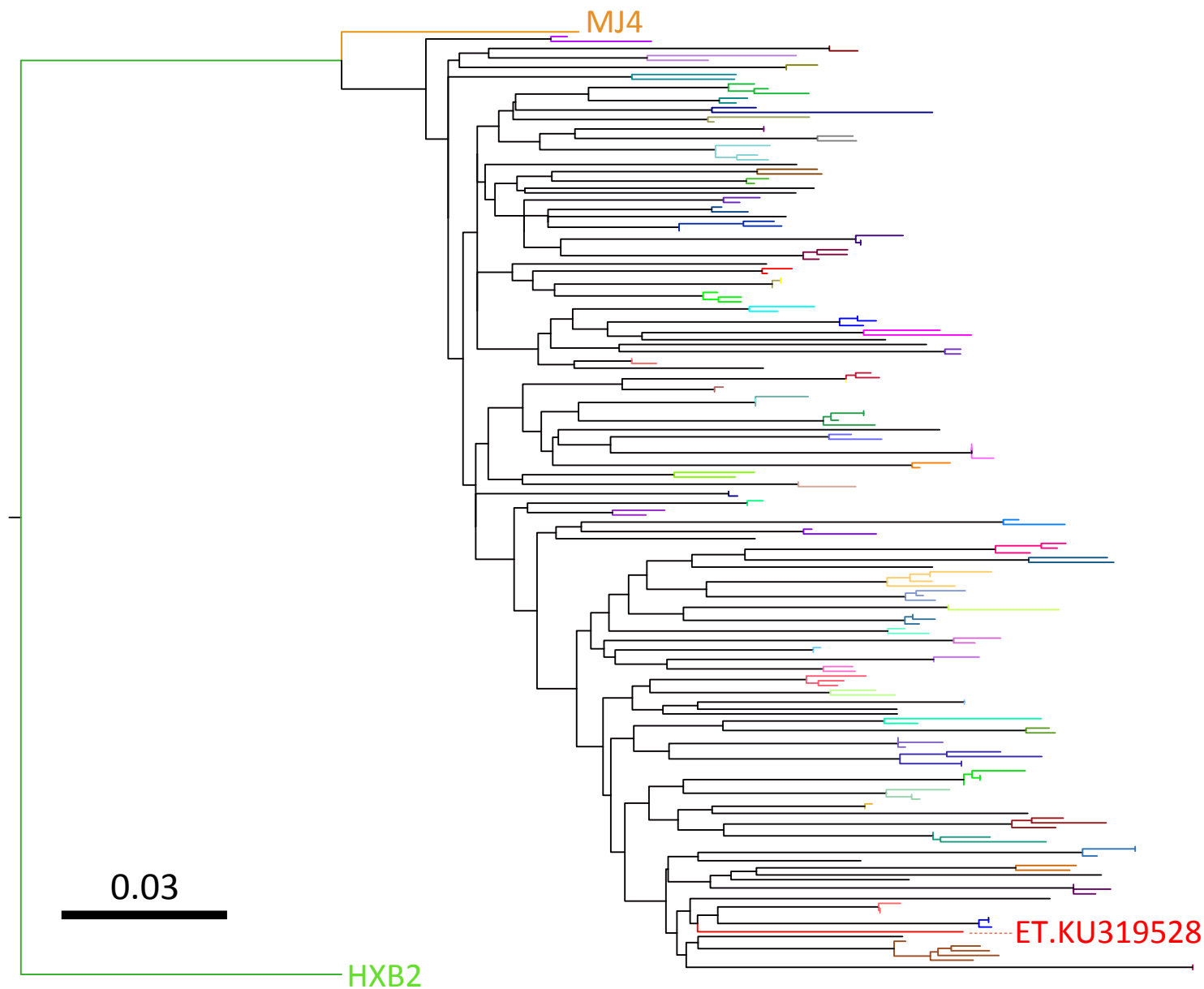


Supplemental Table 1. Primers used for HIV-1 Protease and Reverse Transcriptase amplification

Primer Set		First Round		Second Round	
		HXB2 coordinates (start/end)	Sequence (5'→3')	HXB2 coordinates (start/end)	Sequence (5'→3')
Set 1*	F	1979/2005	AAGAAGGGCACMTAGCCARAAAYTGYA	2011/2039	CCTAGGAAAAARGGCTGTTGGAARTGTGG
	R	3333/3301	CCACTAACTTCTGTATGTCATTGACAGTCCAGC	3280/3255	ATAGGCTGTACTGTCCATTTATCAGG
Set 2	F	2008/2031	GCCCCTAGGAAAAAGGGCTGTTGG	2011/2039	CCTAGGAAAAARGGCTGTTGGAARTGTGG
	R	3361/3342	TAAATCTGACTTGCCART	3323/3303	CTGTATRTCATTRACWGTCCA
Set 3	F	1979/2005	AAGAAGGGCACMTAGCCARAAAYTGYA	2011/2039	CCTAGGAAAAARGGCTGTTGGAARTGTGG
	R	3859/3831	GCTCCTACTATGGGTTCTTTYTCYARYTG	3798/3777	CAAACCCCAYTCAGGRATCCA
Set 4	F	1992/2015	AGCCAGAAATTGCAGGGCCCCTAG	2074/2095	AGACAGGCTAATTTTTTAGGGA
	R	3322/3303	TGTATRTCATTGACAGTCCA	3271/3252	ACTGTCCATTTRTCAGGATG

* primary primer set



Supplemental Figure 1. Maximum-likelihood phylogenetic tree of all intact, non-hypermutated sequences isolated from EPHIC participants experiencing virologic failure of first-line cART. Scale indicates substitutions per nucleotide site. Drug resistance codons were removed from the alignment prior to phylogenetic inference [48]. Reference strains HXB2 (subtype B, green), MJ4 (subtype C- Botswana, orange) and KU319528 (subtype C- Ethiopia, red) are included. In all cases, replicate sequences from the same participant cluster together.