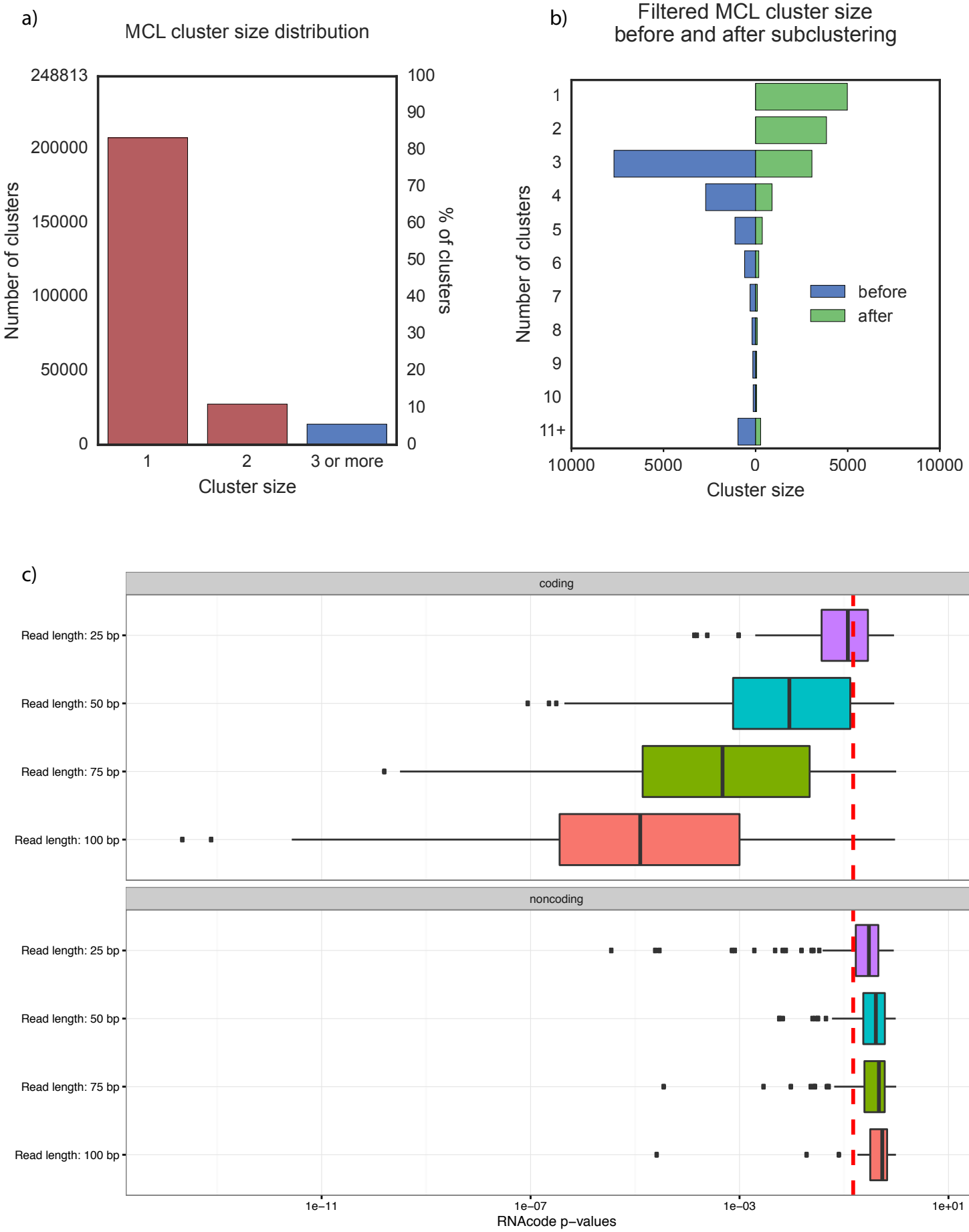
Discovering viral genomes in human metagenomic data by predicting unknown protein families

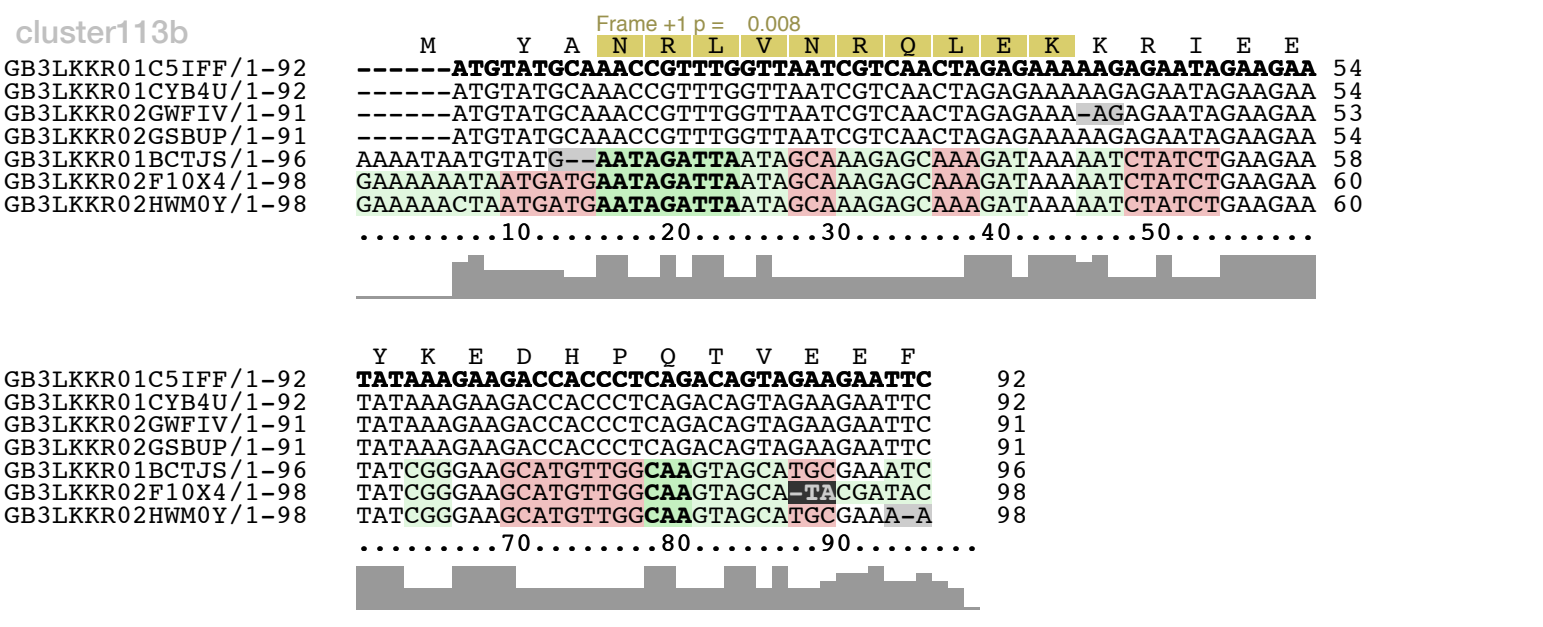
Mauricio Barrientos-Somarribas, David N. Messina, Christian Pou, Fredrik Lysholm, Annelie Bjerkner, Tobias Allander, Björn Andersson and Erik L.L. Sonnhammer

Supplementary Material

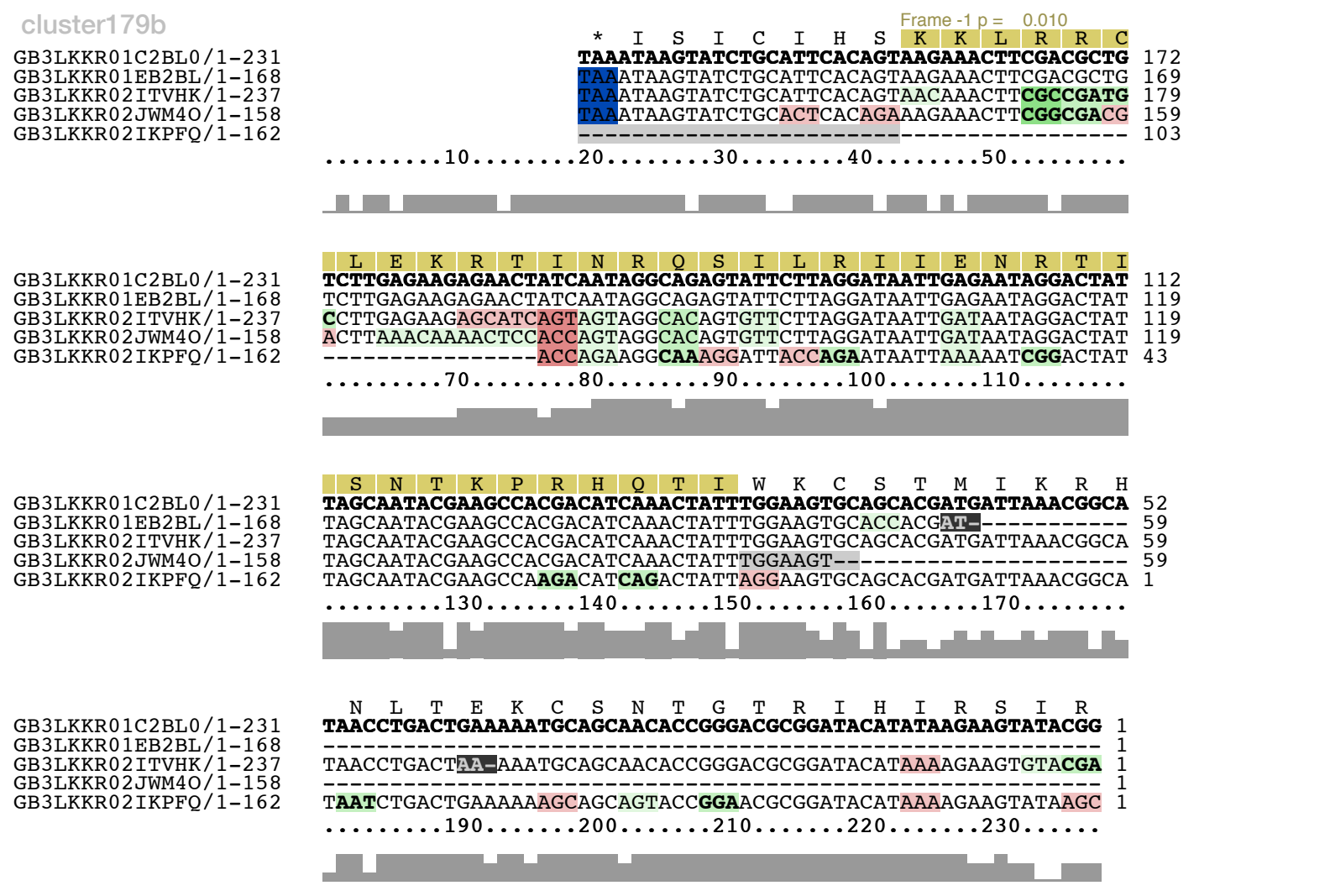
Supplementary Figure S1. Detection of high-confidence protein families by clustering and RNAcode calibration. a) Distribution of cluster sizes from MCL. The size distribution was split into three categories: singletons, clusters of size two, and clusters of size 3 and above (candidate for multiple sequence alignment) b) Comparison of cluster size distribution for the filtered MCL clusters (3 < size < 250) before and after subclustering. Cluster size decreases post-subclustering, indicating that the original clusters contained many sequences with low diversity c) Calibration of RNAcode for short sequences. The plot describes the distribution of RNAcode's p-values for simulated alignments of varying lengths from coding and non-coding regions of the *Methanococcus jannaschii* genome. RNAcode separates coding from non-coding sequences up to a length of 50bp with a p-value of 0.15.

