

Table S1: Comparison of transmission chains identified by Sanger and UDS

Clusters identified by Sanger	HCV sub-type	Patient	HIV co-infection	HCV reinfection	Date of 1 st positive HCV viral load or anti-HCV	UDS at 3% of maximum genetic distance	UDS at 4.5% of maximum genetic distance
1	GT3a	1	Yes	No	13/08/2015		
		2	Yes	No	18/09/2015		
		3	Yes	Yes	13/05/2015		
		4	Yes	Yes	27/04/2015		
		5	Yes	No	19/03/2015		
		6	No	No	17/05/2016		
2	GT1a	7	Yes	No	16/10/2014		
		8	No	No	04/08/2015		
3	GT1a	9	Yes	No	09/10/2015		
		10	Yes	Yes	14/08/2015		
		11	Yes	No	20/06/2014		
		12	Yes	No	15/05/2015		
		13	Yes	No	19/05/2015		
		14	No	No	18/03/2014		
4	GT1a	15	Yes	No	07/08/2014		
		16	Yes	No	02/04/2015		
		17	Yes	Yes	27/07/2015		
		18	No	No	24/04/2014		
		19	No	No	03/02/2014		

5	GT1a	20	Yes	No	23/07/2014				
		21	Yes	No	27/06/2015				
		22	No	No	15/09/2014				
6	GT1a	23	Yes	Yes	02/04/2015				
		24	Yes	No	21/09/2015				
		25	Yes	Yes	07/05/2015				
*	GT1a	26	Yes	No	27/12/2014				
*	GT4d	27	Yes	No	08/04/2015				
7	GT4d	28	Yes	Yes	29/12/2014				
		29	No	No	15/05/2015				
		30	Yes	Yes	13/04/2015				
*	GT4d	31	Yes	No	18/09/2014				
8	GT4d	32	Yes	No	12/12/2014				
		33	Yes	Yes	22/01/2016				
		34	Yes	No	16/09/2015				
		27	Yes	No	08/04/2015				
		35	No	No	06/08/2012				
*	GT4d	36	Yes	No	07/01/2016				
9	GT4d	37	Yes	No	14/03/2014				
		38	No	No	20/11/2014				
10	GT4d	39	Yes	No	04/05/2015				
		40	Yes	Yes	07/11/2014				
		41	Yes	No	25/02/2015				

The table presents ten clusters identified by Sanger sequencing and numerated from 1 to 10 (first column).

The same coloured boxes in the two last columns represent individuals involved in the same chain of transmission detected by UDS at 3% and 4.5% of maximum genetic distance (MGD).

*: Individuals additionally detected by UDS in a transmission chain.

Additional transmission chains detected by UDS at 4.5% of MGD compared to the 3% threshold are presented in grey boxes.

UDS at both thresholds of MGD did not detect the transmission chain number 5 found by Sanger sequencing.

Table S2: Hidden transmission chains additionally detected by UDS

Trans- mission chains	Sub- type	Patient	HIV co- infection	HCV re- infection	Date of 1 st positive HCV viral load or anti-HCV	UDS at 3% of maximum genetic distance	UDS at 4.5% of maximum genetic distance
1	GT4d	42	No	No	23/09/2015		
		43	Yes	No	09/01/2015		
2	GT4d	44	Yes	No	01/02/2016		
		45	No	No	05/10/2015		
3	GT1a	46	Yes	Yes	21/09/2015		
		47	Yes	No	11/06/2015		
		48	Yes	No	05/12/2014		

The same coloured boxes in the two last columns represent individuals involved in the same chain of transmission detected by UDS at 3% and 4.5% of maximum genetic distance, respectively.

