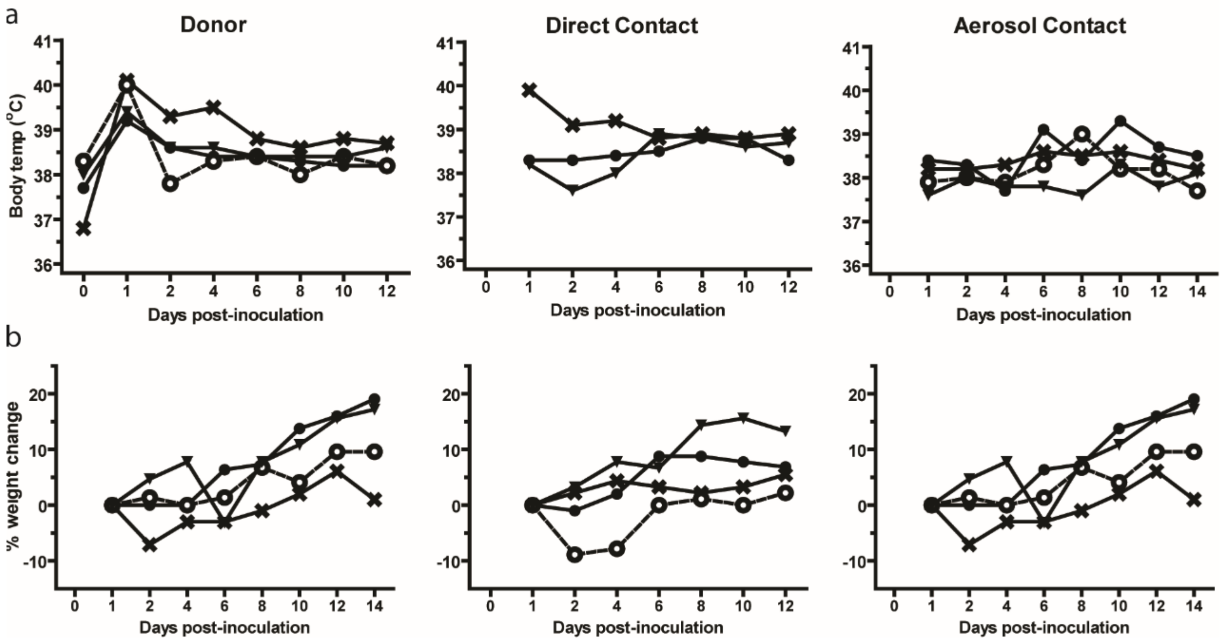
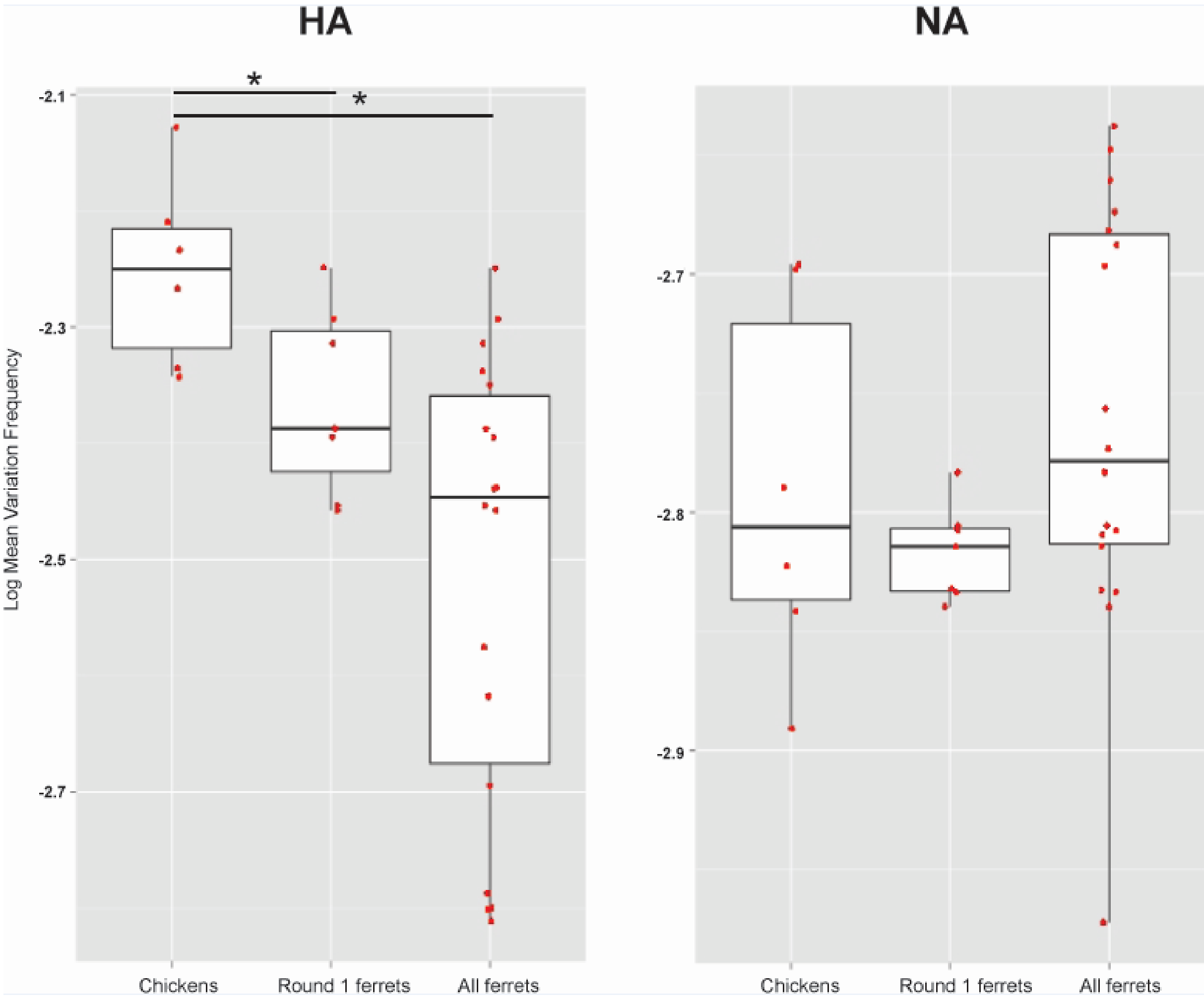
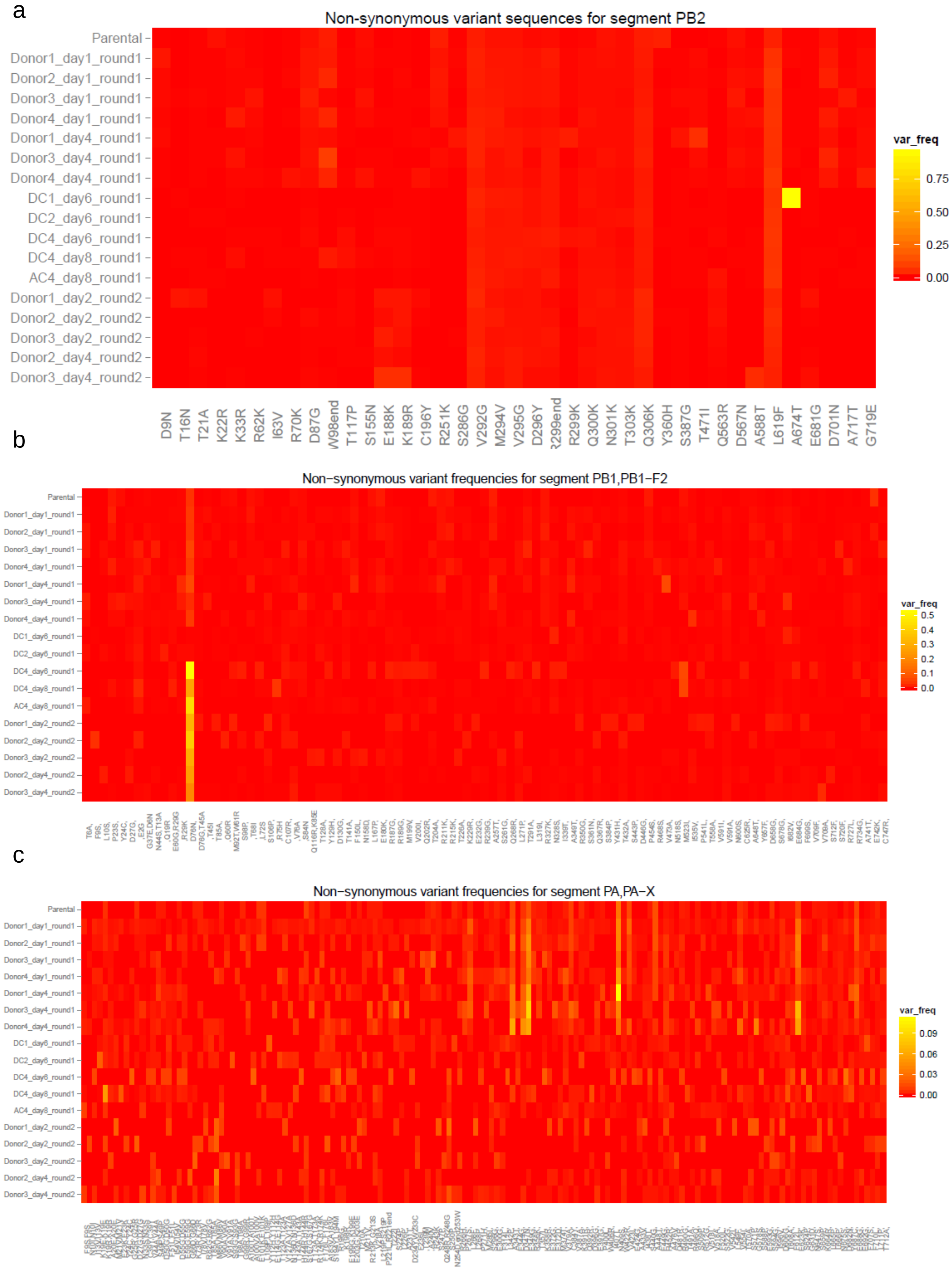