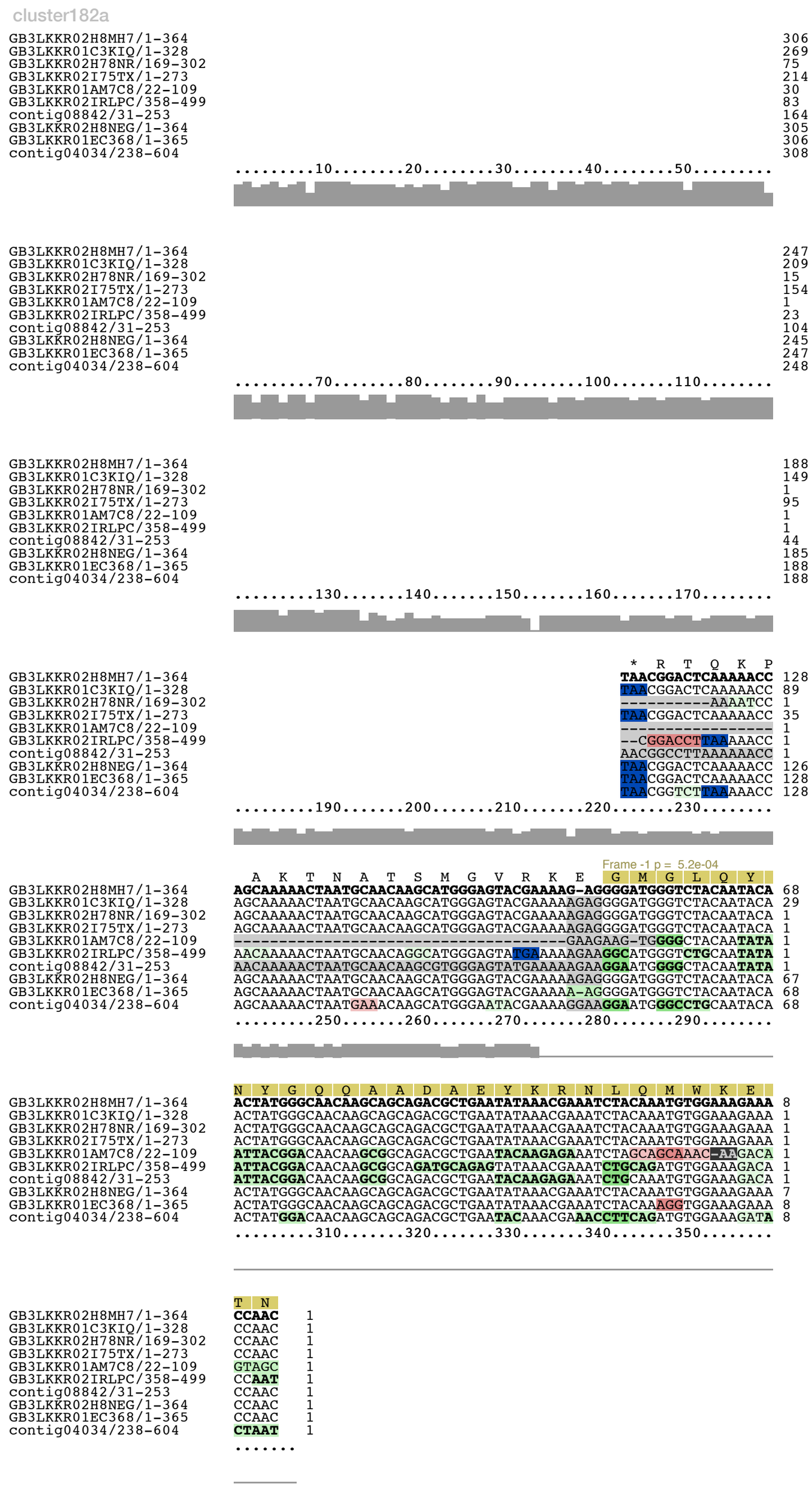

a)
MCL cluster size distribution
248813
200000
150000
100000
50000
0
Number of clusters
100
90
80
70
60
50
40
30
20
10
0
% of clusters
1
2
3 or more
Cluster size
b)
Filtered MCL cluster size
before and after subclustering
Number of clusters
1
2
3
4
5
6
7
8
9
10
11+
before
after
10000
5000
0
5000
10000
Cluster size
c)
coding
Read length: 25 bp
Read length: 50 bp
Read length: 75 bp
Read length: 100 bp
noncoding
Read length: 25 bp
Read length: 50 bp
Read length: 75 bp
Read length: 100 bp
1e−11
1e−07
1e−03
1e+01
RNAcode p−values

Supplementary Figure S2. RNAcode output for the 32 predicted protein families.

