CORRECTION

Correction: Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants

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In [Table 1](#), the residue for 27162 should be 107, not 109. Please see the corrected [Table 1](#) here.

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Table 1. Nonsynonymous mutations occurring at >1% at sites with at least 100 X ORP coverage.

Nt pos.	Residue	Data type	SEED	C1D1	C1D3	C1D5	C2D1	C2D3	C2D5	C3D1	C3D3	C3D5	ORF									
2169	I631L	Consensus	A	0.985	A	1.000	A	0.938	A	0.928	A	0.894	A	0.931	A	0.964	A	0.877	A	0.962	nsp2	
3475	K1066T	ISNV	C	0.015	NA	C	0.062	C	0.074	C	0.072	C	0.106	C	0.069	C	0.036	C	0.123	C	0.038	
		Consensus	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	0.982	A	1.000	A	0.804	nsp3	
6161	L1961V	ISNV	0	NA	NA	NA	0	NA	NA	NA	NA	NA	NA	0.009	NA	0	0	0	0	0.197	nsp3	
		Consensus	G	1.000	G	0.993	0	G	1.000	G	1.000	G	1.000	G	1.000	G	1.000	G	1.000	G		0.892
6172	F1965S	ISNV	NA	T	0.008	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	C	0.108	nsp3	
		Consensus	T	0.858	C	0.593	0	C	0.812	C	0.938	C	0.939	C	0.955	C	0.921	C	1.000	C		1.000
8050	D2591A	ISNV	C	0.142	T	0.417	NA	T	0.188	T	0.062	T	0.061	T	0.045	T	0.079	NA	NA	NA	nsp3	
		Consensus	A	0.941	A	1.000	A	1.000	A	1.000	A	0.622	A	0.998	A	0.994	A	0.912	A	0.923		A
8614	M2779T	ISNV	C	0.060	NA	NA	NA	C	0.378	C	0.002	C	0.002	C	0.006	C	0.088	C	0.077	C	0.078	nsp4
		Consensus	T	1.000	0	0	T	0.942	T	0.845	0	0	0	0	0	0	0.951	T	1.000	T	0.850	
9798	D3174H	ISNV	0	NA	NA	NA	C	0.058	C	0.155	NA	NA	NA	NA	C	0.050	NA	NA	C	0.150	nsp4	
		Consensus	G	0.998	0	0	G	1.000	G	0.896	0	0	0	0	G	1.000	G	1.000	G	1.000		
13234	E4319V	ISNV	A	0.002	NA	NA	C	0.104	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	nsp10	
		Consensus	A	1.000	0	0	A	1.000	A	1.000	0	0	0	0	A	0.855	A	1.000	A	0.940		
23150	E565D	ISNV	0	NA	NA	NA	0	NA	NA	NA	NA	NA	NA	NA	T	0.145	NA	NA	T	0.060	S gene	
		Consensus	G	1.000	0	G	1.000	G	0.884	G	0.884	G	0.948	G	0.877	G	0.814	G	0.875	G		0.931
24474	A1007T	ISNV	0	NA	NA	NA	T	0.116	T	0.052	T	0.052	T	0.123	T	0.186	T	0.125	T	0.069	S gene	
		Consensus	G	1.000	0	G	0.986	G	0.721	G	1.000	G	1.000	G	0.969	G	0.820	G	0.821	G		0.889
24499	N1015T	ISNV	NA	NA	NA	NA	A	0.014	A	0.279	NA	NA	A	0.031	A	0.180	A	0.179	A	0.111	S gene	
		Consensus	A	0.886	0	0	C	0.824	C	0.959	C	1.000	C	1.000	C	0.970	C	1.000	C	1.000		
24502	N1016S	ISNV	C	0.115	NA	NA	A	0.176	A	0.041	NA	NA	NA	A	1.000	A	0.956	A	1.000	A	0.978	S gene
		Consensus	A	0.986	0	0	A	0.967	A	1.000	A	1.000	A	1.000	A	0.956	A	0.944	A	0.845	A	
24538	N1028S	ISNV	G	0.014	NA	NA	G	0.033	NA	NA	NA	NA	NA	G	0.044	NA	NA	G	0.022	G	0.022	orf5
		Consensus	A	0.966	0	0	A	0.710	A	0.803	A	1.000	G	0.698	A	0.944	A	0.845	A	0.845	A	
27162	Y107*	ISNV	G	0.034	NA	NA	G	0.290	G	0.197	NA	NA	A	0.302	G	0.056	G	0.155	G	0.044	orf5	
		Consensus	0	0	0	0	0	0	0	0	G	0.878	G	0.944	0	0	0	0	0	0		0
28464	R204S	ISNV	NA	NA	NA	NA	NA	NA	A	0.122	A	0.056	NA	NA	NA	NA	NA	NA	NA	NA	M gene	
		Consensus	G	1.000	G	0.638	G	0.995	G	0.995	G	0.998	G	0.999	G	0.999	G	0.999	G	0.997		G
28466	S2051	ISNV	NA	T	0.362	T	0.100	T	0.005	T	0.001	T	0.001	T	0.001	T	0.001	T	0.002	T	0.020	N gene
