

**Supplementary Table 1. Characteristics of Patients with newly diagnosed Human Immunodeficiency Virus (HIV): Henan, 2018–2021.**

Characteristics	All (N=1228)	2018 (N=90)	2019 (N=318)	2020 (N=602)	2021 (N=218)
Age at diagnosis (years)	35 (7–89)	37.5 (7–81)	37 (15–77)	35 (10–89)	34 (18–78)
< 20 years	31 (2.52)	2 (2.22)	8 (2.52)	14 (2.33)	7 (3.21)
20–49 years	933 (75.98)	65 (72.22)	241 (75.79)	451 (74.92)	176 (80.73)
≥ 50 years	264 (21.50)	23 (25.56)	69 (21.70)	137 (22.76)	35 (16.06)
Sex					
Male	1,097 (89.33)	88 (97.78)	280 (88.05)	528 (87.71)	201 (92.20)
Female	131 (10.67)	2 (2.22)	38 (11.95)	74 (12.29)	17 (7.80)
Ethnicity					
Han	1,038 (84.53)	63 (70.00)	263 (82.70)	528 (87.71)	184 (84.40)
Other	15 (1.22)	2 (2.22)	2 (0.63)	7 (1.16)	4 (1.83)
Unknown	175 (14.25)	25 (27.78)	53 (16.67)	67 (11.13)	30 (13.76)
Geographic location					
Henan province	1,020 (83.06)	81 (90.00)	264 (83.02)	503 (83.55)	172 (78.90)
Zhengzhou	230 (18.73)	19 (21.11)	75 (23.58)	121 (20.10)	15 (6.88)
Other city in Henan	560 (45.60)	17 (18.89)	169 (53.14)	317 (52.66)	57 (26.15)
Unknown city in Henan	230 (18.97)	45 (50.00)	20 (6.60)	65 (11.13)	100 (45.87)
Other/Unknown	208 (16.94)	9 (10.00)	54 (16.98)	99 (16.45)	46 (21.10)
Marriage					
Married	522 (42.51)	39 (43.33)	154 (48.43)	250 (41.53)	79 (36.24)
Single	517 (42.10)	26 (28.89)	109 (34.28)	277 (46.01)	105 (48.17)
Unkown	189 (15.39)	25 (27.78)	55 (17.3)	75 (12.46)	34 (15.60)
Transmission category					

HSX	333 (27.12)	11 (12.22)	48 (15.09)	224 (37.21)	50 (22.94)
MSM	406 (33.06)	27 (30.00)	86 (27.04)	198 (32.89)	95 (43.58)
MTCT	0	0	0	0	0
PL	16 (1.30)	3 (3.33)	3 (0.94)	9 (1.50)	1 (0.46)
IDU	0	0	0	0	0
Other	473 (38.52)	49 (54.44)	181 (56.92)	171 (28.41)	72 (33.03)
Occupation					
Workers	427 (34.77)	30 (33.33)	79 (24.84)	235 (39.04)	83 (38.07)
Non-workers	522 (42.51)	30 (33.33)	155 (48.74)	253 (42.03)	84 (38.53)
Students	64 (5.21)	2 (2.22)	18 (5.66)	32 (5.32)	12 (5.50)
Unknown	215 (17.51)	28 (31.11)	66 (20.75)	82 (13.62)	39 (17.89)
CD4+ T cell count (cells/ $\mu$ L)	923 (75.16)	15 (16.67)	192 (60.38)	505 (83.89)	211 (96.79)
CD4+, median (min/max)	127 (1–1102)	97 (1–424)	113.5 (1–816)	114 (1–1102)	188 (1–999)
HIV Baseline viral load (copies/ml plasma)	895 (72.88)	12 (13.33)	177 (55.66)	502 (83.39)	204 (93.58)
VL, median (min/max)	64,235 (182 – 67,946,648)	56118 (12,076 – 279,162)	64,610 (182 – 67,946,648)	74,977.5 (716 – 62,375,280)	34920 (308 – 20,830,442)

Data are presented as *n* (%) or median (IQR). IQR: Interquartile range; HSX: Heterosexual orientation; MSM: Men who have sex with men; MTCT: Mother-to-child transmission;

PL: Plasmapheresis; IDU: Injection drug use; OTH: Others, including patients whose risk factors were unknown or patients who did not provide information; TDRM: Transmitted drug-resistance mutations; NRTI: Nucleotide reverse transcriptase inhibitors; NNRTI: Non-nucleoside reverse transcriptase inhibitors; PI: Protease inhibitors; INSTI: Integrase strand transfer inhibitors.

