

1. The original Sanger sequencing file in seq format is changed to fasta format with TextEdit. The forward Sanger sequencing files are stored as F000~003.fasta and the reverse Sanger sequencing files are stored as R004~006.fasta, which are shown below:

>F000

```
GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGG
AAGTTCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGCGGATCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACG
GAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCGGTGATCACCGACGAGTACAAGGTGCCCA
GCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGG
CCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGG
TGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACG
AGGTGGCCTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGG
CCCTGGCCCACATGATCAAGTTCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGG
TGCAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGAC
GGCTGGAAAATCTGATCGCCAGCTGCCC GGCGAGAAGAAGAATGGCCCTGTTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTC
AAGAGCAACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGACACCTGCTGGCCCAGATCGGCGACCA
GTACGCCGACCTGTTTTCTATGCAGACTGTCGACGCATCTGCTGACGACATCTGAGAGTGAACACGAGATCACAGCTCCCTTGACCTTATGATCAG
AGAATATCGATCGAGCACCTATCGAGACTGAACTCCTGACTGGA
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>F001

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CTGTATTTTCGATCAGTTCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGGTGCAGA
CCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGG
AAAATCTGATCGCCAGCTGCCC GGCGAGAAGAAGAATGGCCTGTTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCA
ACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCAGATCGGCGACCAAGTACG
CCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCTGAGCG
CCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTT
TCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGA
TGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCC
ACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCC
GCATCCCCTACTACGTGGGCCCTCTGGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAGAGCGAGGAAACCATCACCCCTGCACTTCGA
GGAAGTGTGGACAGGCGCTCGCCAGAGCTCATCGAGCGATGACACTCGATAGACTGCCAACGAGAGGTGCTGCCAGCACAGCTGCTGTA
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>F002

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GGGATCATCTGGAAGTGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCA
TCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGA
AGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCA
CCCCCTGGAACCTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGA
AGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCG
CCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCA
AGAAAATCGAGTGCTTCGACTCCGTGGAATCTCCGGCGTGGAAAGATCGGTTCAACGCCTCCCTGGGCACATACCAGATCTGCTGAAAATTATCA
AGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGG
AACGGCTGAAAACCTATGCCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGC
TGATCAACGGCATCCGGGACAAGCAGTCCGGGCAGACATCCTGGATTTCCTGAAGTCCGACGGCTTCGCAACAGAACTCATGCAGCTGATCACGA
CGACAGCTGACTTAAGAGACATCAGATGCCAGTGTGCGAGGCGATAGCTGCACGAGCAATGGCATCTGTGCAGGCCGCATAGAGCATCTGCGACTG
AGTGTGACAGCTCTGAATGATGACCGCCAAGCCGAAAACCTCTGGTATTCTG
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>F003

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GGCCAGGCTACACGATCTGCTGAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGA
CACTGTTTTCGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGAT
ACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCT
TCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCC
TGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGG
GCCGGCACAAGCCCAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGA
TCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACC
TGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGA
AGGACGACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCAGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCTGTGAAGAAGATGA
AGAACTACTGGCGGCAGCTGCTGAACGCCCAAGCTGATTACCCAGAGAAAGTTTCGACATCTGACCAACGCCGAGAGAGGCGGCCTGAGCGAACTGG
ATAATGCGCTTCATCAGGAGACAGCTGATGAACCCCGCAGATCACAAAGCACGTGGCACAGATCTGACTCCCGGATGACACTTAGTACGACGAGAT
GACAGCCTGATCGGCAGTGAAGTGATCACCTTGAGTTCAGCTTGGGTTCCGATTTCGCAAGAATTCCTAGCTTACCAAATTGC
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>R004

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TCCGTTCTTCGGATCGGACACCAGCTTGGACTTCAGGGTGATCACTTTCACCTCCCGGATCAGCTTGTCAATTCTCGTCGTAATTAGTGTTTCATCCG
GGAGTCCAGGATCTGTGCCACGTGCTTTGTGATCTGCCGGGTTTCCACCAGCTGTCTCTTGATGAAGCCGGCCTTATCCAGTTCGCTCAGGCCGCC
TCTCTCGGCCTTGGTCAGATTGTCGAACCTTCTCTGGGTAATCAGCTTGGCGTTACGACGCTGCCGCCAGTAGTTCTTCATCTTCTTCACGACCTC
TTCGGAGGGCACGTTGTGCTCTTGCCCCGGTTCTTGTCGCTTCTGGTCAGCACCTTGTTGTGATGGAGTCGTCCTTCAGAAAGCTCTGAGGCAC
GATATGGTCCACATCGTAGTCGGACAGCCGTTGATGTCCAGTTCCTGGTCCACGTACATATCCCGCCATTCTGCAGGTAGTACAGGTACAGCTT
CTCGTTCTGCAGCTGGGTGTTTTCCACGGGGTGTTCTTTCAGGATCTGGCTGCCAGCTCTTTGATGCCCTCTTCGATCCGCTTCATTCTCTCGCG
GCTGTTCTTCTGTCCCTTCTGGGTGGTCTGGTTCTCTCTGGCCATTTTCGATCACGATGTTCTCGGGCTTGTCGCCGGCCCATCACTTTCACGAGCTC
GTCCACCACCTTCACTGTCTGCAGGATGCCCTTCTTAATGGCGGGGCTGCCGGCCAGATTGGCAATGTGCTCGTGAGGCTATCGCCCTGGCCGGA
CACCTGGGGCTTTCTGGATGTCCTCTTTAAAGGTACGCTGTGCTGCTGGATCAGCTGCATGAAGTTTCTGTTGGCGAAGCCGTGCGACTTCAGAA
ATCCAGGATTGTCTTGCCGACTGCTTGTCCCGGATGCCGTTGATCAGTTCGGGCTCAGCCTGCCCCAGCCGGTGTATCTCCGCCGCTTCAGCTG
CTTCATCACTTTGTGCTCGAACAGGTGGGGCATAGGTTTTAGCCGTTCTCGATCATCTCTCTGTCTCAAACAGTGTGAGGTGAGCACGATATCT
TTCAGATGTCTCGTTTTCTCATTGGTCAAGCAGTCATGTCCTGATTGCTTCAGCAGAATCGTGATGTGTGCCAGGAGGCGTTGAATCAGACCATC
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>R005

>R006

2. The reverse Sanger sequencing files are changed to the corresponding forward Sanger sequencing files with EMBOS revseq, which are stored as R004~006rev.fasta.

