S2 Table. Multiple sequence alignment of PB2 mRNA fragments from known avian H5N1 influenza A viruses. All sequences were obtained from NCBI's Influenza Virus Resource (http://www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html).

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                 224         235  240           254  1941          1956  1961    1969
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                 224         235  240           254  1941           1956  1961    1969
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AB496989  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
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AY221590  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
EU616850  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGGTCAGGAATGAGAATAC...-3'
CY048448  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCCGGAATGAGAATAC...-3'
GQ122430  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCTGGAATGAGAATAC...-3'
CY034709  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030364  5'-...TGATACCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY048480  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
FM174399  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030324  5'-...TGATACCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030356  5'-...TGATACCTGAAAGAAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY048552  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCCGGAATGAGAATAC...-3'
HM172430  5'-...TGATTCCTGAAAGAAATGAACAAGGGCAGAC---GAATGTAAGAGGCTCAGGAATGAGAATAC...-3'
CY048128  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
HM172428  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ351871  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY048104  5'-...TGATTCCTGAAAGGAATGAACAGGGACAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030244  5'-...TGATACCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AB496988  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
DQ320844  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ992642  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
HM172419  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAAAGGCTCAGGAATGAAAATAC...-3'
GU356580  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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DQ999893  5'-...TAATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGATCAGGAATGAGAATAC...-3'
CY040939  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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FM163437  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AY221589  5'-...TGATTCCTGAAAGGAATGAACAAGGACAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY040955  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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FM163445  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AB496987  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
CY029668  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY030372  5'-...TGATACCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY040979  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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DQ890066  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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GQ122436  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCTGGAATGAGACTAC...-3'
GQ122454  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCTGGAATGAGACTAC...-3'
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CY040995  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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                 224         235  240           254  1941           1956  1961    1969
                  *           *    *             *   *              *    *       *
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DQ992630  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ992629  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY044047  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
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CY048568  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ492829  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCTGGAATGAGAATAC...-3'
CY048488  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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DQ992599  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030450  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAGTGAGAATAC...-3'
CY030506  5'-...TGATTCCTGAAAGGAATGAAAAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ992627  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ992628  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY036170  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY030292  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY044039  5'-...TGATTCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
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CY030252  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY040907  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY029724  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGGATAC...-3'
CY030236  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030284  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
GU083642  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ992688  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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JX420235  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY030340  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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                 224         235  240           254  1941           1956  1961    1969
                  *           *    *              *   *              *    *       *