**Supplementary Table 2. Distribution and prevalence of DR among HIV-1 subtypes in patients newly diagnosed with HIV: Henan, 2018–2021.**

<b>Subtype</b>	<b>Patients</b>	<b>DR</b>
CRF07_BC	427 (34.77)	61 (14.29)
CRF01_AE	387 (31.51)	78 (20.16)
B	315 (25.65)	64 (20.32)
CRF55_01B	41 (3.34)	40 (97.56)
A	14 (1.14)	2 (14.29)
C	10 (0.81)	4 (40.00)
CRF08_BC	9 (0.73)	2 (22.22)
Other/recombinant	25 (2.04)	9 (36.00)
Total	1228 (100.00)	260 (21.17)

Data are presented as *n* (%). CRF: Circulating recombinant forms; DR: Drug resistance; Other/recombinants, including CRF52\_01B, CRF59\_01B, CRF67\_01B, CRF68\_01B, CRF45\_cpx, CRF01\_AE/B, CRF07\_BC/A1, CRF07\_BC/D, CRFA1/B, and CRFA1/C/B.

**Supplementary Table3. Prevalence of drug class-specific mutations in persons newly diagnosed with HIV: Henan, 2018–2021.**

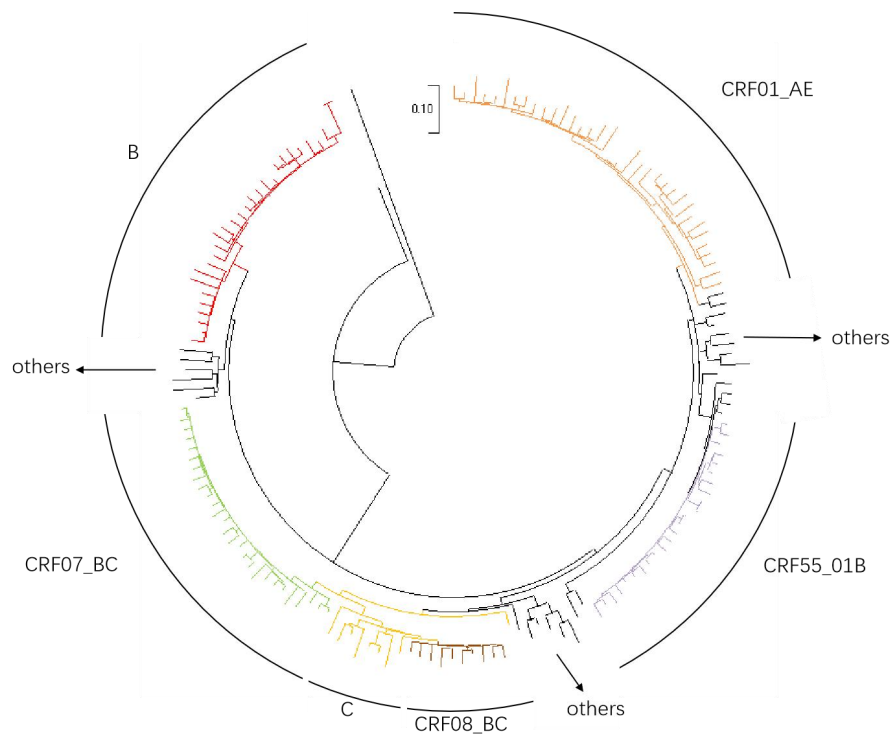
NRTIs ( <i>n</i> =1228)		NNRTIs ( <i>n</i> =1228)		PIs ( <i>n</i> =1228)		INSTIs ( <i>n</i> =827)	
Mutation	Prevalence	Mutation	Prevalence	Mutation	Prevalence	Mutation	Prevalence
Any NRTIs	27 (2.20)	Any NNRTIs	212 (17.26)	Any PIs	34 (2.77)	Any INSTIs	15 (1.81)
M41L	4 (0.33)	A98AG	5 (0.41)	L10F	5 (0.41)	T97A	3 (0.36)
A62V	2 (0.16)	L100I	1 (0.08)	K20T	1 (0.08)	E138AK	3 (0.36)
K65RE	11 (0.90)	K101EH	5 (0.41)	L24I	1 (0.08)	E157Q	8 (0.97)
D67N	2 (0.16)	K103SNRQ	36 (2.93)	L33F	2 (0.16)	D232N	1 (0.12)
K70R	1 (0.08)	V106MI	47 (3.83)	K43T	1 (0.08)		
L74I	1 (0.08)	V108I	4 (0.33)	M46IL	8 (0.65)		
V75M	2 (0.16)	E138QAG	10 (0.81)	I54V	1 (0.08)		
F77L	1 (0.08)	V179DEIT	125 (10.18)	Q58E	21 (1.71)		
M184VI	17 (1.38)	Y181C	7 (0.57)	L76V	1 (0.08)		
L210W	2 (0.16)	Y188HC	2 (0.16)	V82A	1 (0.08)		
T215YFS	5 (0.41)	G190A	2 (0.16)	I84V	1 (0.08)		
K219ENQ	6 (0.49)	G190S	5 (0.41)				
		H221Y	2 (0.16)				
		P225H	2 (0.16)				
		F227L	1 (0.08)				
		M230L	4 (0.33)				
		L234I	2 (0.16)				
		K238T	3 (0.24)				
		P236L	1 (0.08)				

