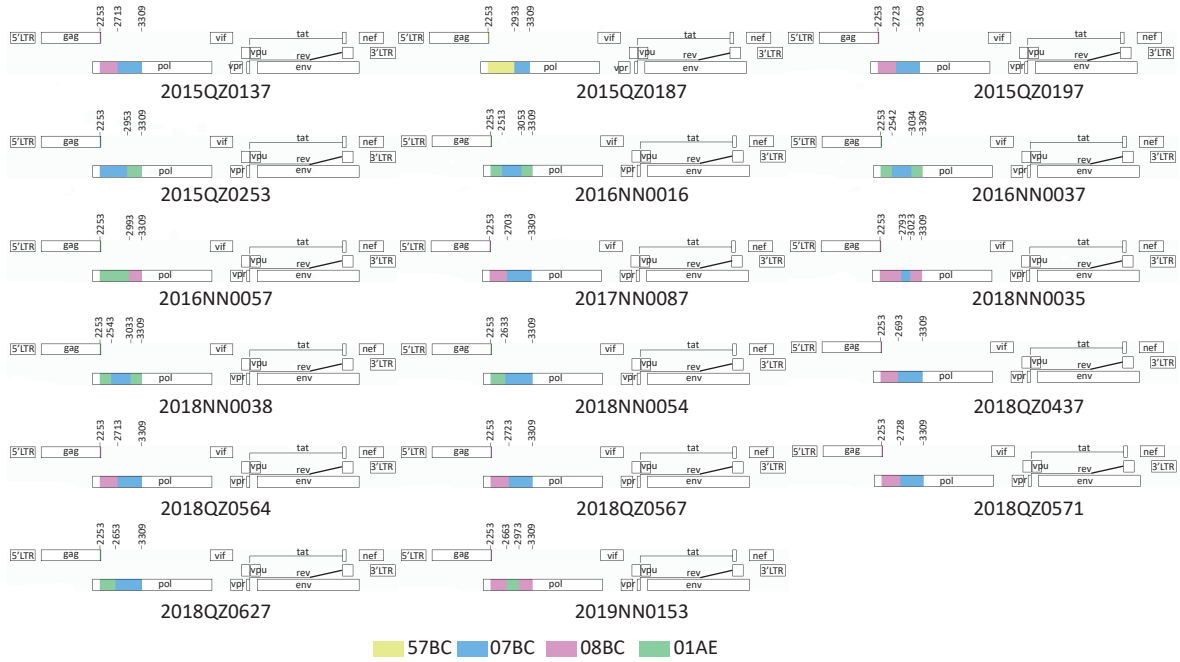
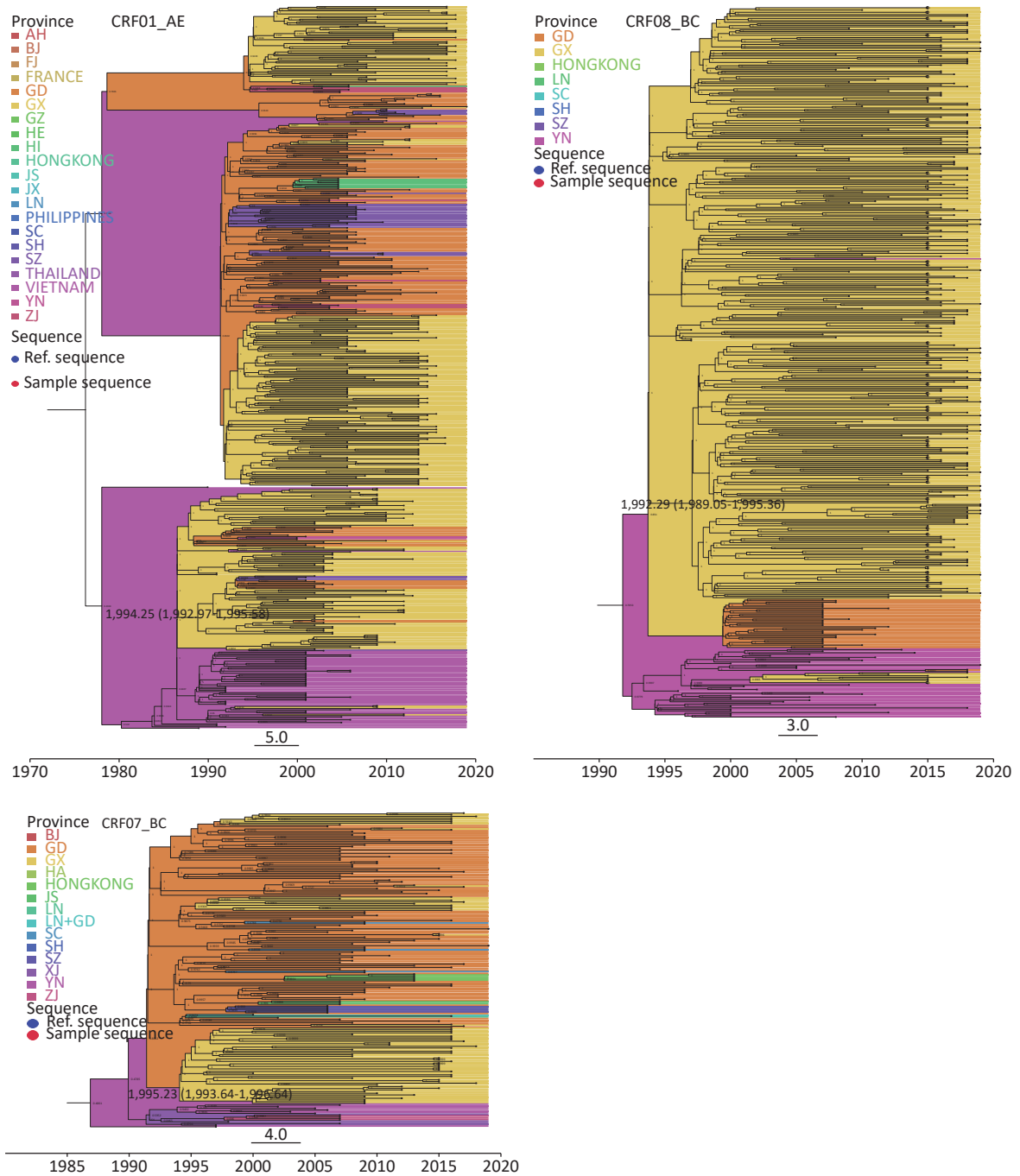


