S2 Fig.

A. Nucleotide substitutions among three *C. abortus hemN* alleles (in boldface; *hemN*_4, *hemN*_21, *hemN*_14 ruminant and avian *C. abortus* alleles) (a)

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                    .10       .20       .30       .40       .50       .60       .70       .80       .90      .100      .110      .120      .130      .140      .150      .160      .170      .180      .190      .200      .210
consensus   CGTGTGAGYYTRGGHRTYCARGATACCCAAKSKGMWGTTCAAGAAGCTGTWCGKMGWCGBCAAWSTYAYGARGARTCDCTNYWWGCTTATSAAMWATTYMRWGASYTARRWTTYRMARGYATHAAYATWGAYYTMATTTAYGGTCTYCCWAARCAAACNMAGKHWASHTTTAMDCAAACVATTSMWSATATYTTASMBATGCGKCCWGAY
hemN_4      CGTGTGAGCTTAGGCGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGGCAAAGTTACGAAGAGTCACTGTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTCATTTACGGTCTTCCAAAACAAACGAAGGTAACATTTACGCAAACGATTGCGGATATTTTACACATGCGTCCTGAC
hemN_21     CGTGTGAGCTTAGGCGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGGCAAAGTTACGAAGAGTCACTGTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTCATTTACGGTCTTCCAAAACAAACGAAGGTAACATTTACGCAAACGATTGCGGATATTTTACACATGCGTCCTGAC
hemN_14     CGTGTGAGCTTAGGCGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGGCAAAGTTACGAAGAGTCACTGTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTCATTTACGGTCTTCCAAAACAAACGAAGGTAACATTTACGCAAACGATTGCGGATATTTTACACATGCGTCCTGAC
hemN_9      CGTGTGAGCTTAGGAGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGTCAAAGTCATGAAGAGTCACTTTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTAATTTACGGTCTTCCAAAACAAACTAAGTTAACATTTACTCAAACGATTGCTGATATTTTACACATGCGGCCTGAC
hemN_11     CGTGTGAGCTTAGGAGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGTCAAAGTCATGAAGAGTCACTTTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTAATTTACGGTCTTCCAAAACAAACTAAGTTAACATTTACTCAAACGATTGCTGATATTTTACACATGCGGCCTGAC
hemN_13     CGTGTGAGCTTAGGAGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGTCAAAGTCATGAAGAGTCACTTTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTAATTTACGGTCTTCCAAAACAAACTAAGTTAACATTTACTCAAACGATTGCTGATATTTTACACATGCGGCCTGAC
hemN_10     CGTGTGAGCTTAGGAGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGTCAAAGTCATGAAGAGTCACTTTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTAATTTACGGTCTTCCAAAACAAACTAAGTTAACATTTACTCAAACGATTGCTGATATTTTACACATGCGGCCTGAC
hemN_12     CGTGTGAGCTTAGGAGTCCAAGATACCCAAGCTGCTGTTCAAGAAGCTGTACGGCGTCGTCAAAGTCATGAAGAGTCACTTTATGCTTATGAAAAATTCCGTGAGTTAGGTTTTGAAAGCATAAATATAGATCTAATTTACGGTCTTCCAAAACAAACTAAGTTAACATTTACTCAAACGATTGCTGATATTTTACACATGCGGCCTAAC
hemN_5      CGTGTGAGCTTAGGGGTTCAAGATACGCAAGCTGCTGTTCAAGAAGCTGTACGGCGACGACAAAGTCATGAAGAATCTCTGCATGCTTATGAGAAGTTTCGTGCTCTAGGTTTTGAGAGTATAAACATTGATTTGATTTATGGTCTCCCCAAGCAAACAAAAGCAACATTTACCCAAACAATCGCTGATATTTTACAGATGCGTCCTGAC
hemN_6      CGCGTGAGCCTAGGAGTACAGGATACCCAAGCTTCTGTTCAAGAGGCGTCGTGCGGCGGCGTCAAAGTTATGAAGAGTCTCTACATGCCTATGAAAAATTCCGAGAGCTAGGTTTTGAGAGTATAAACATAGATTTGATTTACGGACTTCCTAAGCAAACAAAGAAAACATTTTCACAAACCAATTGTAGATATTTTACAGATGCGTCCCGAT
hemN_8      CGTGTAAGCTTGGGAGTACAAGATACCCAAGCTGCCGTACAAGAAGCCGTAAAGCGACGGCAGACCCATGAGGAGTCACGACGTGTGTATGAGAAGTTTAAAGAGCTGGGCTTTACTAGCATCAACATTGATCTAATCTACGGCTTGCCAAAGCAAACCCGTCACACCTTTGCGCAAACTATCCAAGACATCCTCGCAATGCGCCCGGAT
hemN_17     CGTGTAAGCTTGGGAGTACAAGATACCCAAGCTGCCGTACAAGAAGCCGTAAAGCGACGGCAGACCCATGAGGAGTCACGACGTGTGTATGAGAAGTTTAAAGAGCTGGGTTTTACTAGCATCAACATTGATCTAATCTACGGCTTGCCAAAGCAAACCCGTCACACCTTTGCGCAAACTATCCAAGACATCCTCGCAATGCGCCCGGAT
hemN_3      AGGGTTAGCTTAGGCGTTCAAGATACCCAAGCTGATGTTCAAGAAGCTGTACGACGACGCCAATCGCATGAGGAATCTTTAAAGGCATACGAAAAATTTAAGGAACTCGCCTTCCAAAGTATCAATATAGACTTAATTTATGGTCTTCCCAAACAAACCAAGGAGTCCTTTTCTAAAACAATTCAAGATATCTTAGCGATGTATCCAGAT
hemN_16     AGGGTTAGCTTAGGCGTTCAAGATACCCAAGCTGATGTTCAAGAAGCTGTACGACGACGCCAATCGCATGAGGAATCTTTAAAGGCATACGAAAAATTTAAGGAACTCGGCTTCCAAAGTATCAATATAGACTTAATTTATGGTCTTCCCAAGCAAACCAAGGAGTCCTTTTCTAAAACAATTCAAGATATCTTAGCGATGTATCCAGAT
hemN_7      CGTGTCAGCCTTGGAATCCAAGATACTCAATGGGAAGTTCAAGAGGGCGTCCGTAGACGCCAATCCTATGAAGAATCCCTCTTGGCCTATAAACAATTCCGTGATCTGAATTTCACAGGTATCAATATTGATCTTATTTATGGGCTTCCTAAACAAACGCAATCGAGTTTCAAACAAACCATTCAACATATTTTAGATATGCGGCCTGAT
hemN_15     CGTGTGAGTCTGGGTATTCAGGATACCCAATGGGAAGTTCAAGAAGCTGTTCGTAGACGCCAATCTTACGAAGAATCGCTCTTAGCTTATCAACTATTCCGAGACTTAAAATTCACAGGTATTAATATTGACCTCATTTATGGTCTCCCTAAACAAACACAGTCTAGTTTTAAACAAACCATTGAACATATCTTAGATATGCGGCCAGAC
hemN_19     CGTGTGAGTCTGGGTATTCAGGATACCCAATGGGAAGTTCAAGAAGCTGTTCGTAGACGCCAATCTTACGAAGAATCGCTCTTAGCTTATCAACTATTCCGAGACTTAAAATTCACAGGTATTAATATTGACCTCATTTACGGTCTCCCTAAACAAACACAGTCTAGTTTTAAACAAACCATTGAACATATCTTAGATATGCGGCCAGAC
hemN_1      CGTGTGAGTCTGGGTATTCAGGATACCCAATGGGAAGTTCAAGAAGCTGTTCGTAGACGCCAATCTTACGAAGAATCGCTCTTAGCTTATCAACTATTCCGAGACTTAAAATTCACAGGTATTAATATTGACCTCATTTATGGTCTCCCTAAACAAACACAGTCTAGTTTTAAACAAACCATTGAACATATCTTAGATATGCGGCCAGAC
hemN_2      CGTGTGAGTCTGGGTATTCAGGATACCCAATGGGAAGTTCAAGAAGCTGTTCGTAGACGCCAATCTTACGAAGAATCGCTCTTAGCTTATCAACTATTCCGAGACTTAAAATTCACAGGTATTAATATTGACCTCATTTATGGTCTCCCTAAACAAACACAGTCTAGTTTTAAACAAACCATTGAACATATCTTAGATATGCGGCCAGAC
hemN_18     CGTGTGAGTCTGGGTATTCAGGATACCCAATGGGAAGTTCAAGAAGCTGTTCGTAGACGCCAATCTTACGAAGAATCGCTCTTAGCTTATCAACTATTCCGAGACTTAAAATTCACAGGTATTAATATTGACCTCATTTATGGTCTCCCTAAACAAACACAGTCTAGTTTTAAACAAACCATTGAACATATCTTAGATATGCGGCCAGAC
                    .220       .230       .240       .250       .260       .270       .280       .290       .300       .310       .320       .330       .340       .350       .360       .370       .380       .390       .400       .410       .420
consensus   CGYYTAGCSYTWTTYTCHTTYGCTYMWGTWCCWTGGRYHAARCCKCAYCAAAARGCTWTGMRMRMWAVHGAYMTSCCYTCYATGGARGARAAATTCGCSATWTATTCYYAWKCYCGRCATACSYTRAYVMARGMAGGHTAYCARGCYATTGGWHTRGATCATTTTTCTCTWCCBGAWGAYCCWYTAASYATMGCBYTTAARAACAAAACK
hemN_4      CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCCTGGATAAAACCCCATCAGAAAGCTATGAAAGAAAGTGACATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGGCATACGTTAACAAAAGCTGGTTACCAAGCTATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATCGCCTTTAAAAACAAAACT
hemN_21     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCCTGGATAAAACCCCATCAGAAAGCTATGAAAGAAAGTGACATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGGCATACGTTAACAAAAACTGGTTACCAAGCTATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATCGCCTTTAAAAACAAAACT
hemN_14     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCCTGGATAAAACCCCATCAAAAAGCTATGAAAGAAAGTGACATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGGCATACGTTAACAAAAGCTGGTTACCAAGCTATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATCGCCTTTAAAAACAAAACT
hemN_9      CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCATGGATAAAACCTCATCAAAAAGCTATGAAAGAAAGCGATATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGACATACGTTAACGAAAGCAGGTTACCAAGCCATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATAGCGTTTAAAAACAAAACT
hemN_11     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCATGGATAAAACCTCATCAAAAAGCTATGAAAGAAAGCGATATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGACATACGTTAACGAAAGCAGGTTACCAAGCCATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATAGCGTTTAAAAACAAAACT
hemN_13     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCATGGATAAAACCTCATCAAAAAGTTATGAAAGAAAGCGATATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGACATACGTTAACGAAAGCAGGTTACCAAGCCATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATAGCGTTTAAAAACAAAACT
hemN_10     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCATGGATAAAACCTCATCAAAAAGCTATGAAAGAAAGCGATATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGACATACGTTAACGAAAGCAGGTTACCAAGCCATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATAGCTTTTAAAAACAAAACT
hemN_12     CGCTTAGCGTTATTTTCATTTGCTTCTGTTCCATGGATAAAACCTCATCAAAAAGCTATGAAAGAAAGCGATATGCCCTCTATGGAGGAAAAATTCGCCATATATTCTTATGCTCGACATACGTTAACGAAAGCAGGTTACCAAGCCATTGGATTAGATCATTTTTCTCTACCTGAAGACCCATTAAGCATAGCTTTTAAAAACAAAACT
hemN_5      CGCCTAGCGTTGTTTTCATTTGCTTCTGTGCCTTGGATAAAGCCTCATCAAAAAGCTATGAAAGAAAGTGACATGCCCTCCATGGAGGAGAAATTCGCTATATACTCTTATGCACGGCATAAATTAACAAAGTCGGGATATCAGGCAATTGGTTTAGATCATTTTTCACTACCGGAAGATCCTTTAAGCATAGCCTTTAAAAATAAAACT
hemN_6      CGTTTAGCCTTGTTTTCCTTCGCTTCTGTTCCATGGATAAAACCGCACCAAAAAGCAATGAAAGACAGTGATCTGCCCTCTATGGAGGAAAAATTCGCGATATATTCTCATGCACGACATATGTTAACAAAGCCGGGATATCAGGCTATTGGCTTGGATCATTTTTCCCTACCCGAAGACCCTTTAAGCATCGCTTTAAAAATAAAACT
hemN_8      CGTCTGGCATTATTTTCTTATGCTGCAGTCCCTTGGATCAAACCGCACCAAAAAGCAATCAAAGCTACAGATCTTCCCTCTATGGAAGAAAAATTTGCGATATACTCACAATCCCGACATAGCTTAATCAAGGCAGGCTACCAAGCTATTGGGATGGATCATTTTTCTCTTCCCGAAGATCCCTTAACAGTAGCGTTTCATAACAAAACA
hemN_17     CGTCTGGCATTATTTTCTTATGCTGCAGTCCCTTGGATCAAACCGCACCAAAAAGCAATCAAAGCTACAGATCTTCCCTCTATGGAAGAAAAATTTGCGATATACTCACAATCCCGACATAGCTTAATCAAGGCAGGCTACCAAGCTATTGGGATGGATCATTTTTCTCTTCCCGAAGATCCCTTAACAGTAGCGTTTCATAACAAAACA
hemN_3      CGTCTTGCTTTATTTTCTTTTGCCTCAGTTCCATGGATCAAGCCGCACCAAAAAGCCATGAAAGCTTCGGATATGCCTTCTATGGAAGAGAAATTCGCGATTTATTCTCAATCCCGGCATTTACTTACAAAAGCAGGATATCAGGCCATCGGTATGGATCATTTCTCTCTTCCCCATGATCCTCTTACCCTCGCTTTCAAAAACAAAACT
hemN_16     CGTCTTGCTTTATTTTCTTTTGCCTCAGTTCCATGGATCAAGCCGCACCAAAAAGCCATGAAAGCTTCGGATATGCCTTCTATGGAAGAGAAATTCGCGATTTATTCTCAATCCCGGCATTTACTTACAAAAGCAGGATATCAGGCCATCGGTATGGATCATTTCTCTCTTCCCCATGATCCTCTTACCCTTGCTTTCAAAAACAAAACT
hemN_7      CGCTTAGCCCTATTCTCTTTTGCACATGTGCCATGGGTCAAGCCTCATCAAAAAGCTTTACGAACAAAAGACCTTCCCTCTATGGAAGAGAAATTTGCGATTTATTCTCAATCTCGACAAGCCCTTATCCAAGAAGGATACCAGGCTATTGGCCTTGATCATTTTTCTCTTCCTGATGATCCCCTAACTATTGCACTTAAAAACAAAACC
hemN_15     CGCCTAGCCCTTTTCTCCTTCGCTCATGTACCTTGGACTAAGCCGCATCAAAAGGCTTTGCGCACTAAAGATCTCCCTTCCATGGAAGAGAAATTCGCGATTTATTCCCAATCTCGGCATACCCTGATCCAGGAAGGCTACCAGGCTATTGGTCTAGATCATTTTTCTCTTCCGGATGATCCTCTAACTATCGCCCTTAAGAACAAAACG
hemN_19     CGCCTAGCCCTTTTCTCCTTCGCTCATGTACCTTGGGCTAAGCCGCATCAAAAGGCTTTGCGCACTAAAGATCTCCCTTCCATGGAAGAGAAATTCGCGATTTATTCCCAATCTCGGCATACCCTGATCCAGGAAGGCTACCAGGCTATTGGTCTAGATCATTTTTCTCTTCCGGATGATCCTCTAACTATCGCCCTTAAGAACAAAACG
hemN_1      CGCCTAGCCCTTTTCTCCTTCGCTCATGTACCTTGGGCTAAGCCGCATCAAAAGGCTTTGCGCACTAAAGAGCTCCCTTCCATGGAAGAGAAATTCGCGATTTATTCCCAATCTCGGCATACCCTGATCCAGGAAGGCTACCAGGCTATTGGTCTAGATCATTTTTCTCTTCCGGATGATCCTCTAACTATCGCCCTTAAGAACAAAACG
hemN_2      CGCCTAGCCCTTTTCTCCTTCGCTCATGTACCTTGGGCTAAGCCGCATCAAAAGGCTTTGCGCACTAAAGATCTCCCTTCCATGGAAGAGAAATTCGCGATTTATTCCCAATCTCGGCATACCCTGATCCAGGAAGGCTACCAGGCTATTGGTCTAGATCATTTTTCTCTTCCGGATGATCCTCTAACTATCGCCCTTAAGAACAAAACG
hemN_18     CGCCTAGCCCTTTTCTCCTTCGCTCATGTACCTTGGGCTAAGCCGCATCAAAAGGCTTTGCGCACTAAAGATCTCCCTTCCATGGAAGAGAAATTCGCGATTTATTCCCAATCTCGGCATACCCTGATCCAGGAAGGCTACCAGGCTATTGGTCTAGATCATTTTTCTCTTCCGGATGATCCTCTAACTATCGCCCTTAAGAACAAAACG

                    .430
consensus   YTRATTCGDAAT
hemN_4      TTGATTCGAAAT
hemN_21     TTGATTCGAAAT
hemN_14     TTGATTCGAAAT
hemN_9      TTGATTCGGAAT
hemN_11     TTGATTAGGAAT
hemN_13     TTGATTCGGAAT
hemN_10     TTGATTCGGAAT
hemN_12     TTGATTCGGAAT
hemN_5      CTGATTCGTAAT
hemN_6      CTTATTCGCAAT
hemN_8      TTAATTCGTAAT
hemN_17     TTAATTCGTAAT
hemN_3      CTAATCCGCAAC
hemN_16     CTAATCCGTAAC
hemN_7      CTTATTCGAAAT
hemN_15     TTGATTCGTAAT
hemN_19     TTGATTCGTAAT
hemN_1      TTGATTCGTAAT
hemN_2      TTGATTCGTAAT
hemN_18     TTGATTCATAAT
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A. Amino-acid substitutions among three *C. abortus hemN*-encoded protein alleles (b)

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                  1111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990000000000111111111122222222223333333333444444
         123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234
