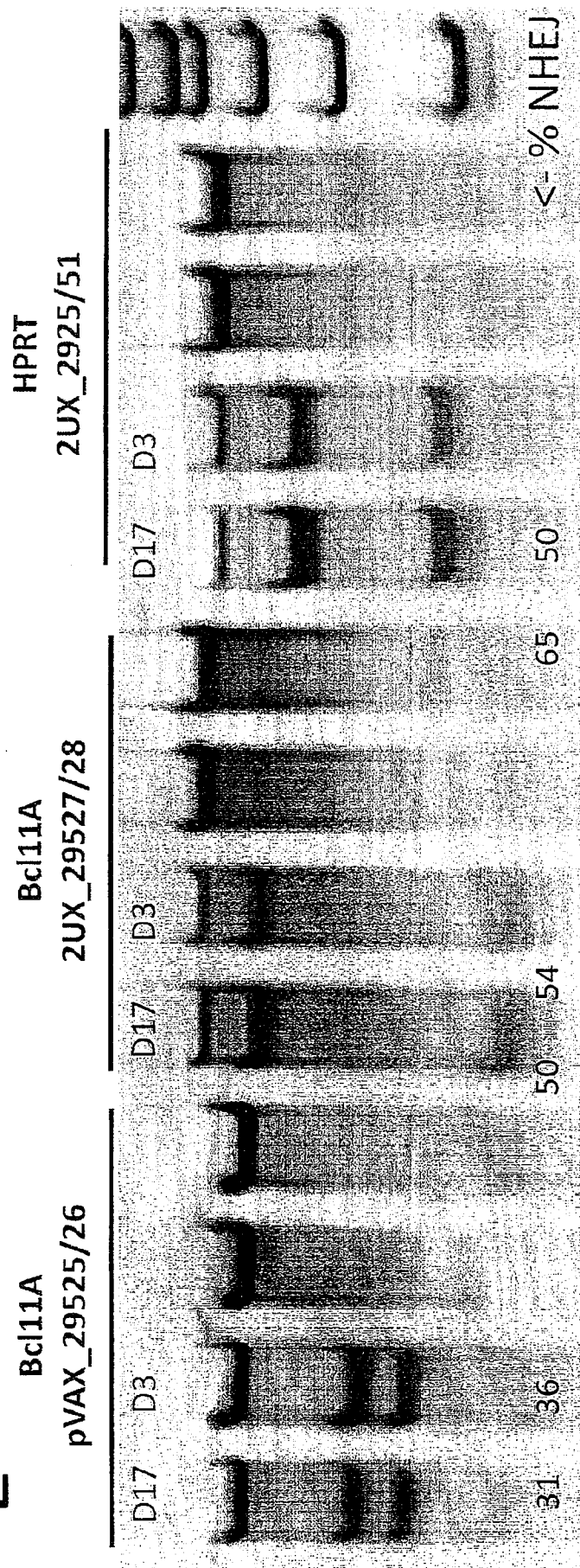


Figure 4

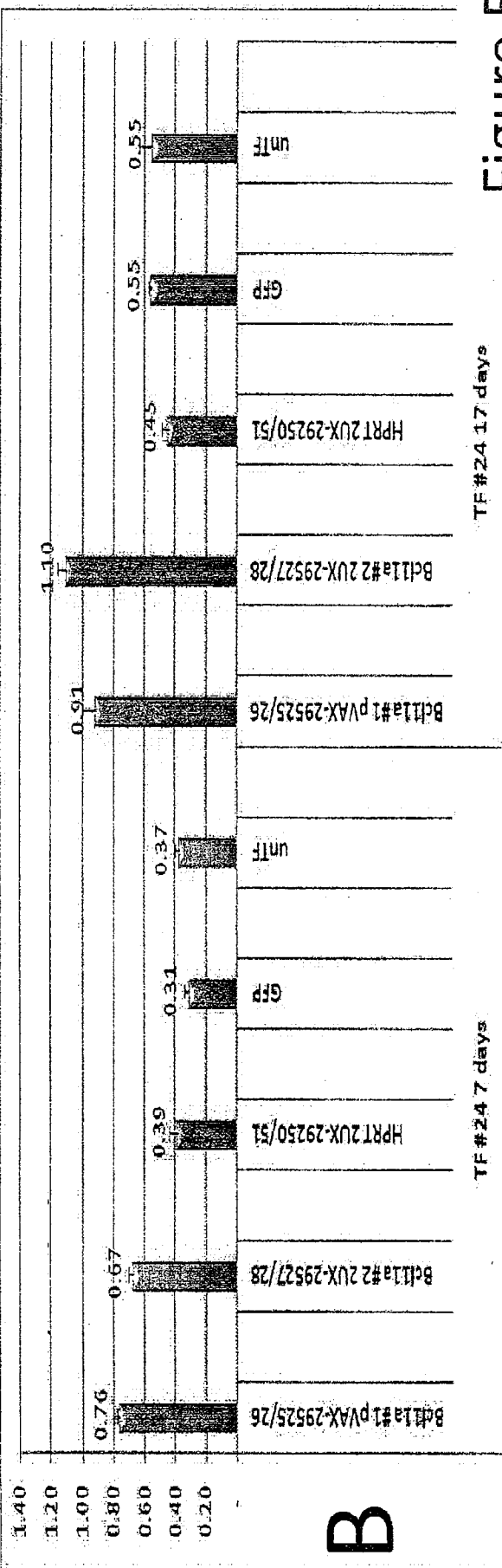