>R004rev

>R005rev

>R006rev

3. EMBOSS needle is used to align the tandemly arranged Sanger sequencing files and the results are shown below. The blue highlight shows the first time that the two sequences match for 50 continuous nucleotides. The numbers in red

highlight indicate the positions of interval for joining to the final merged sequence.

F000.fasta-F001.fasta			
F000	1	GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATAT	50
F001	0	-----	0
F000	51	ACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGAAGT	100
F001	0	-----	0
F000	101	TCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGG	150
F001	0	-----	0
F000	151	GTCGCGGATCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCA	200
F001	0	-----	0
F000	201	GCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGT	250
F001	0	-----	0
F000	251	GGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCA	300
F001	0	-----	0
F000	301	AGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGA	350
F001	0	-----	0
F000	351	GCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAG	400
F001	0	-----	0
F000	401	AACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGC	450
F001	0	-----	0
F000	451	AAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCAC	500
F001	0	-----	0
F000	501	AGACTGGAAGAGTCCTTCCTGGTGAAGAGGATAAGAAGCACGAGCGGCA	550
F001	0	-----	0
F000	551	CCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACC	600
F001	0	-----	0
F000	601	CCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCC	650
F001	0	-----	0
F000	651	GACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGG	700
F001	1	. . -----CTG---TATTT-----CGATC-AGTT-CGGGG	22
F000	701	CCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACA	750
F001	23	 CCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACA	72
F000	751	AGCTGTTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAAC	800
F001	73	 AGCTGTTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAAC	122
F000	801	CCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACT	850
F001	123	 CCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACT	172
F000	851	GAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCC GGCGAGA	900
F001	173	 GAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCC GGCGAGA	222

F000	901	AGAAGAATGGCCCTGTTTCGGAACCTGATTGCCCTGAGCCTGGGCCTGAC	950
F001	223	AGAAGAATGG-CCTGTTTCGGAACCTGATTGCCCTGAGCCTGGGCCTGAC	271
F000	951	CCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGC	1000
F001	272	CCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGC	321
F000	1001	TGAGCAAGGACACCTACGACGACGACCT-GAC-ACCTGCTGGCCCAGATC	1048
F001	322	TGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATC	371
F000	1049	GGCGACCAGTACGCCGACCTGTTTTCTATGC-----AGA--CTGT-CGAC	1090
F001	372	GGCGACCAGTACGCCGACCTG-TTTCT-GGCCGCCAAGAACCTGTCCGAC	419
F000	1091	G-CAT-CTGCTGA-CGACAT-CTGAGAGTGAACA-CGAGATCAC---AGC	1132
F001	420	GCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGC	469
F000	1133	TCCCTTGA---CCT-TATGATCAGAGA-ATATCGATCGAGCACCTATCGA	1177
F001	470	CCCCCTGAGCGCCTCTATGATCA-AGAGATA-CGA-CGAGCACC-ACCAG	515
F000	1196	-----	1196
F001	566	CAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTG	615
F000	1196	-----	1196
F001	616	ACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTG	665
F000	1196	-----	1196
F001	666	GAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGA	715
F000	1196	-----	1196
F001	716	CCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGA	765
F000	1196	-----	1196
F001	766	TCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTAC	815
F000	1196	-----	1196
F001	816	CCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCG	865
F000	1196	-----	1196
F001	866	CATCCCCTACTACGTGGGCCCTCTGGGCCAGGGGAAACAGCAGATTCGCC	915
F000	1196	-----	1196
F001	916	TGGATGACCAGAAGAGCGAGGAAACCATCACCCCCTGCACTTCGAGGAAG	965
F000	1196	-----	1196
F001	966	TGTGGACAGGCGCTCGCCAGAGCTCATCGAGCGATGACACTCGATAGACT	1015
F000	1196	----- 1196	
F001	1016	GCCAACGAGAGGTGCTGCCAGCACAGCTGCTGTA 1049	
F001.fasta-F002.fasta			
F001	1	CTGTATTTTCGATCAGTTCGGGGCCACTTCCTGATCGAGGGCGACCTGAAC	50
F002	0	-----	0
F001	51	CCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGGTGCAGACCTA	100
F002	0	-----	0
F001	101	CAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCA	150

F002	0	-----	0
F001	151	AGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTG	200
F002	0	-----	0
F001	201	ATCGCCCAGCTGCCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGAT	250
F002	0	-----	0
F001	251	TGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGG	300
F002	0	-----	0
F001	301	CCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTG	350
F002	0	-----	0
F001	351	GACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGC	400
F002	0	-----	0
F001	401	CGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGA	450
F002	0	-----	0
F001	451	ACACCGAGATCACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATAC	500
F002	0	-----	0
F001	501	GACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCA	550
F002	0	-----	0
F001	551	GCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCT	600
F002	0	-----	0
F001	601	ACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTC	650
F002	1	-----GG-----GATC	6
F001	651	ATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAAGTCTCGTGAA	700
F002	7	AT-----CTGGAA---GTGGACGGCACCGAGGAAGTCTCGTGAA	43
F001	701	GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA	750
F002	44	GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA	93
F001	751	GCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGG	800
F002	94	GCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGG	143
F001	801	CAGGAAGATTTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAA	850
F002	144	CAGGAAGATTTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAA	193
F001	851	GATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGGCCAGGGGA	900
F002	194	GATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCT-GGCCAGGGGA	242
F001	901	AACAGCAGATTTCGCCTGGATGACCAG-AAGAGCGAGGAAACCATCACCCC	949
F002	243	AACAGCAGATTTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCC	292
F001	950	CT-GCACTTCGAGGAAGT-GTGGACA--GGCGCT--CG-CCAGAGC-TCA	991