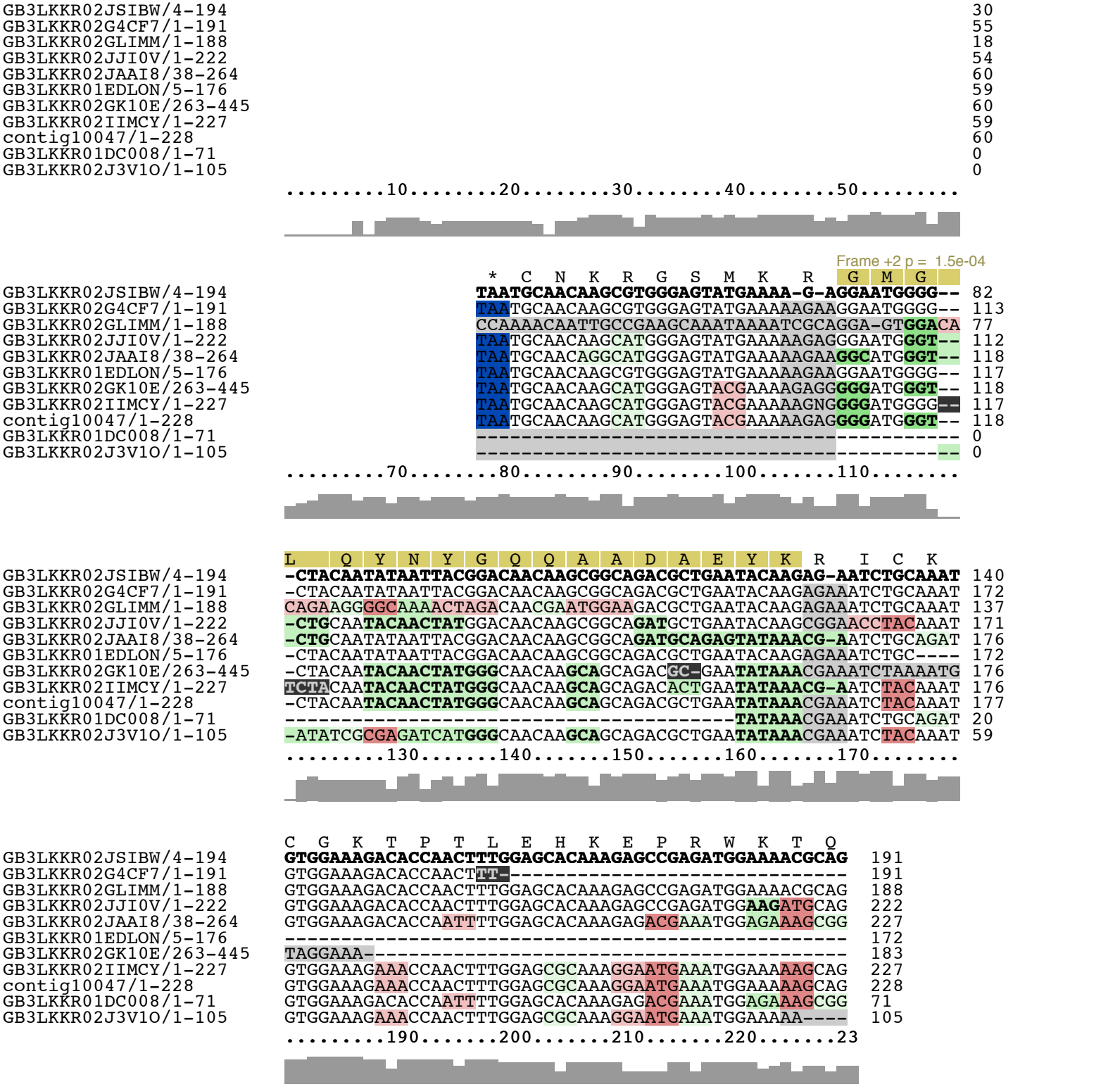

cluster113b
Frame +1 p = 0.008
M Y A N R L V N R Q L E K K R I E E
GB3LKKR01C5IFF/1-92 ------ATGTATGCAAACCGTTTGGTTAATCGTCAACTAGAGAAAAAGAGAATAGAAGAA 54
GB3LKKR01CYB4U/1-92 ------ATGTATGCAAACCGTTTGGTTAATCGTCAACTAGAGAAAAAGAGAATAGAAGAA 54
GB3LKKR02GWFIV/1-91 ------ATGTATGCAAACCGTTTGGTTAATCGTCAACTAGAGAAA-AGAGAATAGAAGAA 53
GB3LKKR02GSBUP/1-91 ------ATGTATGCAAACCGTTTGGTTAATCGTCAACTAGAGAAAAAGAGAATAGAAGAA 54
GB3LKKR01BCTJS/1-96 AAAATAATGTATG--AATAGATTAATAGCAAAGAGCAAAGATAAAAATCTATCTGAAGAA 58
GB3LKKR02F10X4/1-98 GAAAAAATAATGATGAATAGATTAATAGCAAAGAGCAAAGATAAAAATCTATCTGAAGAA 60
GB3LKKR02HWM0Y/1-98 GAAAAACTAATGATGAATAGATTAATAGCAAAGAGCAAAGATAAAAATCTATCTGAAGAA 60
.....10.....20.....30.....40.....50.....
