

**Table S15. Summary of regions of significant constraint found in H7N7 (avian host) influenza A genes, using weighted and ranked codon variability values. Reference sequences used are GenBank KM922674.1, KM922675.1, KM922676.1, KM922677.1, KM922678.1, KM922679.1, KM922680.1, KM922673.1, for segments 1–8, respectively. Citation details may be found in S1 Appendix. \*Denotes a region only found by excluding a potentially interfering signal. *Z*- and *p*-values in parentheses denote values prior to removal of the next most significant signal. If parenthetical values are absent, then such a signal was removed in an earlier step only.**

Gene	Order found	Refseq nt location	<i>Z</i>	<i>p</i>	Comment
PB2	2	7–90	3.04	<0.0001	Packaging-associated(21, 22); conserved RNA structure(18)
	1	2179–2280	5.04	<0.0001	Packaging-associated(4–6, 21, 23, 24); conserved RNA structure(3, 25)
PB1	2	73–99	2.25	0.0265	PB1-F2 initiation – note region is 3' of regions previously associated with packaging; conserved RNA structure(18)
	1	2125–2265	3.99	<0.0001	Packaging-associated(5, 6, 21, 22) – note region described extends 5' of previously described regions; conserved RNA structure(3, 18)
PB1-F2	1	269–331	1.98	0.0001	PB1-N92 initiation region (see main text); conserved RNA structure(18)
PA	3	4–75	3.15	<0.0001	Packaging-associated(6, 22) – but longer than one previously described region
	1	568–741	5.50	<0.0001	Proposed frameshift stimulator (see main text); overlap PA-X(26)
	2	1999–2145	4.23	<0.0001	Packaging-associated(5, 6, 21) – but longer than previously described regions; conserved cRNA structure(18)
PA-X	2	10–75	2.33	0.0017	Packaging-associated(6, 22) – but longer than one previously described region
	1	568–572; 574–748	4.20	<0.0001	Proposed frameshift stimulator (see main text); overlap PA
HA	1	1582–1680	3.24	<0.0001	Packaging-associated(8, 9, 27)
NP	2	7–63	3.06	<0.0001	Packaging-associated(28, 29); conserved RNA structure(3, 18)
	1	1372–1482	4.67	<0.0001	Packaging-associated(28–31) – but longer than previously described region; conserved RNA structure(3, 31)
NA	1	1345–1416	3.91	<0.0001	Packaging-associated(31–33); conserved cRNA structure(18)
M1	1	11–232	3.41	<0.0001	Packaging-associated(7, 16); M2 splice donor; M42 alternate ORF and m4 splice junction(17); conserved RNA structure(3, 14, 15, 18)
M2	Nil found				
NS1	3*	41–46	1.56	0.0312	Packaging-associated(11); splice donor
	4*	95–127	1.24	0.0411	Conserved RNA structure(3, 15, 37, 38)
			(1.20)	(0.1139)	
	2*	146–169	1.64	0.0125	Unclear
		(1.59)	(0.0701)		
	1	512–703	3.51	<0.0001	Splice acceptor; conformationally important region(20); overlapping ORFs
NS2	1	528–581	2.17	0.0235	Conformationally important region(20); overlapping ORFs
	3*	606–620	1.54	0.0475	Overlapping ORFs
			(1.46)	(0.2091)	
	2*	645–704	1.82	0.0459	Overlapping ORFs
		(1.68)	(0.1675)		
	4*	837–848	1.52	0.0151	Packaging-associated(11)