

1801 ctaggacaataaagccacttggttgggaaacagatgattcagggggtcccatgtccatagg  
1861 tgatttgctctatcaacgatttcccccaaagggcgctttgccgaggctggttgggggtgg  
1921 agacttgggataccgcctggcggtggatggaggaggcgatgagggggccctggaagccagc  
1981 ccctgagcctggcggtgtaaggcgattacacatcttccctgggggtcatatcttctgtgagcg  
2041 tttatctttcatgcctgccgcgctaggattttccccctgccgtgcaagacatctttgctc  
2101 ggtctggggagggcgcttagccatttgccccgggtggggggcgctcccgtgttctgc**aaagt**  
2161 **gctctgcacttgcccc**cgggttaggtcccggacggcgccctccagtgccaccactaac  
25 A Y S S V P V  
2221 cccgccctccggggcttcttctcactcgctgtctccactccagGCCTACTCCTCCGTCCCCGG  
32 S N M N S G L G S M N S M N T Y M T M N  
2281 TCAGCAACATGAACTCAGGCCTGGGCTCCATGAACTCCATGAACACCTACATGACCATGA  
52 T M T T S G N M T P A S F N M S Y A N P  
2341 ACACCATGACTACGAGCGGCAACATGACCCCG**CGC**TCCTTCAACATGTCCTATGCCAACCC  
72 G L G A G L S P G A V A G M P G G S A G  
2401 CGGGCCTAGGGGCCGGCCTGAGTCCCGGCGCAGTAGCCGGCATGCCGGGGGGGCTCGGCGG  
92 A M N S M T A A G V T A M G T A L S P S  
2461 GCGCCATGAACAGCATGACTGCGGCCGGCGTGACGGCCATGGGTACGGCGCTGAGCCCGA  
112 G M G A M G A Q Q A A S M N G L G P Y A  
2521 GCGGCATGGGCGCCATGGGTGCGCAGCAGGCGGCCTCCATGAATGGCCTGGGCCCCCTACG  
132 A A M N P C M S P M A Y A P S N L G R S  
2581 CGGCCGCC**ATGAACCCGTGCATGAGCCC**CATGGCGTACGCGCCGTCCAACCTGGGCCGCA  
152 R A G G G G D A K T F K R S Y P H A K P  
2641 GCCGCGCGGGCGGCGGCGGCGACGCCAAGACGTTCAAGCGCAGCTACCCGCACGCCAAGC  
172 P Y S Y I S L I T M A I Q Q A P S K M L  
2701 CGCCCTACTCGTACATCTCGCTCATCACCATGGCCATCCAGCAGGCGCCAGCAAGATGC  
192 T L S E I Y Q W I M D L F P Y Y R Q N Q  
2761 TCACGCTGAGCGAGATCTACCACTGGATCATGGACCTCTTCCCCTATTACCGGCAGAACC  
212 Q R W Q N S I R H S L S F N D C F V K V  
2821 AGCAGCGCTGGCAGAACTCCATCCGCCACTCGCTGTCCTTCAATGACTGCTTCGTCAAGG  
232 A R S P D K P G K G S Y W T L H P D S G  
2881 TGGCAGCTCCCCGGACAAGCCGGGCAAGGGCTCCTACTGGACGCTGCACCCGGACTCCG  
252 N M F E N G C Y L R R Q K R F K C E K Q  
2941 GCAACATGTTTCGAGAACGGCTGCTACTTGCGCCGCCAGAAGCGCTTCAAGTGCAGAGAAGC  
272 P G A G G G G G S G S G G S G A K G G P  
3001 AGCCGGGGGCCGGCGGCGGGGCGGGAGCGGAAGCGGGGGCAGCGGCCAAGGGCGGCC  
292 E S R K D P S G A S N P S A D S P L H R  
3061 CTGAGAGCCGCAAGGACCCCTCTGGCGCCTCTAACCCAGCGCCGACTCGCCCCCTCCATC  
312 G V H G K T G Q L E G A P A P G P A A S  
3121 GGGGTGTGCACGGGAAGACCGGCCAGCTAGAGGGCGCGCCGGCCCCCGGGCCCCGCCCA  
332 P Q T L D H S G A T A T G G A S E L K T  
3181 GCCCCAGACTCTGGACCACAGTGGGGCGACGGCGACAGGGGGCGCTCGGAGTTGAAGA  
352 P A S S T A P P I S S G P G A L A S V P  
3241 CTCCAGCCTCCTCAACTGCGCCCCCATAAGCTCCGGGCCCCGGGGCGCTGGCCTCTGTGC  
372 A S H P A H G L A P H E S Q L H L K G D  
3301 CCGCCTCTACCCGGCACACGGCTTGGCACCCACAGTCCAGCTGCACCTGAAAGGGG  
392 P H Y S F N H P F S I N N L M S S S E Q  
3361 ACCCCCCTACTCCTTCAACCACCCGTTCTCCATCAACAACCTCATGTCCTCCTCGGAGC  
412 Q H K L D F K A Y E Q A L Q Y S P Y G S  
3421 AGCAGCATAAGCTGGACTTCAAGGCATACGAACAGGCACTGCAATACTCGCCTTACGGCT  
432 T L P A S L P L G S A S V T T R S P I E  
3481 CTACGTTGCCCCGCCAGCCTGCCTCTAGGCAGCGCCTCGGTGACCACCAGGAGCCCCATCG  
452 P S A L E P A Y Y Q G V Y S R P V L N T  
3541 AGCCCTCAGCCCTGGAGCCGGCGTACTACCAAGGTGTGTATTCCAGACCCGTCTAAACA  
472 S \*  
3601 CTCCTAG