Y K E D H P Q T V E E F
GB3LKKR01C5IFF/1-92 TATAAAGAAGACCACCCTCAGACAGTAGAAGAATTC 92
GB3LKKR01CYB4U/1-92 TATAAAGAAGACCACCCTCAGACAGTAGAAGAATTC 92
GB3LKKR02GWFIV/1-91 TATAAAGAAGACCACCCTCAGACAGTAGAAGAATTC 91
GB3LKKR02GSBUP/1-91 TATAAAGAAGACCACCCTCAGACAGTAGAAGAATTC 91
GB3LKKR01BCTJS/1-96 TATCGGGAAGCATGTTGGCAAGTAGCATGCGAAATC 96
GB3LKKR02F10X4/1-98 TATCGGGAAGCATGTTGGCAAGTAGCA-TAACGATAC 98
GB3LKKR02HWM0Y/1-98 TATCGGGAAGCATGTTGGCAAGTAGCATGCGAAA-A 98
.....70.....80.....90.....

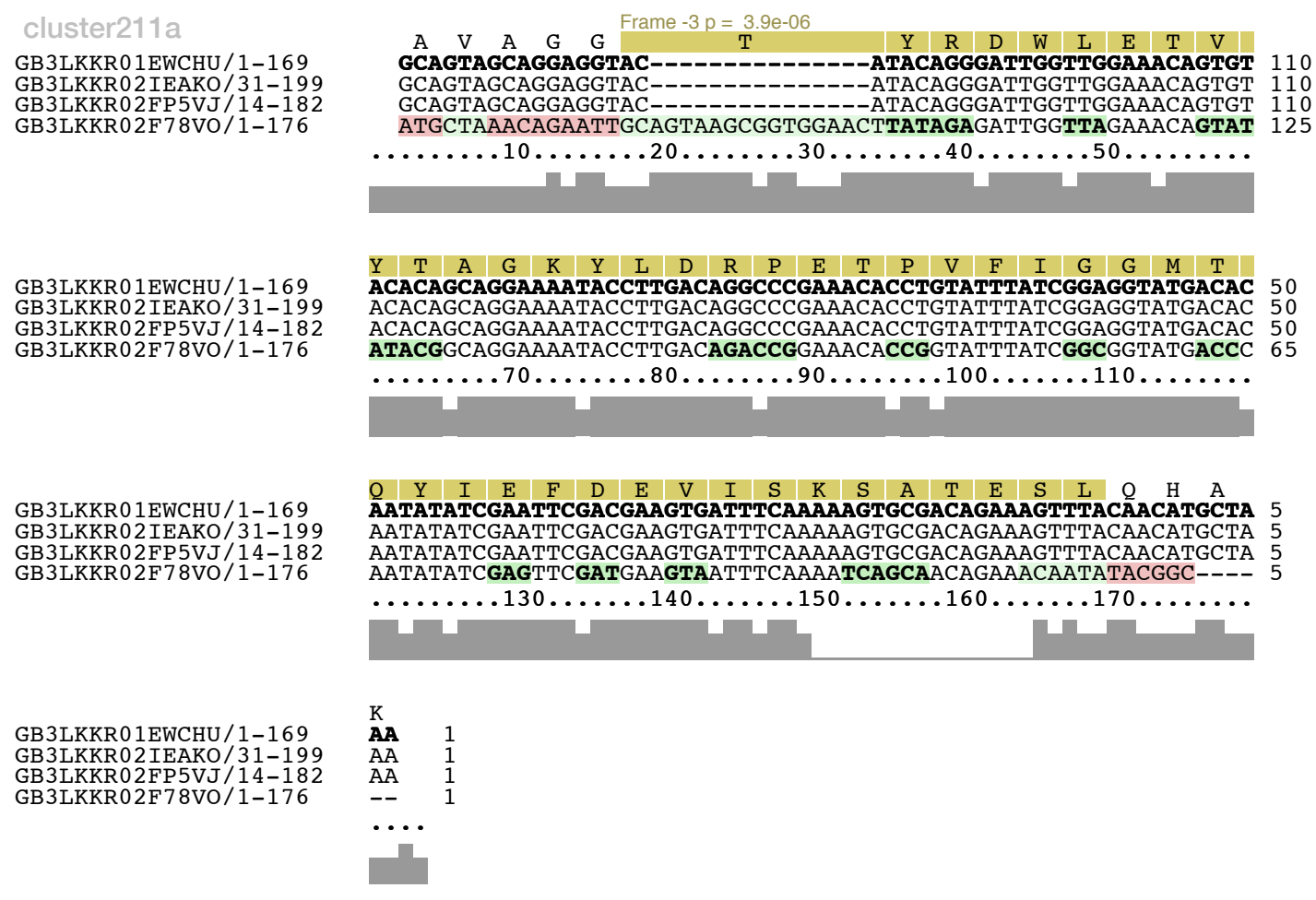
cluster179a
GB3LKKR01D9539/1-314