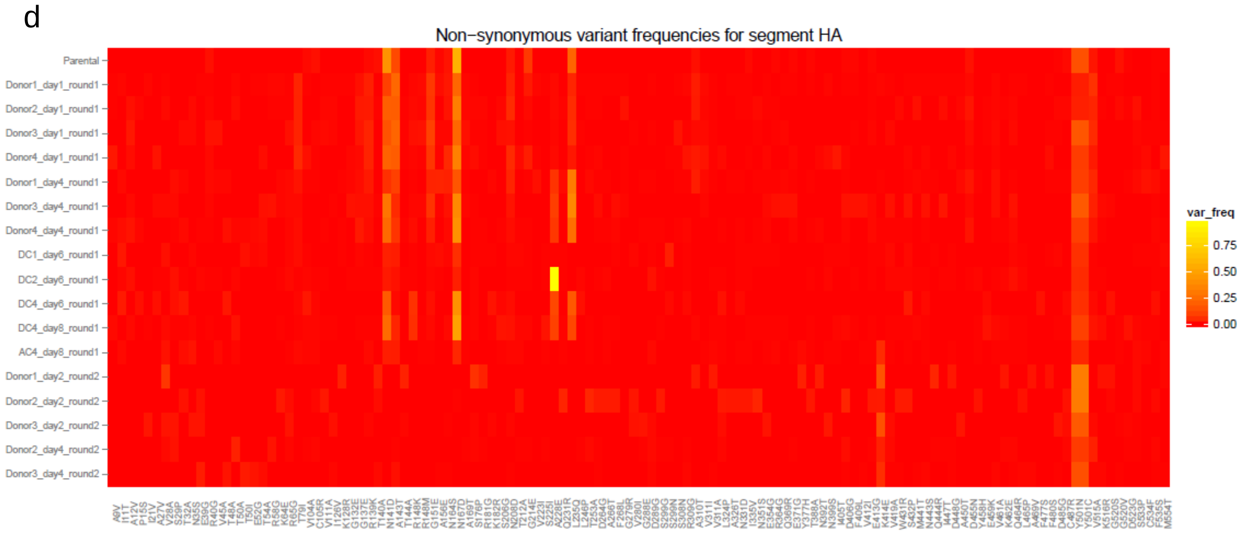
Supplementary Figure 1 | Weight and body temperature of ferrets inoculated with A/Anhui/1/2013 (H7N9) influenza virus. (**a**) Body temperature and (**b**) weight change of ferrets after intranasal inoculation with 10^6 TCID50 of A/Anhui/1/2013 (H7N9) influenza virus, direct contact, and aerosol contact (*n* = 4 per group). Body temperature is shown for only 3 direct contact ferrets, as one temperature probe was faulty.



