

A surveillance cohort study to characterize HIV dynamics in Washington, DC

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Introduction

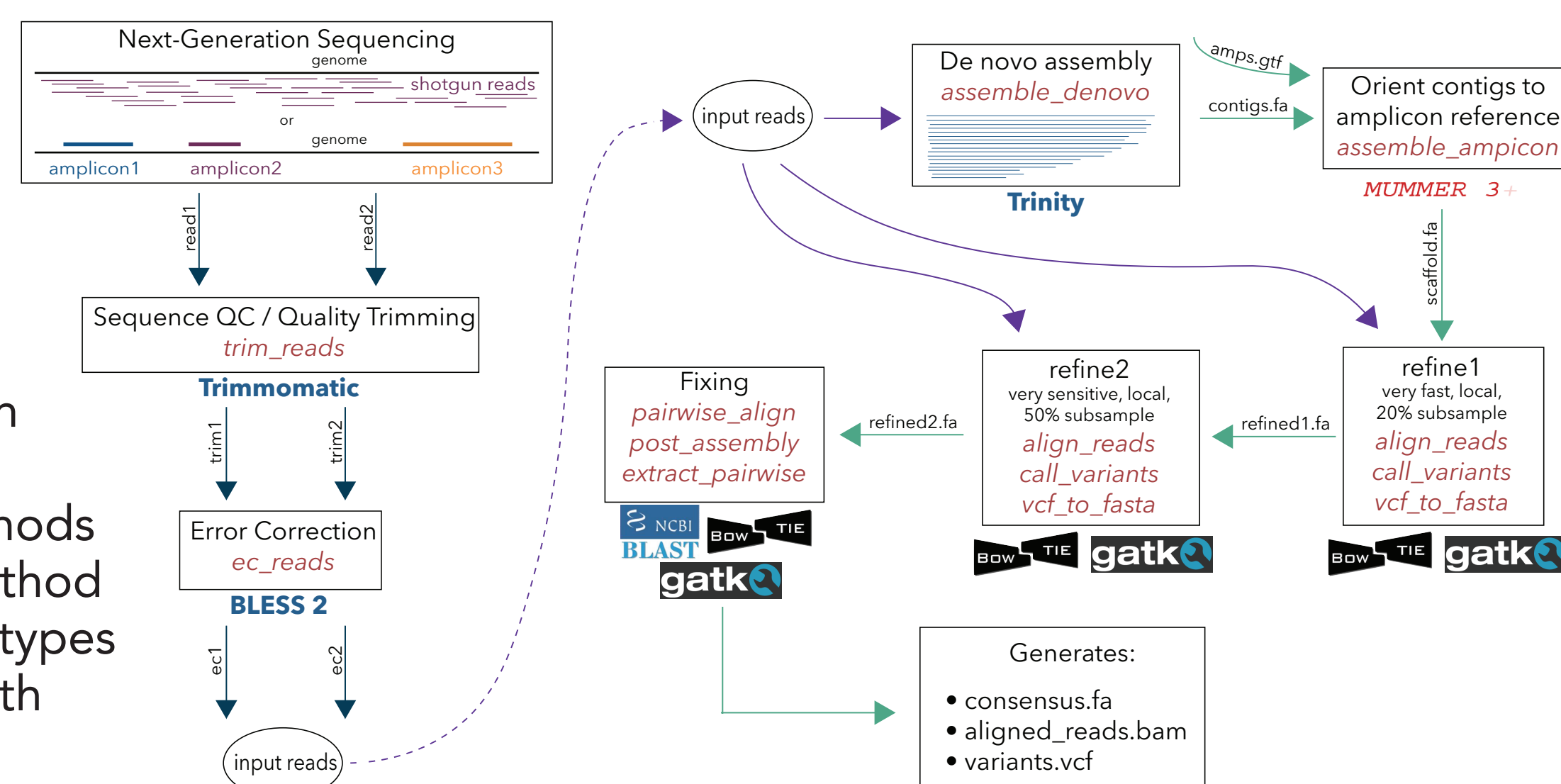
This study coupled patients clinical data with cross-sectional self-reported behavioral data and sequencing results to identify new transmissions networks occurring in the Washington, DC area with respect to demographics, high-risk groups, and geographic distribution.

- Washington, DC has one of the highest HIV prevalences in the US.
- Understanding the current dynamics will aid and provide informative data to guide programs that prevent and reduce the prevalence of HIV in DC.
- A total of 70 participants from the DC Cohort were recruited for this study in 2016 and 2017.
- Participants were comprised mostly of black males (54.3%) and individuals who reported their risk type as heterosexual (40.0%).
- All participants were subtype B.