		Consensus	G	0.999	G	1.000	G	0.996	G	0.920	G	0.997	G	0.999	G	0.999	G	0.998	G	0.997	G	
28567	R8C	ISNV	NA	NA	NA	NA	T	0.080	T	0.004	T	0.001	T	0.001	T	0.001	T	0.002	T	0.002	0.025	N gene
		Consensus	C	0.993	C	0.993	C	0.990	C	0.993	C	0.996	C	0.950	C	0.996	C	1.000	C	1.000	C	
28778	L16P	ISNV	T	0.007	A	0.004	T	0.010	T	0.004	T	0.050	T	0.004	NA	NA	NA	NA	NA	NA	N gene	
		Consensus	T	1.000	T	1.000	T	1.000	T	1.000	T	0.992	T	1.000	T	0.981	T	0.982	T	0.996		T
29734	G390V	ISNV	0	0	0	0	C	0.008	0	C	0.008	0	C	0.020	C	0.018	C	0.004	C	0.005	N gene	
		Consensus	G	1.000	G	1.000	G	0.997	G	0.571	G	0.935	G	0.990	G	0.990	G	1.000	G	1.000		G
29737	S391I	ISNV	NA	T	0.429	C	0.003	T	0.065	A	0.010	A	0.010	A	0.005	NA	NA	NA	NA	T	0.057	N gene
		Consensus	G	0.999	G	1.000	G	0.928	G	0.906	G	0.906	G	0.924	G	1.000	G	0.932	G	1.000	G	
29747	Q394H	ISNV	C	0.001	NA	NA	T	0.072	T	0.094	T	0.076	NA	NA	T	0.063	NA	T	0.083	NA	0.089	N gene
		Consensus	G	0.992	0	G	1.000	G	0.985	G	0.936	G	0.800	G	1.000	G	0.992	G	0.876	G	0.911	
29748	R395C	ISNV	A	0.008	NA	NA	T	0.064	T	0.064	T	0.190	NA	A	0.008	T	0.124	T	0.073	T	0.073	N gene
		Consensus	C	0.950	0	C	1.000	C	0.994	C	0.973	C	1.000	C	1.000	C	0.940	C	0.955	C	0.998	
29748	P406L	ISNV	T	0.050	NA	NA	A	0.006	T	0.027	NA	NA	NA	NA	T	0.058	T	0.045	G	0.002	N gene	
		Consensus	C	1.000	0	0	C	1.000	C	1.000	C	1.000	C	1.000	C	1.000	C	1.000	C	1.000		C
29783	P406L	ISNV	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	NA	NA	T	0.213	T	0.213	N gene
		Consensus	A	1.000	0	0	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	
29784	M407I	ISNV	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	NA	NA	T	0.213	T	0.213	N gene
		Consensus	A	1.000	0	0	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	1.000	A	
29788	I408S	ISNV	T	1.000	0	0	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	0.858	N gene
		Consensus	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	G	
29794	V410S	ISNV	0	0.000	0.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	0.917	T	1.000	N gene
		Consensus	0	0.000	0.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	1.000	T	0.917	
29794	ISNV	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	C	0.083	NA	NA	NA	NA	

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There is an incorrect reference to [Table 1](#) in the second sentence of the first paragraph the Results section, “ORF1ab.” The correct sentence is: The Seed stock had iSNVs present at nts 307–313, part of the nsp1 ORF (residues 9–11). All iSNVs were detected at 4% indicating there is a second genotype present at 4%.

The incorrect value reported in [Table 1](#) also appears in the first sentence of the Results section, “ORF5.” The correct sentence is An iSNV resulting in a stop codon at residue 107 was detected in 12% of reads at nt 27162 for camel C2D5, the only sample for which there was adequate coverage at this site (>100x, S2 Table).

Reference

1. Borucki MK, Lao V, Hwang M, Gardner S, Adney D, Munster V, et al. (2016) Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. PLoS ONE 11(1): e0146251. doi:[10.1371/journal.pone.0146251](https://doi.org/10.1371/journal.pone.0146251) PMID: [26790002](https://pubmed.ncbi.nlm.nih.gov/26790002/)