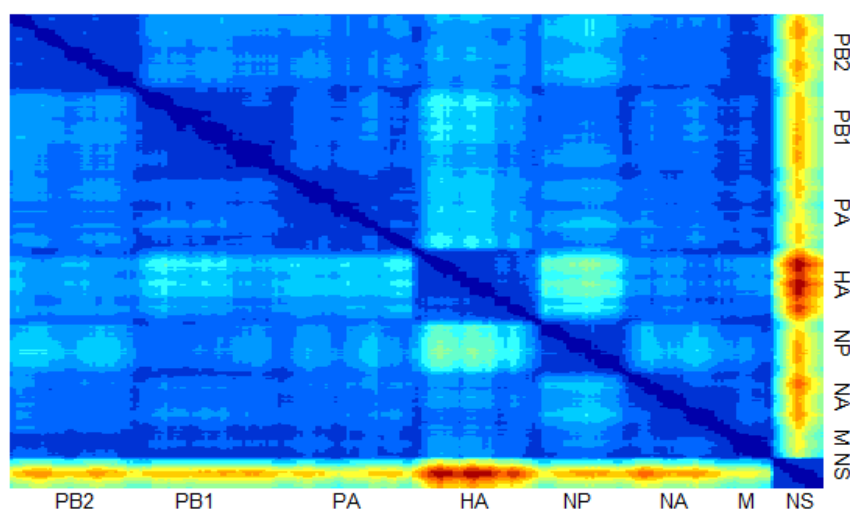
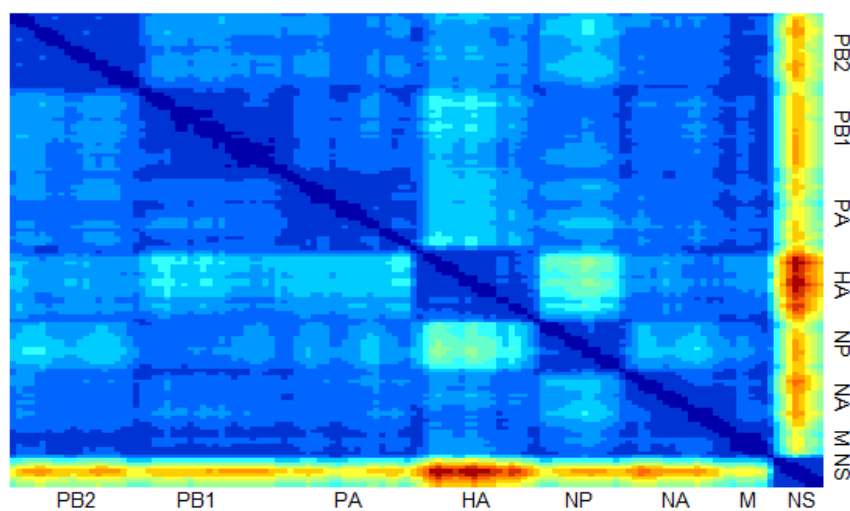
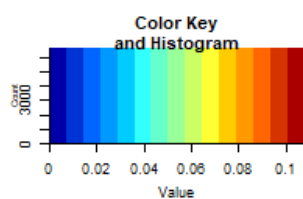


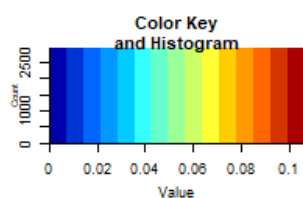
PDD matrix
H7N1
window = 500 step = 50



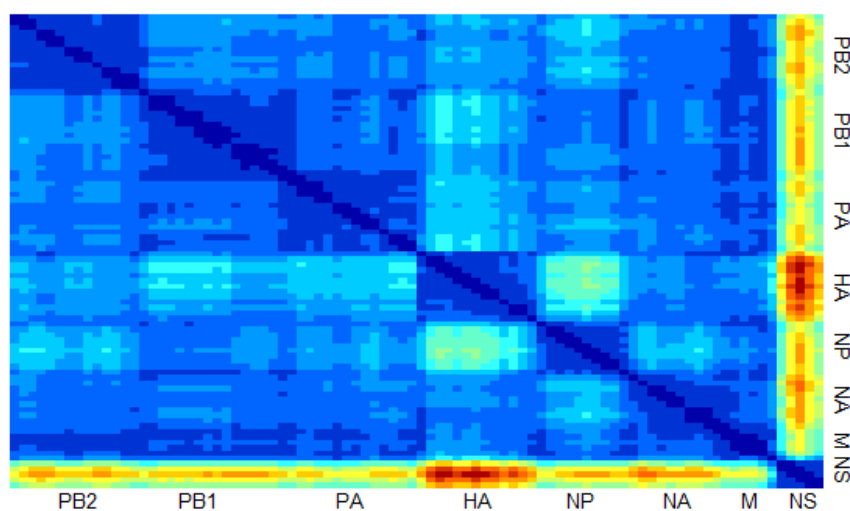
(a)
PDD matrix
H7N1
window = 500 step = 100



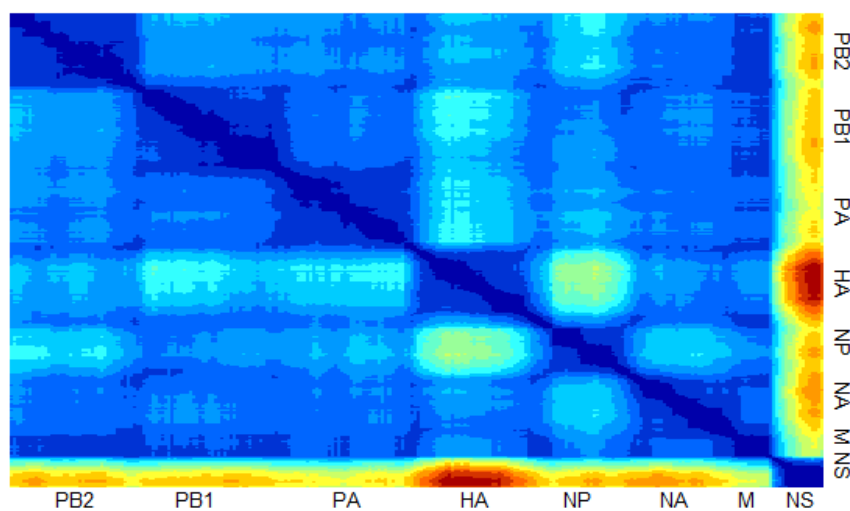
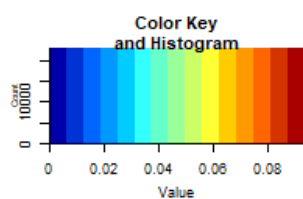
(b)



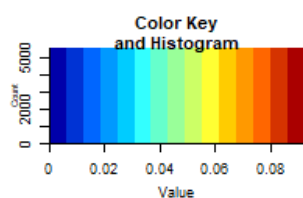
**PDD matrix
H7N1
window = 500 step = 150**



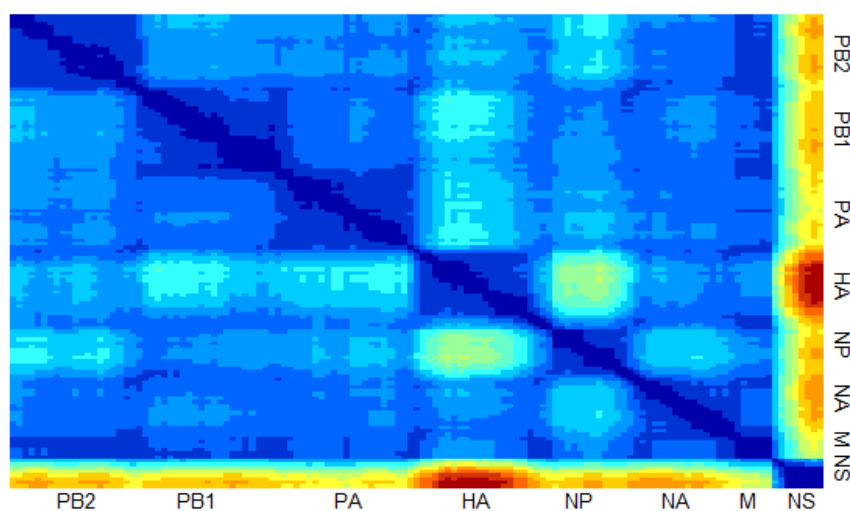
(c)
**PDD matrix
H7N1
window = 750 step = 50**



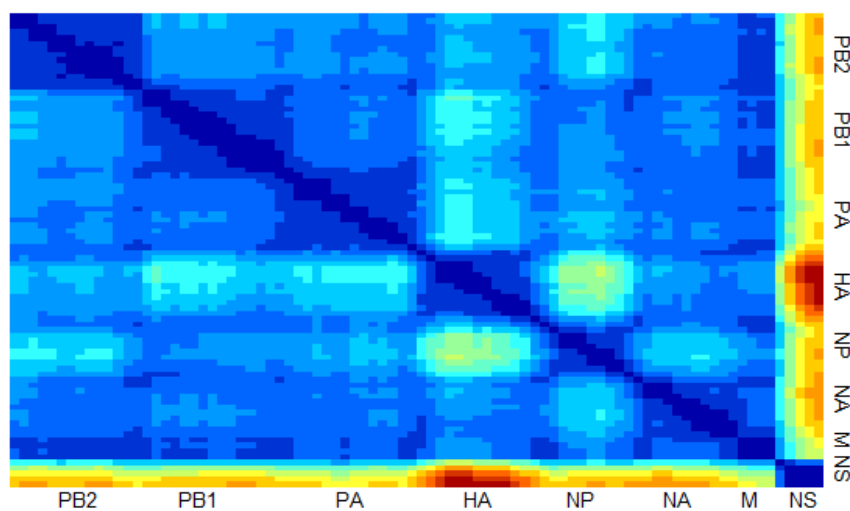
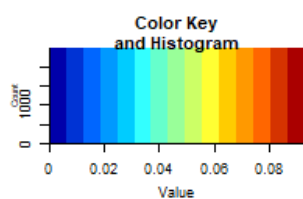
(d)



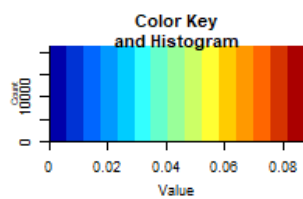
**PDD matrix
H7N1
window = 750 step = 100**



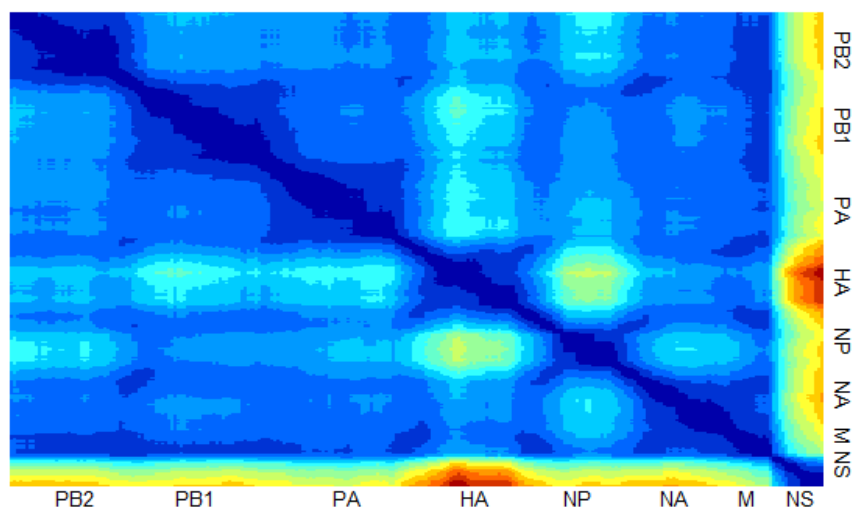
(e)
**PDD matrix
H7N1
window = 750 step = 150**



(f)

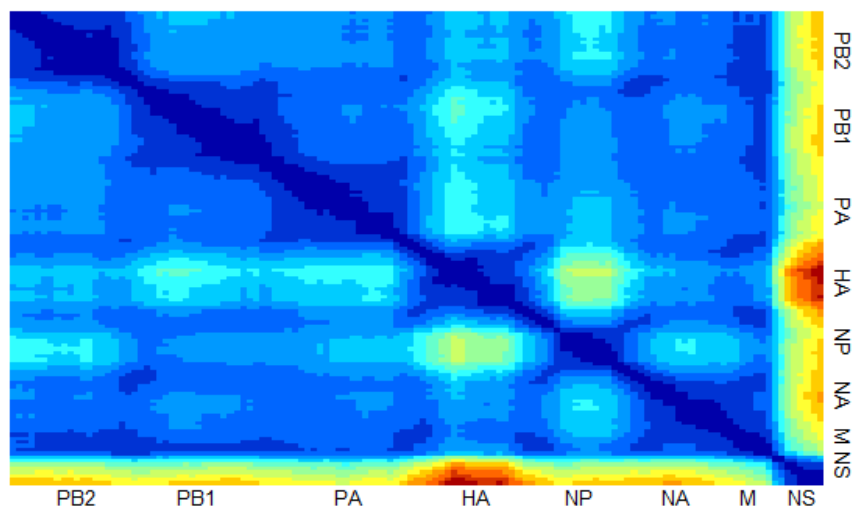
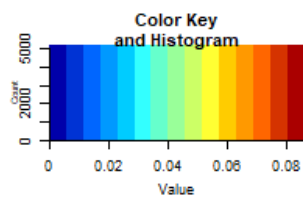


**PDD matrix
H7N1
window = 1000 step = 50**

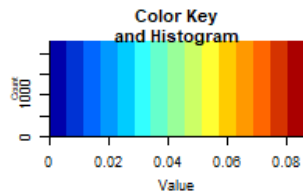


(g)

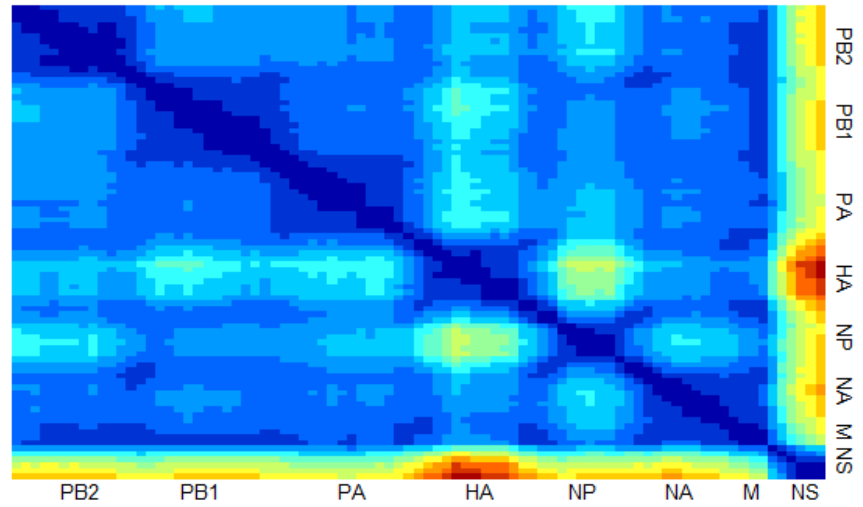
**PDD matrix
H7N1
window = 1000 step = 100**



(h)

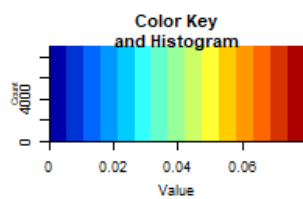


**PDD matrix
H7N1
window = 1000 step = 150**

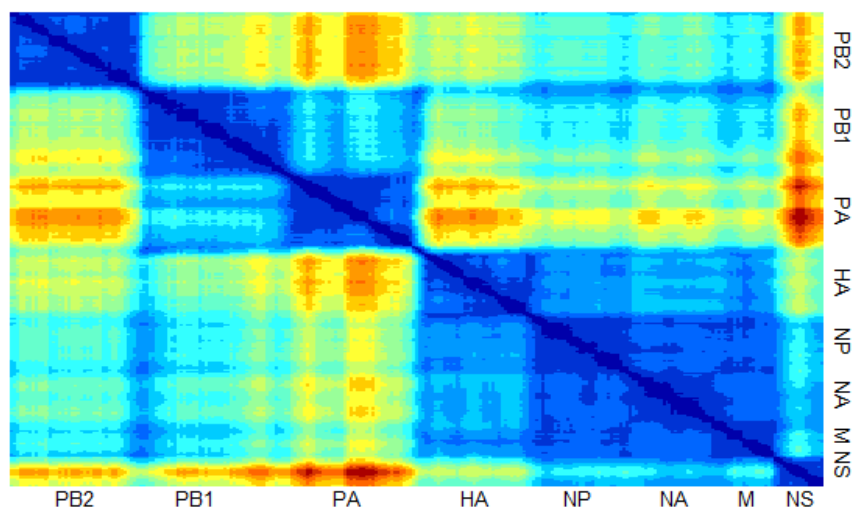


(i)

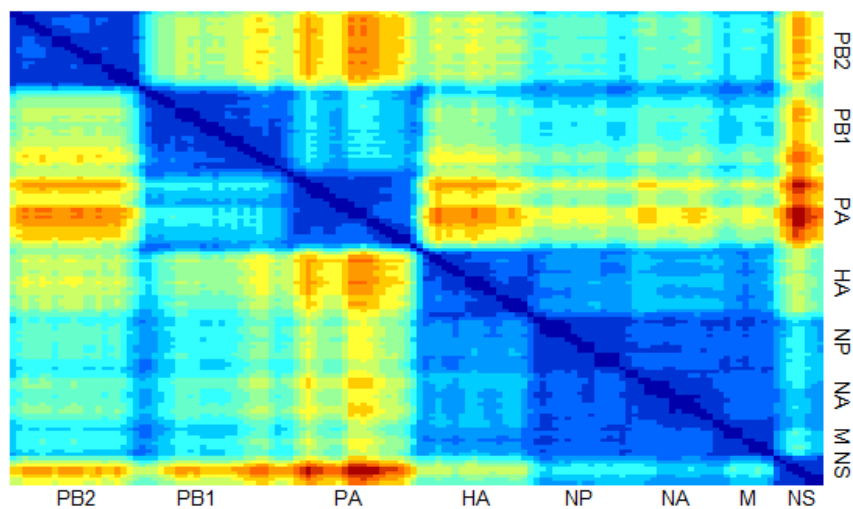
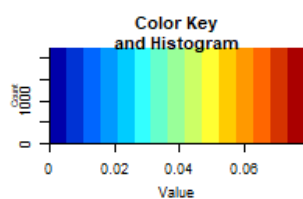
Supplementary Figure S1. Pairwise distance divergence matrix (PDDM) for H7N1 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides . The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.