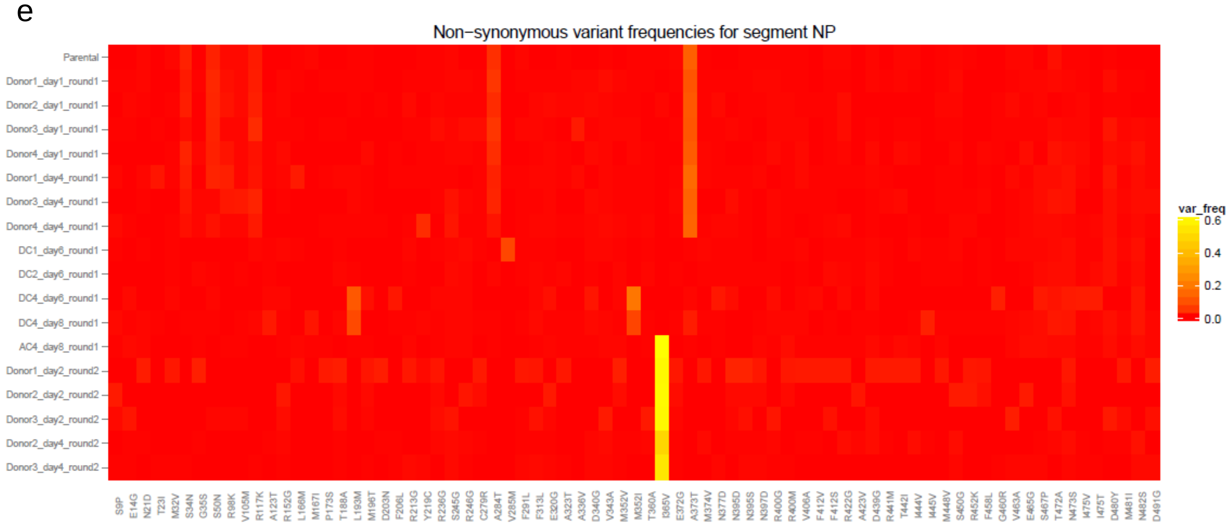
Supplementary Figure 2 | Mean variation frequencies of HA and NA genes after virus replication in chickens and ferrets. "Round 1 ferrets" were inoculated with parental A/Anhui/1/13 (H7N9) influenza virus; "all ferrets" include donor and contact ferrets in rounds 1 and 2. Statistical comparisons were performed by using two-tailed Mann-Whitney U test, $*P < 0.05$.


a
Non-synonymous variant sequences for segment PB2
Parental
Donor1_day1_round1
Donor2_day1_round1
Donor3_day1_round1
Donor4_day1_round1
Donor1_day4_round1
Donor3_day4_round1
Donor4_day4_round1
DC1_day6_round1
DC2_day6_round1
DC4_day6_round1
DC4_day8_round1
AC4_day8_round1
Donor1_day2_round2
Donor2_day2_round2
Donor3_day2_round2
Donor2_day4_round2
Donor3_day4_round2
D9N
T16N
T21A
K22R
K33R
R62K
I63V
R70K
D87G
W98end
T117P
S155N
E188K
K189R
C196Y
R251K
S286G
V292G
M294V
V295G
D296Y
R299end
R299K
Q300K
N301K
T303K
Q306K
Y360H
S387G
T471I
Q563R
D567N
A588T
L619F
A674T
E681G
D701N
A717T
G719E
var_freq
0.75
0.50
0.25
0.00
b
Non-synonymous variant frequencies for segment PB1,PB1-F2
var_freq
0.5
0.4
0.3
0.2
0.1
0.0
c
Non-synonymous variant frequencies for segment PA,PA-X
var_freq
0.09
0.06
0.03
0.00

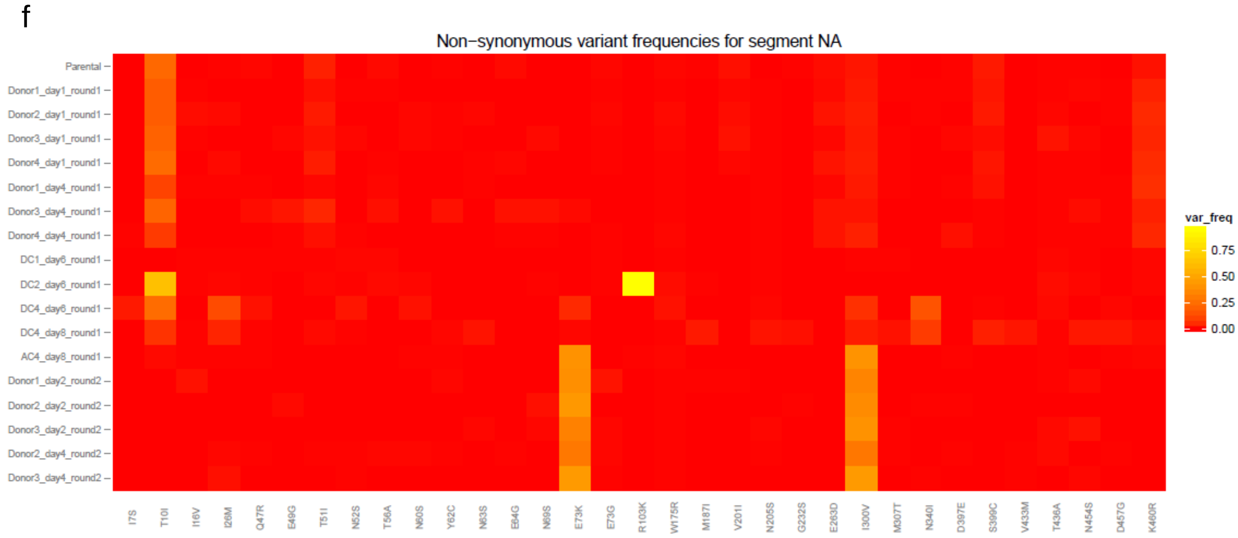
d


Non−synonymous variant frequencies for segment HA
Parental
Donor1_day1_round1
Donor2_day1_round1
Donor3_day1_round1
Donor4_day1_round1
Donor1_day4_round1
Donor3_day4_round1
Donor4_day4_round1
DC1_day6_round1
DC2_day6_round1
DC4_day6_round1
DC4_day8_round1
AC4_day8_round1
Donor1_day2_round2
Donor2_day2_round2
Donor3_day2_round2
Donor2_day4_round2
Donor3_day4_round2
var_freq
0.75
0.50
0.25
0.00

