

Appendix

Table of contents

File	Page
Appendix Table S1: Oligonucleotide sequences for qPCR of indicated mRNAs	1
Appendix Table S2: Composition of human study population for isolation of lung alveolar macrophages	2
Appendix Figure S1: Phyllogenetic Tree PB1-F2 protein sequences	3

Appendix Table S1. Gene specific primers for qPCR and cloning

Gene (RT-qPCR)	Sequence
M1 (viral mRNA)	5'-AGATGAGTCTTCTAACCGAGTCG-3' 5'-TGCAAAAACATCTTCAGTCTCTG-3'
18S	5'-GTAACCCGTTGAACCCATT-3' 5'-CCATCCAATCGGTAGTAGCG-3'
IFN β	5'-TCTGGCACAACAGGTAGTAGGC-3' 5'-GAGAAGCACAACAGGAGAGCAA-3'
IP-10	5'-GGAACCTCCAGTCTCAGCACCA-3' 5'-AGACATCTCTTCTCACCTTC-3'
IL-6	5'-ATGAACTCCTTCTCCACAAGCGC-3' 5'-GAAGAGCCCTCAGGCTGGACTG-3'
CCL2	5'-TCGCCTCCATCATGAAAGTC-3' 5'-TTGCATCTGGCTGAGCGAG-3'
TNF- α	5'-ATGAGCACTGAAAGCATGATCC-3' 5'-GAGGGCTGATTAGAGAGAGGTC-3'
ISG15	5'-TCCTGGTGAGGAATAACAAGGG-3' 5'-GTCAGCCAGAACAGGTCGTC-3'
IL-1 β	5'-CTCGCCAGTGAAATGATGGCT-3' 5'-GTCGGAGATTCGTAGCTGGAT-3'
Caspase-1	5'-AGGATATGGAAACAAAAGTCGGC-3' 5'-AGATAATGAGAGCAAGACGTGTG-3'
Sequence + receptor plasmid	Sequence
NLRP3 + pCAGGS-V5-MCS	5'-GCGTACATGCATCCAAGATGGCAAGCACCCGCTGCAG-3' 5'-GCGTACCTCGAGCTACCAAGAAGGCTCAAAGACG-3'
PYRIN + pCAGGS-V5-MCS	5'-ATCTTACTCGAGAAGATGGCAAGCACCCGCTGCAAG-3' 5'-GTATTGGCTAGCCTATAAACCCATCCACTCCTCTTC-3'
NACHT + pCAGGS-V5-MCS	5'-ATCTTACTCGAGCTGGAGTACCTTTGAGA-3' 5'-GTATTGGCTAGCCTAGATCTTGCAACTTAATTC-3'
LRR + pCAGGS-V5-MCS	5'-ATCTTACTCGAGTCTCAGCAAATCAGGCTG-3' 5'-GTATTGGCTAGCCTACGAGCCAAGAAGGCTCA-3'
Nek7 + pCAGGS-V5-MCS	5'-ATCTTACTCGAGGATGAGCAATCACAAGGAATGCAAG-3' 5'-GTATTGGCTAGCTTAGCTGCTTGCAAGTGCATGCATG-3'
V5-ZsGreen-PB1-F2 + pCAGGS-MCS	5'-ATCTTAGGTACCATGGGTAAGCCTATCCCTAACCTCTCCTCGGTCTC GATTCTACGATGGCCAGTCCAAG-3' 5'-GTATTGGCTAGCTCAGTTTATCCACTCTTG-3'
PB1-F2 H7N9 (Sha) + pCAGGS-Flag-ZsGreen-MCS	5'-ATCTTACTCGAGGAACAGGAACAGGAT-3' 5'-GTATTGGCTAGCTCAGTTTATCCACTCT-3'
PB1-F2 H3N2 (Wyo) + pCAGGS-Flag-ZsGreen-MCS	(Mazel-Sanchez et al., 2018)

Mazel-Sanchez, B., Boal-Carvalho, I., Silva, F., Dijkman, R., and Schmolke, M. (2018). H5N1 Influenza A Virus PB1-F2 Relieves HAX-1-Mediated Restriction of Avian Virus Polymerase PA in Human Lung Cells. *J Virol* 92.

