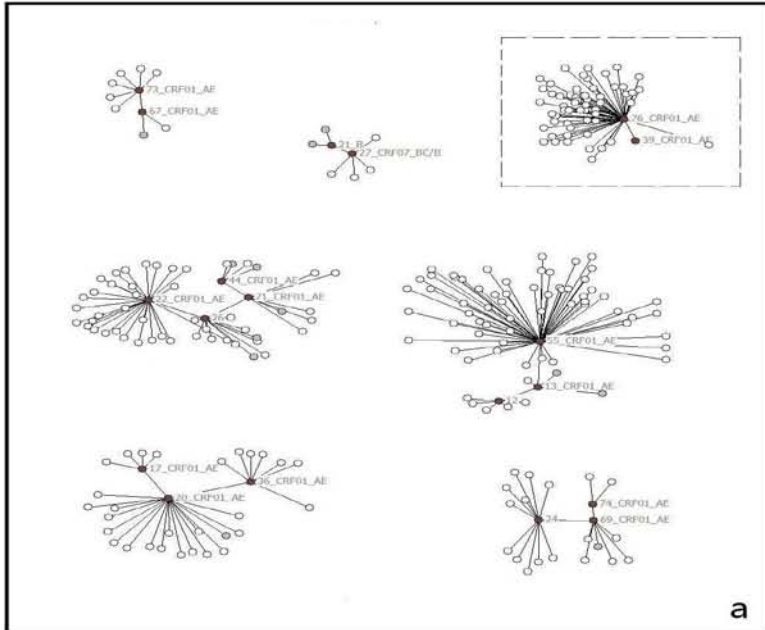
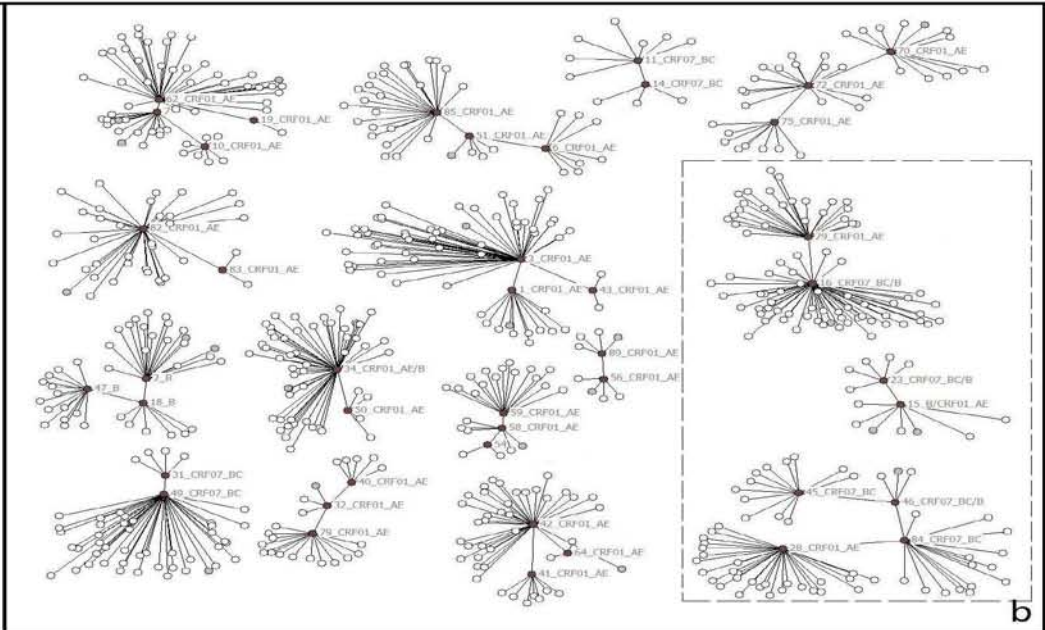