hemN_4   RVSLGVQDTQAAVQEAVRRRQSYEESLYAYEKFRELGFESINIDLIYGLPKQTKVTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_21  RVSLGVQDTQAAVQEAVRRRQSYEESLYAYEKFRELGFESINIDLIYGLPKQTKVTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKTGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_14  RVSLGVQDTQAAVQEAVRRRQSYEESLYAYEKFRELGFESINIDLIYGLPKQTKVTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_9   RVSLGVQDTQAAVQEAVRRRQSHEESLYAYEKFRELGFESINIDLIYGLPKQTKLTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_11  RVSLGVQDTQAAVQEAVRRRQSHEESLYAYEKFRELGFESINIDLIYGLPKQTKLTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_13  RVSLGVQDTQAAVQEAVRRRQSHEESLYAYEKFRELGFESINIDLIYGLPKQTKLTFTQTIADILHMRPDRLALFSFASVPWIKPHQKVMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_10  RVSLGVQDTQAAVQEAVRRRQSHEESLYAYEKFRELGFESINIDLIYGLPKQTKLTFTQTIADILHMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_12  RVSLGVQDTQAAVQEAVRRRQSHEESLYAYEKFRELGFESINIDLIYGLPKQTKLTFTQTIADILHMRPNRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHTLTKAGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_5   RVSLGVQDTQAAVQEAVRRRQSHEESLHAYEKFRALGFESINIDLIYGLPKQTKATFTQTIADILQMRPDRLALFSFASVPWIKPHQKAMKESDMPSMEEKFAIYSYARHKLTKSGYQAIGLDHFSLPEDPLSIAFKNKTLIRN
hemN_6   RVSLGVQDTQASVQEAVRRRQSYEESLHAYEKFRELGFESINIDLIYGLPKQTKKTFSQTIVDILQMRPDRLALFSFASVPWIKPHQKAMKDSDLPSMEEKFAIYSHARHMLTKSGYQAIGLDHFSLPEDPLSIALKNKTLIRN
hemN_8   RVSLGVQDTQAAVQEAVKRRQTHEESRRVYEKFKELGFTSINIDLIYGLPKQTRHTFAQTIQDILAMRPDRLALFSYAAVPWIKPHQKAIKATDLPSMEEKFAIYSQSRHSLIKAGYQAIGMDHFSLPEDPLTVAFHNKTLIRN
hemN_17  RVSLGVQDTQAAVQEAVKRRQTHEESRRVYEKFKELGFTSINIDLIYGLPKQTRHTFAQTIQDILAMRPDRLALFSYAAVPWIKPHQKAIKATDLPSMEEKFAIYSQSRHSLIKAGYQAIGMDHFSLPEDPLTVAFHNKTLIRN
hemN_3   RVSLGVQDTQADVQEAVRRRQSHEESLKAYEKFKELAFQSINIDLIYGLPKQTKESFSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLPHDPLTLAFKNKTLIRN
hemN_16  RVSLGVQDTQADVQEAVRRRQSHEESLKAYEKFKELGFQSINIDLIYGLPKQTKESFSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLPHDPLTLAFKNKTLIRN
hemN_7   RVSLGIQDTQWEVQEAVRRRQSYEESLLAYKQFRDLNFTGINIDLIYGLPKQTQSSFKQTIQHILDMRPDRLALFSFAHVPWVKPHQKALRTKDLPSMEEKFAIYSQSRQALIQEGYQAIGLDHFSLPDDPLTIALKNKTLIRN
hemN_15  RVSLGIQDTQWEVQEAVRRRQSYEESLLAYQLFRDLKFTGINIDLIYGLPKQTQSSFKQTIEHILDMRPDRLALFSFAHVPWTKPHQKALRTKDLPSMEEKFAIYSQSRHTLIQEGYQAIGLDHFSLPDDPLTIALKNKTLIRN
hemN_19  RVSLGIQDTQWEVQEAVRRRQSYEESLLAYQLFRDLKFTGINIDLIYGLPKQTQSSFKQTIEHILDMRPDRLALFSFAHVPWAKPHQKALRTKDLPSMEEKFAIYSQSRHTLIQEGYQAIGLDHFSLPDDPLTIALKNKTLIRN
hemN_1   RVSLGIQDTQWEVQEAVRRRQSYEESLLAYQLFRDLKFTGINIDLIYGLPKQTQSSFKQTIEHILDMRPDRLALFSFAHVPWAKPHQKALRTKELPSMEEKFAIYSQSRHTLIQEGYQAIGLDHFSLPDDPLTIALKNKTLIRN
hemN_2   RVSLGIQDTQWEVQEAVRRRQSYEESLLAYQLFRDLKFTGINIDLIYGLPKQTQSSFKQTIEHILDMRPDRLALFSFAHVPWAKPHQKALRTKDLPSMEEKFAIYSQSRHTLIQEGYQAIGLDHFSLPDDPLTIALKNKTLIRN
hemN_18  RVSLGIQDTQWEVQEAVRRRQSYEESLLAYQLFRDLKFTGINIDLIYGLPKQTQSSFKQTIEHILDMRPDRLALFSFAHVPWAKPHQKALRTKDLPSMEEKFAIYSQSRHTLIQEGYQAIGLDHFSLPDDPLTIALKNKTLIHN
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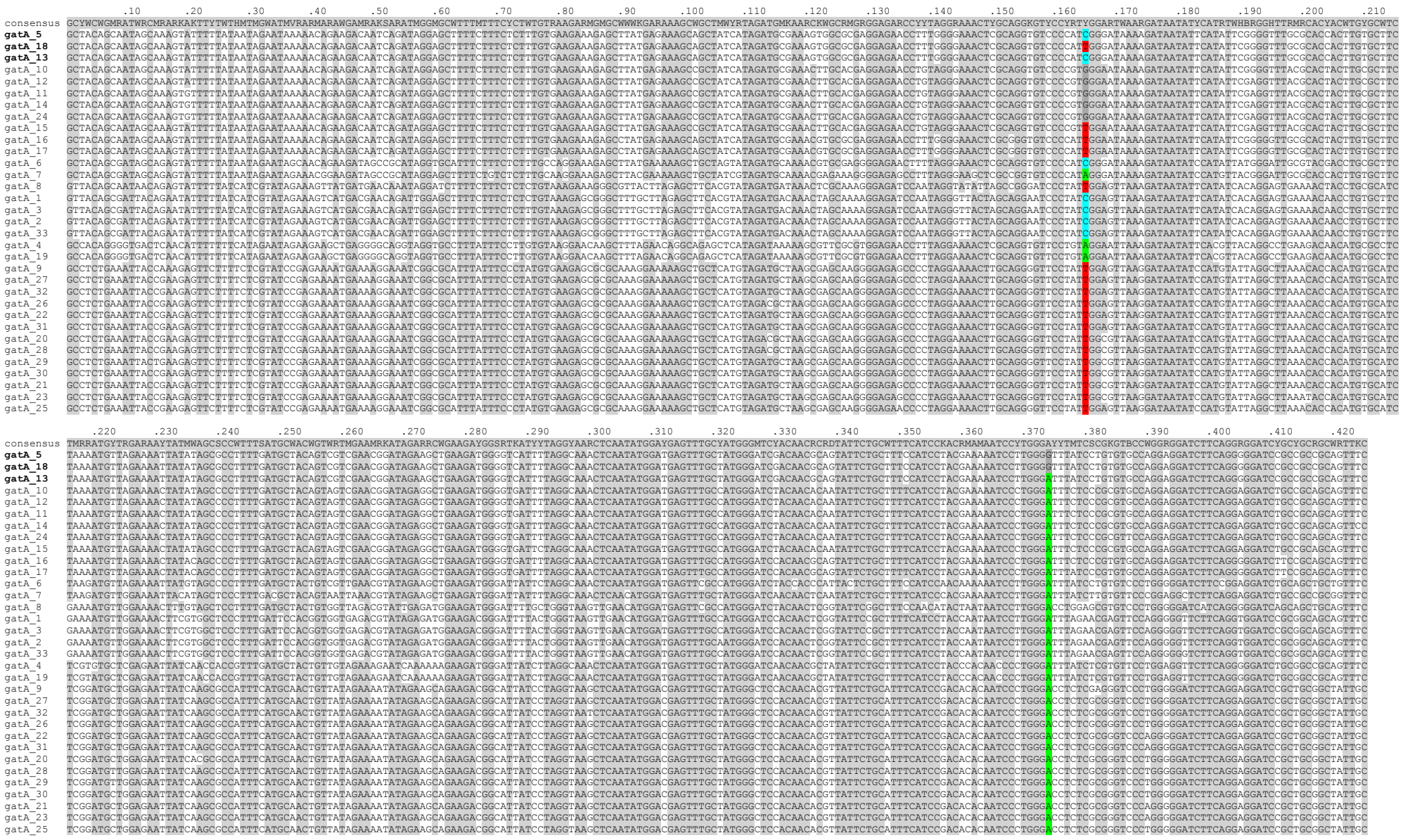
B. Nucleotide substitutions among three *C. abortus gatA* alleles (in boldface; *gatA*_5, *gatA*_18, *gatA*_13 ruminant and avian *C. abortus* alleles) (a)



B. Amino-acid substitutions among three *C. abortus gatA*-encoded protein alleles (b)

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                  1111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990000000000111111111122222222223333333333444
         123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901
gatA_5   ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKVARGEPLGKLAGVPIGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWGLSCVPGGSSGGSAAAV
gatA_18  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKVARGEPLGKLAGVPIGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWGLSCVPGGSSGGSAAAV
gatA_13  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKVARGEPLGKLAGVPIGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDLSCVPGGSSGGSAAAV
gatA_10  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_12  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_11  ATAIAKCFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_14  ATAIAKCFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_24  ATAIAKCFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_15  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKLARGEPVGKLAGVPVGIKDNIHIRGLRTTCASKMLENYIAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSAAAV
gatA_16  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKRARGEPLGKLAGVPIGIKDNIHIRGLRTTCASKMLENYTAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDFSRVPGGSSGGSSAAV
gatA_17  ATAIAKYFYNRIKTEDNQIGAFLSLCEERAYEKAAIIDAKRARGEPLGKLAGVPIGIKDNIHIRGLRTTCASKMLENYTAPFDATVVERIEAEDGVILGKLNMDEFAMGSTTQYSAFHPTKNPWDLSRVPGGSSGGSSAAV
gatA_6   ATAIAEYFYNRIATEDSRIGAFLSLCQERAYEKAASIDAKRARGELLGKLAGVPIGIKDNIHIMGLRTTCASKMLENYVAPFDATVVERIEAEDGIILGKLNMDEFAMGSTTHYSAFHPTKNPWDLSCVPGGSSGGSAAAV
gatA_7   ATAIAEYFYNRIETEDSRIGAFLSLCKERAYEKAAIVDAKRERGEPLGKLAGVPIGIKDNIHVTGLRTTCASKMLENYIAPFDATVIKRIEAEDGIILGKLNMDEFAMGSTTQYSAFHPTKNPWDLSCVPGGSSGGSAAAV
gatA_8   VTAITEYFYHRIESYDEQIGSFLSLCKERALLRASRIDDKLAKGDPIGILAGIPIGVKDNIHITGVKTTCASKMLENFVAPFDATVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFQHTNNPWDLERVPGGSSGGSAAAV
gatA_1   VTAITEYFYHRIESHDEQIGAFLSLCKERALLRASRIDDKLAKGDPIGLLAGIPIGVKDNIHITGVKTTCASKMLENFVAPFDSTVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFHPTNNPWDLERVPGGSSGGSAAAV
gatA_3   VTAITEYFYHRIESHDEQIGAFLSLCKERALLRASRIDDKLAKGDPIGLLAGIPIGVKDNIHITGVKTTCASKMLENFVAPFDSTVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFHPTNNPWDLERVPGGSSGGSAAAV
gatA_2   VTAITEYFYHRIESHDEQIGAFLSLCKERALLRASRIDDKLAKGDPIGLLAGIPIGVKDNIHITGVKTTCASKMLENFVAPFDSTVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFHPTNNPWDLERVPGGSSGGSAAAV
gatA_33  VTAITEYFYHRIESHDEQIGAFLSLCKERALLRASRIDDKLAKGDPIGLLAGIPIGVKDNIHITGVKTTCASKMLENFVAPFDSTVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFHPTNNPWDLERVPGGSSGGSAAAV
gatA_4   ATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGVPVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGIILGKLNMDEFAMGSTTLYSAFHPTHNPWDLSRVPGGSSGGSAAAV
gatA_19  ATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGVPVGIKDNIHVTGLKTTCASRMLENYQPPFDATVVERIKKEDGIILGKLNMDEFAMGSTTLYSAFHPTHNPWDLSRVPGGSSGGSAAAV
