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| logo | CGGTCA CGTGTGGCGTCCGTACTTCTC | | | | | | | | | | CTATTTcccGATA | | | | | | | | | | AGCTCCTCGACTTCAACATAAGCGGCGTCCCTAAGGGTCGATTTAGTG | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| tig00008411:134529-176298() | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 172 | | | |
| tig00008216:94751-135048(-) | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 175 | | | |
| tig00002380:120727-159743() | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 177 | | | |
| tig00008216:53978-94751(-) | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 179 | | | |
| tig00002380:1146-40745() | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 176 | | | |
| tig00008411:94672-134529() | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 173 | | | |
| tig00008411:217104-257759() | TCATGCCTCTTTTCAc | GC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCA | AACTTACAGATGA | 165 | | | |
| tig00008411:257759-297618() | TCATGCCTCTTTTCAc | GC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 174 | | | |
| tig00002380:80433-120727() | TCATGCCTCTTTTCAc | GC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 159 | | | |
| tig00008215:19898-58526(-) | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 176 | | | |
| tig00008215:58526-97877(-) | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 172 | | | |
| tig00008216:21673-53978(-) | | | | | | | 51 | | | |
| tig00008411:14398-55544() | TAGTGTCTATGCCTCTT | TCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 172 | | | | |
| tig00008215:97877-137448(-) | TCATGCCTCTTTTCAc | CG | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 174 | | | | |
| tig00008411:55544-94672() | TCATGCCTCTTTTCAc | CGC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 177 | | | |
| tig00002380:40745-80433() | TCATGCCTCTTTTCAc | CG | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 175 | | | |
| tig00008411:176298-217104() | TCATGCCTCTTTT | TCAC | ACCAC | GAAGATGAAAGCAAAGATCGGCTAAATAC | CGTGTCTCATCTAGAAGTGGG | AACTTACAGATGA | 172 | | | |
| tig00008215:0-19898(-) | | | | | | | 0 | | | |
| tig00008216:0-21673(-) | | | | | | | 0 | | | |
| tig00008411:297618-338078() | CAAGATGTAATACAGAGT | CCAG | TATGACAGACTTGA | AACTTTTAAAAACTAGG | AAAGTAA | | | | | |

