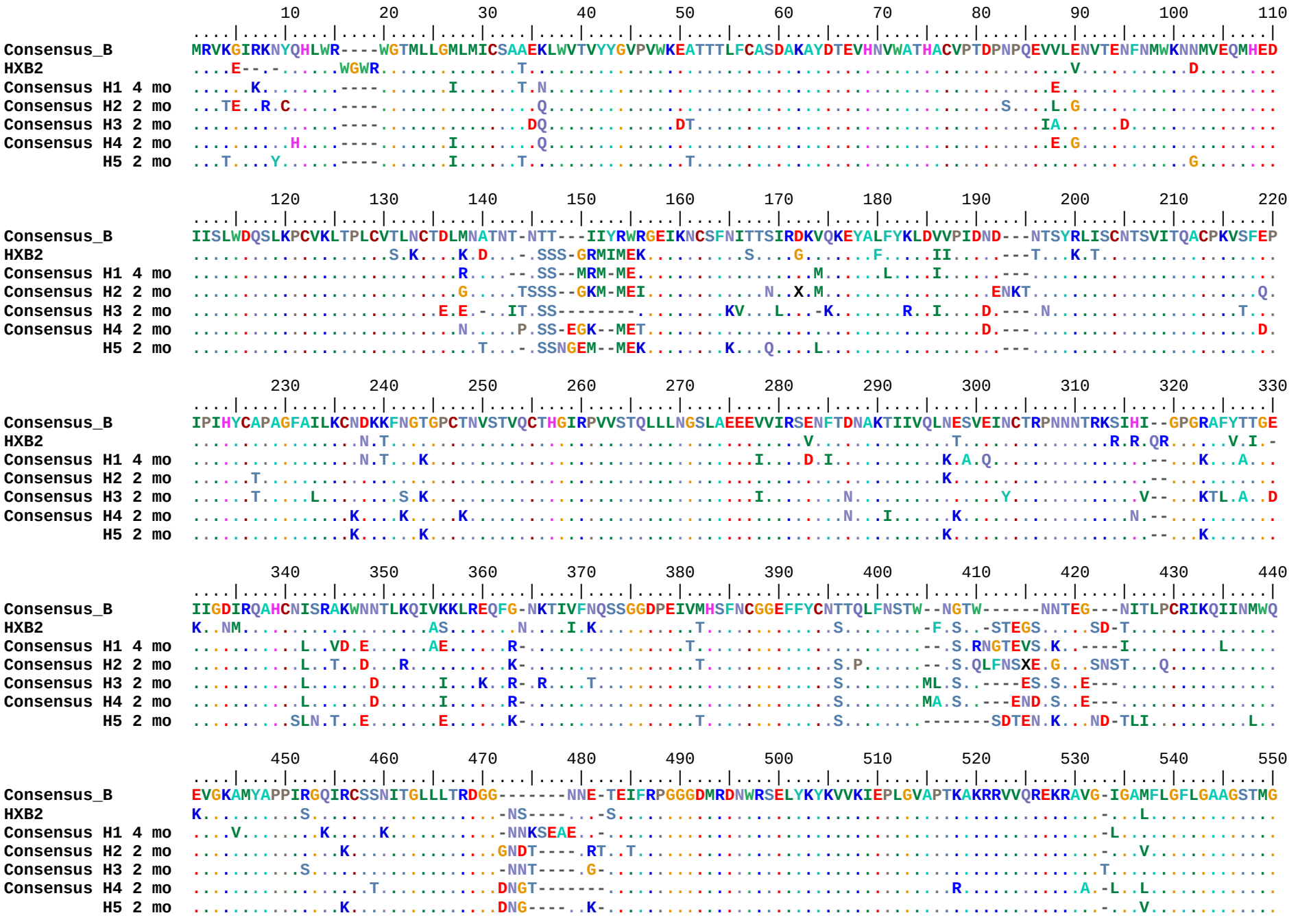
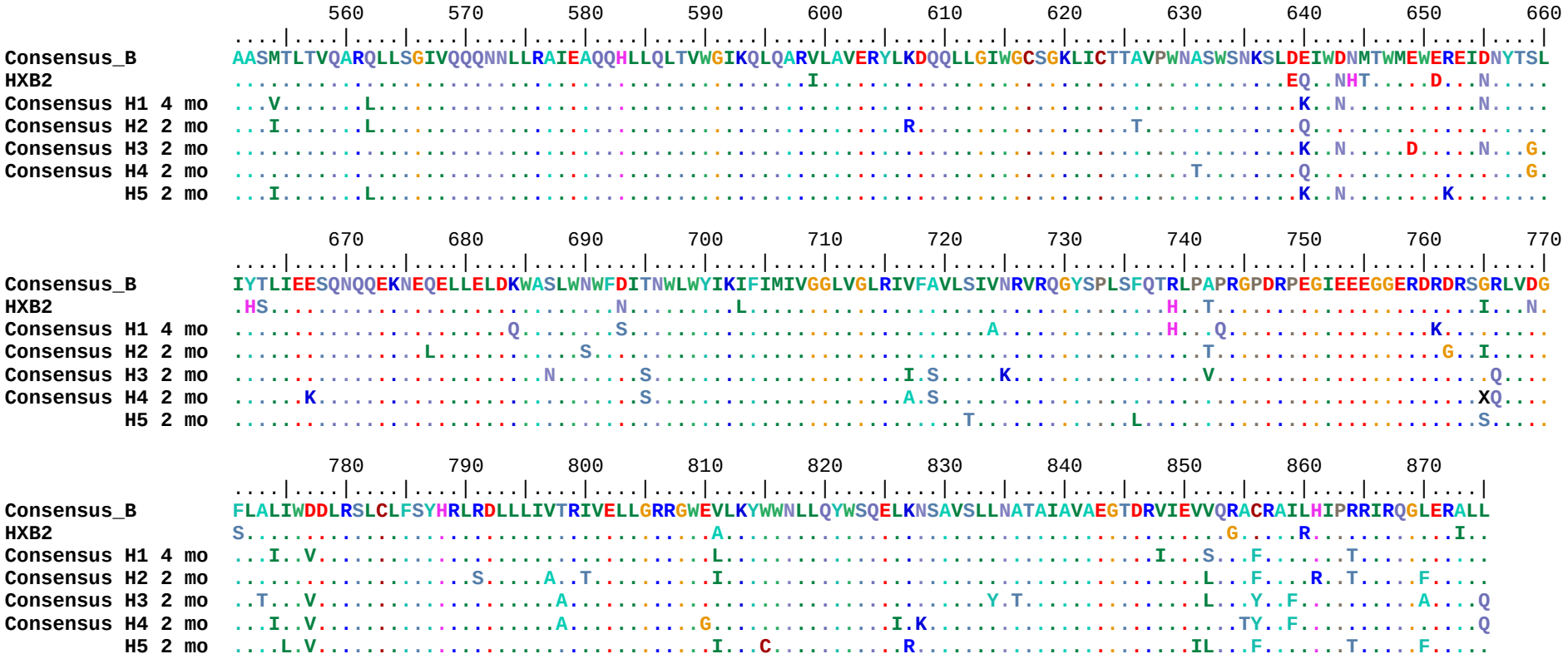

10 20 30 40 50 60 70 80 90 100 110
Consensus_B MRVKGIRKNYQHLWR----WGTMLLGMLMICSAAEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVTENFNMWKNNMVEQMHED
HXB2 ....E---.....WGWR.....T.....V.....D.....
Consensus H1 4 mo .....K.....----.....I.....T.N.....E.....
Consensus H2 2 mo ...TE..R.C.....----.....Q.....S....L.G.....
Consensus H3 2 mo .....----.....DQ.....DT.....IA.....D.....