Supplementary Table S1. Detail information of HIV-1 unique recombinant forms of 17 sample from 535 IDUs in Guangxi, China

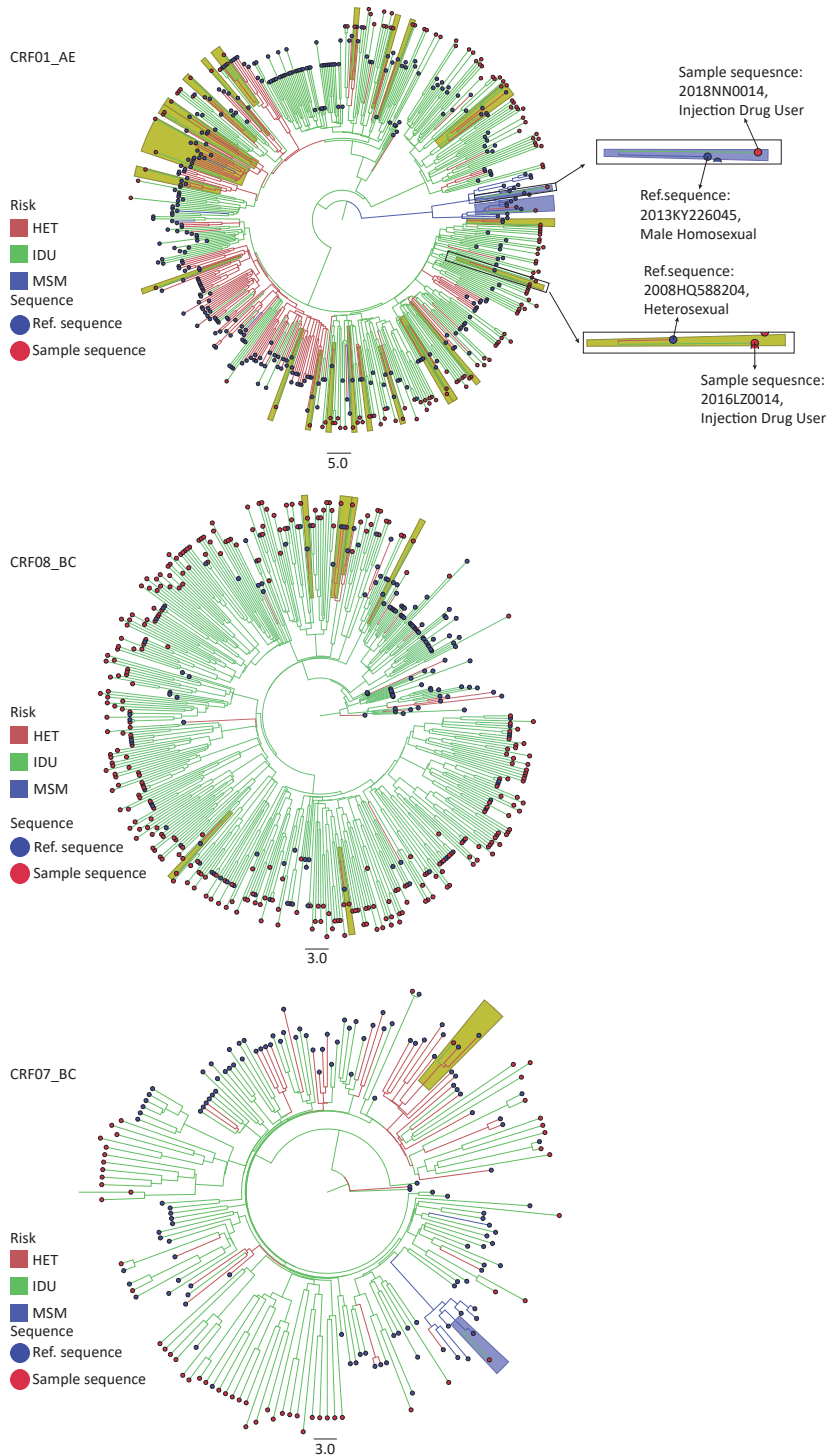
Sequence name	Ethnicity	Sex	Fragment start position	Breakpoint interval	Fragment end position	Fragment subtype
2015QZ0137	Han	Male	2253	2253-2713	2713	08_BC
			2713	2713-3309	3309	07_BC
2019NN0153	Zhuang	Male	2253	2253-2663	2663	08_BC
			2663	2663-2973	2973	01_AE
			2973	2973-3309	3309	08_BC
2016NND0016	Han	Female	2253	2253-2513	2513	01_AE
			2513	2513-3053	3053	07_BC
			3053	3053-3309	3309	01_AE
2018NN0035	Han	Male	2253	2253-2793	2793	08_BC
			2793	2793-3023	3023	07_BC
			3023	3023-3309	3309	08_BC
2016NND0037	Han	Male	2253	2253-2542	2542	01_AE
			2542	2542-3034	3034	07_BC
			3034	3034-3309	3309	01_AE
2018NN0038	Han	Male	2253	2253-2543	2543	01_AE
			2543	2543-3033	3033	07_BC
			3033	3033-3309	3309	01_AE
2018NN0054	Han	Male	2253	2253-2633	2633	01_AE
			2633	2633-3309	3309	07_BC
2016NND0057	Han	Male	2253	2253-2993	2993	01_AE
			2993	2993-3309	3309	08_BC
2017NND0087	Han	Male	2253	2253-2703	2703	08_BC
			2703	2703-3309	3309	07_BC
2018QZ0437	Han	Male	2253	2253-2693	2693	08_BC
			2693	2693-3309	3309	07_BC
2015QZ0187	Han	Male	2253	2253-2933	2933	57_BC
			2933	2933-3309	3309	07_BC
2015QZ0197	Han	Male	2253	2253-2723	2723	08_BC
			2723	2723-3309	3309	07_BC
2015QZ0253	Han	Male	2253	2253-2953	2953	07_BC
			2953	2953-3309	3309	01_AE
2018QZ0564	Han	Male	2253	2253-2713	2713	08_BC
			2713	2713-3309	3309	07_BC
2018QZ0567	Han	Male	2253	2253-2723	2723	08_BC
			2723	2723-3309	3309	07_BC
2018QZ0571	Han	Male	2253	2253-2728	2728	08_BC
			2728	2728-3309	3309	07_BC
2018QZ0627	Han	Male	2253	2253-2653	2653	01_AE
			2653	2653-3309	3309	07_BC