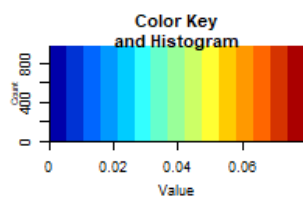
**PDD matrix
H7N2
window = 500 step = 50**



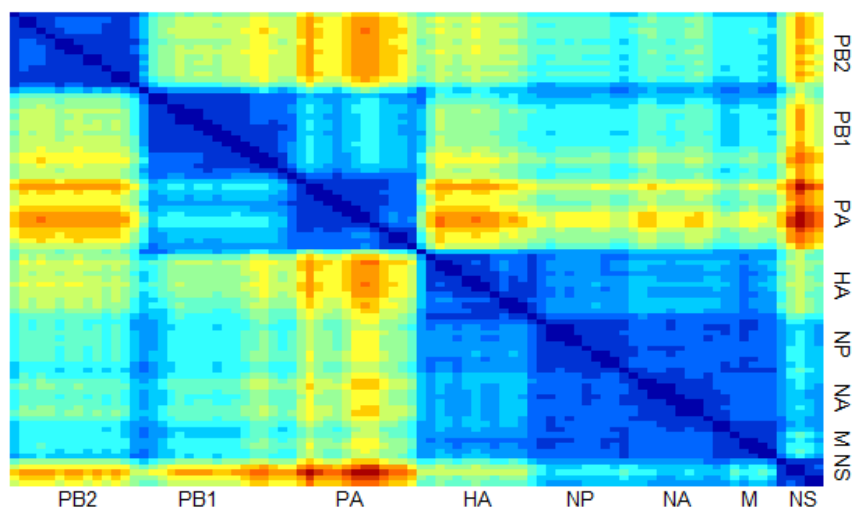
(a)
**PDD matrix
H7N2
window = 500 step = 100**



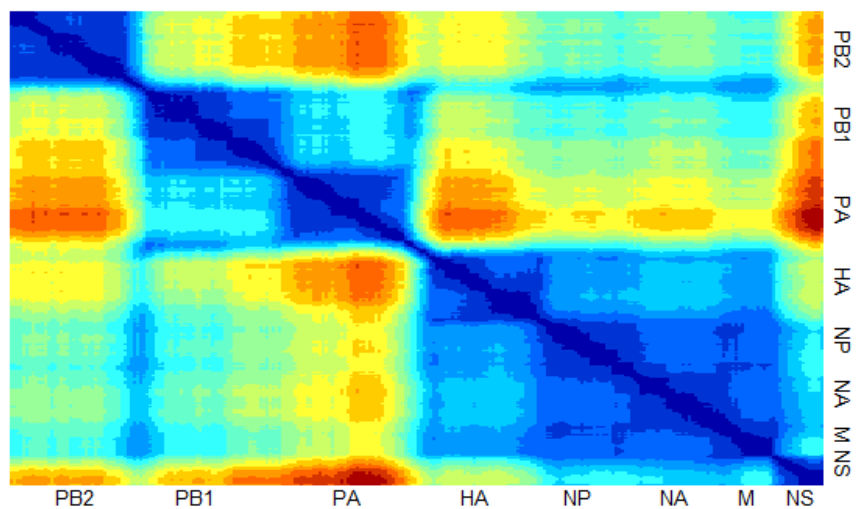
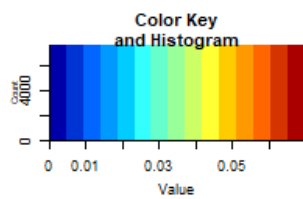
(b)



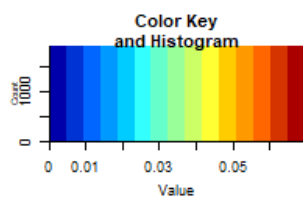
**PDD matrix
H7N2
window = 500 step = 150**



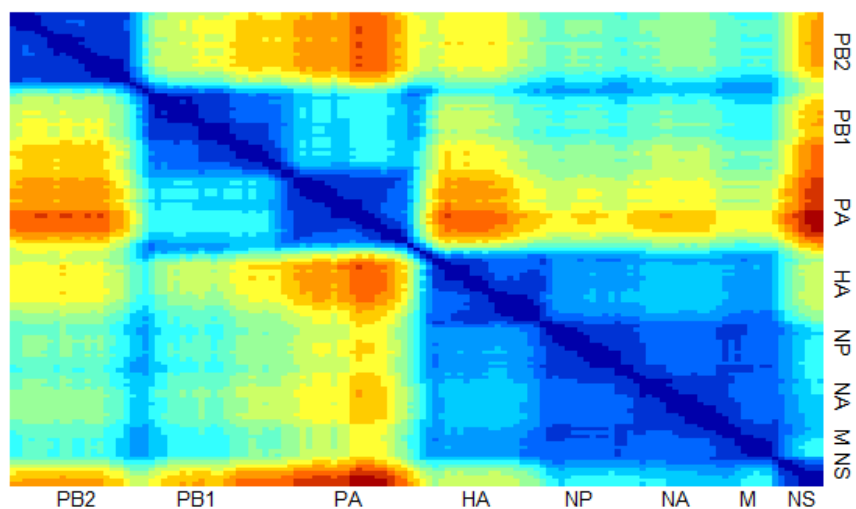
(c)
**PDD matrix
H7N2
window = 750 step = 50**



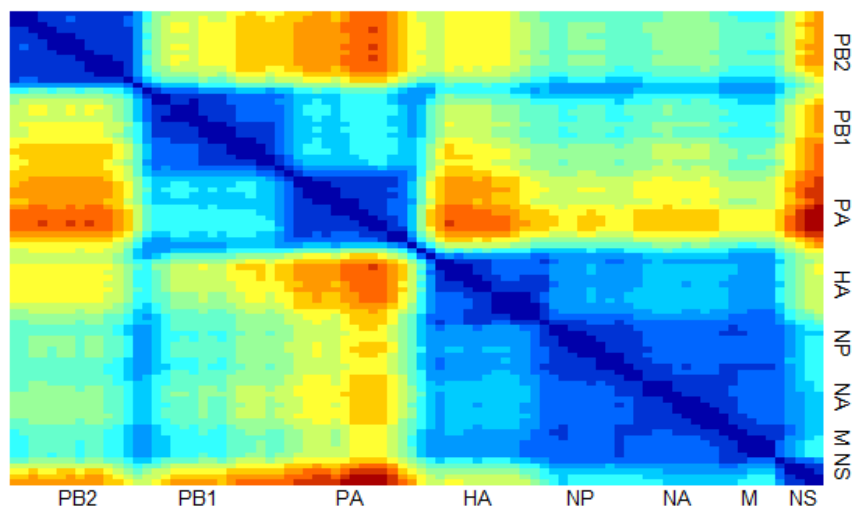
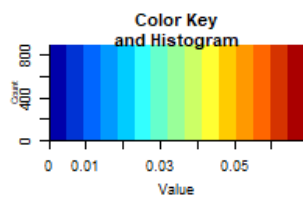
(d)



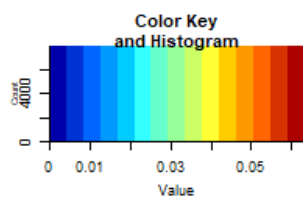
**PDD matrix
H7N2
window = 750 step = 100**



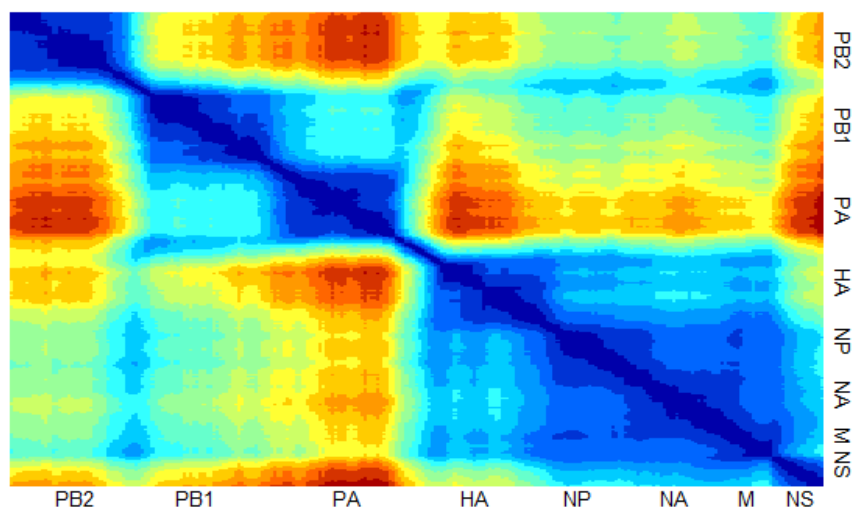
(e)
**PDD matrix
H7N2
window = 750 step = 150**



(f)

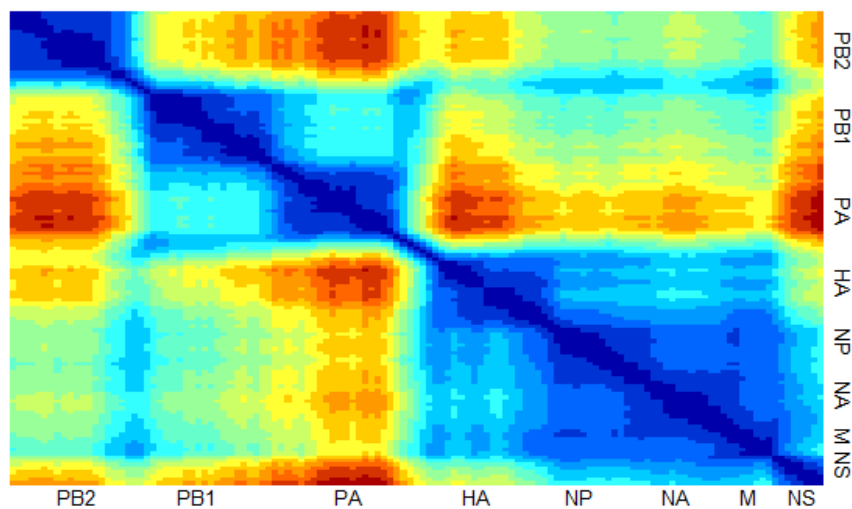
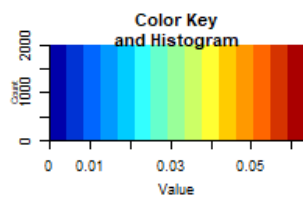


**PDD matrix
H7N2
window = 1000 step = 50**

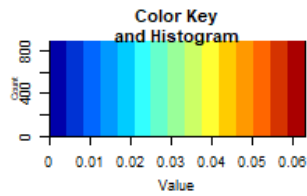


(g)

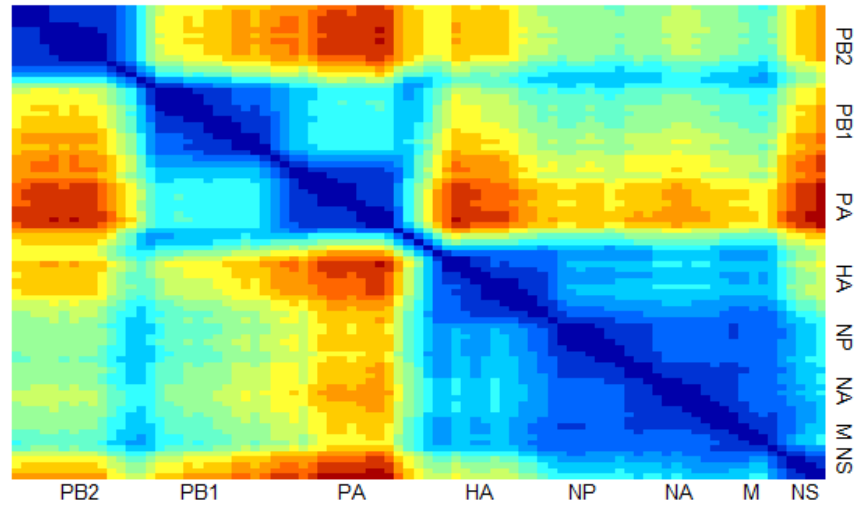
**PDD matrix
H7N2
window = 1000 step = 100**



(h)

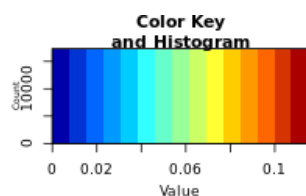


PDD matrix
H7N2
window = 1000 step = 150

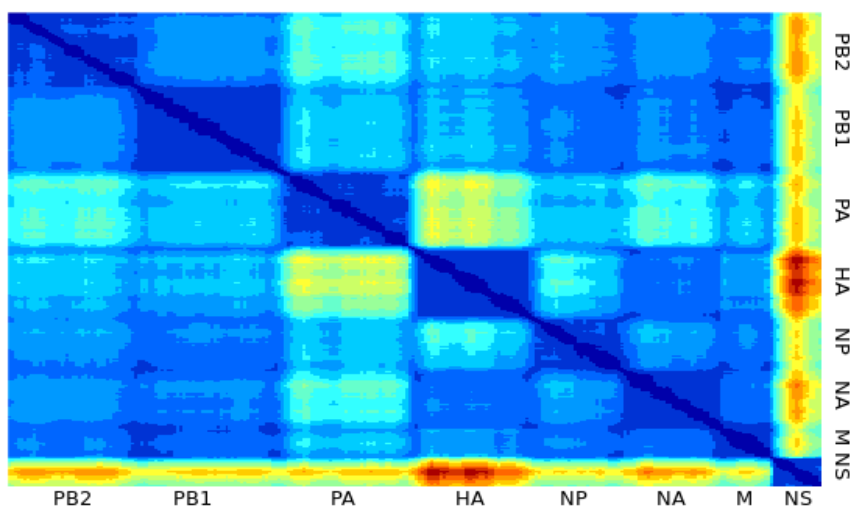


(i)

Supplementary Figure S2. Pairwise distance divergence matrix (PDDM) for H7N2 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

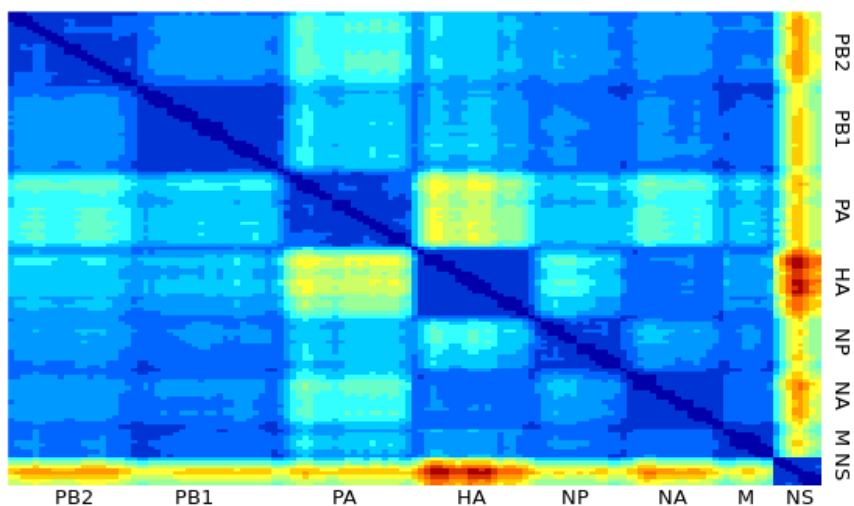
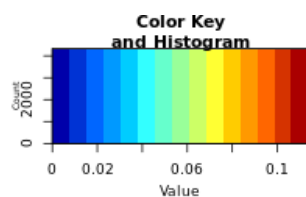


**PDD matrix
H7N3
window = 500 step = 50**

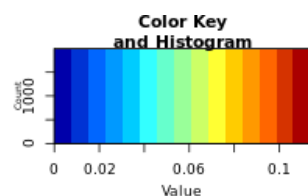


(a)

