

Supplementary Table 1

A. Details of quasi-species population at day 9

Reference NA	Pos	Ref	Var	Frq1	Frq2	Frq3	Pst1	Pst2	Pst3	Fvar	Rvar	Ftot	Rtot	Pval	Qval
BRISBANE_15_2011_pdm09-NA-332645	131	A	G	1	-	1	1.0889	-	1.1667	190	21	192	21	0.958268	1
BRISBANE_15_2011_pdm09-NA-332645	135	G	T	1	-	1	1.0889	-	1.1667	187	20	187	20	1	1
BRISBANE_15_2011_pdm09-NA-332645	244	T	C	0.9736	1	1	1.0029	0.9883	1.0061	265	380	268	380	0.980006	1
BRISBANE_15_2011_pdm09-NA-332645	316	A	G	1	1	1	1.0061	1.0198	1.0017	376	320	376	325	0.957118	1
BRISBANE_15_2011_pdm09-NA-332645	486	C	T	1	1	1	1.0974	1.2828	1.1235	258	232	261	237	0.982049	1
BRISBANE_15_2011_pdm09-NA-332645	627	C	T	1	0.9801	1	1.1397	0.9995	1.1525	169	191	174	193	0.956532	1
BRISBANE_15_2011_pdm09-NA-332645	823	T	C	-	0.8297	0.5468	-	1.1398	1.0341	89	101	160	178	0.972977	1
BRISBANE_15_2011_pdm09-NA-332645	961	A	G	0.9905	1	1	1	1.3169	1.0022	369	306	371	306	0.985918	1
BRISBANE_15_2011_pdm09-NA-332645	1131	A	G	1	-	1	1.2061	-	1.1333	171	70	171	70	1	1
BRISBANE_15_2011_pdm09-NA-332645	1134	C	T	1	-	1	1.2061	-	1.1333	171	76	171	76	1	1
BRISBANE_15_2011_pdm09-NA-332645	1191	T	A	1	1	0.9946	1.1333	1.1291	1	359	226	361	228	1	1
BRISBANE_15_2011_pdm09-NA-332645	1248	C	T	1	1	0.9937	1.1291	0.9999	0.9995	453	456	455	462	0.975173	1
BRISBANE_15_2011_pdm09-NA-332645	1288	C	A	0.0054	0.0063	-	0.9746	0.9347	-	3	1	499	512	0.613338	1
BRISBANE_15_2011_pdm09-NA-332645	1291	C	G	0.0054	0.0063	-	0.9746	0.9347	-	2	1	517	520	0.995703	1
BRISBANE_15_2011_pdm09-NA-332645	1294	A	G	1	1	*	0.9991	0.9995	*	514	543	515	543	1	1
BRISBANE_15_2011_pdm09-NA-332645	1297	G	A	0.0063	0.0028	*	0.9347	0.9045	*	1	1	400	550	1	1

Quasi-species frequencies were estimated by first mapping the high-throughput sequencing data to reference NA (Brisbane 15 2011) and then inferring NA haplotypes from mapped reads [12]. The spreadsheet contains frequencies for each detected nucleotide change relative to reference sequence.

B. Sequences of each inferred NA haplotype in the influenza virus population with corresponding frequencies at day 9

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