

Figure S1. Alignments of sequences obtained from Swiss and US AmFV isolates. The following genes were used for designing diagnostic PCR assays: AmFV_112 (*Bro* gene), AmFV_28 (thymidylate synthase gene) and AmFV_221 (ribonucleotide reductase gene). Primers positions are underlined in bold characters.

1. AmFV_112 (Bro gene)

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: AmFV_112 1497 bp
Sequence 2: US 1497 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 98.33
Guide tree file created: [clustalw.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences: 2 Score:28110
Alignment Score 10157

CLUSTAL 2.1 multiple sequence alignment

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AmFV_112_CH_      ATGGATTCAAAGGTTTATACCTATGAAGATCAAGAGGTTACTGTACTTAGTTGTTTAGAC
US_BRO            ATGGAGTCAAAGGTTTATACCTATGAAGATCAAGAGGTTACTGTACTTAGTTGTTTAGAC
*****

AmFV_112_CH_      GAAAACAATGTACGTTTTTATTATCTAATAACGTTTCTTGCTATTTTTGGTCTAAAAAAC
US_BRO            GAAAACAATGTACGTTTTTATTATCTAATAACGTTTCTTGCTATTTTTGGTCTAAAAAAC
*****

AmFV_112_CH_      CGACGTTTCGTACATAAGAACACGCTTACAAAATCTGCAAAAACCGCAAAGATATTTCTT
US_BRO            CAACGTTTCGTACATAAGAACACGCTTACAAAATCTGCAAAAACCGCAAAGATATTTCTT
* *****

AmFV_112_CH_      CGATATCTATCCGAATTTAATGTATCGAGCGTCTTACCCAGAGAATTCGGTTTTTGTGAGT
US_BRO            CGATATCTATCTGAATTCATGTATCGAGTGTCTTACCAGAGAATTCGGTTTTTGTGAGT
*****

AmFV_112_CH_      GCTGCTGGATTAAAAGAAATTATATCAAAGTTACAACATGAGAAAAACATTTTTGGATT
US_BRO            GCTGCCGGATTAAGAGAAATTATATCAAAGTTACAACATGAGAAAAAAATTTATTTGATT
*****

AmFV_112_CH_      ACCTTGTTGAAGAGAATTTTTCGTGATTATAAAGAAAGTAGTTGGTCAAACAAAAACGAC
US_BRO            ACCTTTTGAAGAGGATTTTTCGTGATTATAAAGAAAGTAGTTGGTCAAACAAAAACGAC
*****

AmFV_112_CH_      ATTTTAATGAAAAAGGTAACCTTTTGAAGGATATTCTTTTGACTTGGTGAAGATAATTGGT
US_BRO            ATTTTAATGAAAAAGGTAACCTTTTGAAGGATATTCTTTTGACTTGGTGAAGATAATTGGT
*****

