ابتدا لازم به توضیح است که هایلات زرد نشانه محلهای مشترک برای توالی یابی با پرایمرهای forward و reverse است. حروف سبز داخل توالی ها نشان دهنده توالی اگزون 4 است با 105 نوکلوتید و 35 اسید آمینه و حروف قرمز نشان دهنده محل های جهش می باشد.حروف سبز داخل بلاست شده های نشان دهنده جهش های نامحسوس و بی اثر است.

**Pattern A:** **ACG**

7 (sample number)-pink (Forward)\_F\_Ex4p53.ab1

AAATAACGGCGGGTTGTGTGTACTGCGTGGCAATGAGCCTATGAACTTACTTTTTTCCGCTGGCTGGAAGACTGTCCGAATAAATCGCACCAATTGCCAAACCCTCCTGCCCAAGCTGCCCTGGCACCAGCCACCTCC**TGG**CCC**CTG**TCG**TCC**TTT**GTC**CCC**TCC**CAA**AAA**ACC**TAC**CCT**GGC**AAC**TAC**GGT**TTC**CGT**CTC**GGG**TTC**CTG**CAT**TCC**GGA**ACA**GCC**AAG**TCT**GTG**ACC**TGC**ACG**GTCATTGGCCCTGGGGAGCCGGCTTCCCTATCAGTGCCTGGCCATACGGCCTAGGCTTTTGTGGGTCTGAGGTCCTCCCACTGCTGGGTGTGGGGGCCTCAGTTCAATATGAGGAAGTACGAAGTCTATTATGGCGGGTAGTTCTTTGTTAG

7 (sample number)-blue (Reverse)\_R\_Ex4p53.ab1

CAATAATCGAGTGATTCAGGGCCACTGAC**CGT**GCA**GGT**CAC**AGA**CTT**GGC**TGT**TCC**GGA**ATG**CAG**GAA**CCC**GAG**ACG**GAA**ACC**GTA**GTT**GCC**ACG**GTA**GGT**CTT**CTG**GGA**GGG**GAC**AAA**GGA**CGA**CAG**GGG**CCA**CGAGGTGGTTGGCGCCAGGGCACTTTGGCCAGGAGGCTCTGGCATTTGGGGCGCTTCATTCGGACACTCATCCAGCCAGGTGACCACATCTTCTGAGTACGGGAACAGGTCATCCACAGGTGCGGAGAGCTCGGAGGACTACAGACGGGAGGAGTTGCACCAGAAGGCCARelated Information

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** | **Frame** |
| 265 bits(143) | 2e-75() | 179/197(91%) | 0/197(0%) | Plus/Minus |  |

Query 60 CTGGCTGGAAGACTGTCCGAATAAATCGCACCAATTGCCAAACCCTCCTGCCCAAGCTGC 119

 ||||||||| || ||||||||| || ||| |||| ||||| | ||||||| |||| |||

Sbjct 213 CTGGCTGGATGAGTGTCCGAATGAAGCGCCCCAAATGCCAGAGCCTCCTGGCCAAAGTGC 154

Query 120 CCTGGCACCAGCCACCTCCTGGCCCCTGTCGTCCTTTGTCCCCTCCCAAAAAACCTACCC 179

 |||||| ||| ||||||| ||||||||||||||||||||||||||||| || |||||||

Sbjct 153 CCTGGCGCCAACCACCTCGTGGCCCCTGTCGTCCTTTGTCCCCTCCCAGAAGACCTACCG 94

Query 180 TGGCAACTACGGTTTCCGTCTCGGGTTCCTGCATTCCGGAACAGCCAAGTCTGTGACCTG 239

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 93 TGGCAACTACGGTTTCCGTCTCGGGTTCCTGCATTCCGGAACAGCCAAGTCTGTGACCTG 34

Query 240 CACGGTCATTGGCCCTG 256

 |||||||| ||||||||

Sbjct 33 CACGGTCAGTGGCCCTG 17



**Pattern B:** **TCC**

4(sample number)-pink (Forward)-F\_Ex4p53.ab1

CATACGGTCTTTCTCTGTATACTGCGGGTGATTGATCCAAGCCACTTACTTTTTTCTCCGGGTTGAAAGACCGTCCAAATGAAGCGCCCCAAATGCCAAAGCCTCCTGCCCAAGTTGCCCTGGCACCAGCCACCTCC**TGG**CCC**CTG**TCG**TCC**TTT**GTC**CCC**TCC**CAA**AAA**ACC**TAC**CCT**GGA**AAC**TAC**GGT**TTC**CGT**CTC**GGG**TTC**CTG**CAT**TCC**GAA**ACA**GCC**AAG**TCT**GTG**ACC**TGC**ACG**GTCAGGGGCCCTGGGGAGCCGGTTTCCCTATCAGGGCCTGGCCATACAGCCTAGGAA