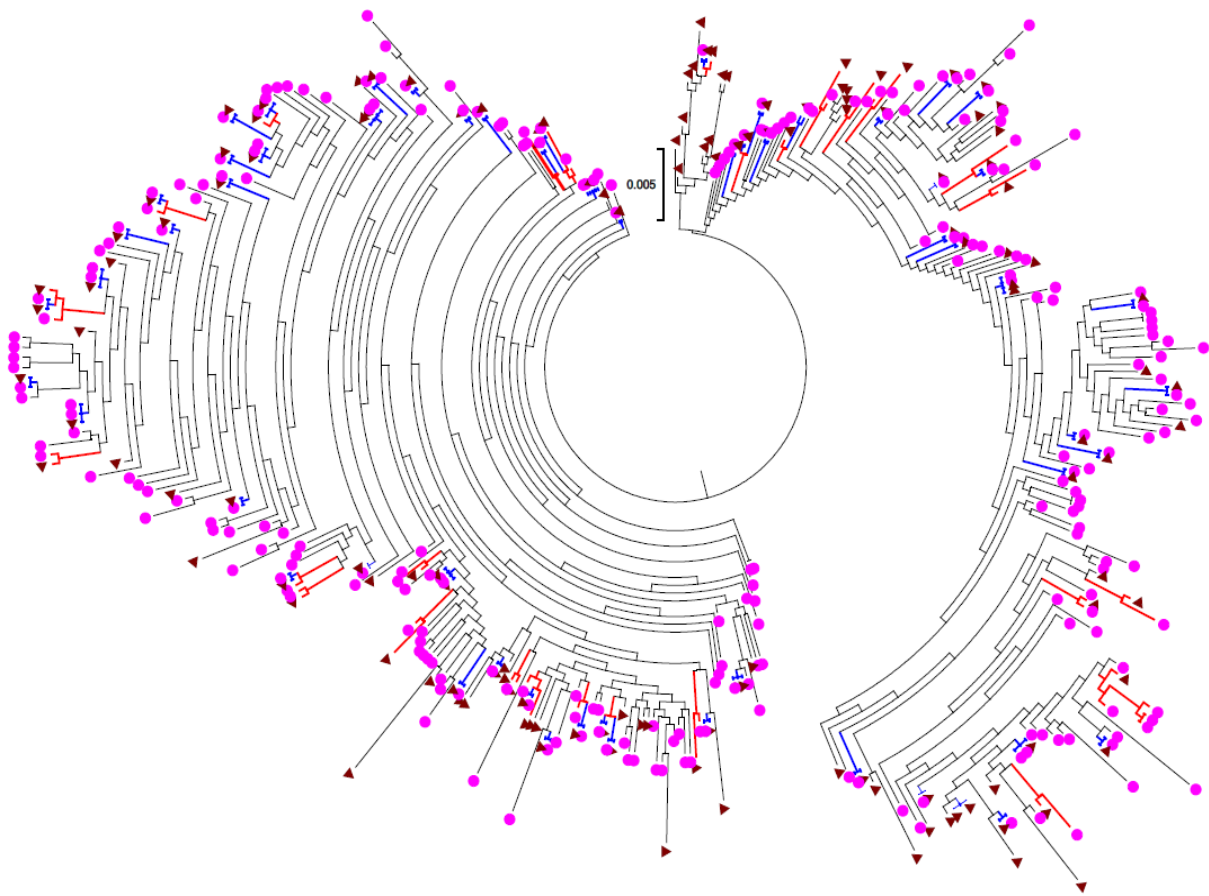


Figure S1: Phylogenetic tree constructed from UDS viral sequences of two individuals, individual 9 (pink circle) and 10 (brown triangle), which were considered as closely related transmission.