AmFV_112_CH_      GATGACGATGATTATTTTACGCTAAACCACTCGAAAAAATTTTGAATTACAAGAAGCTA
US_BRO            GATGACGATGATTATTTTACGCTAAACCACTCGAAAAAATTTTGAATTACAAGAAGCTA
*****
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AmFV_112_CH_ US_BRO	CATAAAGCTATACGAAAGTACGTTTCGCCGAACAATTGTCGTCCATTTAGTTCGTTCGCAC CATAAAGCTATACAAAAGTACGTTTCGCCGAACAATTGTCGTCCATTTAGTTCGTTCGCAC *****
AmFV_112_CH_ US_BRO	ATAGGGGTTATATACACAGGAAAAACAACATCGTTGCCATATCTCAAACCGAATGCAAAC ATAGGGGTTATATACACAGGAAAAACGACATCGTTGCCATATCTCAAACCGAATGCAAAC *****
AmFV_112_CH_ US_BRO	TTTATTAAACACCGCAGGCTTCAACGAATTAATTTTGCATTGACCCAACCTTTTGCGAAG TTTATTAAACACCGCAGGCTTCAACGAATTAATTTTGCATTGACCCAACCTTTTGCGAAG *****
AmFV_112_CH_ US_BRO	CGTTTCAAGGAATGGCTGATCAACGTTATGGATCAATTGCGAGTGGACGGCGAGTACGTG CGTTTCAAGGAATGGCTGATCAACGTTATGGATCAATTGCGAGTGGACGGCGAGTACGTG *****
AmFV_112_CH_ US_BRO	GTTACCCGAGACGCCCATTTGGACATCC <u>AGCAAGACTTGGCCACCATGA</u> ACAACATCTTT GTTACCCGAGACGCCCATTTGGACATCCAGCAAGACTTGGCCACCATGAACAACATCTTT *****
AmFV_112_CH_ US_BRO	GGACAGACACCTCGGACACCTCGATTAGCTGTTCAACCTCTTCAGACGAAACCTCTGGAT GGACAGACACCTCGGACACCTCGATTAGCTGTTCAACCTCTTCAGACGAAACCTCTGGAT *****
AmFV_112_CH_ US_BRO	CAGTTGACTCTATCGGAGTGTCACGACTTGATAATGTTCTTACAAAGAGAAAAACAACCTTA CAGTTGACTCTATCGGAGTGTCACGACTTGATAATGTTCTTACAAAGAGAAAAACAACCTTA *****
AmFV_112_CH_ US_BRO	TACAAACGGAACATACAGAGATATCAAGTCCAACCTACGCCAACGTGTCACTCATCCGGCA TACAAACGGAACATACAGAGATATCAAGTCCAACCTACGCCAACGTGTCACTCATCCGGCA *****
AmFV_112_CH_ US_BRO	GACTACAGTCTCTTCATGTTGCTGTGCGATGAGTGTTGTCCGATCCGTCATTTCGGTTCTCC GACTACAGTCTCTTCATGTTGCTGTGCGATGAGTGTTGTCCGATCCGTCATTTCGGTTCTCC *****
AmFV_112_CH_ US_BRO	ATCTCGAGAGGAAAGGACAAGTATATTCGTAGTATCGAGGCAAAACGTAGGAAATTTGTC ATCTCGAGAGGAAAGGACAAGTATATTCGTAGTATCGAGGCAAAACGTAGGAAATTTGTC *****
AmFV_112_CH_ US_BRO	GCCGCTTGCAAGCAAGACCGGTCTCTGCTGTCTTCCCCGCAAGCCGCGCGGTATCTGCAG GCCGCTTGCAAGCAAGACCGGTCTCTGCTGTCTTCCCCGCAAGCCGCGCGGTATCTGCAG *****
AmFV_112_CH_ US_BRO	ATTACCATCAAAAAGTACAGAACCGCCAACGCGGCGATCTCGTGGATGCGGATTTCGTAAA ATTACCATCAAAAAGTACAGAACCGCCAACGCGGCGATCTCGTGGATGCGGATTTCGTAAA *****
AmFV_112_CH_ US_BRO	GAGTATATAAACTTTTTGGACGACGTGGACTTTACGAATCGTTGCAAGACCGTTTTTTTCG GAGTATATGAACTTTTTGGACGACGTGGACTTTACGAATCGTTGCAAGACCGTTTTTTTCG *****
AmFV_112_CH_ US_BRO	CCACGAGGTTTACGGCCCGCATCGATGGATCCCCTCTTCTCCGATCGGCTGGACGCACAT CCACGAGGTTTACGGCCCGCATCGATGGATCCCCTCTTCTCCGATCGGCTGGACGCACAT *****
AmFV_112_CH_ US_BRO	GACGACCGTGACTCTTTAGAGTGGCTGGACCCCAAAATAGCCGACTTCAAGGGCACGGTC GACGACCGTGACTCTTTAGAGTGGCTGGACCCCAAAATAGCCGACTTCAAGGGCACGGTC *****
AmFV_112_CH_ US_BRO	GAGCGTATGTGCGACAGAGTGTTTCGAAAGGCTCGATCGGGAGACCAACTTGACGACTAAC GAGCGTATGTGCGACAGAGTGTTTCGAAAGGCTCGAGCGGGAGACCAACTTGACGACTAAC *****
AmFV_112_CH_ US_BRO	TCGGCAAGAATAGAGGACGATCCGAGCAAGCCTGGACCGTCTAATGCGGTTGAGTAA TCGGCAAGAATAGAGGACGATCCGAGCAAGCCTGGGCGGTCTAATGCGGTTGAGTAA *****