GB3LKKR01B7VFA/1-313
GB3LKKR01A1AS6/1-174
GB3LKKR01DZB8X/1-177
GB3LKKR02JP9RY/1-314
Frame -2 p = 0.005

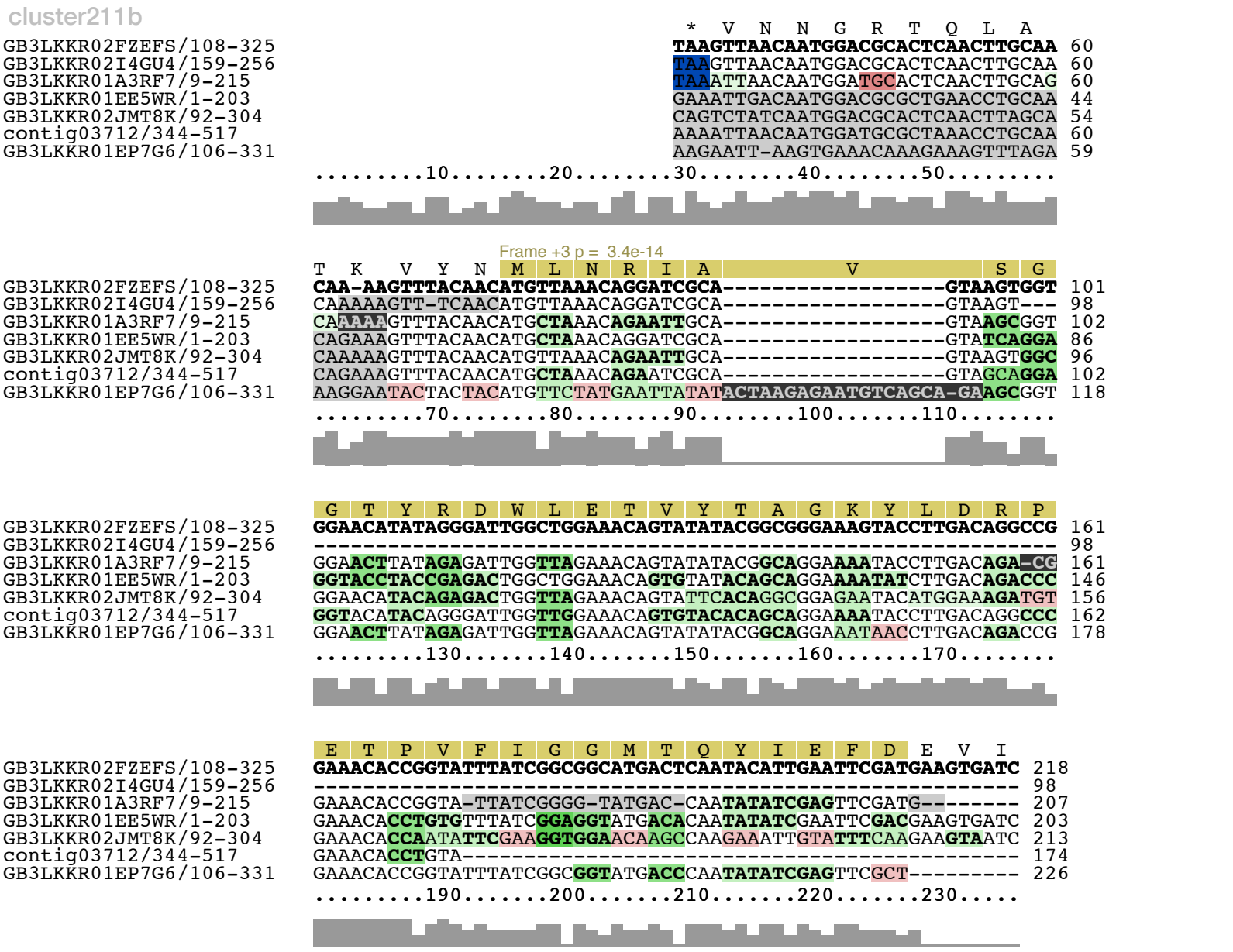

cluster179b
Frame -1 p = 0.010
* I S I C I H S K K L R R C
GB3LKKR01C2BL0/1-231 TAAATAAGTATCTGCATTCACAGTAAGAAACTTCGACGCTG 172
GB3LKKR01EB2BL/1-168 TAAATAAGTATCTGCATTCACAGTAAGAAACTTCGACGCTG 169
GB3LKKR02ITVHK/1-237 TAAATAAGTATCTGCATTCACAGTAACAAACTTCGCCGATG 179
GB3LKKR02JWM4O/1-158 TAAATAAGTATCTGCACTCACAGAAAGAAACTTCGGCGACG 159
GB3LKKR02IKPFQ/1-162 ---------- 103
.....10.....20.....30.....40.....50.....