DRMs: Drug resistance mutations; NRTIs: Nucleoside reverse transcriptase inhibitors; NNRTIs: Non-nucleoside reverse transcriptase inhibitors; PIs: Protease inhibitors; INSTIs: Integrase strand transfer inhibitors.

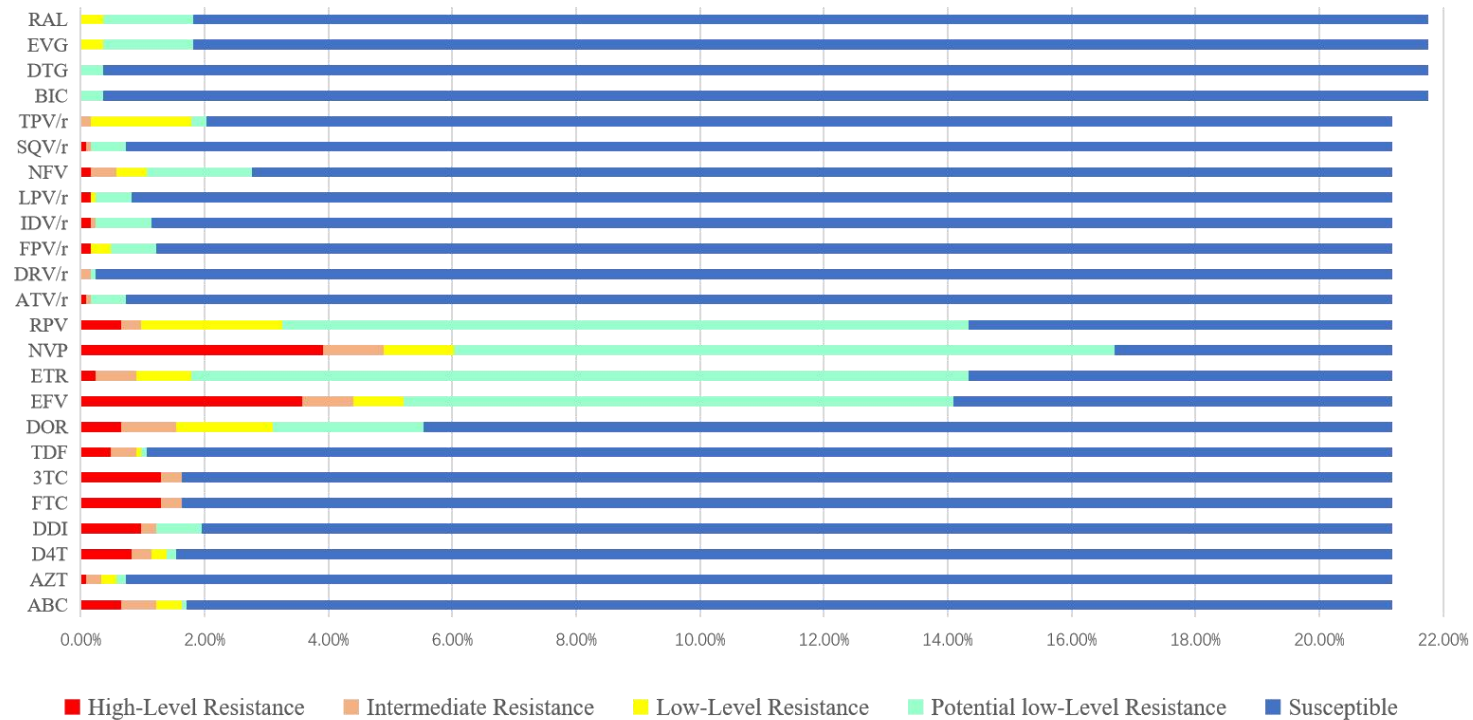
**Supplementary Table 4. Distribution of transmission routes stratified by age among patients newly diagnosed with HIV-1: Henan, 2018–2021.**

