

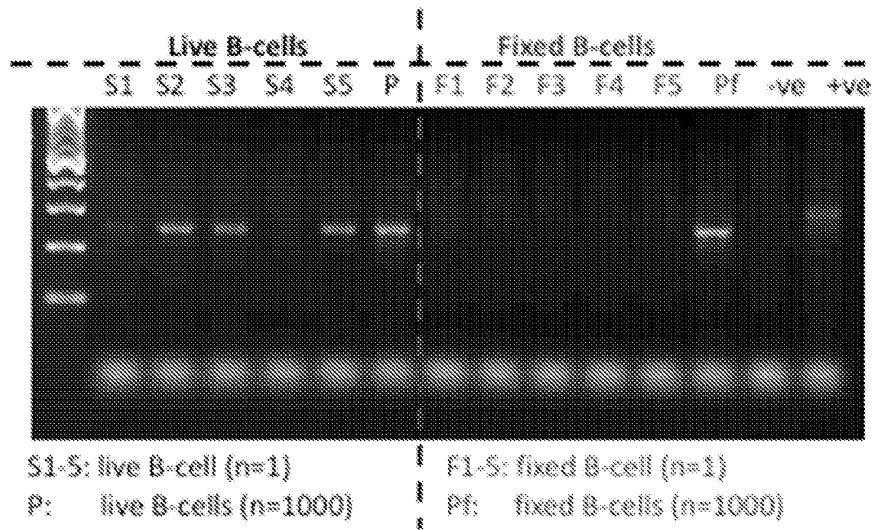


FIGURE 1

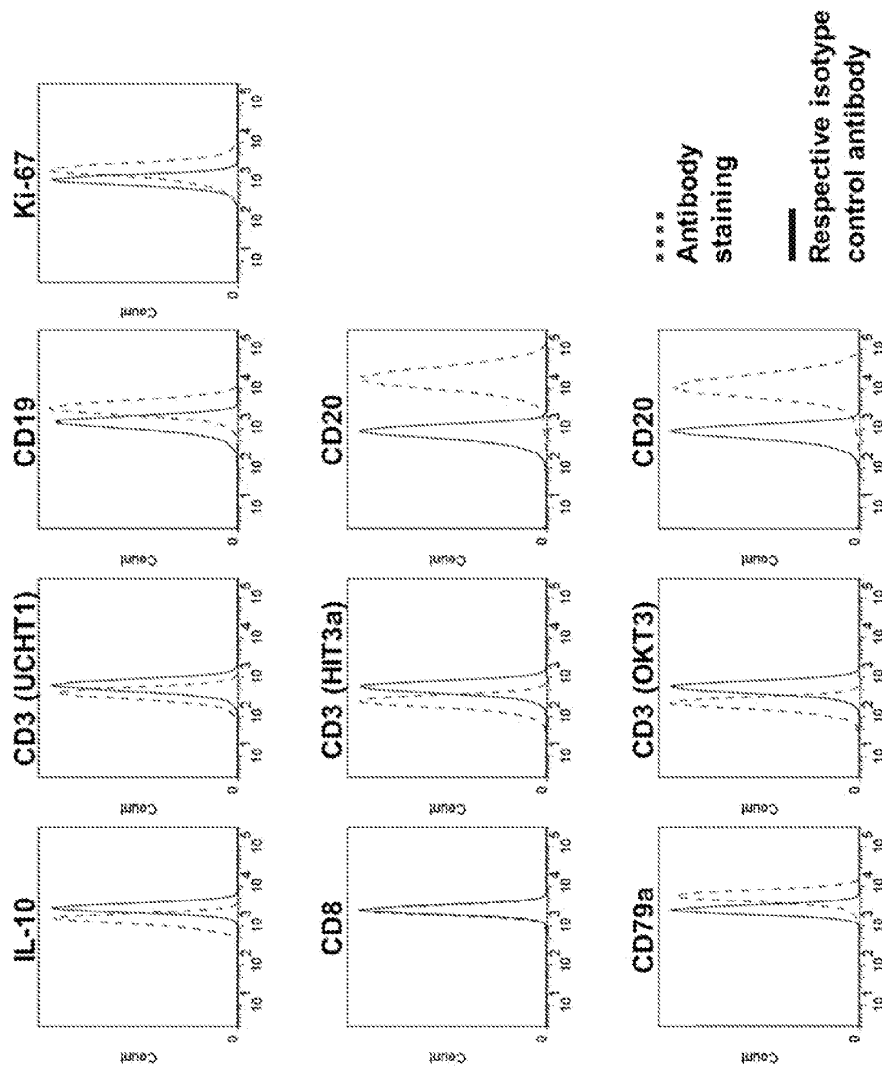


FIGURE 2A

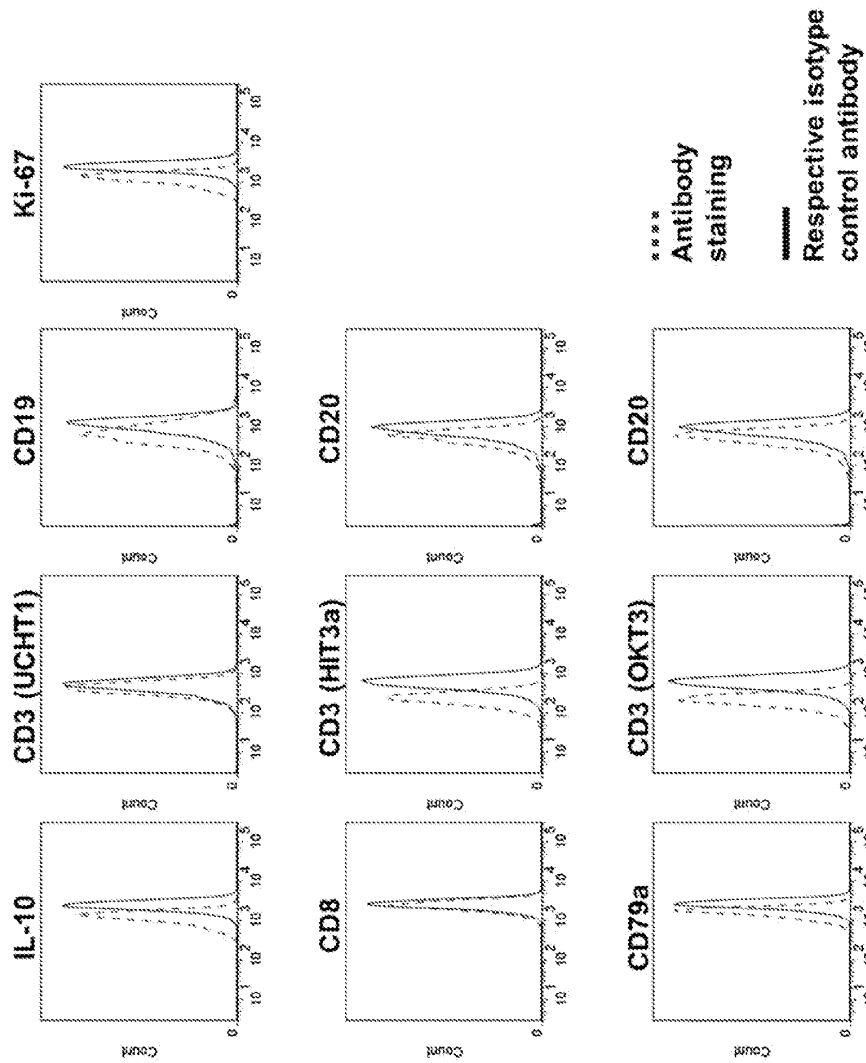