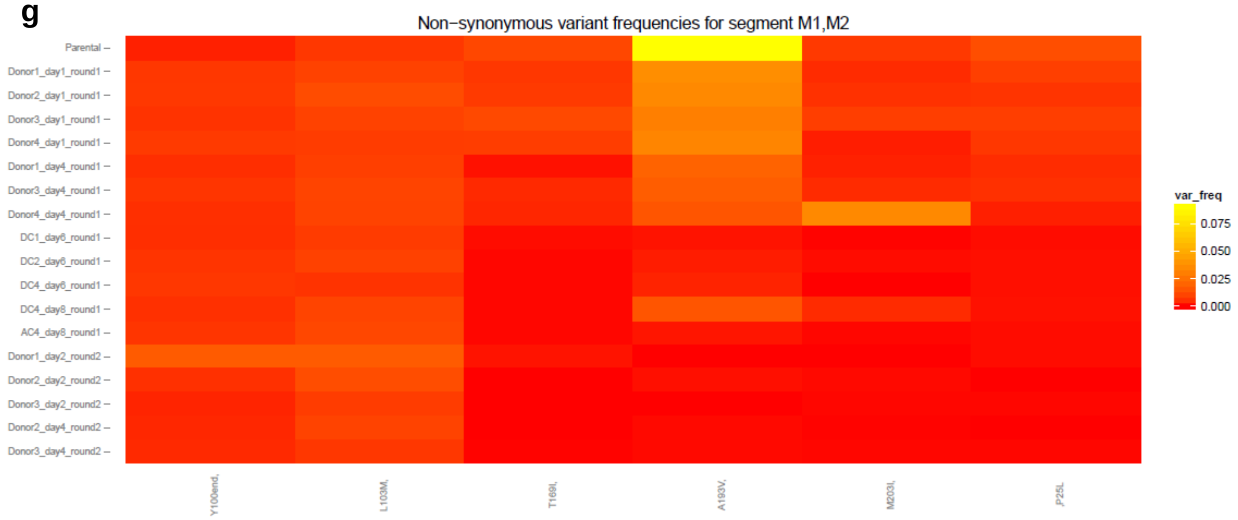
e


Non−synonymous variant frequencies for segment NP
Parental
Donor1_day1_round1
Donor2_day1_round1
Donor3_day1_round1
Donor4_day1_round1
Donor1_day4_round1
Donor3_day4_round1
Donor4_day4_round1
DC1_day6_round1
DC2_day6_round1
DC4_day6_round1
DC4_day8_round1
AC4_day8_round1
Donor1_day2_round2
Donor2_day2_round2
Donor3_day2_round2
Donor2_day4_round2
Donor3_day4_round2
var_freq
0.6
0.4
0.2
0.0

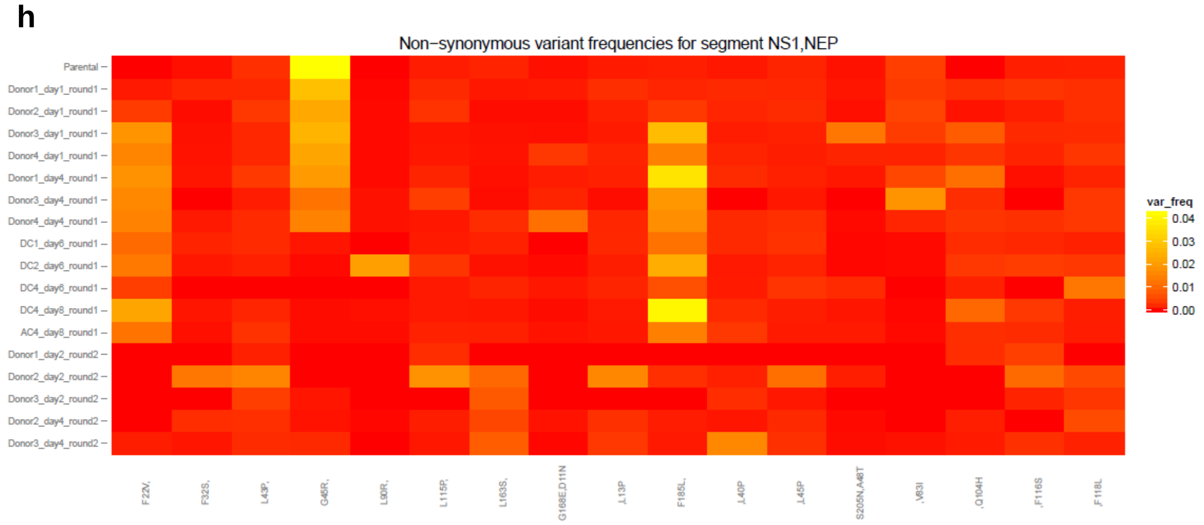
f


Non−synonymous variant frequencies for segment NA
Parental
Donor1_day1_round1
Donor2_day1_round1
Donor3_day1_round1
Donor4_day1_round1
Donor1_day4_round1
Donor3_day4_round1
Donor4_day4_round1
DC1_day6_round1
DC2_day6_round1
DC4_day6_round1
DC4_day8_round1
AC4_day8_round1
Donor1_day2_round2
Donor2_day2_round2
Donor3_day2_round2
Donor2_day4_round2
Donor3_day4_round2
I7S
T10I
I16V
I26M
Q47R
E49G
T51I
N52S
T56A
N60S
Y62C
N63S
E64G
N69S
E73K
E73G
R103K
W175R
M187I
V201I
N205S
G232S
E263D
I300V
M307T
N340I
D397E
S399C
V433M
T436A
N454S
D457G
K460R
var_freq
0.75
0.50
0.25
0.00