gatA_9   ASEITKEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_27  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_32  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGNLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_26  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_22  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_31  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_20  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYHAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_28  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_29  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_30  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_21  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_23  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
gatA_25  ASEITEEFFSRIRENEKEIGAFISLCEERAKEKAAHVDAKRARGEPLGKLAGVPIGVKDNIHVLGLNTTCASRMLENYQAPFHATVIENIEAEDGIILGKLNMDEFAMGSTTRYSAFHPTHNPWDLSRVPGGSSGGSAAAI
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C. Nucleotide substitutions among four *C. abortus fumC* alleles (in boldface; *fumC*_5, *fumC*_18, *fumC*_17, *fumC*_14 ruminant or avian *C. abortus* alleles) (a)

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           .10       .20       .30       .40       .50       .60       .70       .80       .90      .100      .110      .120      .130      .140      .150      .160      .170      .180      .190      .200      .210
consensus  ATTGTTKCTGCTDCWGATGARATTMTMKMMGGMRRWTTTGAWGARCAYTTYCCTYTAAARGTTTGGCARACAGGWAGYGGMACKCAAWSMAATATGAATGTSAAYGAGGTGATTGCKAATYTAGCWATTCARCGTCAYGGDGGDGWKYTWGGWAGYAAAMMWCCMRTRCAYCCYAATGATCAYGTRAATAAATCYCARTCYTCWAATGAT
fumC_5     ATTGTTTCTGCTTCTGATGAGATTATCGCAGGCAATTTTGATGAACATTTCCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGAGGGGTTTTAGGTAGCAAAACACCCATACATCCTAATGATCATGTAAATAAATCTCAATCTTCAAATGAT
fumC_18    ATTGTTTCTGCTTCTGATGAGATTATCGCAGGCAATTTTGATGAACATTTCCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGAGGGGTTTTAGGTAGCAAAACACCCATACATCCTAATGATCATGTAAATAAATCTCAATCTTCAAATGAT
fumC_17    ATTGTTTCTGCTTCTGATGAGATTATCGCAGGCAATTTTGATGAACATTTCCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGAGGGGTTTTAGGTAGCAAAACACCAATACATCCTAATGATCATGTAAATAAATCCCAATCTTCAAATGAT
fumC_14    ATTGTTTCTGCTTCTGATGAGATTATCGCAGGCAATTTTGATGAACATTTCCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGAGGGGTTTTAGGTAGCAAAACACCAATACATCCTAATGATCATGTAAATAAATCCCAATCTTCAAATGAT
fumC_10    ATTGTTTCTGCTTCTGATGAGATTATAGCAGGCAATTTTGATGAGCATTTTCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTGTTTTAGGTAGCAAAACACCAATACACCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_12    ATTGTTTCTGCTTCTGATGAGATTATAGCAGGCAATTTTGATGAGCATTTTCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTGTTTTAGGTAGCAAAACACCAATACACCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_15    ATTGTTTCTGCTTCTGATGAGATTATAGCAGGCAATTTTGATGAGCATTTTCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTGTTTTAGGTAGCAAAACACCAATACACCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_11    ATTGTTTCTGCTTCTGATGAGATTATAGCAGGAAATTTTGAAGAGCATTTTCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTATTTTAGGTAGCAAAACACCAATACACCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_13    ATTGTTTCTGCTTCTGATGAGATTATAGCAGGCAATTTTGATGAAGAGCATTTTCCTCTAAAAGTTTGGCAGACAGGTAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTATTTTAGGTAGCAAAACACCAATACACCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_16    ATTGTTTCCGCTTCTGATGAGATTATAACAGGCAATTTTGATGAGCACTTTCCTCTAAAAGTTTGGCAGACAGGCAGTGGAACGCAATCAAATATGAATGTGAACGAGGTGATTGCGAATCTAGCTATTCAACGTCACGGTGGTGTTTTAGGTAGCAAAACACCAATACATCCTAATGATCATGTAAATAAATCCCAATCTTCTAATGAT
fumC_7     ATTGTCTCTGCTGCTGACGAGATTTTAGAAGGTAATTTTGATGAACATTTTCCTTTAAGGGTGTGGCAAACGGGAAGCGGGACGCAATCTAATATGAATGTGAATGAAGTGATCGCGAATCTAGCCATTCAACGTCACGGAGGAGTCGTTGGCAGTAAAACACCGATACATCCTAATGATCATGTGAATAAATCCAGTCTTCTAATGAT
fumC_6     ATTGTTTCTGCTGCTTCTGAGATTCTTGAAGGCGGATTTGAGGAGCATTTTCCTTTAAAGGTATGGCAAACGGGCAGCGGCACGCAATCCAACATGAATGTAAATGAGGTTATTGCTAATTTAGCTATTCAACGTCATGGAGGGGTTGTAGGTAGTAAAACACCGATACATCCTAATGATCATGTCAATAAATCCCAATCTTCGAATGAT
fumC_9     ATCGTTTCCGCAGCCGATAAGATCCTTCAGGGGGGGTATGAAGAGCATTTTCCTTTAAGGGTTTGGCAAACGGGAAGTGGAACACAGACAAATATGAATGTCAATGAGGTGATAGCAAACCTTGCCATTCATAGTCATGGGGGAGTTTTGGGAAGTAAATCCCCTATACACCCTAATGATCATGTGAATAAATCTCAGTCTTCAAATGAT
fumC_20    ATCGTTTCCGCAGCCGATAAGATCCTTCAGGGGGGTATGAAGAGCATTTTCCTTTAAGGGTTTGGCAAACGGGAAGTGGAACACAGACAAATATGAATGTCAATGAGGTGATAGCAAACCTTGCCATTCATAGTCATGGGGGAGTTTTGGGAAGTAAATCCCCTATACACCCTAATGATCATGTGAATAAATCTCAGTCTTCAAATGAT
fumC_4     ATTGTTGCTGCTGCCGATGAGATTTTAGAGGGAGGTTTTGAAGAGCATTTCCCTTTAAAAGTTTGGCAGACAGGGAGCGGCACACAATCTAATATGAATGTGAATGAGGTGATTGCGAATCTTGCCATTCGTCATCACGGAGGGGTGTTAGGCAGTAAGGATCCTATCCATCCTAATGATCATGTGAATAAGTCCCAATCGTCCAATGAT
fumC_8     ATTGTGGCTGCTTCGGATGAAATTCTTTCCGGAGGATTAGAGGAACACTTCCCTTTAAAGGTATGGCAAACAGGAAGTGGAACCCAAAGCAATATGAATGTGAATGAGGTAATCGCTAATTTAGCGATTAAACGTCACGGAGGGGAGCTAGGAAGTAAAAATCCTGTGCATCCCAATGATCATGTGAATAAATCACAGTCTTCTAACGAT
fumC_2     ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCAGCGTCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
fumC_19    ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCACGCGTCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAA CCCAGTCCTCAAATGAT
fumC_22    ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCACGCGTCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
fumC_1     ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCACGCGTCGTGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
fumC_3     ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCACGCGTCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
fumC_21    ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCACGCGTCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
fumC_23    ATTGTTGCTGCTACAGATGAAATTCTCTCCGGAGAATTTGATGAACACTTCCCTTTAAAGGTTTGGCAGACAGGAAGCGGCACTCAAAGCAATATGAATGTCAATGAGGTGATTGCTAATTTAGCAATTCAGCATCATGGGGGAGAGCTTGGAAGTAAACATCCCGTGCATCCCAATGATCACGTGAATAAATCCCAGTCCTCAAATGAT
           .220      .230      .240      .250      .260      .270      .280      .290      .300      .310      .320      .330      .340      .350      .360      .370      .380      .390      .400      .410      .420
consensus  GTKTTCCCHACRGCWATGCATATWGCTGCRGTVMWRAGTMTRAARRRWMWYTMATTCCKGCWYTGGAWCATTTAMARMRRGYKWTWGATGCTAARGYTKYDGARTTTSSWSRWKRTRTMAARATTGGMAGAACRCATTTRATGGATGCWGTTCCWATGACWYTWGGRC  ARGARTTTTCTGGKTAYAGTWGYCARWTRCRTMAWTGTT
