**SUPPLEMENTARY**

**MEDIA**

**TABLE 1 LB media (18)**

|  |  |
| --- | --- |
| Materials | Methods |
| Tryptone  Yeast extract  Sodium chloride (NaCl)  dH2O | 1) Dissolve the following in dH2O while stirring using a stir plate: 10 g tryptone, 5 g yeast extract, 10 g NaCl  2) Top up to 1 L with dH2O  3) Autoclave on liquid cycle 2  4) Store on bench  \*Add 1.5% agar prior to autoclave if making plates |

**TABLE 2 M9S media (19)**

|  |  |
| --- | --- |
| Materials | Methods |
| NaCl  Na2HPO  KH2PO4  NH4Cl  MgSO4•7H2O  dH2O  Sucrose  Thiamine (2mg/mL in dH2O)  Biotin | 1) Dissolve the following in dH2O while stirring using a stir plate: 0.5 g NaCl, 7 g  Na2HPO4, 3 g KH2PO4, 1 g NH4Cl and 0.7 g MgSO4•7H2O  2) Add sucrose so that the final concentration would be 20% in 1 L  3) Top up to 1 L with dH2O  4) Autoclave on liquid cycle 2  5) Add thiamine to 2µg/mL and biotin to 0.008% prior to use  \*Add 1.5% agar prior to autoclave if making plates |

**TABLE 3 L Media (12)**

|  |  |
| --- | --- |
| Materials | Methods |
| Glucose  Tryptone  Yeast extract  NaCl  2M CaCl2 in dH2O  dH2O | 1) Dissolve the following in 900 mL dH2O while stirring using a stir plate: 10 g NaCl, 1 g  glucose, 10 g tryptone, 5 g yeast extract and 1 mL of 2 M CaCl2 solution  2) Top up to 1 L with dH2O  4) Autoclave on liquid cycle 2  \*Add 1.5% agar prior to autoclave if making plates |

**Sequences of *ompC* gene from DAE219 N1-N19 isolates**

**> E.coli BW25113 (obtained from Genbank database)**

**TTAGAACTGGTAAACCAGACCCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACGAGTGAACTGG**

**TTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTTGTTGAAGTAGTAGGTAGCAC**

**CAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCCACGACCCAGGTTTTTACCTTTAGACTGCAG**

**GTAAGCCAGGGACGGACGCAGACCGAAGTCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTG**

**TTCGCCCAACCCAGGGAACCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGT**

**TGTTAGCGTCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTAATCATAAGTG**

**ATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTTGTTAGTTACGCCACTAGTAA**

**AGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTGAACAGCAAAGTTCAGGCCGTCAACCAGACC**

**GAAGAAGTCAGTGTTACGGTAGGTCGCGAAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAG**

**GTGTCACCACCGAATTCTGGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGAC**

**CGTAGTCGAAAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTCAGTAACCTGA**

**GTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTGGTCGCCATCTACATCTTTGTTGTCAGAGAAATAGT**

**GCAGGCCGTCTACTTTACCGTACAGATCTAATTTGTTGCCGTCTTTGTTGTAAACTTCAGCAGCGTTTGC**

**TGCGCCTGCTACCAGCAGAGCTGGGACCAGGAGGGACAGTACTTTAACTTTCAT**

**> *E.coli* BW25113 (sequenced with our samples)**

**CCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCAC**

**GAGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTT**

**TGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGC**

**CACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGT**

**CGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAAC**

**CTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGT**

**CGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGG**

**TGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGT**

**AATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGT**

**TGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACT**

**GAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGA**

**AGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTG**

**GCAGTACGTCGGTCCAGGAAGTTACGTCATNNCAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCANACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGNTCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTGGTCGCCATCTACATC**

**TTTGTNGTCAGANAAATAGTGCNNNCGTCTACTTTACCGTACAGATCTAATTTGTTGCCG**

**TCNTTTGTNGTAAACTTCAGCAGCGTTNGCTGCGCNGCTNCAGCAGANCTGGG**

**> DAE219 N1**

**GAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

**GTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

**AACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAA**

**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGNTCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTNNNCTTGAAGCCAAGACGCATG**