Methods

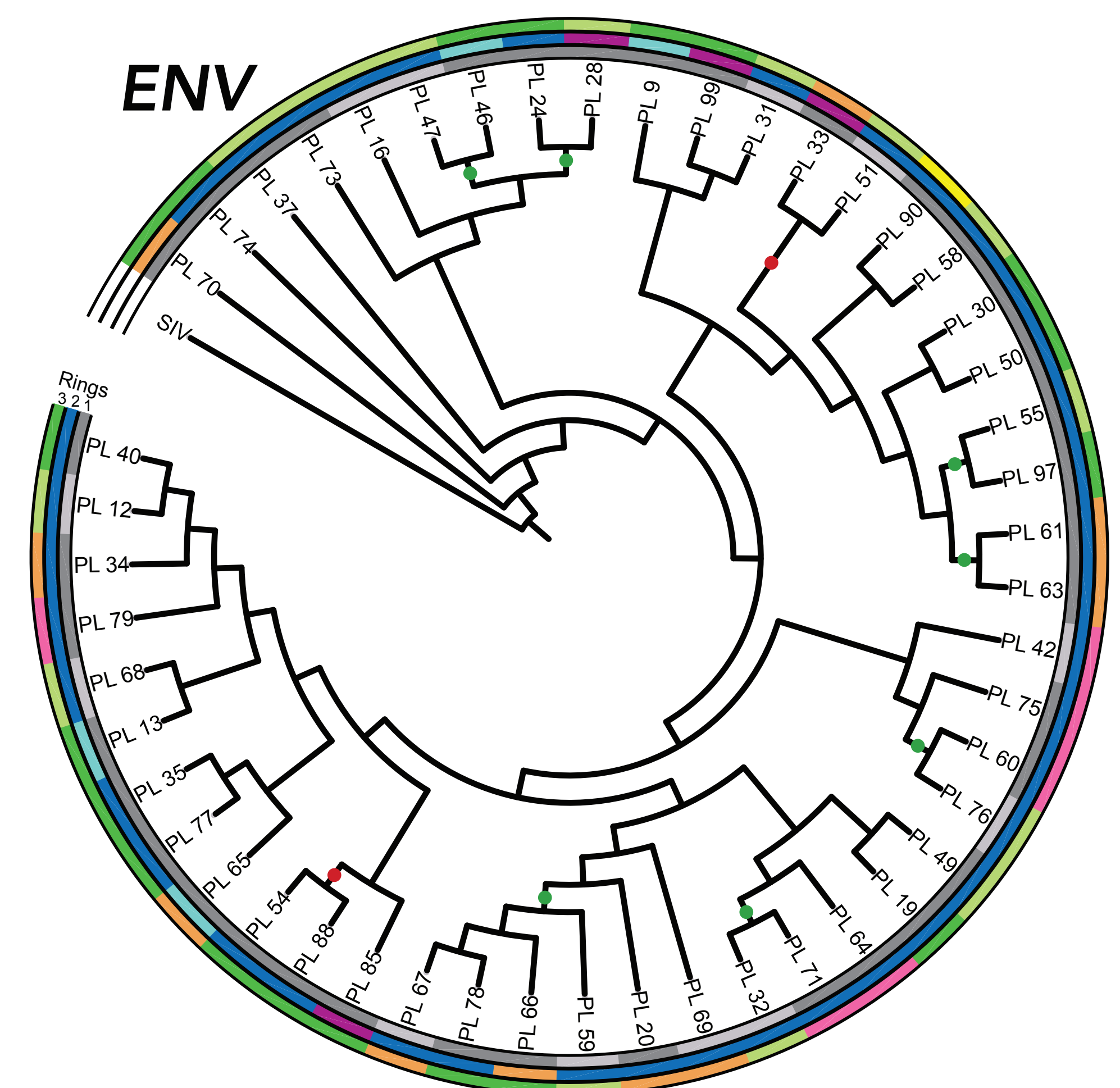