fumC_5     GTATTCCCAACAGCTATGCATATTGCTGCAGTCATGAGTCTGAAGAAGAAACTCATTCCTGCTCTGGATCATTTACAGAGGGCGTTAGATGCTAAGGTTGCGGAATTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGGC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_18    GTATTCCCAACAGCTATGCATATTGCTGCAGTCATGAGTCTGAAGAAGAAACTCATTCCTGCTCTGGATCATTTACAGAGGGCGTTAGATGCTAAGGTTGCGGAATTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGGC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_17    GTATTCCCAACAGCTATGCATATTGCTGCAGTAATGAGTCTGAAGAAGAAACTCATTCCTGCTCTGGATCATTTACAGAGGGCGTTAGATGCTAAGGTTGCGGAATTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGGC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_14    GTATTCCCAACAGCTATGCATATTGCTGCAGTCATGAGAAGAAACTCATTCCTGCTCTGGATCATTTACAGAGGGCGTTAGATGCTAAGGTTGCGGAATTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGGC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_10    GTGTTCCCCACAGCTATGCATATTGCTGCAGTGATGAGTCTGAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGGGCGTTAGATGCTAAGGTTGCTGAGTTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AAGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_12    GTGTTCCCCACAGCTATGCATATTGCTGCAGTGATGAGTCTGAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGGGCGTTAGATGCTAAGGTTGCTGAGTTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AAGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_15    GTGTTCCCCACAGCTATGCATATTGCTGCAGTGATGAGTCTGAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGGGCGTTAGATGCTAAGGTTACTGAGTTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_11    GTGTTCCCCACAGCTATGCATATTGCTGCAGTGATGAGTCTGAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGGGCGTTAGATGCTAAGGTTGCTGAGTTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_13    GTGTTCCCCACAGCTATGCATATTGCTGCAGTGATGAGTCTGAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGGGCGTTAGATGCTAAGGTTGCTGAGTTTCGAGATTGTGTCAAGATTGGCAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_16    GTGTTCCCAACAGCTATGCATATTGCTGCAGTGATTAGTCTAAAGAAGAAATTAATTCCTGCTCTGGATCATTTACAGCGAGCGTTAGATGCTAAGGTTGCTGAATTTCGAGATTGTGTCAAGATTGGAAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGGC  AGGAATTTTCTGGTTACAGTAGCCAAATACGTCAATGTT
fumC_7     GTGTTTCCAACAGCTATGCATATGGCGGCTGTGATTAGCATTAAGAAGAAATTGATTCCTTCTATGGATCATTTACAACGGGCTTTGGATGCTAAGGTTGCTGAATTTCGAGACTGCGTTAAGATAGGAAGAACCCATTTAATGGATGCTGTTCCTATGACATTAGGTC  AGGAATTTTCTGGTTACAGTAGTCAGATTCGTCAGTGTT
fumC_6     GTTTTCCCTACAGCTATGCATATTGCTGCGGTGATTAATCTGAAGAAAAAGCTCATTCCCGCTATGGATCATTTGCAAAGGGCATTAGATGCTAAGGTAGCTGAATTTCGTGACTGCGTAAAGATAGGAAGAACACATTTAATGGATGCTGTTCCTATGACATTAGGAC  AGGAGTTTTCTGGTTATAGTAATCAGATACGTCAATCCT
fumC_9     GTGTTCCCTACAGCTATGCATATTGCTGGAGTCTTGAGTGTGAAAAATCGACTTATCCCTGCGATTGATCATATGCTGAATAGTTTAAGCCATAAGGTGGATGAATTTCGTCATGATATAAAAATTGGTCGTACACATCTTATGGATGCGGTTCCTATGACTTTAGGGC  AGGAGTTTTCCGGTTATCATTCCCAAATATTTCAGTGTT
fumC_20    GTGTTCCCTACAGCTATGCATATTGCTGGAGTCTTGAGTGTGAAAAATCGGCTCATCCCTGCGATTGATCATATGCTGAATAGTTTAAGCCATAAGGTGGATGAATTTCGTCATGATATAAAAATTGGTCGTACACATCTTATGGATGCGGTTCCTATGACTTTAGGGC  AGGAGTTTTCCGGTTATCATTCCCAAATATTTCAGTGTT
fumC_4     GTTTTCCCTACAGCAATGCATATCGCTGCTGTGATTAGTTTAAAAAATAAGTTAATTCCAGCTTTAGATCATATGATTCGGGTGTTAGATGCTAAAGTGGAAGAATTTCGTCATGATGTAAAGATAGGACGGACCCATCTTATGGATGCGGTGCCTATGACGTTGGGTC  AGGAATTTTCTGGTTATAGCAGTCAATTGCGTCACTGCT
fumC_8     GTTTTCCCTACGGCCATGCATATAGCTGCTGTGCAAAGTATAAAAGGTCTTTAATACCGGCATTAGAACATTTACAAAAAAACCTTGATGCCAAAGCTTTAGAGTTTTCTAGAGACATTAAAATTGGAAGAACACATCTAATGGATGCCGTTCCAATGACTCTAGGGC  AAGAGTTTTCTGGGTACAGTCATCAGTTACGTAGTTGTT
fumC_2     GTTTTCCCAACGGCAATGCATATAGCTGCGGTTCAAAGTATAAAAGGATCTTTAATTCCGGTATTGGAACATTTAAAAAAAGTTGTTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGTAGTTCCAATGACTCTTGGGCAAAAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_19    GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGTATTGGAACATTTAAAAAAAGTTGTTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGTAGTTCCAATGACTCTTGGGCAAAAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_22    GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGCATTGGAACATTTAAAAAAAGTTATTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGCAGTTCCAATGACTCTTGGGC  AAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_1     GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGCATTGGAACATTTAAAAAAAGTTATTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGCAGTTCCAATGACTCTTGGGC  AAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_3     GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGCATTGGAACATTTAAAAAAAGTTATTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGCAGTTCCAATGACTCTTGGGC  AAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_21    GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGCATTGGAACATTTAAAAAAAGTTATTGATGCTAAAGCTTTAGAGTTTGCTCGAGATATAAAAATTGGAAGAGCGCATTTGATGGATGCAGTTCCAATGACTCTTGGGC  AAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
fumC_23    GTTTTCCCAACGGCAATGCATATAGCTGCGGTACAAAGTATAAAAGGATCTTTAATTCCGGCATTGGAACATTTAAAAAAAGTTATTGATGCTAAAGCTTTGGAGTTTGCTCGAGATATAAAAATTGGAAGAACGCATTTGATGGATGCAGTTCCAATGACTCTTGGGC  AAGAGTTTTCTGGGTATAGTTGTCAGTTGCATAATTGTT
           .430      .440      .450      .460
consensus  TAGAGMGRRTVGSWTTTTCTYTDACDCAYMTSTATGARTTRGCBATW
fumC_5     TAGAGAGAGTGGCTTTTTCGCTGACGCACATGTATGAATTAGCGATA
fumC_18    TAGAGAGAGTGGCTTTTTCCCTGACGCACATGTATGAATTAGCGATA
fumC_17    TAGAGAGAGTGGCTTTTTCGCTGACGCACATGTATGAATTAGCGATA
fumC_14    TAGAGAGAGTGGCTTTTTCGCTGACGCACATGTATGAATTAGCGATA
fumC_10    TAGAGAGAGTCGCTTTTTCTCTTACACACATGTATGAGTTAGCCATA
fumC_12    TAGAAAGAGTCGCTTTTTCTCTTACACACATGTATGAGTTAGCCATA
fumC_15    TAGAGAGAGTCGCTTTTTCTCTTACACACATGTATGAGTTAGCCATA
fumC_11    TAGAGAGAGTCGCTTTTTCTCTTACACACATGTATGAGTTAGCCATA
fumC_13    TAGAGAGAGTCGCTTTTTCTCTTACACACATGTATGAGTTAGCCATA
fumC_16    TAGAGAGAGTGGCTTTTTCTCTTACACACATGTATGAATTGGCCATA
fumC_7     TAGAAAGAGTCGCCTTTTCTCTTACACATATGTATGAGTTAGCTATA
fumC_6     TAGAGAGGGTAGCGTTTTCCCTTACGCATATGTATGAGTTAGCTATA