FIGURE 2B

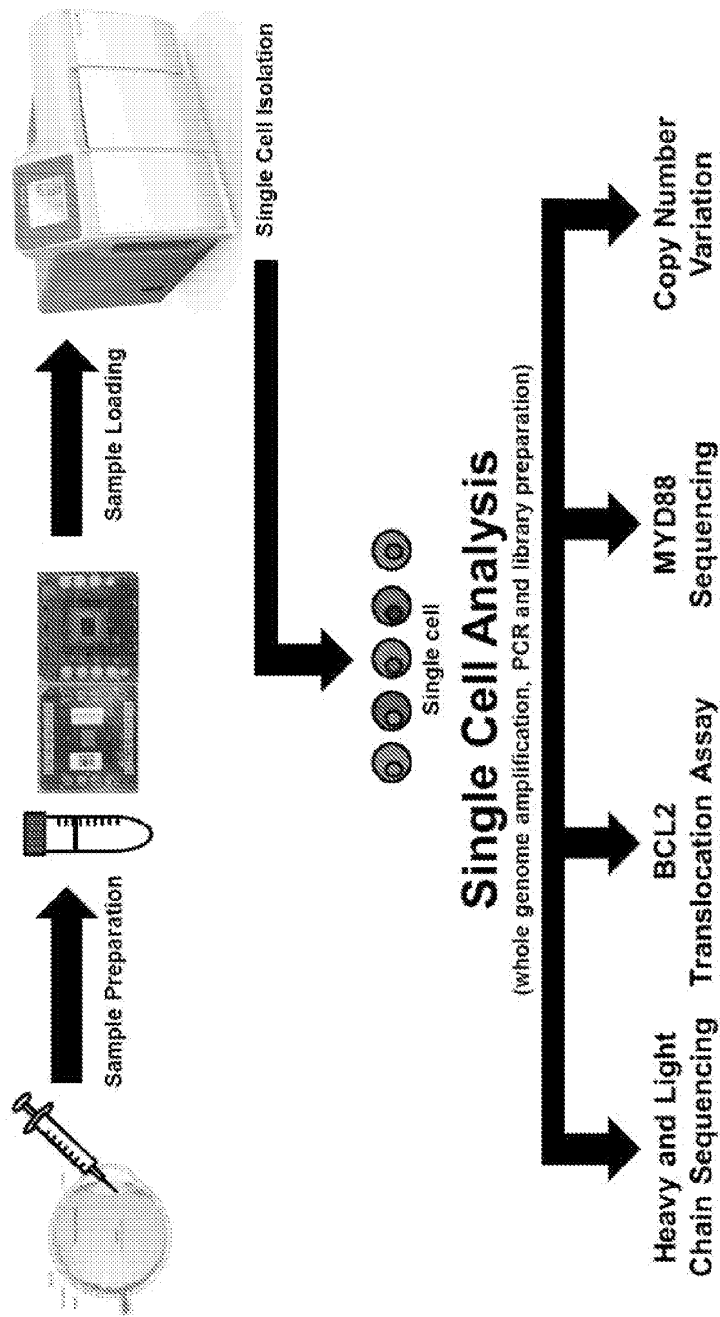


FIGURE 3

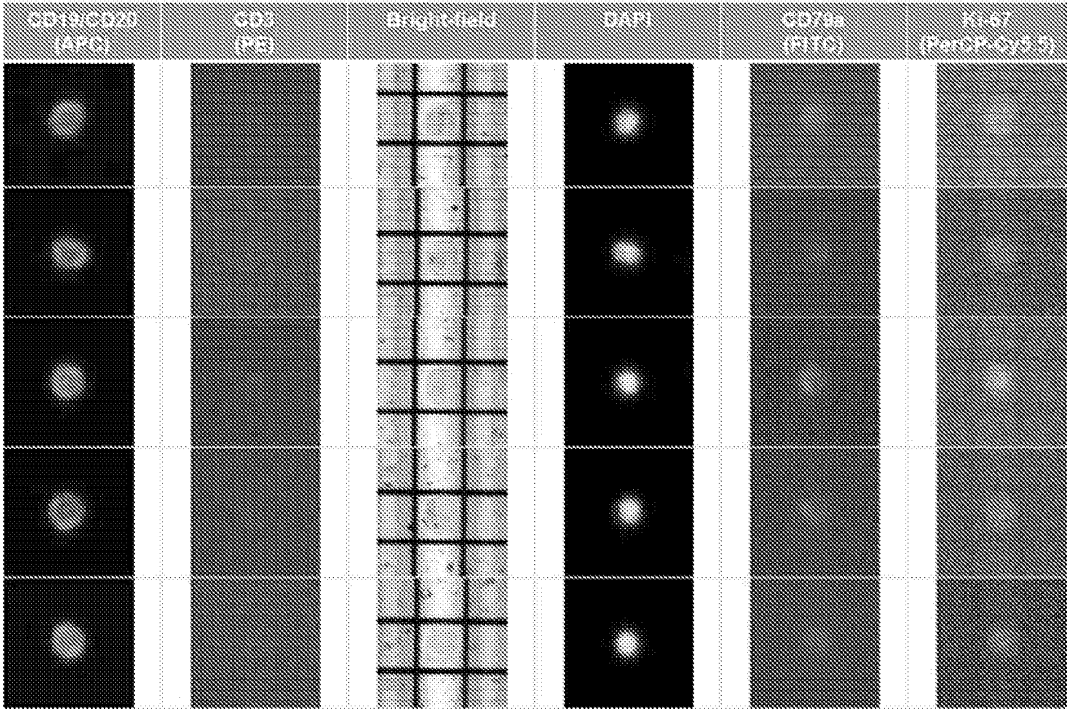


FIGURE 4

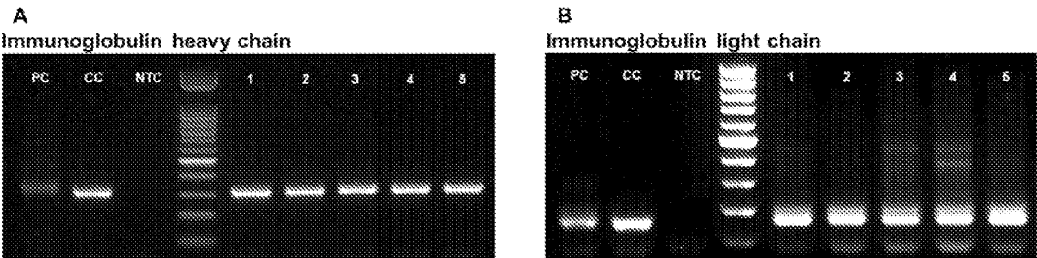