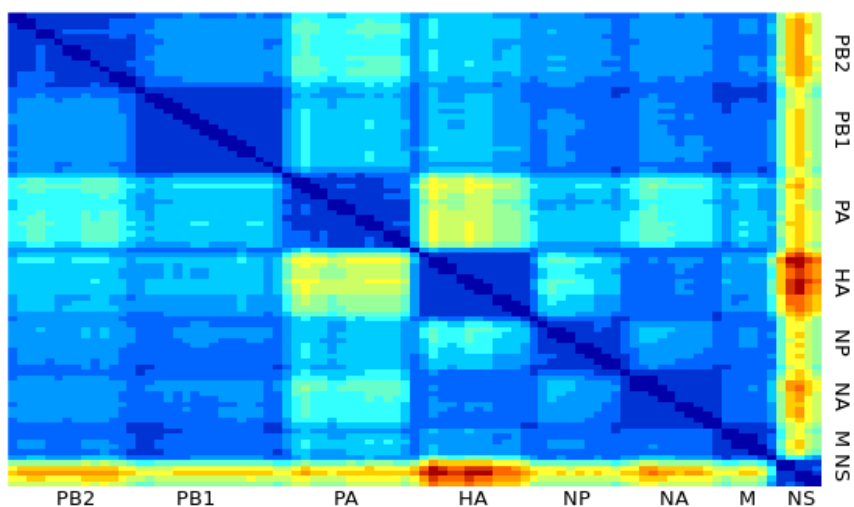
**PDD matrix
H7N3
window = 500 step = 100**



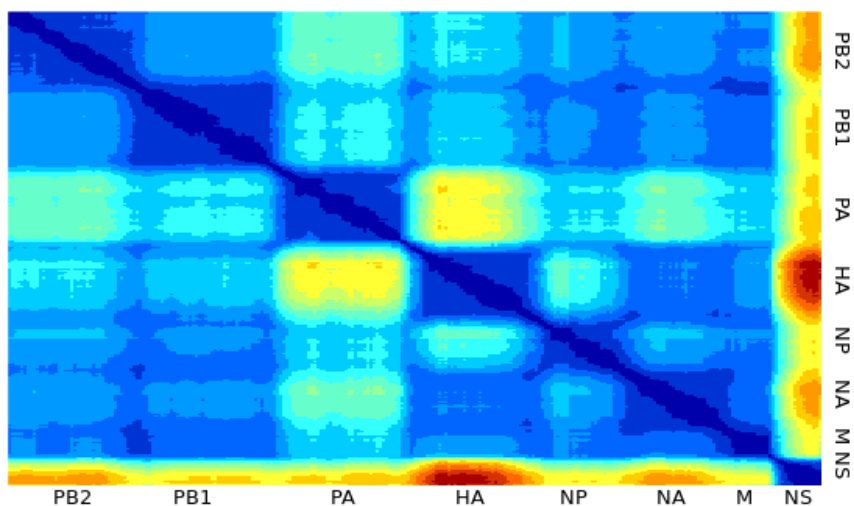
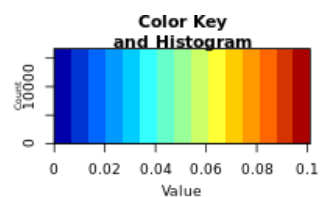
(b)



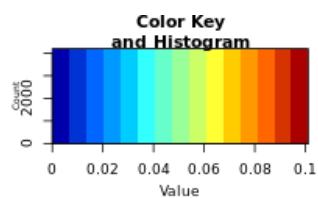
**PDD matrix
H7N3
window = 500 step = 150**



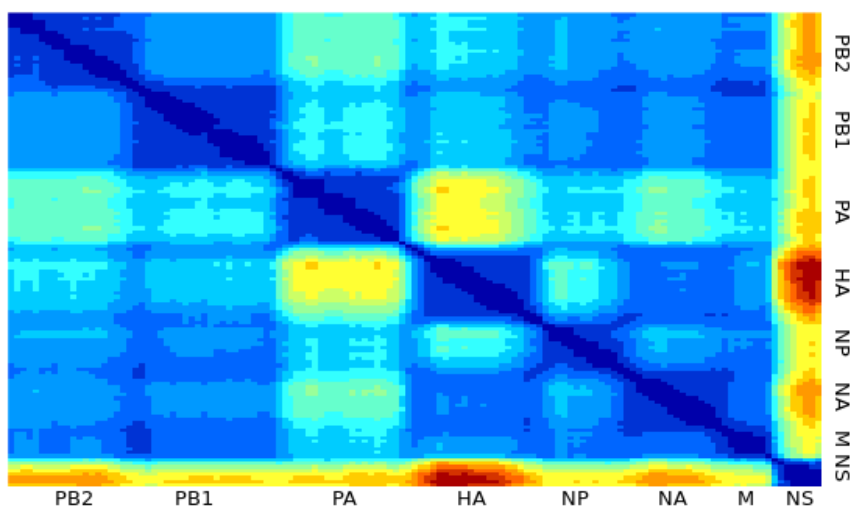
(c)
**PDD matrix
H7N3
window = 750 step = 50**



(d)

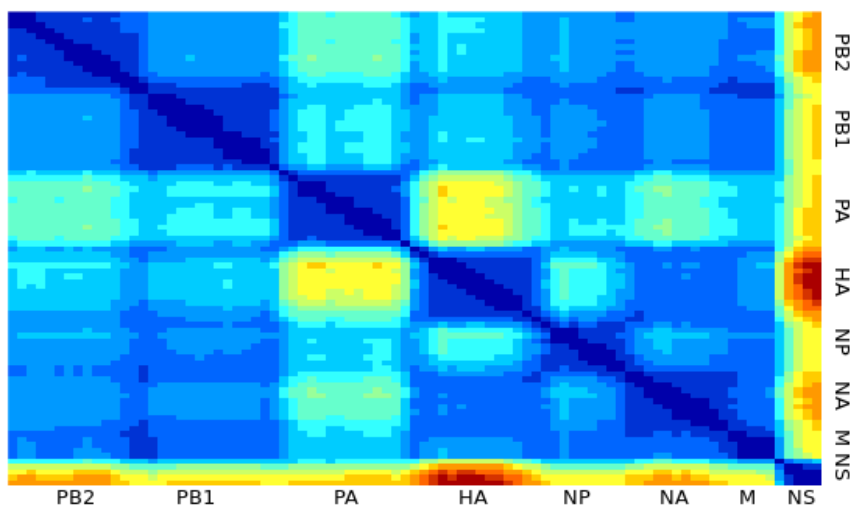
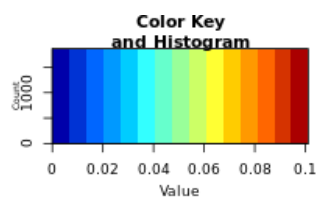


**PDD matrix
H7N3
window = 750 step = 100**

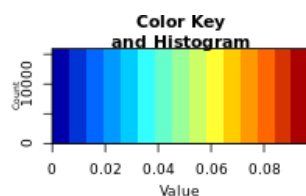


(e)

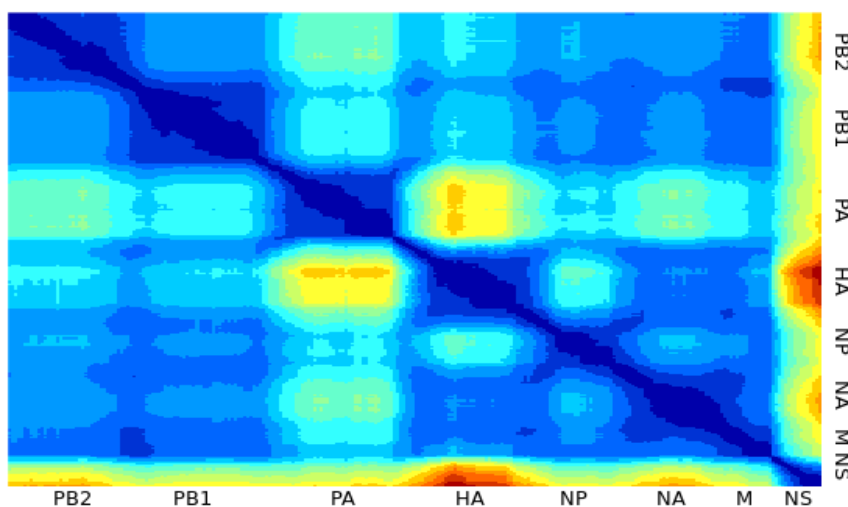
**PDD matrix
H7N3
window = 750 step = 150**



(f)

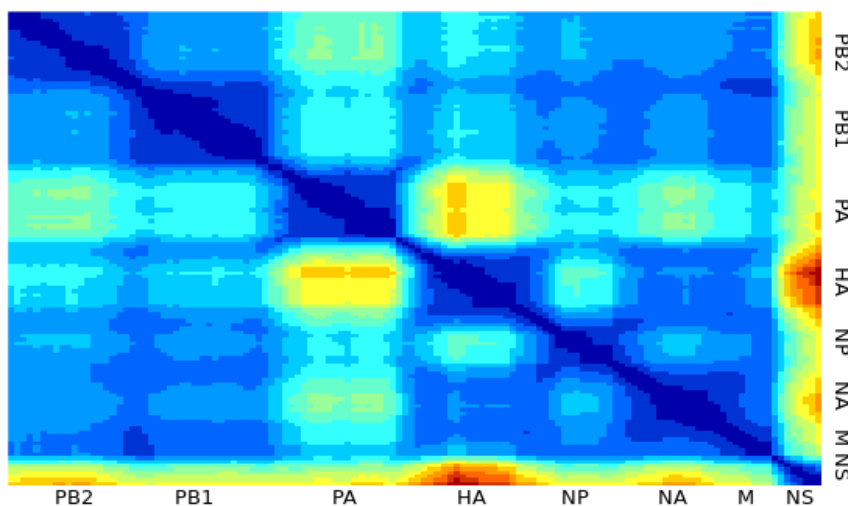
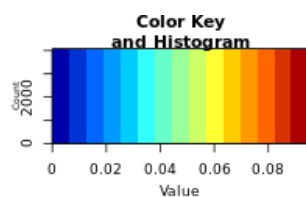


**PDD matrix
H7N3
window = 1000 step = 50**

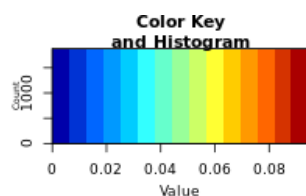


(g)

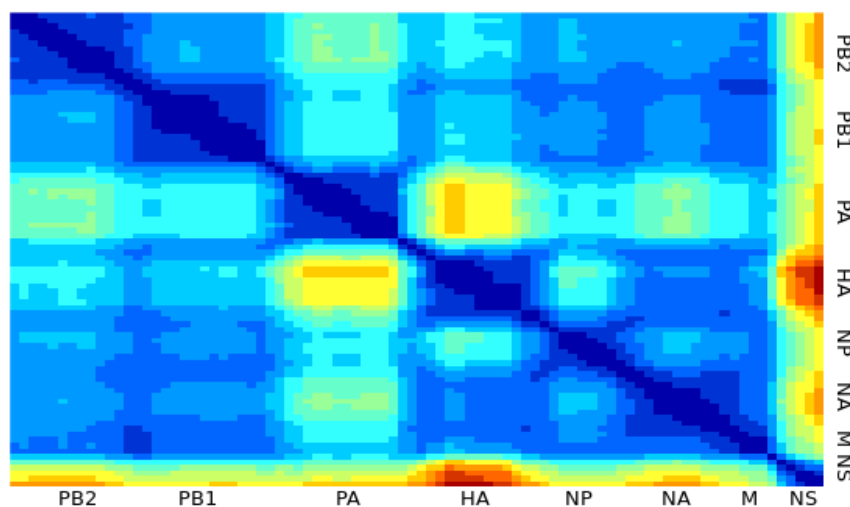
**PDD matrix
H7N3
window = 1000 step = 100**



(h)

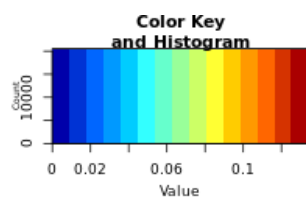


**PDD matrix
H7N3
window = 1000 step = 150**

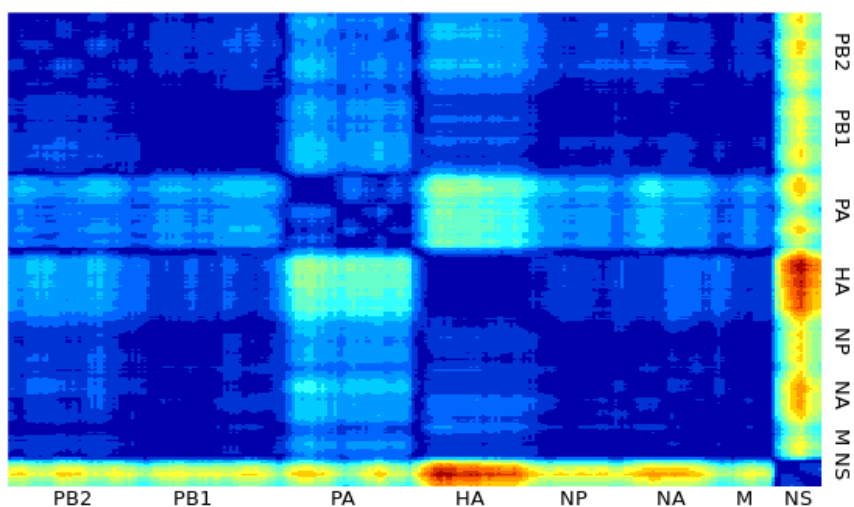


(i)

Supplementary Figure S3. Pairwise distance divergence matrix (PDDM) for H7N3 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

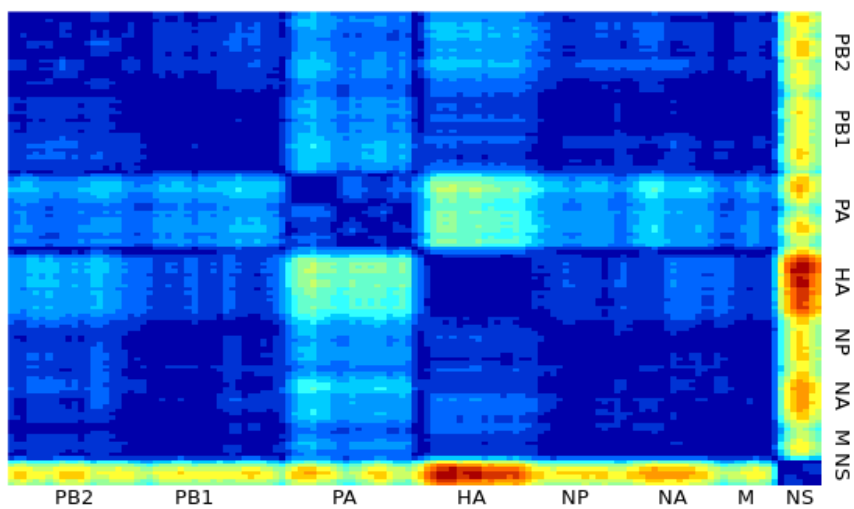
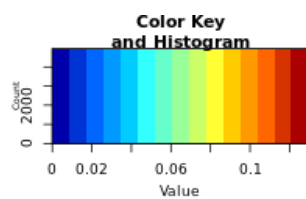


**PDD matrix
H7N4
window = 500 step = 50**

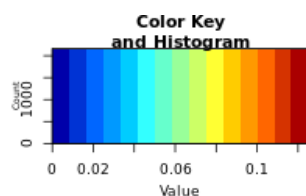


(a)

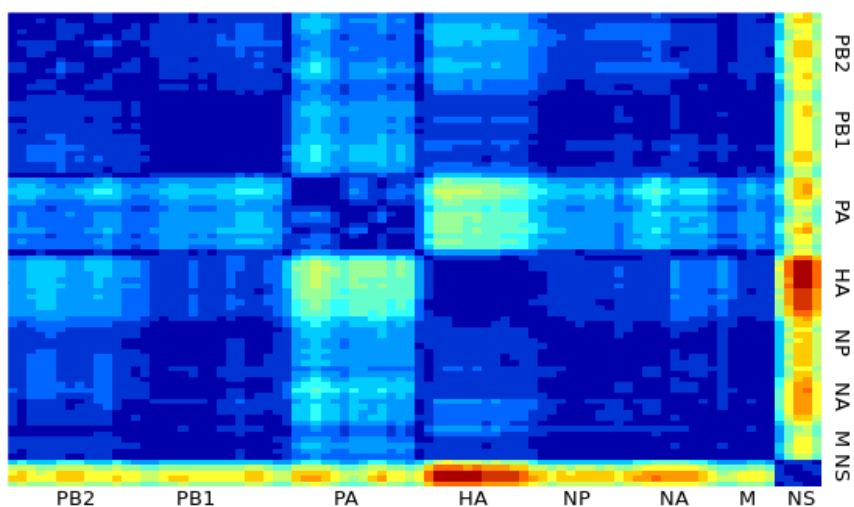
**PDD matrix
H7N4
window = 500 step = 100**



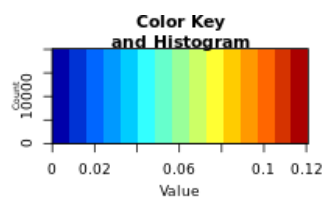
(b)



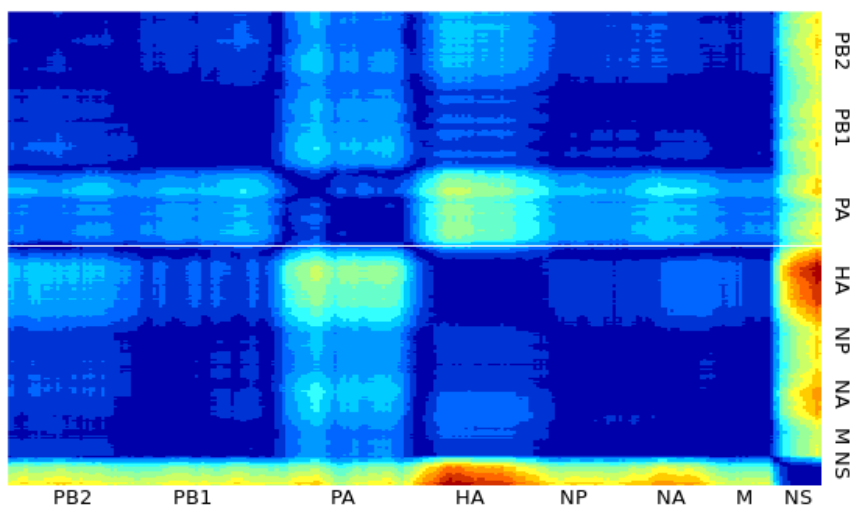
**PDD matrix
H7N4
window = 500 step = 150**



