Supporting Information

Zhang and Nuss 10.1073/pnas.0807225105

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Nucleotide alignment of full-length CHV1-EP713 RNA (713) and predominant ~8 kb DI RNA (713 defect).

Majority   GCCTATGGGTGGTCTACATAGGTGAGCATGCGTTGCTCGATATAGACCGCCATTATTGGTAACACGCTTGAAGTGTTCTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                  10        20        30        40        50        60        70        80
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCCTATGGGTGGTCTACATAGGTGAGCATGCGTTGCTCGATATAGACCGCCATTATTGGTAACACGCTTGAAGTGTTCTC         80
713 defect GCCTATGGGTGGTCTACATAGGTGAGCATGCGTTGCTCGATATAGACCGCCATTATTGGTAACACGCTTGAAGTGTTCTC         80

Majority   ATCCGGAGAAAGTGATTTGCTTTCTTCCATGAGGCTCCCTGGAGGGATTGTCCAATAATGGTTGATAATTTTGGTTGCTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                  90       100       110       120       130       140       150       160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATCCGGAGAAAGTGATTTGCTTTCTTCCATGAGGCTCCCTGGAGGGATTGTCCAATAATGGTTGATAATTTTGGTTGCTG        160
713 defect ATCCGGAGAAAGTGATTTGCTTTCTTCCATGAGGCTCCCTGGAGGGATTGTCCAATAATGGTTGATAATTTTGGTTGCTG        160

Majority   CACAACCGGGGCTTTGCCCGGGGATTTCATCCCGTTCAAGGTGAGGCCCTTGTAGTAACCTCTCCCCGCTGCGTGAGCGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 170       180       190       200       210       220       230       240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CACAACCGGGGCTTTGCCCGGGGATTTCATCCCGTTCAAGGTGAGGCCCTTGTAGTAACCTCTCCCCGCTGCGTGAGCGA        240
713 defect CACAACCGGGGCTTTGCCCGGGGATTTCATCCCGTTCAAGGTGAGGCCCTTGTAGTAACCTCTCCCCGCTGCGTGAGCGA        240

Majority   ATACATAAGTTCACCCAGTACTGACAGTGTCAGCGCCGCACGTGCGTGAAACGTGTGACTCGCAGACTGAAGCGACCTAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 250       260       270       280       290       300       310       320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATACATAAGTTCACCCAGTACTGACAGTGTCAGCGCCGCACGTGCGTGAAACGTGTGACTCGCAGACTGAAGCGACCTAT        320
713 defect ATACATAAGTTCACCCAGTACTGACAGTGTCAGCGCCGCACGTGCGTGAAACGTGTGACTCGCAGACTGAAGCGACCTAT        320

Majority   GGTGAAAACGGATGTACCATCTAGCTGTGGAGTAGTGACCCTAGAAGCTAATCCGATGGTTCCACCAGTCGTTGTTTGCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 330       340       350       360       370       380       390       400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGTGAAAACGGATGTACCATCTAGCTGTGGAGTAGTGACCCTAGAAGCTAATCCGATGGTTCCACCAGTCGTTGTTTGCC        400
713 defect GGTGAAAACGGATGTACCATCTAGCTGTGGAGTAGTGACCCTAGAAGCTAATCCGATGGTTCCACCAGTCGTTGTTTGCC        400

Majority   GGCAAACGCCACAAACGGTTTCGTGCTTTGCGTGAAGAAGCACGGTCTCTTAAGAGTTCATTGGTACGGTTGACCCCGAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 410       420       430       440       450       460       470       480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCAAACGCCACAAACGGTTTCGTGCTTTGCGTGAAGAAGCACGGTCTCTTAAGAGTTCATTGGTACGGTTGACCCCGAA        480
713 defect GGCAAACGCCACAAACGGTTTCGTGCTTTGCGTGAAGAAGCACGGTCTCTTAAGAGTTCATTGGTACGGTTGACCCCGAA        480

Majority   CGAGGTCCGAACATAATGGCTCAATTAAGAAAACCCAGTCAGAGTCTGGTGCTCTCTGAAAGTGTTGATCCTACTACAGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 490       500       510       520       530       540       550       560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGAGGTCCGAACATAATGGCTCAATTAAGAAAACCCAGTCAGAGTCTGGTGCTCTCTGAAAGTGTTGATCCTACTACAGT        560
713 defect CGAGGTCCGAACATAATGGCTCAATTAAGAAAACCCAGTCAGAGTCTGGTGCTCTCTGAAAGTGTTGATCCTACTACAGT        560

Majority   GGATCCTTTCGTCAGCGTGAGGACGGAAGAGGTGGTCCCTGCGGGTTGCATAACCCTATGGGAGTACAGAGACTCATGTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 570       580       590       600       610       620       630       640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGATCCTTTCGTCAGCGTGAGGACGGAAGAGGTGGTCCCTGCGGGTTGCATAACCCTATGGGAGTACAGAGACTCATGTG        640
713 defect GGATCCTTTCGTCAGCGTGAGGACGGAAGAGGTGGTCCCTGCGGGTTGCATAACCCTATGGGAGTACAGAGACTCATGTG        640

Majority   GCGACGTGCCTGGCCCGTTGTCGCATGGTGATCTCCGGCGTTTGCGCACCCCTGACGGGGTATGTAAGTGCCAGGTCCAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 650       660       670       680       690       700       710       720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCGACGTGCCTGGCCCGTTGTCGCATGGTGATCTCCGGCGTTTGCGCACCCCTGACGGGGTATGTAAGTGCCAGGTCCAC        720
713 defect GCGACGTGCCTGGCCCGTTGTCGCATGGTGATCTCCGGCGTTTGCGCACCCCTGACGGGGTATGTAAGTGCCAGGTCCAC        720

Majority   TTTGAGTTGCCGACCGTGCTCAAGAGTGGTTCCACCGGAACGGTCCCGGAACACCCCGCGGTGTTGGCTGCCTTCATTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 730       740       750       760       770       780       790       800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTTGAGTTGCCGACCGTGCTCAAGAGTGGTTCCACCGGAACGGTCCCGGAACACCCCGCGGTGTTGGCTGCCTTCATTGG        800
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Fig. S1. Nucleotide alignment of full-length CHV1-EP713 RNA (713) and predominant ≈8 kb DI RNA (713 defect).

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713 defect TTTGAGTTGCCGACCGTGCTCAAGAGTGGTTCCACCGGAACGGTCCCGGAACACCCCGCGGTGTTGGCTGCCTTCATTGG       800

Majority   CAGGCCTCGCCGGTGTTCCTTGGAACAACGTACGAAGGAGTTGGATTCCCGATTCCTTCAGTTGGTGCATGGTGGCCTCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                  810       820       830       840       850       860       870       880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGGCCTCGCCGGTGTTCCTTGGAACAACGTACGAAGGAGTTGGATTCCCGATTCCTTCAGTTGGTGCATGGTGGCCTCC       880
713 defect CAGGCCTCGCCGGTGTTCCTTGGAACAACGTACGAAGGAGTTGGATTCCCGATTCCTTCAGTTGGTGCATGGTGGCCTCC       880

Majority   CTGCGAGGCCATCATACATGATTGCGCGCCCGCCCAGGCCAGTTCGAGGCCTGTGCTCATCTCGGAACGGTTCCCTTGCT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                  890       900       910       920       930       940       950       960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTGCGAGGCCATCATACATGATTGCGCGCCCGCCCAGGCCAGTTCGAGGCCTGTGCTCATCTCGGAACGGTTCCCTTGCT       960
713 defect CTGCGAGGCCATCATACATGATTGCGCGCCCGCCCAGGCCAGTTCGAGGCCTGTGCTCATCTCGGAACGGTTCCCTTGCT       960

Majority   CAGTTTGGGCAGGGCTACTGTTATCTCTCGGCCATTGTAGACAGCGCAAGATGGCGCGTCGCCCGTACCACCGGTTGGTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                  970       980       990      1000      1010      1020      1030      1040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGTTTGGGCAGGGCTACTGTTATCTCTCGGCCATTGTAGACAGCGCAAGATGGCGCGTCGCCCGTACCACCGGTTGGTG      1040
713 defect CAGTTTGGGCAGGGCTACTGTTATCTCTCGGCCATTGTAGACAGCGCAAGATGGCGCGTCGCCCGTACCACCGGTTGGTG      1040

Majority   TGTACGTGTGGCAGACTATCTTAGGCTGCTACAATGGGTTGGTCGCCGGTCCTTTGGCTCCTTTCAGATTGAGAAAAGCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1050      1060      1070      1080      1090      1100      1110      1120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGTACGTGTGGCAGACTATCTTAGGCTGCTACAATGGGTTGGTCGCCGGTCCTTTGGCTCCTTTCAGATTGAGAAAAGCG      1120
713 defect TGTACGTGTGGCAGACTATCTTAGGCTGCTACAATGGGTTGGTCGCCGGTCCTTTGGCTCCTTTCAGATTGAGAAAAGCG      1120

Majority   CCGTCGACCATGTTTATCACGTGGTCGTCGACGCTGAGTATCAGTCTGAGCAGGATGGGGCCCTTTTCTACCAAGCCATT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1130      1140      1150      1160      1170      1180      1190      1200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCGTCGACCATGTTTATCACGTGGTCGTCGACGCTGAGTATCAGTCTGAGCAGGATGGGGCCCTTTTCTACCAAGCCATT      1200
713 defect CCGTCGACCATGTTTATCACGTGGTCGTCGACGCTGAGTATCAGTCTGAGCAGGATGGGGCCCTTTTCTACCAAGCCATT      1200

Majority   TTGGGTTTGGCCGAGAAGGATCCCCTTGCCCGGATTGGCGGCCGATTGAACCCGCTCGCTGCCGAGTTTGCGCCCGGCAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1210      1220      1230      1240      1250      1260      1270      1280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGGGTTTGGCCGAGAAGGATCCCCTTGCCCGGATTGGCGGCCGATTGAACCCGCTCGCTGCCGAGTTTGCGCCCGGCAG      1280
713 defect TTGGGTTTGGCCGAGAAGGATCCCCTTGCCCGGATTGGCGGCCGATTGAACCCGCTCGCTGCCGAGTTTGCGCCCGGCAG      1280

Majority   CGCCCTTAGGGTTGAACCTGTGACTCCACAGGTTACCCGCCGTAAAGGTTCGACTCGGATGACTGGTCGTGACCCAACCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1290      1300      1310      1320      1330      1340      1350      1360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGCCCTTAGGGTTGAACCTGTGACTCCACAGGTTACCCGCCGTAAAGGTTCGACTCGGATGACTGGTCGTGACCCAACCA      1360
713 defect CGCCCTTAGGGTTGAACCTGTGACTCCACAGGTTACCCGCCGTAAAGGTTCGACTCGGATGACTGGTCGTGACCCAACCA      1360

Majority   TTGTCTCCGTTGGCAAGGTTGGTATGGCCATCACCAGCATCCAGGATGCTCTTGTGGCTACGGAGTTGAGGAACGTCAAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1370      1380      1390      1400      1410      1420      1430      1440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGTCTCCGTTGGCAAGGTTGGTATGGCCATCACCAGCATCCAGGATGCTCTTGTGGCTACGGAGTTGAGGAACGTCAAT      1440
713 defect TTGTCTCCGTTGGCAAGGTTGGTATGGCCATCACCAGCATCCAGGATGCTCTTGTGGCTACGGAGTTGAGGAACGTCAAT      1440

Majority   TTCGGCCGTCGTGACACGGAAGCTGAGTGTCGTCGCCTTTGGGCGAGATACGAAGTGAACGACTATTTCCGTCGTCACAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1450      1460      1470      1480      1490      1500      1510      1520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTCGGCCGTCGTGACACGGAAGCTGAGTGTCGTCGCCTTTGGGCGAGATACGAAGTGAACGACTATTTCCGTCGTCACAA      1520
713 defect TTCGGCCGTCGTGACACGGAAGCTGAGTGTCGTCGCCTTTGGGCGAGATACGAAGTGAACGACTATTTCCGTCGTCACAA      1520