Consensus H4 2 mo .....H.....----.....I.....Q.....E.G.....
H5 2 mo ...T....Y.....----.....I.....T.....T.....G.....
120 130 140 150 160 170 180 190 200 210 220
Consensus_B IISLWDQSLKPCVKLTPLCVTLNCTDLMNATNT-NTT---IIYRWRGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDND---NTSYRLISCNTSVITQACPKVSFEP
HXB2 .....S.K....K.D...-.SSS-GRMIMEK.....S....G.....F.....II.....---T...K.T.....
Consensus H1 4 mo .....R.....---.SS--MRM-ME.....M.....L....I.....---.....
Consensus H2 2 mo .....G.....TSSS--GKM-MEI.....N..X.M.....ENKT.....Q.
Consensus H3 2 mo .....E.E.-..IT.SS--------.....KV...L...-K.....R..I....D.----.N.....T...
Consensus H4 2 mo .....N.....P.SS-EGK--MET.....D.---.....D.
H5 2 mo .....T...-.SSNGEM--MEK.....K...Q....L.....---.....
230 240 250 260 270 280 290 300 310 320 330
Consensus_B IPIHYCAPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTDNAKTIIVQLNESVEINCTRPNNNTRKSIHI--GPGRAFYTTGE
HXB2 .....N.T.....V.....T.....R.R.QR.....V.I.-
Consensus H1 4 mo .....N.T...K.....I....D.I.....K.A.Q.....---...K...A...
Consensus H2 2 mo .....T.....K.....--.....
Consensus H3 2 mo .....T.....L.....S.K.....I.....N.....Y.....V----.KTL.A..D
Consensus H4 2 mo .....K....K.....K.....N...I.....K.....N.--.....
H5 2 mo .....K.....K.....K.....---...K.....
340 350 360 370 380 390 400 410 420 430 440
Consensus_B IIGDIRQAHCNISRAKWNNTLKQIVKKLREQFG-NKTIVFNQSSGGDPEIVMHSFNCGGEFFYCNTTQLFNSTW--NGTW------NNTEG---NITLPCRIKQIINMWQ
HXB2 K..NM.....AS.....N....I.K.....T.....S.....-F.S..-STEGS.....SD-T.....
Consensus H1 4 mo .....L..VD.E.....AE.....R-.....T.....---S.RNGTEVS.K.-----I.....L.....
Consensus H2 2 mo .....L..T..D...R.....K-.....T.....S.P.....---S.QLFNSXE.G...SNST...Q.....
Consensus H3 2 mo .....L.....D.....I...K..R-.R....T.....S.....ML.S.-----ES.S..E---.....
Consensus H4 2 mo .....L.....D.....I.....R-.....S.....MA.S.---END.S..E---.....
H5 2 mo .....SLN.T..E.....E.....K-.....T.....S.....-------SDTEN.K...ND-TLI.....L..
450 460 470 480 490 500 510 520 530 540 550
Consensus_B EVGKAMYAPPIRGQIRCSSNITGLLLTRDGG-------NNE-TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVG-IGAMFLGFLGAAGSTMG
HXB2 K.....S.....-NS------S.....-...L.....
Consensus H1 4 mo ....V.....K.....K.....-NNKSEAE..-.....-L.....
Consensus H2 2 mo .....K.....GNDT-----RT..T.....-...V.....
Consensus H3 2 mo .....S.....-NNT-----G-.....T.....
Consensus H4 2 mo .....T.....DNGT-----.....R.....A.-L..L.....
H5 2 mo .....K.....DNG-----K-.....-...V.....



Supplementary Figure 1: Consensus gp160 sequences of the earliest virus variants from each patient aligned to the consensus B and HXB2 Env sequences. Since isolation of clonal virus variants was not successful for the earliest time point in individual H5, a single *env* sequence was generated from proviral DNA in patient PBMC from this time point. In those cases where no single residue was present in at least 50 % of the sequences from one patient, an X is shown.