Anotação Gênica de tecido tumoral e normal de próstata.

Gene: FOXA1

Dentre os genes de tecido tumoral, os genes FOXA1, SATB1, ZXDC estão envolvidos com fatores de transcrição e se mostraram mais relevantes para o estudo. Foi visto também que, a partir da função nos fatores de transcrição, os genes FOXA1 e ZXDC estão mais regulados em linhagens de células luminais no câncer de mama do que em células mesenquimais do câncer.

Seq. Escolhida: região intro-exon do Exon 2, e o Exon 2 inteiro, onde a mutação está localizada.

SNP missense - Pos. 497 do mRNA: GCG -> GTG / Pos. 62: Ala -> Val

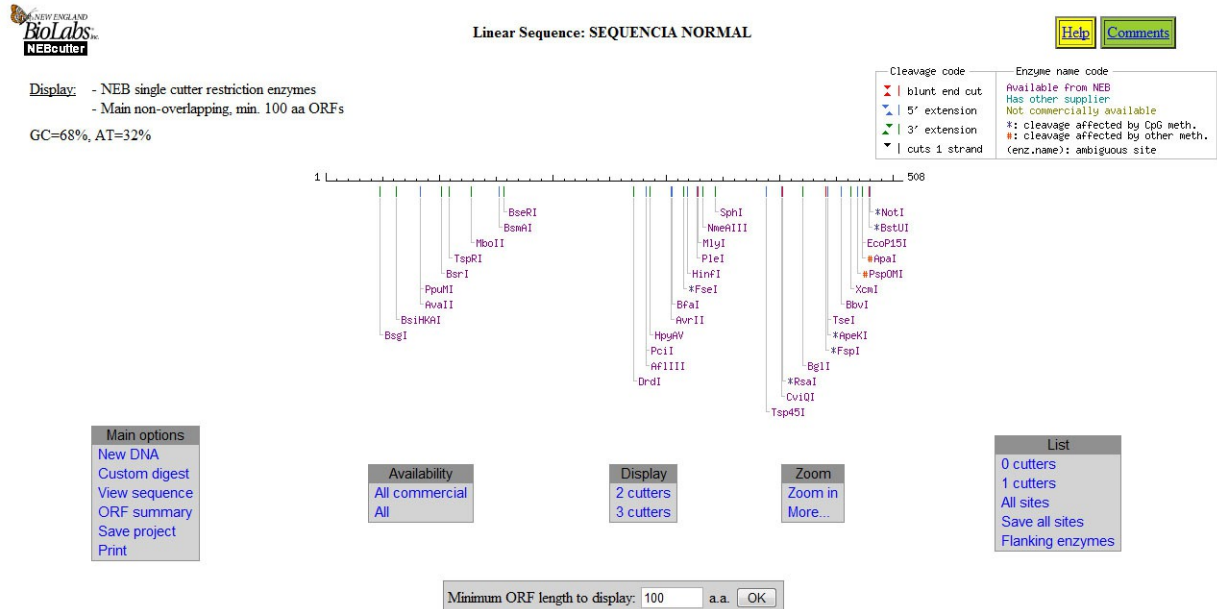
Região escolhida para o Fprimer: 5'-aaagtgcctctgcacttgcccc-3'  
Seq. Fprimer: 5'-aaagtgcctctgcacttgcccc-3' - Tm = 64°