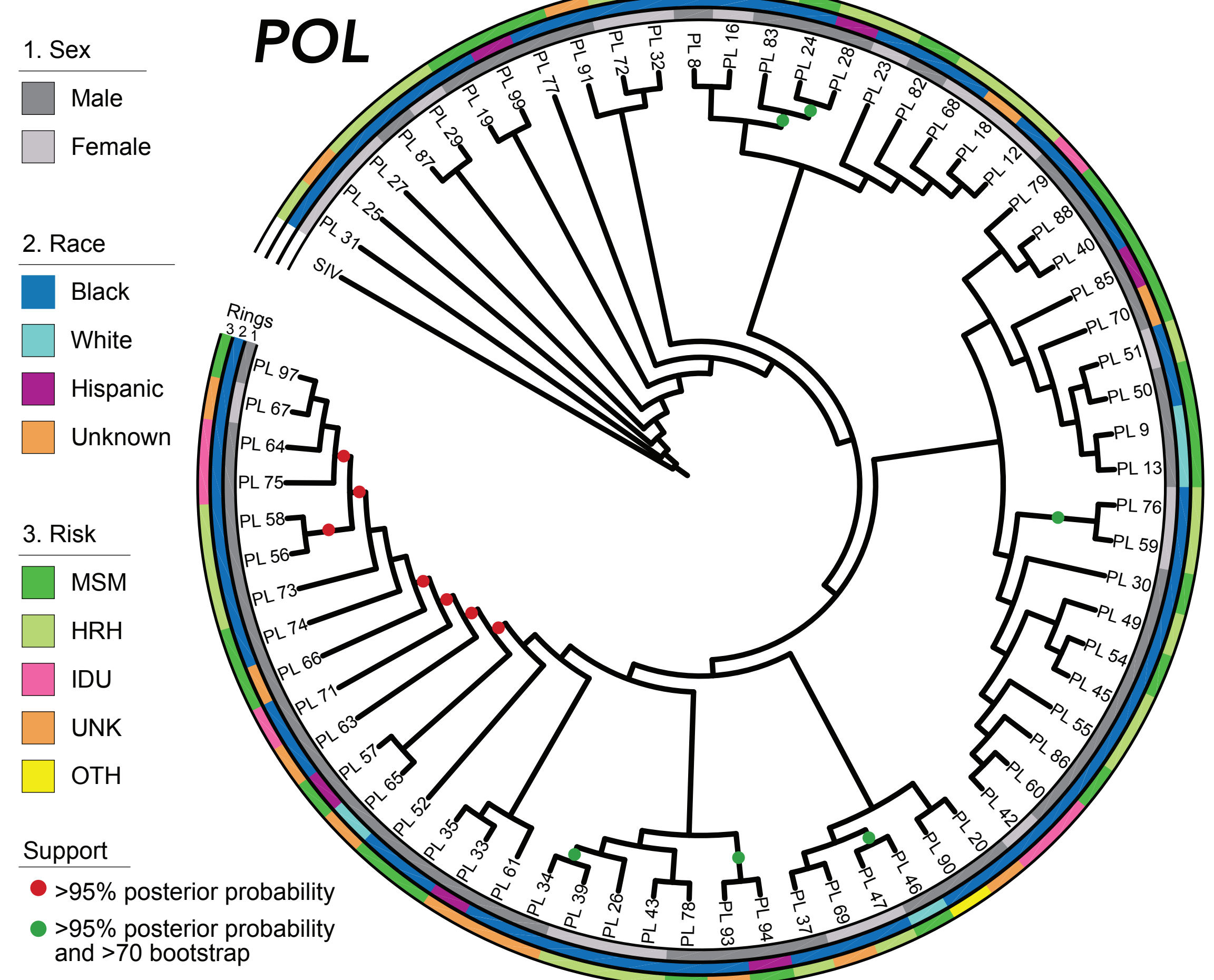
Sequence data was processed with **HAPHIPE**.