F002	293	CTGGAACCTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCA	342
F001	992	TCGAGC-GATGAC--AC-TCGAT-AGA--CTG-CCAACGAG-AGGTGCTG	1032
F002	343	TCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGAAGGTGCTG	392

F001	1033	CC--AGCACAG-CTGCTGTA-----	1049
F002	393	CCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGAC	442
F001	1049	-----	1049
F002	443	CAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCG	492
F001	1049	-----	1049
F002	493	GCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAA	542
F001	1049	-----	1049
F002	543	GTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTT	592
F001	1049	-----	1049
F002	593	CGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGG	642
F001	1049	-----	1049
F002	643	GCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGAC	692
F001	1049	-----	1049
F002	693	AATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACT	742
F001	1049	-----	1049
F002	743	GTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACC	792
F001	1049	-----	1049
F002	793	TGTTGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGC	842
F001	1049	-----	1049
F002	843	TGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTC	892
F001	1049	-----	1049
F002	893	CGGGCAGACATCCTGGATTTCTGAAGTCCGACGGCTTCGCAACAGAAAC	942
F001	1049	-----	1049
F002	943	TCATGCAGCTGATCACGACGACAGCTGACTTAAGAGACATCAGATGCCAG	992
F001	1049	-----	1049
F002	993	TGTCGCAGGCGATAGCTGCACGAGCAATGGCATCTGTGCAGGCCGCATAG	1042
F001	1049	-----	1049
F002	1043	AGCATCTGCGACTGAGTGTGACAGCTCTGAATGATGACCGCCAAGCCGAA	1092
F001	1049	-----	1049
F002	1093	AACTCTGGTATTCG 1106	
F002.fasta-F003.fasta			
F002	1	GGGATCATCTGGAAGTGGACGGCACCGAGGAACTGCTCGTGAAGCTGAAC	50
F003	0	-----	0
F002	51	AGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCC	100
F003	0	-----	0
F002	101	CCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAG	150
F003	0	-----	0
F002	151	ATTTTACCATTTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTG	200

F003	0	-----	0
F002	201	ACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAG	250
F003	0	-----	0
F002	251	ATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGA	300
F003	0	-----	0
F002	301	TCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGG	350
F003	0	-----	0
F002	351	ATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCA	400
F003	0	-----	0
F002	401	CAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGA	450
F003	0	-----	0
F002	451	AATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAG	500
F003	0	-----	0
F002	501	AAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGT	550
F003	0	-----	0
F002	551	GAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCG	600
F003	0	-----	0
F002	601	TGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACA---	647
F003	1	----- --GGC-CAGGC	8
F002	648	TACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGA	697
F003	9	TA-CACGATCTGCTG--AATTATCAAGGACAAGGACTTCCTGGACAATGA	55
F002	698	GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTG	747
F003	56	GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTG	105
F002	748	AGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTC	797
F003	106	AGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTC	155
F002	798	GACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGG	847
F003	156	GACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGG	205
F002	848	CAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGGC	897
F003	206	CAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCA	255
F002	898	AGAC-ATCCTGGATTTCTGAAGTCCGACGGCTTCG-CAACAGAAAC-TC	944
F003	256	AGACAATCCTGGATTTCTGAAGTCCGACGGCTTCGCCAACAGAACTTC	305
F002	945	ATGCAGCTGAT-CACGACGACAG-CTGAC---TTAAGA-GACATC---AG	985
F003	306	ATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAA	355
F002	986	ATGCCA-GTGTC--GC--AGGCGATAG-CTGCACGAGCA-ATGGC--ATC	1026
F003	356	AGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC	405
F002	1027	TGTGCAGGCCG-----CAT-----AGAGCAT-CTGC-GAC--TGA----	1057
F003	406	TG-GCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGT	454
F002	1058	-GTGTGAC-AGCTC-TGAA--TGAT-GACCG--CCAAG-CCGAAAAC-TC	1097

F003	455	. . .	503
F002	1098	TGGTATTTCG-----	1106
F003	504	. --GTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAG	551
F002	1106	-----	1106
F003	552	AACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGG	601
F002	1106	-----	1106
F003	602	CAGCCAGATCCTGAAAGAACACCCCGTGAAAAACACCCAGCTGCAGAACG	651
F002	1106	-----	1106
F003	652	AGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGAC	701
F002	1106	-----	1106
F003	702	CAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGT	751
F002	1106	-----	1106
F003	752	GCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAAGTGCTGACCA	801
F002	1106	-----	1106
F003	802	GAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTC	851
F002	1106	-----	1106
F003	852	GTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCCAAGCTGA	901
F002	1106	-----	1106
F003	902	TTACCCAGAGAAAGTTCGACATCTGACCAACGCCGAGAGAGGCGGCCTGA	951
F002	1106	-----	1106
F003	952	GCGAACTGGATAATGCGCTTCATCAGGAGACAGCTGATGAACCCCGCAGA	1001
F002	1106	-----	1106
F003	1002	TCACAAAGCACGTGGCACAGATCTGACTCCCGGATGACACTTAGTACGAC	1051
F002	1106	-----	1106
F003	1052	GAGATGACAGCCTGATCGGCAGTGAAGTGATCACCTTGAGTTCAGCTTG	1101
F002	1106	----- 1106	
F003	1102	GGTTCCGATTCGCAAAGAATTCCTAGCTTACCAAATTGC 1140	
F003.fasta-R004rev.fasta			
F003	1	-----GGCCAGGCTACACGA-TCTGCTGAA-T	25
R004rev	1	. . .	50
F003	26	TATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGG	75
R004rev	51		95
F003	76	AAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAG	125
R004rev	96		143
F003	126	GAACGGCTGAAAACCTATG-CCCACCTGTTTCGACGACAAAGTGATGAAGC	174
R004rev	144		193
F003	175	AGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTG	224
R004rev	194	AGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTG	243

F003	225	ATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCT	274
R004rev	244	ATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTT-CT	292
F003	275	GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG	324
R004rev	293	GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG	342
F003	325	ACAGCCTGACCTTTAAAGAGGACATCCAGAAAG-CCCAGGTGTCCGGCCA	373
		.	