Majority   GGCCGAACTCCTCAAGTTCGATGCGCGCCTTCGGTCGCGCATGGCCAAGAAACCTGCGTCGTCACGGGCCCGCCCGTCCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 1530      1540      1550      1560      1570      1580      1590      1600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCCGAACTCCTCAAGTTCGATGCGCGCCTTCGGTCGCGCATGGCCAAGAAACCTGCGTCGTCACGGGCCCGCCCGTCCG      1600
713 defect GGCCGAACTCCTCAAGTTCGATGCGCGCCTTCGGTCGCGCATGGCCAAGAAACCTGCGTCGTCACGGGCCCGCCCGTCCG      1600

Majority   ACGCAAAGATTCAGTGCATAGGGTGGCGTGATCGCCACCTGTTGCCACAACGCCTTGCTGGTCTCTCCAAACAAGGCCGT
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           ---------+---------+---------+---------+---------+---------+---------+---------+
                    1610      1620      1630      1640      1650      1660      1670      1680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ACGCAAAGATTCAGTGCATAGGGTGGCGTGATCGCCACCTGTTGCCACAACGCCTTGCTGGTCTCTCCAAACAAGGCCGT       1680
713 defect ACGCAAAGATTCAGTGCATAGGGTGGCGTGATCGCCACCTGTTGCCACAACGCCTTGCTGGTCTCTCCAAACAAGGCCGT       1680

Majority   TCCCTCGTCTGGTCGCGGTTCGCGACCAGCAACATCAGACGCAAGACTCCGCCTTGTGTCGTCAACCCCAGTGCGGACCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    1690      1700      1710      1720      1730      1740      1750      1760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCCCTCGTCTGGTCGCGGTTCGCGACCAGCAACATCAGACGCAAGACTCCGCCTTGTGTCGTCAACCCCAGTGCGGACCC       1760
713 defect TCCCTCGTCTGGTCGCGGTTCGCGACCAGCAACATCAGACGCAAGACTCCGCCTTGTGTCGTCAACCCCAGTGCGGACCC       1760

Majority   CGTCGTCCATAACTGGAAGGATTCCGCTGCCCTGGCAGTGAAGAAAATCGCCGAAGCACGCCGGCGACAAGAAATTCGCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    1770      1780      1790      1800      1810      1820      1830      1840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGTCGTCCATAACTGGAAGGATTCCGCTGCCCTGGCAGTGAAGAAAATCGCCGAAGCACGCCGGCGACAAGAAATTCGCG       1840
713 defect CGTCGTCCATAACTGGAAGGATTCCGCTGCCCTGGCAGTGAAGAAAATCGCCGAAGCACGCCGGCGACAAGAAATTCGCG       1840

Majority   CTGCAGCCTACGCCGAGCGGGCCAAAGCTCGGGGGCAGACCAATGTCGTTGCTTCCATTTCGGAAGCAATTGAAACCACT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    1850      1860      1870      1880      1890      1900      1910      1920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTGCAGCCTACGCCGAGCGGGCCAAAGCTCGGGGGCAGACCAATGTCGTTGCTTCCATTTCGGAAGCAATTGAAACCACT       1920
713 defect CTGCAGCCTACGCCGAGCGGGCCAAAGCTCGGGGGCAGACCAATGTCGTTGCTTCCATTTCGGAAGCAATTGAAACCACT       1920

Majority   CTACGGCGGAATAAAACCCGCTTTGCCTTGGATGGTCTTCATCTGGCGGCATCTGCCATTGTCACGACCCGGTTGAGGTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    1930      1940      1950      1960      1970      1980      1990      2000
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTACGGCGGAATAAAACCCGCTTTGCCTTGGATGGTCTTCATCTGGCGGCATCTGCCATTGTCACGACCCGGTTGAGGTC       2000
713 defect CTACGGCGGAATAAAACCCGCTTTGCCTTGGATGGTCTTCATCTGGCGGCATCTGCCATTGTCACGACCCGGTTGAGGTC       2000

Majority   GTGGAACCAAGAGGAAATTCGTGCTGGTCGCGAATTTCGTAAATCAACCACTTCCTGGATATGGAGGCATGTGCCTTCAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2010      2020      2030      2040      2050      2060      2070      2080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTGGAACCAAGAGGAAATTCGTGCTGGTCGCGAATTTCGTAAATCAACCACTTCCTGGATATGGAGGCATGTGCCTTCAT       2080
713 defect GTGGAACCAAGAGGAAATTCGTGCTGGTCGCGAATTTCGTAAATCAACCACTTCCTGGATATGGAGGCATGTGCCTTCAT       2080

Majority   CAATCCAGGACGCCCTGAACCTGACTTCGGTCAGGGACAAGCTCGACCCCGGCCGCGCGTTTGGTTACGTGCAGGCTGCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2090      2100      2110      2120      2130      2140      2150      2160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAATCCAGGACGCCCTGAACCTGACTTCGGTCAGGGACAAGCTCGACCCCGGCCGCGCGTTTGGTTACGTGCAGGCTGCG       2160
713 defect CAATCCAGGACGCCCTGAACCTGACTTCGGTCAGGGACAAGCTCGACCCCGGCCGCGCGTTTGGTTACGTGCAGGCTGCG       2160

Majority   GTTGCGCAGGGCATGTCCGACTTCCGGAGGGCAAAGCGGGCATTGGCGATCGTCGCCAAGCCCGTAATCCGGAACATCCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2170      2180      2190      2200      2210      2220      2230      2240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTTGCGCAGGGCATGTCCGACTTCCGGAGGGCAAAGCGGGCATTGGCGATCGTCGCCAAGCCCGTAATCCGGAACATCCG       2240
713 defect GTTGCGCAGGGCATGTCCGACTTCCGGAGGGCAAAGCGGGCATTGGCGATCGTCGCCAAGCCCGTAATCCGGAACATCCG       2240

Majority   TGACCCCTATGAGCACGGGTTTGTCAAGCGAGATGGTAAGCTTCGCCATTCTCGCGACGCATTTAATAAGAAGCTGCGTA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2250      2260      2270      2280      2290      2300      2310      2320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGACCCCTATGAGCACGGGTTTGTCAAGCGAGATGGTAAGCTTCGCCATTCTCGCGACGCATTTAATAAGAAGCTGCGTA       2320
713 defect TGACCCCTATGAGCACGGGTTTGTCAAGCGAGATGGTAAGCTTCGCCATTCTCGCGACGCATTTAATAAGAAGCTGCGTA       2320

Majority   CAAAGGCCGTGGCCGCCACGAAGGTCCACAAAATAAAATTTTAATGTATAAGGAAGCCGAACGACCTATTGAAGTGTGGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2330      2340      2350      2360      2370      2380      2390      2400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAAAGGCCGTGGCCGCCACGAAGGTCCACAAAATAAAATTTTAATGTATAAGGAAGCCGAACGACCTATTGAAGTGTGGC       2400
713 defect CAAAGGCCGTGGCCGCCACGAAGGTCCACAAAATAAAATTTTAATGTATAAGGAAGCCGAACGACCTATTGAAGTGTGGC       2400

Majority   GAACACAGGTCATGGACGGGCCAACATGGACTGCCCTTTCTGAGTCGTGCAGGGACAGGTTGTTCTTTGCATCCGGGGAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2410      2420      2430      2440      2450      2460      2470      2480
           ---------+---------+---------+---------+---------+---------+---------+---------+
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713        GAACACAGGTCATGGACGGGCCAACATGGACTGCCCTTTCTGAGTCGTGCAGGGACAGGTTGTTCTTTGCATCCGGGGAA        2480
713 defect GAACACAGGTCATGGACGGGCCAACATGGACTGCCCTTTCTGAGTCGTGCAGGGACAGGTTGTTCTTTGCATCCGGGGAA        2480

Majority   GGTGGTGAGCACATGACGCTCGATATCATCCAGCCTGATTCGTACACCAAGATACGCTTATTTCGCAGCGGTCGGTTCGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2490      2500      2510      2520      2530      2540      2550      2560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGTGGTGAGCACATGACGCTCGATATCATCCAGCCTGATTCGTACACCAAGATACGCTTATTTCGCAGCGGTCGGTTCGA        2560
713 defect GGTGGTGAGCACATGACGCTCGATATCATCCAGCCTGATTCGTACACCAAGATACGCTTATTTCGCAGCGGTCGGTTCGA        2560

Majority   GGTGTCGGTTGACGGAAAGAGTTTTGGCCAGGGCGGCAACCGTTATAGATTCGTCTTTCGCTATGACTCTTTGCTGTCGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2570      2580      2590      2600      2610      2620      2630      2640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGTGTCGGTTGACGGAAAGAGTTTTGGCCAGGGCGGCAACCGTTATAGATTCGTCTTTCGCTATGACTCTTTGCTGTCGA        2640
713 defect GGTGTCGGTTGACGGAAAGAGTTTTGGCCAGGGCGGCAACCGTTATAGATTCGTCTTTCGCTATGACTCTTTGCTGTCGA        2640

Majority   CACCTTTTGGATATCCTGCCGAGGACAAGGAAATAGCGCTTCAGGATTACAATCACAAGCAGTTGCTGGGTGAGATGTTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2650      2660      2670      2680      2690      2700      2710      2720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CACCTTTTGGATATCCTGCCGAGGACAAGGAAATAGCGCTTCAGGATTACAATCACAAGCAGTTGCTGGGTGAGATGTTC        2720
713 defect CACCTTTTGGATATCCTGCCGAGGACAAGGAAATAGCGCTTCAGGATTACAATCACAAGCAGTTGCTGGGTGAGATGTTC        2720

Majority   TTGAAGCTTCCTGACTCCTATGTTGACGGGAGACCGATCGCTGAGGCTTTCTTTCGTTACGTTGACGACCTGAAATGGGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2730      2740      2750      2760      2770      2780      2790      2800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGAAGCTTCCTGACTCCTATGTTGACGGGAGACCGATCGCTGAGGCTTTCTTTCGTTACGTTGACGACCTGAAATGGGA        2800
713 defect TTGAAGCTTCCTGACTCCTATGTTGACGGGAGACCGATCGCTGAGGCTTTCTTTCGTTACGTTGACGACCTGAAATGGGA        2800

Majority   TGTCGGCGTGTTCCGTGACCGCAGGTCGCTAACGGAACTTCATTTACCAGCATCATCTGGTTTAACAACTGCACAAGTTT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2810      2820      2830      2840      2850      2860      2870      2880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGTCGGCGTGTTCCGTGACCGCAGGTCGCTAACGGAACTTCATTTACCAGCATCATCTGGTTTAACAACTGCACAAGTTT        2880
713 defect TGTCGGCGTGTTCCGTGACCGCAGGTCGCTAACGGAACTTCATTTACCAGCATCATCTGGTTTAACAACTGCACAAGTTT        2880

Majority   CGGTGGCCAAACTCGAATGGCCGCCACTACCTATCATCCAGGCCCAGCCGACAATACTAGCCGGTATCATTGACAACTTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2890      2900      2910      2920      2930      2940      2950      2960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGGTGGCCAAACTCGAATGGCCGCCACTACCTATCATCCAGGCCCAGCCGACAATACTAGCCGGTATCATTGACAACTTC        2960
713 defect CGGTGGCCAAACTCGAATGGCCGCCACTACCTATCATCCAGGCCCAGCCGACAATACTAGCCGGTATCATTGACAACTTC        2960