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DQ992712  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGATCAGGAATGAGAATAC...-3'
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CY030942  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY030950  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY029572  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY036250  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
CY029596  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY029604  5'-...TGATCCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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CY048184  5'-...TGATTCCTGAAAGGAATGAACAGGGACAGAC---GAATGTGAGAGGCTCCGGAATGAGAATAC...-3'
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GQ122552  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCTGGAATGAGAATAC...-3'
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                  *           *    *             *    *             *    *       *
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GU252813  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
KF881435  5'-...TGATTCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
KF881579  5'-...TGATTCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
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AY950283  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AY950279  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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AY950281  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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                 224         235  240           254  1941           1956  1961    1969
                  *           *    *             *   *              *    *       *
JQ277222  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
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DQ997323  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGGATGAGAATAC...-3'
DQ997317  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTAAGAGGCTCAGGGATGAGAATAC...-3'
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KF881593  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
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KF881346  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
KF881667  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGTTCAGGAATGAGAATAC...-3'
DQ997354  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAGAT---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
KF881622  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGTTCAGGAATGAGAATAC...-3'
KF881324  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
DQ997142  5'-...TGATTCCTGAAAGGAATGAACCAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
KF881317  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
KF881701  5'-...TGATCCCTGAAAGAAATGAACAAGGACAGAC---GAATGTTAGAGGCTCAGGAATGAGAATAC...-3'
DQ997225  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AY950280  5'-...TGGTTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
GU727666  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCGGGAATGAGAATAC...-3'
JX534546  5'-...TTGTTCCTGAGAGAAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
GU727674  5'-...TGATTCCCGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCGGGAATGAGAATAC...-3'
DQ997149  5'-...TGATTCCCGAAAGGAATGAGCAAGGGCAGAC---GAATGTGAGAGGATCAGGAATGAGAATAC...-3'
FR687271  5'-...TGATTCCTGAAAGAAATGAACAAGGACAGAC---GAATGTGAGGGGATCAGGAATGAGAATAC...-3'
JX534562  5'-...TGATTCCTGAAAGAAATGAACAAGGCCAGAC---GAATGTGAGAGGCTCGGGAATGAGAATAC...-3'
AF144300  5'-...TGATTCCTGAAAGGAATGAGCAAGGACAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
EU263350  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
EU263342  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
DQ366311  5'-...TGATCCCTGAAAGGAATGAGCAAGGTCAAAC---GAATGTGAGGGGATCAGGAATGAGAATAC...-3'
CY015088  5'-...TGATTCCTGAAAGAAATGAACAAGGGCAGGC---GAATGTAAGAGGCTCAGGAATGAGAATAC...-3'
DQ997101  5'-...TGATTCCCGAAAGGAATGAGCAAGGGCAGAC---GAATGTGAGGGGCTCAGGGATGAGAATAC...-3'
DQ997121  5'-...TGATTCCTGAAAGAAATGAACAAGGGCAGAC---GAATGTAAGAGGGTCAGGGATGAGAATAC...-3'
EU871817  5'-...TGATTCCCGAGAGGAATGAACAAGGGCAAAC---GAATGTAAGAGGATCAGGAATGAGGATAC...-3'
FR687270  5'-...TGATTCCGGAGAGAAATGAACAAGGACAAAC---GAATGTGAGAGGATCAGGATTGAGGATAC...-3'
DQ366335  5'-...TGATCCCTGAACGGAATGAACAGGGACAGAC---AAATGTGAGAGGTTCAGGAATGAGAATAC...-3'
DQ366327  5'-...TGATCCCTGAACGGAATGAACAGGGACAGAC---AAATGTGAGAGGTTCAGGAATGAGAATAC...-3'
DQ997110  5'-...TGATCCCTGAAAGAAATGAACAAGGTCAAAC---GAATGTGAGGGGCTCAGGAATGAGAATAC...-3'
DQ997132  5'-...TGATCCCTGAAAGAAATGAGCAAGGTCAAAC---GAATGTGAGGGGCTCAGGAATGAGAATAC...-3'
DQ366303  5'-...TGATCCCTGAAAGGAATGAGCAAGGTCAAAC---GAATGTGAGGGGATCAGGAATGAGAATAC...-3'
DQ366319  5'-...TGATCCCTGAAAGGAATGAGCAAGGTCAAAC---GAATGTGAGGGGATCAGGAATGAGAATAC...-3'
DQ454106  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGATCAGGAATGAGAATAC...-3'
CY061882  5'-...TGATCCCTGAAAGAAATGAGCAAGGTCAGAC---GAACGTAAGGGGTTCAGGAATGAGAATAC...-3'
CY015126  5'-...TGATCCCTGAAAGAAATGAGCAAGGTCAAAC---GAACGTGAGGGGTTCAGGAATGAGAATAC...-3'
GU596981  5'-...TGGTCCCGGAAAGGAATGAGCAAGGTCAGAC---GAACGTGAGGGGTTCAGGAATGAGAATAC...-3'
FJ031998  5'-...TGATTCCTGAAAGAAATGAACAGGGACAAAC---GAATGTAAGGGGATCAGGAATGAGAATAC...-3'
CY014732  5'-...TGATTCCTGAGAGGAATGAACAAGGACAAAC---GAATGTGAGAGGGTCAGGAATGAGGATAC...-3'
EF392844  5'-...TGATTCCTGAAAGAAATGAACAGGGACAAAC---GAATGTAAGGGGATCAGGAATGAGAATAC...-3'
EF210572  5'-...TGATTCCTGAAAGAAATGAACAGGGACAAAC---GAATGTAAGGGGGTCAGGAATGAGAATAC...-3'
EU871943  5'-...TGATTCCTGAAAGGAATGAACAAGGACAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
FJ868022  5'-...TGATTCCTGAAAGGAATGAAAAAGGGCAGAC---GAATGTGAGAGGATCAGGAATGAGAATAC...-3'
EF112202  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAGAC---GAATGTGAGAGGCTCAGGAATGAGAATAC...-3'
AY856861  5'-...TGATTCCTGAAAGGAATGAACAAGGGCAAAC---GAATGTGAGAGGCTCAGGATTGAGAATAC...-3'
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