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|------------------------------|------------------|--------|---------------|----------------------|------------------------------|-------------------------------|------------------------------|----------------|-------|----------|--------|-----|
| tig00002380:159743-198526() | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACCGGG | CGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | GAAG | AAA | CA | 262 | | | |
| tig00008411:134529-176298() | CAGTTCCTTGCATGGG | CAGAAC | GGGGGACCGGA | CGGAAGCCTGCTTGAGG | AGG...GTGGAAGGAGAGACAGCTTCAG | GAAA | ACA | AA | 258 | | | |
| tig00008216:94751-135048(-) | CAGTTCCTTGCATGGG | CAGAAC | GAGGGGACCGG | ACGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAG...ACAGCTTCAG | GAAA | CAA | AC | 261 | | | |
| tig00002380:120727-159743() | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACG | CGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | GAAG | AAAC | AA | 264 | | | |
| tig00008216:53978-94751(-) | CAGTTCCTTGCATGGG | CAGAAC | GAGGGGACGAGGG | ACGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | G... | AAAC | AA | 265 | | | |
| tig00002380:1146-40745() | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACGAGG | ACGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | G... | AAAC | AA | 260 | | | |
| tig00008411:94672-134529() | CAGTTCCTTGCATGGG | CAGAAC | AGGGACGGGAC | GGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | GAAAC | AAAC | AC | 262 | | | |
| tig00008411:217104-257759() | CAGTTCCTTGCATGGG | CA | AAAGGGGACGAG | GGGAAAC | TGC | GAGGG | AGGAGGGTGAAG | AGAGACAGCTTCAG | GAAGA | AAAC | AA | 249 |
| tig00008411:257759-297618() | CAGTTCCTTGCATGGG | CAGAAC | AGGGACCGG | GGACAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | GAAG | AAAC | AA | 259 | | | |
| tig00002380:80433-120727() | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACCGGGG | CAGCGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAC | AGCTTCAG | GAA | AAAC | AA | 248 | | |
| tig00008215:19898-58526(-) | CAGTTCCTTGCATGGG | CAGAAC | GAGGGGACGAGGG | ACGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGA | GACTTCAG | GAA | AAAC | AA | 261 | | |
| tig00008215:58526-97877(-) | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACCGGA | CGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | AAGAA | AAAC | AA | 260 | | | |
| tig00008216:21673-53978(-) | | | | | | | | | | 51 | | |
| tig00008411:14398-55544() | CAGTTCCTTGCATGGG | CAGAAC | GAGGGGAC | CAGGG | ACGGAAGCCTGCTTGAGG | GAGGAGGGTGAAGAGAGAGACAGCTTCAA | GAA | AAAC | AA | 260 | | |
| tig00008215:97877-137448(-) | CAGTTCTTGCATGGG | CAGAAC | GGGGA | CCGGG | ACGGAAGCCTGCTTGAGG | AGGTGGAAGGAGACAGCTTCAG | GAA | AG | AAAC | AA | 254 | |
| tig00008411:55544-94672() | CAGTTCCTTGCATGGG | CAGAAC | GAGGGGAC | CGGA | ACGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | G... | AAAC | AA | 262 | | |
| tig00002380:40745-80433() | CAGTTCCTTGCATGGG | CAGAAC | AGGGGACCGGG | CGGAAGCCTGCTTGAGG | AGGAGGGTGAAGGAGA | ACAGCTTCAG | AAGA | AAAC | AA | 263 | | |
| tig00008411:176298-217104() | CAGTTCCTTGCATGGG | CAGAAG | AGGGGACCGGG | GACGCG | AAGCCTGCTAGGGG | AGGAGGGTGAAGGAGAGACAGCTTCAG | G... | AAG | AA | 258 | | |
| tig00008215:0-19898(-) | | | | | | | | | | 0 | | |