Majority   AAGATTTGCTTCCCCGTAAACGGGAAATGGATCTATGGTCAAGGGTTGTCATGGACCAGATACGATGGCGATGCCTCCGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    2970      2980      2990      3000      3010      3020      3030      3040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AAGATTTGCTTCCCCGTAAACGGGAAATGGATCTATGGTCAAGGGTTGTCATGGACCAGATACGATGGCGATGCCTCCGT        3040
713 defect AAGATTTGCTTCCCCGTAAACGGGAAATGGATCTATGGTCAAGGGTTGTCATGGACCAGATACGATGGCGATGCCTCCGT        3040

Majority   TCCAACCTCTCTATTGTCCAACCGACAGCACGCGAGGTTCTGGAACGAGAAGGACATCCCCACCGGCCTGAAGCTTTCAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    3050      3060      3070      3080      3090      3100      3110      3120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCCAACCTCTCTATTGTCCAACCGACAGCACGCGAGGTTCTGGAACGAGAAGGACATCCCCACCGGCCTGAAGCTTTCAA        3120
713 defect TCCAACCTCTCTATTGTCCAACCGACAGCACGCGAGGTTCTGGAACGAGAAGGACATCCCCACCGGCCTGAAGCTTTCAA        3120

Majority   AGGAAGGCTTCATCAAGCTCTGGGCCCAGAAATCTCGCAAGTGGCAGGACCACATGGCGAGATCGATAGGATTAAGTCAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    3130      3140      3150      3160      3170      3180      3190      3200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AGGAAGGCTTCATCAAGCTCTGGGCCCAGAAATCTCGCAAGTGGCAGGACCACATGGCGAGATCGATAGGATTAAGTCAC        3200
713 defect AGGAAGGCTTCATCAAGCTCTGGGCCCAGAAATCTCGCAAGTGGCAGGACCACATGGCGAGATCGATAGGATTAAGTCAC        3200

Majority   GAGGCCGCTGTAGAGTTGGTTCGTGCAACAAGAGTGAACGAAGCAAAGCCCCATCTCGTCCCCATGGAAGAGGCGAAAGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    3210      3220      3230      3240      3250      3260      3270      3280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAGGCCGCTGTAGAGTTGGTTCGTGCAACAAGAGTGAACGAAGCAAAGCCCCATCTCGTCCCCATGGAAGAGGCGAAAGA        3280
713 defect GAGGCCGCTGTAGAGTTGGTTCGTGCAACAAGAGTGAACGAAGCAAAGCCCCATCTCGTCCCCATGGAAGAGGCGAAAGA        3280
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Majority   GGCACCTAGGCAGCAGCTTGTTCCTAGGCGTTCAACTTTCGTCGATAACCATGAGGAGGAGGTTGAGATTGACACCCTTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3290      3300      3310      3320      3330      3340      3350      3360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCACCTAGGCAGCAGCTTGTTCCTAGGCGTTCAACTTTCGTCGATAACCATGAGGAGGAGGTTGAGATTGACACCCTTC        3360
713 defect GGCACCTAGGCAGCAGCTTGTTCCTAGGCGTTCAACTTTCGTCGATAACCATGAGGAGGAGGTTGAGATTGACACCCTTC        3360

Majority   GGGTGCCGGTCGAAGAGGGTCGATGTTTCGAGCTCTTGTTCAATAATCAAGTAACCCCTGCAATTTTCGACAAGAAGCCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3370      3380      3390      3400      3410      3420      3430      3440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGGTGCCGGTCGAAGAGGGTCGATGTTTCGAGCTCTTGTTCAATAATCAAGTAACCCCTGCAATTTTCGACAAGAAGCCA        3440
713 defect GGGTGCCGGTCGAAGAGGGTCGATGTTTCGAGCTCTTGTTCAATAATCAAGTAACCCCTGCAATTTTCGACAAGAAGCCA        3440

Majority   TTGCTTAAAGACGTCCTCGGCGTGTTCGAAGAGAATGTCTGCACGATGGACTCGCTCGAAATCAGTCACAGTGACCAATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3450      3460      3470      3480      3490      3500      3510      3520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGCTTAAAGACGTCCTCGGCGTGTTCGAAGAGAATGTCTGCACGATGGACTCGCTCGAAATCAGTCACAGTGACCAATG        3520
713 defect TTGCTTAAAGACGTCCTCGGCGTGTTCGAAGAGAATGTCTGCACGATGGACTCGCTCGAAATCAGTCACAGTGACCAATG        3520

Majority   CGTGCACATTGTCGCTGGTGAAACCTTCCGGAACTACGATGAAATCAAAGCCGTTCTCGAGGTCATTCTTGAGAACGAGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3530      3540      3550      3560      3570      3580      3590      3600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGTGCACATTGTCGCTGGTGAAACCTTCCGGAACTACGATGAAATCAAAGCCGTTCTCGAGGTCATTCTTGAGAACGAGC        3600
713 defect CGTGCACATTGTCGCTGGTGAAACCTTCCGGAACTACGATGAAATCAAAGCCGTTCTCGAGGTCATTCTTGAGAACGAGC        3600

Majority   CTGACATCCTCGTTGGAGCTGAAGAAGGTTCAGTCGCTGATTATGTGAAAGCGGGCAAACACTTCTTGTTTGAAAACCAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3610      3620      3630      3640      3650      3660      3670      3680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTGACATCCTCGTTGGAGCTGAAGAAGGTTCAGTCGCTGATTATGTGAAAGCGGGCAAACACTTCTTGTTTGAAAACCAC        3680
713 defect CTGACATCCTCGTTGGAGCTGAAGAAGGTTCAGTCGCTGATTATGTGAAAGCGGGCAAACACTTCTTGTTTGAAAACCAC        3680

Majority   CAGTGGGTCAGAAATGGGCTCAAGCTAGCGAAGGGTCTAGCTGAACCTGGCCAAAGGGCCAAAGATAATACCAACCCTTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3690      3700      3710      3720      3730      3740      3750      3760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGTGGGTCAGAAATGGGCTCAAGCTAGCGAAGGGTCTAGCTGAACCTGGCCAAAGGGCCAAAGATAATACCAACCCTTC        3760
713 defect CAGTGGGTCAGAAATGGGCTCAAGCTAGCGAAGGGTCTAGCTGAACCTGGCCAAAGGGCCAAAGATAATACCAACCCTTC        3760

Majority   GACACCTAGGCCGATTGAAGACGCTGACTACATTCATCCTTTTGACAACGGACAGCCCCTCCCGGGCAGGTCCGACCAAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3770      3780      3790      3800      3810      3820      3830      3840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GACACCTAGGCCGATTGAAGACGCTGACTACATTCATCCTTTTGACAACGGACAGCCCCTCCCGGGCAGGTCCGACCAAT        3840
713 defect GACACCTAGGCCGATTGAAGACGCTGACTACATTCATCCTTTTGACAACGGACAGCCCCTCCCGGGCAGGTCCGACCAAT        3840

Majority   GGGTCAGCGGCTTTGAAGTGACGAGGTTACGTCACCATGACGAAATGCCACACATTAGGAGTGTGAGGAACACGGGCATC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3850      3860      3870      3880      3890      3900      3910      3920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGGTCAGCGGCTTTGAAGTGACGAGGTTACGTCACCATGACGAAATGCCACACATTAGGAGTGTGAGGAACACGGGCATC        3920
713 defect GGGTCAGCGGCTTTGAAGTGACGAGGTTACGTCACCATGACGAAATGCCACACATTAGGAGTGTGAGGAACACGGGCATC        3920

Majority   CATGGGCTACCTGGGGATTTCTTGTCGAATTACCCTAGACTGCCTACGCCTGTATTTCATCGCCTCCGCGATTTGTGGGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 3930      3940      3950      3960      3970      3980      3990      4000
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CATGGGCTACCTGGGGATTTCTTGTCGAATTACCCTAGACTGCCTACGCCTGTATTTCATCGCCTCCGCGATTTGTGGGA        4000
713 defect CATGGGCTACCTGGGGATTTCTTGTCGAATTACCCTAGACTGCCTACGCCTGTATTTCATCGCCTCCGCGATTTGTGGGA        4000

Majority   TGATGTCATCGGCATACTGATGAAGCTTGAATTCGGGGACAATTGTTCACCGGTGCTCAACGTGACTGCTAATGCAGACT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 4010      4020      4030      4040      4050      4060      4070      4080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGATGTCATCGGCATACTGATGAAGCTTGAATTCGGGGACAATTGTTCACCGGTGCTCAACGTGACTGCTAATGCAGACT        4080
713 defect TGATGTCATCGGCATACTGATGAAGCTTGAATTCGGGGACAATTGTTCACCGGTGCTCAACGTGACTGCTAATGCAGACT        4080

Majority   GGGTTCGGTCAGAGACGACGATAAATTTTATCTCTGACCAACCCGGCAAGGCTCAGTCACGTCCTCGCGAAGATGGGGGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 4090      4100      4110      4120      4130      4140      4150      4160
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           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGGTTCGGTCAGAGACGACGATAAATTTTATCTCTGACCAACCCGGCAAGGCTCAGTCACGTCCTCGCGAAGATGGGGGT       4160
713 defect GGGTTCGGTCAGAGACGACGATAAATTTTATCTCTGACCAACCCGGCAAGGCTCAGTCACGTCCTCGCGAAGATGGGGGT       4160

Majority   TTTGACATCCTCGTTCCTTGCAGGGGCATCGCAACCCGAAGCATCAGGCTTCTGCCTCTATTCATCAGACTGCCAAACCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4170      4180      4190      4200      4210      4220      4230      4240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTTGACATCCTCGTTCCTTGCAGGGGCATCGCAACCCGAAGCATCAGGCTTCTGCCTCTATTCATCAGACTGCCAAACCG       4240
713 defect TTTGACATCCTCGTTCCTTGCAGGGGCATCGCAACCCGAAGCATCAGGCTTCTGCCTCTATTCATCAGACTGCCAAACCG       4240

Majority   TTTCAGGGCCGTGGCTTTGTTAAACGGTAGGCAGTCTGATTATGACAATTATGGTTGGCCAGTGTTCAATCCGGTCATCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4250      4260      4270      4280      4290      4300      4310      4320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTTCAGGGCCGTGGCTTTGTTAAACGGTAGGCAGTCTGATTATGACAATTATGGTTGGCCAGTGTTCAATCCGGTCATCC       4320
713 defect TTTCAGGGCCGTGGCTTTGTTAAACGGTAGGCAGTCTGATTATGACAATTATGGTTGGCCAGTGTTCAATCCGGTCATCC       4320

Majority   CATTGCCTCAGATGGACTCCTTCTACGTGGAGGCCGTCGCCGCTGGCAGATCAATGTACCCACCTGGTTTCCTCCTAGGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4330      4340      4350      4360      4370      4380      4390      4400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CATTGCCTCAGATGGACTCCTTCTACGTGGAGGCCGTCGCCGCTGGCAGATCAATGTACCCACCTGGTTTCCTCCTAGGT       4400
713 defect CATTGCCTCAGATGGACTCCTTCTACGTGGAGGCCGTCGCCGCTGGCAGATCAATGTACCCACCTGGTTTCCTCCTAGGT       4400

Majority   AGGTATGACGCACTAGAGTATCTAGTGCACACTGCGACGGTGTATGGCGCTGAGGAAGCCTTCTTGCTTCCGTTCACGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4410      4420      4430      4440      4450      4460      4470      4480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AGGTATGACGCACTAGAGTATCTAGTGCACACTGCGACGGTGTATGGCGCTGAGGAAGCCTTCTTGCTTCCGTTCACGCA       4480
713 defect AGGTATGACGCACTAGAGTATCTAGTGCACACTGCGACGGTGTATGGCGCTGAGGAAGCCTTCTTGCTTCCGTTCACGCA       4480