L E K R T I N R Q S I L R I I E N R T I
GB3LKKR01C2BL0/1-231 TCTTGAGAAGAGAACTATCAATAGGCAGAGTATTCTTAGGATAATTGAGAATAGGACTAT 112
GB3LKKR01EB2BL/1-168 TCTTGAGAAGAGAACTATCAATAGGCAGAGTATTCTTAGGATAATTGAGAATAGGACTAT 119
GB3LKKR02ITVHK/1-237 CCTTGAGAAGAGCATCAGTAGTAGGCACAGTGTTCTTAGGATAATTGATAATAGGACTAT 119
GB3LKKR02JWM4O/1-158 ACTTAAACAAAACTCCACCAGTAGGCACAGTGTTCTTAGGATAATTGATAATAGGACTAT 119
GB3LKKR02IKPFQ/1-162 ----------ACCAGAAGGCAAAGGATTACCAGAATAATTAAAAATCGGACTAT 43
.....70.....80.....90.....100.....110.....
S N T K P R H Q T I W K C S T M I K R H
GB3LKKR01C2BL0/1-231 TAGCAATACGAAGCCACGACATCAAACTATTTGGAAGTGCAGCACGATGATTAAACGGCA 52
GB3LKKR01EB2BL/1-168 TAGCAATACGAAGCCACGACATCAAACTATTTGGAAGTGCACCACGATG---------- 59
GB3LKKR02ITVHK/1-237 TAGCAATACGAAGCCACGACATCAAACTATTTGGAAGTGCAGCACGATGATTAAACGGCA 59
GB3LKKR02JWM4O/1-158 TAGCAATACGAAGCCACGACATCAAACTATTTGGAAGT---------- 59