fumC_9     GTGAGCGCATAGCGTTTTCTCTGACGCATATGTATGAATTAGCCTTA
fumC_20    GTGAGCGCATAGCGTTTTCTCTGACGCATATGTATGAATTAGCCTTA
fumC_4     TAGAGAGTATAGCATTTTCTTTAGCTCATTTATATGAACTTGCGATT
fumC_8     TGGAGCGTATAGGTTTTTCCTTAACCCATCTTTACGAATTAGCGATT
fumC_2     TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_19    TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_22    TAGAGTGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_1     TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_3     TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_21    TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
fumC_23    TAGAGCGGATAGGATTTTCTTTAACTCACCTCTATGAGTTGGCTATT
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C. Sequence alignment among *C. abortus fumC*-encoded protein alleles (b)

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                 1111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990000000000111111111122222222223333333333444444444455555555
        1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
fumC_5  IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_18 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_17 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_14 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_10 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_12 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_15 IVSASDEIIAGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVTEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_11 IVSASDEIIAGNFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGILGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_13 IVSASDEIIAGNFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGILGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVMSLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_16 IVSASDEIITGNFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVLGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVISLKKKLIPALDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_7  IVSAADEILEGNFDEHFPLRVWQTGSGTQSNMNVNEVIANLAIQRHGGVVGSKTPIHPNDHVNKSQSSNDVFPTAMHMAAVISIKKKLIPSMDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSSQIRQCLERVAFSLTHMYELAI
fumC_6  IVSAASEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGVVGSKTPIHPNDHVNKSQSSNDVFPTAMHIAAVINLKKKLIPAMDHLQRALDAKVAEFRDCVKIGRTHLMDAVPMTLGQEFSGYSNQIRQSLERVAFSLTHMYELAI
fumC_9  IVSAADKILQGGYEEHFPLRVWQTGSGTQTNMNVNEVIANLAIHSHGGVLGSKSPIHPNDHVNKSQSSNDVFPTAMHIAGVLSVKNRLIPAIDHMLNSLSHKVDEFRHDIKIGRTHLMDAVPMTLGQEFSGYHSQIFQCCERIAFSLTHMYELAL
fumC_20 IVSAADKILQGGYEEHFPLRVWQTGSGTQTNMNVNEVIANLAIHSHGGVLGSKSPIHPNDHVNKSQSSNDVFPTAMHIAGVLSVKNRLIPAIDHMLNSLSHKVDEFRHDIKIGRTHLMDAVPMTLGQEFSGYHSQIFQCCERIAFSLTHMYELAL
fumC_4  IVAAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPTAMHIAAVISLKNKLIPALDHMIRVLDAKVEEFRHDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLESIAFSLAHLYELAI
fumC_8  IVAASDEILSGGLEEHFPLKVWQTGSGTQSNMNVNEVIANLAIKRHGGELGSKNPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLQKNLDAKALEFSRDIKIGRTHLMDAVPMTLGQEFSGYSHQLRSCLERIGFSLTHLYELAI
fumC_1  IVAATDEILSGEFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRRGGELGSKHPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLKKVIDAKALEFARDIKIGRTHLMDAVPMTLGQEFSGYSCQLHNCLERIGFSLTHLYELAI
fumC_21 IVAATDEILSGEFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGELGSKHPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLKKVIDAKALEFARDIKIGRAHLMDAVPMTLGQEFSGYSCQLHNCLERIGFSLTHLYELAI
fumC_3  IVAATDEILSGEFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGELGSKHPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLKKVIDAKALEFARDIKIGRTHLMDAVPMTLGQEFSGYSCQLHNCLERIGFSLTHLYELAI
fumC_22 IVAATDEILSGEFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQRHGGELGSKHPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLKKVIDAKALEFARDIKIGRTHLMDAVPMTLGQEFSGYSCQLHNCLEWIGFSLTHLYELAI
fumC_23 IVAATDEILSGEFDEHFPLKVWQTGSGTQSNMNVNEVIANLAIQHHGGELGSKHPVHPNDHVNKSQSSNDVFPTAMHIAAVQSIKGSLIPALEHLKKVIDAKALEFARDIKIGRTHLMDAVPMTLGQEFSGYSCQLHNCLERIGFSLTHLYELAI
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D. Nucleotide substitutions among three *C. abortus enoA* alleles (in boldface; *enoA*_8, *enoA*_16, *enoA*_14 ruminant or avian *C. abortus* alleles) (a)

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                .10       .20       .30       .40       .50       .60       .70       .80       .90      .100      .110      .120      .130      .140      .150      .160      .170      .180      .190      .200      .210
consensus GGBATGCAYGCHRMHAAYGGYYTSSAATTYCAAGAATTTATGATYCGYCCDATWRGVGCDCMYTCYMTRMMMGARGCKGTRYSBATGGGDGCWGAWGTHTTYMAYRCYTTRAAAAAMMTCYTMMAKDMWMRWCABYTVKCTACAGGWTDGGHGATGAAGGMGGMTTYGCTCCDMAHYTWVVHTCYAAYKCHGAAGCTYTRGABCTWCTY
enoA_8    GGTATGCATGCAAACAACGGCCTGCAATTTCAAGAATTTATGATTCGCCCTATAGGCGCACATTCTCTACAAGAAGCTGTACGTATGGGTGCCGATGTGTTCCATACATTGAAAAACCTTCTCAATGATAAACATCTCGCTACAGGAGTGGGAGATGAAGGCGGATTTGCTCCACAATTAAAATCTAACTCTGAAGCTTTAGACCTTCTT
enoA_16    GGTATGCATGCAAACAACGGCCTGCAATTTCAAGAATTTATGATTCGCCCTATAGGCGCACATTCTCTACAAGAAGCTGTACGTATGGGTGCCGATGTGTTCCATACATTGAAAAACCTTCTCAATGATAAACATCTCGCTACAGGAGTGGGAGATGAAGGCGGATTTGCTCCACAATTAAAATCTAACTCTGAAGCTTTAGACCTTCTT
enoA_14    GGTATGCATGCAAACAACGGCCTGCAATTTCAAGAATTTATGATTCGCCCTATAGGCGCACATTCTCTACAAGAAGCTGTACGTATGGGTGCCGATGTGTTCCATACATTGAAAAACCTTCTCAATGATAAACATCTCGCTACAGGAGTGGGAGATGAAGGCGGATTTGCTCCACAATTAAAATCTAACTCTGAAGCTTTAGACCTTCTT
enoA_13    GGCATGCATGCAGACAATGGTCTTCAATTTCAAGAATTTATGATTCGCCCTATAGGTGCACATTCTCTAAAAGAAGCTGTGCGTATGGGTGCTGATGTTTTCCATGCGTTGAAAAAACTGCTCAACGATAGACATCTCGCTACAGGAGTTGGAGATGAAGGCGGATTTGCTCCAAACTTAACATCTAACTCTGAAGCTTTAGACCTTCTT
enoA_15    GGCATGCATGCAGACAATGGTCTTCAATTTCAAGAATTTATGATTCGCCCTATAGGTGCACATTCTCTAAAAGAAGCTGTGCGTATGGGTGCTGATGTTTTCCATGCGTTGAAAAAACTGCTCAACGATAGACATCTCGCTACAGGAGTTGGAGATGAAGGCGGATTTGCTCCAAACTTAACATCTAACTCTGAAGCTTTAGACCTTCTT
enoA_10    GGTATGCATGCCAATAATGGACTACAATTCCAAGAATTTATGATTCGTCCTATCGGAGCAACATCAATAAAAGAGGCGGTACGTATGGGAGCAGATGTTTTTCACACTCTGAAAAAACTCCTCAACGATAAGAACCTCGCTACGGGAGTGGGAGATGAGGGAGGATTTGCTCCTCAACTCAAATCCAACTCTGAAGCTTTAGATCTTCTT