R004rev	343	ACAGCGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCA	392
F003	374	GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA	423
R004rev	393	GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA	442
F003	424	TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA	473
R004rev	443	TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA	492
F003	474	GTGATGGGCCGGCACAAGCCCCGAGAACATCGTGATCGAAATGGCCAGAGA	523
R004rev	493	GTGATGGGCCGGCACAAGCCCCGAGAACATCGTGATCGAAATGGCCAGAGA	542
F003	524	GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC	573
R004rev	543	GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC	592
F003	574	GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC	623
R004rev	593	GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC	642
F003	624	CCCGTGGAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT	673
R004rev	643	CCCGTGGAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT	692
F003	674	GCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGC	723
R004rev	693	GCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGC	742
F003	724	TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC	773
R004rev	743	TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC	792
F003	774	GACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCGGGGCAA	823
		.	
R004rev	793	GACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCGGGGCAA	842
F003	824	GAGCGACAACGTGCCCTCCGAAGAGGTCTGTGAAGAAGATGAAGAACTACT	873
R004rev	843	GAGCGACAACGTGCCCTCCGAAGAGGTCTGTGAAGAAGATGAAGAACTACT	892
F003	874	GGCGGCAGCTGCTGAACGCCCAAGCTGATTACCCAGAGAAAGTTTCGAC-A	922
R004rev	893	GGCGGCAGCTGCTGAACG-CCAAGCTGATTACCCAGAGAAAGTTTCGACAA	941
F003	923	TCTGACCAACGCCGAGAGAGGCGGCCTGAGCGAACTGGATAATGC--GCT	970
		. .	
R004rev	942	TCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCT	991
F003	971	TCATCAGGAGACAGCTGATG--AACCCCGCAGATCACAAAGCACGTGGCA	1018
		. . .	
R004rev	992	TCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCA	1041
F003	1019	CAGATC--TGA TCCCGGATG-ACACTTAGTACGACGAG-ATGACAGCCT	1064
			
R004rev	1042	CAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAAATGACAAGCT	1091
F003	1065	GATC--GGCAGTG-AAGTGATCACCTTGAGTTC-AGCTTGGGT-TCCGA	1109
			
R004rev	1092	GATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCT--GGTGTCCGA	1139
F003	1110	TTCGCAAAGAATTCTAGCTTACCAAATTGC 1140	
		. .	

R004rev	1140	TCCG--AAGAA--CCGA-----	1152	
R004rev.fasta-R005rev.fasta				
R004rev	1	GATGGTCTGATTCAACGCCTCCTGGGCACACATCACGATTCTGCTGAAGC	50	
R005rev	0	-----	0	
R004rev	51	AATCAGGACATGACTGCTTGACCAATGAGAAAACGAGACATCTGAAAGAT	100	
R005rev	0	-----	0	
R004rev	101	ATCGTGCTGACCTGACACTGTTTGAGGACAGAGAGATGATCGAGAACGGC	150	
R005rev	0	-----	0	
R004rev	151	TGAAAACCTATGCCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAA	200	
R005rev	0	-----	0	
R004rev	201	GCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACG	250	
R005rev	0	-----	0	
R004rev	251	GCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCG	300	
R005rev	0	-----	0	
R004rev	301	ACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCGTG	350	
R005rev	0	-----	0	
R004rev	351	ACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCAGGGCGATA	400	
R005rev	0	-----	0	
R004rev	401	GCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAG	450	
R005rev	0	-----	0	
R004rev	451	GGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGG	500	
R005rev	0	-----	0	
R004rev	501	CCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGA	550	
R005rev	0	-----	0	
R004rev	551	CCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAA	600	
R005rev	0	-----	0	
R004rev	601	GAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGA	650	
R005rev	0	-----	0	
R004rev	651	AAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATG	700	
R005rev	0	-----	0	
R004rev	701	GGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGCTGTCCGAC	750	
R005rev	0	-----	0	
R004rev	751	TACGATGTGGACCATATCGTGCCTCAGAGCTTTTCTGAAGGACGACTCCAT	800	
R005rev	1	-----GCTTTCTGAAGGACGACTCCAT	22	
R004rev	801	CGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACA	850	
R005rev	23	CGAC-ACAAGGTGCTGACCAGAAGCGACA--GACCGGGGC-AGAGCGAC-	67	
R004rev	851	ACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAG	900	
R005rev	68	ACGTGCCCTCCGAAGA-GTCGTG-AGAAGATGAAGAACTACTGGCGGCAG	115	

R004rev	901	CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAA	950
R005rev	116	CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAA	165
R004rev	951	GG-CCGAGAGAGGGCGCCTGAGCGAACTGGATAAGG-CCGGCTTCATCAA	998
R005rev	166	GGCCCGAGAGAGGGCGG-CTGAGCGAACTGGATAAGGCCCGGCTTCATCAA	214
R004rev	999	GAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCC	1048
R005rev	215	GAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCC	264
R004rev	1049	TGGA CTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGG	1098
R005rev	265	TGGA CTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGG	314
R004rev	1099	GAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGAT---CCGAA	1145
R005rev	315	GAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAA	364
R004rev	1146	GAACCGA-----	1152
R005rev	365	G-----GATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACCTACCACCAC	410
R004rev	1152	-----	1152
R005rev	411	GCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAA	460
R004rev	1152	-----	1152