Região escolhida para o Rprimer: 5'-ATGAACCCGTGCATGAGCCC-3'  
Seq. Rprimer: 3'-GGGCTCATGCACGGGTTTCAT-5' - Tm = 64°

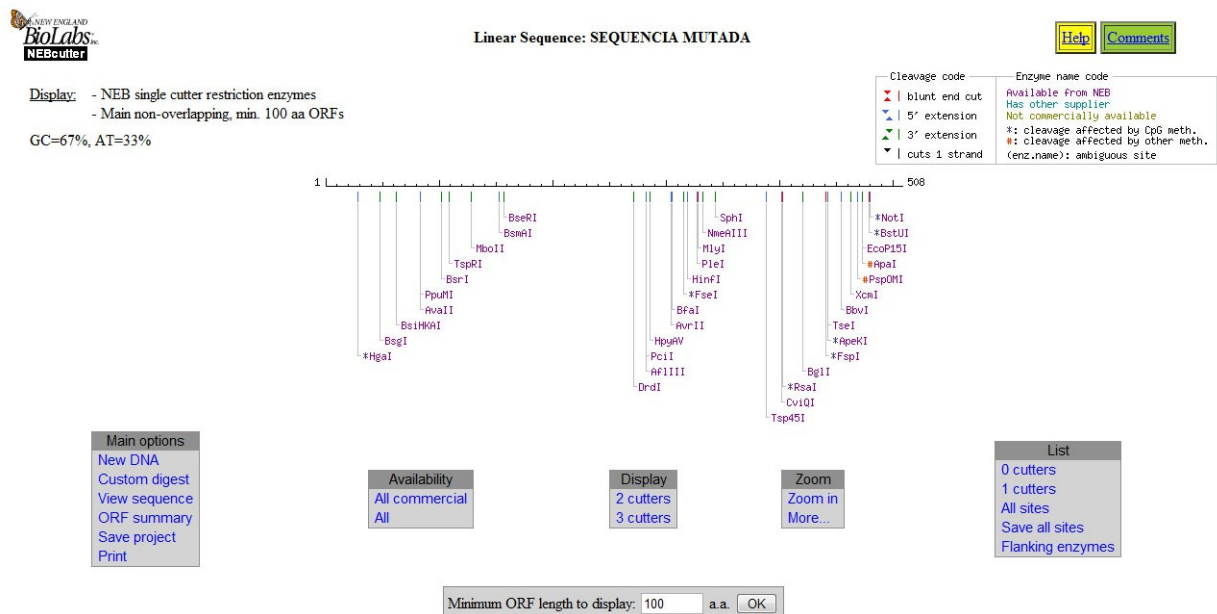
Região Amplificada - aprox. 452pb visando que a SNP escolhida esteja aproximadamente no meio da sequência a ser amplificada.

Mapa de Restrição feito pelo <http://tools.neb.com/NEBcutter2/>

## Sequencia NORMAL:



## Sequencia MUTADA:



Após fazer o mapa de restrição da sequencia normal e da sequencia com mutação, foi observado que a sequencia mutada teve um sitio de restrição adicionado logo no inicio da sequencia, e manteve os demais sitios que a sequencia normal possui.