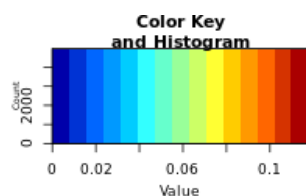
(c)



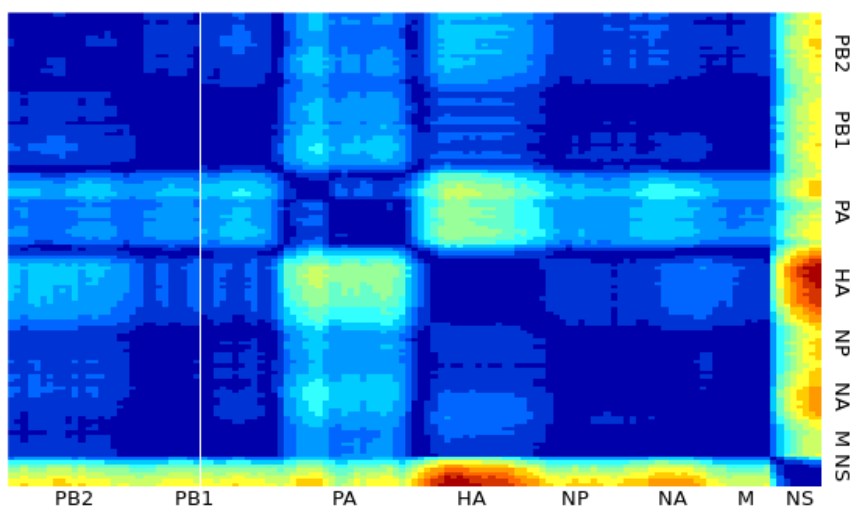
**PDD matrix
H7N4
window = 750 step = 50**



(d)

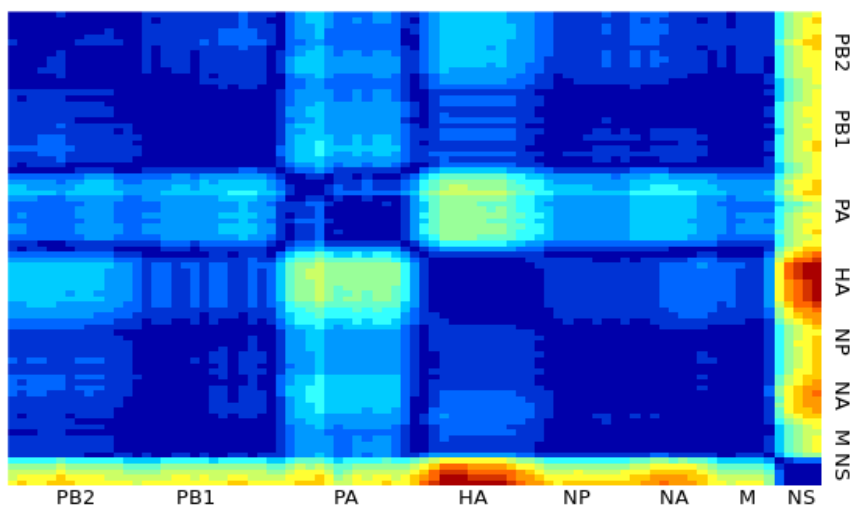
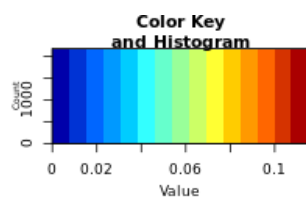


**PDD matrix
H7N4
window = 750 step = 100**

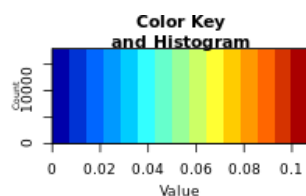


(e)

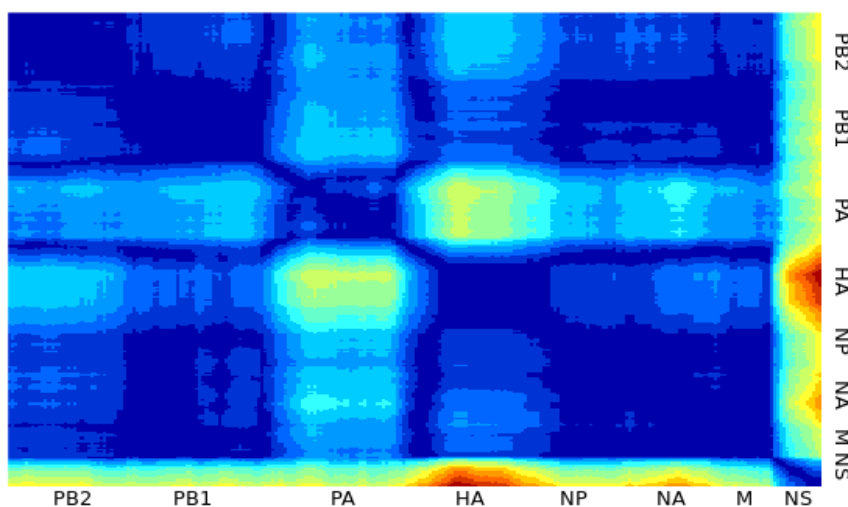
**PDD matrix
H7N4
window = 750 step = 150**



(f)

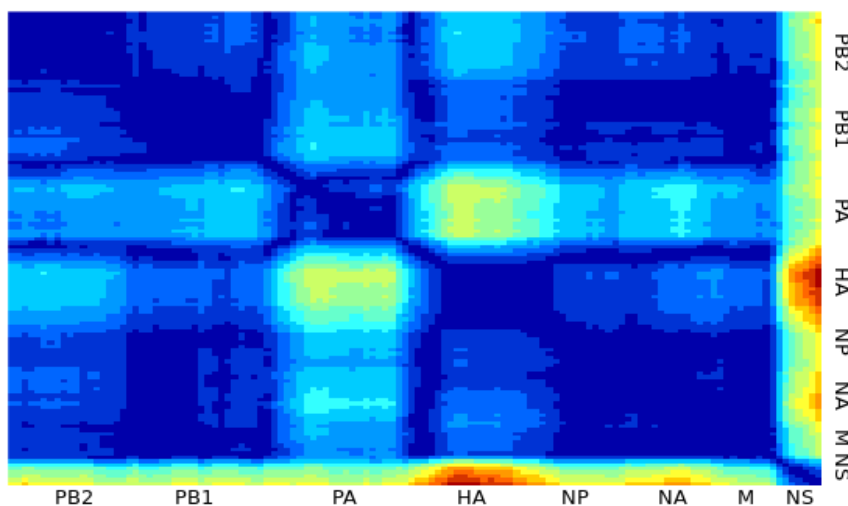
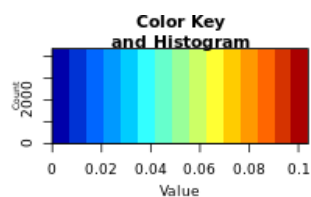


**PDD matrix
H7N4
window = 1000 step = 50**

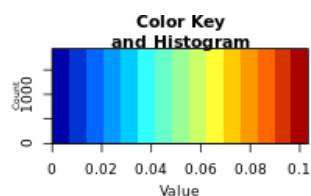


(g)

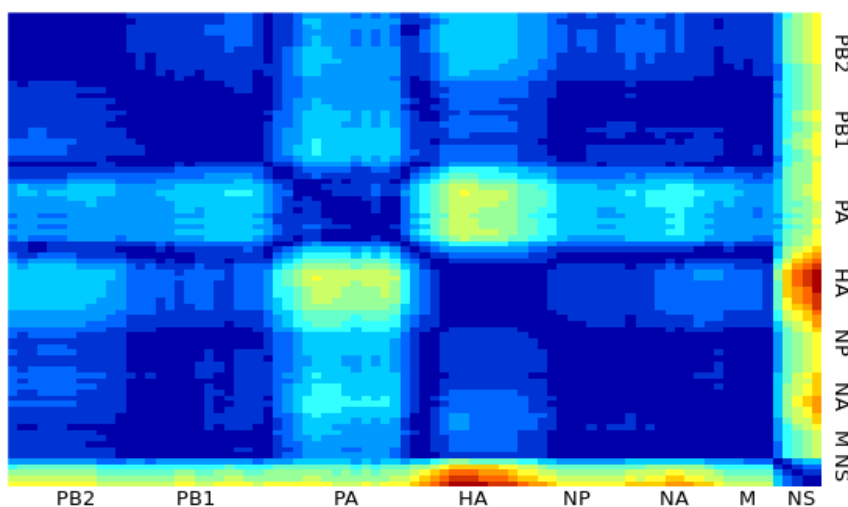
**PDD matrix
H7N4
window = 1000 step = 100**



(h)

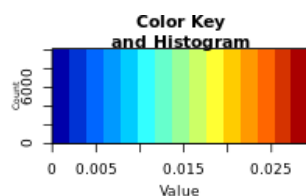


**PDD matrix
H7N4
window = 1000 step = 150**

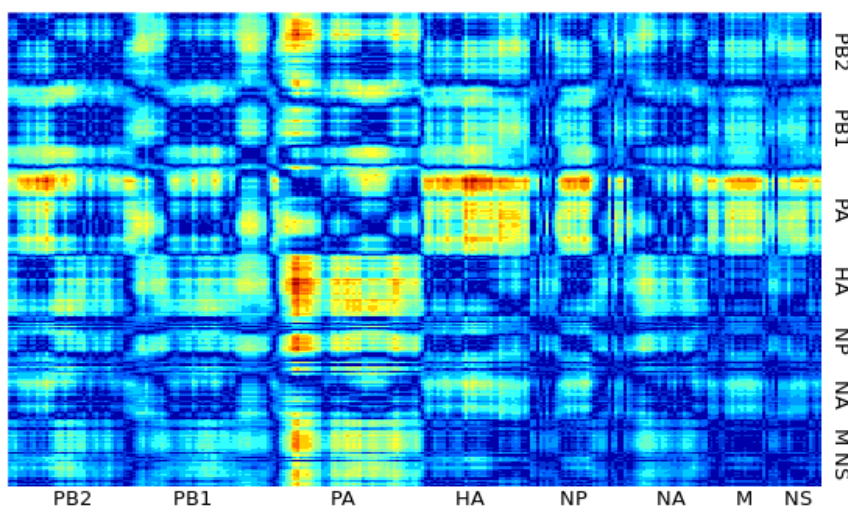


(i)

Supplementary Figure S4. Pairwise distance divergence matrix (PDDM) for H7N4 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

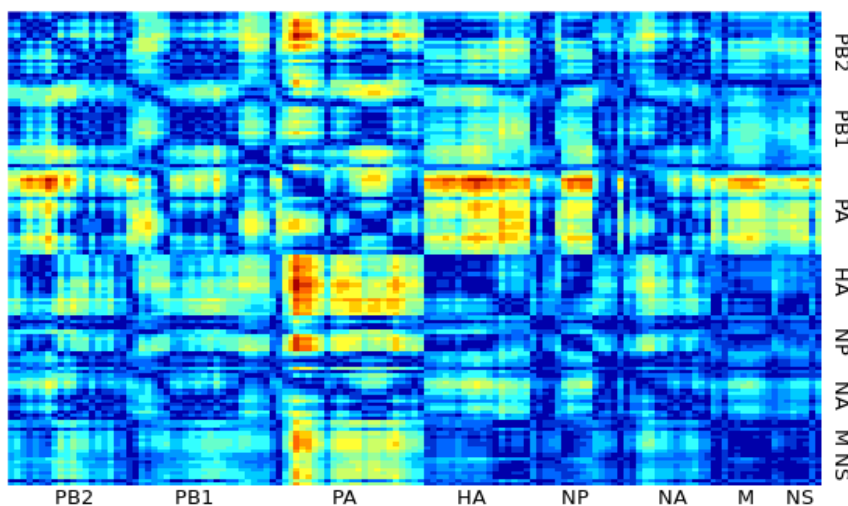
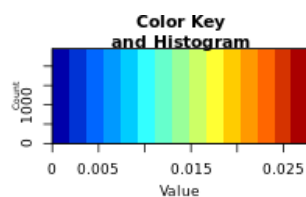


**PDD matrix
H7N5
window = 500 step = 50**

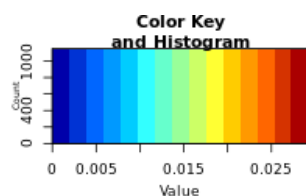


(a)

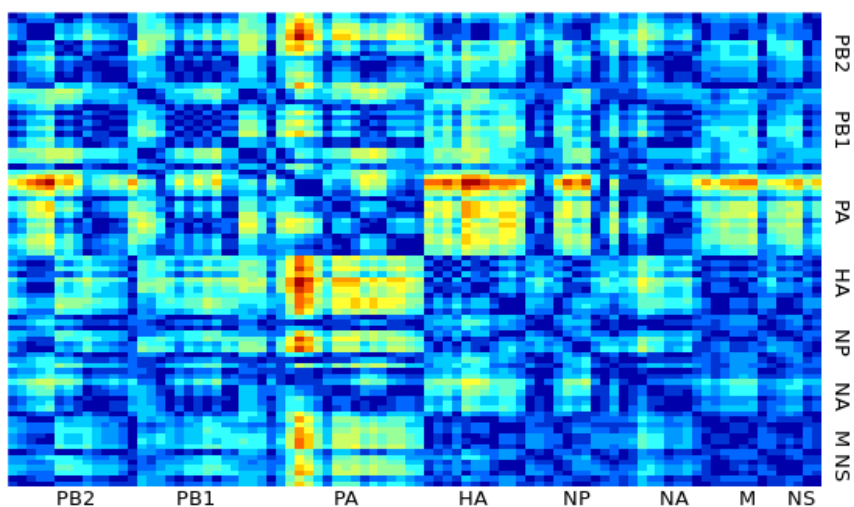
**PDD matrix
H7N5
window = 500 step = 100**



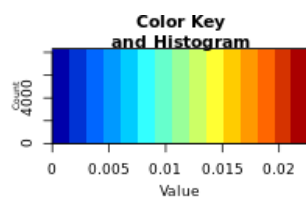
(b)



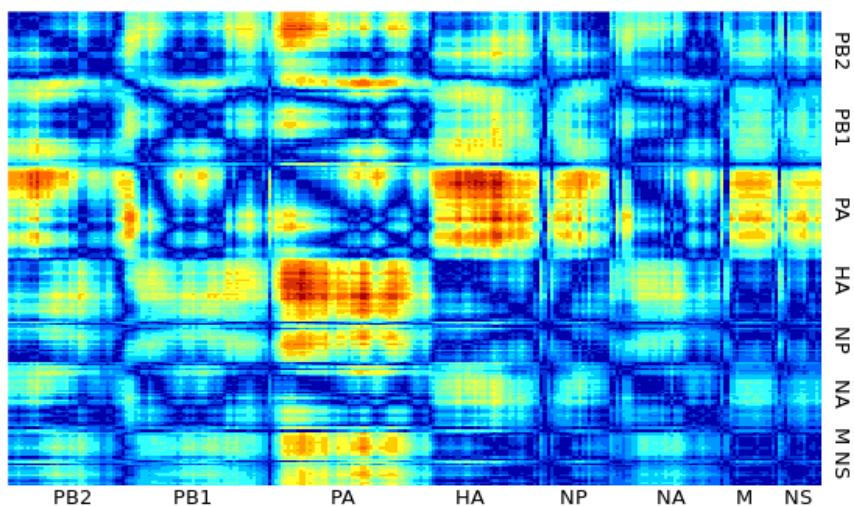
**PDD matrix
H7N5
window = 500 step = 150**



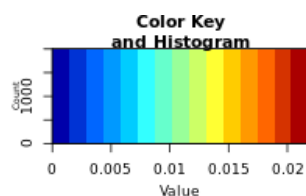
(c)



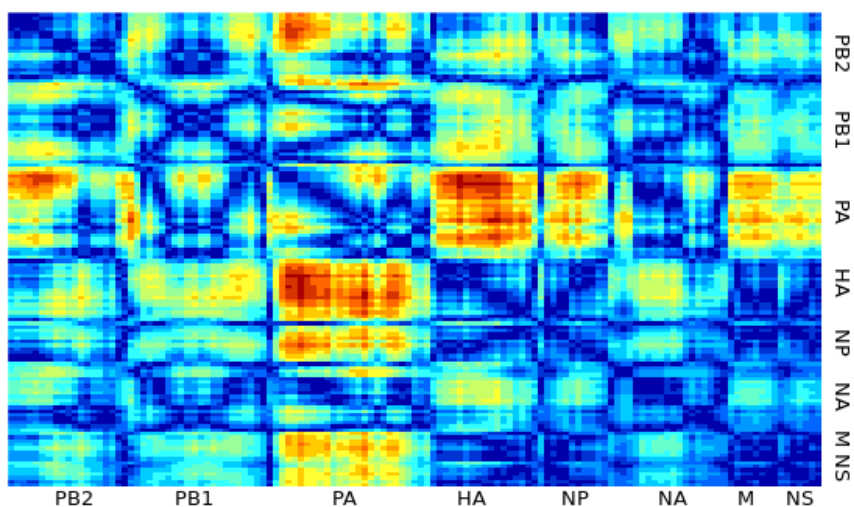
**PDD matrix
H7N5
window = 750 step = 50**