2. AmFV_28 (thymidylate synthase gene)

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: AmFV_28 1833 bp
Sequence 2: US_TS 1833 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 98.9634
Guide tree file created: [clustalw.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences: 2 Score: 34599
Alignment Score 13792

CLUSTAL-Alignment file created [clustalw.aln]

clustalw.aln

CLUSTAL 2.1 multiple sequence alignment

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AmFV_28      ATGAGTGCATCGAATCCTATTGAGATCAACTCTATCACTCAAACGAACGGGAATGCGGAA
US_TS        ATGAGTGCATCGAATCCTATTGAGATCAACTCGATCACTCAAACGAACGGGAATGCGGAA
*****

AmFV_28      CATCTTATTGATGACACTTACGGCCGGAACGAGACGCCTAACACCGGCGACACAGCACAA
US_TS        CATCTTATTGATGACACTTACGGCCGGAACGAGACGCCTAACACCGGCGACACAGCACAA
*****

AmFV_28      CTCGTGCGCATCGCCAGACACGCCAAAAACGACAGAACTCCAGAAGTAGAAACGGCAACA
US_TS        CTCGTGCGCATCGCCAGACACGCCAAAAACGACAGAACTCCAGAAGTAGAAACGGCAACA
*****

AmFV_28      ACGCCCGCCCAAATCAACACAGCCATCAATCGACCAACGAACGTAAGCCCTCAACATCCG
US_TS        ACGCCCGTCCAAATCAACACAGCCATCAATCGACCAACGAACGTAAGCCCTCAACATCCG
*****

AmFV_28      CCAAACCGCCACGAAAGTCGATCGTGAATCCTCCGACTACTCCAAACGAAACACAAAAC
US_TS        CCAAACCGCCACGAAAGTCGATCGTGAATCCTCCGACTACTCCAAACGAAACACAAAAC
*****

AmFV_28      GACCAACTAAGAACCTCACGCACCGACCAACCAAAACGCCAACCAACCGCCAATTAAGC
US_TS        GACCAACTAAGAACCTCACACACCGACCAACCAAAACGCCAACCAACCGCCAATTAAGC
*****

AmFV_28      AAATTAAGCAACCCGCAGAGAGGTCCAAACTCCCCAAACCATCCACCAAGCGACTTTGTC
US_TS        AAATTAAGCAACCCGCAGAGAGGTCCAAACTCCCCAAACCGTCCACCAAGCGACTTTGTC
*****

AmFV_28      AGAAACTCCTCCTCGAACAACTCGAACTGCTCACCACAAACAACTCTAAACGCGGGGTC
US_TS        AGAAACTCCTCCTCGAACAACTCGAACTGCTCACCACAAACAACTCTAAACGCGAGGTC
*****

AmFV_28      ACCACCAACTGGAACCACGCATTACCCTACGCTCCAGGCCACACACACAACAGAACAACG
US_TS        ACCACCAACTGGAACCACGCATTACCCTACGCTCCAGGTCACACACACAACAGAACAACG
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AmFV_28      AACCACCTCGTTGAACAACAAGTGGGACGAGTGGAACCGCGAACTCAGTCGAATCGAGAGA
US_TS        AACCACCTCGTTGAACAACAAGTGGGACGAGTGGAACCGCGAACTCAGTCGAATCGAGAGA
*****