Supplementary Figure S1. Recombination patterns and parental origin in 1.2 kb *pol* region of 17 sample from 535 IDUs in Guangxi, China. The genome map of the *pol* gene DNA sequence of 17 recombinant sample was generated using the Online Recombinant HIV-1 Drawing Tool (https://www.hiv.lanl.gov/content/sequence/DRAW_CRF_recom_mapper.html).



Supplementary Figure S2. This figure illustrated time-scaled phylogeographic history of three HIV-1 subtypes (CRF01_AE, CRF08_BC, CRF07_BC) for IDU in Guangxi. Background colours around branches represented the most probable origin province of the parental node of each branch. The names of the origin provinces were indicated by the colour of the legend in the upper left corner. The values of probability inferred by Bayesian skygrid demographic model estimation for the most probable ancestral location were specified at the corresponding nodes. The probable time of introduction for these three key subtypes with an effective population size circulating in Guangxi IDU was indicated at key nodes. Red and blue dots at the ends of branches denoted the sequences of study participants and references, respectively. The Bayesian MCC trees were visualised through the FigTree software v1.4.3 (<http://beast.bio.ed.ac.uk>). The figure editing was using Adobe Illustrator 2020 (V 24.0.1.341).



Supplementary Figure S3. This figure illustrated HIV transmission risk category link of three HIV-1 subtypes (CRF01_AE, CRF07_BC, CRF08_BC) for IDU in Guangxi. The transmission risk category of the strains is color-coded as shown in the inset. Red and blue dots at the ends of branches denoted sequences of study participants and references, respectively. Background colors around branches represent the most probable origin of the parental node of each branch. The Bayesian MCC trees were visualized through the FigTree software v1.4.3 (<http://beast.bio.ed.ac.uk>). The figure editing was using Adobe Illustrator 2020 (V 24.0.1.341).