FIGURE 5

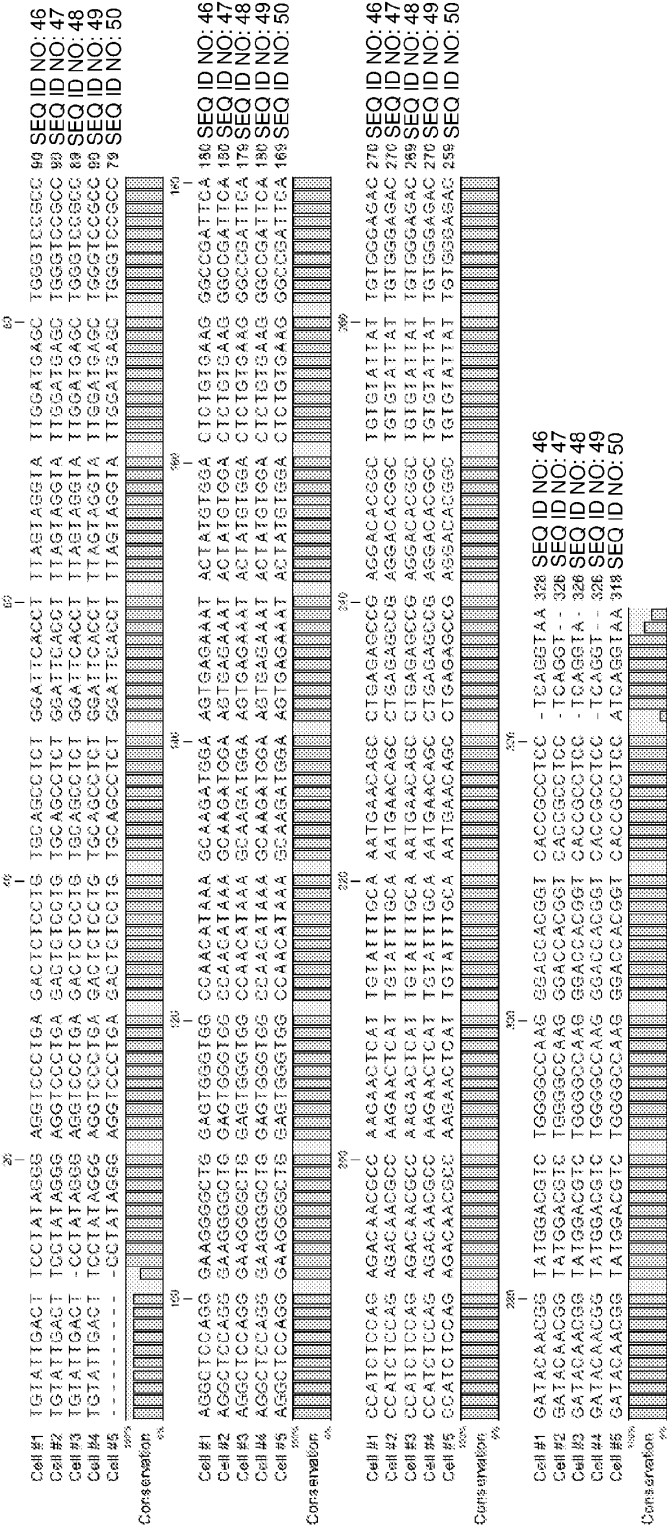


FIGURE 6A

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      -FR2- T867-----C8K3- T867-----
A K N S L V L Q H N S L R A E O T A V V Y C G R R Y G H P D
187 GCACAGAACCTATTGTATTTGCAATGACAGCCCTGACAGCCCTGATGATATTATTTGGGAGACGATACACGGTATGGAC 27%
Query_1 1000/3.7*11
V 97.6% (246/252)
A K N S L V L Q H N S L R A E O T A V V Y C A R 254
SEQ ID NO: 52
SEQ ID NO: 51
SEQ ID NO: 53

```

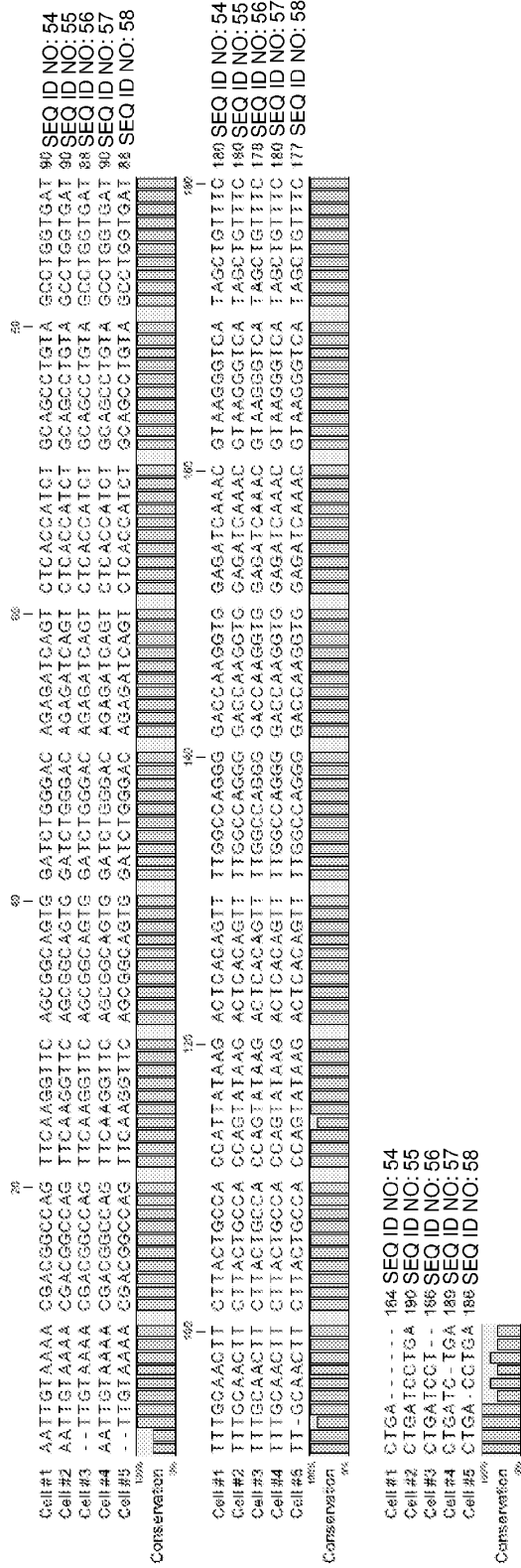


FIGURE 7A

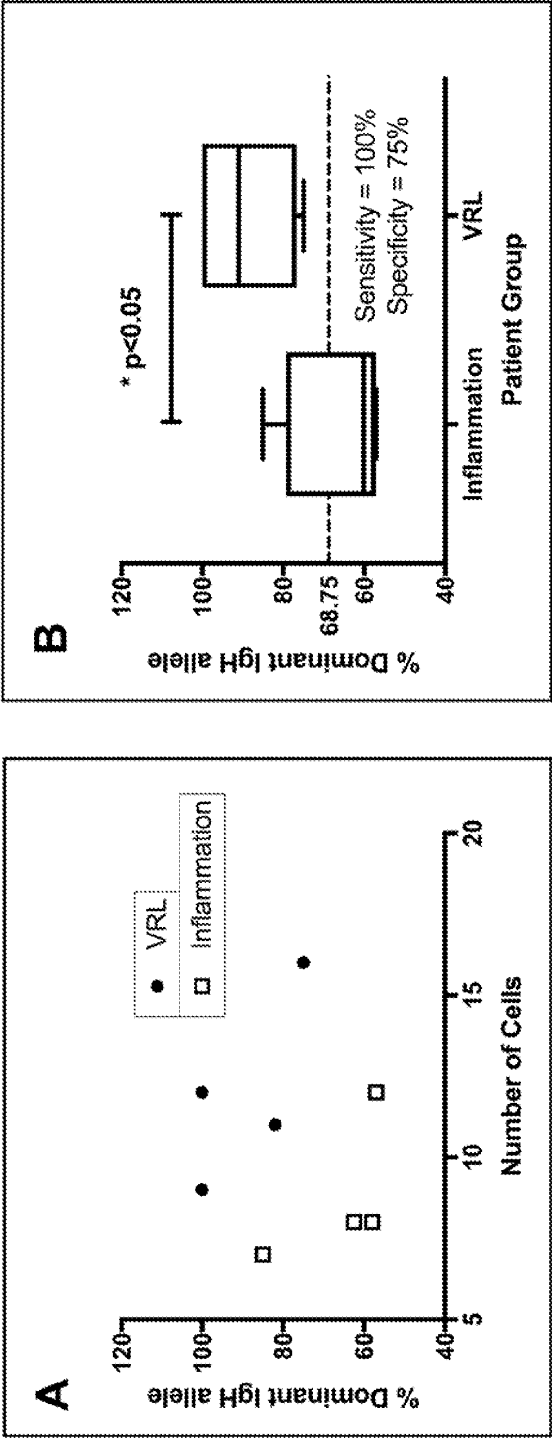


FIGURE 8

