File 6. Tree reconstructions and topology tests for *gag*, *pol* and *env* data sets including the DRC lineage.

Fig. A6. HIV-1 Maximum likelihood trees for the structural genes *gag*, *pol* and *env*. The numbers at the nodes represent the bootstrap support percentages based on 100 replicates. The DRC sequences are indicated with a rectangle.

Table A6. *p*-values for one-sided Kishino-Hasegawa test, the Shimodaira-Hasegawa test and the approximately unbiased test.

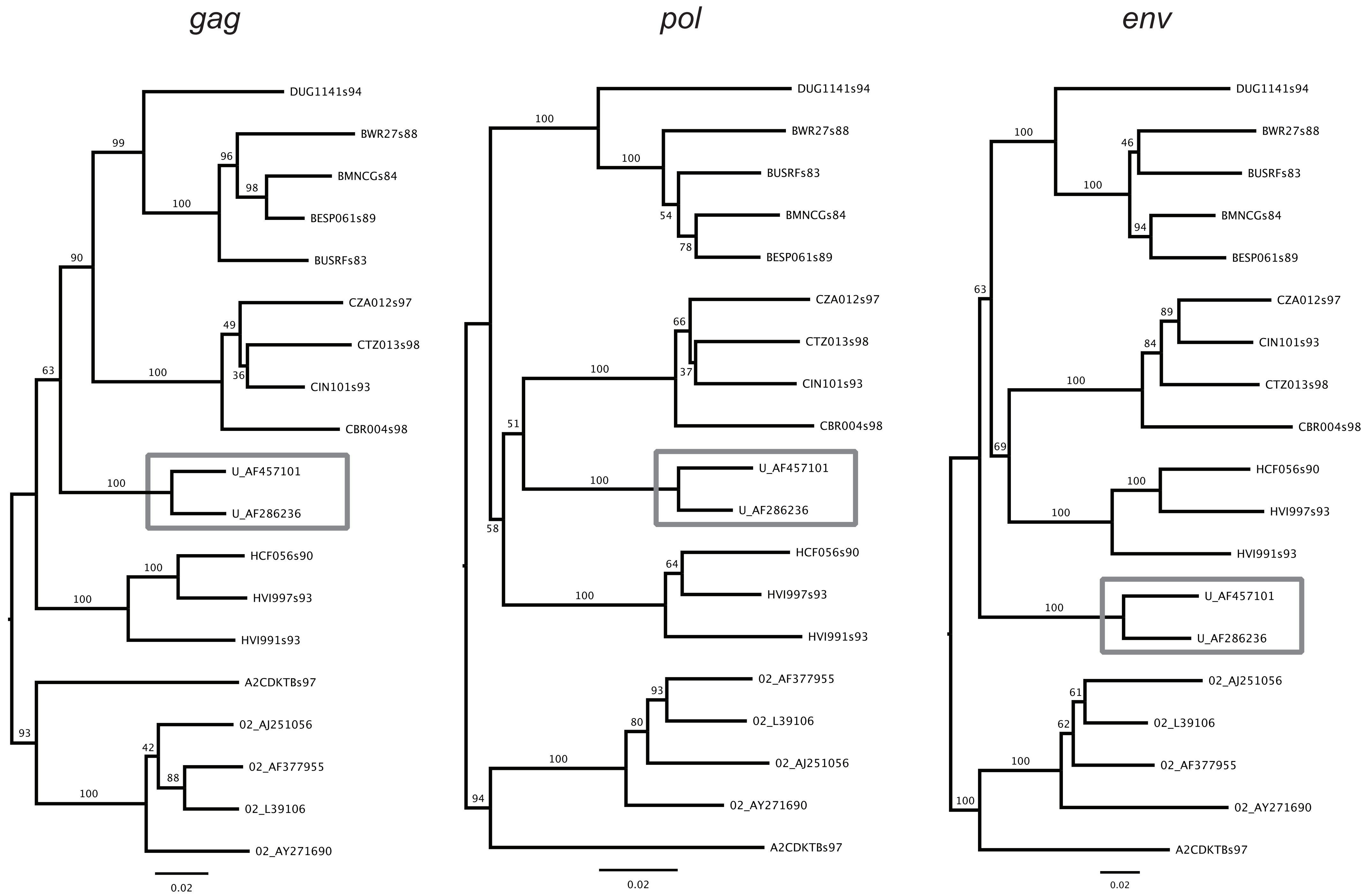
gag
DUG1141s94
BWR27s88
BMNCGs84
BESP061s89
BUSRFs83
CZA012s97
CTZ013s98
CIN101s93
CBR004s98
U_AF457101
U_AF286236
HCF056s90
HVI997s93
HVI991s93
A2CDKTBs97
02_AJ251056
02_AF377955
02_L39106
02_AY271690
99
96
98
100
90
49
36
100
63
100
100
100
93
42
88
100
0.02
pol
DUG1141s94
BWR27s88
BUSRFs83
BMNCGs84
BESP061s89
CZA012s97
CTZ013s98
CIN101s93
CBR004s98
U_AF457101
U_AF286236
HCF056s90
HVI997s93
HVI991s93
02_AF377955
02_L39106
02_AJ251056
02_AY271690
A2CDKTBs97
100
100
54
78
66
37
100
51
100
58
64
100
93
80
100
94
0.02
env
DUG1141s94
BWR27s88
BUSRFs83
BMNCGs84
BESP061s89
CZA012s97
CIN101s93
CTZ013s98
CBR004s98
HCF056s90
HVI997s93
HVI991s93
U_AF457101
U_AF286236
02_AJ251056
02_L39106
02_AF377955
02_AY271690
A2CDKTBs97
100
46
100
94
63
89
84
100
69
100
100
100
61
62
100
100
0.02

Table A6. *p*-values for tree incongruence tests

	Data								
	gag			pol			env		
Tree	KH	SH	AU	KH	SH	AU	KH	SH	AU
gag	(Best ML tree)			0.208	0.329	0.228	0.025*	0.026*	0.035*
pol	0.006**	0.008**	0.002**	(Best ML tree)			0.032*	0.021*	0.027*
env	0.035*	0.039*	0.048*	0.026*	0.030*	0.017*	(Best ML tree)		

KH, one-sided Kishino-Hasegawa test; SH, Shimodaira-Hasegawa test; AU, approximately unbiased test. * significant at the 0.05 level; ** significant at the 0.01 level