A

RT gene sequences

```
                        10         20         30         40         50         60         70         80
consensus D     EDWGPCAEHG EHHIRIPRTP ARVTGGVFLV DKNPHNTAES RLVVDFSQFS RGNYRVSWPK FAVPNLQSLT NLLSSNLSWL
SL05_2001       .......... .......... .......... .......... .......... .......... .......... .........--
SL02_2010       .......... .......... .......... .......... ..-------- ---------- ---------- ----------
                        90        100        110        120        130        140        150        160
consensus D     SLDVSAAFYH LPLHPAAMPH LLVGSSGLSR YVARLSSNSR IFNHQHGTMQ NLHDYCSRNL YVSLLLLYQT FGRKLHLYSH
SL05_2001       ---------- ---------- ---------- -------H-- ---------- ----S----- ---------- --Q-------
SL02_2010       ---------- ---------- ---------- -------H-- ---------- ----S----- ---------- --Q-------
                                                                                                K
                       170        180        190        200        210        220        230        240
consensus D     PIILGFRKIP MGVGLSPFLL AQFTSAICSV VRRAFPHCLA FSYMDDVVLG AKSVQHLESL FTAVTNFLLS LGIHLNPNKT
SL05_2001       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
SL02_2010       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                       250        260        270        280        290        300        310        320
consensus D     KRWGYSLNFM GYVIGCYGSL PQDHIIQKIK ECFRKLPVNR PIDWKVCQRI VGLLGFAAPF TQCGYPALMP LYACIQSKQA
SL05_2001       -------H-- -----..... .......... .......... .......... .......... .......... ..........
SL02_2010       -------H-- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                       330        340
consensus D     FTFSPTYKAF LCKQYLNLYP VARQ
SL05_2001       .......... .......... ....
SL02_2010       --------.. .......... ....
```

B

HBsAg gene sequences

```
                        10         20         30         40         50         60         70         80
consensus D     MENITSGFLG PLLVLQAGFF LLTRILTIPQ SLDSWWTSLN FLGGTTVCLG QNSQSPTSNH SPTSCPPTCP GYRWMCLRRF
SL05_2001       .......... .......... .......... .......... .......... .......... .......... ----------
SL02_2010       .......... .......... .......... ....------ ---------- ---------- ---------- ----------
                        90        100        110        120        130        140        150        160
consensus D     IIFLFILLLC LIFLLVLLDY QGMLPVCPLI PGSSTTSTGP CRTCTTPAQG TSMYPSCCCT KPSDGNCTCI PIPSSWAFGK
SL05_2001       ---------- ---------- ---------- ---------- -K-------- ---------- -L--R----- ----------
                                                                                    P
SL02_2010       ---------- ---------- ---------- ---------- -K-------- ---------- -L-ER----- ----------
                                                                                    P D
                       170        180        190        200        210        220
consensus D     FLWEWASARF SWLSLLVPFV QWFVGLSPTV WLSVIWMMWY WGPSLYSILS PFLPLLPIFF CLWVYI*
SL05_2001       ---------- --------S- ---------- ---------- ---------- ---------- ---A---
                                   F                                                   V
SL02_2010       ---------- --------S- ---------- ---------- ---------- ---------- -------
                                   F
```