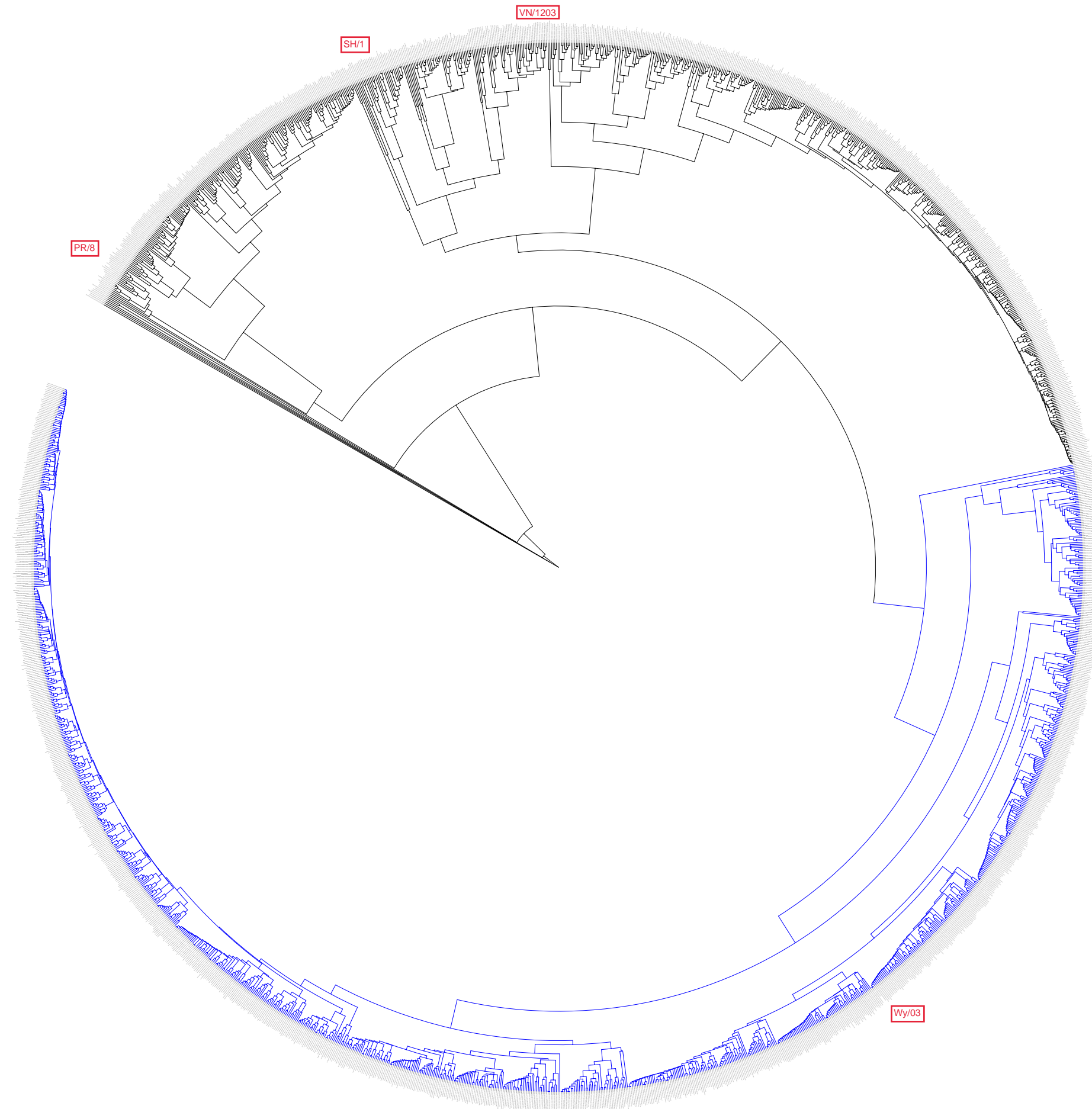
Appendix Table S2. Clinical characteristics of the study population

Patient ID	hAMV1	hAMV2	hAMV3	hAMV4	hAMV5
Age (years)	1.2	1.3	16.4	16.4	16.8
Sex	Female	Female	Female	Female	Female
Reason for BAL	Suspected foreign body aspiration	Surfactant B defect, post LTx surveillance	CF, post LTx surveillance	PAH, post LTx surveillance	CF, early post LTx surveillance
Time post LTx (months)	n.a.	9	2	3	0.25
Clinical findings	Insuspicious respiratory tract, apple piece in upper esophagus	Insuspicious respiratory tract	Insuspicious respiratory tract	Insuspicious respiratory tract	Desquamative bronchitis
Cytology of BAL portion 3					
<i>AM (%)</i>	94	94	96	97	91
<i>Lymphocytes (%)</i>	3	3	3	2	7
<i>Granulocytes (%)</i>	3	3	1	1	2
Medication					
<i>Prednisolon (mg/kg/d)</i>	None	0.1	0.2	0.2	0.6
<i>MMF (mg/kg/d)</i>	None	45	33	33	45
<i>Tacrolimus (trough level, µg/l)</i>	None	4.6	24	16	22
<i>Antibiotics</i>	None	None	None	None	Meropenem, Tobramycin

LTx, lung transplantation; CF, cystic fibrosis; PAH, pulmonary arterial hypertension; n.a., not applicable; MMF, mycophenolate mofetil

Tree scale: 0.1

Appendix Figure S1: Phylogenetic Tree PB1-F2 protein sequences. P



Phylogenetic Tree Obtained from of PB1-F2 protein Sequences of Influenza A virus Selected from Various Epidemic Periods, After Removal of Partial Sequences. The Multiple sequence alignment and NJ was performed in MAFFT (Kuraku et al., 2013) using default parameters. The Newick resulting tree was formatted in MEGA7 (Molecular Evolutionary Genetics Analysis) (Kumar et al., 2016). Sequences obtained for Wyoming formed a large cluster colored in blue. The tree is not rooted and drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Positions of PB1-F2 from viruses/PB1-F2s used in this study are indicated.