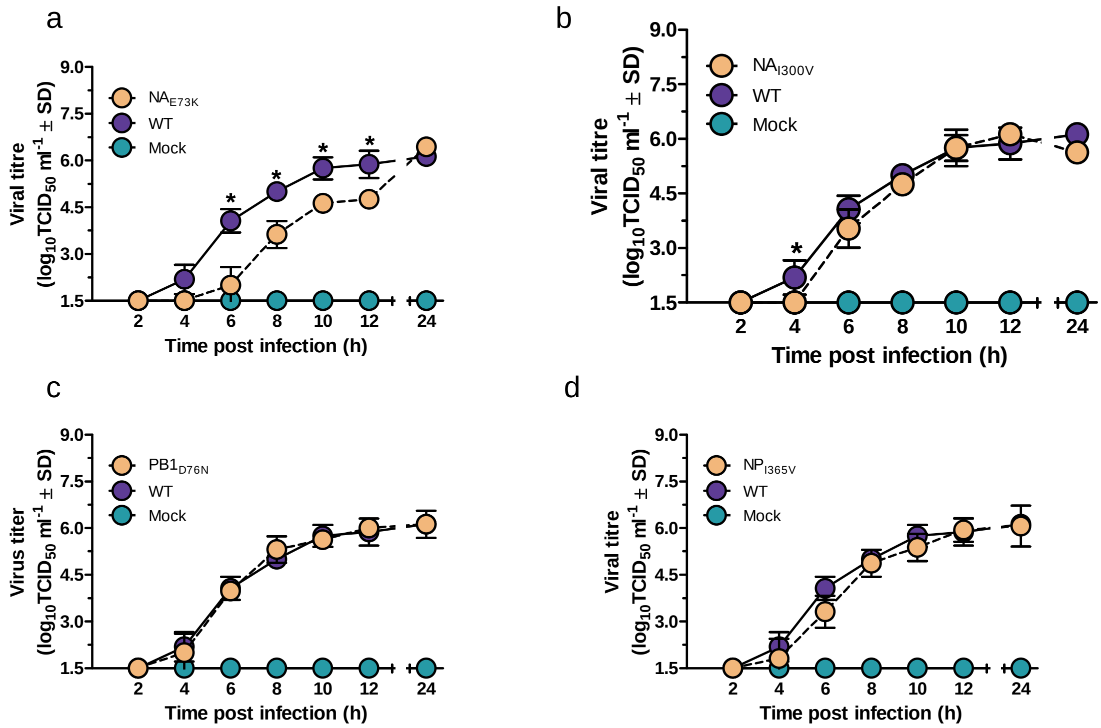
g



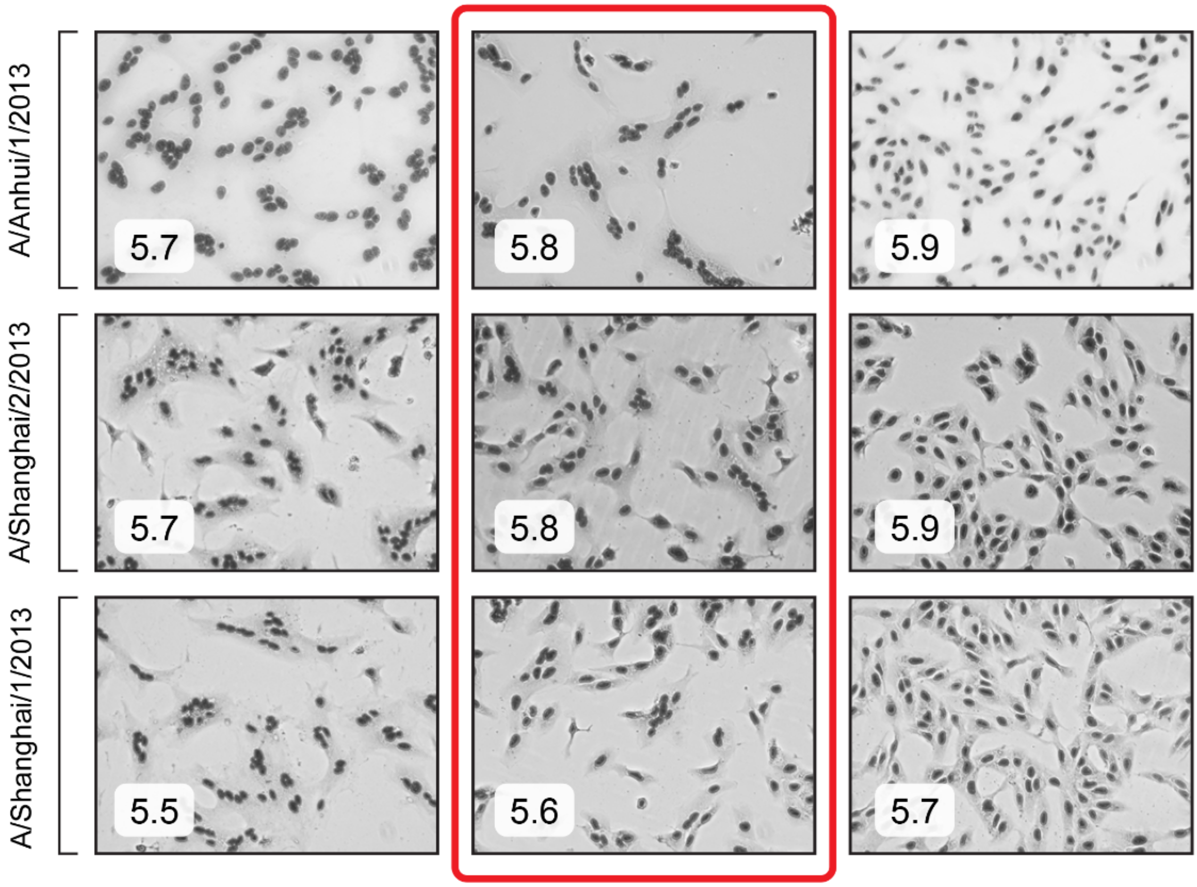
h



Supplementary Figure 3 | Heat map of variations in the whole genome of A/Anhui/1/2013 (H7N9) influenza virus in ferrets. Non-synonymous variant sequences for segments PB2 (a); PB1, PB1-F2 (b); PA, PA-X (c); HA (d); NP (e); NA (f); M1, M2 (g); and NS1, NEP (h) are shown. Parental virus is compared with viruses obtained in experimental rounds 1 and 2. Rows represent viruses from donor, direct contact (DC) and aerosol contact (AC) ferrets. Columns represent amino acid positions (counted from the start codon). Mutations in PA, M1, and NS1 genes are shown in black while those in PA-X, M2, and NS2 are in purple. Mutations with frequency > 0.01 are shown.



Supplementary Figure 4 | Effect of identified amino acid substitutions in the NA, PB1, and NP on replication kinetics of A/Anhui/1/2013 (H7N9) influenza viruses *in vitro*. Growth curves of the wild-type and the NA_{E73K} (**a**), NA_{I300V} (**b**), $PB1_{D76N}$ (**c**), and NP_{I365V} (**d**) rg-A/Anhui/1/2013 (H7N9) influenza viruses using MOI 1 $TCID_{50}$ per cell in MDCK cells at 37°C. Values are mean and SD from two independent experiments (n= 4). *<0.05 compared to WT virus by 2-way ANOVA.



Supplementary Figure 5 | Activation pH of the HA proteins of H7N9 influenza viruses.

Vero cells were inoculated with the indicated viruses at an MOI of 5 $TCID_{50/cell}$. Cells were then treated with pH buffers at the indicated pH values, and syncytium formation was monitored. The highest pH at which syncytia were observed (boxed in red) was recorded as the pH of HA activation. Data is representative of two independent experiments.

Supplementary Table 1 | Homology sequence analysis of A/Anhui/1/2013 (H7N9) influenza virus in comparison with H7N9 influenza viruses from birds and environment isolated during the first wave of the outbreak in China, 2013.