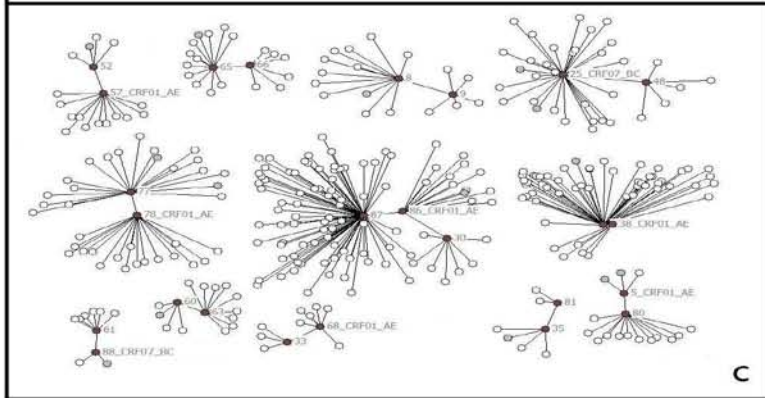
Web Figure 1. Sexual and molecular networks of human immunodeficiency virus (HIV)-infected men who have sex with men(MSM) in Taizhou, China, 2008-2010. (a) Networks (n = 7) of potential HIV transmission pairs or clusters: Each of the seven networks excluding the one inside the small dashed square contained at least two HIV-infected MSM who were determined to be potential HIV transmission pairs. The network placed inside the small dashed square is that of an HIV-infected MSM whose wife was also infected with the same HIV subtype. (b) Networks (n = 16) of behaviorally linked (i.e., having unprotected sex) HIV-infected MSM pairs or clusters who either had discordant HIV subtypes (3 clusters) or had the same HIV subtype but did not qualify to be determined as potential HIV transmission pairs (13 pairs or clusters). (c) Networks (n = 12) of behaviorally linked HIV-infected MSM pairs or clusters with HIV genotypes unidentifiable for at least one HIV-infected MSM within each pair or cluster. (d) Networks (n = 14) of HIV-infected MSM whose risky contacts were not HIV-infected or not tested for HIV. *Dark dots* represent the 100 HIV-infected MSM and one HIV-infected wife (no.39); *Grey dots* represent risky contacts of HIV-infected MSM who were tested to be HIV-negative; *Circles* represent reported risky contacts of HIV-infected MSM who did not receive HIV testing.