(d)

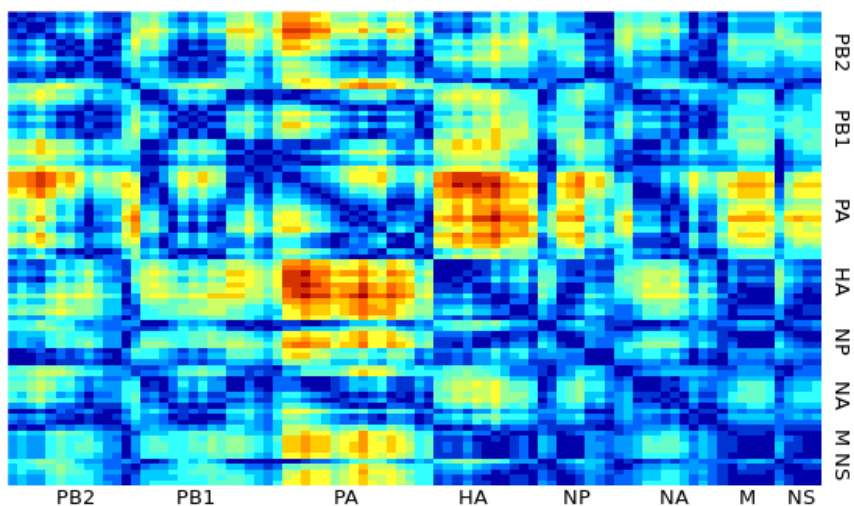
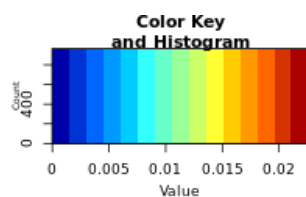


**PDD matrix
H7N5
window = 750 step = 100**

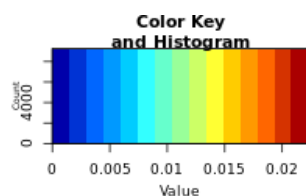


(e)

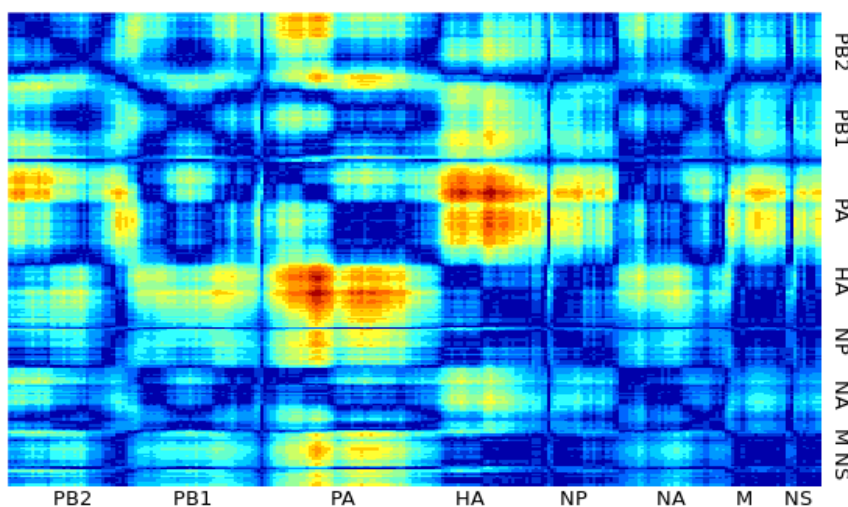
**PDD matrix
H7N5
window = 750 step = 150**



(f)

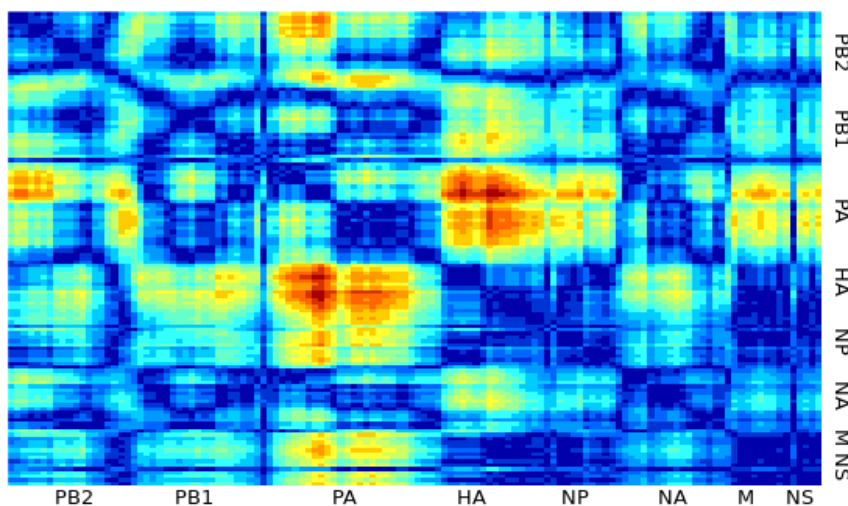
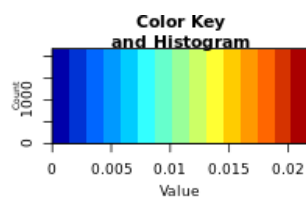


**PDD matrix
H7N5
window = 1000 step = 50**

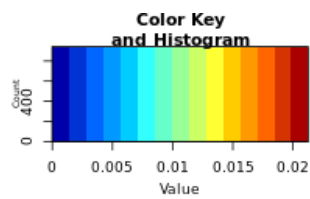


(g)

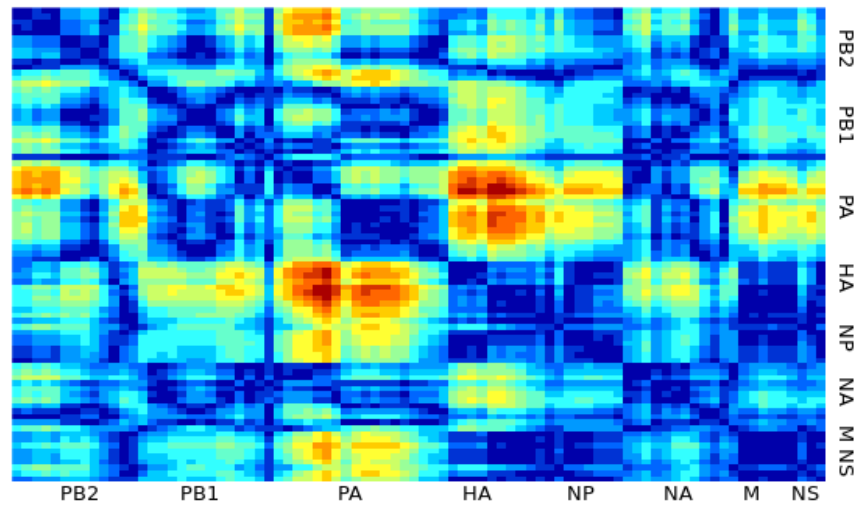
**PDD matrix
H7N5
window = 1000 step = 100**



(h)

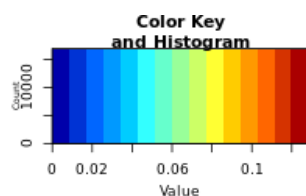


**PDD matrix
H7N5
window = 1000 step = 150**

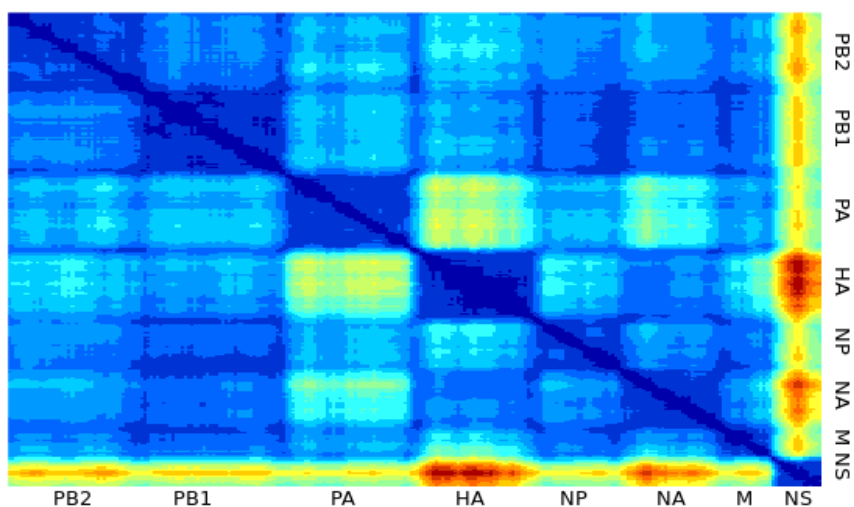


(i)

Supplementary Figure S5. Pairwise distance divergence matrix (PDDM) for H7N5 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

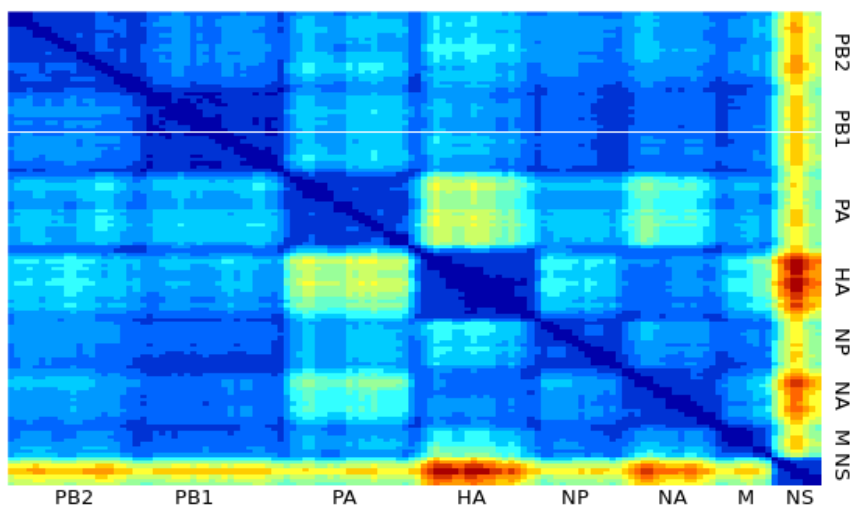
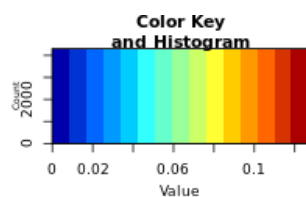


**PDD matrix
H7N6
window = 500 step = 50**

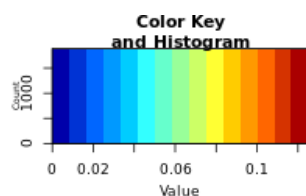


(a)

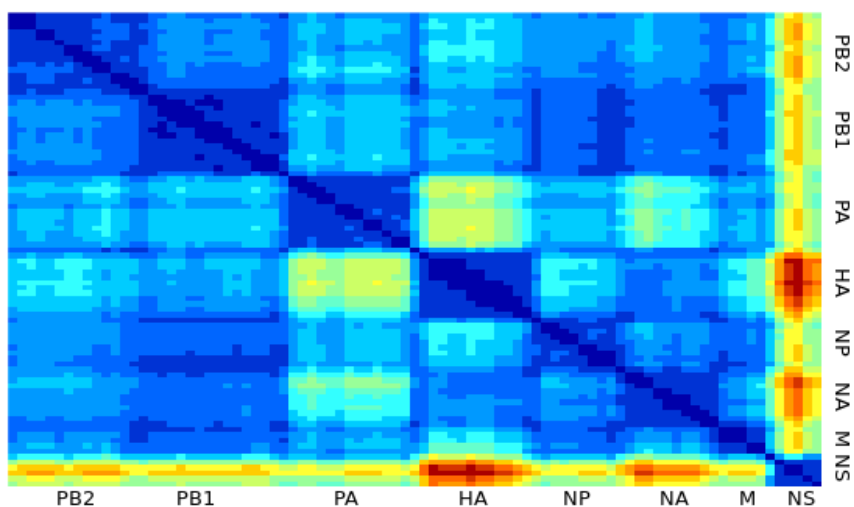
**PDD matrix
H7N6
window = 500 step = 100**



(b)

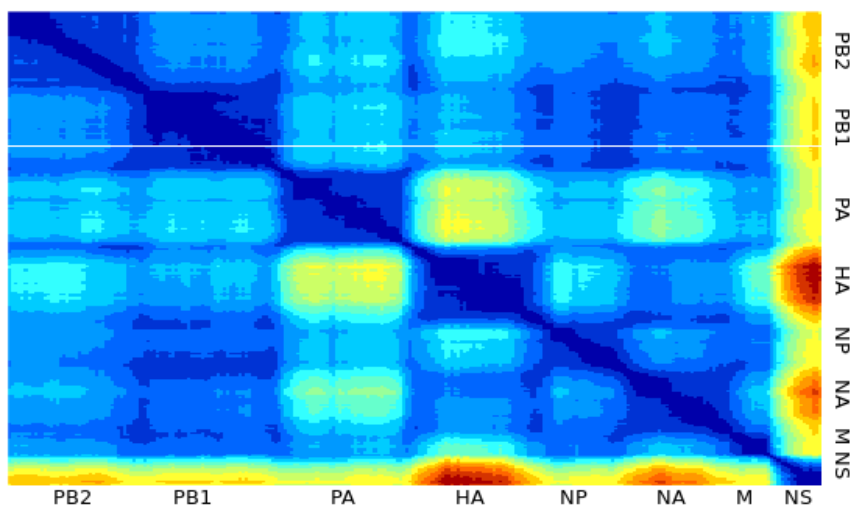
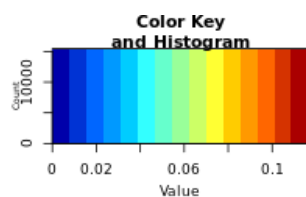


**PDD matrix
H7N6
window = 500 step = 150**

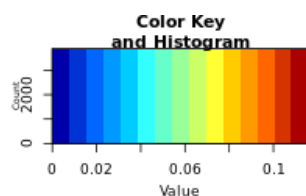


(c)

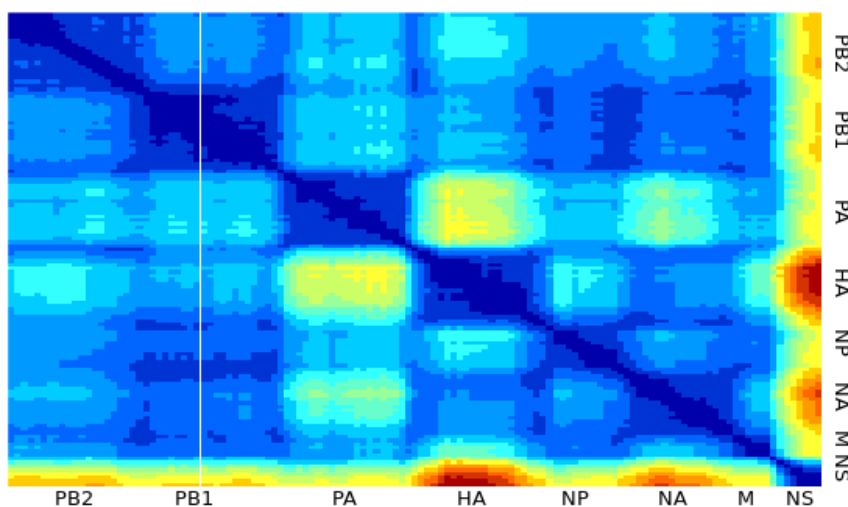
**PDD matrix
H7N6
window = 750 step = 50**



(d)

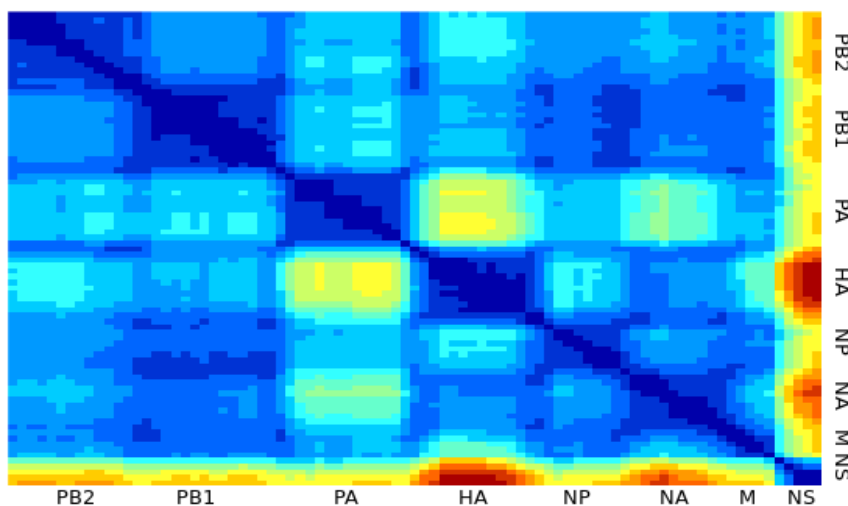
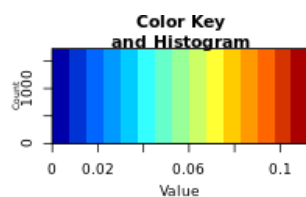


**PDD matrix
H7N6
window = 750 step = 100**

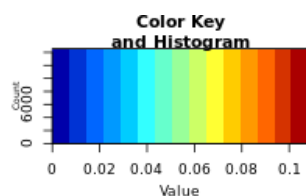


(e)