AmFV_28      CGCGTACAAACGATCAACGAGACCTTCAAAAACATTGGTGAGATGAGCACGGAACCAAGT
US_TS        CGCGTACAAACGATCAACGAGACCTTCAAGAACATTGGTGAGATGAGCACGGAACCAAGT
*****

AmFV_28      GAAACTGAAAACCCCAATCAAAGTACCAGCGTAGCGAGCATCAACAATCTTGTCAC TGAC
US_TS        GAAACTGAAAACCCCAATCAAAGTACCAGCGTAGCGAGCATCAACAATCTTGTCAC TGAC
*****

AmFV_28      ATCGACAGCGACATTATGGGCAACACATCCATCGACGCAACCGAAAAGGCGAGACTCCTC
US_TS        ATCGACAGCGACATTATGGGCAACACATCCATCGACGCAACCGAAAAGGCAAGACTCCTC
*****

AmFV_28      GCGATGATCGCCTCCACACCGGGACTGGAGAACGACGAGCCGGACAACGTCAACGTGAAC
US_TS        GCGATGATCGCCTCCACACCGGGACTGGAGAACGACGAGCCGGACAACGTCAACGTGGAC
*****

AmFV_28      GAGGTGAAAAACCTTCCCGATGTTTCGATCCGACAACCGATACCACAACGATGCTCAAACC
US_TS        GAGGTGAAAAACCTTCCCGATGTTTCGATCCGACAACCGATACCACAACGATGCTAAAACC
*****

AmFV_28      GATACTATCGACCGATTTCGGTCTGACCGACCCGCAGTTTCGACGACACATGGAACGACCGC
US_TS        GATACTATCGACCGATTTCGGTCTGACCGACCCGCAGTTTCGACGACACATGGAACGACCGC
*****

AmFV_28      ATGTACCAACAACCTCGTACGAAAAGTACTGAAACGAGGCGAACAACGGGACGACCGCACG
US_TS        ATGTACCAACAACCTCGTACGAAAAGTACTGAAACGAGGCGAACAACGGGACGACCGCACG
*****

AmFV_28      GGCACGGGAACTCGCGCCCTGTTCGGCGAGCTGCTCGAATTTGATCTTCGAGGTAATCGG
US_TS        GGCACGGGAACTCGCGCCCTGTTCGGCGAGCTGCTCGAATTTGATCTTCGAGGTAATCGG
*****

AmFV_28      CTGCCATTGCTCAACTGCCGCCGCTCTCGTTCAAGTCCATTCTCGAGGAAGTCTGTGG
US_TS        CTGCCATTGCTCAACTGCCGCCGCTCTCGTTCAAGTCCATTCTCGAGGAAGTCTGTGG
*****

AmFV_28      TTCTTGCGCGGGGAGACCGACAGCAAAATACTGGAACGCCGAGGTGTACATATCTGGACC
US_TS        TTCTTGCGCGGGGAGACCGACAGCAAAATACTGGAACGCCGAGGTGTACATATCTGGACC
*****

AmFV_28      GAACATGCGACCCGAGACGTCTTGACGAAAAGAGGCTTTCCATCGCGGCGGGAAGGCGAC
US_TS        GAACATGCGACCCGAGACGTACTGACGAAAAGAGGCTTTCCATCGCGGCGGGAAGGCGAC
*****

AmFV_28      ATCGGACCGCTCTACGGATTCCAATGGCGGTTTCGCCGACTGCGCTACACCAACTGTGAA
US_TS        ATCGGACCGCTCTACGGATTCCAATGGCGGTTTCGCCGACTGCGCTACACCAACTGTGAA
*****

AmFV_28      GCCAACTATGCGGCCCAAAAACGAACGAGAGGGTATGACCAAATCGCTTACATTTTAGAC
US_TS        GCCAACTATGCGGCCCAAAAACGAACGAGAGGGTACGACCAAATCGCTTACATTTTAGAC
*****