Majority   TCATGTGAGAGTGTATCCCCCTCCCCGTCCAGGGAGGGAGATTCCTTTCGGCTCGTGGTGCAAGAACTACAAGTTCGAAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4490      4500      4510      4520      4530      4540      4550      4560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCATGTGAGAGTGTATCCCCCTCCCCGTCCAGGGAGGGAGATTCCTTTCGGCTCGTGGTGCAAGAACTACAAGTTCGAAG       4560
713 defect TCATGTGAGAGTGTATCCCCCTCCCCGTCCAGGGAGGGAGATTCCTTTCGGCTCGTGGTGCAAGAACTACAAGTTCGAAG       4560

Majority   CAGAAAGGTTTTGGTATGACGCGGACTGGAAACTGAGGGTCCACGAAACCAACCACGATTTTGACAGGTTAATCGAAATA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4570      4580      4590      4600      4610      4620      4630      4640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGAAAGGTTTTGGTATGACGCGGACTGGAAACTGAGGGTCCACGAAACCAACCACGATTTTGACAGGTTAATCGAAATA       4640
713 defect CAGAAAGGTTTTGGTATGACGCGGACTGGAAACTGAGGGTCCACGAAACCAACCACGATTTTGACAGGTTAATCGAAATA       4640

Majority   ACAAAAACCTGTCGCCGCAACCCCCCCGAAGAAAACTTGCAAGCAAAACTGGAGGACACCGCGCGCAAGGTGTGTAGTGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4650      4660      4670      4680      4690      4700      4710      4720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ACAAAAACCTGTCGCCGCAACCCCCCCGAAGAAAACTTGCAAGCAAAACTGGAGGACACCGCGCGCAAGGTGTGTAGTGT       4720
713 defect ACAAAAACCTGTCGCCGCAA-------------------------------------------------------------        4659

Majority   ATGGCAATATAACATCATGATCGCTTCATCTGTCGCGTTTCTAGTGCCATTATACTTCACACTCTATGTGCCGTACCTGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4730      4740      4750      4760      4770      4780      4790      4800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATGGCAATATAACATCATGATCGCTTCATCTGTCGCGTTTCTAGTGCCATTATACTTCACACTCTATGTGCCGTACCTGC       4800
713 defect --------------------------------------------------------------------------------       4659

Majority   AATTCTACTTGCATGTTGACCCAGGCGATTACATATTGCTTCCACCGGTGCTCTGGTTGGTCTGGACCAATCTTTGCTAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4810      4820      4830      4840      4850      4860      4870      4880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AATTCTACTTGCATGTTGACCCAGGCGATTACATATTGCTTCCACCGGTGCTCTGGTTGGTCTGGACCAATCTTTGCTAC       4880
713 defect --------------------------------------------------------------------------------       4659

Majority   GGCTACGCGTGTGACGCCTGGTGCCGTTTATTTTTCTTCGTAGAGGAGGCGGGAAAGAAAGAACTTGTCCATTCAAGTGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    4890      4900      4910      4920      4930      4940      4950      4960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCTACGCGTGTGACGCCTGGTGCCGTTTATTTTTCTTCGTAGAGGAGGCGGGAAAGAAAGAACTTGTCCATTCAAGTGA       4960
713 defect ------------------------------TTTTTCTTCGTAGAGGAGGCGGGAAAGAAAGAACTTGTCCATTCAAGTGA       4710
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Majority   GGAGTTTTCCAGTGACCCGTCATCCACGCTCTTGATCCCGACAATGGGAACAAGAGGAGATCACGTGCCACCACGGTTCT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   4970      4980      4990      5000      5010      5020      5030      5040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGAGTTTTCCAGTGACCCGTCATCCACGCTCTTGATCCCGACAATGGGAACAAGAGGAGATCACGTGCCACCACGGTTCT        5040
713 defect GGAGTTTTCCAGTGACCCGTCATCCACGCTCTTGATCCCGACAATGGGAACAAGAGGAGATCACGTGCCACCACGGTTCT        4790

Majority   TCGCCAACATGGCGGTCCTCGCAGGTGTCAAGACCCATCTCTTGAAACTGCAGACTGCGACGTACGGCGATTTGGAGAAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5050      5060      5070      5080      5090      5100      5110      5120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCGCCAACATGGCGGTCCTCGCAGGTGTCAAGACCCATCTCTTGAAACTGCAGACTGCGACGTACGGCGATTTGGAGAAC        5120
713 defect TCGCCAACATGGCGGTCCTCGCAGGTGTCAAGACCCATCTCTTGAAACTGCAGACTGCGACGTACGGCGATTTGGAGAAC        4870

Majority   CTCAAGAAAGGGAAGCTCGGAAGCTTGTTGCCAGGCTATCTTCAGAACCATTACTCGGTGCTGAGGGGTTACAAAGCCGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5130      5140      5150      5160      5170      5180      5190      5200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTCAAGAAAGGGAAGCTCGGAAGCTTGTTGCCAGGCTATCTTCAGAACCATTACTCGGTGCTGAGGGGTTACAAAGCCGC        5200
713 defect CTCAAGAAAGGGAAGCTCGGAAGCTTGTTGCCAGGCTATCTTCAGAACCATT----------------------------        4921

Majority   GTTCACTCCGCATGTCGAGCTTGACATGCCGAACGCAACTTCGTACAACTTAGCACCGCCTCGCAGCTACATCAACAAGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5210      5220      5230      5240      5250      5260      5270      5280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTTCACTCCGCATGTCGAGCTTGACATGCCGAACGCAACTTCGTACAACTTAGCACCGCCTCGCAGCTACATCAACAAGA        5280
713 defect --------------------------------------------------------------------------------        4921

Majority   TACGGTACCTGACCGATGAAAATCGGTCGGGCGCCAGTATGATTGATCGCGCTGTGTCCTGGTTCGCCGAAGAACTGGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5290      5300      5310      5320      5330      5340      5350      5360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TACGGTACCTGACCGATGAAAATCGGTCGGGCGCCAGTATGATTGATCGCGCTGTGACCTGGTTCGCCGAAGAACTGGCA        5360
713 defect ---------------------------------------------------------CCTGGTTCGCCGAAGAACTGGCA        4945

Majority   GACACGTTCTGGCCCGACTGGCAAATTGGTTGCCTTAGAGGTTGCAATTTACCGCGTTCCGCGGATGGTGTTTCCCTGAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5370      5380      5390      5400      5410      5420      5430      5440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GACACGTTCTGGCCCGACTGGCAAATTGGTTGCCTTAGAGGTTGCAATTTACCGCGTTCCGCGGATGGTGTTTCCCTGAT        5440
713 defect GACACGTTCTGGCCCGACTGGCAAATTGGTTGCCTTAGAGGTTGCAATTTACCGCGTTCCGCGGATGGTGTTTCCCTGAT        5025

Majority   CACCAAACAACCCAACCTTAAAACAGGGAAAATCGGATGGCTACATGGCTCCGCTGATCCAGCTGTGGTGCCTAAGGACA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5450      5460      5470      5480      5490      5500      5510      5520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CACCAAACAACCCAACCTTAAAACAGGGAAAATCGGATGGCTACATGGCTCCGCTGATCCAGCTGTGGTGCCTAAGGACA        5520
713 defect CACCAAACAACCCAACCTTAAAACAGGGAAAATCGGATGGCTACATGGCTCCGCTGATCCAGCTGTGGTGCCTAAGGACA        5105

Majority   TCAGGGACAAGTACCCCCTGGTTCCGAACGGTGACCACAACGAGATCTTCAGGCATTATGATAAGATTTACATGCCTGGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5530      5540      5550      5560      5570      5580      5590      5600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCAGGGACAAGTACCCCCTGGTTCCGAACGGTGACCACAACGAGATCTTCAGGCATTATGATAAGATTTACATGCCTGGT        5600
713 defect TCAGGGACAAGTACCCCCTGGTTCCGAACGGTGACCACAACGAGATCTTCAGGCATTATGATAAGATTTACATGCCTGGT        5185

Majority   GGAGCCGGTGCCGTCCAAACCGCAATCGCTTGTGGATGCGAAGTCGTCGTCACAGACGTCAACCTTGACAGAGATTATCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5610      5620      5630      5640      5650      5660      5670      5680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGAGCCGGTGCCGTCCAAACCGCAATCGCTTGTGGATGCGAAGTCGTCGTCACAGACGTCAACCTTGACAGAGATTATCA        5680
713 defect GGAGCCGGTGCCGTCCAAACCGCAATCGCTTGTGGATGCGAAGTCGTCGTCACAGACGTCAACCTTGACAGAGATTATCA        5265

Majority   CACAATGCCTACGCAGAAAGACTTTCACCAACCCTCCATACTGCCATACTTCGCATGGCTGTGGAGGCAAGGGTTTGATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5690      5700      5710      5720      5730      5740      5750      5760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CACAATGCCTACGCAGAAAGACTTTCACCAACCCTCCATACTGCCATACTTCGCATGGCTGTGGAGGCAAGGGTTTGATG        5760
713 defect CACAATGCCTACGCAGAAAGACTTTCACCAACCCTCCATACTGCCATACTTCGCATGGCTGTGGAGGCAAGGGTTTGATG        5345

Majority   TTAAACTGCCACGCGTGTTGCTCGTCATAGGCTGGCTGAAGTTTCATTACTCCATCCGCTACAAGCATCTGGAATTCGCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
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                   5770      5780      5790      5800      5810      5820      5830      5840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTAAACTGCCACGCGTGTTGCTCGTCATAGGCTGGCTGAAGTTTCATTACTCCATCCGCTACAAGCATCTGGAATTCGCC       5840
713 defect TTAAACTGCCACGCGTGTTGCTCGTCATAGGCTGGCTGAAGTTTCATTACTCCATCCGCTACAAGCATCTGGAATTCGCC       5425

Majority   GCTGACTTCGTCATCAGGGCTGGGTTGTTCTGGTGGTATGGGTGCTTGCACCTACTACCATTCATGGCAGCCGCGATCAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5850      5860      5870      5880      5890      5900      5910      5920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCTGACTTCGTCATCAGGGCTGGGTTGTTCTGGTGGTATGGGTGCTTGCACCTACTACCATTCATGGCAGCCGCGATCAT       5920
713 defect GCTGACTTCGTCATCAGGGCTGGGTTGTTCTGGTGGTATGGGTGCTTGCACCTACTACCATTCATGGCAGCCGCGATCAT       5505

Majority   GGCACCAAGGTTCGTTAAGAAGTACTTGGTTGGCATGGCGTGGTTAACTGAACCCGGTCTCCTAATGCTGAAGGCGCTGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   5930      5940      5950      5960      5970      5980      5990      6000
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCACCAAGGTTCGTTAAGAAGTACTTGGTTGGCATGGCGTGGTTAACTGAACCCGGTCTCCTAATGCTGAAGGCGCTGT       6000
713 defect GGCACCAAGGTTCGTTAAGAAGTACTTGGTTGGCATGGCGTGGTTAACTGAACCCGGTCTCCTAATGCTGAAGGCGCTGT       5585

Majority   GGCGTTTTCCAATTTTCATGGTCACCCCAAGGTGGATGCTGCCGTTCATTGTAACGGTTTCGGTATACAATTGGTGGTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6010      6020      6030      6040      6050      6060      6070      6080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCGTTTTCCAATTTTCATGGTCACCCCAAGGTGGATGCTGCCGTTCATTGTAACGGTTTCGGTATACAATTGGTGGTGG       6080
713 defect GGCGTTTTCCAATTTTCATGGTCACCCCAAGGTGGATGCTGCCGTTCATTGTAACGGTTTCGGTATACAATTGGTGGTGG       5665

Majority   CCGTTATCCCAAGACGGGCTCAACTACGCGAGCAAACGGTTTGAATTGATCTTCGAACCGGTAACTCGGGGTAAGCACAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6090      6100      6110      6120      6130      6140      6150      6160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCGTTATCCCAAGACGGGCTCAACTACGCGAGCAAACGGTTTGAATTGATCTTCGAACCGGTAACTCGGGGTAAGCACAC       6160
713 defect CCGTTATCCCAAGACGGGCTCAACTACGCGAGCAAACGGTTTGAATTGATCTTCGAACCGGTAACTCGGGGTAAGCACAC       5745