| tig00008216:0-21673(-) | | | | | | | | | | 0 | | |
| tig00008411:297618-338078() | TTGCACTGACTTGATG | CAGAA | TTGGTGC | ATTAACAT | ATGTATACATTACAT | ACGTATACAT | GTGCCAT | GCTGTGTGT | GCTGC | CACCCATT | AACTCG | 279 |
| consensus | cagttcttgc | catggg | cagaac | gggac | gg | cggaagcctgcttgagg | aggaggggtgaaggagagacagcttcag | aa | aa | | | |

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|------------------------------|-------|------------------------------------|----------------------------------|-------------------------------|--------------|-------------|-------------|-------|------|-----|
| tig00002380:159743-198526() | A | ...AATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | GTC | CAAGTTT | ACC | 338 | | |
| tig00008411:134529-176298() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATC...ACACTGAACACCC | C | ... | GTCACAAGTTT | ACC | 335 | | |
| tig00008216:94751-135048(-) | AC | ...GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACAAGTTT | ACC | 338 | | |
| tig00002380:120727-159743() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACAAGTTT | ACC | 343 | | |
| tig00008216:53978-94751(-) | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACAAGTTT | ACC | 344 | | |
| tig00002380:1146-40745() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACAAGTTT | ACC | 339 | | |
| tig00008411:94672-134529() | | ...GAATACTGTCGGACACAGCACTGACTACC | GG | TGATGAAATCATCTGCACACTGAACACCC | ... | GTCACAAGTTT | ACC | 336 | | |
| tig00008411:217104-257759() | AACA | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACAAGTTT | TACC | 329 | | |
| tig00008411:257759-297618() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GG | TGATGAAATCATCTGCACACTGAACACCC | ... | GTCACAAGTTT | ACC | 337 | | |
| tig00002380:80433-120727() | ACACA | GAATACTGTCGGACACAGCACTGACTACC | CGGTGATGAAATCATCTGCACACTGAACACCC | ... | C | GTCACAAGTTT | ACC | 329 | | |
| tig00008215:19898-58526(-) | | ...CTGAATACTGTCGGACACAGCACTGACTACC | CGGTGATGAAATCATCTGCACACTGAACACCC | ... | C | GTCACAAGTTT | TACC | 340 | | |
| tig00008215:58526-97877(-) | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | C | GTC | CAAGTTT | ACC | 339 | |
| tig00008216:21673-53978(-) | | ...ACTGT | | | | | | 56 | | |
| tig00008411:14398-55544() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAAC | CGGTACAAGTTTACC | AT | GTCACA | GTC | T | GCT | 352 |
| tig00008215:97877-137448(-) | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCAC | TGAAC | ACCC | ... | GTCACAAGTTT | ACC | 334 | |
| tig00008411:55544-94672() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTGCACACTGAACACCC | ... | ... | GTCACA | GTTT | ACC | 340 | |
| tig00002380:40745-80433() | AC | ...GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATC | ... | CTGAACACCC | ... | GTCACAAGTTT | ACC | 334 | |
| tig00008411:176298-217104() | ACAC | GAATACTGTCGGACACAGCACTGACTACC | GGGTGATGAAATCATCTG | ... | CACTGAACACCC | ... | GTCACAAGTTT | ACC | 335 | |
| tig00008215:0-19898(-) | | | | | | | | 0 | | |
| tig00008216:0-21673(-) | | | | | | | | 0 | | |
| tig00008411:297618-338078() | ACAT | ...TTAGCATTAAGGCATATCTGCTAATGCT | ...ATCCCTCCCCGGTCTCTCC | CACCCCACAACA | ... | GTC | CC | AGAGT | GTGA | 355 |
| consensus | ac | ...gaatactgtcggacacagcactgactacc | gggtgatgaaatcatctgcacactgaacaccc | | | gtcacaagttt | acc | | | |

