



NC038882 CATCCTCTGAGCCCGCCCCCTTCTGGC''''''TGCCCCCCCGACTCC''''''GACGTTGAGTC 7199
NC004102 CATCCTCTGAGCCCGCCCCCTTCTGGC''''''TGCCCCCCCGACTCC''''''GACGTTGAGTC 7199
NC009823 CGGGC''''GCTGCCGATTCCGGCAGTCAGACGCCTCCTGATGAGTTGGCCCTTTCGGAGACAGGTTTC 7199
NC009824 CGACA-CACAGTCCAGCACTACTTCCAAGGTCCCCCTTCTCCGGGAGGGGAG''TCCGACTCAGAGTC 7199
NC009825 ---C---CGAGCTCAGACCGT---GATACAGACCTTACCACCCCAACT--GAGACCACAGAC-TCGGGCC 7117
NC009826 -----CCAGGATTCTGCGTT---GG-GTACTAGCAGCCAACACGAT-----TCGGGGC-CTGAGGA 7139
NC009827 -----CCGAGCTCCGGCCTC---GGAGGGTCAATAGCCGGCCCATCA-----TCTCCTGAC-CCGACAA 7153
NC030791 -----AGGAGGCACCCCCC---AGCGACTCCGCCATTAGTCTGGAT-----TCACCGGCGGCAATGA 7130



KP641125 CCTACGCCTGGGGCGGTCTTGAGCCT''TTCGTCAGCTCCAGATTTTTGACACTCCACCTCCTCCTTA 6365
KP641123 CCTACGCCTGGGGCGGCCTTGAGCCT''TTCGTCAGCTCCAGATTTTTGACACTCCACCTCCTCCTTA 6365
KP641127 CCTACGCCTGGGGCGGCCTTGAGCCT''TTCGTCAGCTTCAGATGTTTGACACTCCACCTCCTCCTTA 6365
KP641124 CCTACGCCTGGGGCGGCCTTGAGCCT''TTCGTCAGCTCCAAATGTTTGACACTCCACCTCCTCCTTA 6365
KP641126 CCTACGCCTGGGGCGGCCTTGAGCCT''TTCGTCAGCTCCAAATGTTTGACACTCCACCTCCTCCTTA 6365
MH027953 CCTATGCCTGGGGCGGTCTTGAGCCT''TTCGTCAGCTTGAAATGTTTGACACTCCACCTCCCTCCTTA 6365
KP265950 ''''TTCTGGGCGGGGTTGCAGCC''TTCGGCCAATTACAGGTGTTTGAAACTCCACCACCCCTTA 6365
KP265948 ''''TTCTGGGCGGGGCTGCAACCC''TTCGGCCAATTACAGGTGTTTGAAACTCCACCACCCCTTA 6365
KP265943 ''''TTCTGGGCGGGGCTGCAACCT''TTCGGCCAATTACAGGTGTTTGAAACTCCACCACCCCTTA 6365
KP265947 ''''TTTGGGCGGGCCTGCAGCCT''TTCGGACAAATTACAGGTTTTTGAGACTCCACCACCCCTTA 6365
KP265946 ''''TTTGGGCGGGCCTGCAGCCT''TTCGGACAAATTACAGGTTTTTGAGACTCCACCACCCCTTA 6365
MG781019 CCTACTTCTGGGGTGGACTTGAGCCC''TTCGCCAGTTGCAGATGTTTGACACTCCACCTCCACCTTA 6365
MG781018 CCTATTTCTGGGGTGGACTTGAGCCC''TTCGCCAGTTGCAGATGTTTGACACTCCACCTCCACCTTA 6365
MG257793 ''''TTCTGGGCGGGGCTGCAGCCT''TTCGGACAAATTACAGGTATTTGACACTCCACCACCTCCTTA 6365
MG257794 ''''TTCTGGGCGGGGCTGCAGCCT''TTCGGACAAATTACAGGTATTTGACACTCCACCACCTCCTTA 6365
MH027948 ''''TTCTGGGCGGGTTCAGCCT''TTCGGTCAACTCCAGGTGTTTGACACTCCACCTCCTCCTTA 6365
MN266283 CTTACTTCTGGGGCGGTCTCGAGCCC''TTCGTCAACTTCAGATGTTTGACACTCCACCACCTCCTTA 6365
MN266285 CCTACTTCTGGGGCGGCCTTGAGCCT''TTCGCCAACTTCAGATGTTTGACACTCCACCTCCTCCTTA 6365
MN266284 CCTACTTCTGGGGCGGCCTTGAGCCT''TTCGCCAACTTCAGATGTTTGACACTCCACCTCCTCCTTA 6365
MZ221927 CCTACTTTGGGGGGGGCTTGAACCT''TTCGCCAACTGCAGATGTTTGACACTCCACCTCCACCTTA 6365
MZ540979 CCTACTTTGGGGGGGGCTTGAACCC''TTCGCCCTACTGCAGATGTTTGACACTCCACCTCCACCTTA 6365
MZ540980 CCTACTTTGGGGGGGGCTTGAACCC''TTCGCCCTACTGCAGAGTTTGACACTCCACCTCCACCTTA 6365
MN691105 ''''TTCTGGAGCGGTCTGACGCCGAGCTCGGTCAACTCCAAATCTTTGACACCCCGCCGCCACCGTA 6365



NC038425 TAACAATTACTTTAAACTTTTGCTTGTGCTTTTAGCTTATTCAGGCTTAGTTTCTTGT'''''''' 1188
NC024889 TAATAATTACTTTAAATTATGCTTATTACTCTTGGCTTATTCTGGCTTAGTTTCTTGTACT'''''' 1188
MT955624 AAATAATTACTTTAAGCTTTTGCCTGTTGCTTTTAGCTATTCTGGCTTAGTTTCTTGTGGGAACGATAAT 1188
MT955623 AAATAATTACTTTAAGCTTTTGCCTGTTGCTTCTAGCTATTCTGGCTTAGTTTCTTGT''''''GAT 1188
MT955622 AAATAATTACTTTAAGCTTTTGCCTGTTGCTTCTAGCTATTCTGGCTTAGTTTCTTGT''''''GAT 1188
MH027992 CAATAATTACTTTAAACTTTTGCTTATTGCTTTTAGCTTATTCGGCATTAGTTTCTTGTGATGAT'''' 1188
MN734124 TAACAATTACTTTAAGCTTTTGTCTGCTGCTTTTAGCTTACTCAGGCTTAGTTTCTTGTGAT'''' 1188
MK644936 TAACAATTATTTCAAGCTTTTGCTTACTTTTTGGCATATTCTGGCTTGTTTCTTGTGGCACCTCAGAA 1188
KX056116 TAACAATTACTTTAAACTTTTGCTTATTGCTTTTAGCTTATTCAGGCTTAGTTTCTTGTAAAT'''' 1188
KX421286 TAATAATTACTTTAAGCTTTTGCCTATTGCTTTTGGCGTATTCTGGCTTAGTTTCTTGTGATTCT''ACA 1188
KT880192 AAACAATTACTTCAAGCTGTGTTTACTGCTTTTAGCTTATTCTGCCTTGTTTCTGT''''''GAA 1188

Figure S1. Multiple sequence alignment showing the example of variation in genomics of hepaciviruses in bovine, humans, and equine.