AmFV_28      GAACTGACTGCTCGTCCACACAGTCGTCTGTTGCTCAACTCGTGGAATGTAGCCGAC
US_TS        GAACTGACTGCTCGTCCACACAGTCGTCTGTTGCTCAACTCCTGGAATGTAGCCGAC
*****

AmFV_28      ATCGCCGAAATGGTGTTGCCGCCCTTGTCACGTTATGTTTCAACTCTTTGCCGACAATGCT
US_TS        ATCGCCGAAATGGTGTTGCCGCCCTTGTCACGTCATGTTTCAACTCTTTGCCGACAATGCT
*****

AmFV_28      AACGAACTGTCAGGAATGCTGTACTCGCGCAGCGCAGACATCGGTCTTGTTTACCGTTC
US_TS        AACGAACTGTCAGGAATGCTGTACTCGCGCAGCGCGGACATCGGTCTTGTTTACCGTTC
*****

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AmFV_28	AATATTGCGTCCTACGCCATCTTGCTACACGCCATAGCCAAAAAAGTGGGTCGAACAGCC
US_TS	AATATTGCGTCCTACGCCATCTTGCTACACGCCATAGCCAAAAAAGTGGGTCGAACAGCC

AmFV_28	AAAACGTTGAAGGTGATCATCGGTGATGCCCACATCTACAACGACCACATCGACGCAATG
US_TS	AAAACGTTGAAGGTGATCATCGGTGATGCCCACATCTACAACGACCACATCGACGCAATG

AmFV_28	ACCGAGATTGCGGCTCGCGAACCACGACCATCACCACGCGTTTACATCGACAGCAGGTCG
US_TS	ACCGAGATTGCGGCTCGCGAACCACGACCATCACCACGCGTTTACATCGACAGCAGGTCG

AmFV_28	TTCGACAAACCGCTCCACGAATACTCGACCGACTTTTTCCACCTGTTCAACTACCACCCA
US_TS	TTCGACAAACCGCTCCACGAATACTCGACCGACTTTTTCCACCTGTTCAACTACCACCCA

AmFV_28	CACGAACCCGTTTCGTATGCGCGTGTCGGTATAG
US_TS	CACGAACCCGTTTCGTATGCGCGTGTCGGTATAG

3. AmFV_221 (ribonucleotide reductase gene)

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: AmFV_221 2649 bp
Sequence 2: US_RR 2634 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score: 98.4055
Guide tree file created: [clustalw.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences: 2 Score:49515
Alignment Score 19334

CLUSTAL-Alignment file created [clustalw.aln]