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consensus

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tig00008216:0-21673(-)
tig00008411:297618-338078()
consensus

| CTGTcACCC AGGCTGCGGTGCGGTGGCTCTCTCGGCTCACTGAAACCT CTGCTTCCCGG TTCCAGTGATTCTTCTTcGGTAGCTGGGATT | | | | | | | | | | |
|---|-----------------------|--------------------------|------------------|-------------------|-------------|------|--------|-----|-----|--|
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 687 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 670 | |
| ... | AGGCTG | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | GATT | | | 656 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | ATT | | | 684 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 668 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | ATT | | | 671 | |
| CT... | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 669 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | GATT | | | 614 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 673 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | ATT | | | 681 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | ATT | | | 676 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | ATT | | | 667 | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | 65 | |
| CTCTGTcAC | CCAGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | TCCTGCTGGG | ATT | | | 673 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GTAGCTGGG | ATT | | | 637 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | ATT | | | 677 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | CGGTAGCTGGG | GATT | | | 651 | |
| CTGTcACCC | AGGCTGCGGTGCGGTGGCT | CTCTCGGCTCACTGAAACCT | CTGCTTCCCGG | TTCCAGTGATTCTTCTT | GGTAGCTGGG | GATT | | | 677 | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | 0 | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | 0 | |
| ATATATAATTA | ACAAAATAAAAAATA | TTATTCACTCTTTTAAAGAACATT | TACTAAATTCACAGAT | ATTACCCGAAGT | TTAGAAA | GTCA | CCTAAG | AAC | 723 | |
| ctgtcacc | aggctgcggtgcggtggc | ctctcggctcactgaaacct | ctgcttcccg | ttccagtgattcttctt | ggtagctggg | att | | | | |

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tig00008216:21673-53978(-)
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tig00008215:0-19898(-)
tig00008216:0-21673(-)
tig00008411:297618-338078()
consensus

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 tig00008216:0-21673(-)
 tig00008411:297618-338078()
 consensus

| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CG | GGG | ATT | CAG | CTT | TAA | CGC | GGC | CT | GCC | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|------|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|---|--|-----|
| ... | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CG | GGG | ATT | CAG | CTT | TAA | CGC | GGC | CT | GCC | 853 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CGCC | GGG | ATT | CAG | CTT | TAA | AGC | GGC | CT | ACC | 854 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GCCG | GG | ATT | CAG | CTT | TAA | AGC | GGC | CT | GCC | 841 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GC | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 861 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GC | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 839 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CGC | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 849 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CG | GG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 846 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | AGCG | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | ACC | 796 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GCC | GG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 849 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | CGCC | GAG | ATT | CAG | CTT | TAA | AGC | GGC | CT | GCC | 860 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | ..C | GGG | ATT | CAG | CTT | TAA | AG | CTG | GGC | CT | GCC | 852 | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GCC | GGG | ATT | CAG | CTT | TAA | AG | CTG | GG | CT | GCC | 845 | | | | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 72 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | ..GC | GGG | ATT | CAG | CTT | TAA | AGC | GGC | CT | GCC | 852 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | AGC | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 815 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | AG | ..GAT | TTT | CAG | CTT | TAA | A | GGG | GGC | CT | GCC | 855 | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | GC | GGG | ATT | CAG | CTT | TAA | AGC | GGC | CT | GCC | 819 | | | | | |
| ACA | AAT | GAT | CCA | CTT | CT | TGG | CT | CCA | AGT | GCT | TGAA | CGAC | AGG | CT | TAG | AGCG | GGG | ATT | CAG | CTT | TAA | A | GGC | CT | GCC | 861 | | | | | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 0 | | | | | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 0 | | | | | |
| TG | AA | AG | T | CC | CTT | CA | TT | CT | G | AAT | GT | CT | G | CAG | T | AG | T | T | G | GGG | AG | CAG | T | AG | T | T | CC | AT | C | | 906 |
| aca | aat | gat | cca | ctt | ct | tgg | ct | cca | agt | gct | tgaa | cgac | agg | ct | tag | ... | ggg | att | cag | ctt | taa | ... | gcg | ggc | ct | gcc | | | | | |

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tig00008216:94751-135048(-)
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tig00008216:0-21673(-)
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consensus

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 tig00008216:21673-53978(-)
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 tig00008215:97877-137448(-)
 tig00008411:55544-94672()
 tig00002380:40745-80433()
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 tig00008216:0-21673(-)
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tig00008411:257759-297618()
tig00002380:80433-120712()
tig00008215:19898-58526(-)
tig00008215:58526-97877(-)
tig00008216:21673-53978(-)
tig00008411:14398-55544()
tig00008215:97877-137448(-)
tig00008411:55544-94672()
tig00002380:40745-80433()
tig00008411:176298-217104()
tig00008215:0-19898(-)
tig00008216:0-21673(-)
tig00008411:297618-338078()
consensus

AGTGTGTGTTCCcGTGAG_gTGATTTCcTAAAGAAATGGTACTGTACACTGA_cGCAGTGGCTcAGTCTGTATcCcGAGGTcAGGAGTTCcGAG

tig00002380:159743-198526()
 tig00008411:134529-176298()
 tig00008216:94751-135048(-)
 tig00002380:120727-159743()
 tig00008216:53978-94751(-)
 tig00002380:1146-40745()
 tig00008411:94672-134529()
 tig00008411:217104-257759()
 tig00008411:257759-297618()
 tig00002380:80433-120727()
 tig00008215:19898-58526(-)
 tig00008215:58526-97877(-)
 tig00008216:21673-53978(-)
 tig00008411:14398-55544()
 tig00008215:97877-137448(-)
 tig00008411:55544-94672()
 tig00002380:40745-80433()
 tig00008411:176298-217104()
 tig00008215:0-19898(-)
 tig00008216:0-21673(-)
 tig00008411:297618-338078()
 consensus

ACCAGCCC GGCCA CGTGGTGAAACCCGGTCTCTACTGAAA TACGAAATGGAGTCAGGCGCGTGGGCAGGCACCTGTAACCCGAGCTAC

tig00002380:159743-198526()
tig00008411:134529-176298()
tig00008216:94751-135048(-)
tig00002380:120727-159743()
tig00008216:53978-94751(-)
tig00002380:1146-40745()
tig00008411:94672-134529()
tig00008411:217104-257759()
tig00008411:257759-297618()
tig00002380:80433-120727()
tig00008215:19898-58526(-)
tig00008215:58526-97877(-)
tig00008216:21673-53978(-)
tig00008411:14398-55544()
tig00008215:97877-137448(-)
tig00008411:55544-94672()
tig00002380:40745-80433()
tig00008411:176298-217104()
tig00008215:0-19898(-)
tig00008216:0-21673(-)
tig00008411:297618-338078()
consensus