enoA_9     GGGATGCACGCAAATAACGGTTTGCAATTCCAAGAGTTTATGATTCGTCCTATCGGAGCAACTTCTCTAAAAGAAGCTGTACGGATGGGCGCTGATGTTTTTCATTCTTTGAAAAATATCCTCAATGAAAAAAACTTAGCTACAGGGGTTGGTGATGAAGGAGGCTTTGCTCCACAACTAAAATCTAACTCTGAAGCATTAGATCTTCTT
enoA_5     GGCATGCATGCCGATAACGGCTTGGGTTCCAAGAATTTATGATCCGTCCTATTGGAGCCTCTTCCATCAAAGAAGCTGTCAACATGGGTGCTGACGTTTTTCATACTTTGAAAAAATTACTCCATGAAAGAGGCTTATCTACTGGAGTGGGTGACGAAGGAGGCTTCGCCCCGAATCTTGCTTCTAATGAAGAAGCTCTAGAGCTCCTA
enoA_6     GGCATGCATGCCGATAACGGCTTGGAGTTCCAAGAATTTATGATCCGTCCTATTGGAGCCTCTTCCATCAAAGAAGCTGTCAACATGGGTGCTGACGTTTTTCATACTTTGAAAAAATTACTCCATGAAAGAGGCTTATCTACTGGAGTGGGTGACGAAGGAGGCTTCGCCCCGAATCTTGCTTCTAATGAAGAAGCTCTAGAGCTCCTA
enoA_7     GGCATGCATGCCGATAACGGCTTGGAGTTCCAAGAATTTATGATCCGTCCTATTGGAGCCTCTTCCATCAAAGAAGCTGTCAACATGGGTGCTGACGTTTTTCATACTTTGAAAAAATTACTCCATGAAAGAGGCTTATCTACTGGAGTGGGTGACGAAGGAGGCTTCGCCCCGAATCTTGCTTCTAATGAAGAAGCTCTAGAGCTCCTA
enoA_17    GGCATGCATGCCGATAACGGCTTGGAGTTCCAAGAATTTATGATCCGTCCTATTGGAGCCTCTTCCATCAAAGAAGCTGTCAACATGGGTGCTGACGTTTTTCATACTTTGAAAAAATTACTCCATGAAAGAGGCTTATCTACTGGAGTGGGTGACGAAGGAGGCTTCGCCCCGAATCTTGCTTCTAATGAAGAAGCTCTAGAGCTCCTA
enoA_12    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGGGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCGGATGTATTCCATGCTTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_18    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGGGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCGGATGTATTCCATGCTTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_22    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGGGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCGGATGTATTCCATGCTTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_23    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGGGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCAGATGTATTCCATGCTTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_19    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGGGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCAGATGTATTCCATGCCTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_20    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGAGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCAGATGTATTCCATGCCTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACTTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_21    GGGATGCACGCAGATAATGGCCTGGAATTTCAAGAATTTATGATCCGTCCGATTGGAGCGCACTCTATGCACGAGGCGGTATCTATGGGGGCAGATGTATTCCATGCCTTGAAAAACCTCTTAAAGTCACGTCATTTAGCTACAGGAGTAGGCGATGAAGGAGGCTTTGCTCCGAACGTACGCTCCAATGCAGAAGCTTTAGAGCTTCTC
enoA_11    GGCATGCATGCAACAAATGGCCTCCAATTTCAAGAATTTATGATCCGTCCTATTAGCGCTCCTTCCCTAACAGAAGCTGTGCGCATGGGAGCAGAAGTTTTTCACACTTTGAAAAAAATCTTACAAAATCGGCAACTTTCTACAGGAGTCGGAGATGAAGGCGGATTCGCTCCCCAACTCGCTTCCAATTCAGAGGCGCTTGACCTTCTC
enoA_2     GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAAAAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAGAATCGACAGCTGGCTACAGGTGTTGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC
enoA_3     GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAACAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAGAATCGACAGCTGGCTACAGGTGTTGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC
enoA_25    GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAACAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAGAATCGACAGCTGGCTACAGGTGTTGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC
enoA_4     GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAACAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAAAATCGACAGCTGGCTACAGGTGTTGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC
enoA_1     GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAACAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAGAATCGACAGCTGGCTACAGGTGTTGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC
enoA_24    GGTATGCATGCTACAAATGGTCTCCAATTCCAAGAATTTATGATTCGTCCAATTAGCGCTCCTTCTCTAACAGAGGCTGTGCGGATGGGAGCAGAAGTCTTCAACGCCTTAAAAAAAATCTTACAGAATCGACAGCTGGCTACAGGTGTCGGTGATGAAGGCGGATTTGCTCCTAATCTTGCCTCTAATGCCGAAGCTCTGGATCTACTC

                .220      .230      .240      .250      .260      .270      .280      .290      .300      .310      .320      .330      .340      .350      .360      .370      .380
consensus DTRMYWGCWATHGAARMHGCAGGHTTYVHVCCTRGVRARGADRTYTCTYTAGCTCTHGAYTGYGCWGCWTCYTCTTTYTAYRAWRCMVMRRMWRAAACYTAYSAHGGSARRHMBTMTSMWGMWCARRTVGVBATWCTYRMMGADYTHTGYGAKCRBTWTCCTATAGAYTCY
enoA_8     GTATTAGCTATTGAGAAAGCCGGTTTCCAGCCTGGCGAGGAGATCTCTTTAGCTCTTGACTGTGCTGCATCTTCTTTCTACGATACAAAAACAGAAACTTACGCAGGGAAAAACTCTCAAGAACAAGTCGGCATACTCGCCGATCTTTGTGATCGTTATCCTATAGACTCT
enoA_16     GTATTAGCTATTGAGAAAGCCGGTTTCCAGCCTGGCGAGGAGATCTCTTTAGCTCTTGACTGTGCTGCATCTTCTTTCTATCGATACAAAAACAGAAACTTACGCAGAGAAAAACTCTCAAGAACAAGTCGGCATACTCGCCGATCTTTGTGATCGTTATCCTATAGACTCT
enoA_14     GTATTAGCTATTGAGAAAGCCGGTTTCCAGCCTGGCGAAGAGATCTCTTTAGCTCTTGACTGTGCTGCATCTTCTTTCTACGATACAAAAACAGAAACTTACGCAGGGAAAAACTCTCAAGAACAAGTCGGCATACTCGCCGATCTTTGTGATCGTTATCCTATAGACTCT
enoA_13     TTACTAGCTATTGAAAAAGCAGGTTTCCAGCCTGGCGAGGAGATCTCTTTAGCTCTTGACTGTGCTGCATCTTCTTTCTACGATACAAAAACAAAAACTTACGAAGGGAAAAACTCTCAAGAACAAGTCAGCATACTCGCCGATCTTTGTGATCGTTATCCTATTGACTCT
enoA_15     TTACTAGCTATTGAAAAAGCAGGTTTCCAGCCTGGCGAGGAGATCTCTTTAGCTCTTGACTGTGCTGCATCTTCTTTCTACGATACAAAAACAAAAACTTACGAAGGGAAAAACTCTCAAGAACAAGTCAGCATACTCGCCGATCTTTGTGACCGTTATCCTATTGACTCT
enoA_10     GTATTAGCTATTGAAAAATCTGGTTTCCAACCGGGGAAAGAAATTTCACTAGCTCTTGATTGCGCAGCATCTTCTTTCTATTGATACCAAAACAAAAACTTACGAGGGTAAGAGCTATCAAGAACAAGTAGAAATACTTGCAGATCTTTGCGACCGTTATCCTATTGATTCC
enoA_9      GTACTTGCTATCGAAAAAGCAGGTTTCCAACCTGGAGAAGACATCTCCCTAGCTCTCGATTGCGCAGCTTCTCCTTCTATGATACGAAAGCAGAAACCTATGATGGAAAGAGCTATGAAGAACAAGTGAACATACTTGCCGATCTCTGTGATCGCTATCCTATCGATTCT
enoA_5      TTGCTGGCTATTGAAAAAGCAGGCTTTACTCCAGGAAAAGATATATCGCTAGCCTTAGACTGCGCAGCATCCTCATTCTATAACGTAAAAACAGGCACGTATGATGGGAGGCACTATGAAGAGCAAATCGCAATCCTTTCTAATTTATGTGATCGCTATCCTATAGACTCC
enoA_6      TTGCTGGCTATTGAAAAAGCAGGCTTTACTCCAGGAAAAGATATATCGCTAGCCTTAGACTGCGCAGCATCCTCATTCTATAACGTAAAAACAGGCACGTATGATGGGAGGCACTATGAAGAGCAAATCGCAATCCTTTCTAATTTATGTGATCGCTATCCTATAGACTCC