H7N9 virus (isolated form birds and environment)	Date of isolation	Segment[a]	Accession No.[b]	% Nucleotide sequence homology with A/Anhui/1/2013[c]	% Amino acid sequence homology with A/Anhui/1/2013
A/Chicken/Shanghai/S1053/2013	2013-04-03	PB2	EPI440682	99.8	99.8
		PB1	EPI440683	100.0	100.0
		PA	EPI440681	99.8	99.6
		HA	EPI440685	99.3	98.7
		NP	EPI440678	100.0	100.0
		NA	EPI440684	99.8	100.0
		MP	EPI440680	99.9	100.0
		NS	EPI440679	99.9	100.0
A/Chicken/Zhejiang/SD033/2013	2013-04-11	PB2	EPI457746	99.9	99.7
		PB1	EPI457747	100.0	100.0
		PA	EPI457745	100.0	100.0
		HA	EPI457749	99.9	100.0
		NP	EPI457742	100.0	100.0
		NA	EPI457748	99.9	99.8
		MP	EPI457744	98.3	99.3
		NS	EPI457743	99.9	100.
A/Environment/Shanghai/S1088/2013	2013-04-03	PB2	EPI440690	99.9	99.8
		PB1	EPI440691	100.0	100.0
		PA	EPI440689	99.4	98.7
		HA	EPI440693	99.4	99.1
		NP	EPI440686	100.0	100.
		NA	EPI440692	99.9	100.0
		MP	EPI440688	99.7	99.8
		NS	EPI440687	99.9	100.0
A/Pigeon/Shanghai/S1069/2013	2013-04-02	PB2	EPI440698	99.8	99.7
		PB1	EPI440699	100.0	100
		PA	EPI440697	99.8	99.6
		HA	EPI440701	99.8	100.0

		NP	EPI440694	98.8	99.7
		NA	EPI440700	99.8	99.8
		MP	EPI440696	99.8	100
		NS	EPI440695	96.9	99.4
A/Pigeon/Shanghai/S1423/2013	2013-04-03	PB2	EPI457626	99.9	99.8
		PB1	EPI457627	100.0	100.0
		PA	EPI457625	97.8	98.7
		HA	EPI457629	99.8	99.7
		NP	EPI457622	100.0	100.0
		NA	EPI457628	99.8	100.0
		MP	EPI457624	99.9	99.8
		NS	EPI457623	99.9	100.0

[a] PB2: RNA polymerase basic subunit 2; PB1: RNA polymerase basic subunit 1; PA: RNA polymerase acidic subunit; HA: haemagglutinin; NP: nucleoprotein; NA: neuraminidase; MP: matrix gene; NS: non-structural gene.

[b] Sequence data used in this table were downloaded from GISAID, Global Initiative on Sharing Avian Influenza Data (http://platform.gisaid.org)

[c] Homology analysis was performed using BioEdit software (http://www.mbio.ncsu.edu/bioedit/bioedit.html) Sequence Identity Matrix tool.

Supplementary Table 2 | Genetic diversity of A/Anhui/1/2013 (H7N9) influenza viruses in chickens.

Animal number	**Dpi**	**Gene segment**							
		PB2	**PB1**	**PA**	**HA**	**NP**	**NA**	**M**	**NS**
(Parental virus)	**N/A**	—[b]	—	—	N141D (0.4211), A143T (01250), N167D (0.5824), L235Q (0.2182), Y501N (0.1454), Y501C (0.1457)	A373T (0.1277)	T10I (0.2283)	—	—
1	3	N100D (0.4203), K627R (0.1687), L665P (0.125530625	N346S (0.125), V421A (0.3125), V609A (0.1355)	T210N (0.4737), A255G (0.3125), E377G (0.100)	N141D (0.6923), N167D (0.7945), Q444L (0.1477), Y501N (0.1874), Y501C (0.1884)	R26G (0.4809), R98K (0.1094), A284T (0.1975), A428T (0.1407)	T50K (0.1250), K139N (0.1677)	—[a]	—
	5	R70G (0.1102)	—	P28L (0.1070), S184N (0.7272), Q654stop (0.1698), R663G (0.1709)	N141D (0.4201), A143T (0.1203), G151E (0.1761), N167D (0.4350), Y501N (0.1935), Y501C (0.1935)	R99K (0.2261), A373T (0.1207), R446K (0.1058)	—	—	—

2	3	K48R (0.1020), W98stop (0.72), D275E (0.125)	—	E623K (0.3325)	N141D (0.4225), A143T (0.1509), N167D (0.5347), N208D (0.1339), A310T (0.1724), G475D (0.36951), Y501N (0.1598), Y501C (0.1598)	—	—	—	—
	5	—	—	—	N141D (0.6972), N167D (0.5634), Y501Y (0.1596), Y501C (0.1586)	—	T10I (0.2241)	M165I (0.1438), M192I (0.1846), A193V (0.1969)	—
3	3	M90T (0.2526)	K54E (0.6257), M523I (0.6470), Q569K (0.1161)	Y110H (0.1724)	N141D (0.7217), N167D (0.6614), L235Q (0.8971), Y501N (0.2537), Y501C (0.2529), G520V (0.1451)	A284T (0.1267),	—	—	—

5	—	F94L (0.1726), L108F (0.1274)	—	N141D (0.2786), N167D (0.3247), L235Q (0.1111), K414R (0.1111), Y501N (0.46939), Y501C (0.4694)	A373T (0.1265)	S119P (0.1097)	—	—

Three 6-week-old, specific pathogen–free chickens were inoculated with 10^6 EID_{50} of virus in 0.5 ml PBS via natural routes (nares, trachea, eyes). RNA was extracted from oropharyngeal swabs on the indicated days post-inoculation (dpi) and influenza virus genes were amplified and sequenced. Shown are all amino acid variations that differed from the consensus parental sequence and were present at a frequency ≥ 0.1.

—, no nonsynonymous mutations were observed at a frequency ≥ 0.1.

Supplementary Table 3 | Ferret serum hemagglutination inhibition titers.

A/Anhui/1/2013 (H7N9) virus	Serum HI titer (HAU 50 μl^{-1})											
	After inoculation				**After direct contact**				**After aerosol contact**			
	D1	**D2**	**D3**	**D4**	**DC1**	**DC2**	**DC3**	**DC4**	**AC1**	**AC2**	**AC3**	**AC4**
Parental	160	80	40	160	160	320	160	40	<	<	10	40
AC	80	160	<	ND	ND	ND	ND	ND	<	<	<	ND

Titers are reciprocal values. HAU, hemagglutinating units. D, donor; DC, direct contact; AC aerosol contact; <, below the lower limit of detection (10 HAU/50 µl); ND, not determined.

Supplementary Table 4 | Variation frequency of A/Anhui/1/2013 (H7N9) influenza virus after inoculation of ferrets and chickens.

