

***Epidemiology and Infection***

**The characteristics of pretreatment HIV-1 drug resistance in Western Yunnan, China**

M. Chen<sup>1,\*</sup>, Q. M. Zhu<sup>2,\*</sup>, H. Xing<sup>3,\*</sup>, H. C. Chen<sup>1</sup>, X. M. Jin<sup>1</sup>, L. J. Dong<sup>1</sup>, J. Dai<sup>1</sup>, M. Yang<sup>1</sup>, C. Y. Yang<sup>2</sup>, M. H. Jia<sup>1</sup>, Y. L. Ma<sup>1</sup>

1. Institute for AIDS/STD Control and Prevention, Yunnan Center for Disease Control and Prevention, Kunming, Yunnan, China
2. Division for AIDS/STD Control and Prevention, Lincang Center for Disease Control and Prevention, Lincang, Yunnan, China
3. National Center for AIDS/STD Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China

**SUPPLEMENTARY MATERIAL**

Supplemental Table S1. The distribution of subjects successfully genotyped.

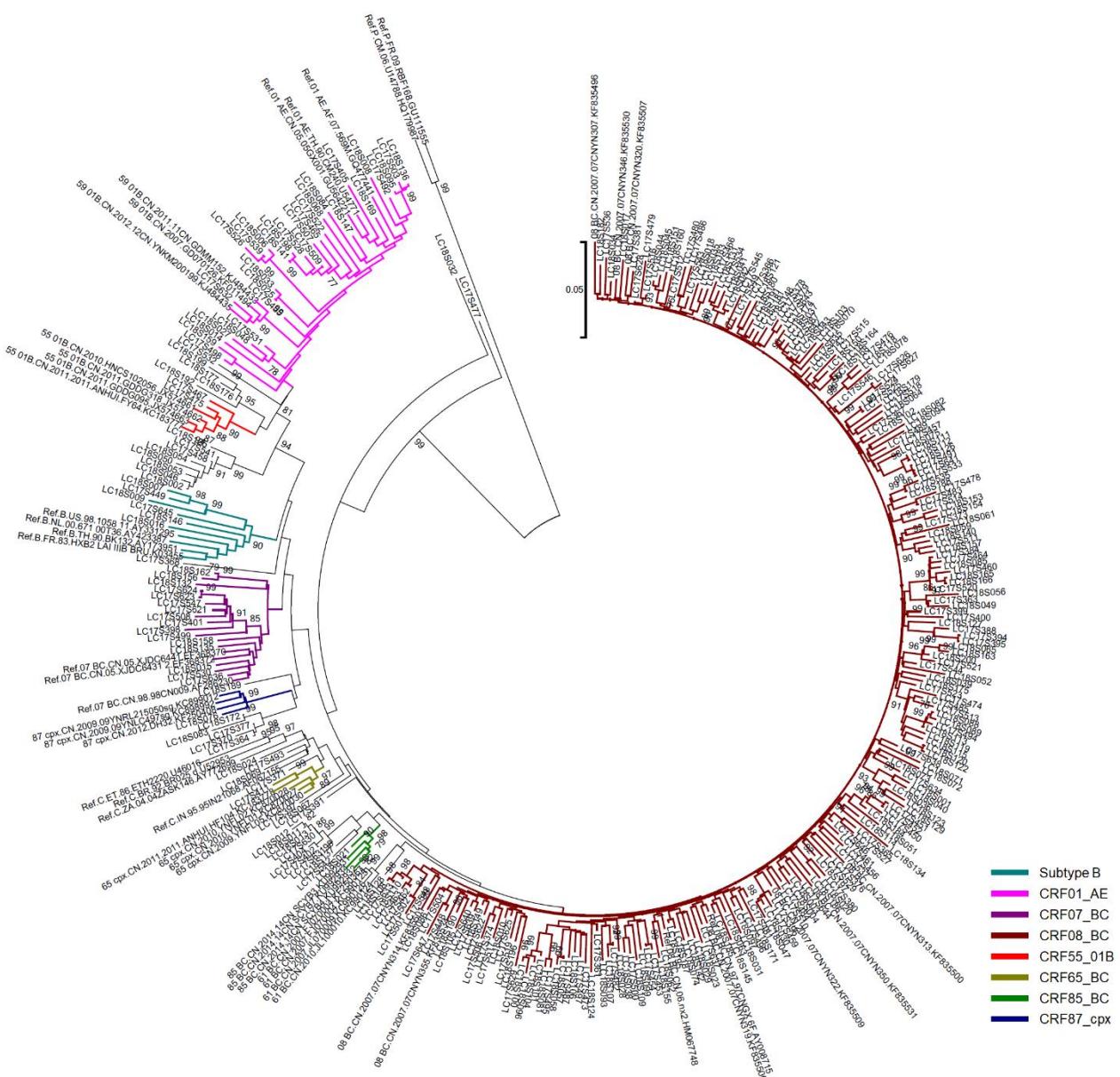
	Subjects with pol sequence	<i>P</i>
Total	372	322
Gender		0.640
Male	223	199
Female	149	123
Age		0.482
≤40	234	194
≥41	138	128
Race/ethnicity		0.878
Han	210	184
Others	162	138
Marital Status		0.900
Unmarried	99	83
Married	205	176
Divorced/Widowed	68	63
CD4		0.930
<200	104	94
200-349	133	119
350-499	69	56
≥500	66	53
Infection Routes		0.988
Heterosexual contact	347	302
Intravenous drug injection	17	13
Homosexual contact	3	3
Unknown	5	4

