## Supplementary Data

Network attribute Distance threshold	Primary analysis	Sensitivity analysis		
		1.0%	2.0%	1.5%
Drug resistance associated mutation codons	Retained	Retained	Retained	Removed
No. of U.S. sequences that clustered	13,145	8,010	17,494	12,822
% of U.S. sequences that clustered	32	19	42	31
No. of U.S. sequences that clustered internationally	457	177	1,019	449
% of U.S. sequences that clustered internationally	3.5	2.2	5.8	3.5
No. of clusters	9,814	7,406	11,027	9,070
% of foreign-born persons that linked to country of birth	35	47	35	37
Significant correlates of international linkage	Race/ethnicity, transmission category, country of birth, year of HIV diagnosis, U.S. region	Race/ethnicity, country of birth, year of HIV diagnosis, U.S. region	Race/ethnicity, country of birth, year of HIV diagnosis, U.S. region	Race/ethnicity, transmission category, country of birth year of HIV diagnosis, U.S. region

## SUPPLEMENTARY TABLE S1. SENSITIVITY OF THE U.S./INTERNATIONAL TRANSMISSION NETWORK ANALYSIS TO CLUSTERING PARAMETERS