

Supplementary Material

Table S1: HTLV-1 and HTLV-2 nucleotide sequences deposited in GenBank and used as references in this study.

Access number	Types and subgroups	Isolate	Geographic origin
DQ070891	1aA	SNT43	Brazil
KY928524	1aA	BRSP71066-15	Brazil
DQ005547	1aA	FNN100	Brazil
DQ005550	1aA	FNN153	Brazil
Y16475	1aA	Qu1_Peru	Peru
Y16479	1aA	Me2_Peru	Peru
AY818430	1aA	2472LE	Cameroon
D23694	1aA	Ainu	Japan
KY928524	1aA	CA423	Brazil
KY928525	1aA	BRSP87092-14	Brazil
EU108722	1aA	CA253	Brazil
EU108721	1aA	CA422	Brazil
U53074	1aB	TA6	Taiwan
U53075	1aB	TA7	Taiwan
LC210070	1aB	JPNBr177	Japan
J02029	1aB	ATK	Japan
M37299	1aB	H5	Japan
KJ544830	1aC	PH906	Senegal
D23693	1aC	GH78	Japan
D13784	1aC	HS35	Caribbean islands
U12804	1aD	Bo	Algeria
U12805	1aD	OD	Mauritania
DQ235698	1aD	BD89112	Senegal
AY818427	1b	1503MV	Cameroon
AY026855	1b	2656ND	Central Africa
AY818423	1b	979MO	Cameroon
AY818425	1b	1380MV	Cameroon
AY818426	1b	1443MV	Cameroon
AY818429	1b	1842LE	Cameroon
AY818432	1b	2810YI	Cameroon
AY818433	1b	1127MO	Cameroon
AY818424	1b	1259NG	Cameroon

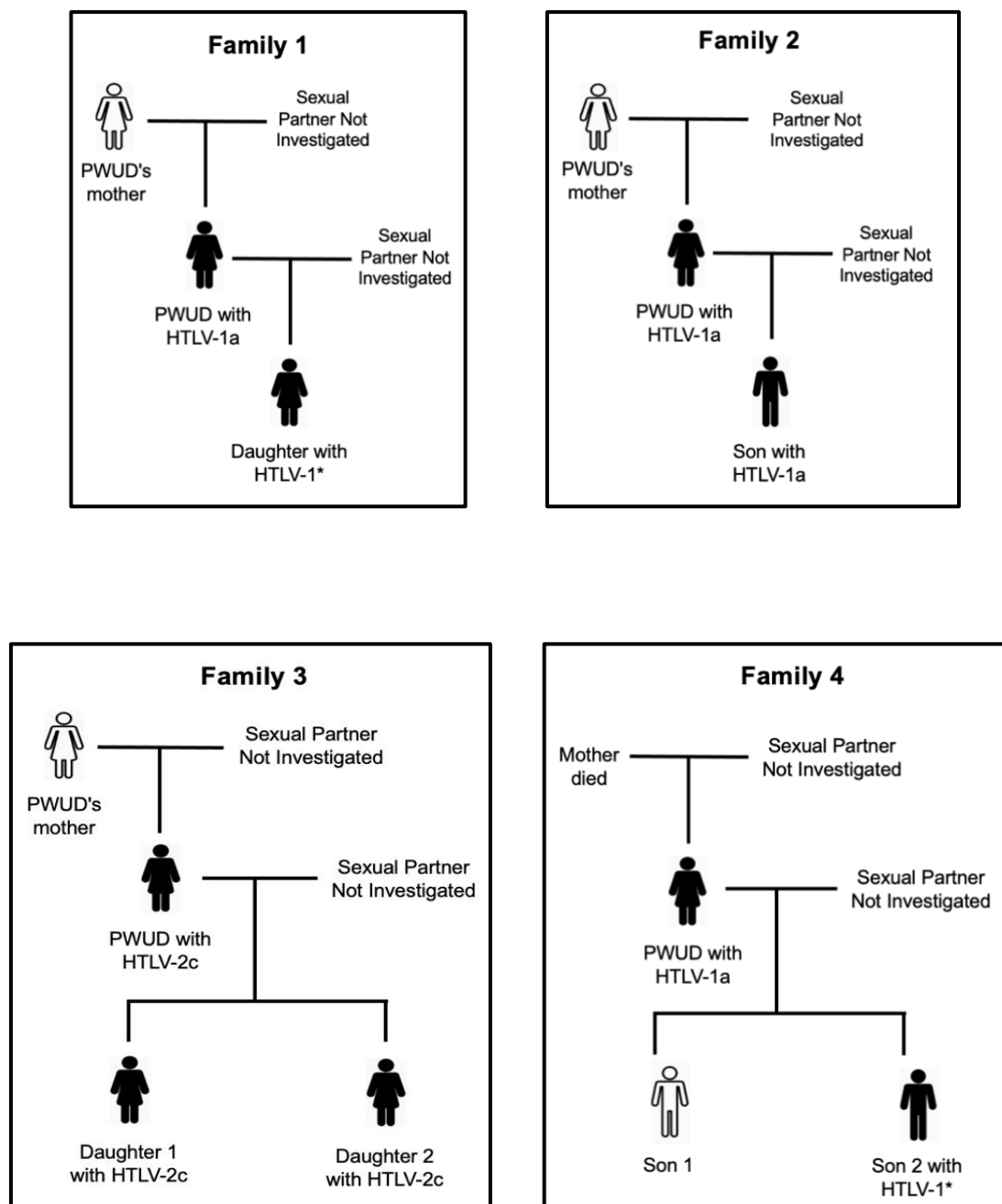
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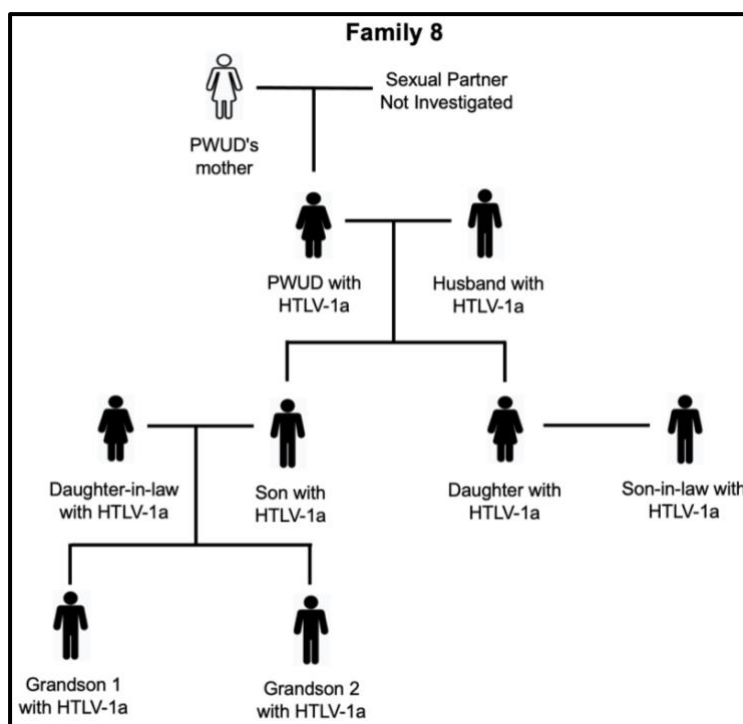