<b>Age group</b>	<b>Transmission category</b>	
<20 ( <i>n</i> = 31)	HSX	7 (22.58)
	MSM	14 (45.16)
	PL	1 (3.23)
	OTH	9 (29.03)
20–29 ( <i>n</i> = 351)	HSX	126 (35.90)
	MSM	125 (35.61)
	OTH	100 (28.49)
30–39 ( <i>n</i> = 346)	HSX	95 (27.46)
	MSM	161 (46.53)
	IDU	1 (0.29)
	PL	4 (1.16)
	OTH	86 (24.86)
	HSX	52 (22.03)
40–49 ( <i>n</i> = 236)	MSM	80 (33.90)
	PL	2 (0.85)
	OTH	102 (43.22)
	HSX	53 (20.08)
≥50 ( <i>n</i> = 264)	MSM	73 (27.65)
	PL	10 (3.79)
	OTH	128 (48.48)

HSX: Heterosexual orientation; MSM: Men who have sex with men; MTCT: Mother-to-child transmission; PL: Plasmapheresis; IDU: Injection drug use; OTH: Others: Including patients whose risk factors were unknown or patients who did not provide information.



**Supplementary Figure 1.** Phylogenetic tree based on pol sequence was constructed using Molecular Evolutionary Genetic Analysis (MEGA) software (version X) based on Maximum Likelihood method and General Time Reversible model with 1000 bootstrap replicates. Different subtypes are shown in different colors.



**Supplementary Figure 2.** Predicted resistance to antiretroviral drugs among HIV-1 nucleotide sequences with transmitted drug-resistance-associated mutation: Henan, 2018–2021. ABC: Abacavir; AZT: Zidovudine; D4T: Stavudine; DDI: Didanosine; FTC: Emtricitabine; 3TC: Lamivudine; TDF: Tenofovir; DOR: Doravirine; EFV: Efavirenz; ETR: Etravirine ; NVP: Nevirapine; RPV: Rilpivirine; ATV/r: Atazanavir/r; DRV/r: Darunavir/r; FPV/r: Fosamprenavir/r; LPV/r: Lopinavir/r; NFV: Nelfinavir; SQV/r: Saquinavir/r; TPV/r: Tipranavir/r; BIC: Bictegravir; DTG: Dolutegravir; EVG: Elvitegravir; RAL: Raltegravir.