DRUG-RESISTANT MUTATION 3

Sequence Alignment

Alignment between the input query sequence and the genotype D consensus reference sequence. Amino acid and nucleotide sequence numbers refer to HBV polymerase numbering.

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      10----------------------------20----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _G__E__H__H__I__R__I__P__R__T__P__A__R__V__T__G__G__V__F__L_
Consensus   ggagaacatcacatcaggattcctaggacccctgctcgtgttacaggcggggtttttctt
Input       ------------------------------------------------------------
            --|---------|---------|---------|---------|---------|-------
            -30--------40--------50--------60--------70--------80-------

            30----------------------------40----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _V__D__K__N__P__H__N__T__A__E__S__R__L__V__V__D__F__S__Q__F_
Consensus   gttgacaagaatcctcacaataccgcagagtctagactcgtggtggacttctctcaattt
Input       -------t....g...g.---.--..c.-.....a....a.c.-...-----..-g..aa
            --|---------|---------|---------|---------|---------|-------
            -90--------100-------110-------120-------130-------140------

            50----------------------------60----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _S__R__G__N__Y__R__V__S__W__P__K__F__A__V__P__N__L__Q__S__L_
Consensus   tctaggggaactaccgtgtgtcttggccaaaattcgcagtccccaacctccaatcactc
Input       .-.--------..gt...c.t...c..----..a.----a.-----..a..att...-.g
            --|---------|---------|---------|---------|---------|-------
            -150-------160-------170-------180-------190-------200------

            70----------------------------80----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _T__N__L__L__S__S__N__L__S__W__L__S__L__D__V__S__A__A__F__Y_
Consensus   accaacctcctgtcctccaacttgtcctggttatcgctggatgtgtctgcggcgttttat
Input       g.t--g..ag...a........g..t.----.-....g...--------..t.c...gt.
            --|---------|---------|---------|---------|---------|-------
            -210-------220-------230-------240-------250-------260------

            90----------------------------100----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _H__L__P__L__H__P__A__A__M__P__H__L__L__V__G__S__S__G__L__S_
Consensus   catcttcctcttcatcctgctgctatgcctcatcttcttgttggttcttctggactatca
Input       t.-.g...-.g...-g.-....-a....ga.cc.c..--.cg..g..gct...gg---.t
            --|---------|---------|---------|---------|---------|-------
            -270-------280-------290-------300-------310-------320------

            110----------------------------120----------------------------
            -|------------------------------|----------------------------
Input       _-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _R__Y__V__A__R__L__S__S__N__S__R__I__F__N__H__Q__H__G__T__M_
Consensus   aggtatgttgcccgtttgtcctctaattccaggatcttcaaccaccagcacgggaccatg
Input       --....cg.-...c-..c.....----.g.c.t.c.g..--.g....-.gg...t...c.
            --|---------|---------|---------|---------|---------|-------
            -330-------340-------350-------360-------370-------380------

            130----------------------------140----------------------------
            -|------------------------------|----------------------------
Input       _-__.__A__R__S__R__S__G__A__.__-__S__S__G__.__I__I__.__S__S_
Consensus   _Q__N__L__H__D__S__C__S__R__N__L__Y__V__S__L__L__L__L__Y__Q_
Consensus   cagaacctgcacgactcctgctcaaggaacctctatgtatccctcctgttgctgtaccaa
Input       .-.g-t..c.c..--..t...-.t-----t...-..c.-g..g.....c.t.gc.--.--
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            --|---------|---------|---------|---------|---------|-------
            -390-------400-------410-------420-------430-------440------

            150----------------------------160---------------------------
            -|-----------------------------|-------------------------169
Input       _F__L__N__H__H__F__._F__F__G__R__._L__F__T__S__R__._T__T_
Consensus   _T__F__G__R__K__L__H__L__Y__S__H__P__I__I__L__G__F__R__K__I_
Consensus   accttcggacggaaattgcacctgtattcccatcccatcatcctgggctttcggaaaatt
Input       ....ct.c..-.---.....--..g.ca..a.c............t...a.at..g.gg
            --|---------|---------|---------|---------|---------|-------
            -450-------460-------470-------480-------490-------500------

            170----------------------------1801-------------------------
             -|----------------------------|--------------------------
Input       _.__R__.__.__A__W__G__-__-__C__I__V__P__.__-__-__S__V__.__R_
Consensus   _P__M__G__V__G__L__S__P__F__L__L__A__Q__F__T__S__A__I__C__S_
Consensus   cctatgggagtgggcctcagcccgtttctcctggctcagtttactagtgccatttgttca
Input       a..c.t...c.----.........----a......ct.c..g...-...-----....t.
            --|---------|---------|---------|---------|---------|-------
            -510-------520-------530-------540-------550-------560------

            190----------------------------200---------------------------
            -|-----------------------------|---------------------------
Input       _T__.__-__.__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-__-_
Consensus   _V__V__R__R__A__F__P__H__C__L__A__F__S__Y__M__D__D__V__V__L_
Consensus   gtggttcgtagggctttcccccactgtttggctttcagttatatggatgatgtggtattg
Input       aa.ac.g.g....t.g.t---a.ag...a......---g...ta...g.c....c..a.t
            --|---------|---------|---------|---------|---------|-------
            -570-------580-------590-------600-------610-------620------

            210----------------------------220---------------------------
            -|-----------------------------|---------------------------
Input       _-__P__R__G__A__P__-__-__-__-__.__.__.__R__S__P__R__-__-__-_
Consensus   _G__A__K__S__V__Q__H__L__E__S__L__F__T__A__V__T__N__F__L__L_
Consensus   ggggccaagtctgtacagcatcttgagtccctttttaccgctgttaccaattttcttttg
Input       ---.----.....cg..c....a.c.tg.a.........t...---..t.a--..a.c--
            --|---------|---------|---------|---------|---------|-------
            -630-------640-------650-------660-------670-------680------

            230----------------------------240---------------------------
            -|-----------------------------|---------------------------
Input       _-__.__C__L__-__.__I__-__-__-__C__R__S__V__C__T__.__.__.__L_
Consensus   _S__L__G__I__H__L__N__P__N__K__T__K__R__W__G__Y__S__L__H__F_
Consensus   tctttgggtatacatttaaaccctaacaaaacaaaaagatggggttactctttacatttc
Input       .-c..--.---------------.------------.c..----g.-.c.---..t....
            --|---------|---------|---------|---------|---------|-------
            -690-------700-------710-------720-------730-------740------

                                250---------------
                                -|----------------
                     Input       _C__T__L__H__-__.
                     Consensus   _M__G__Y__V__I__G
                     Consensus   atgggctatgtcattgg
                     Input       .-a.c..ca.g.c...n
                                 --|---------|----
                                 -750-------760---
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Figure S3. Dual-drug-resistant mutation observed in cases of HBV-related HCC from North India. The input sequence (yellow) bears the amino acid T in place of the expected I, as observed in the reference sequence (green) at codon 169 (blue). The mutation I169T has been associated with the entecavir resistance mutations in lamivudine-resistant patients, and is believed to play a secondary role in entecavir resistance. Again, at codon 181 (blue) there is a mutation from A→V, which is associated with resistance to adefovir and/or lamivudine.