Supplementary data 1. Sequence of isolated *env-tm* gene and the BLASTx result from NCBI

GCCGTGGGGATGGTCATATTCCTTCTCGTGTTAGCTATCATGGCGATGACAGCATCTGTCACCGCAGCTGCTACGC
TCGTGAAGCAACACGCCACGGCACAAGTAGTGGGGAGACTGAGCACGAATCTAACTTATATCACTAAGATACAGA
ATCAATACCTGCACCTGTTTCAAAATCTGAACACACGAGTTAATAATCTACATCATAGGGTTACTTACCTTGAGTTT
TTGGCAGAAGTCCATGAGGTACAAACTGGGCTAGGGTGTGTGCCGAGAGGAAGATATTGCCATTTTGACTGGCGC
CCAGAGGAGGTAGGATTAAACATGACGCTCTGGAATTCTACCACCTGGCAACAATGGATGTCCTACTACGATCAG
ATAGAAGAAAACATATGGAATTTGAAATACAATTGGTCTGAGGCCTTAGAGAAAGGAAAGAGTAATACTGACGGT
TTGGAGCCGGATGTCTTCCGATACTTGGCAGACCTATCCTCCAGTTTTACATGGGGTAGTTGGGTGGATAAGCTTG
TATGGCTAGCTTATATACTTTTGGCTTATTTTGCATTTAAGGTCCTCCAGTGCATCATGTCAAACTTGGGCGCTCAA
ACACGGTATCAGTTGCTGAATGCGCAAGAGGATACCGACCCTGCAGGGGACGGAGACCAGCCAGACGACCACCG
ATCCGGAGACACCCCTCGTTCTGGGGTACCCTCCGGGGGCTGGTCTCAGAAGCTCAGCGAAGGCAAGAAGATCGG
ATGTCTGATCTTGAGAACAGAATGGCAGAATTGGAGGAACGATTTGAGGACCTTGCGCTGGTTGACTCTGGGGGG
AAAAATCCTGCAGCTCCCGCTCAGTCTGTTAGTCCTCCTAGTTCGAATCCTTTTGCATATTCTCTCTCCCACTTTTCA
AAATCAAAGAGGGTGGACTGTGGGGAGAAAGGGAACAGGTGGGGACGACCGGGAGCTTTCCCCGGAGCTGGAAT
ATCTGAGTTGGACTGGATCGAGTCAGGAGATGGTGGAGATGAGAGACCTAAAGGAGGAAGATATCCCCGAGGAG
GGAATACGCCCAGTTGAGATG

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
RecName: Full=Envelope glycoprotein; AltName: Full=Env polyprotein; Contains: RecName: Full=Surface protein; Short=SU; AltName: Full=Glycopr	736	736	100%	0.0	100%	Q82857.1
envelope protein [Jembrana disease virus]	736	736	100%	0.0	100%	ABB72000.1
envelope protein [Jembrana disease virus]	736	736	100%	0.0	100%	ABB72001.1

Supplementary data 2. Alignment between the synthetic transgene and sequencing result from inserted gene produced in -Clustal 2.1 online software (https://www.genome.jp/tools-bin/clustalw)

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CLUSTAL 2.1 multiple sequence alignment


transgene_env_tm                ATGGCCGTGGGAATGGTGATCTTCCTGCTGGTGCTGGCCATCATGGCCAT
1st_BASE_sequencing_env_tm      ATGGCCGTGGGAATGGTGATCTTCCTGCTGGTGCTGGCCATCATGGCCAT
                                **************************************************

transgene_env_tm                GACCGCCTCCGTGACCGCCGCTGCTACCCTGGTGAAGCAGCACGCCACCG
1st_BASE_sequencing_env_tm      GACCGCCTCCGTGACCGCCGCTGCTACCCTGGTGAAGCAGCACGCCACCG
                                **************************************************

transgene_env_tm                CCCAAGTTGTGGGCAGACTGAGCACCAACCTGACCTACATCACCAAGATC
1st_BASE_sequencing_env_tm      CCCAAGTTGTGGGCAGACTGAGCACCAACCTGACCTACATCACCAAGATC
                                **************************************************

transgene_env_tm                CAGAACCAGTACCTGCACCTGTTCCAGAACCTGAACACCCGGGTGAACAA
1st_BASE_sequencing_env_tm      CAGAACCAGTACCTGCACCTGTTCCAGAACCTGAACACCCGGGTGAACAA
                                **************************************************

transgene_env_tm                CCTGCACCACCGGGTGACCTACCTGGAGTTCCTGGCCGAAGTTCACGAAG
1st_BASE_sequencing_env_tm      CCTGCACCACCGGGTGACCTACCTGGAGTTCCTGGCCGAAGTTCACGAAG
                                **************************************************

transgene_env_tm                TTCAGACCGGCCTGGGCTGCGTGCCCAGAGGAAGATACTGCCACTTCGAC
1st_BASE_sequencing_env_tm      TTCAGACCGGCCTGGGCTGCGTGCCCAGAGGAAGATACTGCCACTTCGAC
                                **************************************************