**TANGTCTGGTCGCNTCTACATCTTTNNNGTCNNAGAAANNANTGCANNNNCTACTTTACC**

**GTACAGATCTAANTTNNNNCGNCTTTNNTNGTAAACTTCANCA**

**> DAE219 N2**

**ACCCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCA**

**CGAGTGAACTGGTTGTCNTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTT**

**TTGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAG**

**CCACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAG**

**TCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAA**

**CCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCG**

**TCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCG**

**GTGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCG**

**TAATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCG**

**TTGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTAC**

**TGAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCG**

**AAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTANGTGTCACCACCGAATTCT**

**GGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCG**

**AAAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTT**

**TCGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGGTCAGCTG**

**GTCAGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTTGAAGCCAAGACG**

**CATGTAGGTCTGGTCGCNTCTACATCTTTNTTGTC**

**> DAE219 N3**

**CCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCAC**

**GAGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTT**

**TGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGC**

**CACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGT**

**CGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAAC**

**CTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGT**

**CGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGG**

**TGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGT**

**AATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGT**

**TGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACT**

**GAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGA**

**AGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTG**

**GCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGA**

**AAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTT**

**CGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGT**

**CAGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTNNTCTTGAAGCCANNANGCAT**

**GTNNTCTGGTCGCCATCTACATCTTTGTNGTCAGAGAAATAGTGC**

**> DAE219 N4**

**GACCCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

**GTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

**AACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAA**

**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGNCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAAGANGCATGTAGGTCTTGAAGCCAAGANGCAT**