| Sequence | Position |
|---------------|----------|
| TCGGGAGGCTGGG | 1301 |
| TCGGGAGGCTGGG | 1308 |
| TCGGGAGGCTGGG | 1289 |
| TCGGGAGGCTGGG | 1309 |
| TCGGGAGGCTGGG | 1258 |
| TCGGGAGGCTGGG | 1295 |
| TCGGGAGGCTGGG | 1293 |
| TCGGGAGGCTGGG | 1248 |
| TCGGGAGGCTGGG | 1293 |
| TCGGGAGGCTGGG | 1303 |
| TCGGGAGGCTGGG | 1290 |
| TCGGGAGGCTGGG | 1282 |
| TCGGGAGGCTGGG | 170 |
| TCGGGAGGCTGGG | 1294 |
| TCGGGAGGCTGGG | 1261 |
| TCGGGAGGCTGGG | 1301 |
| TCGGGAGGCTGGG | 1242 |
| TCGGGAGGCTGGG | 1304 |
| TCGGGAGGCTGGG | 0 |
| TCGGGAGGCTGGG | 0 |
| TCGGGAGGCTGGG | 1310 |

tig00002380:159743-198526()
 tig00008411:134529-176298()
 tig00008216:94751-135048(-)
 tig00002380:120727-159743()
 tig00008216:53978-94751(-)
 tig00002380:1146-40745()
 tig00008411:94672-134529()
 tig00008411:217104-257759()
 tig00008411:257759-297618()
 tig00002380:80433-120727()
 tig00008215:19898-58526(-)
 tig00008215:58526-97877(-)
 tig00008216:21673-53978(-)
 tig00008411:14398-55544()
 tig00008215:97877-137448(-)
 tig00008411:55544-94672()
 tig00002380:40745-80433()
 tig00008411:176298-217104()
 tig00008215:0-19898(-)
 tig00008216:0-21673(-)
 tig00008411:297618-338078()
 consensus

[illegible]

logo

| | | |
|------------------------------|--|------|
| tig00002380:159743-198526() | CAGATATACAA.GAAAGAA..AAGAAAGAAA.....TGTTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1453 |
| tig00008411:134529-176298() | CAGATATACAA.GAAGAAA..AAGAAAAGAAAAAT..GAGAAAAGGCCTGTATTGCTACTGGGCTGGGGCCTTCTCT..CTGTCTGTTTCTCT | 1474 |
| tig00008216:94751-135048(-) | CAGATATACAAAGAAAGAAA..AAGAAAGAGAGAAA.TGAAAGAAAGGCCTGTATTGCTACTGGGCT.GGGCCTTCTCT..CT.TTTGTCTCTCT | 1459 |
| tig00002380:120727-159743() | CAGATATACAAGAAAGAAA..AAGAAAGAAAGAAA.GAAATGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1480 |
| tig00008216:53978-94751(-) | TATACAAAGAAAGAAAAGAA..AAGAAAGAAAGAAATGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1431 |
| tig00002380:1146-40745() | CAGATATACAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA.TGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1469 |
| tig00008411:94672-134529() | CAGATA.TACAAAGAAAGAA..AAGAAAGAAAGAAA.TGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1463 |
| tig00008411:217104-257759() | CAGATAGCAAAGAAAGAA..AAGAAAGAGA.AAA.TGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1424 |
| tig00008411:257759-297618() | AAGACA.....AAGA..AAGAAAGAGA..AA.TGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCTGTCTGTCTCTGTCTCT | 1452 |
| tig00002380:80433-120727() | CATACAGAT.ATACAAAGAA.GAAAAGAAAGAAAGAAAGAAAGAAAGGCCTGTATTGCTAGAA.....AGGGCCTTCT....CTGTCTGTTTCTCT | 1474 |
| tig00008215:19898-58526(-) | CAGATATAC..AAGAAAGAA..AGAAAGAAAGAAAGAAATGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCT....CTGTCTGTTTCTCT | 1461 |
| tig00008215:58526-97877(-) | CAT.....GGCACTATATTGCTGGG...CTAAGACCT.....CTGTCTGTTTCTCT | 1389 |
| tig00008216:21673-53978(-) | | 188 |
| tig00008411:14398-55544() | GATATACAAAGAAAGAAA..GAAAAGAAAGAAAGAAATGAAAGAAAGGCCTGTATTGCTACTGGGCTGGGGCCTTCTCT..CTGTCTGTTTCTCT | 1458 |
| tig00008215:97877-137448(-) | CAGATATA..CAAGAAAGA..AAAGAAAGAAAGAAATGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1424 |
| tig00008411:55544-94672() | CAGATATACAAGAAAGAAAGAAAGAAAAAGAAA.....TCTGTATTATCT.....GCTCTCTCT..CTGTCTGTCTCTGT | 1450 |
| tig00002380:40745-80433() | CAGATATACAAGAAAGAAAGAAAGAAAGAAAGAAATGAAAGAAAGGCCTGTATTGCTACTGGGCTAGGGCCTTCTCT..CTGTCTGTTTCTCT | 1416 |
| tig00008411:176298-217104() | CAGATATACAAGAAAGAA..AAGAAAGAAAGAAA.....GAAAGGCCTGTATTCTACT.....GGCCTTCTCTG..TTTCTCTGTCTTT | 1470 |
| tig00008215:0-19898(-) | | 0 |
| tig00008216:0-21673(-) | | 0 |
| tig00008411:297618-338078() | TACAACTAATATGCAAAATACAAACTGGCTATCAC.....TACCATTCGATAATGGAAATTAGCTCTCCTGCA..TACCTGATGACCT | 1475 |
| consensus | cagata.a.a.a.a.aa..aa.aaa.a.a.aa....a..aaaggcactgtattgctactgggct.gggccttctct..ctgtctgtttctct | |