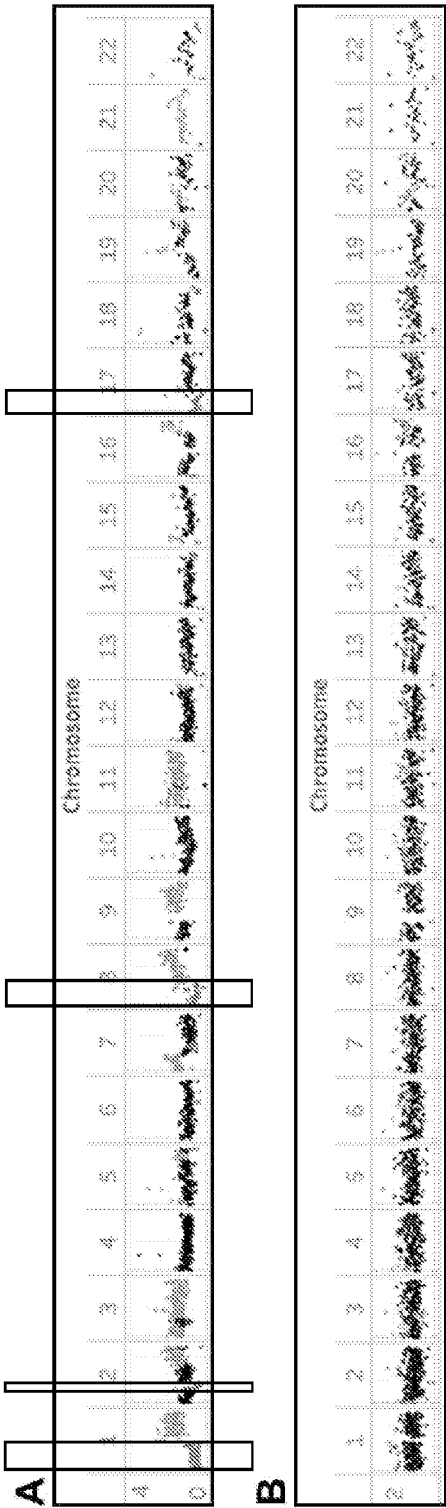


FIGURE 9A

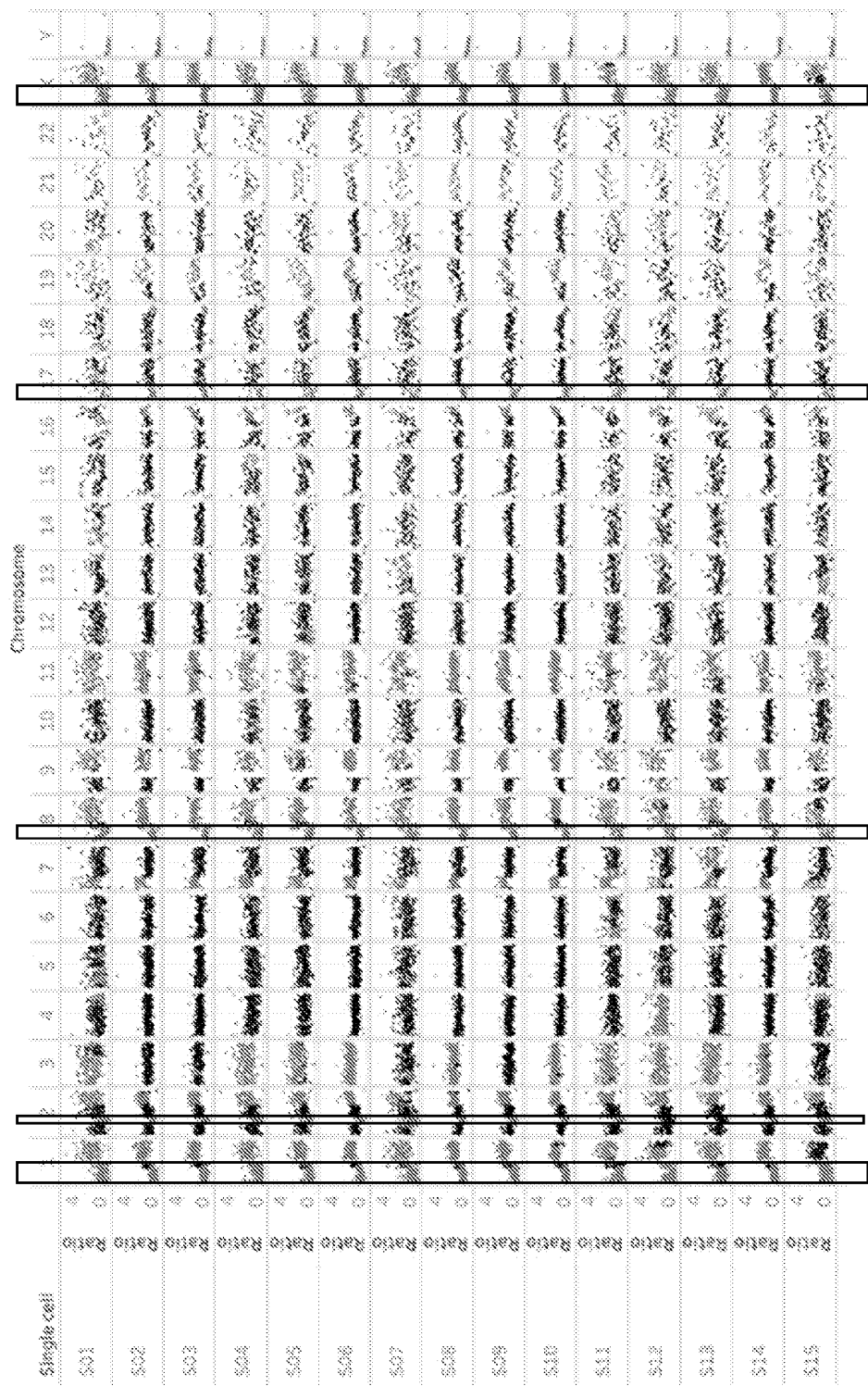


FIGURE 9B

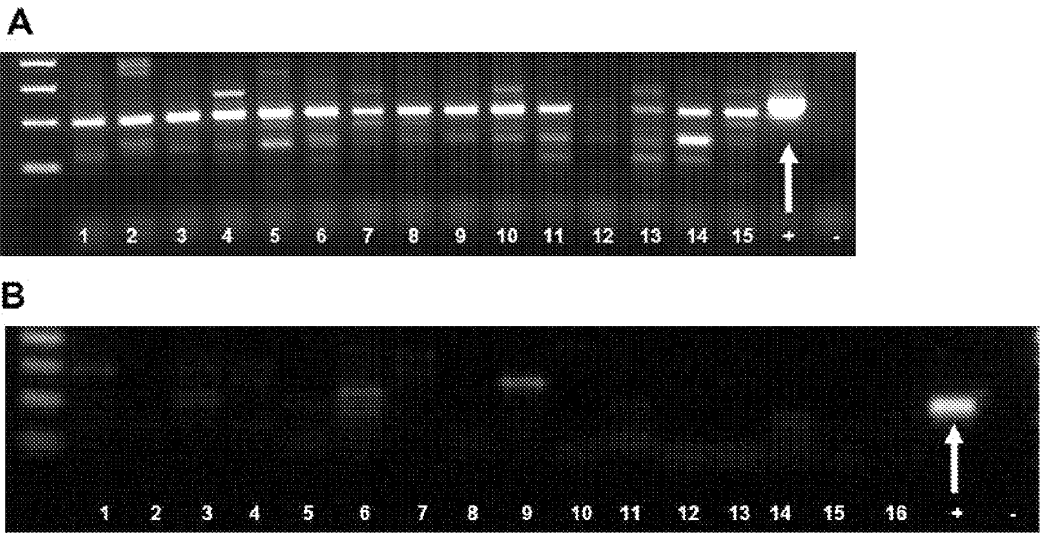