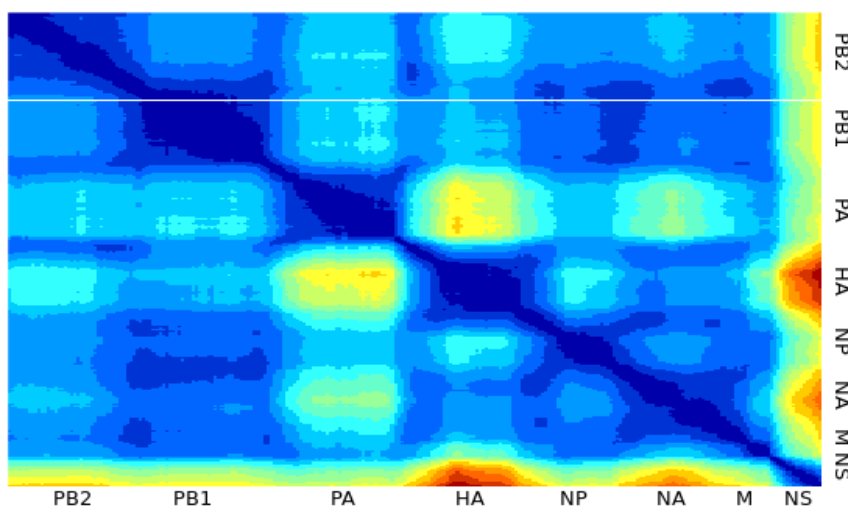
**PDD matrix
H7N6
window = 750 step = 150**



(f)

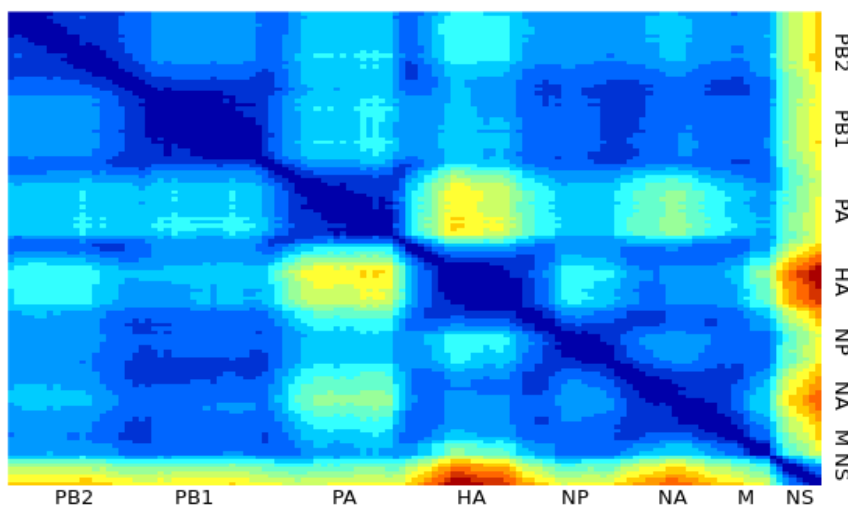
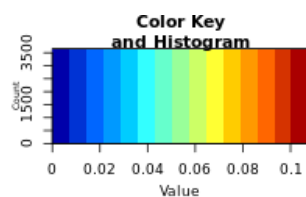


**PDD matrix
H7N6
window = 1000 step = 50**

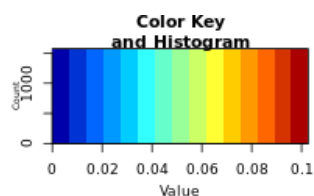


(g)

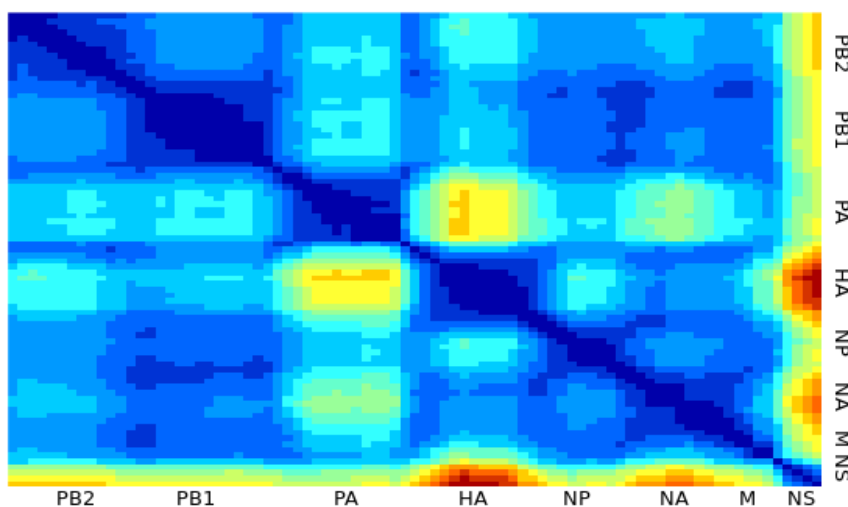
**PDD matrix
H7N6
window = 1000 step = 100**



(h)

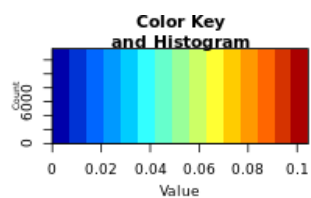


**PDD matrix
H7N6
window = 1000 step = 150**

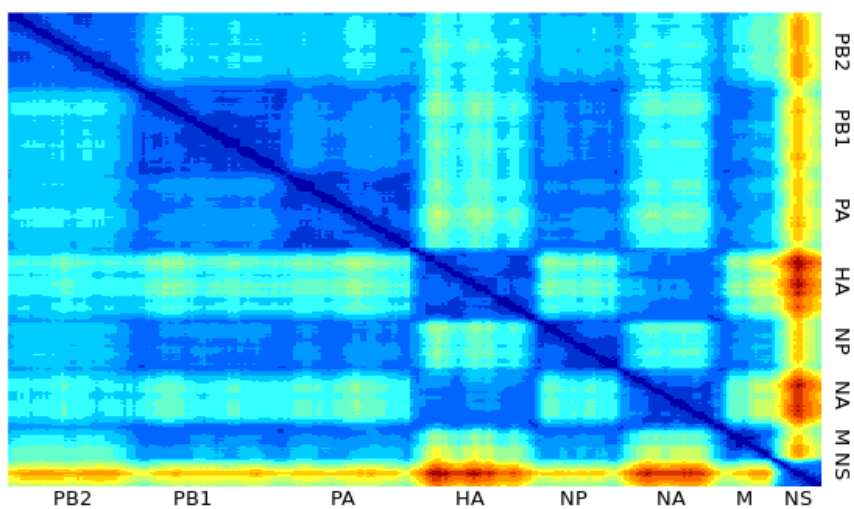


(i)

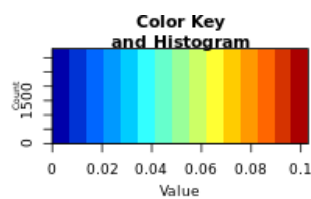
Supplementary Figure S6. Pairwise distance divergence matrix (PDDM) for H7N6 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.



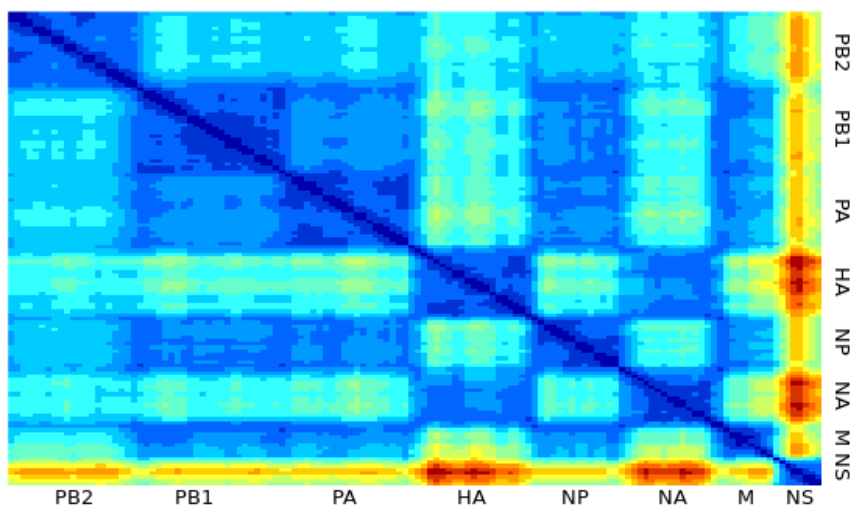
**PDD matrix
H7N7
window = 500 step = 50**



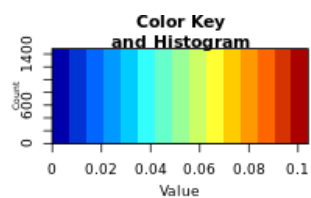
(a)



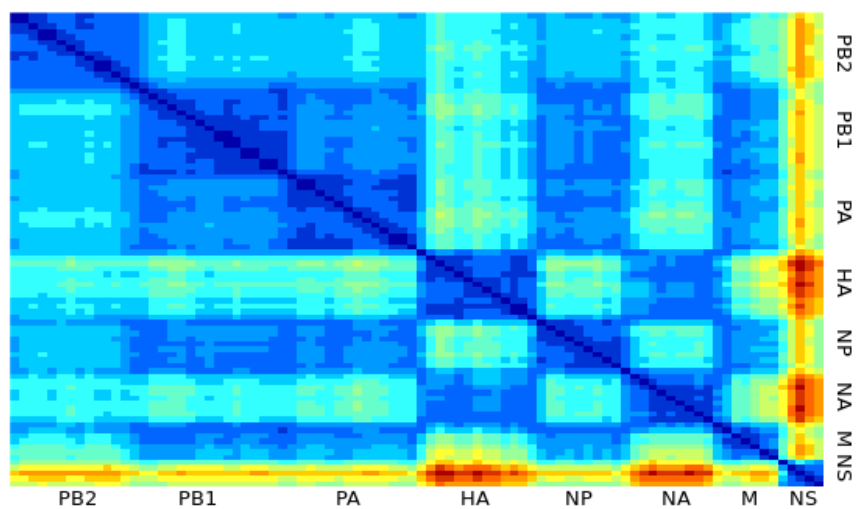
**PDD matrix
H7N7
window = 500 step = 100**



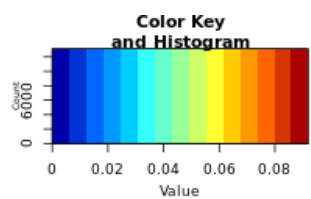
(b)



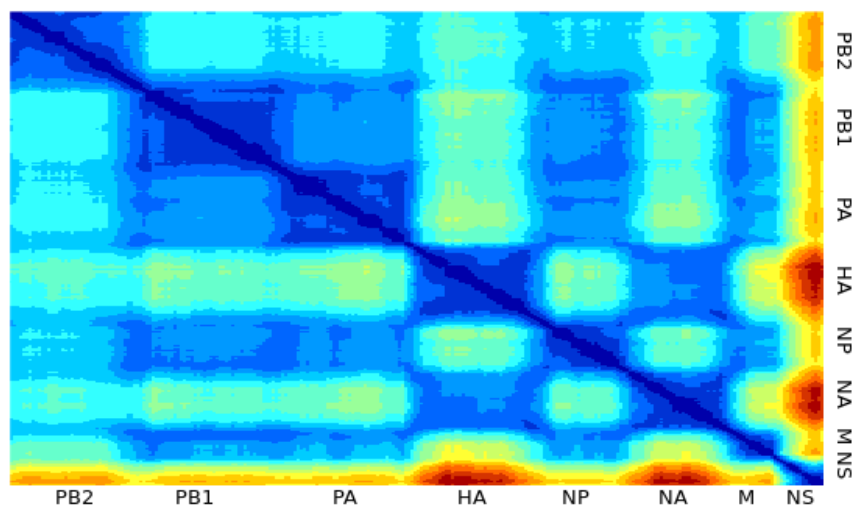
**PDD matrix
H7N7
window = 500 step = 150**



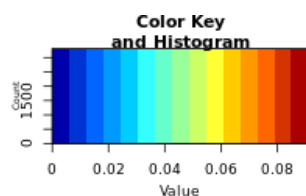
(c)



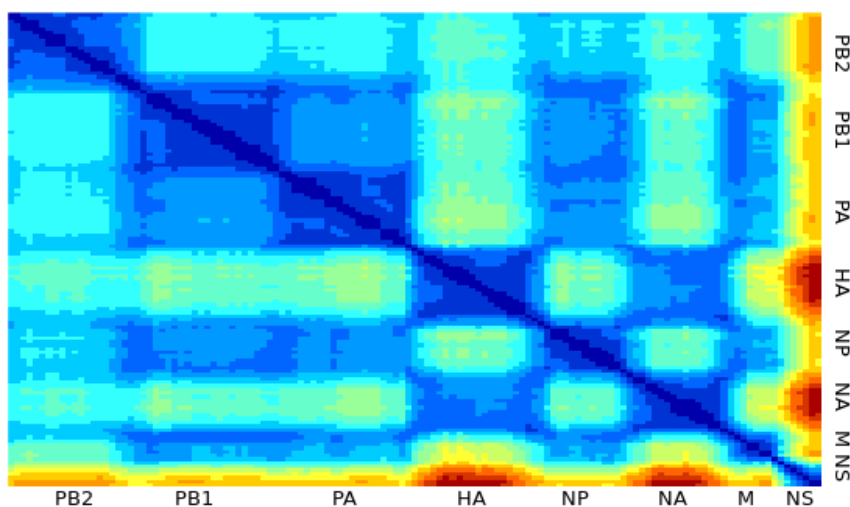
**PDD matrix
H7N7
window = 750 step = 50**



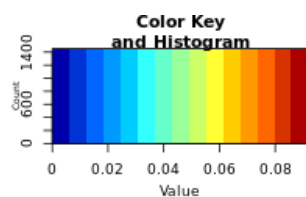
(d)



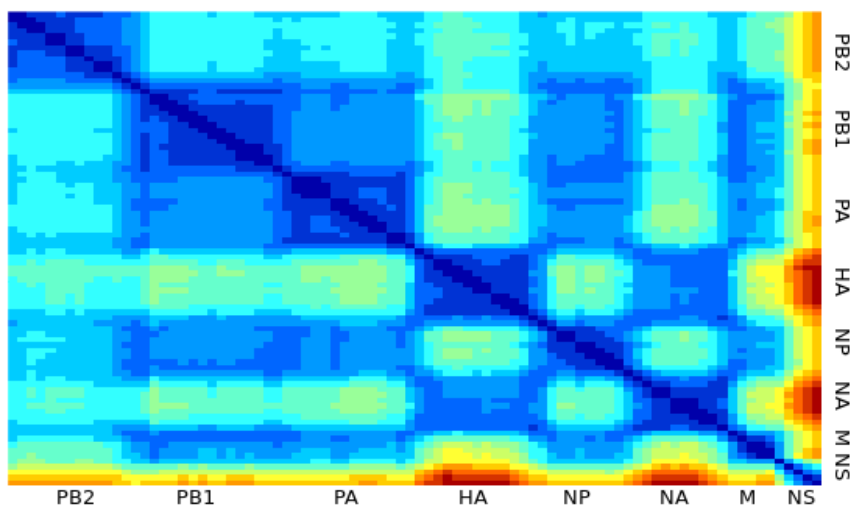
**PDD matrix
H7N7
window = 750 step = 100**



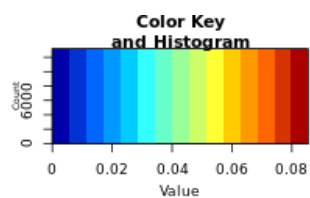
(e)



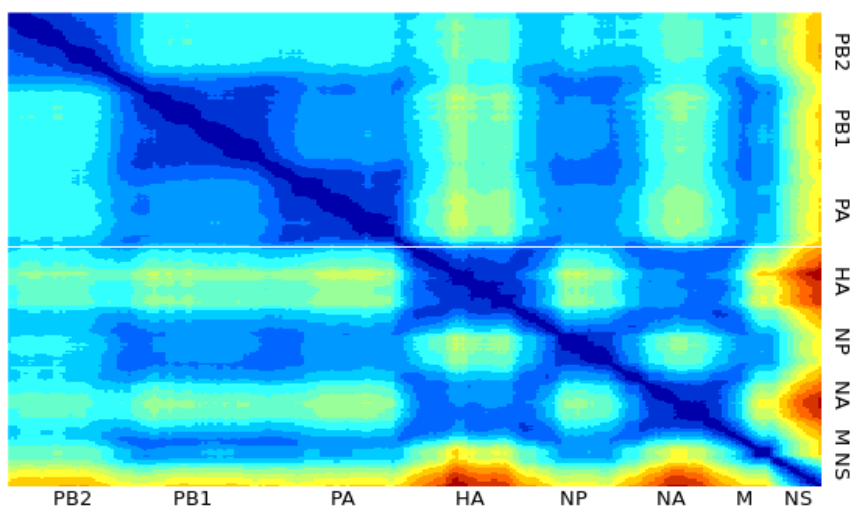
**PDD matrix
H7N7
window = 750 step = 150**



(f)