**GTNNNCTGGTCGNCATCTACNTCTTNNTNTCAGANAANTANTGCAGGCGTCTACTTTACC**

**GTACNGATCTAATTTGTNCNTCTTGTT**

**> DAE219 N6**

**GACCCNGAGCTACGATGTTATCANTGTTGATGCCAGCGTCAC**

**GAGTGAACTGGTTGTCNTCNAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTT**

**TGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGC**

**CACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGT**

**CGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAAC**

**CTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGT**

**CGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGG**

**TGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGT**

**AATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGT**

**TGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACT**

**GAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGA**

**AGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTG**

**GCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGA**

**AAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTT**

**CGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGT**

**CAGTAACCTGAGTTTCACCTTTGAAGNCNAGACGCATGTAGGTCTTGAAGCCAAGANGCA**

**TGTNNTCTGGTCGCCATCTACATCTTTGTTGTCAGANAAAATAGTGCAGNCGTCTACTTT**

**ACCGTACAGATCTATTTG**

**> DAE219 N7 (resolved by forward and reverse sequencing)**

**GACCCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACGAGTGAACTGGTTGTCGT**

**CCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTTGTTGAAGTAGTAGGTAG**

**CACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCCACGACCCAGGTTTTTAC**

**CTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTCGAACTGGTACTGAGCAA**

**CAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACCTACGCGAGTTGCGTTGT**

**AGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTCGTATTTCAGACCACCAG**

**TGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGTGTTCTGAGCATCAGTAC**

**GTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTAATCATAAGTGATAGAAC**

**CGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTTGTTAGTTACGCCACTAG**

**TAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTGAACAGCAAAGTTCAGGC**

**CGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAAGCCGTTACCACGCTGCT**

**GCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGGCAGTACGTCGGTCCAGG**

**AAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAAAGAACCCACATCCTGGA**

**ATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTCGTTTTCAGCGCTGTTGC**

**CCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTCAGTAACCTGAGTTTCAC**

**CTTTGAAGCCAAGACGCATGTAGGTCTTGAAGCCAAGACGCATGTAGGTCTGGTCGCCAT**

**CTACATCTTTGTTGTCAGAGAAATAGTGCAGGCCGTCTACTTTACCGTACAGATCTAATT**

**TGTTGCCGTCTTTGTTGTAAACTTCAGCAGCGTTTGCTGCGCCTGCTACCAGCAGAGCTG**

**GGACCAGGAGGGACAGTACTTTAACTTTCATGTTATTAAC**

**> DAE219 N8**

**GACCCNGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

**GTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

**AACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAA**

**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTTGAANNCCAGACGCAT**

**GTAGGTCTGGTCGCCATCTACATCTTTGNNGTCAGANNAANTAGTGCNGNNGTCTACTTT**

**ACNGTACAGATCTAATTTGTTGCCGTCNTTTNTNGTAAACTTCAGCAGCGTTTGCTG**

**> DAE219 N9**

**GAGCTACGATGTTATCAGTGTTGATGCCAG**

**CGTCACGAGTGAACTGGTTGNCNTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACA**

**TGTTTTTGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGT**

**CGTAGCCACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGAC**

**CGAAGTCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCA**

**GGGAACCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGT**

**TAGCGTCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAG**

**CAGCGGTGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAAC**

**CTTCGTAATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCAC**

**GACCGTTGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCT**

**GGTACTGAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGG**

**TCGCGAAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGA**

**ATTCTGGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGT**

**AGTCGAAAGAACCCACATCCTGGAATTTCAGANCTGCGAATGCCACACGGGTCCAGGAGT**

**TGTTTTCGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCA**

**GCTGGTCAGTAACCTGAGTTTCACCTTTGAAGCCAGANGCATGTAGGTCTTGAAGCCAAN**

**ACGCATGTAGGTCTGGTCGCCATCTACNTNNTTTGTTGTCANANAAATA**

**> DAE219 N10 (resolved by forward and reverse sequencing)**

**GACCCAGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACGAGTGAACTGGTTGTCGT**

**CCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTTGTTGAAGTAGTAGGTAG**

**CACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCCACGACCCAGGTTTTTAC**

**CTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTCGAACTGGTACTGAGCAA**

**CAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACCTACGCGAGTTGCGTTGT**

**AGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTCGTATTTCAGACCACCAG**

**TGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGTGTTCTGAGCATCAGTAC**

**GTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTAATCATAAGTGATAGAAC**

**CGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTTGTTAGTTACGCCACTAG**

**TAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTGAACAGCAAAGTTCAGGC**

**CGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAAGCCGTTACCACGCTGCT**

**GCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGGCAGTACGTCGGTCCAGG**

**AAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAAAGAACCCACATCCTGGA**

**ATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTCGTTTTCAGCGCTGTTGC**

**CCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTCAGTAACCTGAGTTTCAC**

**CTTTGAAGCCAAGACGCATGTAGGTCTTGAAGCCAAGACGCATGTAGGTCTGGTCGCCAT**

**CTACATCTTTGTTGTCAGAGAAATAGTGCAGGCCGTCTACTTTACCGTACAGATCTAATT**

**TGTTGCCGTCTTTGTTGTAAACTTCAGCAGCGTTTGCTGCNCCTGCTACCAGCAGAGCTG**

**GGACCAGGAGGGACAGTACTTTAACTTTCATGTTATTAAC**

**> DAE219 N11**

**GACCCNGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACGAG**

**TGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTTGT**

**TGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCCAC**

**GACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTCGA**

**ACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACCTA**

**CGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTCGT**

**ATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGTGT**

**TCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTAAT**

**CATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTTGT**

**TAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTGAA**

**CAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAAGC**

**CGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGGCA**

**GTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAAAG**

**AACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTCGT**

**TTTCAGCGCTGTTGCCCTGGNTCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTCAG**

**TAACCTGAGTTTCACCTTTGAAGCCAAGANGCATGTNNNCNTGAAGCCAAGACGCATGTA**

**GGNCTGGTCGCCATCTACATCTTT**

**> DAE219 N12**

**GANCCNGAGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

**GTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

**AACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAA**

**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGNATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGNCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCANANGCATGTAGGNCTGGTCGCCATCTACATCT**

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**TT**

**> DAE219 N13**

**GACCCNGNGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

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**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

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**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAGACGCATGTAGGTCTGGTCGCCATCTACATCT**