Majority   GTTTTCCTACCCATTCGGGCACTGGTGTTTGCGTGACACCAACTCGATGATTGTTTACGAAGGAAAATTTGTCAACCCAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6170      6180      6190      6200      6210      6220      6230      6240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTTTTCCTACCCATTCGGGCACTGGTGTTTGCGTGACACCAACTCGATGATTGTTTACGAAGGAAAATTTGTCAACCCAA       6240
713 defect GTTTTCCTACCCATTCGGGCACTGGTGTTTGCGTGACACCAACTCGATGATTGTTTACGAAGGAAAATTTGTCAACCCAA       5825

Majority   GTGAGACCTCAATCGGGTCTCCCTTCAAGTTGTCGAAGTCCGTTAGACCGGTCCGACCTGGCGCAGTGTTCCACCTGGTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6250      6260      6270      6280      6290      6300      6310      6320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTGAGACCTCAATCGGGTCTCCCTTCAAGTTGTCGAAGTCCGTTAGACCGGTCCGACCTGGCGCAGTGTTCCACCTGGTG       6320
713 defect GTGAGACCTCAATCGGGTCTCCCTTCAAGTTGTCGAAGTCCGTTAGACCGGTCCGACCTGGCGCAGTGTTCCACCTGGTG       5905

Majority   CCTTTCCACGTCCAGAAGCTTCTGGATTCAATGGATGAGGCACCACTACCTTACAGCGCGAATCACAATTGCACGACCGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6330      6340      6350      6360      6370      6380      6390      6400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCTTTCCACGTCCAGAAGCTTCTGGATTCAATGGATGAGGCACCACTACCTTACAGCGCGAATCACAATTGCACGACCGT       6400
713 defect CCTTTCCACGTCCAGAAGCTTCTGGATTCAATGGATGAGGCACCACTACCTTACAGCGCGAATCACAATTGCACGACCGT       5985

Majority   GATCCTCAAGGGGATCATGTACCGTAGTGCACTAGGTTTTGTATTCGCGTATATGGTTTCGTGGGCGGTGTACCTGGTCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6410      6420      6430      6440      6450      6460      6470      6480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GATCCTCAAGGGGATCATGTACCGTAGTGCACTAGGTTTTGTATTCGCGTATATGGTTTCGTGGGCGGTGTACCTGGTCC       6480
713 defect GATCCTCAAGGGGATCATGTACCGTAGTGCACTAGGTTTTGTATTCGCGTATATGGTTTCGTGGGCGGTGTACCTGGTCC       6065

Majority   TCCGGCCTCCTCAAGCCGCGGCTACCGTTTATCACTGGGTGTATCCCGAGCGATCGTGGGACACATCAAGGCTGTATCAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6490      6500      6510      6520      6530      6540      6550      6560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCCGGCCTCCTCAAGCCGCGGCTACCGTTTATCACTGGGTGTATCCCGAGCGATCGTGGGACACATCAAGGCTGTATCAT       6560
713 defect TCCGGCCTCCTCAAGCCGCGGCTACCGTTTATCACTGGGTGTATCCCGAGCGATCGTGGGACACATCAAGGCTGTATCAT       6145

Majority   CTGCTGCTGGGTTTCGCAGCAGGTGGCACGGTGCCAATGGAAGTGATAGACGAAGAGCACGTTGAGGAAAAGCCTTCGGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   6570      6580      6590      6600      6610      6620      6630      6640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTGCTGCTGGGTTTCGCAGCAGGTGGCACGGTGCCAATGGAAGTGATAGACGAAGAGCACGTTGAGGAAAAGCCTTCGGT       6640
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713 defect CT---GCTGGGTTTCGCAGCAGGTGGCACGGTGCCAATGGAAGTGATAGACGAAGAGCACGTTGAGGAAAAGCCTTCGGT       6222

Majority   TGCTGGTCAGTCAGAGCCAGCCGCCGAAATCGACAATGACAAAATTTCTGACTATGACCAAGAATGGTGGGGGAGTCAAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    6650      6660      6670      6680      6690      6700      6710      6720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGCTGGTCAGTCAGAGCCAGCCGCCGAAATCGACAATGACAAAATTTCTGACTATGACCAAGAATGGTGGGGGAGTCAAG       6720
713 defect TGCTGGTCAGTCAGAGCCAGCCGCCGAAATCGACAATGACAAAATTTCTGACTATGACCAAGAATGGTGGGGGAGTCAAG       6302

Majority   ACAGTATTGACACAGTGGTTAACGACCTGTGTTACTTGCTGTCCTTCCTGAAAGATACGGCGATCCCTGAAGAGGTCAAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    6730      6740      6750      6760      6770      6780      6790      6800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ACAGTATTGACACAGTGGTTAACGACCTGTGTTACTTGCTGTCCTTCCTGAAAGATACGGCGATCCCTGAAGAGGTCAAA       6800
713 defect ACAGTATTGACACAGTGGTTAACGACCTGTGTTACTTGCTGTCCTTCCTGAAAGATACGGCGATCCCTGAAGAGGTCAAA       6382

Majority   CTCGATGTAGTCGAACTGGCTTACTCCCAGCTTGTCCAGGACGAAAAGGAACGCATACCAGAACCGAAGGGAACTAAGAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    6810      6820      6830      6840      6850      6860      6870      6880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTCGATGTAGTCGAACTGGCTTACACCCAGCTTGTCCAGGACGAAAAGGAACGCATACCAGAACCGAAGGGAACTAAGAT       6880
713 defect CTCGATGTAGTCGAACTGGCTTAC--------------------------------------------------------       6407

Majority   TCTGGACATGCCGAATTGGAAGCCTGGCAACTGGGCCAAGTTAATAGTCGAGACGCATCGGGTGCTCTCCCAGTTTACTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    6890      6900      6910      6920      6930      6940      6950      6960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCTGGACATGCCGAATTGGAAGCCTGGCAACTGGGCCAAGTTAATAGACGAGACGCATCGGGTGCTCTCCCAGTTTACTC       6960
713 defect ----------------------------------------TTAATA---GAGACGCATCGGGTGCTCTCCCAGTTTACTC       6443

Majority   AATATACACCGCGAGTTCTCAACGAACTCGTCGTGTGGTTGAAAGGACTAGGGGAGAACCTCTATAGGGTCGCTGAACCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    6970      6980      6990      7000      7010      7020      7030      7040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AATATACACCGCGAGTTCTCAACGAACTCGTCGTGTGGTTGAAAGGACTAGGGGAGAACCTCTATAGGGTCGCTGAACCC       7040
713 defect AATATACACCGCGAGTTCTCAACGAACTCGTCGTGTGGTTGAAAGGACTAGGGGAGAACCTCTATAGGGTCGCTGAACCC       6523

Majority   ATTCTTATGCTATTAGTACGTGCGATGAGAGCTGCCAAATCCGTGAGTGATCGTGCCACACGTTCCGTATATCACTGCCT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7050      7060      7070      7080      7090      7100      7110      7120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATTCTTATGCTATTAGTACGTGCGATGAGAGCTGCCAAATCCGTGAGTGATCGTGCCACACGTTCCGTATATCACTGCCT       7120
713 defect ATTCTTATGCTATTAGTACGTGCGATGAGAGCTGCCAAATCCGTGAGTGATCGTGCCACACGTTCCGTATATCACTGCCT       6603

Majority   CTGCCATTGGCTAGACGTGATGTATGGCGGCTCCGCCCCTACCAGGGTGAAGACCGTGTGGGGACTCACAGGCCTGGTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7130      7140      7150      7160      7170      7180      7190      7200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTGCCATTGGCTAGACGTGATGTATGGCGGCTCCGCCCCTACCAGGGTGAAGACCGTGTGGGGACTCACAGGCCTGGTGG       7200
713 defect CTGCCATTGGCTAGACGTGATGTATGGCGGCTCCGCCCCTACCAGGGTGAAGACCGTGTGGGGACTCACAGGCCTGGTGG       6683

Majority   CTTCTGGCATGACCAGTCAGAAAGCCATACTCGCTCAGAACATAGCAATGATGGAATACCAGGGCAGAGGGAATTTCCTT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7210      7220      7230      7240      7250      7260      7270      7280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTTCTGGCATGACCAGTCAGAAAGCCATACTCGCTCAGAACATAGCAATGATGGAATACCAGGGCAGAGGGAATTTCCTT       7280
713 defect CTTCTGGCATGACCAGTCAGAAAGCCATACTCGCTCAGAACATAGCAATGATGGAATACCAGGGCAGAGGGAATTTCCTT       6763

Majority   GATGATTATGACAACTTTGTCTCCAACATCAAGGAACCCGGGAAAGGACTACCTGGTATAAACACCATCGGAGGGCCACA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7290      7300      7310      7320      7330      7340      7350      7360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GATGATTATGACAACTTTGTCTCCAACATCAAGGAACCCGGGAAAGGACTACCTGGTATAAACACCATCGGAGGGCCACA       7360
713 defect GATGATTATGACAACTTTGTCTCCAACATCAAGGAACCCGGGAAAGGACTACCTGGTATAAACACC--------------       6829

Majority   ACGACGTCCGATTCGATACAAGAACCCTGTCATGTCTCACCAGGCTGCCGAAATCTGTGGATTGAAGCCTGGGGAGTATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7370      7380      7390      7400      7410      7420      7430      7440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ACGACGTCCGATTCGATACAAGAACCCTGTCATGTCTCACCAGGCTGCCGAAATCTGTGGATTGAAGCCTGGGGAGTATG       7440
713 defect --------------------------------------------------------------------------------       6829

Majority   AAGTGGATGATAGGTATCAGGAAAGGATAAACGATTACCTTGCGGAAGGGATCCCGCAGGCAGTCGATGGCGTCCTCTTT
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           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7450      7460      7470      7480      7490      7500      7510      7520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AAGTGGATGATAGGTATCAGGAAAGGATAAACGATTACCTTGCGGAAGGGATCCCGCAGGCAGTCGATGGCGTCCTCTTT       7520
713 defect --------------------------------------------------------------------------------       6829

Majority   GGAGACAGGAATCCCGACAGGATCGCGCGATCCATAAGCCGATATGAACCCGAATACTCTGGCTGTTCGCCTGAGGACAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7530      7540      7550      7560      7570      7580      7590      7600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGAGACAGGAATCCCGACAGGATCGCGCGATCCATAAGCCGATATGAACCCGAATACTCTGGCTGTTCGCCTGAGGACAA       7600
713 defect --------------------------------------------------------------------------------       6829

Majority   GGCCTTGGTGGAGGATACCGCCAGGGCCATGTTCGAACAATGGCCAGAAGTGTTCGCCGATCGAGACATCATGCTCCCTA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7610      7620      7630      7640      7650      7660      7670      7680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCCTTGGTGGAGGATACCGCCAGGGCCATGTTCGAACAATGGCCAGAAGTGTTCGCCGATCGAGACATCATGCTCCCTA       7680
713 defect --------------------------------------------------------------------------------       6829

Majority   AAGGTGTAGAACTTTACATCAAAGAGAAGTACTCGGCGGGCACCCCGTTCATAAGCTCGTTCTATAAGAGTAGAAAGGCT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7690      7700      7710      7720      7730      7740      7750      7760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AAGGTGTAGAACTTTACATCAAAGAGAAGTACTCGGCGGGCACCCCGTTCATAAGCTCGTTCTATAAGAGTAGAAAGGCT       7760
713 defect --------------------------------------------------------------------------------       6829

Majority   CTTAAGCAAGCTGGTGTCATGGATGTGATCCGTAAAAACGCACTGGAGTGCATCAGTACCGGTAAATACCCTACGCAATT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7770      7780      7790      7800      7810      7820      7830      7840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTTAAGCAAGCTGGTGTCATGGATGTGATCCGTAAAAACGCACTGGAGTGCATCAGTACCGGTAAATACCCTACGCAATT       7840
713 defect --------------------------------------------------------------------------------       6829