clustalw.aln

CLUSTAL 2.1 multiple sequence alignment

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AmFV_221      ATGAGCTTGCCCGCGATAATTGATCAGAGTATTGCGGGCGCTCAGAGCATTCGAGGTGAA
US_RR         ATGAGCTTGCCCGCGATAATTGATCAAAGTATTGCGGGTGTTCAGAGCATTCGAGGTGAA
*****
AmFV_221      CAAACGACGAATCTTGACAGCGACATTAAGGAAGCTTCCTCAGACTCGCAAGACACCGAT
US_RR         CAAACGACGAATCTTGACAGCGACATTAAGGAAGATTCTCAGACTCGCAAGACACCGAT
*****
AmFV_221      TCCACAGTCGTTCCCATCTACCCGCACCACTTGGCTTTGCCGACGAGTCCGAGATAGCA
US_RR         TCCACAGTCGTTCCCATCTACCCGCACCACTTGGCTTTGCCGACGAGTCCGAGATAGCA
*****
AmFV_221      GAACCGACTATCGAGCCAACTACCACACCGACCGCCGATCTTACCACCGTTGAGCCTACC
US_RR         GAACCGACTATCGAGCCAACTACCACACCGACCGCCGAGCTTACCACCGTTGAGCCTACC
*****
AmFV_221      GCTGAGCTCACCGTTGAGCCTACCGCTGAGCTTACCGCTGAGCTTACCGCTGATCCGACC
US_RR         GCTGAGCTCACCGTTGAGCCTACCGCTGAGCTTACCG-----CTGATCCGACC
*****
AmFV_221      GGAGCCGAACCTCGAACCGATCGTGGATCTACCCAAAGTCCCGATCGAAGAACCAGCAGTG
US_RR         AGAGCCGAACCTCGAACCGATCGTGGATCTACCCAAATCCCGATCGAAGAACCAGCAGTG
*****
AmFV_221      GTAGTGTGCGACGACACATACAAACACGTACACCGAAACCAACGATTTCGACGGATGAC
US_RR         GTAGTGTGCGACGACACATACCAACACGTACACCGAAACCAACGATTTCGACGGATGAC
*****
AmFV_221      GATTTTCCCGATTTTGCGGACTTTCGTGGCGCTAGTATCGTCGATCGTTCCGAATCTCCC
US_RR         GATTTTCCCGATTTTGCGGACTTTCGTGGCGCTAGTATCGTCGATCGTTCCGAATCTCCC
*****
AmFV_221      CGACCTGGGGGAACACCGCCCGCCGCCTATATAGAGCGCTCGTCCTCACCAGTGATACAGA
```

US_RR	CGACCTGGGGGAACACCGCCGCCGGCCTATATAGAGCGCTCGTCCTCACCGGTGTACAGA *****
AmFV_221 US_RR	ACCTTACCTTCTGTGTATACGGACGATTTCGACCAACGACGTTTCGATCTACGAAGGAATA ATCCTACCTTCTGTGTATACGGACGATTTCGACCAACGACGTTTCGATCTACGAAGGAATA * *****
AmFV_221 US_RR	ACACGTTTCGGTGAATCGATCGTCTCGGTTGACACAAGCTCCACCGATCCGACAAAACCG ACACGTTTCGGTGAATCGATCGTCTCGGTTGACACAAGCTCCACCGATCCGACAAAACCG *****
AmFV_221 US_RR	CTCAACTTTGCCGAAGTGTGGCGCGACAGCATAACATACACCACTGTTACCTCGTCTGATC CTCAACTTTGCCGAAGTGTGGCGCGACAGCATAACATACACCGCTGTTACCTCGTCTGATC *****
AmFV_221 US_RR	CGGAATCAACGATTTCGCAACACCGACTTTTACAACGTTTAAACCTATGGAGGCACAACGT CGGAATCAACGATTTCGCAACACCGACTTTTACAACGTTTAAACCTATGGAGGCACAACGT *****
AmFV_221 US_RR	CCCTTACGCAAATCACCACAAATAAATTTACTCGAATCGATTGCAAAAGACTCGTCGGAC CCCTTACGCAAATCACCACAAATAAATTTACTCGAATCGATTGCAAAAGACTCGTCGGAC *****