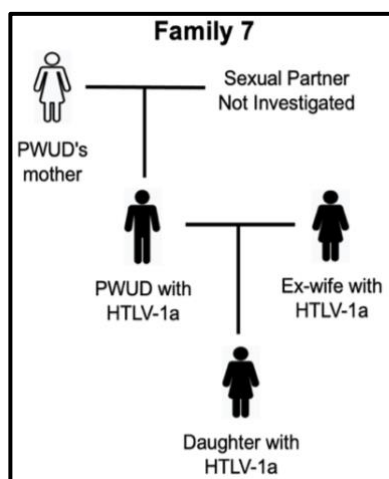
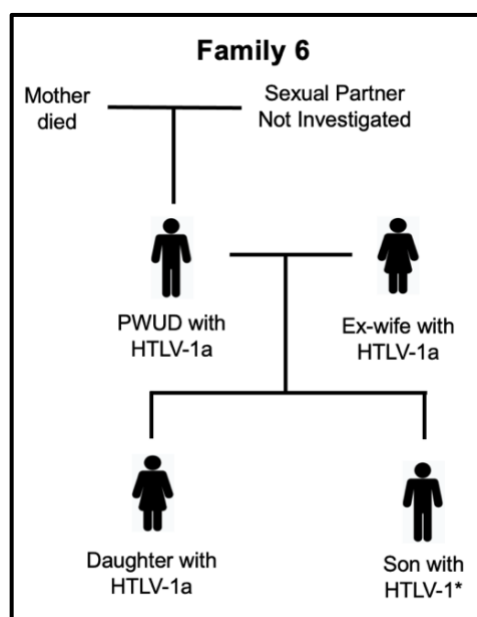
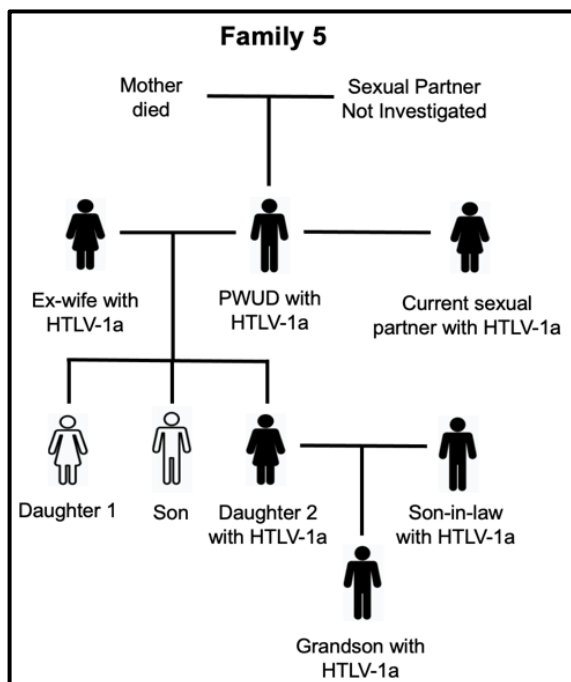
Y17016	1b	Lib1	Gabon
Y17017	1b	Lib2	Gabon
L76307	1b	PH236	Gabon
L76306	1b	SDen	Gabon
Z32527	1b	ITIS	Congo/Zaire
L76312	1b	H23	Cameroon
L02534	1c	Me15	Melanesia
L76310	1d	PYG19	Central African Republic
Y17014	1e	Efe1	Congo/Zaire
U10258	2a	NOR2N	Norway
JN247462	2a	LA8A	Indonesia
JN247456	2a	09IDSKAH-1-2	Indonesia
JN247461	2a	PUEB_2	Indonesia
Y14365	2d	Pygmy2	Congo/Zaire
U10266	2b	SPAN130	Spain
U10254	2b	ITA47A	Italy
AY442388	2b	SP25	Spain
