

**S1 Table. Multiple sequence alignment of PB2 mRNA fragments from known human H5N1 influenza A viruses.**

All sequences were obtained from NCBI's Influenza Virus Resource (<http://www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html>).

	222	235	240	255	1945	1956	1961	1970
	*	*	*	*	*	*	*	*
CY111595	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
HM172413	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
EU263988	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
EU146846	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTTAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
HM114566	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114542	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114550	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114558	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
GQ232441	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114582	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114614	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
HM114606	5'-. . . .	AATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
HM114598	5'-. . . .	AATGATCCCTGAAAGGAAT	GAGCAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
CY088766	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
EU434701	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
EU434693	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
AF115291	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . .	3'	
AF084261	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . .	3'	
AF084262	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . .	3'	
AF084263	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . .	3'	
AF115290	5'-. . . .	GATGATCCCTGAAAGGAAT	GATCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . .	3'	
CY098659	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098576	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098582	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098571	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098613	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098607	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098638	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098619	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098645	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098652	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098678	5'-. . . .	GATGGTTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098692	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGGATACT. . . .	3'	
CY098672	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . .	3'	
CY098706	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAT	GAGAATACT. . . .	3'	

	222	235	240	255	1945	1956	1961	1970
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CY098734	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAGGGGCAGACA	-----	GTGAGGGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098748	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAGGGGCAGACA	-----	GTGAGGGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098720	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGGGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098727	5'-. . . . .	TATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098755	5'-. . . . .	TATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGGGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098665	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098625	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098631	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098594	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098588	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098685	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098713	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
CY098699	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGTTTCAGGAAT	GAGAATACT. . . -3'		
JN588925	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JN588929	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AB598126	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JQ714243	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
HQ664943	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EU146634	5'-. . . . .	AATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY651721	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JN588926	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EF456776	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGATCAGGAAT	GAGAATACT. . . -3'		
EF467807	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EF467805	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EF467806	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY576381	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
GU052096	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
GU052104	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . -3'		
GU052149	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAAC	-----	GTGAGGGGATCAGGAAT	GAGAATACT. . . -3'		
DQ360837	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGATCAGGAAT	GAGAATACT. . . -3'		
JN588924	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY576380	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JN588923	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EU146687	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JN588928	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098741	5'-. . . . .	TATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
JN588927	5'-. . . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY116643	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAGCAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AB212050	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		

	222	235	240	255	1945	1956	1961	1970
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AB212051	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY626149	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY627898	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EF587274	5'-. . . .	GATGGTTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
GQ466181	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AY627892	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
HM006756	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
HQ200462	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
HQ200422	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
HM172451	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY098600	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
EF541126	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AB462292	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
DQ835310	5'-. . . .	GATGATCCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF036363	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258840	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258846	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AJ404632	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258839	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258838	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258845	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258844	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258837	5'-. . . .	GATGATCCCTGAAAGGAAT	GATCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
AF258843	5'-. . . .	GATGATCCCTGAAAGGAAT	GAGCAAGGTCAAACT	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017675	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014167	5'-. . . .	GATGATTCCTGAAAGGAAT	GAGCAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017659	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017651	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017667	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017685	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017635	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY017643	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014367	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014325	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014348	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
DQ535731	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014322	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014352	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		
CY014346	5'-. . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTCAGGAAT	GAGAATACT. . . -3'		



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CY014512	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
AY818126	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	AGGAATGAGAATACT	. . . . .	-3'
EU146655	5'-. . . . .	AATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014520	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014320	5'-. . . . .	AATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014175	5'-. . . . .	AATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
DQ372598	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGATC	AGGAATGAGAATACT	. . . . .	-3'
JX235396	5'-. . . . .	AATGATTCCTGAAAGGAAT	GAACAAGGGCAGACA	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014468	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
EU146776	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014269	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014277	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014285	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014392	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014436	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
EU146800	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
CY014476	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
EU146774	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'
HM172438	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	AGGAATGAGAATACT	. . . . .	-3'
CY014293	5'-. . . . .	GATGATTCCTGAAAGGAAT	GAACAAGGGCAGACG	-----	GTGAGAGGCTC	TGGAATGAGAATACT	. . . . .	-3'