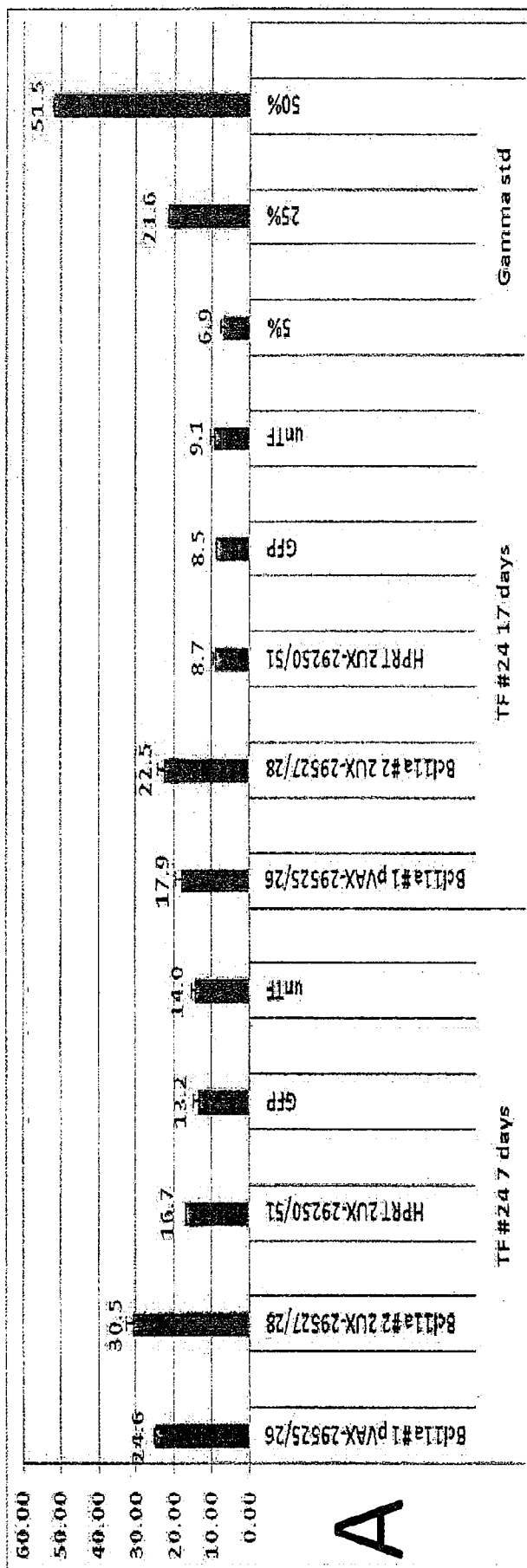
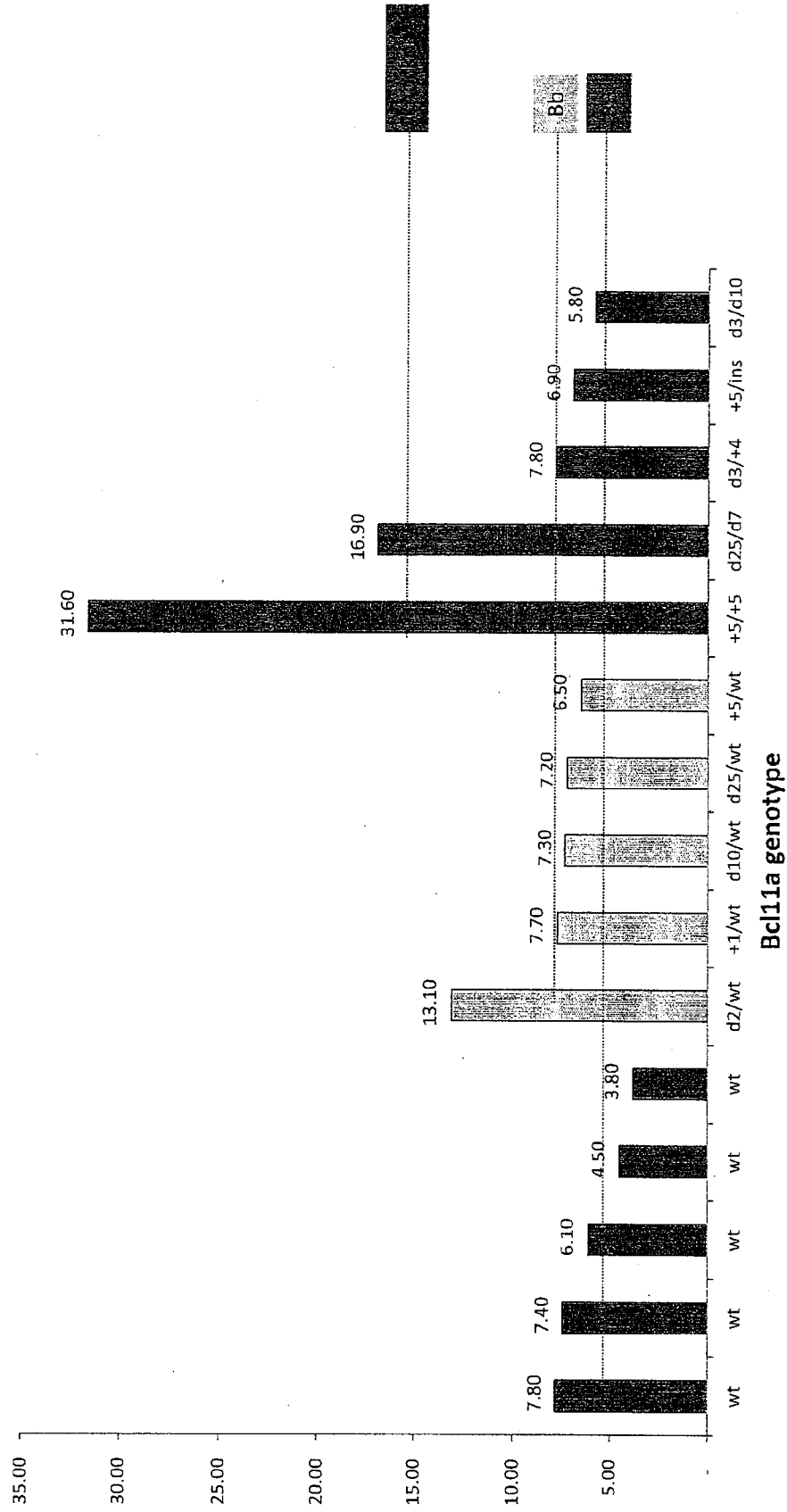


