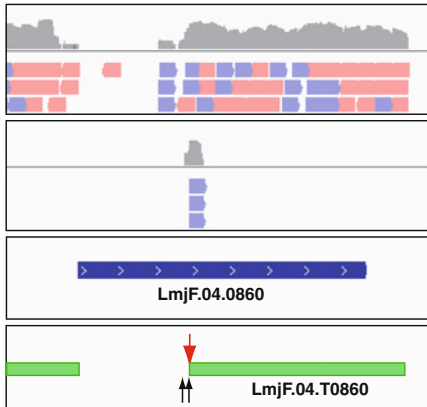


A



B

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1  ATGAGGCGGT  GCGTCATGGC  CAAGGGCGAG  GATCCCGCTC  ATGTGGCGGG  CTGGGACGAC
   M R R C   V M A   K G E   D P A H   V A G   W D D
61  CGTCAGGACG  CGGTCGAGTG  GTGGTGGACG  GAGGCAAACG  ACTCCAGGGG  ACGCCAACGA
   R Q D A   V E W   W W T   E A N D   S R G   R Q R
121 TTGGAAGCTG  CTGCTGCTGT  GGGCGGCGCG  GCGGCGTCTC  CAACTGTGGG  TCTCCCTCTT
   L E A A   A A V   A A A   A A S S   T V G   L P L
181 TTTCCGCGCT  TCTCACCAGG  CCGACGACGA  CGACGCCGCC  CGCCCCCCCC  CCCCCCTCCT
   F P R F   S P G   R R R   R R R P   P A P   P P P
241 CCTCTCCTC  TGTTCTCTAG  CCGCCACCTC  CACAGCATGC  CGTGTTATG  GTGCACATGC
   P P P L   F L S   R H L   H S M P   W L W   C T C
301 GTCAAGATGC  AGATGTACTA  CACGCCTACT  GCTCTCACGT  GTCCTCTCTC  CAACTCTCTC
   V K M Q   M Y Y   T P T   A L T C   P L S   N S L
361 GCTGCGCATG  TGGGCCACAT  CATCGTTGGC  GTGGCGGCGC  TGCTGCCTTA  TTTCTATGCTC
   A A H V   G H I   I V G   V A A L   L P Y   S M L
421 CTCTTTCTCA  CTGTGATGTG  CAACCCGCGC  AAACATGAGC  CCGTGTCTCG  AGCACAGCGG
   L F L T   V M C   N P R   K H E P   V L R   A Q R
481 ATACGTTGGT  TGACTTTCCA  CTCGCTCATG  TTCCGACTTC  TTCGATGCAT  CACCGCCTCG
   I R W L   T F H   S L   F R L L   R C I   T A S
541 CCGGCTGTGG  CAGCAAGCGT  CGCAGTCGCA  GCAGCCCAA  CACCGACCAG  CCTGCGCCCT
   P A V A   C R G   V H L   A P S V   L A A   S A P
601 GCTGCGGTGT  GCCGCCGTGG  TGTTCACCTA  GCACCGTCCG  TACTAGCCGC  GTCGGCACCA
   A A V C   R R G   V H L   A P S V   L A A   S A P
661 CCGCCGCGCG  CGCAGCAGCG  ACTTCCGCCG  CAGTACCGGC  AAGCACCGCC  AAGCACCGCC
   P P P P   Q Q Q   Q Q P   T S A A   V P A   S T A
721 ACGTCGACGA  CGACCATCGC  GGCTGGTCCC  TACCGCCGCG  TCGGGAATGT  GTTCATCGTT
   T S T T   T I A   A G P   Y R R V   G N V   F I V
781 ACGTGTCATG  ACCACCCCTT  CAAGTTCTCG  TGGGAGGTGA  ACCGCATGCT  GCGCGAGCTC
   T C I D   H P F   K F S   W E V N   R M L   R E L
841 CGCTGGAGT  TCATGGGGCA  GACTACCGTC  GTGCCGGACA  TCCCGCCAGT  GCGAAAGCGA
   R L E F   M G Q   T T V   V P D I   P P V   R K R
901 ATTTGGCGGG  TGCGCCACGT  TGTCCGCGTC  GACCAGCTCG  ACCTCGACGA  AGCGAAGGCG
   I W R V   R H V   V R V   D Q L D   L D E   A K A
961 CTCATCGGGA  TTCCGGAGCA  CATCTCATT  CGTGATTGG  CGGGGCAGAT  CCCACCAACG
   L I G I   P E H   I S F   R D L A   G Q I   P P T
1021 TTTGGCCGGG  GCGGCTCCGT  CGCCAACCCG  CACATGCGCA  GCAAGATGAA  CTTTATGCGA
   F G R G   G S V   A N P   H M R S   K M N   F M R
1081 CTGCGGCGCA  TGCGGCTGCG  TGACGTGATC  CACCGCGATC  AGCTTGAGAA  ACGGCTCCTG
   L R R M   R L R   D V M   H R D Q   L E K   R L L
1141 GAAGAAAGGC  ATCATGCACT  GCAGCAGCAG  CAGCAGCAGC  AGCAGGGTGG  TGGCGAAGCA
   E E R H   H A L   Q Q Q   Q Q Q   Q G G   G E A
1201 GCAGCAGCAG  CAGCAGCGAC  GACTGCGTAA
   A A A A   A A T   T A *

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C

LmjF.04.T0860 MFRLRLRCITASPAVAASVAVAAQTPTSLRPAAVCRRGVHLAPSVLAASAPPPPPQQQQQPT
Tb927.9.8290 MMRRMWVPTFS-----AQ-----QQHLEHAMGLKMLTYASTPSGSG-V-T

LmjF.04.T0860 SAAVPASTATSTTT-IAAGPYRRVGNVFIIVTCHDPFKFSWEVNRMLRELRLFEFMGQTTVVV
Tb927.9.8290 SAASNEEMNLHDAAIAPGPYRRVGNVFIIVHCDDHPFKHSWEVNRMLRELRLFEFKGQTTIVP

LmjF.04.T0860 DIPPVRKRIWRVRHVVRVDQLDLDEAKALIGIPEHISFRDLAQIPPTFGRGGSVANPHMRS
Tb927.9.8290 DIPQVRKRIWRVRHIVKVDVLDLDEAKALIGVPEHISFTDLASQLPPSFGRVKAVPSPVIRS

LmjF.04.T0860 KMNFMLRLRRMLRDVMHRDQLEKRLLEERHHAQQQQQQQGGGEEAAAAAATTA
Tb927.9.8290 KMNFMLRLRRMLRDVLRDALELRLLLEKRSAMKNAEQQKHAQKDERTDNKEGEKC 218