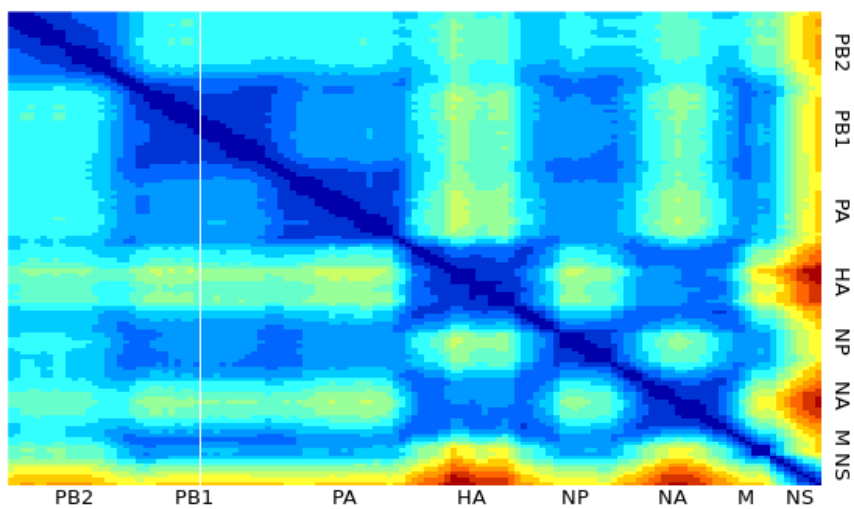
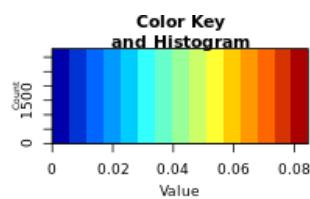


**PDD matrix
H7N7
window = 1000 step = 50**

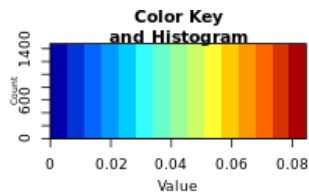


(g)

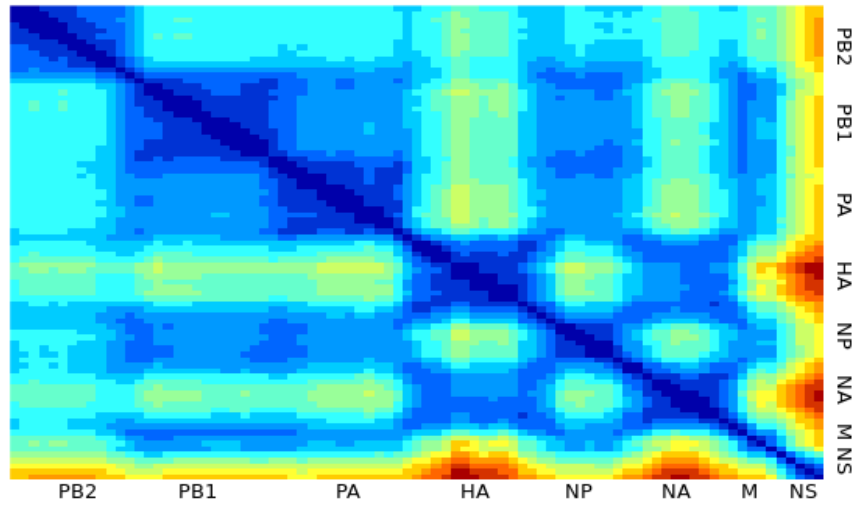
**PDD matrix
H7N7
window = 1000 step = 100**



(h)

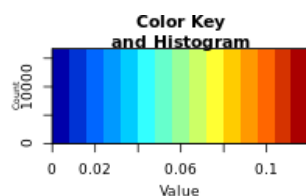


**PDD matrix
H7N7
window = 1000 step = 150**

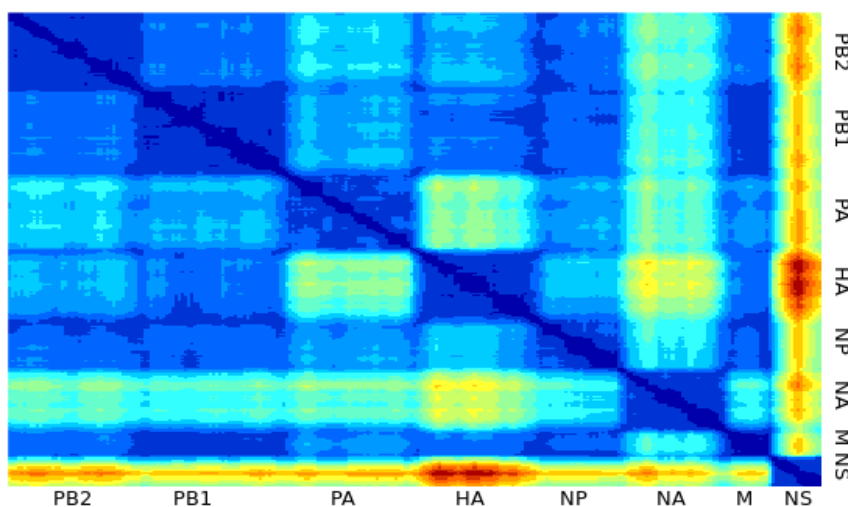


(i)

Supplementary Figure S7. Pairwise distance divergence matrix (PDDM) for H7N7 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

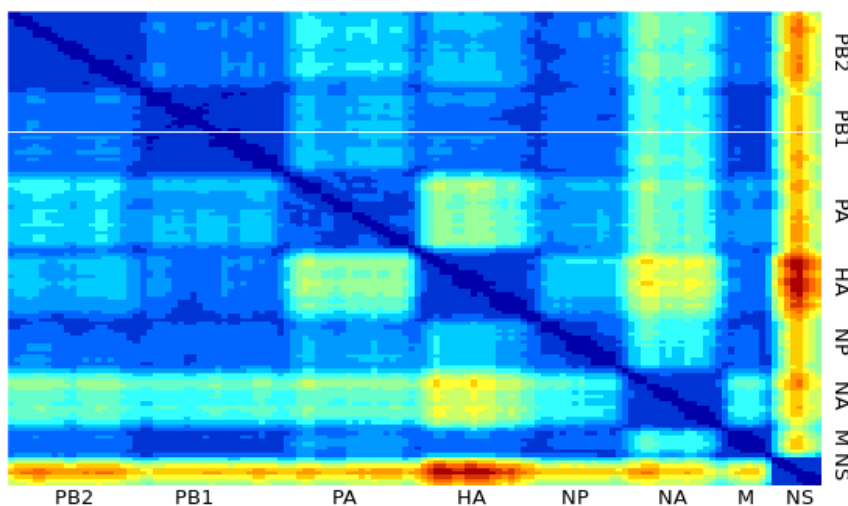
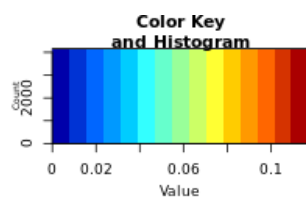


**PDD matrix
H7N8
window = 500 step = 50**

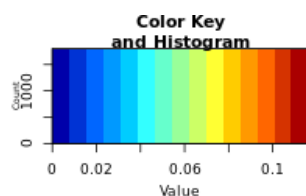


(a)

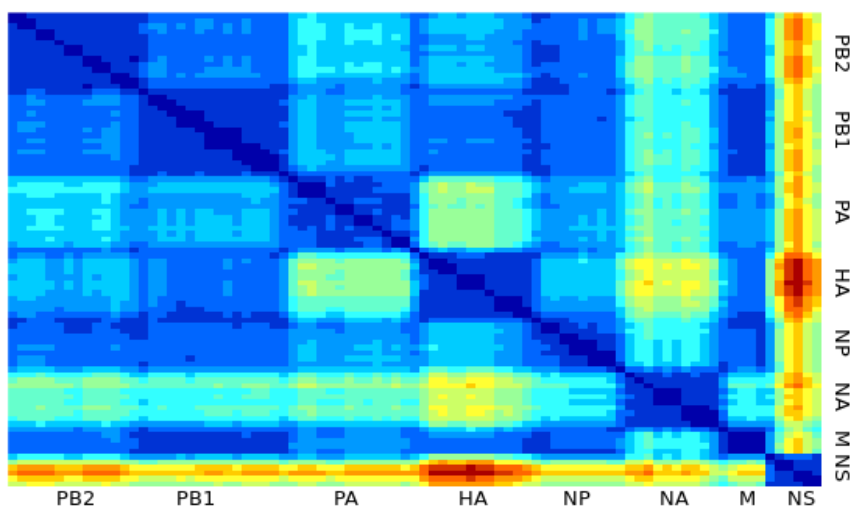
**PDD matrix
H7N8
window = 500 step = 100**



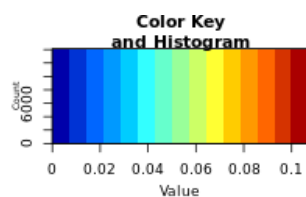
(b)



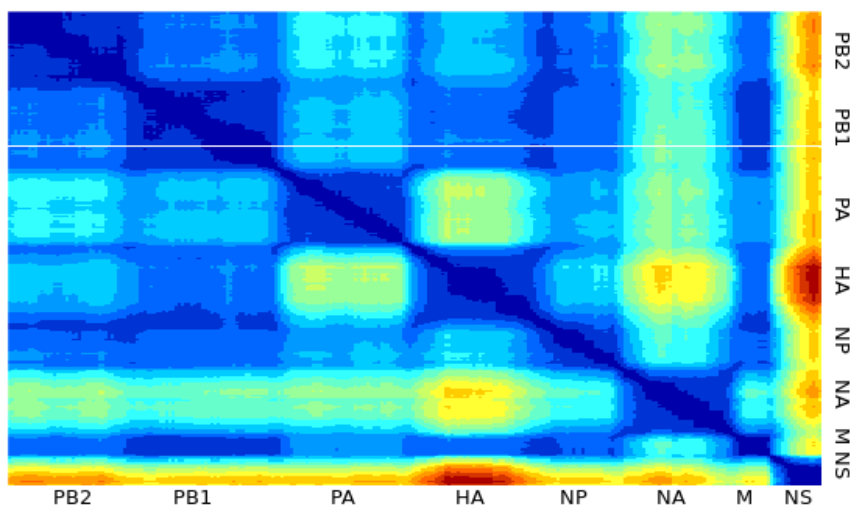
**PDD matrix
H7N8
window = 500 step = 150**



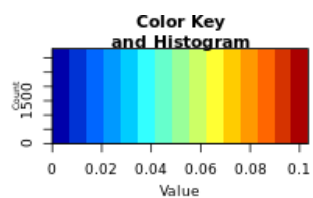
(c)



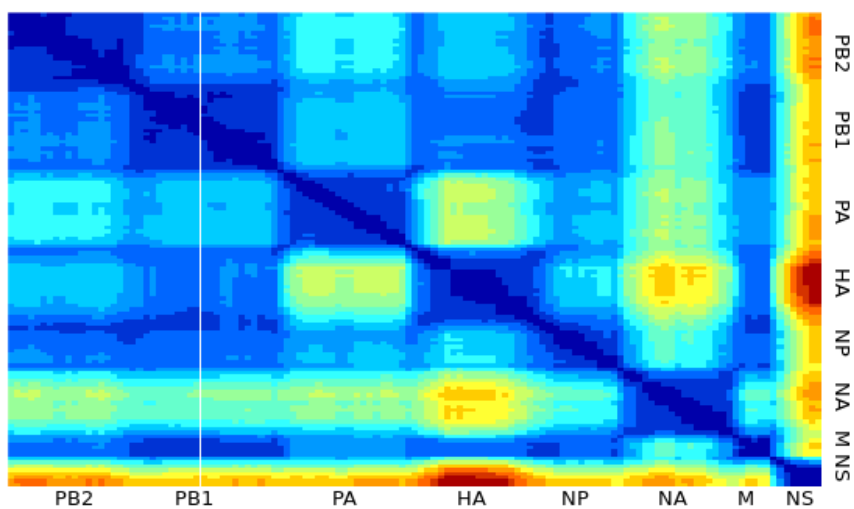
**PDD matrix
H7N8
window = 750 step = 50**



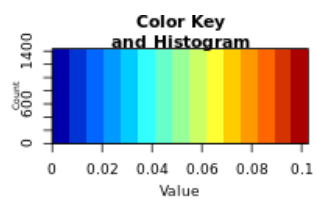
(d)



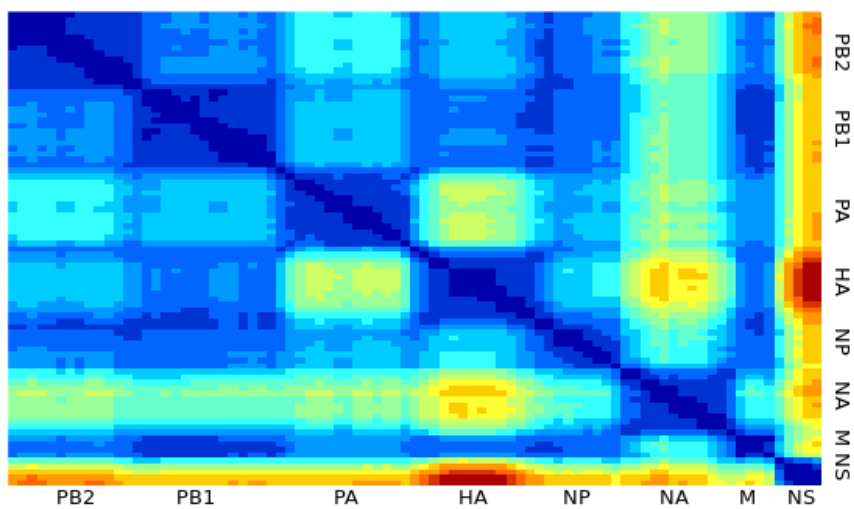
**PDD matrix
H7N8
window = 750 step = 100**



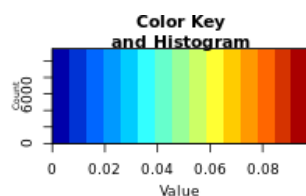
(e)



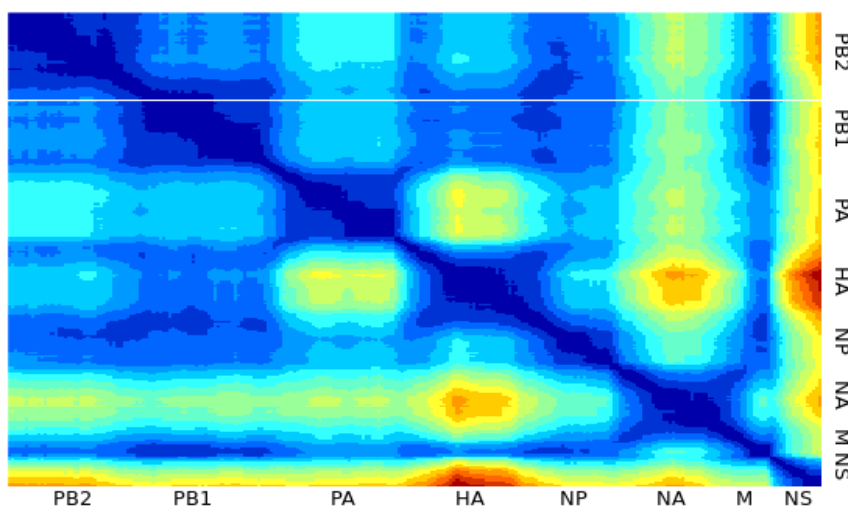
**PDD matrix
H7N8
window = 750 step = 150**



(f)

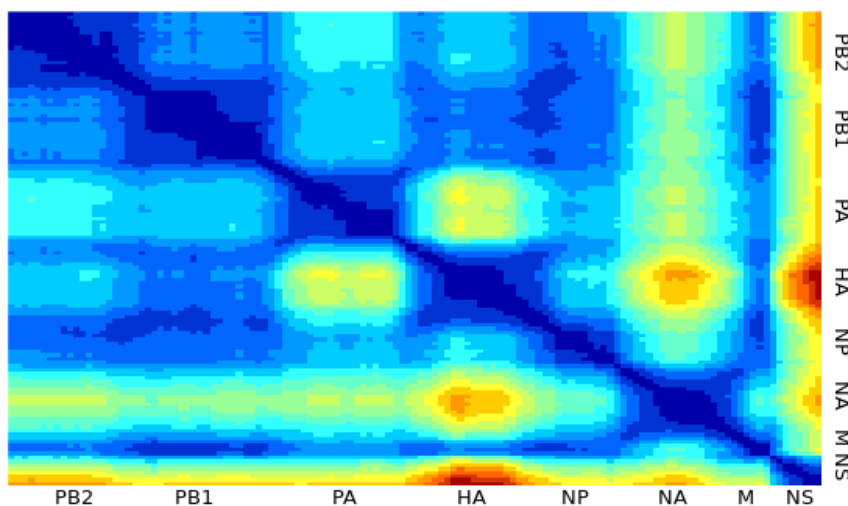
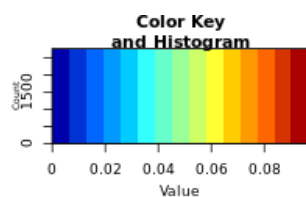


**PDD matrix
H7N8
window = 1000 step = 50**

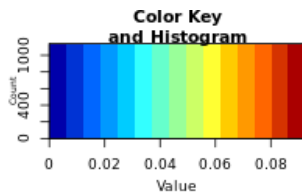


(g)