Majority   TTACCACGCGTTCGCGAAGTCACAAGCGGTTCCTGGCCAACCTTTGTTGGCTCCCCGCATGAAGGACTTGCGAACGGTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7850      7860      7870      7880      7890      7900      7910      7920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTACCACGCGTTCGCGAAGTCACAAGCGGTTCCTGGCCAACCTTTGTTGGCTCCCCGCATGAAGGACTTGCGAACGGTGG       7920
713 defect --------------------------------------------------------------------------------       6829

Majority   TCTCCGAGGATCTATCCGCTTACATGGTCGACCAGATCTTTCAGATCGAGGCCAACAAGCGAATAACCTGGGAAACGTAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    7930      7940      7950      7960      7970      7980      7990      8000
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCTCCGAGGATCTATCCGCTTACATGGTCGACCAGATCTTTCAGATCGAGGCCAACAAGCGAATAACCTGGGAAACGTAC       8000
713 defect --------------------------------------------------------------------------------       6829

Majority   GGTGCCGGTTCTGGCATGCCTTTGTCACAATCGATGGCTCGCATTTGGGACGAGCTGCATGATTTGAGGAAACGCGAAGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8010      8020      8030      8040      8050      8060      8070      8080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGTGCCGGTTCTGGCATGCCTTTGTCACAATCGATGGCTCGCATTTGGGACGAGCTGCATGATTTGAGGAAACGCGAAGG       8080
713 defect --------------------------------------------------------------------------------       6829

Majority   AGGGCAGTTCATCATTGCTGATGCGACTGCCTACGACTCAAACTGTAAACCAGCATTGTTCCATGGGGCTGGCAAACTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8090      8100      8110      8120      8130      8140      8150      8160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AGGGCAGTTCATCATTGCTGATGCGACTGCCTACGACTCAAACTGTAAACCAGCATTGTTCCATGGGGCTGGCAAACTGG       8160
713 defect --------------------------------------------------------------------------------       6829

Majority   TTGAGTTAGGTTTCCAAAATCATCCGAGTGGCAAAGGACGACAATTCGCACAAGTTGTCCAGTGCAAATTCGAGGCCATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8170      8180      8190      8200      8210      8220      8230      8240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGAGTTAGGTTTCCAAAATCATCCGAGTGGCAAAGGACGACAATTCGCACAAGTTGTCCAGTGCAAATTCGAGGCCATG       8240
713 defect --------------------------------------------------------------------------------       6829

Majority   CAAAATGCATGGGTCATGGGGATAACCGAACCTTCCTATACCGCCTTGACTTTCCACGTCCCTGACGTGGCGGTGAGGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8250      8260      8270      8280      8290      8300      8310      8320
           ---------+---------+---------+---------+---------+---------+---------+---------+
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713        CAAAATGCATGGGTCATGGGGATAACCGAACCTTCCTATACCGCCTTGACTTTCCACGTCCCTGACGTGGCGGTGAGGCA       8320
713 defect --------------------------------------------------------------------------------       6829

Majority   TGAACTGGAATCCAAGTACCCTGCACACTTTGCGACGTTCAGCGAGCTTCTGGCTCACAATAATGTGAACGTCACTGAGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8330      8340      8350      8360      8370      8380      8390      8400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGAACTGGAATCCAAGTACCCTGCACACTTTGCGACGTTCAGCGAGCTTCTGGCTCACAATAATGTGAACGTCACTGAGT       8400
713 defect --------------------------------------------------------------------------------       6829

Majority   GGAAGAGGTTATCTTGGGAGGAACGGAAAGCATGTGCTCGTGACATGCAGGCCGTTCCTGGCAAGGTTTTCCTTACCAAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8410      8420      8430      8440      8450      8460      8470      8480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGAAGAGGTTATCTTGGGAGGAACGGAAAGCATGTGCTCGTGACATGCAGGCCGTTCCTGGCAAGGTTTTCCTTACCAAT       8480
713 defect --------------------------------------------------------------------------------       6829

Majority   GATCCAGCATTGCGATTGCAAGGCTCGTCATGGCAAGGTTCTTTCACCACCGAACCCAAAAGGGACGAATTCCGGAAATA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8490      8500      8510      8520      8530      8540      8550      8560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GATCCAGCATTGCGATTGCAAGGCTCGTCATGGCAAGGTTCTTTCACCACCGAACCCAAAAGGGACGAATTCCGGAAATA       8560
713 defect --------------------------------------------------------------------------------       6829

Majority   CCAAACTTATTTCTATGATTCGAAGGCGGCAATGAGAGAAGATATAAAGCGTATTGTCTTCGCCAATCGCGAAGTCATAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8570      8580      8590      8600      8610      8620      8630      8640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCAAACTTATTTCTATGATTCGAAGGCGGCAATGAGAGAAGATATAAAGCGTATTGTCTTCGCCAATCGCGAAGTCATAT       8640
713 defect --------------------------------------------------------------------------------       6829

Majority   CCAACGTCCACCACAAGAACCGTGGTGGAGGCACTGGTCAGAGTGCCACTTCGTGGGACAATACAGCTACATTCAAACTT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8650      8660      8670      8680      8690      8700      8710      8720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCAACGTCCACCACAAGAACCGTGGTGGAGGCACTGGTCAGAGTGCCACTTCGTGGGACAATACAGCTACATTCAAACTT       8720
713 defect --------------------------------------------------------------------------------       6829

Majority   GGCGTCATCAGCGCCTGGGCACGCGCTACTGGTAAACCGCCCAAAGATTTCTTTTGTTCAAACAGGCTCTACAATACGAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8730      8740      8750      8760      8770      8780      8790      8800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGCGTCATCAGCGCCTGGGCACGCGCTACTGGTAAACCGCCCAAAGATTTCTTTTGTTCAAACAGGCTCTACAATACGAG       8800
713 defect --------------------------------------------------------------------------------       6829

Majority   CGATGACACAGTGTGGTGGTCTAAGGACCTGTTATCCTCTGCCGAGGTTGATCGCTTCAAGCAAGCTGCCGCCGATTTTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8810      8820      8830      8840      8850      8860      8870      8880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGATGACACAGTGTGGTGGTCTAAGGACCTGTTATCCTCTGCCGAGGTTGATCGCTTCAAGCAAGCTGCCGCCGATTTTG       8880
713 defect --------------------------------------------------------------------------------       6829

Majority   GCATCCTGCTTGAGATCGGGTCGACCAAGAAGATAACAGAAGTGGAATACTTATCGAAGTTGCCACGTCGCCCAACCGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8890      8900      8910      8920      8930      8940      8950      8960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCATCCTGCTTGAGATCGGGTCGACCAAGAAGATAACAGAAGTGGAATACTTATCGAAGTTGCCACGTCGCCCAACCGCA       8960
713 defect --------------------------------------------------------------------------------       6829

Majority   GAAGATTCAGCGGACTATCGGGCATGGAGGCAGGGAAGGATCGAGAACATGCGATCCTCAGGCCGGTTCAGTGAAGAGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    8970      8980      8990      9000      9010      9020      9030      9040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAAGATTCAGCGGACTATCGGGCATGGAGGCAGGGAAGGATCGAGAACATGCGATCCTCAGGCCGGTTCAGTGAAGAGCA       9040
713 defect --------------------------------------------------------------------------------       6829

Majority   GCTTCTCTCCATTGAACGCGAGCAACTACCTCAATTCCTGATGGTCCAGAACCCCACGGCTATTCTAATGCGAAGGACTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    9050      9060      9070      9080      9090      9100      9110      9120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCTTCTCTCCATTGAACGCGAGCAACTACCTCAATTCCTGATGGTCCAGAACCCCACGGCTATTCTAATGCGAAGGACTG       9120
713 defect --------------------------------------------------------------------------------       6829
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Majority   CTTTCCGTTATTATCAGAGCAGTCCCTCGAAGTTCCTGTACACCTCGTGTGAACGGGGTGCCGGTCACGCACTCGTGACG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9130      9140      9150      9160      9170      9180      9190      9200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTTTCCGTTATTATCAGAGCAGTCCCTCGAAGTTCCTGTACACCTCGTGTGAACGGGGTGCCGGTCACGCACTCGTGACG       9200
713 defect --------------------------------------------------------------------------------       6829

Majority   GCATTCCAGCCCGCACTGTACAAGAGGTTCGCAATTGAGTACGCCGAGGACCTGAATCGTCTCTGCAAGGAGCACCACAT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9210      9220      9230      9240      9250      9260      9270      9280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCATTCCAGCCCGCACTGTACAAGAGGTTCGCAATTGAGTACGCCGAGGACCTGAATCGTCTCTGCAAGGAGCACCACAT       9280
713 defect --------------------------------------------------------------------------------       6829

Majority   CAATCAGCGCTACGAGCTCGTCAGTCAACAAGATAGGATGAAGATGCAGGTTATAAACGTGAACCCGAACTGGAAACGGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9290      9300      9310      9320      9330      9340      9350      9360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAATCAGCGCTACGAGCTCGTCAGTCAACAAGATAGGATGAAGATGCAGGTTATAAACGTGAACCCGAACTGGAAACGGA       9360
713 defect --------------------------------------------------------------------------------       6829

Majority   ACTTCAAGTTGTCACCAAGACAAGAAGCATTCCTTCGGTGGATCAGGCAGGCCAAGTTTCCATCTTATCGACAAGTTCTA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9370      9380      9390      9400      9410      9420      9430      9440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ACTTCAAGTTGTCACCAAGACAAGAAGCATTCCTTCGGTGGATCAGGCAGGCCAAGTTTCCATCTTATCGACAAGTTCTA       9440
713 defect --------------------------------------------------------------------------------       6829

Majority   GACATACACCTCAGGATAAGGGATCCTGACCCATCCGCGCATGATCGCTTTATCGCCAAACTGGATCGCGCTTGGCGCAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9450      9460      9470      9480      9490      9500      9510      9520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GACATACACCTCAGGATAAGGGATCCTGACCCATCCGCGCATGATCGCTTTATCGCCAAACTGGATCGCGCTTGGCGCAA       9520
713 defect --------------------------------------------------------------------------------       6829

Majority   TCCAGATGAGGGGATCCGTGATATAGTGGACGGGGTGTATCGCTACACGGACATGATACCTGAGGAGTTTAAAAGGTTCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9530      9540      9550      9560      9570      9580      9590      9600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCCAGATGAGGGGATCCGTGATATAGTGGACGGGGTGTATCGCTACACGGACATGATACCTGAGGAGTTTAAAAGGTTCA       9600
713 defect --------------------------------------------------------------------------------       6829

Majority   TGCCGTCTACGGACATGCTGTATGCCGAGAATCCGTGGCACACTCACAACCAGTATGTGGAGAAATTCATATACCTCAAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9610      9620      9630      9640      9650      9660      9670      9680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGCCGTCTACGGACATGCTGTATGCCGAGAATCCGTGGCACACTCACAACCAGTATGTGGAGAAATTCATATACCTCAAG       9680
713 defect --------------------------------------------------------------------------------       6829

Majority   TTGCTGGAAACCACGACCGTTGACGAGCTCACGTTCGCCCAATTTGATGCCGTCGCTAAGGAGTCCCCTTACGGCATCTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9690      9700      9710      9720      9730      9740      9750      9760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGCTGGAAACCACGACCGTTGACGAGCTCACGTTCGCCCAATTTGATGCCGTCGCTAAGGAGTCCCCTTACGGCATCTG       9760
713 defect --------------------------------------------------------------------------------       6829