L77237	2b	DP	Southern Europe
L77242	2b	130	Southern Europe
L77240	2b	JL	Southern Europe
L77243	2b	324	Southern Europe
L77244	2b	RVP	Southern Europe
L77239	2b	JA	Southern Europe
L77241	2b	JAN	Southern Europe
AY622979	2b	PortVs	Portugal
AY509602	2c	BH339	Brazil
MH194240	2c	BrPa_Kat116	Brazil
MH194234	2c	BrPa_Dju214	Brazil
U10253	2c	BRAZ.A21	Brazil
L42509	2c	KAY73	Brazil
AF306730	2c	TYR8680	Brazil
AF306728	2c	GTY9274	Brazil
AF306734	2c	BBD4410	Brazil
KX198746	2c	PI46	Brazil
AF306724	2c	Bel3948	Brazil
AY920499	2c	Bel-11935	Brazil
AY920500	2c	Bel-11507	Brazil
GU573734	2c	Bel-10562	Brazil
KY928552	2c	BRSP96617-14	Brazil
KY928551	2c	BRSP92116-1	Brazil
AF306726	2c	BEL9083	Brazil

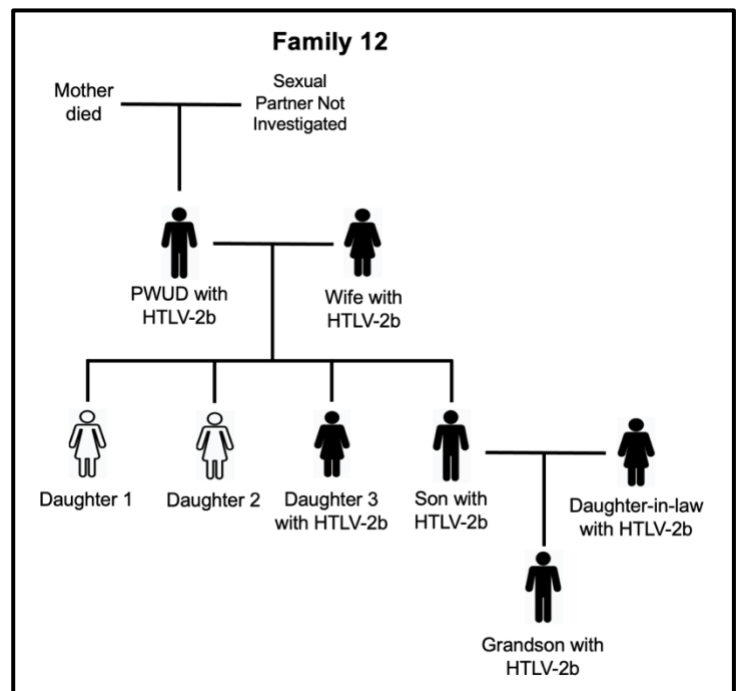
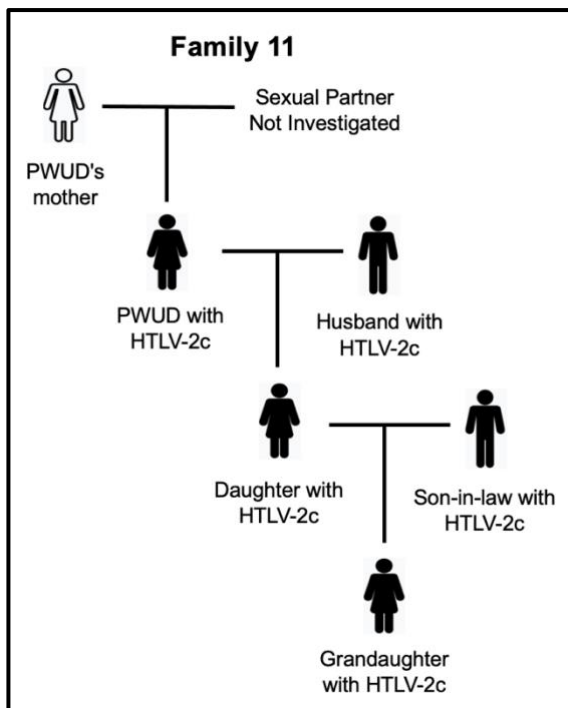
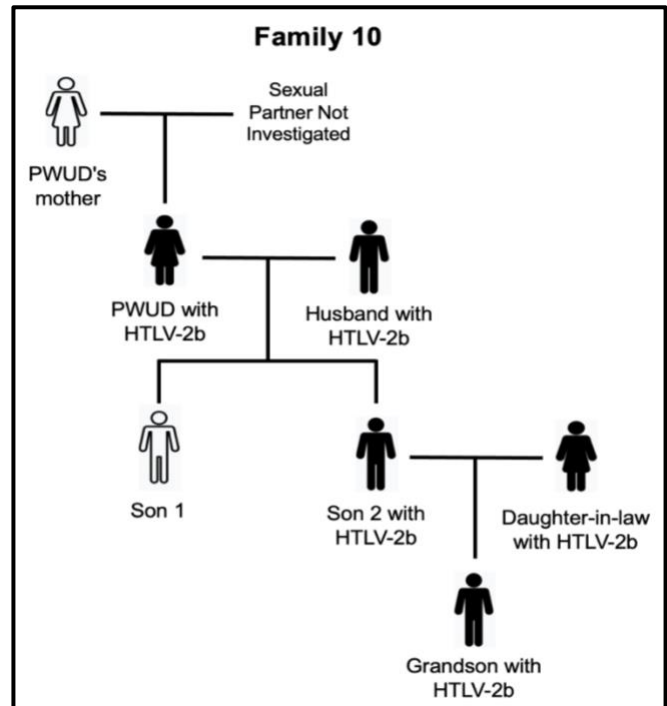
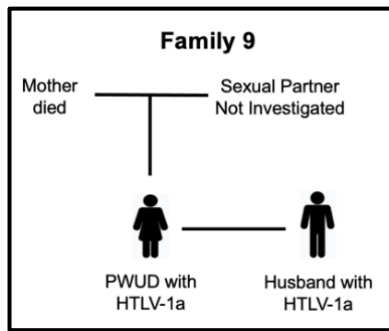
Table S2: Evolutionary models and other information used to reconstruct phylogenetic trees and identify HTLV-1 and HTLV-2 subtypes and subgroups in this study.

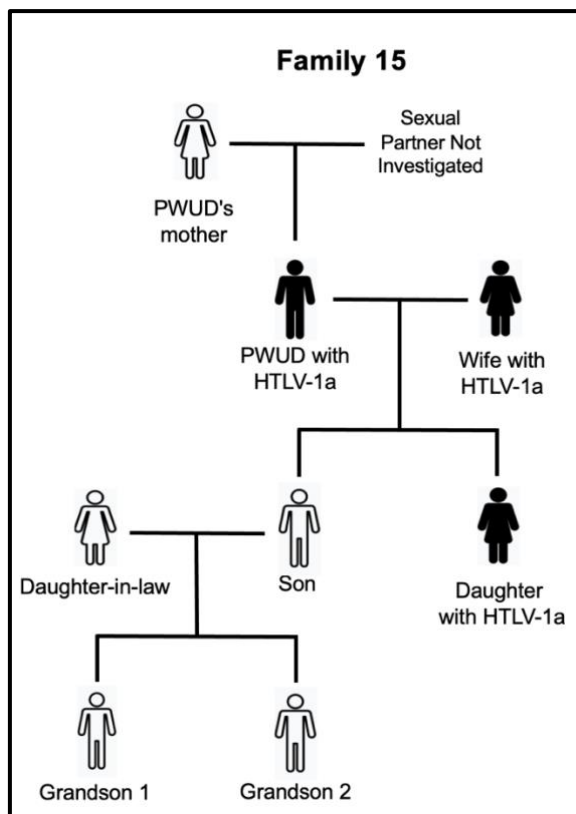
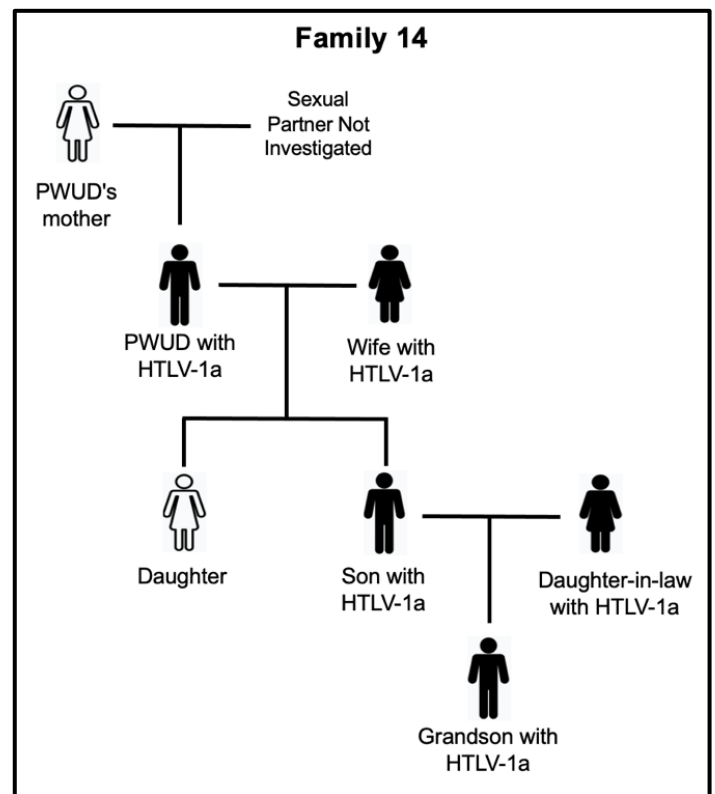
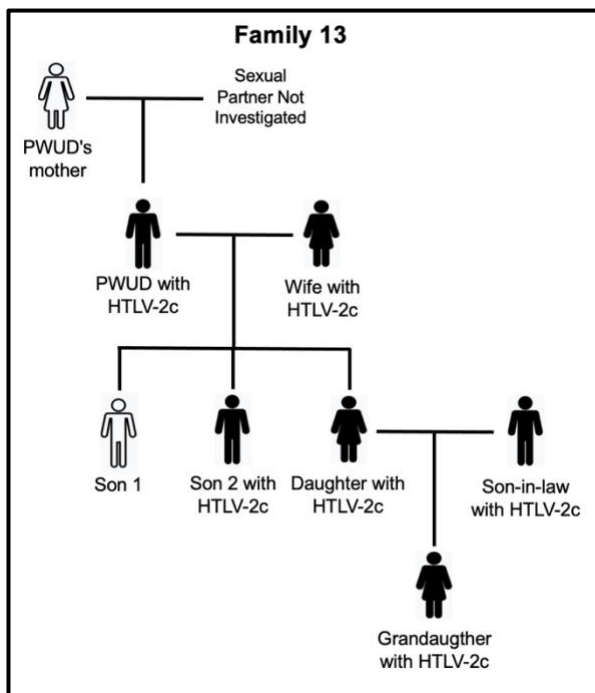
HTLV-1:	
Model of nucleotides substitution	HKY85
Log-likelihood	-1429.86578
Discrete gamma model	Yes
Gamma shape parameter	0.149
Transition/transversion ratio	10.906310
HTLV-2:	
Model of nucleotides substitution	GTR
Log-likelihood	-1176.16034
Discrete gamma model	Yes
Gamma shape parameter	0.253
GTR relative rate parameters	A <-> C: 0.71638 A <-> G: 5.71992 A <-> T: 0.05875 C <-> G: 0.80443 C <-> T: 3.64217 G <-> T: 1.00000

Figure S1: Schematic representation of 15 families that have a person who used illicit drugs (PWUD) with HTLV-1/HTLV-2 infection in northern Brazil.









* Proviral DNA was not detected in this participant's sample.