Figure 5

FIGURE 6



Reference	GGCCAGCCCTTGCCCTTGACCAATAGCCTTGACAAGGCAAACTTGACCAATAG
wt (26)	GGCCAGCCCTTGCCCTTGACCAATAGCCTTGACAAGGCAAACTTGACCAATAG
Δ 1bp (1)	GGCCAGCCCTTGCCCTTGACC-ATAGCCTTGACAAGGCAAACTTGACCAATAG
Δ 4bp (1)	GGCCAGCCCTTGCCCTT---AATAGCCTTGACAAGGCAAACTTGACCAATAG
Δ 6bp (2)	GGCCAGCCCTTGCCCTTGAC-----CCTTGACAAGGCAAACTTGACCAATAG
Δ 6bp (1)	GGCCAGCCCTTGCCCTTGACCAATAGC-----AAGGCAAACTTGACCAATAG
Δ 13bp (9)	GGCCAGCCCTTGCCCTTGAC-----AAGGCAAACTTGACCAATAG
+1bp (1)	GGCCAGCCCTTGCCCTTGACCAAAATAGCCTTGACAAGGCAAACTTGACCAATA
+3bp (1)	GGCCAGCCCTTGCCCTTGACCAATAGCAGCCTTGACAAGGCAAACTTGACCAA
+5bp (3)	GGCCAGCCCTTGCCCTTGACCAATAGAAATAGCCTTGACAAGGCAAACTTGACC