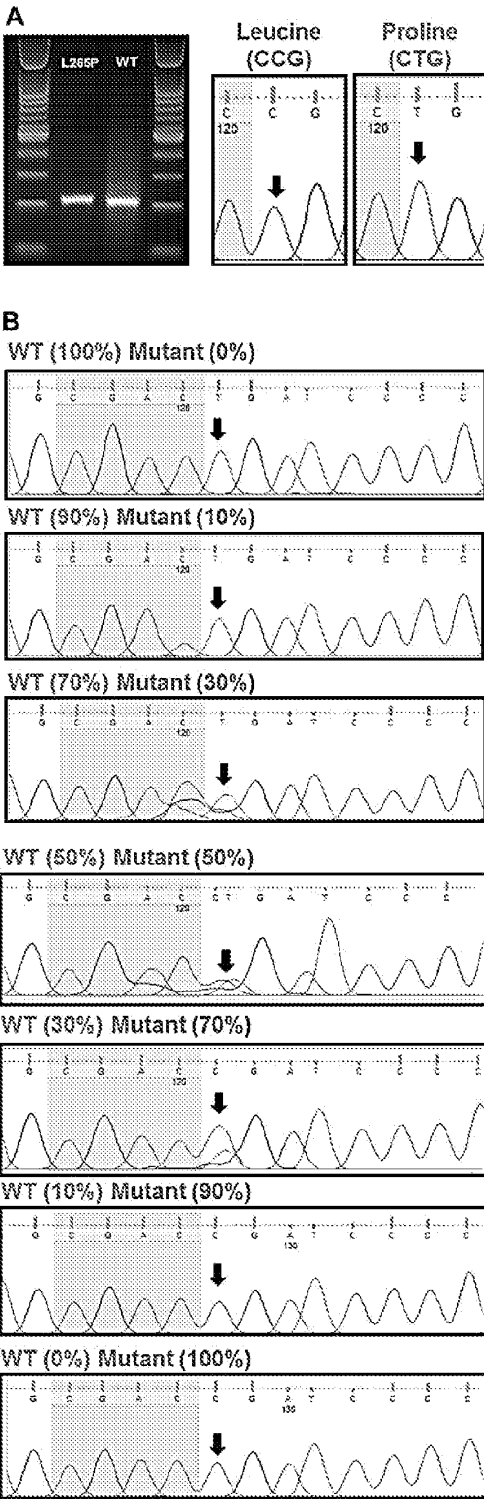


FIGURE 10



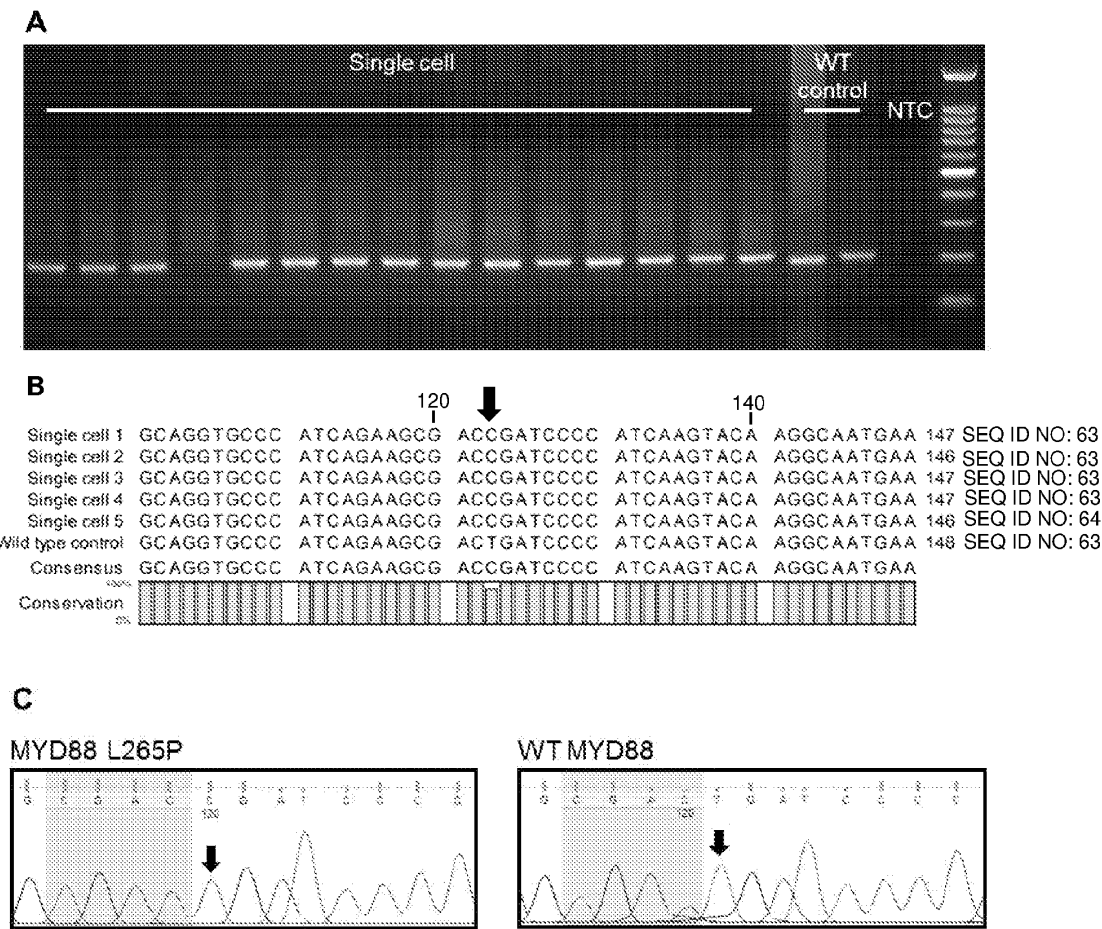


FIGURE 12

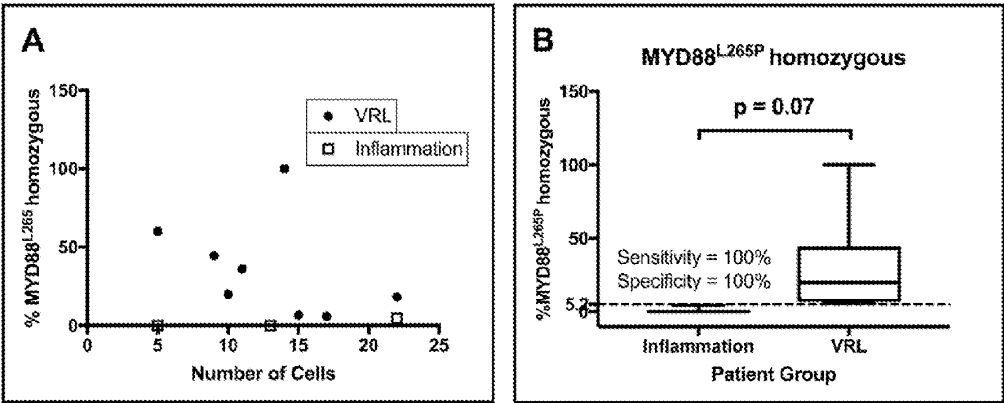


FIGURE 13