R005rev	461	GTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACG	510
R004rev	1152	-----	1152
R005rev	511	ACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACC	560
R004rev	1152	-----	1152
R005rev	561	GCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGAT	610
R004rev	1152	-----	1152
R005rev	611	TACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACG	660
R004rev	1152	-----	1152
R005rev	661	GCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTG	710
R004rev	1152	-----	1152
R005rev	711	CGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGT	760
R004rev	1152	-----	1152
R005rev	761	GCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCG	810
R004rev	1152	-----	1152
R005rev	811	ATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGC	860
R004rev	1152	-----	1152
R005rev	861	TTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGA	910
R004rev	1152	-----	1152
R005rev	911	AAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCA	960
R004rev	1152	-----	1152
R005rev	961	CCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTCTGAAGC	1010
R004rev	1152	----- 1152	
R005rev	1011	CAAGCACAGTGAGG 1024	

R005rev.fasta-R006rev.fasta

R005rev	1	GCTTTCTGAAGGACGACTCCATCGACACAAGGTGCTGACCAGAAGCGACA	50
R006rev	0	-----	0
R005rev	51	GACCGGGGCAGAGCGACACGTGCCCTCCGAAGAGTCGTGAGAAGATGAAG	100
R006rev	0	-----	0
R005rev	101	AACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAAGTT	150
R006rev	0	-----	0
R005rev	151	CGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGG	200
R006rev	0	-----	0
R005rev	201	CCCGGCTTCATCAAGAGACAGCTGGTGAAACCCGGCAGATCACAAAGCA	250
R006rev	0	-----	0
R005rev	251	CGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATG	300
R006rev	0	-----	0
R005rev	301	ACAAGCTGATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTG	350
R006rev	0	-----	0
R005rev	351	TCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGC GCGAGATCAACAA	400
R006rev	0	-----	0
R005rev	401	CTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCC	450
R006rev	0	-----	0
R005rev	451	TGATCAAAAAGTACCCTAAGCTGGAAAGCGA--GTTCGTG-TACGGC-GA	496
R006rev	1	 -----GCT-GAAGGCGAAGTTTCGAGTTACGACGGA	30
R005rev	497	CTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCG-AGCAGGAA	545
R006rev	31	 CTACAA-GAGTACGACGTAC-GAAGATGATCGGCAAGAGCGAAGCCAGAA	78
R005rev	546	ATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAG-CAACATCATGAACT	594
R006rev	79	 ATCCGCCAAGCTA-CGCCAAGTACTTCTTCTACAGCCACCATCATGAACT	127
R005rev	595	TTTTCAAGACCGAGATTACCCTGGCCAACG-GCGAGATCC-GGAAGCGGC	642
R006rev	128	. TTTTCAAGA-CGAGATTACCCT-GCCAACGAGCGAGATCCAGAAAGCGGC	175
R005rev	643	CTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGC	692
R006rev	176	. . . CTCTGATCGAGAC-ATCGGCGAAACCCGGGAGATCGTGTGGGATAAGAGC	224
R005rev	693	CGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCAAGTGAATAT	742
R006rev	225	 CGGGATTTTG-CACCGTGCGGAAAGTGCTGAGCATGCCCAAGTGAATAT	273
R005rev	743	CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC	792
R006rev	274	 CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC	323
R005rev	793	TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGAC	842
R006rev	324	 TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGAC	373
R005rev	843	CCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCT	892
R006rev	374	 CCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCT	423
R005rev	893	GGTGGTGGCCAAAGTGGAAGGGCAAGTCCAAGAACTGAAGAGTGTGA	942

R006rev	424	 GGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGA	473
R005rev	943	AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAAT	992
R006rev	474	 AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAAT	523
R005rev	993	CCCATCGAC-TTCT-GAAGCCAAGCAC-----AGTG----AGG-----	1024
R006rev	524	 CCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCT	573
R005rev	1024	-----	1024
R006rev	574	GATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGA	623
R005rev	1024	-----	1024
R006rev	624	AGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCC	673
R005rev	1024	-----	1024
R006rev	674	CTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAA	723
R005rev	1024	-----	1024
R006rev	724	GCTGAAGGGCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAAC	773
R005rev	1024	-----	1024
R006rev	774	AGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCC	823
R005rev	1024	-----	1024
R006rev	824	AAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTA	873
R005rev	1024	-----	1024
R006rev	874	CAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCC	923
R005rev	1024	-----	1024
R006rev	924	ACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTT	973
R005rev	1024	-----	1024
R006rev	974	GACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGA	1023
R005rev	1024	-----	1024
R006rev	1024	CGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCG	1073
R005rev	1024	-----	1024
R006rev	1074	ACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAG	1123
R005rev	1024	-----	1024
R006rev	1124	CTTGCGGCCGCACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGC	1173
R005rev	1024	-----	1024
R006rev	1174	TAACAAAGCCCGAAAGAGCGATTTCC	1199

4. The numbers with red highlight are F000 (1-700), F001 (23-700), F002 (44-697), F003 (56-174), R004rev (194-900), R005rev (116-742), R006rev (274-1199), which are shown in red highlight in the corresponding Sanger sequencing files as below.

