Suppl. Table S1. MS data of the influenza A virus polymerase complex (Set 2: no nuclease treatment).

gi number [a]	Protein Name	Sequence coverage (%)	Number of unique peptides	PA [c]	PA-PB1 [c]	3P [c]	3P-WSN	3P-CA/04
50313055	PA [Influenza A virus (A/Viet Nam/1203/2004(H5N1))]	74.47	55	809 [b]	732	337		
50296440	PB1 [Influenza A virus (A/Viet Nam/1203/2004(H5N1))]	67.34	40	0	673	286		
50296548	PB2 [[Influenza A virus (A/Viet Nam/1203/2004(H5N1))]	52.59	34	0	0	171		
227977114	PA [Influenza A virus (A/California/04/2009(H1N1))]	51.96	33					396
253828525	PB1 [Influenza A virus (A/California/04/2009(H1N1))]	68.96	40					487
227977116	PB2 [Influenza A virus (A/California/04/2009(H1N1))]	51.38	34					258
194352383	PA[Influenza A virus (A/WSN/1933(H1N1))]	42.60	28				487	
194352385	PB1[Influenza A virus (A/WSN/1933(H1N1))]	66.71	37				467	
194352388	PB2[Influenza A virus (A/WSN/1933(H1N1))]	49.80	33				563	

a) NCBI gi number (sequence record identifier)

b) Numbers represent the spectral counts for each protein averaged across technical replicates.

c) A/Viet Nam/1203/2004(H5N1)

Note: The labels “PA-PB1” and “3P” refer to purified complexes expected to contain PA and PB1 or PA, PB1 and PB2, respectively.