

MGAS27556 sof 2100 AACAGCTCTCGAGGAAAAATAAAGAAGAAGAGAACAAAACGTTCTACACCTACAGAAAATGAAAACCTGTGCACAGAAAAATCATTCAAACTACT 2199
 MGAS26786 sof 2099 AACAGCTCTCGAGGAAAAATAAAGAAGAAGAGAACAAAACGTTCTACACCTACAGAAAATGAAAACCTGTGCACAGAAAAATCATTCAAACTACT 2198
 MGAS27027 sof 2101 AACAGCTCTCGAGGAAAAATAAAGAAGAAGAGAACAAAACGTTCTACACCTACAGAAAATGAAAACCTGTGCACAGAAAAATCATTCAAACTACT 2200

 MGAS27556 sof 2200 ACCTACGAAATTAATGAACAAAAGTTGAAGGGAACAACTTGGTGATGTTAGTCTGACATACAGTAAATCAAGGTTCTGTACCACAGATTGATGGCC 2299
 MGAS26786 sof 2199 ACCTACGAAATTAATGAACAAAAGTTGAAGGGAACAACTTGGTGATGTTAGTCTGACATACAGTAAATCAAGGTTCTGTACCACAGATTGATGGCC 2298
 MGAS27027 sof 2201 ACCTACGAAATTAATGAACAAAAGTTGAAGGGAACAACTTGGTGATGTTAGTCTGACATACAGTAAATCAAGGTTCTGTACCACAGATTGATGGCC 2300

 MGAS27556 sof 2300 ATGTTATTGAGCCACAAGCACCGACATTACCTAAGTTACCTCCTGTTATTGAGCATGGCCCTAACCTTGAGTATGAGGAAGAACAGGTTATCAGTTACC 2399
 MGAS26786 sof 2299 ATGTTATTGAGCCACAAGCACCGACATTACCTAAGTTACCTCCTGTTATTGAGCATGGCCCTAACCTTGAGTATGAGGAAGAACAGGTTATCAGTTACC 2398
 MGAS27027 sof 2301 ATGTTATTGAGCCACAAGCACCGACATTACCTAAGTTACCTCCTGTTATTGAGCATGGCCCTAACCTTGAGTATGAGGAAGAACAGGTTATCAGTTACC 2400

 MGAS27556 sof 2400 ACTTAAACATGGCAGCAATGCCACGACACACAAGTGACAATTGAAGAAGACACAGTTCTCAACGTCAGATATCCTTGTAGGCGGTCAGAGTGGACC 2499
 MGAS26786 sof 2399 ACTTAAACATGGCAGCAATGCCACGACACACAAGTGACAATTGAAGAAGACACAGTTCTCAACGTCAGATATCCTTGTAGGCGGTCAGAGTGGACC 2498
 MGAS27027 sof 2401 ACTTAAACATGGCAGCAATGCCACGACACACAAGTGACAATTGAAGAAGACACAGTTCTCAACGTCAGATATCCTTGTAGGCGGTCAGAGTGGACC 2500

 MGAS27556 sof 2500 GTTGACATCACCGAAGATACCCAACCGATTGTCCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGCACCTAACGTCAGATGTCTTGTG 2599
 MGAS26786 sof 2499 GTTGACATCACCGAAGATACCCAACCGATTGTCCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGCACCTAACGTCAGATGTCTTGTG 2598
 MGAS27027 sof 2501 GTTGACATCACCGAAGATACCCAACCGATTGTCCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGCACCTAACGTCAGATGTCTTGTG 2600

 MGAS27556 sof 2600 GTGGTCAAAGTGAGCCAATCGATATCACTGAAGATACCCAACCAAGTGTGTCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGTACCTCAACG 2699
 MGAS26786 sof 2599 GTGGTCAAAGTGAGCCAATCGATATCACTGAAGATACCCAACCAAGTGTGTCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGTACCTCAACG 2698
 MGAS27027 sof 2601 GTGGTCAAAGTGAGCCAATCGATATCACTGAAGATACCCAACCAAGTGTGTCAGGCTCAATGACGCGACAGTTGTGAGGAAGACACAGTACCTCAACG 2700

 MGAS27556 sof 2700 TCCAGATATCCTTGTGGCGGTCAAAGTGATCCAATCGATATCACCGAAGATACCCAACCGATTGTGAGGCTCAATGACGCTACTGTTATCGAAGAA 2799
 MGAS26786 sof 2699 TCCAGATATCCTTGTGGCGGTCAAAGTGATCCAATCGATATCACCGAAGATACCCAACCGATTGTGAGGCTCAATGACGCTACTGTTATCGAAGAA 2798
 MGAS27027 sof 2701 TCCAGATATCCTTGTGGCGGTCAAAGTGATCCAATCGATATCACCGAAGATACCCAACCGATTGTGAGGCTCAATGACGCTACTGTTATCGAAGAA 2800

 MGAS27556 sof 2800 GATACGAAACAAAACGCTTCTTCCACTTTGATAACGAGCCACAAGCACAGAAAACCTAAAGAGCAACATCTCTCAGCTTACCACAAGCTCCAGTCT 2899
 MGAS26786 sof 2799 GATACGAAACAAAACGCTTCTTCCACTTTGATAACGAGCCACAAGCACAGAAAACCTAAAGAGCAACATCTCTCAGCTTACCACAAGCTCCAGTCT 2898
 MGAS27027 sof 2801 GATACGAAACAAAACGCTTCTTCCACTTTGATAACGAGCCACAAGCACAGAAAACCTAAAGAGCAACATCTCTCAGCTTACCACAAGCTCCAGTCT 2900

 MGAS27556 sof 2900 ATAAGGCAGCTCATCACTTGCCCTGCATCTGGAGACAAACGTGAAGCATCCTTTACAATTGTTGCTCTAACAAATATTGGAGCTGCAGGTTTGTCTCAGCAA 2999
 MGAS26786 sof 2899 ATAAGGCAGCTCATCACTTGCCCTGCATCTGGAGACAAACGTGAAGCATCCTTTACAATTGTTGCTCTAACAAATATTGGAGCTGCAGGTTTGTCTCAGCAA 2998
 MGAS27027 sof 2901 ATAAGGCAGCTCATCACTTGCCCTGCATCTGGAGACAAACGTGAAGCATCCTTTACAATTGTTGCTCTAACAAATATTGGAGCTGCAGGTTTGTCTCAGCAA 3000

 MGAS27556 sof 3000 AAAACGTCGCGACACCGAAGAAAATAA 3027
 MGAS26786 sof 2999 AAAACGTCGCGACACCGAAGAAAATAA 3026
 MGAS27027 sof 3001 AAAACGTCGCGACACCGAAGAAAATAA 3028
