

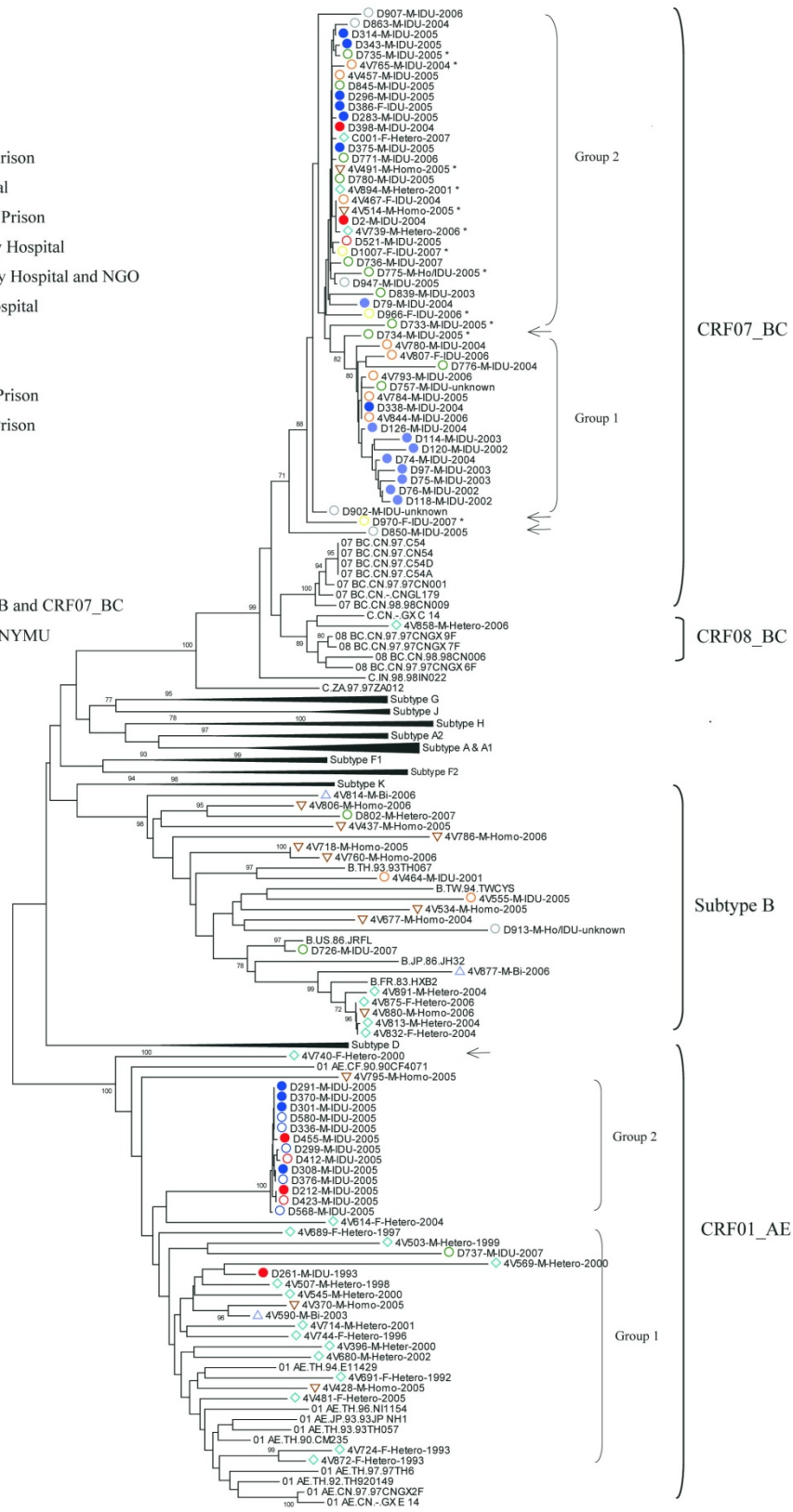
Supplemental Digital Content 6 – Figure 3. Phylogenetic analysis of the HIV-1 strains found in the various Taiwanese risk groups. **(A)** A maximum likelihood tree based on *env* (7077-7619 nucleotide residues of HXB2) nucleotide sequences. **(B)** A maximum likelihood tree based on *pol* (2253-3214 nucleotide residues of HXB2) nucleotide sequences.

- Northern region of Taiwan**
- ○ IDUs from Taipei DC and Prison
 - IDUs from Taipei City Hospital
 - IDUs from Taoyuan Woman's Prison
 - ▽ Homosexuals from Taipei City Hospital
 - ◇ Heterosexuals from Taipei City Hospital and NGO
 - △ Bisexuals from Taipei City Hospital

- Central region of Taiwan**
- IDUs from Taichung DC and Prison
 - ○ IDUs from Yunlin Second Prison

- Southern region of Taiwan**
- IDUs from Tainan DC
 - IDUs from Kaoshung Prison

- * Dually infected with subtype B and CRF07_BC
- ● ● Reference strains from NYMU



Supplementary Figure 3A.

- Northern region of Taiwan**
- IDUs from Taipei City Hospital
 - IDUs from Sindian Drug Abuser Treatment Center
 - IDUs from Taoyuan Woman's Prison
 - ▽ Homosexuals from Taipei City Hospital
 - ◇ Heterosexuals from Taipei City Hospital
- Central region of Taiwan**
- IDUs from Taichung Prison
 - ◇ Heterosexuals from Yunlin Second Prison
 - ◇ Heterosexuals from China Medical University Hospital
- Southern region of Taiwan**
- IDUs from Kaoshung Prison



Supplementary Figure 3B.