Figure 7

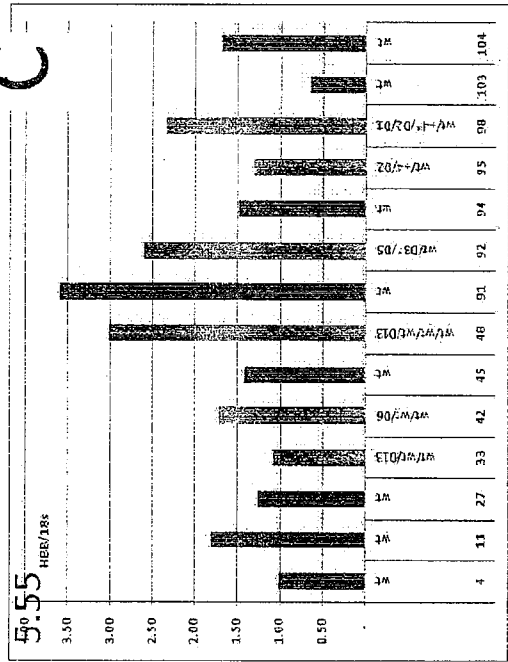
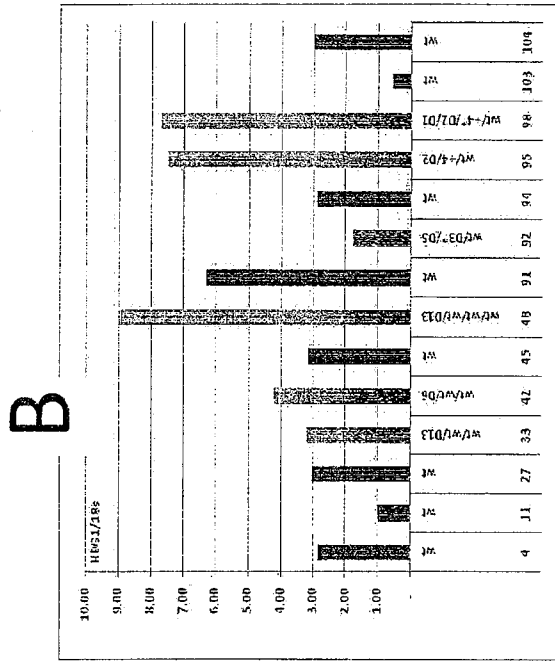
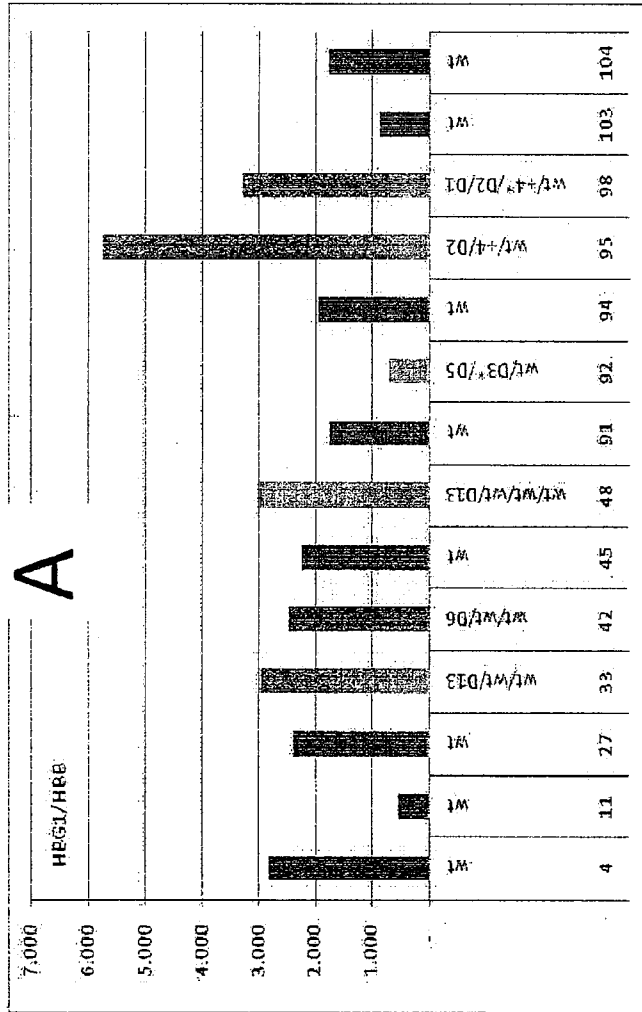


Figure 8

base # relative to
transcription start

(=HBGA) 703 TAGCTAAAGGGAAGAAATAATTAGAGAAAAATGGAATGACTGAAATCGGAACAAGGCAAGGCTATAAAAAAATTAATGCAGTATCCTCTTGGGGGC -203
 HBG1 699 TAGCTAAAGGGAAGAAATAATTAGAGAAAAATGGAATGACTGAAATCGGAACAAGGCAAGGCTATAAAAAAATTAATGCAGTATCCTCTTGGGGGC -203
 (=HBGG)

HPFH mutations:

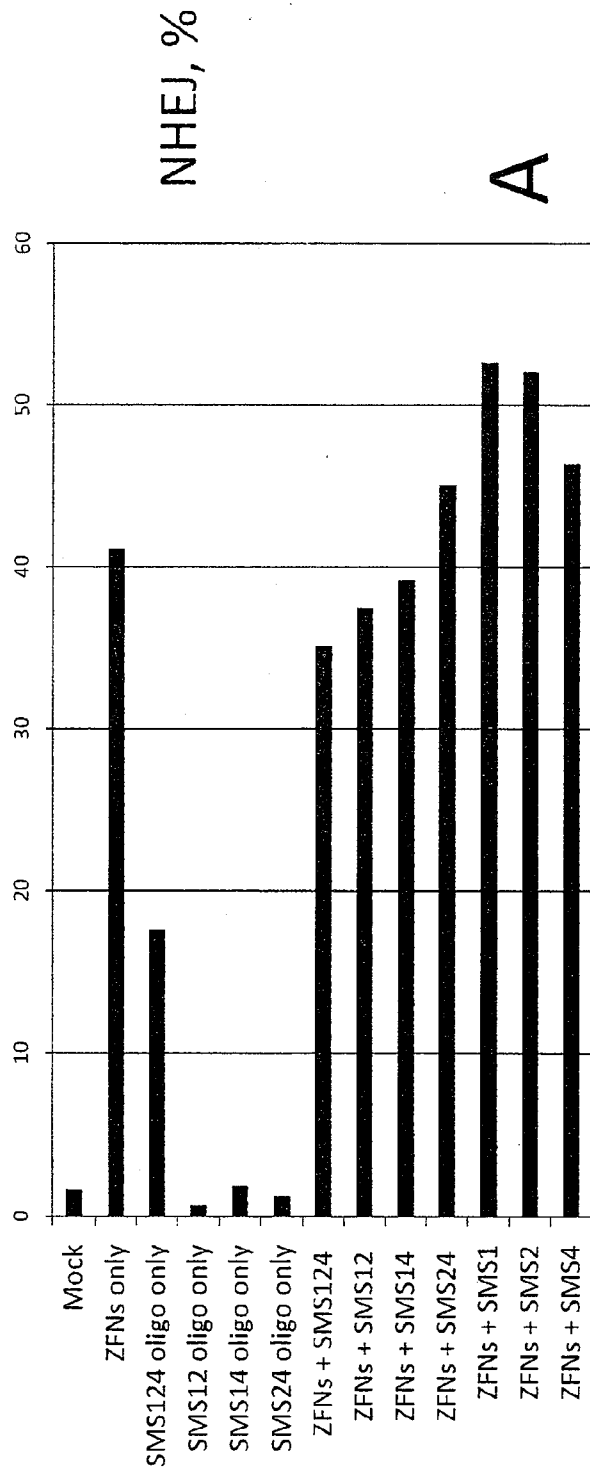
-202 -198 -175 -158 -117 -114 -110
 1.6-3.9 1.6 12-16 3-10 4.7-4.8
 14-24 18-28 37-40
 HBG1 799 C C C T T C C C C A C A C A C T A T C T C A A T G C A A A T A T C T G T C T G A A A C G G T C C C T G G C T A A A C T C C A C C C A T G G G T T G G C C A G C C T T G C C T T G A C C A A T A G C C C T T G A
 HBG2 799 C C C T T C C C C A C A C A C T A T C T C A A T G C A A A T A T C T G T C T G A A A C G G T C C C T G G C T A A A C T C C A C C C A T G G G T T G G C C A G C C T T G C C T T G A C C A A T A G C C C T T G A
 11-14 T 0.6-0.8
 3.8-11 A