>F000

GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGG
AAGTTCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTGCGGATCCCCAAAGAAGAAGCGGAAGGTCTGGTATCCACG
GAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCA
GCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTTCGACAGCGGCCGAAACAGCCGAGG
CCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGG
TGGACGACAGCTTCTTCCACAGACTGGAAGAGTCTTCTGCTGGTGGAAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACG

AGGTGGCCTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGG
CCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGG
TGCAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGAC
GGCTGGAAAATCTGATCGCCAGCTGCCC GGCGAGAAGAAGAATGGCCCTGTTTCGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTC
AAGAGCAACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGACACCTGCTGGCCCAGATCGGCGACCA
GTACGCCGACCTGTTTTCTATGCAGACTGTCGACGCATCTGCTGACGACATCTGAGAGTGAACACGAGATCACAGCTCCCTTGACCTTATGATCAG
AGAATATCGATCGAGCACCTATCGAGACTGAACTCCTGACTGGA

> F001

CTGTATTTCGATCAGTTCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGGTGCAGA
CCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGG
AAAATCTGATCGCCCAGCTGCCC GGCGAGAAGAAGAATGGCCCTGTTTCGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCA
ACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAAGTACG
CCGACCTGTTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCCTGAGCG
CCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTT
TCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTTCATCAAGCCCATCCTGGAAAAGA
TGGACGGCACCGAGGAACTGCTCGTGAACTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCC
ACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCC
GCATCCCCTACTACGTGGGCCCTCTGGGCCAGGGGAAACAGCAGATTCGCTGGATGACCAGAAGAGCGAGGAAACCATCACCCCCTGCACTTCGA
GGAAGTGTGGACAGGCGCTCGCCAGAGCTCATCGAGCGATGACACTCGATAGACTGCCAACGAGAGGTGCTGCCAGCACAGCTGCTGTA

>F002

GGGATCATCTGGAAGTGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCA
TCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGA
AGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCTGGATGACCAGAAAGAGCGAGGAAACCATCA
CCCCCTGGAACCTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGA
AGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGGAATGAGAAAGCCCG
CCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCA
AGAAAATCGAGTGCTTCGACTCCGTGGAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCA
AGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGG
AACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGC
TGATCAACGGCATCCGGGACAAGCAGTCCGGGCAGACATCCTGGATTTCTGAAGTCCGACGGCTTCGCAACAGAACTCATGCAGCTGATCACGA
CGACAGCTGACTTAAGAGACATCAGATGCCAGTGTGCGAGGCGATAGCTGCACGAGCAATGGCATCTGTGCAGGCCGCATAGAGCATCTGCGACTG
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>F003

GGCCAGGCTACACGATCTGCTGAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGA
CACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGAT
ACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCT
TCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCC
TGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGG
GCCGGCACAAGCCCAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGA
TCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACC
TGCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGA
AGGACGACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCAGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCTGAAGAAGATGA
AGAACTACTGGCGGCAGCTGCTGAACGCCCAAGCTGATTACCCAGAGAAAGTTCGACATCTGACCAACGCCGAGAGAGGCGGCCTGAGCGAACTGG
ATAATGCGCTTCATCAGGAGACAGCTGATGAACCCCGCAGATCACAAAGCACGTGGCACAGATCTGACTCCCGGATGACACTTAGTACGACGAGAT
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>R004rev

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CAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGAT
TTCTGAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTG
TCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGAC
GAGCTCGTGAAAGTGATGGGCCGGCACAAGCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGC
CGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAG
AAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATC
GTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCAGGGGCAAGAGCGACAACGTGCCCTCCGAA
GAGGTCTGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGA
GGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCC
CGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATCCGAAGAACCGA

> R005rev

GCTTTCTGAAGGACGACTCCATCGACACAAGGTGCTGACCAGAAGCGACAGACCGGGGCAGAGCGACACGTGCCCTCCGAAGAGTCGTGAGAAGAT
GAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACT
GGATAAGGCCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGT
ACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAG
TGCGCGAGATCAACAACTACCACCACGCCACGACGCCTACCTGAACGCCGTCTGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCG
AGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCT
ACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGG
AGATCGTGTGGGATAAGGGCCGGGATTTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAGACCGAGGTGCAGACAG
GCGGCTTCAGCAAAGAGTCTATCCTGCCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCG
ACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCA
CCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTCTGAAGCCAAGCACAGTGAGG

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> R006rev
GCTGAAGGCGAAGTTTCGAGTTACGACGGACTACAAGAGTACGACGTACGAAGATGATCGGCAAGAGCGAAGCCAGAAATCCGCCAAGCTACGCCA
AGTACTTCTTCTACAGCCACCATCATGAACTTTTTCAAGACGAGATTACCCTGCCAACGAGCGAGATCCAGAAAGCGGCCTCTGATCGAGACATCG
GCGAAACCCGGGAGATCGTGTGGGATAAGAGCCGGGATTTTGCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGA
GGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTA
CGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCT
GCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGAT
CATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGC
CCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGT
GGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCT
GTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCCTGCCGC
CTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCT
GTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAGCTTGCGGCCGCACTCGAGCACCACCACCA
CCACCACTGAGATCCGGCTGCTAACAAAGCCCCGAAAGAGCGATTTC
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5. The nucleotides in red highlight in step 4 are joined via copy and paste to obtain the merged Sanger sequence, as shown below.

