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Electronic Supplementary Material

Development of multi-analyte suspension assay for simultaneously efficient detection of avian influenza virus A subtypes

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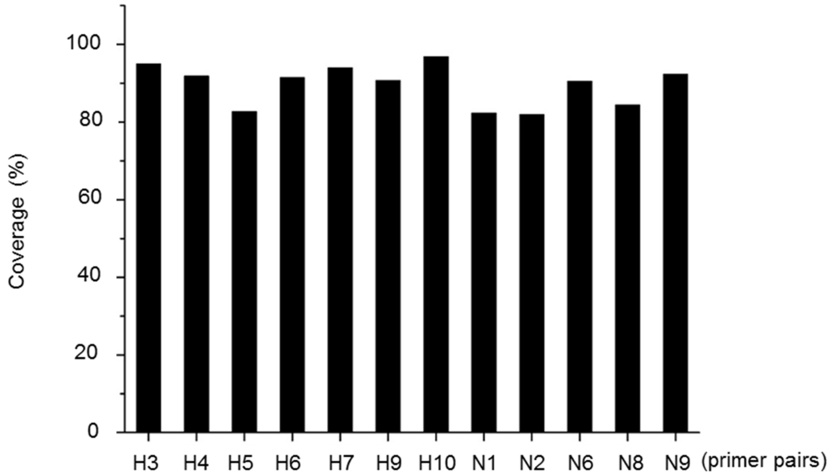

Supplementary Figure S1. The coverage of each primer pairs. We use 12 subtypes of AIVs sequences as template database to run a virtual PCR amplification to predict successful amplicons with 19 pairs of designed primers. The percentages of predicted amplicons represent the coverage (sensitivity) of each primer pairs. The coverage of each primer pairs ranged from 82% to 97%.

Supplementary Table S1. Accession numbers of 27,549 Asian AIVs subtypes sequences downloaded from NCBI and GISAID database.

Supplementary Table S2. Subtype-specific primers evaluated by thermodynamics-based MFEprimer-2.0.

	Predicted amplicons										
data base	H3	H4	H5	H6	H7	H9	H10	N1	N2	N6	N8	N9
H3	262/276	0	0	0	0	0	0	0	0	0	0	0
H4	0	257/280	0	0	0	0	0	0	0	0	0	0
H5	0	0	5874/7107	0	0	0	0	0	0	0	0	0
H6	0	0	0	1445/1581	0	0	0	0	0	0	0	0
H7	0	0	0	0	700/745	0	0	0	0	0	0	0
H9	0	0	0	0	0	4272/4711	0	0	0	0	0	0
H10	0	0	0	0	0	0	93/96	0	0	0	0	0
N1	0	0	0	0	0	0	0	4103/4986	0	0	0	0
N2	0	0	0	0	0	0	0	0	3933/4799	0	0	0
N6	0	0	0	0	0	0	0	0	0	1453/1605	0	0
N8	0	0	0	0	0	0	0	0	0	0	546/647	0
N9	0	0	0	0	0	0	0	0	0	0	0	663/716