

contig2-contig3
TAGGCAGTGGAGTGGGCGAGTACTGAAGCTTGGCGCCGTAATATTGGCACAGGCTATTAATTTCTCAGTAACACATCATTTGGGGTATATAATAATAAA
G S G V G S T E A W R R N I G T G Y N F S V T H H W 96

contig2-contig3
TTCAATTTAAATTGCACGAATATAATTGTCGTTATTAAATAGAACCACTTAATGAAAAATCCTCAGAACCTGTACGACAAACTTGTACACACAT
E P P N E K S S E P V T T K L V P H 192

contig2-contig3

CCGCAAAACCTAATTCCGGTATCTATGTGGGATTTAGACACTTTGGAGCAAGGCGATCTGCCAACAGTAGCTCTATGACACCCAGCTTAAAGT

Contig2-183f

contig2t

288

contig2-contig3
GAACTGTCCGCTAAACACCCCTAATGGT AGTACCAAAACGTGCTTTCAAGCAACAGATAGT AACCACGAAGCAACCCCAAGGTGTCTGCTTGT AACAAA
E T V A K H P N G S T K R A F K Q Q I V T T K N P K V S A C N K 364

contig2-contig3
 AAAAAAAAAAAGGCGGATCGACGTCGAGATCAAGCCGAAGATTAACATCGAGAGAAGGAGGAAAAAGCAAAAGCGCCAGCAATCAAGTGAAGAAAAA
 480

Contig2 - 5287

CGCCACCAACACAACTTAGATGATGAAGAAGCGT CGACCAATGGT TGAACCAAAAT AAACGGCAGCTGCAAAAT TCT AGTACGGCCGGCGGCAAGCAATT

contig2-contig3
CTAGGAATTAAGCCAATGTAATAAATTTCTGGTTTAAAGTGAATCAGTGAATTGAGGTTCTAATCTTCTTAACAAATAATCCGCAATTTCCAATCTTCT
LGNKANVKNSSGLSESVNSSSNLPNKNPHFQSSS
672

contig2-contig3
 GTTGACCACTGGTTACTCAAGCAATGCAGCTTCTTCAGAAAGTGTCATGTCCTAGCTGAATACAAAAAGCTGAAAGACGGGAACGCCAATG
 V A P W F T Q S N A A S S E G V P C L A E I Q K A E R R E R Q M 768

contig2-contig3
GAACAGCGT AAAATGCGCGCTGTTT CACAACGAGTTCGTGCT AGTGT AACTGCTGCTGTTGAAGCATTGATTCCTTGTTAATATGAACGTAACCT
E Q R K M R L F H K R V R A S A N A A V E A F D S L L K W N V P

Contig3-701f

GT AAGGAGCCTCCCGTTAAAGCTTTTGGCGAAT ACAAGCAGAAGAAGCTAAGTGTTTAGCCAATGAAAAAATATGTTGAAGCAGCGTCGCAAT
V R D V P V K S F A E I Q A E E A K C L A N E K N M L K Q R R N

contig2-contig3
1050
AAACAGGAACGACGACACGACACTGTTACGAGTGCACACAAGTAAATACGGGTGGAGGGCCACCAATAAATATTTCGGGTGTATGTTCAAGCACAATA
K Q E Q Q H T T T V T S A T S N T G G H N N I S A V C S S T K

Contig3-156f

Contig2-Contig3

A W G S T N T T V F W D K S I K F S A V V A A N N N S G G K *

1152

contig2-contig3
AACCAATCTTCAACCGGACAACAAAACCTTTCACCAGTCTGGCTATGCCCGGTAAAGCAACCATTTGCAGTTAGTGGGCTATCACAACCCAGCAGCTA
Contig3-156t
contig3f

config2-config3 AAT ACCGTACGATAATAGAGATAGATGTAGATAAATAATTGAGTAATGCACCGCGATCTTAGGTCTATTGGCCCTCTCCTAACTCACAGGACT 134

contig2-contig3
CACTTAGCCCCAGCATATTGATGAAGTCTAATATCTGCTGGGTACTAGCGAGGCGATGTGATCCCTATCCGAANCATGTGATCCAAGGGCCTTCG1441

contig2-contigs3 ACCAGCGCCTGCAGACTGCATGCAGT CGACTAGCAGGTGCT CCGGGGTTTCAGGCT CCCTGT CGCAAAACGACAGGTATCGCAATGATGAT AGG 1536

contig2-contig3
CCCATGTTAGATAGATGSCCTTTTCATTTGCACTGGGCGGTGTAAATGCGACCAAGAAAGCCTAAGTTTATCCCTTGGAGGTT
Contig3-701f
1615