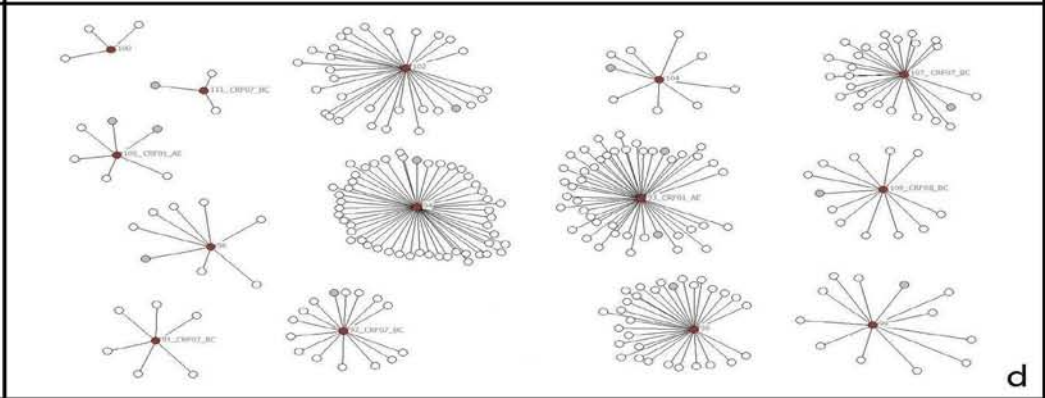
a



b

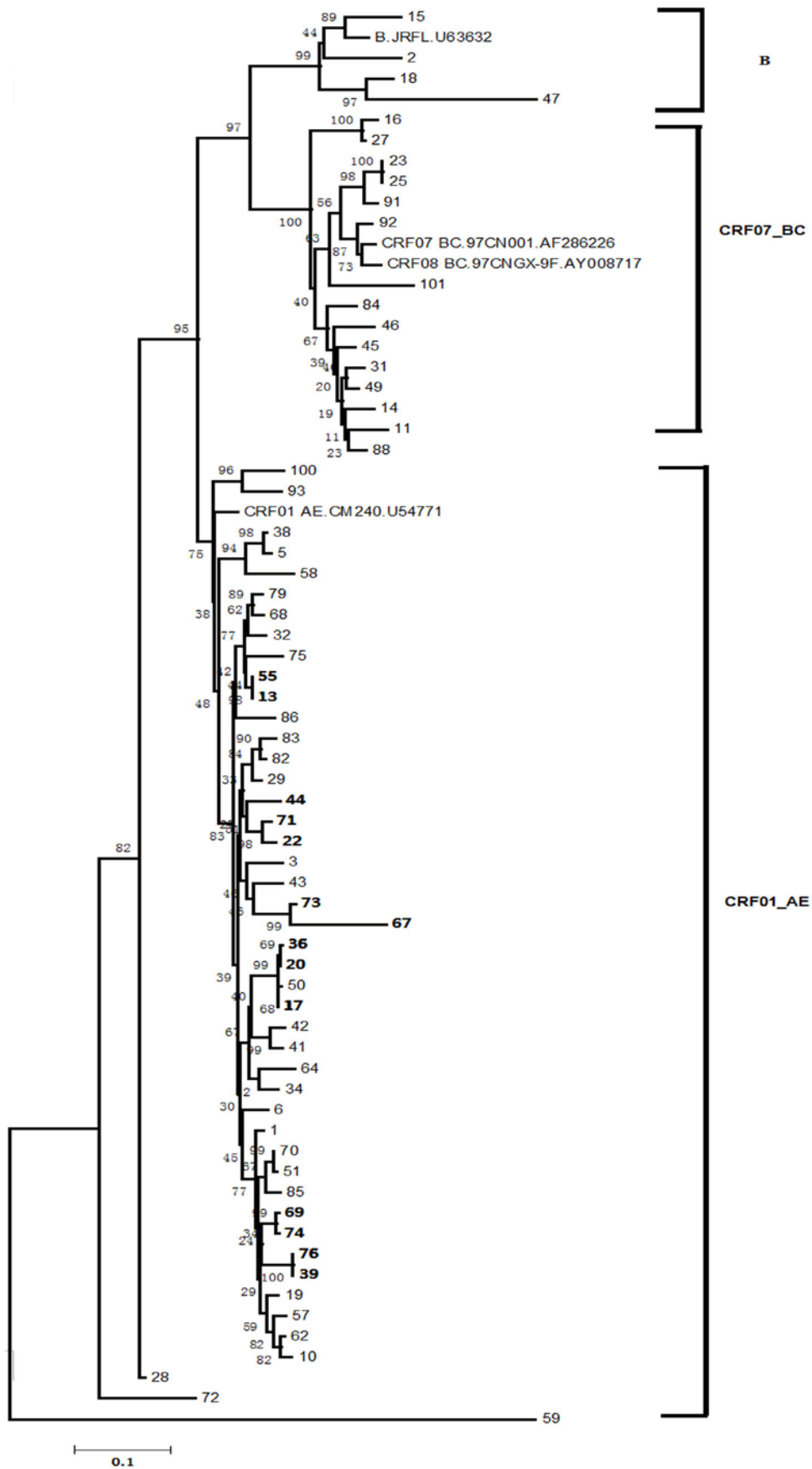


c

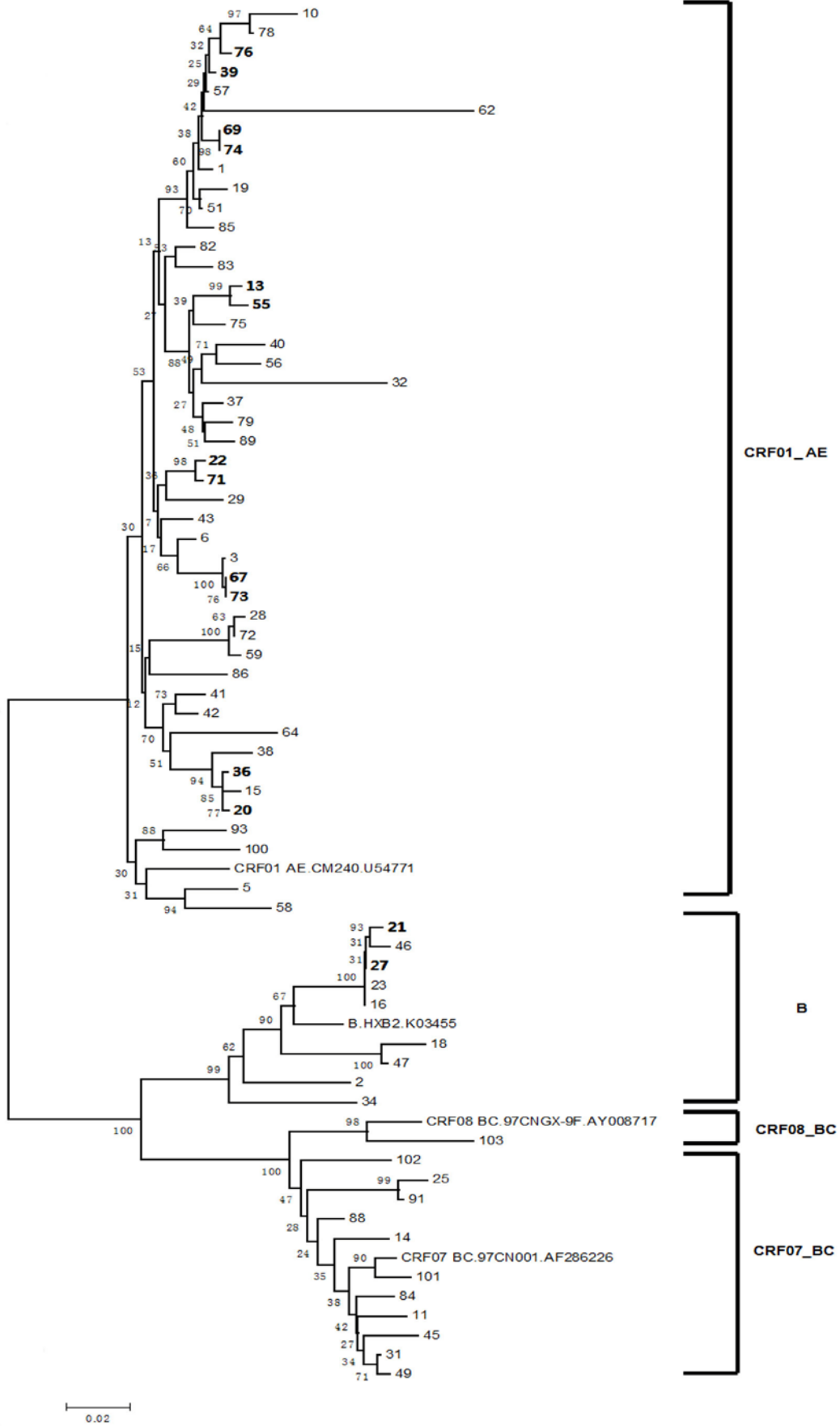


d

Web Figure 2. Phylogenetic analyses of human immunodeficiency virus (HIV)-infected men who have sex with men(MSM) in Taizhou, China, 2008-2010. The numbers are concordant with those in Web Figure 1. The seven potential HIV transmission pairs or clusters are shown *in bold*.



(a). Phylogenetic tree of *env* gene



(b). Phylogenetic tree of *gag* gene