4(sample number)-blue (Reverse)\_R\_Ex4p53.ab1

CGGTGCCTTCTTCCCTGGACCACTGAC**CGT**GCA**GGT**CAC**AGA**CTT**GGC**TGT**TCC**GGA**ATG**CAG**GAA**CCC**GAG**ACG**GAA**ACC**GTA**GTT**GCC**AGG**GTA**GGT**CTT**CTG**GGA**GGG**GAC**AAA**GGA**CGA**CAG**GGG**CCA**GGAGGTGGCTGGTGCCAGGGCAGCTTGGGCAGGAGGCTCTGGCATTTGGGGCGCTTCATTCGGACACTCATCCAGCCAGGTGACAACATCTTCTGAGTACGGGAGCAGGTCATCCACAGGTGCGGAGAGCTCGGAGGACTACAGACGGGAGGAGTTGCATCAGAAGGCCCA

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** | **Frame** |
| 287 bits(155) | 3e-82() | 177/188(94%) | 0/188(0%) | Plus/Minus |  |

Query 73 GTCCAAATGAAGCGCCCCAAATGCCAAAGCCTCCTGCCCAAGTTGCCCTGGCACCAGCCA 132

 |||| ||||||||||||||||||||| ||||||||||||||| |||||||||||||||||

Sbjct 197 GTCCGAATGAAGCGCCCCAAATGCCAGAGCCTCCTGCCCAAGCTGCCCTGGCACCAGCCA 138

Query 133 CCTCCTGGCCCCTGTCGTCCTTTGTCCCCTCCCAAAAAACCTACCCTGGAAACTACGGTT 192

 |||||||||||||||||||||||||||||||||| || ||||||||||| ||||||||||

Sbjct 137 CCTCCTGGCCCCTGTCGTCCTTTGTCCCCTCCCAGAAGACCTACCCTGGCAACTACGGTT 78

Query 193 TCCGTCTCGGGTTCCTGCATTCCGAAACAGCCAAGTCTGTGACCTGCACGGTCAGGGGCC 252

 |||||||||||||||||||||||| |||||||||||||||||||||||||||||| || |

Sbjct 77 TCCGTCTCGGGTTCCTGCATTCCGGAACAGCCAAGTCTGTGACCTGCACGGTCAGTGGTC 18

Query 253 CTGGGGAG 260

 | ||| ||

Sbjct 17 CAGGGAAG 10



**Pattern C:** **TAG**

22 (sample number)-pink (Forward)\_F\_Ex4p53.ab1

GATCAGTCTTCTCTCGATACTGCGAGTGACTGATCCGTACTCTTAAGATGTTGCCACCTGGTTGGATGAGTGTCCGAATGAAGCGCCCCAAATGCCAGAGCCTCCTGCCCAAGCTGCCCTGGCACCAGCCACCTCC**TGG**CCC**CTG**TCG**TCC**TTT**GTC**CCC**TCC**CAG**AAG**ACC**TAC**CCT**GGC**AAC**TAC**GGT**TTC**CGT**CTC**GGG**TTC**CTG**CAT**TCC**GGA**ACA**GCC**AAG**TCT**GTG**ACC**TGC**ACG**GTCAGTGGCCCTGGGGAGCCGGCTTCCCTATCAGTGCCTGGCCATACAGCCTAGGAAA

22 (sample number)-blue (Reverse)\_R\_Ex4p53.ab1

CTTGGCGGAGCGCTCTAGGGCCCTGAC**CGT**GCA**GGT**CAC**AGA**CTT**GGC**TGT**TCC**GGA**ATG**CAG**GAA**CCC**GAG**ACG**GAA**ACC**GTA**GTA**GCC**AGG**GTA**GGT**CTT**CTG**GGA**GGG**GAC**AAA**GGA**CGA**CAG**GGG**CCA**GGAGGTGGCTGGTGCCAGGGCAGCTTGGGCAGGAGGCTCTGGCATTTGGGGCGCTTCATTCGGACACTCATCCAGCCAGGTGACAACATCTTCTGAGTACGGGAGCAGGTCATCCACAGGTGCGGAGAGCTCGGAGGACTACAGACGGGAGGAGTTGCATCAGAAGGCCCA

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** | **Frame** |
| 370 bits(200) | 3e-107() | 213/219(97%) | 1/219(0%) | Plus/Minus |  |

Query 35 CCGTACTCTTAAGATGTTGCCACCTGGTTGGATGAGTGTCCGAATGAAGCGCCCCAAATG 94

 |||||||| ||||||||| ||||||| ||||||||||||||||||||||||||||||||

Sbjct 234 CCGTACTCAGAAGATGTTGTCACCTGGCTGGATGAGTGTCCGAATGAAGCGCCCCAAATG 175

Query 95 CCAGAGCCTCCTGCCCAAGCTGCCCTGGCACCAGCCACCTCCTGGCCCCTGTCGTCCTTT 154

 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 174 CCAGAGCCTCCTGCCCAAGCTGCCCTGGCACCAGCCACCTCCTGGCCCCTGTCGTCCTTT 115

Query 155 GTCCCCTCCCAGAAGACCTACCCTGGCAACTACGGTTTCCGTCTCGGGTTCCTGCATTCC 214

 ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||

Sbjct 114 GTCCCCTCCCAGAAGACCTACCCTGGCTACTACGGTTTCCGTCTCGGGTTCCTGCATTCC 55

Query 215 GGAACAGCCAAGTCTGTGACCTGCACGGTCAGTGGCCCT 253

 |||||||||||||||||||||||||||||||| ||||||

Sbjct 54 GGAACAGCCAAGTCTGTGACCTGCACGGTCAG-GGCCCT 17