Animal model	Experiment round	Group	Animal no.	DPI	Total variation frequency (log)	HA variation frequency (log)	NA variation frequency (log)
N/A	N/A	Parental virus	N/A	N/A	-2.905440162	-2.338603516	-2.972306897
Ferrets	1	Donor	D1	1	-2.806927772	-2.457879004	-2.833868038
				4	-2.742696441	-2.453907496	-2.805941954
			D2	1	-2.816327184	-2.387386966	-2.783279964
			D3	1	-2.769769832	-2.394822726	-2.81441596
				4	-2.776612542	-2.292597553	-2.807442559
			D4	1	-2.802506048	-2.24905896	-2.832470569
				4	-2.774978978	-2.313737707	-2.839594171
		Direct Contact	DC1	6	-2.772057833	-2.438035302	-2.756583119
			DC2	6	-2.748001965	-2.439238638	-2.773588496
			DC4	6	-2.841064242	-2.811259698	-2.637607146
				8	-2.779612706	-2.787387123	-2.696347657
		Aerosol Contact	AC4	8	-2.837547661	-2.349990787	-2.809618722
	2	Donor	D1-2	2	-2.832660393	-2.617216784	-2.660533406
			D2-2	2	-2.846847365	-2.575942667	-2.687619251
				4	-2.847458857	-2.694908903	-2.673835236
			D3-2	2	-2.851934700	-2.801427075	-2.681704602

				4	-2.841801531	-2.799644372	-2.647563697
Chickens	N/A	N/A	1	3	-2.634408252	-2.233465376	-2.841465687
				5	-2.675060293	-2.127884799	-2.891189157
			3	3	-2.67762697	-2.209500848	-2.697862833
				5	-2.736429542	-2.342424772	-2.822763484
			4	3	-2.659243758	-2.335177799	-2.695671659
				5	-2.764034125	-2.266838626	-2.789758423

Three- to 4-month-old male ferrets were inoculated intranasally with 10^6 $TCID_{50}$ of virus. Four 6-week-old, specific-pathogen-free chickens were inoculated with 10^6 50% egg infectious doses (EID_{50}). Viral genes were amplified and sequenced from RNA extracted from nasal washes (ferrets) or oropharyngeal swabs (chickens) on the indicated day pi. Mean variation frequency for each sample was calculated using positions that are variable in at least one of the examined samples. If a site has a minor variant frequency above zero in any of the samples this was included in the nominator and the denominator of the proportion was the total number of variable sites that was variable in all samples. Variation frequency was expressed as the negative log.
DPI, day post-inoculation when mutation was detected; N/A, not applicable.

Supplementary Table 5 | Genetic diversification of A/Anhui/1/2013 (H7N9) influenza viruses during two rounds of experiments in ferrets.

Experiment round	Ferret group	Ferret no.	DPI	Gene segment							
				PB2	PB1	PA	HA	NP	NA	MP	NS
1	(Parental virus)	N/A	N/A	—	—	—	N141D (0.4211), A143T (0.1250), N167D (0.5824), L235Q (0.2182), Y501N (0.1454), Y501C (0.1457)	A373T (0.1277)	T10I (0.2283)	—	—
	Donor	D1	1	—	—	—	A143T (0.2322), N167D (0.2251)	A373T (0.1036)	T10I (0.1838)	—	—
			4	—	—	N409S (0.1130)	N167D (0.1619), L235Q (0.3133)	A373T (0.1530)	T10I (0.1019)	—	—
		D2	1	—	—	—	N141D (0.1936), A143T (0.1922), N167D (0.3266)	A373T (0.1123)	T10I (0.1822)	—	—
		D3	1	—	—	—	N141D (0.1561), A143T (0.2241), N167D (0.2254), Y501N (0.1688), Y501C (0.1628)	A373T (0.1078)	T10I (0.2023)	—	—
			4	—	—	—	N141D (0.2861), A143T (0.1873), N167D (0.3769), L235Q (0.3691), Y501N (0.1782), Y501C (0.1782)	A373T (0.1371)	T10I (0.2098)	—	—
		D4	1	—	—	—	N141D (0.2087), N167D (0.3380)	A373T (0.1199)	T10I (0.2392)	—	—
			4	—	—	—	N141D (0.2391), N167D (0.4117), L235Q (0.2562)	A373T (0.1408)	—	—	—
	Direct Contact	DC1	6	A674T (0.9712)	—	—	—	—	—	—	—
	Direct Contact	DC2	6	—	—	—	A228E (0.9880)	—	T10I (0.6308),	—	—

									R103K (0.9576)		
		DC4	**6**	–	D76N (0.5316)	–	N141D (0.1818), N167D (0.4178), A228E (0.1173), L235Q (0.1737)	L193M (0.1111), M352I (0.1887)	T10I (0.2404), I26M (0.1266), N340I (0.1511)	–	–
			8	–	D76N (0.2793)	–	N141D (0.2464), N167D (0.5005), A228E (0.1004), L235Q (0.1174)	–	–	–	–
	Aerosol Contact	**AC4**	**8**	–	D76N (0.4320)	–	–	I365V (0.6387)	E73K (0.4058), I300V (0.4103)	–	–
2	**Donor**	**D1-2**	**2**	–	D76N (0.3177)	–	K414E (0.1563), Y501N (0.3182), Y501C (0.3182)	I365V (0.6163)	E73K (0.3941), I300V (0.3451)	–	–
	Donor	**D2-2**	**2**	–	D76N (0.3887)	–	Y501N (0.3137), Y501C (0.3137)	I365V (0.6236)	E73K (0.4348), I300V (0.3739)	–	–
			4	–	D76N (0.2604)	–	–	I365V (0.4976)	E73K (0.2933), I300V (0.2848)	–	–
		D3-2	**2**	–	D76N (0.2993)	–	K414E (0.1455), Y501N (0.1783), Y501C (0.1719)	I365V (0.6174)	E73K (0.3309), I300V (0.4053)	–	–
			4		D76N (0.2016)		Y501N (0.1449), Y501C (0.1439)	I365V (0.5547)	E73K (0.4471), I300V (0.4426)		

Three to 4-month-old male ferrets were inoculated intranasally with 10^6 $TCID_{50}$ of virus. Viral genes were amplified and sequenced from RNA extracted from nasal washes on the indicated day pi. Shown are all amino acid variations that differed from the consensus parental sequence and were present at a frequency of ≥ 0.1. Numbers in parentheses indicate the frequency at which each mutation occurred under each condition.

DPI, day post inoculation when mutation was detected; NA, not applicable; –, no nonsynonymous mutations were detected at a frequency ≥0.1.

Supplementary Table 6 | List of primers used in the study.