Majority   CATGAATACGATAAAGTTCTGGGAAGACCTAAGAGACCCTGACTATCTGAAGGATCTCTTGGCCTCCGAGGCCATGATAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9770      9780      9790      9800      9810      9820      9830      9840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CATGAATACGATAAAGTTCTGGGAAGACCTAAGAGACCCTGACTATCTGAAGGATCTCTTGGCCTCCGAGGCCATGATAG       9840
713 defect --------------------------------------------------------------------------------       6829

Majority   ATAAGGTGCGCATCTACCAAGGCATGACTGTCATCATCTCGGCCATGTATTTCGCAATGCATTGGGTCGAGCTGTTTATT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9850      9860      9870      9880      9890      9900      9910      9920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATAAGGTGCGCATCTACCAAGGCATGACTGTCATCATCTCGGCCATGTATTTCGCAATGCATTGGGTCGAGCTGTTTATT       9920
713 defect --------------------------------------------------------------------------------       6829

Majority   CAGTCACTGTTCTTGATAGGGCCATTATATAATCTATTCATGTGGTCGTTCTGGGGATTGTCAAAAGTCTACGGACTGGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                   9930      9940      9950      9960      9970      9980      9990      10000
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           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGTCACTGTTCTTGATAGGGCCATTATATAATCTATTCATGTGGTCGTTCTGGGGATTGTCAAAAGTCTACGGACTGGC      10000
713 defect --------------------------------------------------------------------------------       6829

Majority   GAACACGTTTTATTGGCATGGTAAAGCCCGCTCGAGCAGAGAAATCAGCTCGATCCTGCCAAGAGACCCATACATGTGGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10010     10020     10030     10040     10050     10060     10070     10080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAACACGTTTTATTGGCATGGTAAAGCCCGCTCGAGCAGAGAAATCAGCTCGATCCTGCCAAGAGACCCATACATGTGGT      10080
713 defect --------------------------------------------------------------------------------       6829

Majority   CTAAACGTTTCGTCAGCACGATGGCTGATTTCATCCCTGAACGATTTGCTCTCGGTATCGTTCCCGTGACCTTGGTCTTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10090     10100     10110     10120     10130     10140     10150     10160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTAAACGTTTCGTCAGCACGATGGCTGATTTCATCCCTGAACGATTTGCTCTCGGTATCGTTCCCGTGACCTTGGTCTTG      10160
713 defect --------------------------------------------------------------------------------       6829

Majority   GATGGTCTCGCCGAGATCATCGAAGTTCTATTTGGGCGCATGTGGAGACTGTTTGCGAATCTGAAATCGGTAGGCACCGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10170     10180     10190     10200     10210     10220     10230     10240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GATGGTCTCGCCGAGATCATCGAAGTTCTATTTGGGCGCATGTGGAGACTGTTTGCGAATCTGAAATCGGTAGGCACCGA      10240
713 defect --------------------------------------------------------------------------------       6829

Majority   CTTCAGTGACGCACGATCTGGCAAATCGTTAAATGTGCCGTCCAATCCTTGGGCCGCGTACGCCCACACGTACGCAACAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10250     10260     10270     10280     10290     10300     10310     10320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CTTCAGTGACGCACGATCTGGCAAATCGTTAAATGTGCCGTCCAATCCTTGGGCCGCGTACGCCCACACGTACGCAACAA      10320
713 defect --------------------------------------------------------------------------------       6829

Majority   AAGCCATCGAGCACGGTCACGTTACTGTAGCCGCAAAAACCGCTTCCGGTAAGTCCACTTTCTTCCCCGCAGCGGTGTGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10330     10340     10350     10360     10370     10380     10390     10400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AAGCCATCGAGCACGGTCACGTTACTGTAGCCGCAAAAACCGCTTCCGGTAAGTCCACTTTCTTCCCCGCAGCGGTGTGG      10400
713 defect --------------------------------------------------------------------------------       6829

Majority   GCGGAGAGGAGGAACATCGGAATCAAGAAACTGTGGATCGTTATGCCAAGGAAGATCCTCCGCGATAACTGGGAGATTCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10410     10420     10430     10440     10450     10460     10470     10480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GCGGAGAGGAGGAACATCGGAATCAAGAAACTGTGGATCGTTATGCCAAGGAAGATCCTCCGCGATAACTGGGAGATTCC      10480
713 defect --------------------------------------------------------------------------------       6829

Majority   ATTTGACATCCGATCTCAAATCGTGAAACGGGGCAAAACACTAGACCCATCGGCCGATATCTACGTGACCACGTACGGAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10490     10500     10510     10520     10530     10540     10550     10560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATTTGACATCCGATCTCAAATCGTGAAACGGGGCAAAACACTAGACCCATCGGCCGATATCTACGTGACCACGTACGGAC      10560
713 defect --------------------------------------------------------------------------------       6829

Majority   ATTTCCGAACGAGGATAGGTGGACTGGTCCCGAGGGACAACCTGGTGTTCTTCGATGAGTTTCACGAAATGGACGGTTTC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10570     10580     10590     10600     10610     10620     10630     10640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATTTCCGAACGAGGATAGGTGGACTGGTCCCGAGGGACAACCTGGTGTTCTTCGATGAGTTTCACGAAATGGACGGTTTC      10640
713 defect --------------------------------------------------------------------------------       6829

Majority   ATGCTACAGGACGTGGAAGACTGGAAAGGACCAACCATCTTCATGAGTGCAACTCCTGTTGCACTTCATGGAATGGCCGG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10650     10660     10670     10680     10690     10700     10710     10720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        ATGCTACAGGACGTGGAAGACTGGAAAGGACCAACCATCTTCATGAGTGCAACTCCTGTTGCACTTCATGGAATGGCCGG      10720
713 defect --------------------------------------------------------------------------------       6829

Majority   CATCCCTTTTCTTGAGCCAACACTGCCAAAGCGTTTCAATCTTACCGTTTACAAGGTTGATTCCGATGACGTGTTGGAAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10730     10740     10750     10760     10770     10780     10790     10800
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CATCCCTTTTCTTGAGCCAACACTGCCAAAGCGTTTCAATCTTACCGTTTACAAGGTTGATTCCGATGACGTGTTGGAAA      10800
713 defect --------------------------------------------------------------------------------       6829
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Majority   TGTGGAACCGGGCTCGGAATCAGTTTGCTGATCAGCCCGAATTGTTGGCCCGCCCAATGATCATAGTCCCCACATATAAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10810     10820     10830     10840     10850     10860     10870     10880
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGTGGAACCGGGCTCGGAATCAGTTTGCTGATCAGCCCGAATTGTTGGCCCGCCCAATGATCATAGTCCCCACATATAAC      10880
713 defect --------------------------------------------------------------------------------       6829

Majority   GAACTCAAGAAGACGATTGCTGGATTGGAGAACTTGGACAGGTCTATCACGTGGCATGAGGTGAGCAGTAATAGCCCCCT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10890     10900     10910     10920     10930     10940     10950     10960
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAACTCAAGAAGACGATTGCTGGATTGGAGAACTTGGACAGGTCTATCACGTGGCATGAGGTGAGCAGTAATAGCCCCCT      10960
713 defect --------------------------------------------------------------------------------       6829

Majority   CGTGCCTAAGACTGGTGGCCTCGTGTGCACGCCATATGTACAAACTGGCATCGATATCAAACCCGCGCCGTCGATCTTGA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    10970     10980     10990     11000     11010     11020     11030     11040
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CGTGCCTAAGACTGGTGGCCTCGTGTGCACGCCATATGTACAAACTGGCATCGATATCAAACCCGCGCCGTCGATCTTGA      11040
713 defect --------------------------------------------------------------------------------       6829

Majority   TCGACAGCGGCCGAGATGTCATTGTGCATAAGGGTAGGCTAGTCACACCCCACCCCTATACGGACGAGAAGACCAACGAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11050     11060     11070     11080     11090     11100     11110     11120
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TCGACAGCGGCCGAGATGTCATTGTGCATAAGGGTAGGCTAGTCACACCCCACCCCTATACGGACGAGAAGACCAACGAA      11120
713 defect --------------------------------------------------------------------------------       6829

Majority   CAGAGGGTCAATCGTGTCGGTAGGACGATGGATGGTGTGGTCATACAGCCGCAACTGGCTGGCACAGGCAACCCTCCTGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11130     11140     11150     11160     11170     11180     11190     11200
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAGAGGGTCAATCGTGTCGGTAGGACGATGGATGGTGTGGTCATACAGCCGCAACTGGCTGGCACAGGCAACCCTCCTGT      11200
713 defect --------------------------------------------------------------------------------       6829

Majority   CAAGTATCCTAGTGGGATTTTCTTTTCTTCAGAGTTAGTCGCGGGGCAGTACAAGGTCCCCCGATTAACTAAAGTCAATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11210     11220     11230     11240     11250     11260     11270     11280
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAAGTATCCTAGTGGGATTTTCTTTTCTTCAGAGTTAGTCGCGGGGCAGTACAAGGTCCCCCGATTAACTAAAGTCAATG      11280
713 defect ------------------------------------------------------------------AACTAAAGTCAATG       6843

Majority   GTTGTGTCCACCCGGAACTGCCGTACATGTCAATCAAGTACACATCCGAGCTTTCAGACCCCGCTAAAGCAAGGGAGGAG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11290     11300     11310     11320     11330     11340     11350     11360
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTTGTGTCCACCCGGAACTGCCGTACATGTCAATCAAGTACACATCCGAGCTTTCAGACCCCGCTAAAGCAAGGGAGGAG      11360
713 defect GTTGTGTCCACCCGGAACTGCCGTACATGTCAATCAA-------------------------------------------       6879

Majority   GAACAAAGCGTGACGAAATCGCTCCTGTTTATCCATCTCATGGCATTGGCGGGCGTCAGGCAGTCCGAATGGGCCTTGCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11370     11380     11390     11400     11410     11420     11430     11440
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAACAAAGCGTGACGAAATCGCTCCTGTTTATCCATCTCATGGCATTGGCGGGCGTCAGGCAGTCCGAATGGGCCTTGCG      11440
713 defect --------------------------------------------------------------------------------       6879

Majority   TTACAATCGATACTTTGAACTTCACCTTCCTTTCGGGGAAGATGAAGATCATTTGGAGCGCATCTTAACGTCGGGTAAAC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11450     11460     11470     11480     11490     11500     11510     11520
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTACAATCGATACTTTGAACTTCACCTTCCTTTCGGGGAAGATGAAGATCATTTGGAGCGCATCTTAACGTCGGGTAAAC      11520
713 defect ----------------------------------------------------------------------------AAAC       6884

Majority   TGAGGTATGCTAACCACATACCAGTTGACATGGCCATGCAGTTGCTGGGCAACGGGCACGTTACATGGGGCATCGGTGGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    11530     11540     11550     11560     11570     11580     11590     11600
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TGAGGTATGCTAACCACATACCAGTTGACATGGCCATGCAGTTGCTGGGCAACGGGCACGTTACATGGGGCATCGGTGGC      11600
713 defect TGAGGTATGCTAACCACATACCAGTTGACATGGCCATGCAGTTGCTGGGCAACGGGCACGTTACATGGGGCATCGGTGGC       6964

Majority   GTCCCCACAATAACGCGACCAAGATATCCTTGTGATGGGATGTGGGTGGAGGATCCCTCCTCCCGTAAGTCATATGCGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
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                 11610     11620     11630     11640     11650     11660     11670     11680
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GTCCCCACAATAACGCGACCAAGATATCCTTGTGATGGGATGTGGGTGGAGGATCCCTCCTCCCGTAAGTCATATGCGCA      11680
713 defect GTCCCCACAATAACGCGACCAAGATATCCTTGTGATGGGATGTGGGTGGAGGATCCCTCCTCCCGTAAGTCATATGCGCA       7044