Transmission clusters were assessed with both ML and Bayesian phylogenetic methods and a network method (HIV-Trace). Haplotypes were predicted with PredictHaplo.



Phylogenetics

Cladogram of the POL and ENV concatenated genes of Washington, DC showing sex, race/ethnicities, and risk factors in rings.



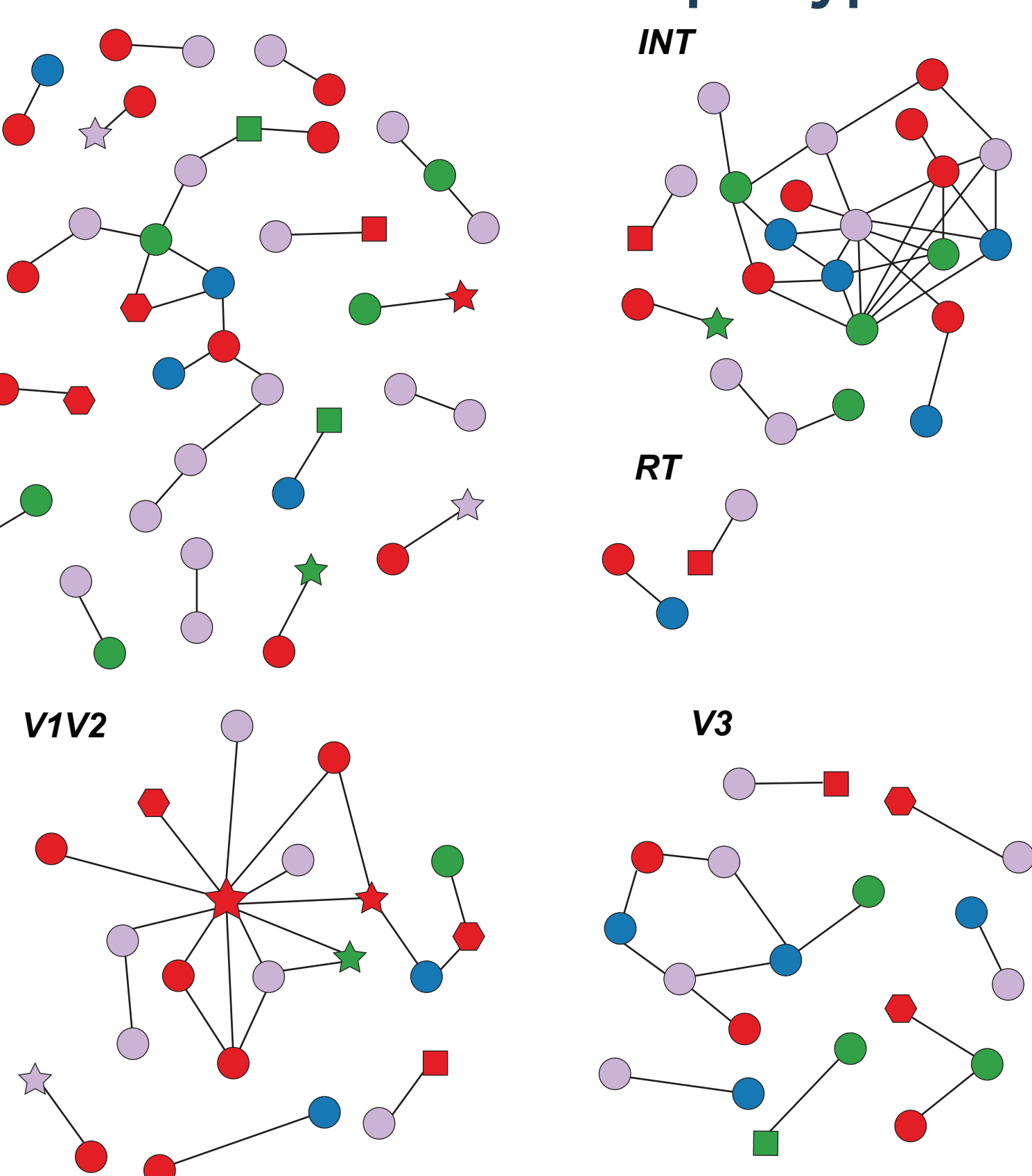
Phylogenetic methods (>70 bootstrap and >95% posterior probability) grouped 15.7% of the sequences into 5 transmission clusters in POL and 22.8% of the sequences into 7 clusters in ENV.

Transmission Clusters

Consensus Sequences

- Risk: HRH (purple), IDU (blue), MSM (red), UNK (green)
- Race/ethnicity: Black (dark grey), White (light grey), Hispanic (purple), Unknown (orange)

Reconstructed Haplotypes



- A participant can have multiple haplotypes and often a different number of haplotypes depending on the gene region.
- Using haplotypes, additional transmission networks are identified. This better captures the diversity and complexity that HIV is known for.
- If a person has multiple haplotypes for a gene, usually only one of their haplotypes is found to have a connection to someone else's. However, there may be a different connection between individuals for other genes.

Each gene tells a different transmission story.

Drug Resistance Mutations

	IN	IN	PR	PR	NRTI	NNRTI	PR SDRMs	RT SDRMs	PI TSMs	NRTI TSMs	NNRTI TSMs	DRM Codons	FUBAR Codons
	Major	Access.	Major	Access.									
PR	NA	NA	0/0/0	1/1/1	NA	NA	0/0/0	NA	0/0/0	NA	NA	1	2
RT	NA	NA	NA	NA	19/37/18	12/15/9	NA	24/44/19	NA	1/1/1	1/1/1	22	3
INT	3/6/6	9/9/3	NA	NA	NA	NA	NA	NA	NA	NA	NA	9	4

Number of sequences/total mutations/unique mutations conferring resistance to antiretroviral drugs.

- 24 sequences showed at least two different DRMs with a prevalence of 34.3%.
- No DRMs were found in ARV treatment naive participants.