logo

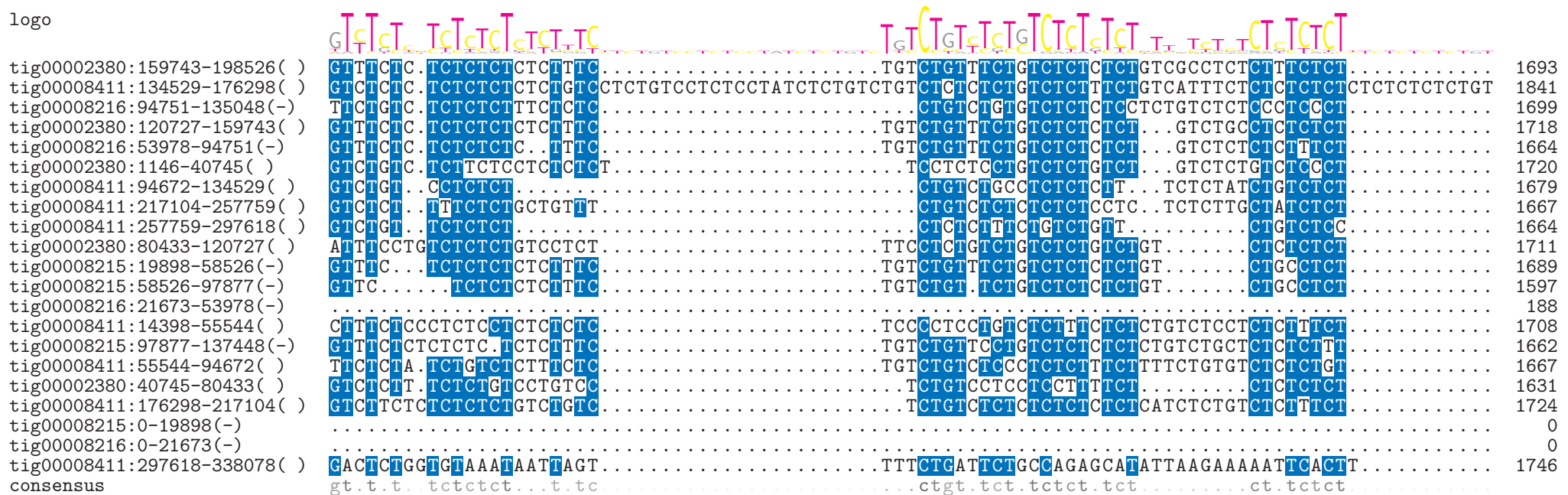
| | | |
|------------------------------|--|------|
| tig00002380:159743-198526() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT....TTCTTTCTTTCTGTCTC | 1534 |
| tig00008411:134529-176298() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTCTGTCT..CTGTCTGTCT..TGTCTGTCTCTTTCTTTCTTTCTGTCTC | 1564 |
| tig00008216:94751-135048(-) | G.T.TCTGTCTCTGTCTTTCTCTGTCTGTGTCTCTTT..CTCTGTCTGT....CTCTCTCTC.TGTCTGTCTCT..TTCTCTCTCTTTCTGTCTC | 1543 |
| tig00002380:120727-159743() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT....TTCTTTCTTTCTGTCTC | 1561 |
| tig00008216:53978-94751(-) | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGT....CTCT....TTCTTTCTTTCTGTCTC | 1508 |
| tig00002380:1146-40745() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT....TTCTTTCTTTCTGTCTC | 1550 |
| tig00008411:94672-134529() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTGT.....CTTTCTTTCTTTCTCTC | 1542 |
| tig00008411:217104-257759() | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCT.T.....CTCTTTCTTTCTTTCT | 1502 |
| tig00008411:257759-297618() | C.TGTTTCATCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..T.....CTTT.....CTTTCTTTCTGTCTC | 1525 |
| tig00002380:80433-120727() | C.TGTTTCGTCTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCT..CTGTCTGTCTCT...TTCTTTCTTTCTGTCTC | 1556 |
| tig00008215:19898-58526(-) | C.TGTTTCGTCTCTGTCTTTCTCT..CTGTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT...TTCTTTCTTTCTGTCTC | 1542 |
| tig00008215:58526-97877(-) | C..ATTTCGTCTCTGTCTTTCTCT..CT..GTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTGT....CTCTTTCTTTCTGTCTC | 1468 |
| tig00008216:21673-53978(-) | | 188 |
| tig00008411:14398-55544() | C.TGTTTCGTCTCTGTCTTTCTCT..CT..GTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCTCT..TGTCTGTCTCT...TTCTTT..CTTTCTGTCTT | 1540 |
| tig00008215:97877-137448(-) | C.TGTTTCGTCTCTGTCTTTCTCT..CT..GTGTCTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT...TTCTTT..CTTTCTGTCTC | 1505 |
| tig00008411:55544-94672() | C.TGTCTGTCTCTTTCTTTCTCT....CTGTCTTTTGT..CCTCTCTGT....CTGTCTG...TGTCTGTCTTC...TATCTTACTCTGTCTC | 1528 |
| tig00002380:40745-80433() | C.TGTTTCGTCTCTGTCTTTCTCT....CTGTGTCTTT..CTCTGTCTGT....CTGTCTGTCT..TGTCTGTCTCT....TTCTTTCTTTCTGTCTC | 1495 |
| tig00008411:176298-217104() | C.TGTCT..TCTCTGTCTCTGTCTGTCTGTCTGTCTTCTTCTTTCT..TTCTGTCTCTGTCTTTGTCTGTCT...TCTGTCTCT....TCTCTCTTTCTCTGTCTC | 1552 |
| tig00008215:0-19898(-) | | 0 |
| tig00008216:0-21673(-) | | 0 |
| tig00008411:297618-338078() | AAATGCTTAACTCTAACTCTCT....TTTCACTTTGATTGGAAAC.....TTGTTACAATAGAGTTT....TTTACCTCAAAGCTCTT | 1551 |
| consensus | c.tggttcgtctctgtctttctct...gtgtctcttt.ctctgtctgt...ctgtctgtc.tgtctgtct.t.....tt.ctttctgtctc | |

[illegible]

logo

Sequence logo showing nucleotide conservation across 1685 sequences. The y-axis represents the log-odds of a nucleotide being at a position, with a scale from 0 to 1685. The x-axis shows positions from 1 to 1685. The logo is color-coded: C (blue), G (green), T (red), and A (yellow). The sequence is highly conserved, with a strong preference for T and C in the first 100 positions, and a strong preference for A and G in the last 100 positions. The consensus sequence is shown at the bottom: c..tc tgtct .ctctc.ct..ct..c t.tct.

logo



logo