enoA_7      TTGCTGGCTATTGAAAAAGCAGGCTTTACTCCAGGAAAAGATATATCGCTAGCCTTAGACTGCGCAGCGTCCTCATTCTATAACGTAAAAACAGGCACGTATGATGGGAGGCACTATGAAGAGCAAATCGCAATCCTTTCTAATTTATGTGATCGCTATCCTATAGACTCC
enoA_17     TTGCTGGCTATTGAAAAAGCAGGCTTTACTCCAGGAAAAGATATATCGCTAGCCTTAGACTGCGCAGCATCCTCATTCTATAACGTAAAAACAGGCACGTATGATGGAAGGCACTATGAAGAGCAAATCGCTATCCTTTCTAATTTATGTGATCGCTATCCTATAGACTCC
enoA_12     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAAGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGTGACAAAAACCTATCACGGCAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAACGGTTTCCTATAGACTCT
enoA_18     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAAGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGCAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAGCGGTTTCCTATAGACTCT
enoA_22     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAAGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGCAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAGCGGTTTCCTATAGACTCT
enoA_23     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAAGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGCAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAGCGGTTTCCTATAGACTCT
enoA_19     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAAGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGTAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAGCGGTTTCCTATAGACTCT
enoA_20     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAGGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGTAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAACGGTTTCCTATAGACTCT
enoA_21     ATGACTGCAATAGAAGCCGCAGGTTTTGTCCCTGGGGAGGAGGTTTCTTTAGCTCTAGATTGCGCAGCATCTTCTTTTTACGAAGCAGCGACAAAAACCTATCACGGTAGACCTTATGATGCACAGATAGAGATTCTTAAAGAGCTTTGCGAGCGGTTTCCTATAGACTCT
enoA_11     TTGGCTGCTATTGAAAAAGGCTGGCTTTATCCCTGGAGAGGATATTTCTTTAGCTCTCGAGTTGCGCAGCTTCCTCGTTTTACAGAATACTCAGGATAAAACTTATGATTGCTGTACTCACAGAATTATGCGATCGCTATCCTATAGATTCT
enoA_2      TTAACAGCAATCGAAACTGCAGGATTCACACCTAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
enoA_3      TTAACAGCAATCGAAACTGCAGGATTCACACCTAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
enoA_25     TTAACAGCAATCGAAACTGCAGGATTCACACCCAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
enoA_4      TTAACAGCAATCGAAACTGCAGGATTCACACCTAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
enoA_1      TTAACAGCAATCGAAACTGCAGGATTCACACCTAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
enoA_24     TTAACAGCAATCGAAACTGCAGGATTCACACCTAGAGAAGATATTTCTTTAGCTCTCGACTGCGCTGCTTCTTCTTTCTATAATACCCAAGATAAAACCTATGATGGGAAATCGTATGCAGATCAAGTGGGTATACTTGCAGAACTCTGTGAGCACTATCCTATAGATTCT
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D. Amino-acid substitutions among *enoA*-encoded protein alleles (b)

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                                                                                                                   1111111111111111111111111111
                  1111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990000000000111111111122222222
         1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567
enoA_8   GMHANNGLQFQEFMIRPIGAHSLQEAVRMGADVFHTLKNLLNDKHLATGVGDEGGFAPQLKSNSEALDLLVLAIEKAGFQPGEEISLALDCAASSFYDTKTETYAGKNSQEQVGILADLCDRYPIDS
enoA_16  GMHANNGLQFQEFMIRPIGAHSLQEAVRMGADVFHTLKNLLNDKHLATGVGDEGGFAPQLKSNSEALDLLVLAIEKAGFQPGEEISLALDCAASSFYDTKTETYAEKNSQEQVGILADLCDRYPIDS
enoA_14  GMHANNGLQFQEFMIRPIGAHSLQEAVRMGADVFHTLKNLLNDKHLATGVGDEGGFAPQLKSNSEALDLLVLAIEKAGFQPGEEISLALDCAASSFYDTKTETYAGKNSQEQVGILADLCDRYPIDS
enoA_13  GMHADNGLQFQEFMIRPIGAHSLKEAVRMGADVFHALKKLLNDRHLATGVGDEGGFAPNLTSNSEALDLLLLAIEKAGFQPGEEISLALDCAASSFYDTKTKTYEGKNSQEQVSILADLCDRYPIDS
enoA_15  GMHADNGLQFQEFMIRPIGAHSLKEAVRMGADVFHALKKLLNDRHLATGVGDEGGFAPNLTSNSEALDLLLLAIEKAGFQPGEEISLALDCAASSFYDTKTKTYEGKNSQEQVSILADLCDRYPIDS
enoA_10  GMHANNGLQFQEFMIRPIGATSIKEAVRMGADVFHTLKKLLNDKNLATGVGDEGGFAPQLKSNSEALDLLVLAIEKSGFQPGKEISLALDCAASSFYDTKTKTYEGKSYQEQVEILADLCDRYPIDS
enoA_9   GMHANNGLQFQEFMIRPIGATSLKEAVRMGADVFHSLKNILNEKNLATGVGDEGGFAPQLKSNSEALDLLVLAIEKAGFQPGEDISLALDCAASSFYDTKAETYDGKSYEEQVNILADLCDRYPIDS
enoA_5   GMHADNGLGFQEFMIRPIGASSIKEAVNMGADVFHTLKKLLHERGLSTGVGDEGGFAPNLASNEEALELLLLAIEKAGFTPGKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDS
enoA_6   GMHADNGLEFQEFMIRPIGASSIKEAVNMGADVFHTLKKLLHERGLSTGVGDEGGFAPNLASNEEALELLLLAIEKAGFTPGKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDS
enoA_7   GMHADNGLEFQEFMIRPIGASSIKEAVNMGADVFHTLKKLLHERGLSTGVGDEGGFAPNLASNEEALELLLLAIEKAGFTPGKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDS
enoA_17  GMHADNGLEFQEFMIRPIGASSIKEAVNMGADVFHTLKKLLHERGLSTGVGDEGGFAPNLASNEEALELLLLAIEKAGFTPGKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDS
enoA_12  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAVTKTYHGRPYDAQIEILKELCERFPIDS
enoA_18  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_22  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_23  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_19  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_20  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNLRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_21  GMHADNGLEFQEFMIRPIGAHSMHEAVSMGADVFHALKNLLKSRHLATGVGDEGGFAPNVRSNAEALELLMTAIEAAGFVPGEEVSLALDCAASSFYEAATKTYHGRPYDAQIEILKELCERFPIDS
enoA_11  GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFHTLKKILQNRQLSTGVGDEGGFAPQLASNSEALDLLLAAIEKAGFIPGEDISLALDCAASSFYNTQDKTYDGKSAADQVAVLTELCDRYPIDS
enoA_2   GMHATNGLQFQEFMIRPISAPSLKEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
enoA_3   GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
enoA_25  GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
enoA_4   GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
enoA_1   GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
enoA_24  GMHATNGLQFQEFMIRPISAPSLTEAVRMGAEVFNALKKILQNRQLATGVGDEGGFAPNLASNAEALDLLLTAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYADQVGILAELCEHYPIDS
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