```
>gene
GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGG
AAGTTCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTGCGGGATCCCCAAGAAGAAGCGGAAGGTGGTATCCACG
GAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCA
GCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGG
CCACCCGGCTGAAGAGAACCAGCCAGAAGAAGATACACCAGACGGAAGAACCAGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGG
TGGACGACAGCTTCTTCCACAGACTGGAAGAGTCTTCTGCTGGTGGAAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACG
AGGTGGCCTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGG
CCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGG
TGCAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGAC
GGCTGGAAAATCTGATCGCCAGCTGCCCAGCGGAGAGAAGAAGTGGCCTGTTTCGGAACCTGATTGCCCTGAGCCTGGGCTGACCCCCAATTCA
AGAGCAACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCAGATCGGCGACC
AGTACGCCGACCTGTTTCTGGCCGCAAGAACCCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCC
TGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAG
AGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGG
AAAAGATGGACGGCACCGAGGAACCTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACC
AGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTACCCATTCTGAAGGACAACCGGGAAGAGATCGAGAAGATCCTGA
CCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTTCGCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCTGGA
ACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCCTGCCAACGAGAAGGTGCTGC
CCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCTGA
GCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCG
AGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGG
ACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGA
AAACCTATGCCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACG
GCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAG
CGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA
TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCA
GAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGA
AAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGG
ACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCG
ACAAGAACCAGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCTGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTA
CCCAGAGAAAGTTCGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCCGGCTTCATCAAGAGACAGCTGGTGGAAACC
CGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATC
ACCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACCTACCACCACGCCCACGACGCCTAC
CTGAACGCCGTCTGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAG
ATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTG
GCCAACGCGGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGG
AAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGC
GATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAA
GTGGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGAC
TTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGA
ATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAG
CTGAAGGGCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTC
TCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAAT
ATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAA
GAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAG
CGGAAGGTCTGAAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCCTGAGATCCGGCTGCTAACAAAGCCCCGAAAGAGCGATTTC
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6. The sequence obtained with the script is shown below.

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>merged
GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGG
AAGTTCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGGGTGCGGGATCCCCAAGAAGAAGCGGAAGGTGGTATCCACG
GAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCA
GCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGG
CCACCCGGCTGAAGAGAACCAGCCAGAAGAAGATACACCAGACGGAAGAACCAGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGG
TGGACGACAGCTTCTTCCACAGACTGGAAGAGTCTTCTGCTGGTGGAAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACG
AGGTGGCCTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGG
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CCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGG
TGCAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGAC
GGCTGGAAAATCTGATCGCCCAGCTGCCCCGGCGAGAAGAAGAATGGCCTGTTTCGAAAACCTGATTGCCCTGAGCCTGGGCTGACCCCCAATTCA
AGAGCAACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACC
AGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCC
TGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAG
AGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGG
AAAAGATGGACGGCACCAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACC
AGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAGATCGAGAAGATCCTGA
CCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTTCGCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCTGGA
ACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGAAGGTGCTGC
CCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGA
GCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCG
AGTGCTTCGACTCCGTGGAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGG
ACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGA
AAACCTATGCCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACG
GCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAG
CGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA
TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCGAGAACATCGTGATCGAAATGGCCA
GAGAGAACCAGACCACCAGAAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGA
AAGAACACCCCGTGGAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGG
ACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCG
ACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTA
CCCAGAGAAAGTTCGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCCGGCTTCATCAAGAGACAGCTGGTGGAACCC
CGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATC
ACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACCTACCACCACGCCCACGACGCCTAC
CTGAACGCCGTCTGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAG
ATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCTG
GCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGG
AAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGC
GATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAA
GTGGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGAC
TTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGA
ATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAACGAACCTGGCCCTGCCCTCCAAATATGTGAACTTCTGTACCTGGCCAGCCACTATGAGAAG
CTGAAGGGCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTC
TCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAAT
ATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAA
GAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAG
CGGAAGGTCTGAAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCTGAGATCCGGCTGCTAACAAAGCCCGAAAGAGCGATTTCC

7. The manual joined sequence is aligned to the script merged sequence with EMBOSS needle and the results is shown below. As can be seen, the two sequence are identical.

gene	1	GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATAT	50
merged	1	GCTGACTCTTCCCTCTAGAATAATTTTGTTTAACTTTAAGAAGGAGATAT	50
gene	51	ACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGAAGT	100
merged	51	ACCATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGAAGT	100
gene	101	TCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGG	150
merged	101	TCTGTTCCAGGGGCCCCATATGGCTAGCATGACTGGTGGACAGCAAATGG	150
gene	151	GTCGCGGATCCCCAAAGAAGAAGCGGAAGGTCTGGTATCCACGGAGTCCCA	200
merged	151	GTCGCGGATCCCCAAAGAAGAAGCGGAAGGTCTGGTATCCACGGAGTCCCA	200
gene	201	GCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGT	250
merged	201	GCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGT	250
gene	251	GGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCAGCAAGAAATTCA	300
merged	251	GGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCAGCAAGAAATTCA	300
gene	301	AGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGA	350
merged	301	AGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGA	350
gene	351	GCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAG	400
merged	351	GCCCTGCTGTTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAG	400

gene	401	AACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGC	450
merged	401	AACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGC	450
gene	451	AAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCAC	500
merged	451	AAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCAC	500
gene	501	AGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCA	550
merged	501	AGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCA	550
gene	551	CCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACC	600
merged	551	CCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACC	600
gene	601	CCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCC	650
merged	601	CCACCATCTACCACCTGAGAAAGAACTGGTGGACAGCACCGACAAGGCC	650
gene	651	GACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGG	700
merged	651	GACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGG	700
gene	701	CCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACA	750
merged	701	CCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACA	750
gene	751	AGCTGTTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTTCGAGGAAAAC	800
merged	751	AGCTGTTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTTCGAGGAAAAC	800
gene	801	CCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACT	850
merged	801	CCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACT	850
gene	851	GAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCC GGCGAGA	900
merged	851	GAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCC GGCGAGA	900
gene	901	AGAAGAATGGCCTGTTTCGGAACCTGATTGCCCTGAGCCTGGGCCTGACC	950
merged	901	AGAAGAATGGCCTGTTTCGGAACCTGATTGCCCTGAGCCTGGGCCTGACC	950
gene	951	CCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCT	1000
merged	951	CCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCT	1000
gene	1001	GAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCG	1050
merged	1001	GAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCG	1050