Primer	Description	Sequence (5’ → 3’)
N9 E73K F	E73K site-directed mutagenesis	CAAACATCACCAACATCCAAATGAAAGAGAGAACAAG
N9 E73K R	E73K site-directed mutagenesis	GAAATTCCTGCTTGTTCTCTCTTTCATTTGGATGTTG
N9 I300V F	I300V site-directed mutagenesis	GCAGGGCTCAAATAGACCAGTGGTTCAGATAGACCC
N9 I300V R	I300V site-directed mutagenesis	GTGTCATTGCTACTGGGTCTATCTGAACCACTGGTCTATTTG
N9 ClaI/- F	ClaI site deletion	GTGGACCAGCAATAGTATAGTTTCGATGTGTTCCAGTACAG
N9 ClaI/- R	ClaI site deletion	CCAGGAATTCTGTACTGGAACACATCGAAACTATACTATTGC
PB2 K627E F	K627E site-directed mutagenesis	CCATTTGCAGCAGCCCCGCCGGAGCAGAGTAGG
PB2 K627E R	K627E site-directed mutagenesis	CGGCGGGGCTGCTGCAAATGGTAATAGCTT
PB1 D76N F	D76N site-directed mutagenesis	ATTGATGGACCATTACCTGAGAACAACGAGCCGA
PB1 D76N R	D76N site-directed mutagenesis	CTCAGGTAATGGTCCATCAATTGGATTGAGT
I365V F	I365V site-directed mutagenesis	GCTATCCACTAGAGGGGTTCAAGTTGCTTCAAAT
I365V R	I365V site-directed mutagenesis	TTGAACCCCTCTAGTGGATAGCTGTCCTCTT
N9 ClaI F	N-terminal ClaI restriction site insertion for pCAAGS cloning	TTACCATCGATATGAATCCAAATCAGAAGATTC
N9 NheI HA-tag R	C-terminal NheI restriction site and HA-tag insertion	TTTCGCGCTAGCTTAAGCGTAATCTGGAACATCGTATGGGTAGAGGAAGTACTCTATTTTAGCC
N9 NheI R	C-terminal NheI restriction site insertion	TTTCGCGCTAGCTTAGAGGAAGTACTCTATTTTAGCC

Supplementary Table 7 | List of sialic acid-containing glycans used in glycan arrays

Chart number	Name	NeuAcα-	Type	Sulfated
1	Galβ(1-4)-GlcNAcβ-ethyl-NH_2	–	Type 2	
2	Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	–	N	
3	NeuAca(2-3)-Galβ(1-4)-6-O-sulfo-GlcNAcβ-propyl-NH_2	3	Type 2	6S-GlcNAc
4	NeuAcα(2-3)-Galβ(1-4)-[Fucα(1-3)]-6-O-sulfo-GlcNAcβ-propyl-NH_2	3	Type 2	6S-GlcNAc
5	NeuAcα(2-3)-6-O-sulfo-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	6S-Gal
6	NeuAcα(2-3)-6-O-sulfo-Galβ(1-4)-[Fucα(1-3)]-GlcNAcβ-propyl-NH_2	3	Type 2	6S-Gal
7	NeuAcα(2-3)-Galβ(1-3)-6-O-sulfo-GlcNAcβ-propyl-NH_2	3	Type 1	6S-GlcNAc
8	NeuAca(2-3)-Galβ(1-4)-Glcβ-ethyl-NH_2	3	Lacto	
9	NeuAca(2-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	
10	NeuAca(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	
11	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	
12	NeuAca(2-3)-GalNAcβ(1-4)-GlcNAcβ-ethyl-NH_2	3	LacDiNAc	
13	NeuAca(2-3)-Galβ(1-3)-GlcNAcβ-ethyl-NH_2	3	Type 1	
14	NeuAca(2-3)-Galβ(1-3)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	

15	NeuAca(2-3)-Galβ(1-3)-GlcNAcβ(1-3)-Galβ(1-3)-GlcNAcβ-ethyl-NH_2	3	Type 1
16	NeuAca(2-3)-Galβ(1-3)-GalNAcβ(1-3)-Gala(1-4)-Galβ(1-4)-Glcβ-ethyl-NH_2	3	Lacto
17	NeuAcα(2-3)-Galβ(1-3)-GalNAcα-Thr-NH_2	3	Core 1
18	NeuAcα(2-3)-Galβ(1-3)-[GlcNAcβ(1-6)]-GalNAcα-Thr-NH_2	3	Core 2
19	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-6)-[Galβ(1-3)]-GalNAcα-Thr-NH_2	3	Core 2
20	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-6)-[Galβ(1-3)]-GalNAcα-Thr-NH_2	3	Core 2
21	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-GalNAcα-Thr-NH_2	3	Core 3
22	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-GalNAcα-Thr-NH_2	3	Core 3
23	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-6)]-GalNAcα-Thr-NH_2	3	Core 4
24	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-6)]-GalNAcα-Thr-NH_2	3	Core 4
25	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	3	N
26	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	3	N
27	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	3	N

28	NeuAca(2-3)-[GalNAcβ(1-4)]-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3	Type 2	
29	NeuAca(2-3)-[GalNAcβ(1-4)]-Galβ(1-4)-Glcβ-ethyl-NH_2	3	Ganglio	
30	Galβ(1-3)-GalNAcβ(1-4)-[NeuAca(2-3)]-Galβ(1-4)-Glcβ-ethyl-NH_2	3	Ganglio	
31	NeuAca(2-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ-propyl-NH_2	3	Type 2	
32	NeuAca(2-3)-Galβ(1-3)-[Fuca(1-4)]-GlcNAcβ(1-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ-ethyl-NH_2	3	Type 2	
33	NeuAca(2-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ(1-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ-ethyl-NH_2	3	Type 2	
34	NeuAca(2-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ(1-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ(1-3)-Galβ(1-4)-[Fuca(1-3)]-GlcNAcβ-ethyl-NH_2	3	Type 2	
35	NeuGca(2-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	3-Gc	Type 2	
36	NeuAca(2-6)-Galβ(1-4)-6-O-sulfo-GlcNAcβ-propyl-NH_2	6	Type 2	6S-GlcNAc
37	NeuAca(2-6)-Galβ(1-4)-Glcβ-ethyl-NH_2	6	Lacto	
38	NeuAca(2-6)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	6	Type 2	
39	NeuAca(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	6	Type 2	
40	NeuAca(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	6	Type 2	
41	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-[NeuAcα(2-6)]-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	6	Type 2	
42	NeuAca(2-6)-GalNAcβ(1-4)-GlcNAcβ-ethyl-NH_2	6	LacDiNAc	

43	NeuAcα(2-6)-[Galβ(1-3)]-GalNAcα-Thr-NH_2	6	Core 1
44	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-6)-[Galβ(1-3)]-GalNAcα-Thr-NH_2	6	Core 2
45	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-6)-[Galβ(1-3)]-GalNAcα-Thr-NH_2	6	Core 2
46	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-GalNAcα-Thr-NH_2	6	Core 3
47	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-GalNAcα-Thr-NH_2	6	Core 3
48	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-6)]-GalNAcα-Thr-NH_2	6	Core 4
49	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-6)]-GalNAcα-Thr-NH_2	6	Core 4
50	Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N
51	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N
52	GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N
53	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N
54	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N

55	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	6	N
56	NeuGcα(2-6)-Galβ(1-4)-GlcNAcβ-ethyl-NH_2	6-Gc	Type 2
57	NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	3/6	N
58	NeuAcα(2-6)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-3)-[NeuAcα(2-3)-Galβ(1-4)-GlcNAcβ(1-2)-Manα(1-6)]-Manβ(1-4)-GlcNAcβ(1-4)-GlcNAcβ-Asn-NH_2	3/6	N