10/14

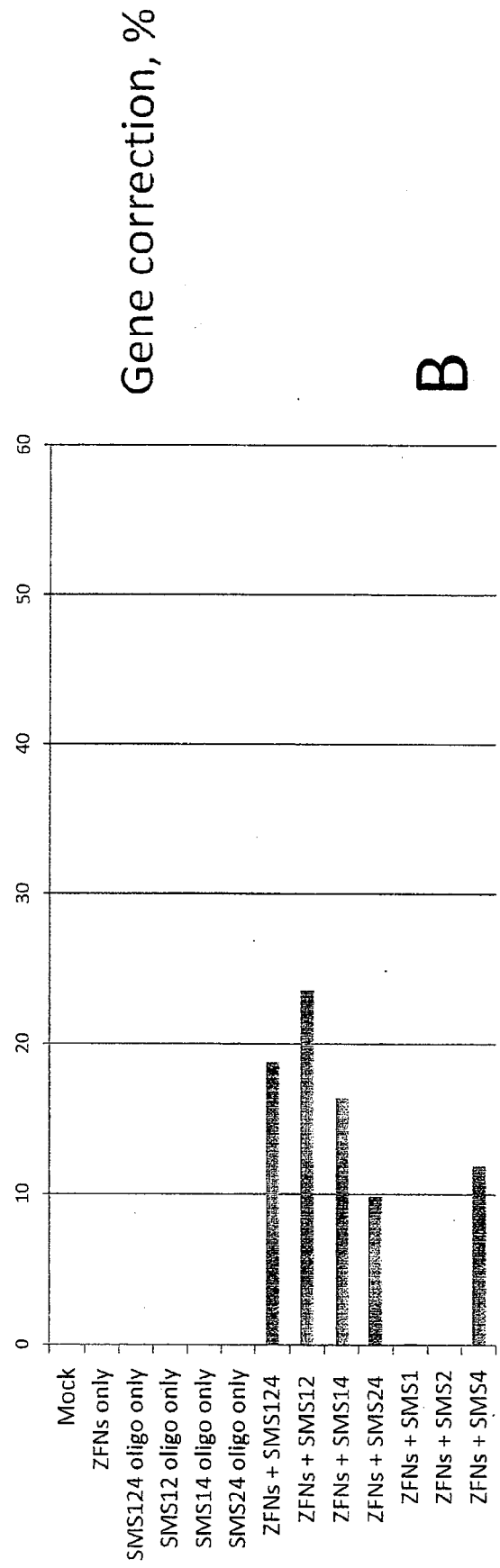
HBG1 899 CAAGGCAAACCTTGACCAATAGTCTTAGAGTATCCAGTGAGGCCAAGGGCCGGCGGCTGGCTAGGGATGAAGAAATAAAAGGAAGCACCCCTTCAGCAGTTCC -3
 HBG2 899 CAAGGCAAACCTTGACCAATAGTCTTAGAGTATCCAGTGAGGCCAAGGGCCGGCGGCTGGCTAGGGATGAAGAAATAAAAGGAAGCACCCCTTCAGCAGTTCC -3
 HBG1 999 ACACACTCGCTTCTGGAAACGCTCTGAGGTTATCAATAAGCTCCTAGTCCAGACGCCCATGGGTCATTTTCACAGAGGAGGACAAAGGCTACTATCACAAGCCTG +98
 HBG2 999 ACACACTCGCTTCTGGAAACGCTCTGAGGTTATCAATAAGCTCCTAGTCCAGACGCCCATGGGTCATTTTCACAGAGGAGGACAAAGGCTACTATCACAAGCCTG +98
 HBG1 1099 TGGGGCAAGGTGAATGTGGAAGATGCTGGAGGAGAAACCCCTGGGAAGGCTAGGCTCTGGTGACCAAGGGAAGGGAAGGACCCCTGTGCCTGGCA +198
 HBG2 1099 TGGGGCAAGGTGAATGTGGAAGATGCTGGAGGAGAAACCCCTGGGAAGGCTAGGCTCTGGTGACCAAGGGAAGGGAAGGACCCCTGTGCCTGGCA +198