Red clades represent sequences with maximum genetic distance (MGD) < 0.5% between the 2 individuals. Blue clades represent identical sequences between the 2 individuals (MGD = 0%)

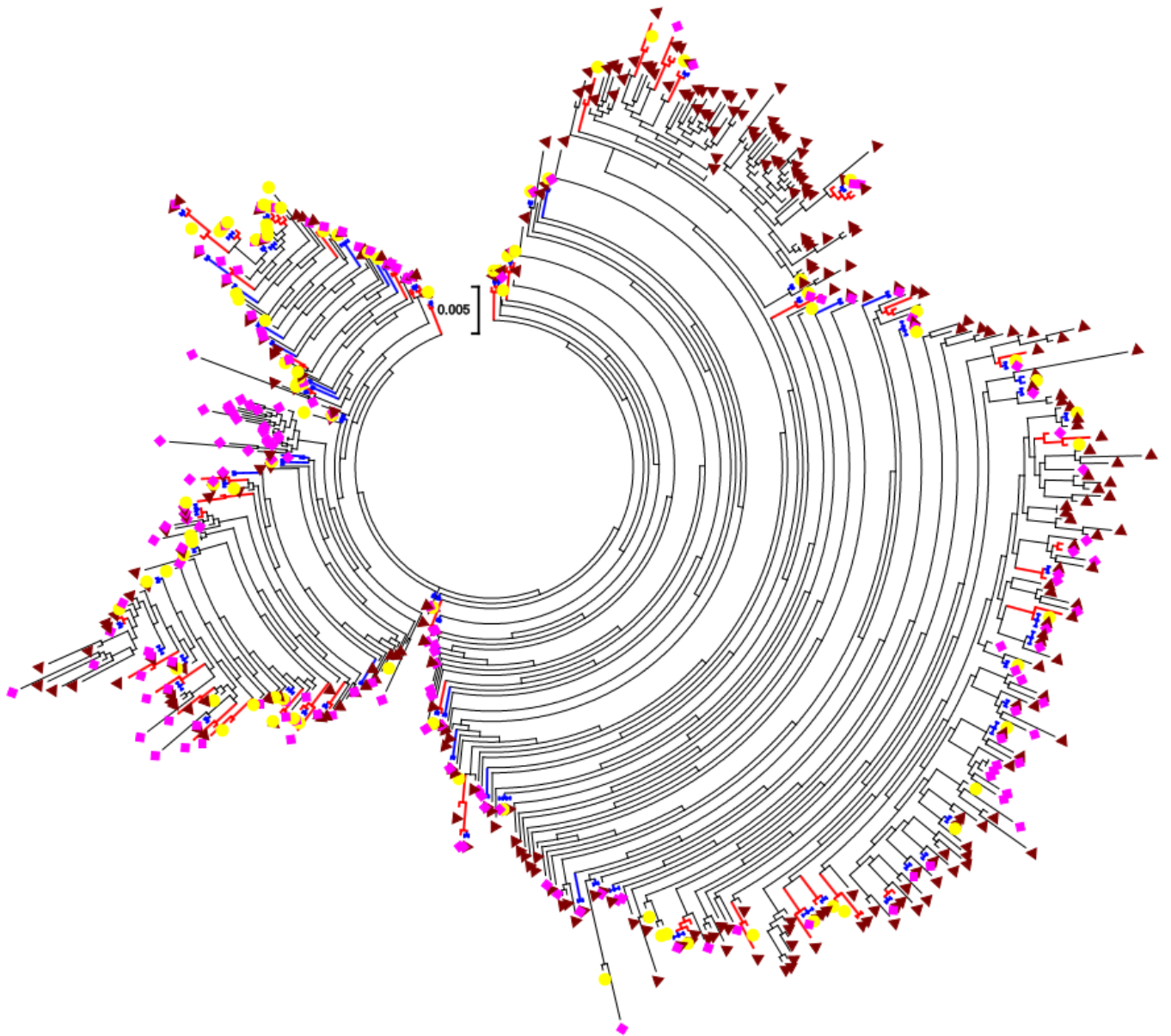


Figure S2: Phylogenetic tree constructed from three individuals, individual 27 (yellow circle), 28 (pink diamond), and 29 (brown triangle) which were considered to belong to closely related transmission events. Blue clades represent identical sequences among the three individuals. Red clades represent sequences with $MGD < 0.5\%$ among the three individuals.