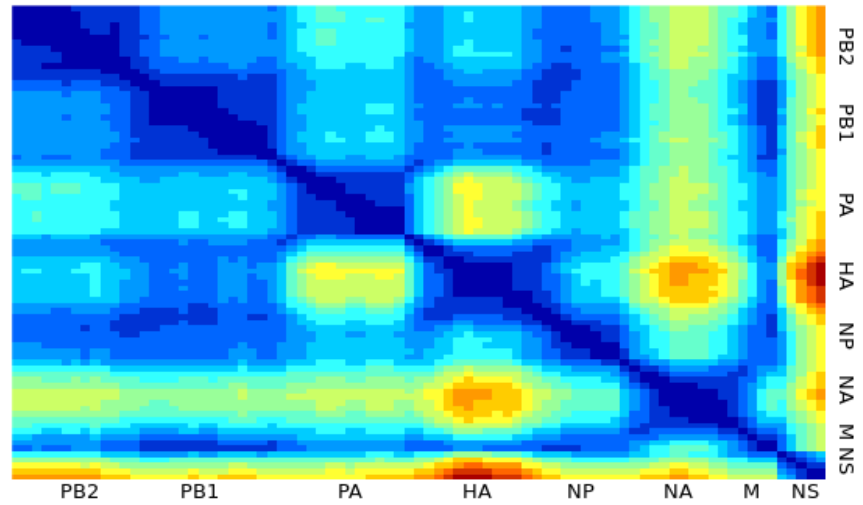
**PDD matrix
H7N8
window = 1000 step = 100**



(h)

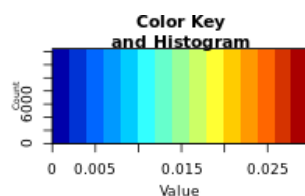


**PDD matrix
H7N8
window = 1000 step = 150**

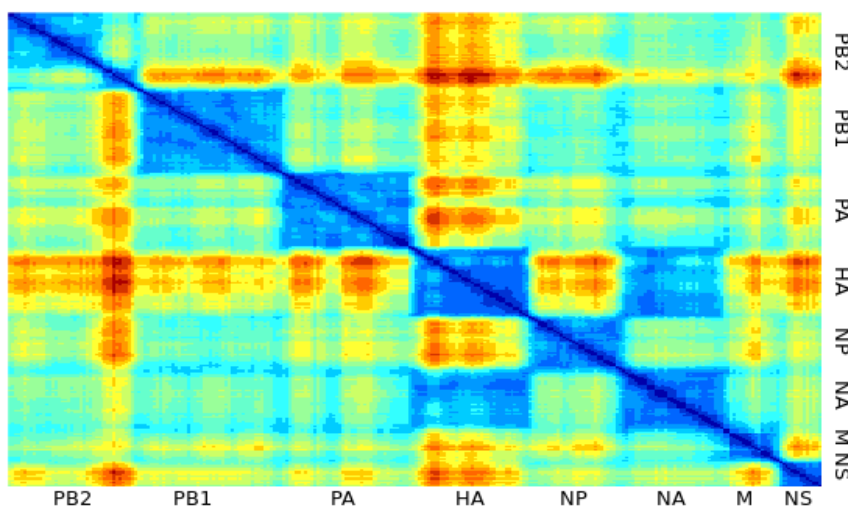


(i)

Supplementary Figure S8. Pairwise distance divergence matrix (PDDM) for H7N8 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.

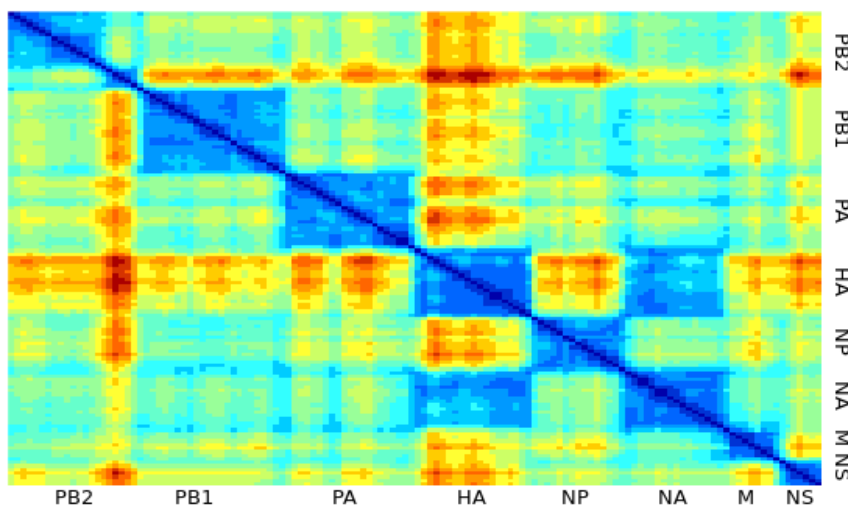
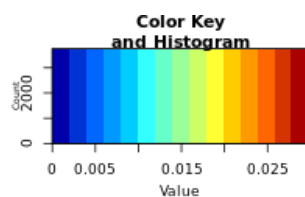


**PDD matrix
H7N9
window = 500 step = 50**

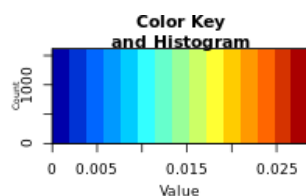


(a)

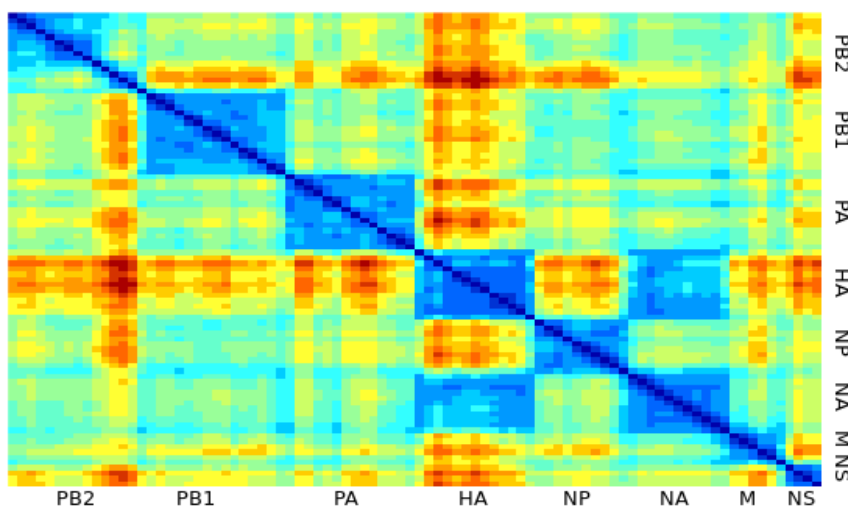
**PDD matrix
H7N9
window = 500 step = 100**



(b)

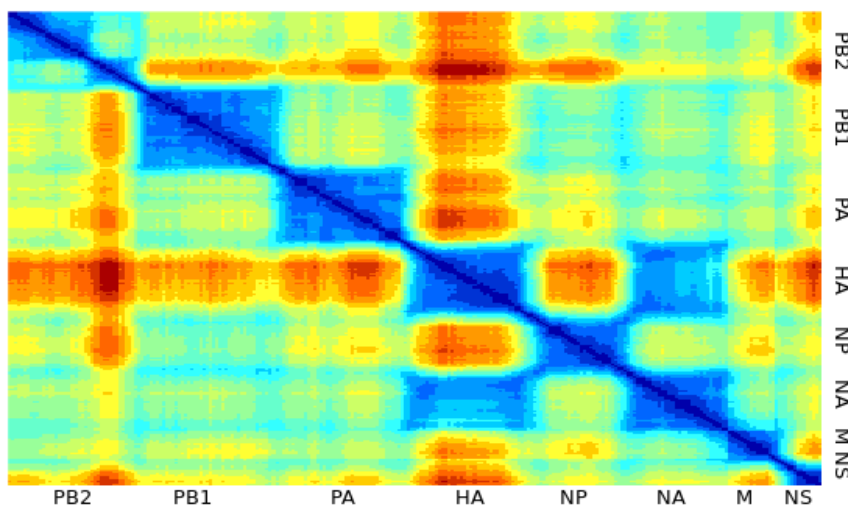
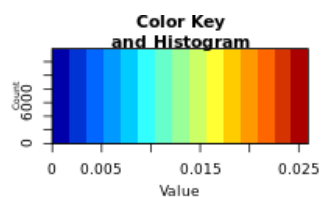


**PDD matrix
H7N9
window = 500 step = 150**

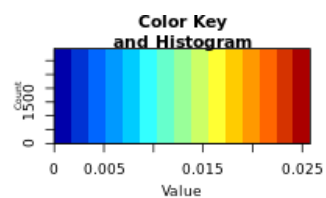


(c)

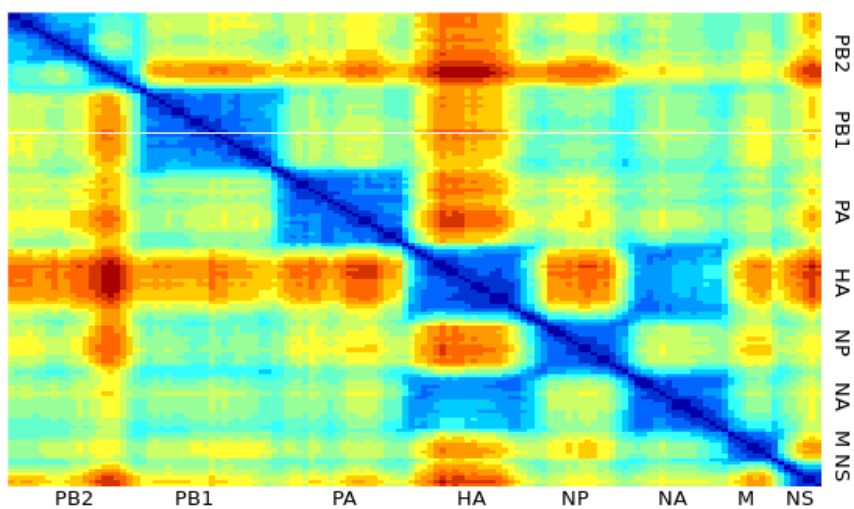
**PDD matrix
H7N9
window = 750 step = 50**



(d)

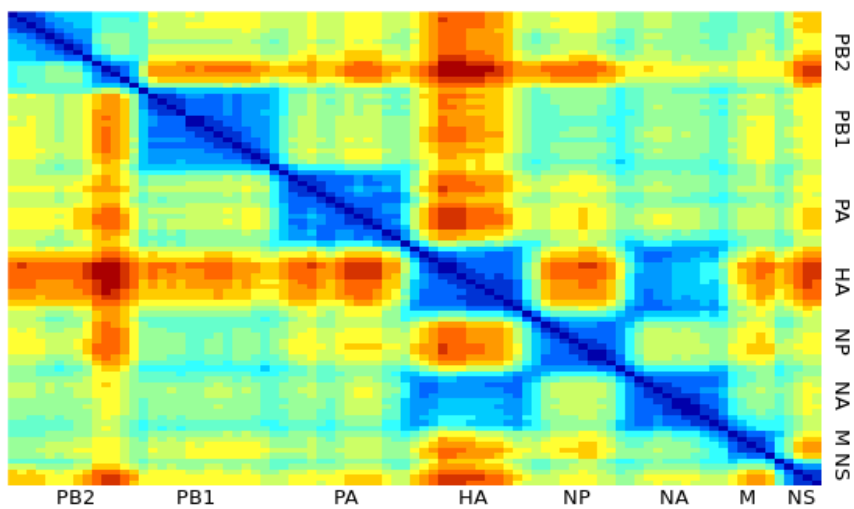
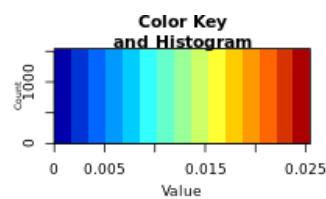


**PDD matrix
H7N9
window = 750 step = 100**

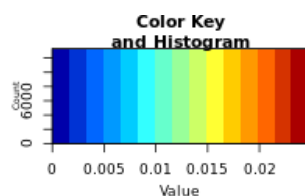


(e)

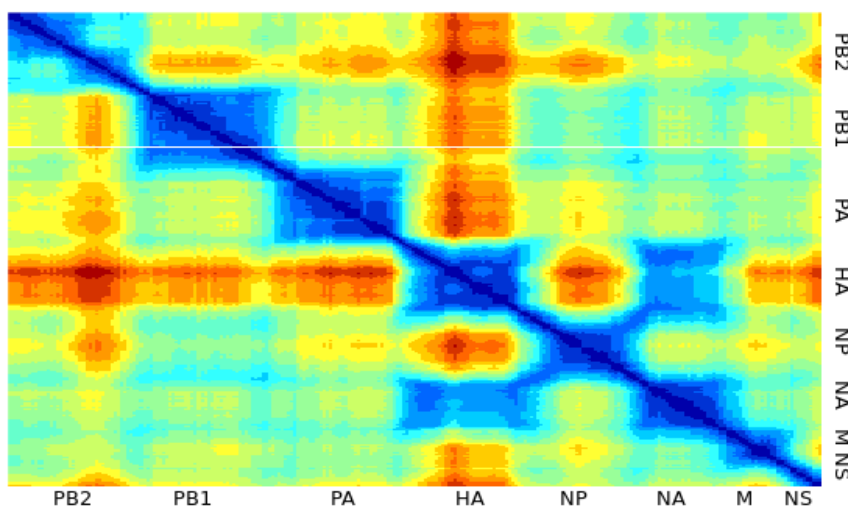
**PDD matrix
H7N9
window = 750 step = 150**



(f)

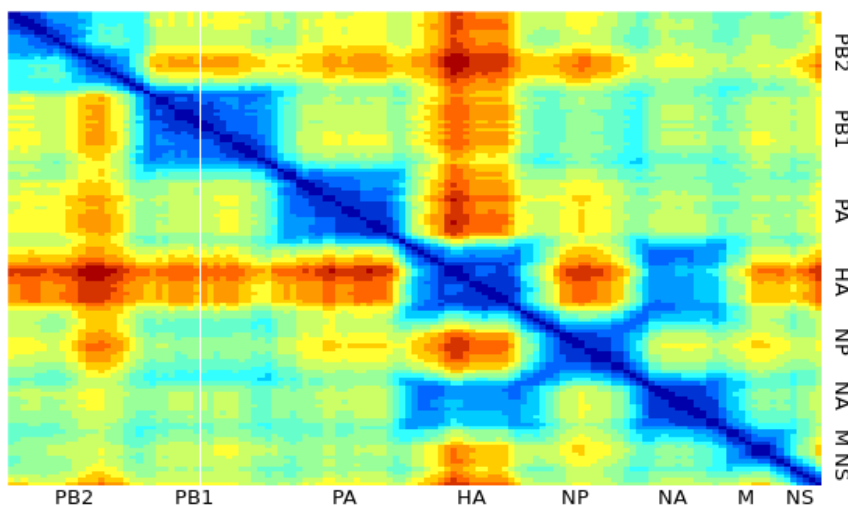
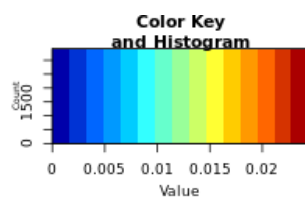


**PDD matrix
H7N9
window = 1000 step = 50**

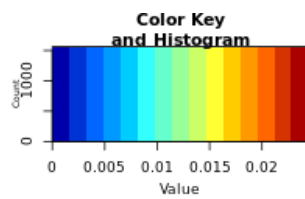


(g)

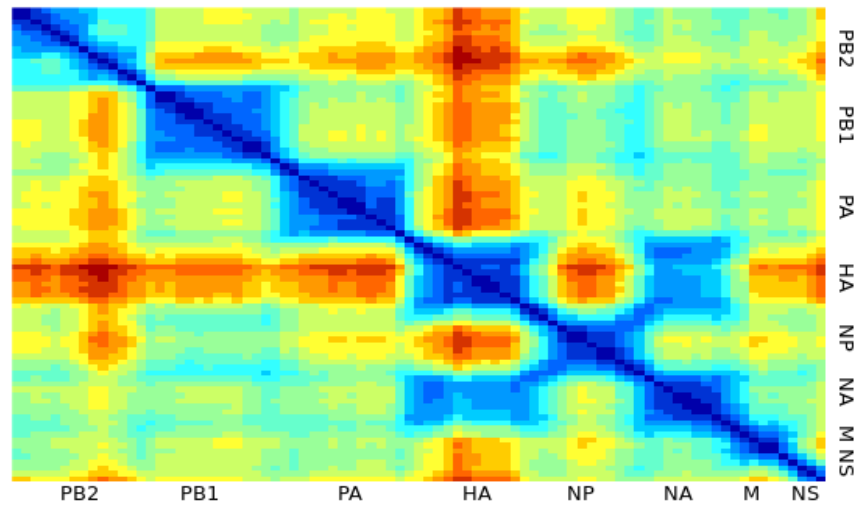
**PDD matrix
H7N9
window = 1000 step = 100**



(h)



**PDD matrix
H7N9
window = 1000 step = 150**



(i)

Supplementary Figure S9. Pairwise distance divergence matrix (PDDM) for H7N9 influenza viruses **(a)** Window = 500 nucleotides, Step = 50 nucleotides **(b)** Window = 500 nucleotides, Step = 100 nucleotides **(c)** Window = 500 nucleotides, Step = 150 nucleotides **(d)** Window = 750 nucleotides, Step = 50 nucleotides **(e)** Window = 750 nucleotides, Step = 100 nucleotides **(f)** Window = 750 nucleotides, Step = 150 nucleotides **(g)** Window = 1000 nucleotides, Step = 50 nucleotides **(h)** Window = 1000 nucleotides, Step = 100 nucleotides **(i)** Window = 1000 nucleotides, Step = 150 nucleotides. The color gradient scale shows the root mean square error (RMSE) values in PDCP is a figure.