**TTGTTGTCNNANNAAATAGTGCAGGCCGTCTACTTTACCGTACAGATCTAATTTGTTGCC**

**GT**

**> DAE219 N14**

**GAGCTACGATGTTATCAGTGTTGATGCCAGCGTCA**

**CGAGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTT**

**TTGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAG**

**CCACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAG**

**TCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAA**

**CCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCG**

**TCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCG**

**GTGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCG**

**TAATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCG**

**TTGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTAC**

**TGAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCG**

**AAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCT**

**GGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCG**

**AAAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTT**

**TCGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGNCGTAACCGGTCAGCTGG**

**TCAGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTGGTCGCNTCTACAT**

**CTTTGTTGTCANANAANAGTGCAGGCCGTCTACTTTACCGTACAGATCTAATTTGTTGCC**

**GTCTTTGTNGTAAACTTCAGCAG**

**> DAE219 N15**

**AGCAGGTTGATTTTGTAGTCAACGTAGGTGGA**

**CATGTTTTTGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTC**

**GTCGTAGCCACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAG**

**ACCGAAGTCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACC**

**CAGGGAACCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTT**

**GTTAGCGTCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTA**

**AGCAGCGGTGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAA**

**ACCTTCGTAATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTC**

**ACGACCGTTGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACC**

**CTGGTACTGAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTA**

**GGTCGCGAAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACC**

**GAATTCTGGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACC**

**GTAGTCGAAAGAACCCACATCCTGGAATTTCANACCTGCGAATGCCACACGGGTCCAGGA**

**GTTGTTTTCGTTTTCAGCGCTGTTGCCCTGGNTCTGATATTCCCACTGGCCGTAACCGGT**

**CAGCTGGTCAGTAACCTGAGTTTCACCTTTGAAGCCAAGANGCATGTAGGTCTGGTCGCC**

**ATCTACATCTTTGTNGTCAGAGAAATAGTGCNGNCGTCTACTTTACCGTACAGATCTAAT**

**TTGTTGCCGTCTTTGTNGNAANCTTCAGCA**

**> DAE219 N16**

**ACCCNGNGCTACGATGTTATCAGTGTTGATGCCAGCGTCAC**

**GAGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTT**

**TGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGC**

**CACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGT**

**CGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAAC**

**CTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGT**

**CGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGG**

**TGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGT**

**AATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGT**

**TGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACT**

**GAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGA**

**AGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTG**

**GCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGA**

**AAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTT**

**CGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGNCGTAACCGGTCAGCTGGT**

**CAGTAACCTGAGTTTCACCTTTGAAGCCANANGCATGTNNTCTGGTCGCNTCTACATCTT**

**TGNTGTCAGANAATAGTGCAGGCCGTCTACTTTACCGTACAGATCTAATTTGTNGCCGTC**

**TTTG**

**> DAE219 N17**

**AGCTACGATGTTATCAGTGTTGATGCCAGC**

**GTCACGAGTGAACTGGTTGNCNTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACAT**

**GTTTTTGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTC**

**GTAGCCACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACC**

**GAAGTCGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAG**

**GGAACCTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTT**

**AGCGTCGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGC**

**AGCGGTGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACC**

**TTCGTAATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACG**

**ACCGTTGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTG**

**GTACTGAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGT**

**CGCGAAGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAA**

**TTCTGGCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTA**

**GTCGAAAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTT**

**GTTTTCGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAG**

**CTGGTCAGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTGGTCGCCATC**

**TACATCTTTGT**

**> DAE219 N18**

**AGCTACGATGTTATCAGTGTTGATGCCAGCGTCACG**

**AGTGAACTGGTTGTNNTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTTT**

**GTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGCC**

**ACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGTC**

**GAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAACC**

**TACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGTC**

**GTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGGT**

**GTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGTA**

**ATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGTT**

**GTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACTG**

**AACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGAA**

**GCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTGG**

**CAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGAA**

**AGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTTC**

**GTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGCCGTAACCGGTCAGCTGGTC**

**AGTAACCTGAGTTTCACCTTTGAAGCCAAGACGCATGTAGGTCTGGTCGCATCTACATCTTTG**

**> DAE219 N19**

**GAGCTACGATGTTATCAGTGTTGATGCCAGCGTCAC**

**GAGTGAACTGGTTGTCGTCCAGCAGGTTGATTTTGTAGTCAACGTAGGTGGACATGTTTT**

**TGTTGAAGTAGTAGGTAGCACCAACATCAACATATTTCAGGATATCTTCGTCGTCGTAGC**

**CACGACCCAGGTTTTTACCTTTAGACTGCAGGTAAGCCAGGGACGGACGCAGACCGAAGT**

**CGAACTGGTACTGAGCAACAGCTTCGAAGTTCTGTGCTTTGTTCGCCCAACCCAGGGAAC**

**CTACGCGAGTTGCGTTGTAGGTCTGGGTGTACTGAGCAGCCAGGTAGATGTTGTTAGCGT**

**CGTATTTCAGACCACCAGTGTAGGTTTCAGCACGGTCGCCGTTACCGATGTAAGCAGCGG**

**TGTTCTGAGCATCAGTACGTTTGGAGCTGGAGATCGCACCACCGATACCGAAACCTTCGT**

**AATCATAAGTGATAGAACCGCCGACGCCGTCGCCGTTTTGACGCAGTGCGTCACGACCGT**

**TGTTAGTTACGCCACTAGTAAAGCCTTCACCAGATGGGTTGCCGTTTTTACCCTGGTACT**

**GAACAGCAAAGTTCAGGCCGTCAACCAGACCGAAGAAGTCAGTGTTACGGTAGGTCGCGA**

**AGCCGTTACCACGCTGCTGCATGAAGTTGTCAGAACCGTAGGTGTCACCACCGAATTCTG**

**GCAGTACGTCGGTCCAGGAAGTTACGTCATAAACAACGCCGTAGTTACGACCGTAGTCGA**

**AAGAACCCACATCCTGGAATTTCAGACCTGCGAATGCCACACGGGTCCAGGAGTTGTTTT**

**CGTTTTCAGCGCTGTTGCCCTGGATCTGATATTCCCACTGGNCGTAACCGGTCAGCTGGT**

**CAGTAACCTGAGTTTCACCTTTGAAGCCANANGCATGTAGGTCTGGTCGCCATCTACATC**

**TTTGNNGTCAGANAAATAGTGCAGNCGTCTACTTTACCGTACAGATCTAATT**