Figure 9

Figure 10



11/14



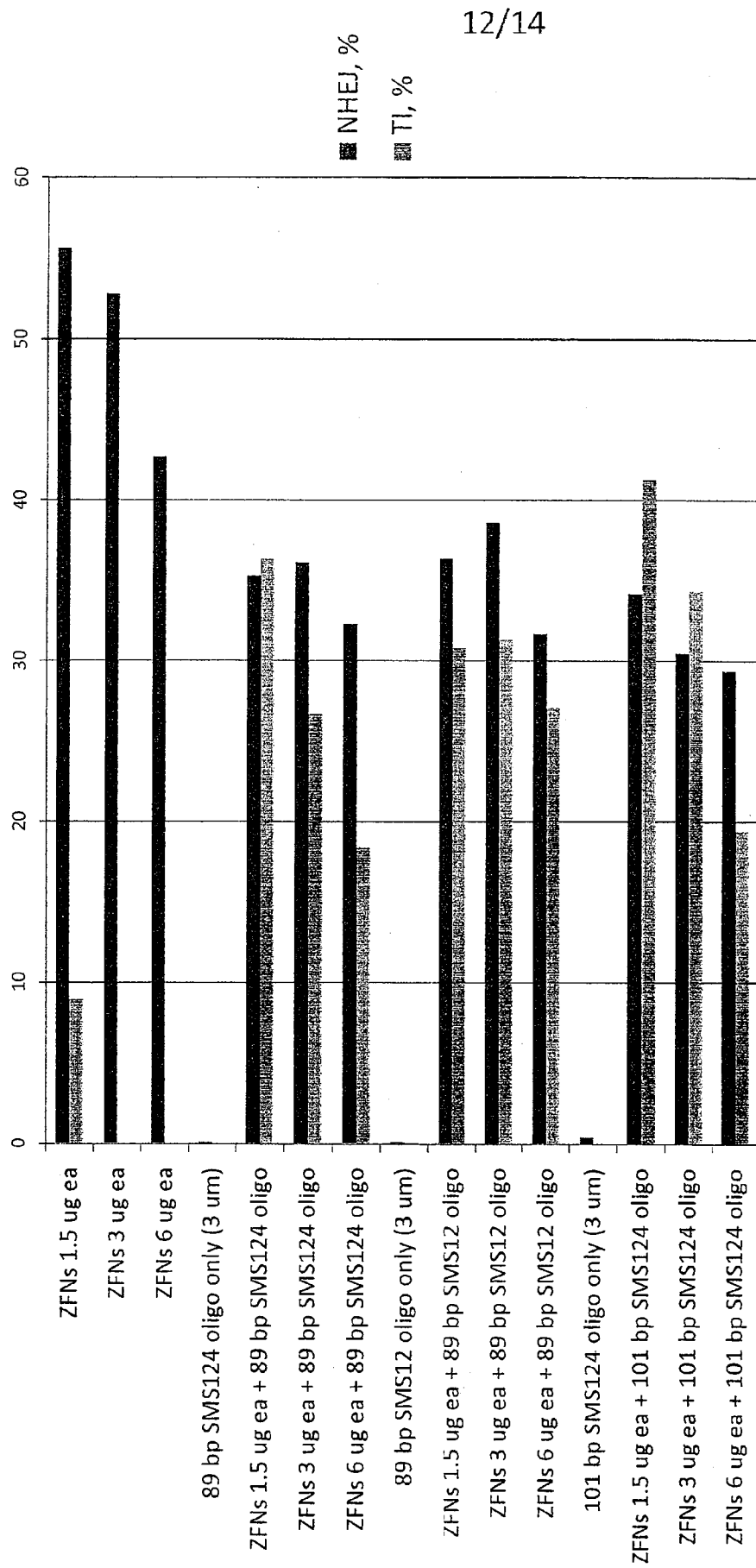


Figure 11

