# Supplemental Digital Content 2. Characterization of partner infections.

## A. <u>SUBTYPE SUMMARY</u>

HIV subtype was determined by phylogenetic analysis of HIV *pol* sequences generated using the ViroSeq HIV-1 Genotyping System (1,302 nucleotide consensus sequences encoding HIV protease and 335 pairs; sequencing analysis failed in six cases. In all 72 cases, the HIV subtypes of the index and partner were consistent with the prevalent subtype(s) in each country. In 70 of the 72 cases, the subtypes of the index and partner were the same. The partner infections were unlinked in the two cases where the subtypes of the index and partner samples were different.

Country	# index- partner pairs with subtyping results	Subtype(s)
US	1	В
Brazil	4	B (N=2), F (N=1) C/BC recombinant (N=1)
Thailand	2	Both CRF02_AE
India	3	All C
Malawi	41	All C
Zimbabwe	9	All C
Botswana	4	All C
Kenya	5	A1 (N=2), D (N=1), A1 index with D partner (N=1), A1
-		index with C partner (N=1)
South Africa	3	All C
TOTAL	72	

## B. RESISTANCE SUMMARY

## Linked infections:

Resistance was detected in 3/46 linked cases (all in the delayed ART arm; in these three cases, the index participant was not on ART at the time of partner diagnosis):

- Two with transmitted resistance
  - o In one case, the index and partner both had K103N
  - o In one case, the index and partner both had V179D and/or V179E
- In one case, the index had K101E in one of two samples; the partner did not have resistance mutations detected

### **Unlinked infections:**

Resistance was detected in 6/26 unlinked cases (all in the early ART arm; in these six cases, the index participant was on ART at the time of partner seroconversion):

- In four cases, resistance was detected in the index only:
  - o K103N, M184V, and Y181C
  - o K103N, V106M, M184V
  - o M184V
  - o K103N and T215S
- In two cases, resistance was detected in the partner only:
  - o K103N
  - o M184V, T215Y, V108I, Y181C