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# Author Correction: A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-020-58410-y>, published online 06 February 2020

This Article contains errors in Table 3. In this Article, data values provided for Participant 16 are incorrect. The correct Table 3 appears below as Table 1.

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Participant	PR/RT		int		env		Viral Load (copies/mL)	ARV Exposure	ARV Regimen Type
	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity			
8	NA	NA	1	0	NA	NA		E	2 NRTI+1 ENH+1 INSTI
9	NA	NA	5	0.066	11	0.038	476	E	
12	1	0	4	0.727	2	0.393	77	E	2 NRTI+1 NNRTI
13	NA	NA	1	0	2	0.302		N	
16	3	0.33	1	0	3	0.415		E	
18	NA	NA	1	0	NA	NA	119149	E	
19	2	0.436	2	0.499	4	0.721	244	N	
20	2	0.479	1	0	2	0.281	5663	E	1 NRTI+1 PI+1 ENH
23	3	0.352	2	0.484	NA	NA	927	E	2 NRTI+1 ENH+1 INSTI
25	1	0	1	0	NA	NA		E	2 NRTI+1 ENH+1 INSTI
26	2	0.452	2	0.466	NA	NA		N	
27	1	0	1	0	NA	NA	11	E	1 PI+1 ENH
29	2	0.464	2	0.25	5	0.62	1	E	2 NRTI+1 ENH+1 INSTI
30	2	0.441	3	0.579	1	0	625	E	
31	3	0.64	3	0.526	2	0.312		E	2 NRTI+1 INSTI
32	2	0.146	2	0.339	2	0.498		E	2 NRTI+1 NNRTI+1 PI+1 ENH
33	1	0	3	0.563	3	0.601		E	2 NRTI+1 ENH+1 INSTI
34	2	0.429	2	0.2	1	0		E	2 NRTI+1 INSTI
35	2	0.385	1	0	3	0.446		E	2 NRTI+1 INSTI
37	2	0.274	1	0	10	0.027	81	E	
39	NA	NA	1	0	NA	NA		E	2 NRTI+1 ENH+1 INSTI
40	2	0.494	4	0.692	3	0.623		E	
42	1	0	2	0.215	2	0.445	13979	E	2 NRTI+1 ENH+1 INSTI
43	1	0	7	0.833	NA	NA	343	E	
45	1	0	10	0.704	NA	NA		E	2 NRTI+1 ENH+1 INSTI
46	2	0.153	3	0.306	2	0.5		N	
47	2	0.263	2	0.42	1	0	2755	E	1 NNRTI+1 PI+1 ENH+1 INSTI
49	2	0.455	1	0	2	0.324	282	E	2 NRTI+1 ENH+1 INSTI
50	1	0	2	0.344	3	0.624	576	E	2 NRTI+1 PI+1 ENH
51	1	0	1	0	3	0.593		E	2 NRTI+1 PI+1 ENH+1 INSTI
52	2	0.439	1	0	NA	NA		E	2 NRTI+1 PI+1 ENH
54	3	0.583	1	0	2	0.491	412	E	2 NRTI+1 PI+1 ENH
55	1	0	1	0	2	0.384		E	1 PI+1 ENH

Continued

Participant	PR/RT		int		env		Viral Load (copies/mL)	ARV Exposure	ARV Regimen Type
	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity			
56	12	0.392	3	0.641	NA	NA	1368	E	2 NRTI+1 ENH+1 INSTI
57	1	0	1	0	NA	NA	12786	E	2 NRTI+1 ENH+1 INSTI
58	1	0	3	0.59	4	0.659	1281	E	2 NRTI+1 ENH+1 INSTI
59	3	0.572	1	0	4	0.705	581	E	2 NRTI+1 INSTI
60	2	0.487	3	0.619	4	0.716		E	2 NRTI+1 PI+1 ENH
61	2	0.27	3	0.632	4	0.679	432	E	
63	3	0.612	6	0.708	1	0	57	E	2 NRTI+1 PI
64	5	0.759	3	0.576	4	0.697		E	
65	2	0.492	2	0.441	3	0.186		E	2 NRTI+1 PI+1 ENH
66	1	0	2	0.49	5	0.602	32	E	2 NRTI+1 ENH+1 INSTI
67	NA	NA	2	0.45	5	0.767		E	2 NRTI+1 NNRTI
68	3	0.564	5	0.736	5	0.758		E	2 NRTI+1 NNRTI
69	1	0	4	0.543	7	0.777	48	E	2 NRTI+1 PI+1 ENH
70	4	0.603	2	0.364	5	0.743	17	N	
71	1	0	4	0.72	6	0.812		E	1 NRTI+1 NNRTI+1 INSTI
72	2	0.209	3	0.614	NA	NA	353	E	2 NRTI+1 NNRTI
73	1	0	3	0.66	2	0.414		E	2 NRTI+1 ENH+1 INSTI
74	1	0	5	0.779	4	0.037	1	E	2 NRTI+1 ENH+1 INSTI
75	1	0	3	0.533	7	0.663		E	2 NRTI+1 PI+1 ENH
76	1	0	1	0	5	0.777	432	E	2 NRTI+1 INSTI
77	4	0.613	4	0.658	6	0.768	113	E	2 NRTI+1 PI+1 ENH+1 INSTI
78	2	0.183	3	0.608	5	0.664	113	E	2 NRTI+1 PI+1 ENH
79	1	0	1	0	2	0.396		E	2 NRTI+1 INSTI
82	1	0	NA	NA	NA	NA		N	
83	2	0.467	NA	NA	NA	NA	554	E	2 NRTI+1 NNRTI
85	2	0.351	1	0	2	0.477	183	E	2 NRTI+1 INSTI
86	2	0.433	1	0	NA	NA		E	2 NRTI+1 PI+1 ENH+1 INSTI
87	2	0.499	NA	NA	NA	NA		E	2 NRTI+1 ENH+1 INSTI
88	1	0	NA	NA	1	0	37	N	
Continued									

Participant	<i>PR/RT</i>		<i>int</i>		<i>env</i>		Viral Load (copies/mL)	ARV Exposure	ARV Regimen Type
	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity	Number of Haplotypes	Haplotype Diversity			
90	3	0.534	2	0.498	3	0.54	8914	E	2 NRTI+1 PI+1 ENH+1 CCR5+1 INSTI
91	1	0	2	0.003	NA	NA	117	E	2 NRTI+1 INSTI
93	2	0.446	1	0	NA	NA	94	E	2 NRTI+1 ENH+1 INSTI
94	1	0	NA	NA	NA	NA	145	E	2 NRTI+1 PI+1 ENH
97	5	0.718	2	0.455	5	0.782		E	2 NRTI+1 INSTI
99	1	0	NA	NA	1	0	184	E	2 NRTI+1 ENH+1 INSTI
Avg	2	0.265	2	0.357	4	0.47			

**Table 1.** Haplotype diversity estimates from PredictHaplo results. A haplotype diversity of 0 indicates no diversity because only a single haplotype was reconstructed by PredictHaplo for the sample. Amplicons that did not pass the filtering thresholds for a sample are indicated by “NA”. ARV exposure is reported at time that blood sample was taken. N: Naïve, E: Experienced, NRTI: Nucleoside reverse transcriptase inhibitors, NNRTI: Non-nucleoside reverse transcriptase inhibitors, ENH: enhancer elements, PI: Protease Inhibitor, INSTI: Integrase Strand Transfer Inhibitor, CCR5: Cysteine-Cysteine Chemokine Receptor 5.



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