AmFV_221 US_RR	GAACACTCTAGCGACGAGAGTGAGATCGTCTCACCGACCATGGTGTCTCGACCCGTTTCGT GAACACTCTAGCGACGAGAGTGAGATCGTCTCACCGACCATGGTGTCTCGACCCGTTTCGT *****
AmFV_221 US_RR	CACGTTTCGCTTCAACTTGAAAGACGACGACTCCGAGTCGGAGCATTCTACTGAGATGGTC CACGTTTCGCTTCAACTTGAAAGACGACGACTCCGAGTCGGAGCATTCTACTGAAATGGTC *****
AmFV_221 US_RR	GAGATCTCGGTAAAGACCGAGAGAGAAGAGTCTGCTGACGACTCGGTGGCGGAATCGATC GAGATCTCGGTAAAGACCGAGAGAGAAGAGTCTGCTGACGACTCGGCGGCGGAATCGAAC *****
AmFV_221 US_RR	GACTCCGAAGAAAACGTACCGTGGCGACAGGAAGGGAGCACGCTGGTCTTGCAAATACCG GACTCCGAAGAAAACGTACCGTGGCGACAGGAAGGGAGCACGTTGGTCTTGCAAATACCG *****
AmFV_221 US_RR	GACCACATTATGGCTCGTCTCTACCGACCGAAGAAACAAAAACAGAAACAAAAACAGAAG GACCACATTATGGCTCGTCTCTACCGACCGAAGAAACAAAAACAGAAACAAAAACAGAAG *****
AmFV_221 US_RR	CAAAACCCGCAGAACAAAGCTAAACCAGCAGAACAAAGCCAAACAGCAGAACAAAGCTTGGT CAAAACCCGCAGAACAAAGCTAAACCAGCAGAACAAAGCTAAACCAGCAGAACAAAGCTTGGT *****
AmFV_221 US_RR	CAGCAGAACAGACCTGTACCACAGTTCGATTTCGAGTGATCAAAACGATCGAAATGATTCA CAGCAGAACAGACCCGTACCACAGTTCGATTTCGAGTGATCAAAACGATCGAAATGATTCA *****
AmFV_221 US_RR	ACGGCTTTAGAGGACAAAGACGAGTCGAAACCGGGCTCGATGAGCTCGACAAGCTCACAA ACGGCTTTAGAGGACAAAGACGAGTCGAAACCGTGCTCGA---GCTCGACAAGCTCACAA *****
AmFV_221 US_RR	AAATCTACCGTGCGTACTCGAGCCACGTGGAGCAAACCCGAACGGCCTATTGTGCTGTCA AAATCTACCGTGCGTACTCGAGCCACATGGAGCAAACCCGAACGGCCTATTGTGCTGTCA *****
AmFV_221 US_RR	GTGCCGCCGCTGAGCCACCCATTGACTACTCTGATAGTAGCGACGACGATGACGATGTA GTGCCGCCGCTGAGCCACCCATTGACTACTCTGATAGTAGCGACGACGATGACGATGTA *****
AmFV_221 US_RR	GTGGTGTGTTGACCACAATTTCGAAGAGCGGAAGTCTGATCGAGATCGCCCCGCTTTGTTCGCG GTGGTGTGTTGACCACAATTTCGAAGAGCGGAAGTCTGATCGAGATCGCCCCGCTTTGTTCGCG *****
AmFV_221 US_RR	<u>CGATCCTGCCCCGACGTTCTTCGAAACACGATCACGAGTCGAGCAACTCTGAATCGTCT</u> <u>CGATCCTGCCCCGACGTTCTTCGAAACACGATCACGAGTCGAGCGACTCTGAATCGTCT</u> *****

AmFV_221 US_RR	CACGTTAATCGCATACCCGAGCGCGAGATCGAGAAGGTTACGCGGTTTTGCGATCGTGTT CACGTTAATCGCATACCCGAGCGCGAGATCGAGAAGGTTACGCGGTTACTGCGATCGTGTT *****
AmFV_221 US_RR	CCTGAGCGAACCTCTTTTGAATGGAACCGTCGCCGCTAGTGGAACCGCTGCTCGACGCC CCTGAGCGAACCTCTTTTGAATGGAACCGTCGCCGCTAGTGGAACCGCTGCTCGACGCC *****
AmFV_221 US_RR	ACTAAAGATGAGGAGCGGTTTCGTCTTGTTCCTCCGTTTCAGCATCCCGACATCTACGACATG ACTAAAGATGAGGAGCGGTTTCGTCTTGTTCCTCCGTTTCAGCATCCCGACATCTACGACATG *****