Supplemental Table S2. The DRMs detected in the sequences with HIV-1 drug resistance.

Sequences	DR	NRTI		NNRTI		PI	
		DRM	DR level	DRM	DR level	DRM	DR level
LC17S371	Yes	-	S	H221HY	L	I50IV	I
LC17S374	Yes	T69D	I	E138EG,V179D	L	-	S
LC17S411	Yes	K65KR	H	V179D	P	-	S
LC17S448	Yes	K65KR	H	Y188YC	H	-	S
LC17S450	Yes	-	S	Y188YF	H	-	S
LC17S465	Yes	-	S	K101E	I	-	S
LC17S467	Yes	-	S	E138EG,V179E	L	-	S
LC17S473	Yes	K65KR,D67DN	H	E138A	S	-	S
LC17S476	Yes	D67DN	L	-	S	-	S
LC17S500	Yes	-	S	V179DE,G190A	H	-	S
LC17S503	Yes	-	S	H221HY	L	-	S
LC17S514	Yes	-	S	E138A,P225H	I	-	S
LC17S626	Yes	-	S	-	S	I47IV	L
LC17S643	Yes	K65KR	H	-	S	-	S
LC18S029	Yes	-	S	K103KN,E138EG	H	-	S
LC18S031	Yes	-	S	K101E,E138A	I	-	S
LC18S072	Yes	M41L	L	-	S	-	S
LC18S078	Yes	-	S	K103N	H	-	S
LC18S081	Yes	K65KR	H	E138A	S	-	S
LC18S096	Yes	-	S	K101E,E138A	I	-	S
LC18S134	Yes	T215D	L	V106I,V179E,Y188L,H221Y	H	K20T	S
LC18S153	Yes	-	S	P225H	I	-	S
LC18S154	Yes	-	S	P225H	I	-	S
LC18S191	Yes	M41L	L	-	S	-	S

S: susceptible; P: potential low-level resistance; L: low-level resistance; I: intermediate resistance; H: high-level resistance

high-level resistance



**Supplementary Figure S1. Neighbor-joining phylogenetic tree of the partial *pol* gene.** The scale bar indicates 5% nucleotide sequence divergence. Values on the branches represent the percentage of 1000 bootstrap replicates.