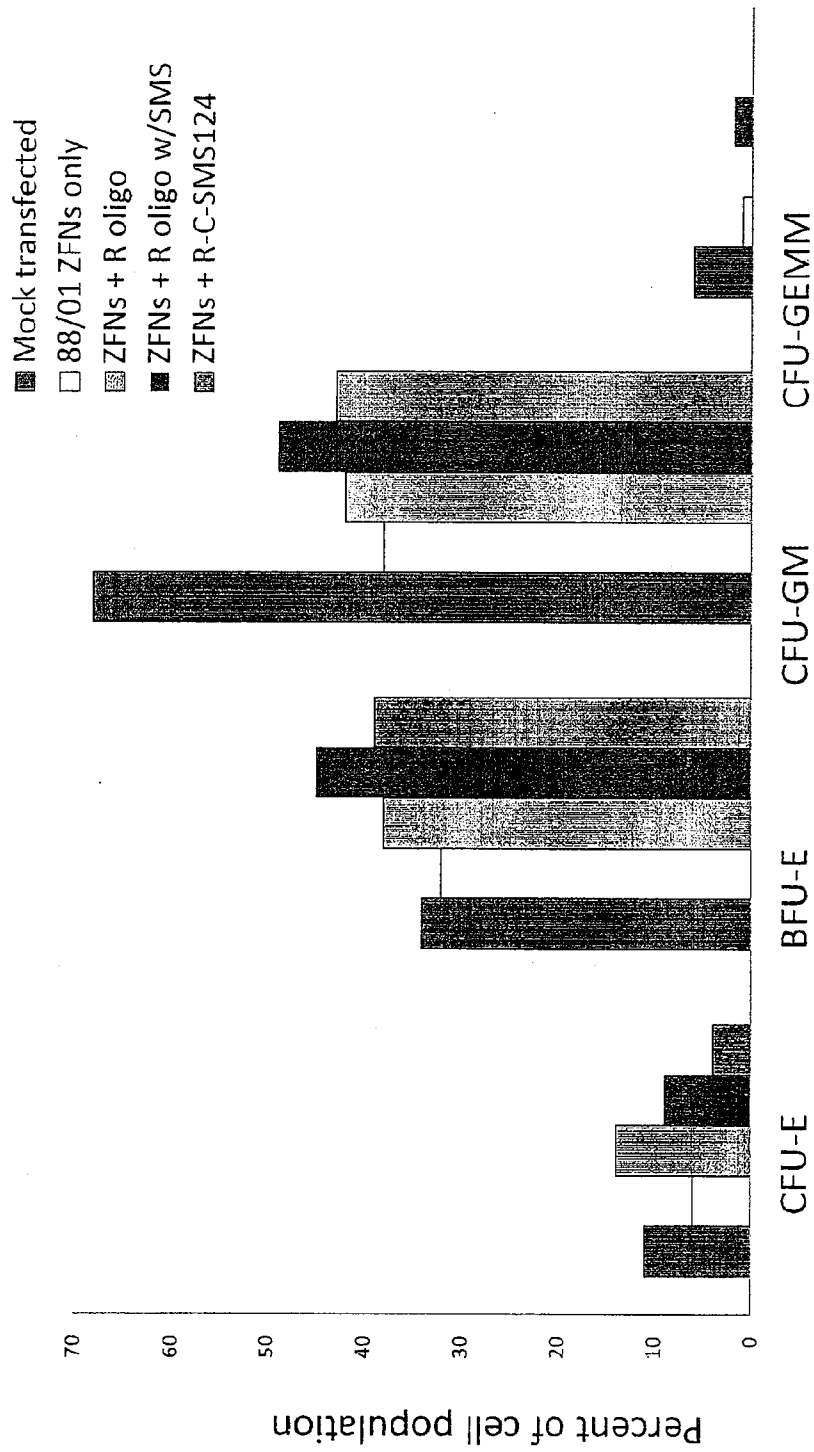


Figure 12

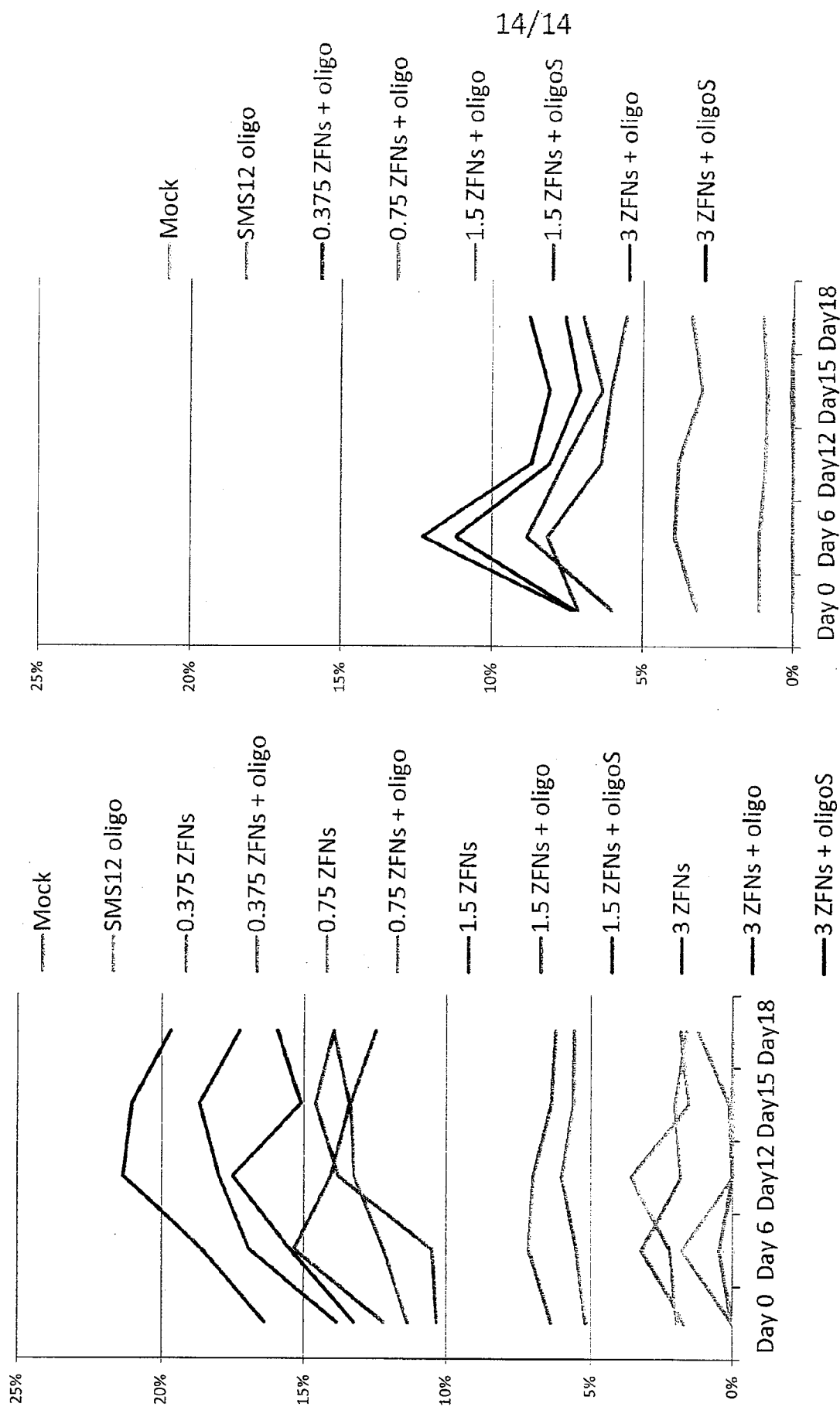


Figure 13