

**Genetic diversity, seasonality and transmission network of human metapneumovirus: identification of a unique sub-lineage of the fusion and attachment genes**

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**Supplementary Table 1.** Inter-person genetic distances and cutoff values estimated based on a set of human metapneumovirus (HMPV) reference sequences representing all known genotypes and sub-lineages.

Gene	Genotype/sub-lineage (n)	Genetic distance <sup>a</sup>		
		Lower 2.5% percentile (95% CI)	Lower 5.0% percentile (95% CI)	Selected cutoff values
<b>F</b>	A1 (6)	.002 (.002-.007)	.002 (.002-.007)	.002
	A2a (15)	.002 (.002-.003)	.002 (.002-.004)	
	A2b (11)	.003 (.002-.005)	.004 (.002-.007)	
	Novel sub-lineage of A2 (8)	.002 (.002-.002)	.002 (.002-.003)	
	B1 (12)	.003 (.002-.007)	.004 (.003-.010)	
	B2 (14)	.002 (.002-.004)	.004 (.002-.005)	
<b>G</b>	A1 (5)	.012 (.012-.046)	.012 (.012-.046)	.012
	A2a (16)	.014 (.002-.017)	.016 (.014-.023)	
	A2b (9)	.018 (.018-.029)	.018 (.018-.032)	
	Novel sub-lineage of A2 (5)	.021 (.021-.037)	.021 (.021-.037)	
	B1 (4)	.040 (.040-.059)	.040 (.040-.055)	
	B2 (6)	.028 (.028-.055)	.028 (.028-.055)	

<sup>a</sup> expressed in nucleotide substitutions per site.