transgene_env_tm                TGGAGGCCCGAGGAAGTTGGCCTGAACATGACCCTGTGGAACTCCACCAC
1st_BASE_sequencing_env_tm      TGGAGGCCCGAGGAAGTTGGCCTGAACATGACCCTGTGGAACTCCACCAC
                                **************************************************

transgene_env_tm                CTGGCAGCAGTGGATGAGCTACTACGACCAGATCGAGGAGAACATCTGGA
1st_BASE_sequencing_env_tm      CTGGCAGCAGTGGATGAGCTACTACGACCAGATCGAGGAGAACATCTGGA
                                **************************************************

transgene_env_tm                ACCTGAAGTACAACTGGAGCGAGGCCCTGGAGAAGGGCAAGAGCAACACC
1st_BASE_sequencing_env_tm      ACCTGAAGTACAACTGGAGCGAGGCCCTGGAGAAGGGCAAGAGCAACACC
                                **************************************************

transgene_env_tm                GACGGCCTGGAGCCCGACGTGTTCAGATACCTGGCCGACCTGAGCAGCTC
1st_BASE_sequencing_env_tm      GACGGCCTGGAGCCCGACGTGTTCAGATACCTGGCCGACCTGAGCAGCTC
                                **************************************************

transgene_env_tm                CTTCACCTGGGGCTCCTGGGTGGACAAGCTGGTGTGGCTGGCCTACATCC
1st_BASE_sequencing_env_tm      CTTCACCTGGGGCTCCTGGGTGGACAAGCTGGTGTGGCTGGCCTACATCC
                                **************************************************

transgene_env_tm                TGCTGGCCTACTTCGCCTTCAAAGTTCTGCAGTGCATCATGAGCAACCTG
1st_BASE_sequencing_env_tm      TGCTGGCCTACTTCGCCTTCAAAGTTCTGCAGTGCATCATGAGCAACCTG
                                **************************************************

transgene_env_tm                GGCGCCCAGACCCGGTACCAGCTGCTGAACGCCCAAGAAGACACCGACCC
1st_BASE_sequencing_env_tm      GGCGCCCAGACCCGGTACCAGCTGCTGAACGCCCAAGAAGACACCGACCC
                                **************************************************

transgene_env_tm                CGCCGGCGATGGCGATCAGCCTGATGACCACCGGTCCGGCGACACCCCTA
1st_BASE_sequencing_env_tm      CGCCGGCGATGGCGATCAGCCTGATGACCACCGGTCCGGCGACACCCCTA
                                **************************************************

transgene_env_tm                GGAGTGGAGTGCCCTCCGGCGGATGGAGCCAGAAGCTGTCCGAGGGCAAG
1st_BASE_sequencing_env_tm      GGAGTGGAGTGCCCTCCGGCGGATGGAGCCAGAAGCTGTCCGAGGGCAAG
                                **************************************************

transgene_env_tm                AAGATCGGCTGCCTGATCCTGCGGACCGAGTGGCAGAACTGGCGGAACGA
1st_BASE_sequencing_env_tm      AAGATCGGCTGCCTGATCCTGCGGACCGAGTGGCAGAACTGGCGGAACGA
                                **************************************************

transgene_env_tm                CCTGCGGACCCTGCGGTGGCTGACCCTGGGAGGAAAGATCCTGCAGCTGC
1st_BASE_sequencing_env_tm      CCTGCGGACCCTGCGGTGGCTGACCCTGGGAGGAAAGATCCTGCAGCTGC
                                **************************************************

transgene_env_tm                CCCTGAGCCTGCTGGTGCTCCTGGTGAGAATCCTGCTGCACATCCTGAGC
1st_BASE_sequencing_env_tm      CCCTGAGCCTGCTGGTGCTCCTGGTGAGAATCCTGCTGCACATCCTGAGC
                                **************************************************

transgene_env_tm                CCCACCTTCCAGAACCAGAGGGGCTGGACCGTGGGCAGAAAGGGCACCGG
1st_BASE_sequencing_env_tm      CCCACCTTCCAGAACCAGAGGGGCTGGACCGTGGGCAGAAAGGGCACCGG
                                **************************************************

transgene_env_tm                AGGCGACGACAGAGAGCTGTCCCCCGAGCTGGAGTACCTGAGCTGGACCG
1st_BASE_sequencing_env_tm      AGGCGACGACAGAGAGCTGTCCCCCGAGCTGGAGTACCTGAGCTGGACCG
                                **************************************************


transgene_env_tm                GCTCCTCCCAAGAAATGGTGGAGATGCGGGACCTGAAGGAGGAGGACATC
1st_BASE_sequencing_env_tm      GCTCCTCCCAAGAAATGGTGGAGATGCGGGACCTGAAGGAGGAGGACATC
                                **************************************************

transgene_env_tm                CCCGAGGAGGGCATCCGCCCTGTGGAGATGTAATAA
1st_BASE_sequencing_env_tm      CCCGAGGAGGGCATCCGCCCTGTGGAGATGTAATAA
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