AmFV_221 US_RR	TACAAACGACAAGTGGCCAGTTTTGGACCATGGAGGAGATTGATCTCTCCAAGGACTTG TACAAACGACAAGTGGCCAGTTTTGGACCATGGAGGAGATTGATCTCTCCAAGGACTTG *****
AmFV_221 US_RR	GCCGATTGGAACGAACGACTATCTAGCCATGAACGCGATTCTTCAAATGCATCTTGGCC GCCGATTGGAACGAACGACTATCTAGCCATGAACGCGACTTCTTCAAATGCATCTTGGCC *****
AmFV_221 US_RR	TTCTTTGCACCGAGCGACGGTATCGTCGGTGAGAATCTGGTGACGCGTTTCTACGAAATG TTCTTTGCACCAAGCGACGGTATCGTCGGTGAGAATCTGGTGACGCGTTTCTACGAGATG *****
AmFV_221 US_RR	GT <u>AGTGTAACCGAGGCCGCT</u> ACTTCTACGCGTTCCAAGCCGCAATGGAGAACATTAC GTAGTGTAACCGAGGCCGCTACTTCTACGCGTTCCAAGCCGCAATGGAGAACATTAC *****
AmFV_221 US_RR	GCCGAGGTCTACAGTCAGTTGATCAAGACACTAATTCGAACGAAGACGAACAGCGGTCC GCCGAGGTCTACAGTCAGTTGATCAAGACACTAATTCGAACGAAGACGAACAGCGGTCC *****
AmFV_221 US_RR	ATCTTCTCATCGTTCATGACCACGCCAGGCATCACTGAAAAGACTCGCTGGGCAAAACAG ATCTTCTCATCGTTCATGACCACGCCAGGCATCACTGAAAAGACTCGCTGGGCAAAACAG *****
AmFV_221 US_RR	TGGCTCGAACGAGAAAAATCTCAGCTTCGTCGAGCGACTAGTCGCTTTTGCTGTGGTCGAA TGGCTCGAACGAGAAAAATCTCAGCTTCGTCGAGCGACTAGTCGCTTTTGCTGTGGTCGAA *****
AmFV_221 US_RR	GGACTGTTGTTTAGCGGCAGCTTTCCTCCATCTTCTGGTTGAAAAAGCGTGGACTTATG GGACTGTTGTTTAGCGGCAGCTTTCCTCCATCTTCTGGTTGAAAAAGCGTGGACTTATG *****
AmFV_221 US_RR	CACGGTCTGACCTTTAGTAACGAACGATCAGTCGGGACGAGGGTTGCATTGCGACTTC CACGGTCTGACCTTTAGTAACGAACGATCAGTCGGGACGAGGGTTGCATTGCGACTTC *****
AmFV_221 US_RR	GCCTGTCTTCTCTACACCAACACATCGTGACAAGCTGCCCAACAATGTGATCTACAAC GCCTGTCTTCTCTACACCAACACATCGTGACAAGCTGCCCAACAATGTGATCTACAAC *****
AmFV_221 US_RR	ATCGTACGTGAAGCCGTACATGCTGAGTCCATATTCTTTGGTCATGCACTCCGAAATGGA ATCGTACGTGAAGCCGTACATGCTGAGTCCATCTTCTTTGGTCATGCACTCCGAAACGGA *****
AmFV_221 US_RR	CCGGTCGGTGAGCTCAGCCAACACAACATGATGCAGTATGTTTCGCTTTTGCGCGGACCGT CCGGTCGGTGAGCTCAGCCAACACAACATGATGCAGTATGTTTCGCTTTTGCGCGGACCGT *****
AmFV_221 US_RR	TTGCTCACGGCCCTTGATGTGCCACCTCTGTACTCGGCCACCAATCCGTTTCGATTTTCATG TTGCTCACGGCCCTTGATGTGCCACCTCTGTATTCGGCCACCAATCCGTTTCGATTTTCATG *****
AmFV_221 US_RR	CACATGATCTCGTTGGATGGGAGAACCAACTTCTTTGAACGGCGCGTCGGCGAGTACCGA CACATGATCTCGTTGGATGGGAGAACCAACTTCTTTGAACGGCGCGTCGGCGAGTACCGA *****
AmFV_221	CAGAGTCGTGTTCTAACCGCAAACGAACGCGAGTACGACGAGTCGTTTGGTCTTGACTAC

US_RR

CAGAGTCGTGTTCTAACCGCAAACGAACGCGAGTACGACGAGTCGTTTGGTCTTGACTAC

AmFV_221

GATTTTTAG

US_RR

GATTTTTAG