Majority   CAAGGTACTTCTACACCAGCGGGAACATGCAGAGATCGGCATGTGGCAAGCGCAGGTCAACGAGCTCAGAGCCCAGAACC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 11690     11700     11710     11720     11730     11740     11750     11760
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CAAGGTACTTCTACACCAGCGGGAACATGCAGAGATCGGCATGTGGCAAGCGCAGGTCAACGAGCTCAGAGCCCAGAACC      11760
713 defect CAAGGTACTTCTACACCAGCGGGAACATGCAGAGATCGGCATGTGGCAAGCGCAGGTCAACGAGCTCAGAGCCCAGAACC       7124

Majority   TTGCCCTTCAGTCACAGCTGAGATCAGCATGCACCCGAAGAAGCACAGCAGGTCGCATCTTACGACACACCCGTCCTCCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 11770     11780     11790     11800     11810     11820     11830     11840
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGCCCTTCAGTCACAGCTGAGATCAGCATGCACCCGAAGAAGCACAGCAGGTCGCATCTTACGACACACCCGTCCTCCG      11840
713 defect TTGCCCTTCAGTCACAGCTGAGATCAGCATGCACCCGAAGAAGCACAGCAGGTCGCATCTTACGACACACCCGTCCTCCG       7204

Majority   GATATACCTGTTTGCGGTTAACACAAACCGCCTTCCATTTGTCATTTCCTTTGTCCTTTCCACGGGAGTAGTGACCCCGT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 11850     11860     11870     11880     11890     11900     11910     11920
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GATATACCTGTTTGCGGTTAACACAAACCGCCTTCCATTTGTCATTTCCTTTGTCCTTTCCACGGGAGTAGTGACCCCGT      11920
713 defect GATATACCTGTTTGCGGTTAACACAAACCGCCTTCCATTTGTCATTTCCTTTGTCCTTTCCACGGGAGTAGTGACCCCGT       7284

Majority   GACACGCCAAAACCAGCACCTGAAGTGGATAACTCAAGCCTATGACATGGTCACTGCCCGTCAGTAAAGACGTTAACCCG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 11930     11940     11950     11960     11970     11980     11990     12000
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GACACGCCAAAACCAGCACCTGAAGTGGATAACTCAAGCCTATGACATGGTCACTGCCCGTCAGTAAAGACGTTAACCCG      12000
713 defect GACACGCCAAAACCAGCACCTGAAGTGGATAACTCAAGCCTATGACATGGTCACTGCCCGTCAGTAAAGACGTTAACCCG       7364

Majority   GGAGCTGATTCTGTTAACAGCCGCACCGCGAACGGTACGTAGATTAAATCTACGGTTTTCTGCCTCCTGAGAGATTGGCA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12010     12020     12030     12040     12050     12060     12070     12080
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGAGCTGATTCTGTTAACAGCCGCACCGCGAACGGTACGTAGATTAAATCTACGGTTTTCTGCCTCCTGAGAGATTGGCA      12080
713 defect GGAGCTGATTCTGTTAACAGCCGCACCGCGAACGGTACGTAGATTAAATCTACGGTTTTCTGCCTCCTGAGAGATTGGCA       7444

Majority   GGGGAAACCCGCTGAAGAGTCCAGGACCGAACACGACCACCATTCCGGCGAATGGTTAGGCCTCGGGAGATGCAATTGTG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12090     12100     12110     12120     12130     12140     12150     12160
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGGGAAACCCGCTGAAGAGTCCAGGACCGAACACGACCACCATTCCGGCGAATGGTTAGGCCTCGGGAGATGCAATTGTG      12160
713 defect GGGGAAACCCGCTGAAGAGTCCAGGACCGAACACGACCACCATTCCGGCGAATGGTTAGGCCTCGGGAGATGCAATTGTG       7524

Majority   CCTCATCACCACACCCACGTGACCAATGAGACCAACTCGCAAAGGAGCAGGAAACACAGTGCAACTGTCGGCCAGCAATA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12170     12180     12190     12200     12210     12220     12230     12240
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CCTCATCACCACACCCACGTGACCAATGAGACCAACTCGCAAAGGAGCAGGAAACACAGTGCAACTGTCGGCCAGCAATA      12240
713 defect CCTCATCACCACACCCACGTGACCAATGAGACCAACTCGCAAAGGAGCAGGAAACACAGTGCAACTGTCGGCCAGCAATA       7604

Majority   GGGCTAGAAATACTAAATACCTTTAACTTGGTGGTAGGCGTGTACCGAACGACCCCGGCCCAGAAGACCAGGGCTGATGC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12250     12260     12270     12280     12290     12300     12310     12320
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GGGCTAGAAATACTAAATACCTTTAACTTGGTGGTAGGCGTGTACCGAACGACCCCGGCCCAGAAGACCAGGGCTGATGC      12320
713 defect GGGCTAGAAATACTAAATACCTTTAACTTGGTGGTAGGCGTGTACCGAACGACCCCGGCCCAGAAGACCAGGGCTGATGC       7684

Majority   TTGTTAGGCAACGGCAATAAGACCGAAGCAAGCACAGAGACTGGAAAAGTAAGCCGGATCCGTCGACGTAGGATCGTCTA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12330     12340     12350     12360     12370     12380     12390     12400
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTGTTAGGCAACGGCAATAAGACCGAAGCAAGCACAGAGACTGGAAAAGTAAGCCGGATCCGTCGACGTAGGATCGTCTA      12400
713 defect TTGTTAGGCAACGGCAATAAGACCGAAGCAAGCACAGAGACTGGAAAAGTAAGCCGGATCCGTCGACGTAGGATCGTCTA       7764

Majority   CATGTTCAAGAAATGGGCGAAAAGGGTTGCCCGAAAGTATGGGCTACGCGCTTCGTTGTAAAGCTACCCATACAAAACCC
           ---------+---------+---------+---------+---------+---------+---------+---------+
                 12410     12420     12430     12440     12450     12460     12470     12480
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        CATGTTCAAGAAATGGGCGAAAAGGGTTGCCCGAAAGTATGGGCTACGCGCTTCGTTGTAAAGCTACCCATACAAAACCC      12480
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713 defect CATGTTCAAGAAATGGGCGAAAAGGGTTGCCCGAAAGTATGGGCTACGCGCTTCGTTGTAAAGCTACCCATACAAAACCC       7844

Majority   TTCGGCGCACTCACAACTGAAATGTTAGTGTTTCAACATCTCAGGAGTTTTAGTGTTACCGTCCTGCGCAAGCAAAGATG
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    12490     12500     12510     12520     12530     12540     12550     12560
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        TTCGGCGCACTCACAACTGAAATGTTAGTGTTTCAACATCTCAGGAGTTTTAGTGTTACCGTCCTGCGCAAGCAAAGATG      12560
713 defect TTCGGCGCACTCACAACTGAAATGTTAGTGTTTCAACATCTCAGGAGTTTTAGTGTTACCGTCCTGCGCAAGCAAAGATG       7924

Majority   AGAACTATACCTTTGACAACAAAGGGTATAGGGATCGGAAAGGCCGCTGCAGTAGGATTCAGACAAATAAATTTTCTCTT
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    12570     12580     12590     12600     12610     12620     12630     12640
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        AGAACTATACCTTTGACAACAAAGGGTATAGGGATCGGAAAGGCCGCTGCAGTAGGATTCAGACAAATAAATTTTCTCTT      12640
713 defect AGAACTATACCTTTGACAACAAAGGGTATAGGGATCGGAAAGGCCGCTGCAGTAGGATTCAGACAAATAAATTTTCTCTT       8004

Majority   GAAAATGTCCGCCGTTTTCTTTTGTTGGCTATTCCCTTTCACCGTGCGTACGGTGGGAAGAGAACAACAAAGAAAAAAAA
           ---------+---------+---------+---------+---------+---------+---------+---------+
                    12650     12660     12670     12680     12690     12700     12710     12720
           ---------+---------+---------+---------+---------+---------+---------+---------+
713        GAAAATGTCCGCCGTTTTCTTTTGTTGGCTATTCCCTTTCACCGTGCGTACGGTGGGAAGAGAACAACAAAGAAAAAAAA      12720
713 defect GAAAATGTCCGCCGTTTTCTTTTGTTGGCTATTCCCTTTCACCGTGCGTACGGTGGGAAGAGAACAACAAAGAAAAAAAA       8084

Majority   AAAAAAAAAAAAAA
           ---------+----
                    12730
           ---------+----
713        AAAAAAAAAAAAAA                                                                        12734
713 defect AAAAAAAAAAAAAA                                                                         8098
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Table S1. Primers for defective RNA cDNA cloning and sequencing

Name*	Sequence†	CHV1-EP713 genome map coordinates
CHV1-F	GGATCC**GCGGCCGC**GCCTATGGGTGGTCTACA	1–18
CHV1-R	GGATCC**GCGGCCGC**CTTTGTTGTTCTCTTCCC	12712–12699
CHV1–0.5kR	GGATCC**GCGGCCGC**CTGGGTTTTCTTAATTGA	518–501
CHV1–1kF	GGATCC**GCGGCCGC**ATCTCTCGGCCATTGTAG	983–1000
CHV1–1kR	GGATCC**GCGGCCGC**TTACTACAATGGCCGAGAGAT	1000–983
CHV1–2kF	GGATCC**GCGGCCGC**CACGACCCGGTTGAGGTC	1983–2000
CHV1–2kR	GGATCC**GCGGCCGC**GACCTCAACCGGGTCGTG	2000–1983
CHV1–3kF	GGATCC**GCGGCCGC**GGAAATGGATCTATGGTC	2993–3000
CHV1–3kR	GGATCC**GCGGCCGC**GACCATAGATCCATTTCC	3000–2993
CHV1–4kF	GGATCC**GCGGCCGC**CCTCCGCGATTTGTGGGA	3993–4000
CHV1–4kR	GGATCC**GCGGCCGC**TCCCACAAATCGCGGAGG	4000–3993
CHV1–4.5F	GGATCC**GCGGCCGC**ATGTGAGAGTGTATCCCC	4483–4500
CHV1–5kF	GGATCC**GCGGCCGC**TCCACGCTCTTGATCCCG	4983–5000
CHV1–5kR	GGATCC**GCGGCCGC**CGGGATCAAGAGCGTGGA	5000–4983
CHV1–5.5kR	GGATCC**GCGGCCGC**TCCTTAGGCACCACAGCT	5518–5501
CHV1–6kF	GGATCC**GCGGCCGC**TAATGCTGAAGGCGCTGT	5983–6000
CHV1–6kR	GGATCC**GCGGCCGC**ACAGCGCCTTCAGCATTA	6000–5983
CHV1–6.5F	GGATCC**GCGGCCGC**CGGCCTCCTCAAGCCGCG	6483–6500
CHV1–7kF	GGATCC**GCGGCCGC**CGAACTCGTCGTGTGGTT	6983–7000
CHV1–7kR	GGATCC**GCGGCCGC**AACCACACGACGAGTTCG	7000–6983
CHV1–11kF	GGATCC**GCGGCCGC**GTGTGCACGCCATATGTA	10983–11000
CHV1–11kR	GGATCC**GCGGCCGC**TACATATGGCGTGCACAC	11000–10983
CHV1–11.7kF	GGATCC**GCGGCCGC**AGGTACTTCTACACCAGC	11683–11700
CHV1–11.7kR	GGATCC**GCGGCCGC**CGATCTCTGCATGTTCCC	11701–11718
CHV1–12kF	GGATCC**GCGGCCGC**AGTAAAGACGTTAACCCG	11983–12000
CHV1–12kR	GGATCC**GCGGCCGC**CGGGTTAACGTCTTTACT	12000–11983
CHV1–12.5F	GGATCC**GCGGCCGC**CGGCGCACTCACAACTGA	12483–12500
CHV1–12.5R	GGATCC**GCGGCCGC**TCAGTTGTGAGTGCGCCG	12500–12483

*F, forward orientation; R, reverse orientation.

†GGATCC and GCGGCCGC are BamHI and Not I restriction sites designed for cloning purposes.