gene	1051	GCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCC	1100
merged	1051	GCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCC	1100
gene	1101	ATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCC	1150
merged	1101	ATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCC	1150
gene	1151	CCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGA	1200
merged	1151	CCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGA	1200
gene	1201	CCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAG	1250
merged	1201	CCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAG	1250
gene	1251	ATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGG	1300
merged	1251	ATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGG	1300
gene	1301	AGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGA	1350

merged	1301	AGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGA	1350
gene	1351	TGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTG	1400
merged	1351	TGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTG	1400
gene	1401	CGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCACCT	1450
merged	1401	CGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCACCT	1450
gene	1451	GGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCC	1500
merged	1451	GGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCC	1500
gene	1501	TGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC	1550
merged	1501	TGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCC	1550
gene	1551	TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTTCGCCTGGATGAC	1600
merged	1551	TACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTTCGCCTGGATGAC	1600
gene	1601	CAGAAAGAGCGAGGAAACCATCACCCCCTGGAAGTTCGAGGAAGTGGTGG	1650
merged	1601	CAGAAAGAGCGAGGAAACCATCACCCCCTGGAAGTTCGAGGAAGTGGTGG	1650
gene	1651	ACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGAT	1700
merged	1651	ACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGAT	1700
gene	1701	AAGAACCTGCCCAACGAGAAGGTGCTGCCAAGCACAGCCTGCTGTACGA	1750
merged	1701	AAGAACCTGCCCAACGAGAAGGTGCTGCCAAGCACAGCCTGCTGTACGA	1750
gene	1751	GTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGG	1800
merged	1751	GTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGG	1800
gene	1801	GAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTG	1850
merged	1801	GAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTG	1850
gene	1851	GACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGA	1900
merged	1851	GACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGA	1900
gene	1901	GGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCG	1950
merged	1901	GGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCG	1950
gene	1951	TGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAA	2000
merged	1951	TGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAA	2000
gene	2001	ATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCT	2050
merged	2001	ATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCT	2050
gene	2051	GGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCG	2100
merged	2051	GGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCG	2100
gene	2101	AGGAACGGCTGAAAACCTATGCCCACCTGTTTCGACGACAAAGTGATGAAG	2150
merged	2101	AGGAACGGCTGAAAACCTATGCCCACCTGTTTCGACGACAAAGTGATGAAG	2150
gene	2151	CAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCT	2200
merged	2151	CAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCT	2200
gene	2201	GATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCT	2250
merged	2201	GATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCT	2250
gene	2251	GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG	2300

merged	2251	 GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG	2300
gene	2301	ACAGCGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCA	2350
merged	2301	 ACAGCGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCA	2350
gene	2351	GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA	2400
merged	2351	 GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA	2400
gene	2401	TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA	2450
merged	2401	 TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA	2450
gene	2451	GTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGA	2500
merged	2451	 GTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGA	2500
gene	2501	GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC	2550
merged	2501	 GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC	2550
gene	2551	GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC	2600
merged	2551	 GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC	2600
gene	2601	CCCGTGGAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT	2650
merged	2601	 CCCGTGGAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT	2650
gene	2651	GCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGC	2700
merged	2651	 GCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGC	2700
gene	2701	TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC	2750
merged	2701	 TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC	2750
gene	2751	GACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAA	2800
merged	2751	 GACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAA	2800
gene	2801	GAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACT	2850
merged	2801	 GAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACT	2850
gene	2851	GGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAAT	2900
merged	2851	 GGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAAT	2900
gene	2901	CTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCCGGCT	2950
merged	2901	 CTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCCGGCT	2950
gene	2951	TCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCA	3000
merged	2951	 TCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCA	3000
gene	3001	CAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCT	3050
merged	3001	 CAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCT	3050
gene	3051	GATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATT	3100
merged	3051	 GATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATT	3100
gene	3101	TCCGGAAGGATTTCCAGTTTTACAAAGTGC GCGAGATCAACAAC TACCAC	3150
merged	3101	 TCCGGAAGGATTTCCAGTTTTACAAAGTGC GCGAGATCAACAAC TACCAC	3150
gene	3151	CACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAA	3200
merged	3151	 CACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAA	3200

gene	3201	AAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGT	3250
merged	3201	AAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGT	3250
gene	3251	ACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCT	3300
merged	3251	ACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCT	3300
gene	3301	ACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGA	3350
merged	3301	ACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGA	3350
gene	3351	GATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAA	3400
merged	3351	GATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAA	3400
gene	3401	ACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACC	3450
merged	3401	ACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACC	3450
gene	3451	GTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGA	3500
merged	3451	GTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGA	3500
gene	3501	GGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACA	3550
merged	3501	GGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACA	3550
gene	3551	GCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGC	3600
merged	3551	GCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGC	3600
gene	3601	GGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGT	3650
merged	3601	GGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGT	3650
gene	3651	GGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGA	3700
merged	3651	GGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGA	3700
gene	3701	TCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTG	3750
merged	3701	TCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTG	3750
gene	3751	GAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCC	3800
merged	3751	GAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCC	3800
gene	3801	TAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCT	3850
merged	3801	TAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCT	3850
gene	3851	CTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATAT	3900
merged	3851	CTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATAT	3900
gene	3901	GTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCC	3950
merged	3901	GTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCC	3950
gene	3951	CGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAAGCACTACC	4000
merged	3951	CGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAAGCACTACC	4000
gene	4001	TGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTG	4050
merged	4001	TGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTG	4050
gene	4051	GCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGA	4100
merged	4051	GCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGA	4100
gene	4101	TAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGA	4150
merged	4101	TAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGA	4150

gene	4151	CCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGAC	4200
merged	4151	CCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGAC	4200
gene	4201	CGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCA	4250
merged	4201	CGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCA	4250
gene	4251	CCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGG	4300
merged	4251	CCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGG	4300
gene	4301	GAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAGCTTGCGGCCGCACTC	4350
merged	4301	GAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAGCTTGCGGCCGCACTC	4350
gene	4351	GAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAA	4400
merged	4351	GAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAA	4400
gene	4401	GAGCGATTTCC	4411
merged	4401	GAGCGATTTCC	4411