GB3LKKR02IKPFQ/1-162 TAGCAATACGAAGCCAAGACATCAGACTATTAGGAAGTGCAGCACGATGATTAAACGGCA 1
.....130.....140.....150.....160.....170.....
N L T E K C S N T G T R I H I R S I R
GB3LKKR01C2BL0/1-231 TAACCTGACTGAAAAATGCAGCAACACCGGGACGCGGATACATATAAGAAGTATACGG 1
GB3LKKR01EB2BL/1-168 ---------- 1
GB3LKKR02ITVHK/1-237 TAACCTGACTAA-AAATGCAGCAACACCGGGACGCGGATACATAAAAGAAGTGTACGA 1
GB3LKKR02JWM4O/1-158 ---------- 1
GB3LKKR02IKPFQ/1-162 TAATCTGACTGAAAAAAGCAGCAGTACCGGAACGCGGATACATAAAAGAAGTATAAGC 1
.....190.....200.....210.....220.....230.....

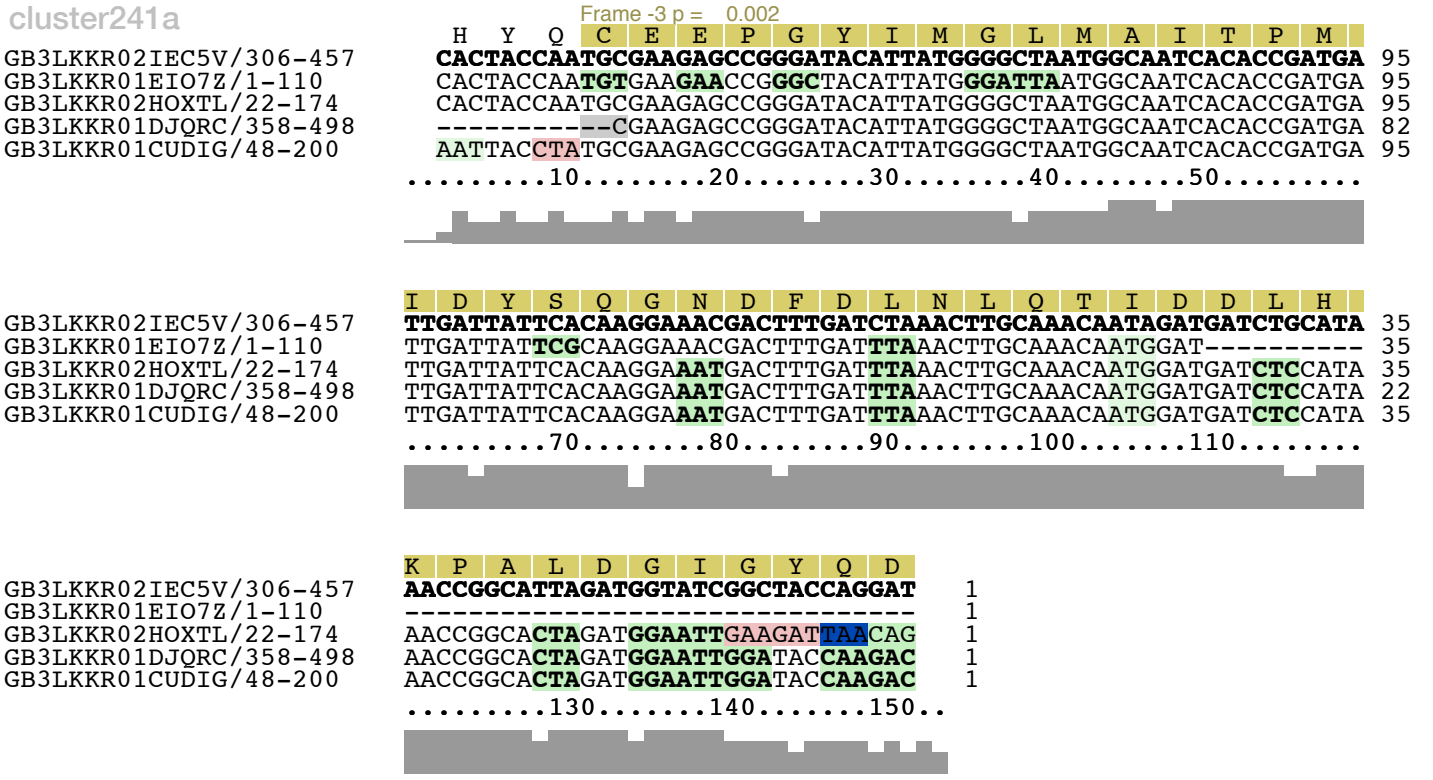

cluster182a
GB3LKKR02H8MH7/1-364
GB3LKKR01C3KIQ/1-328
GB3LKKR02H78NR/169-302
GB3LKKR02I75TX/1-273
GB3LKKR01AM7C8/22-109
GB3LKKR02IRLPC/358-499
contig08842/31-253
GB3LKKR02H8NEG/1-364
GB3LKKR01EC368/1-365
contig04034/238-604
Frame -1 p = 5.2e-04

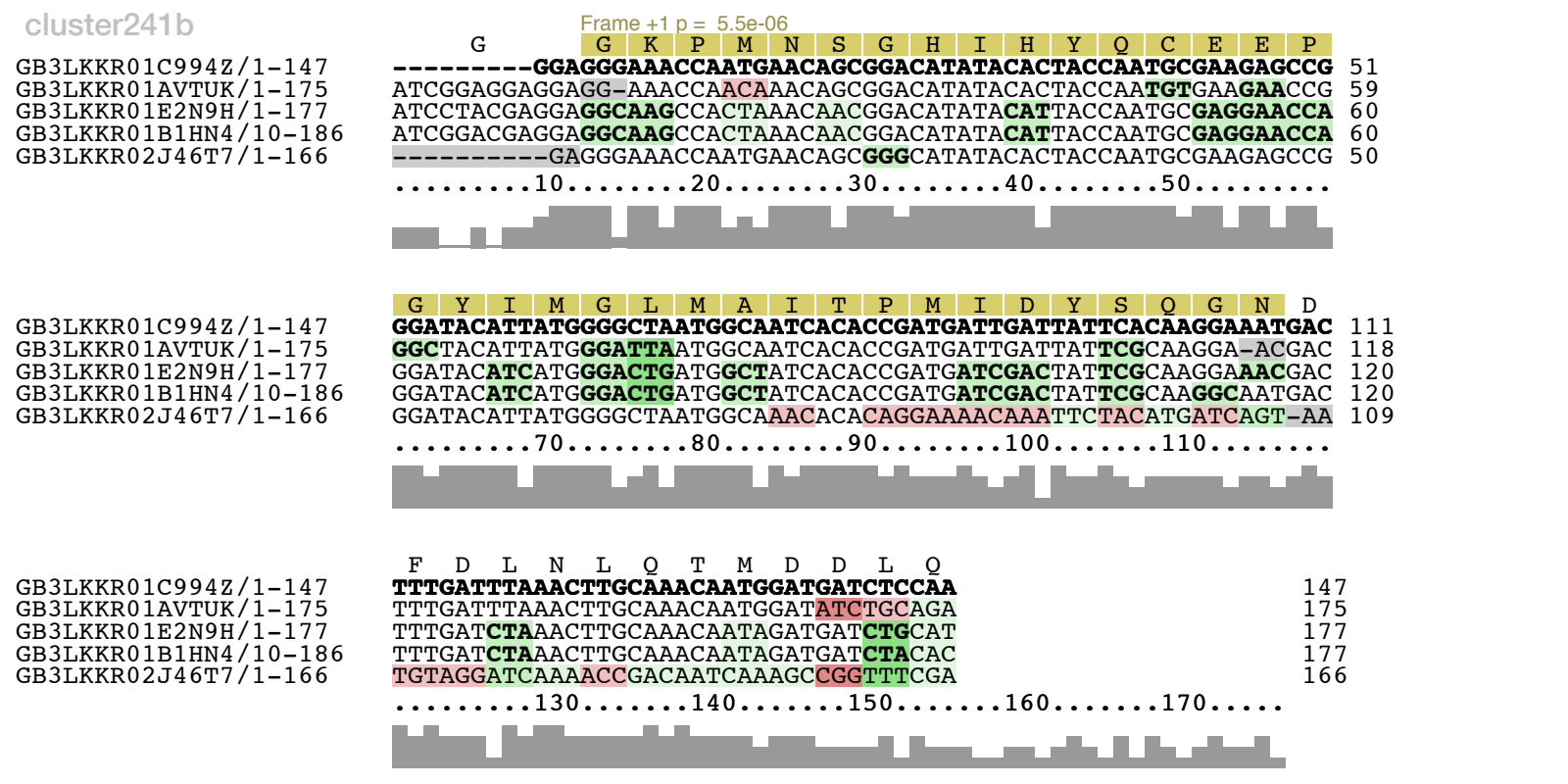
cluster182b

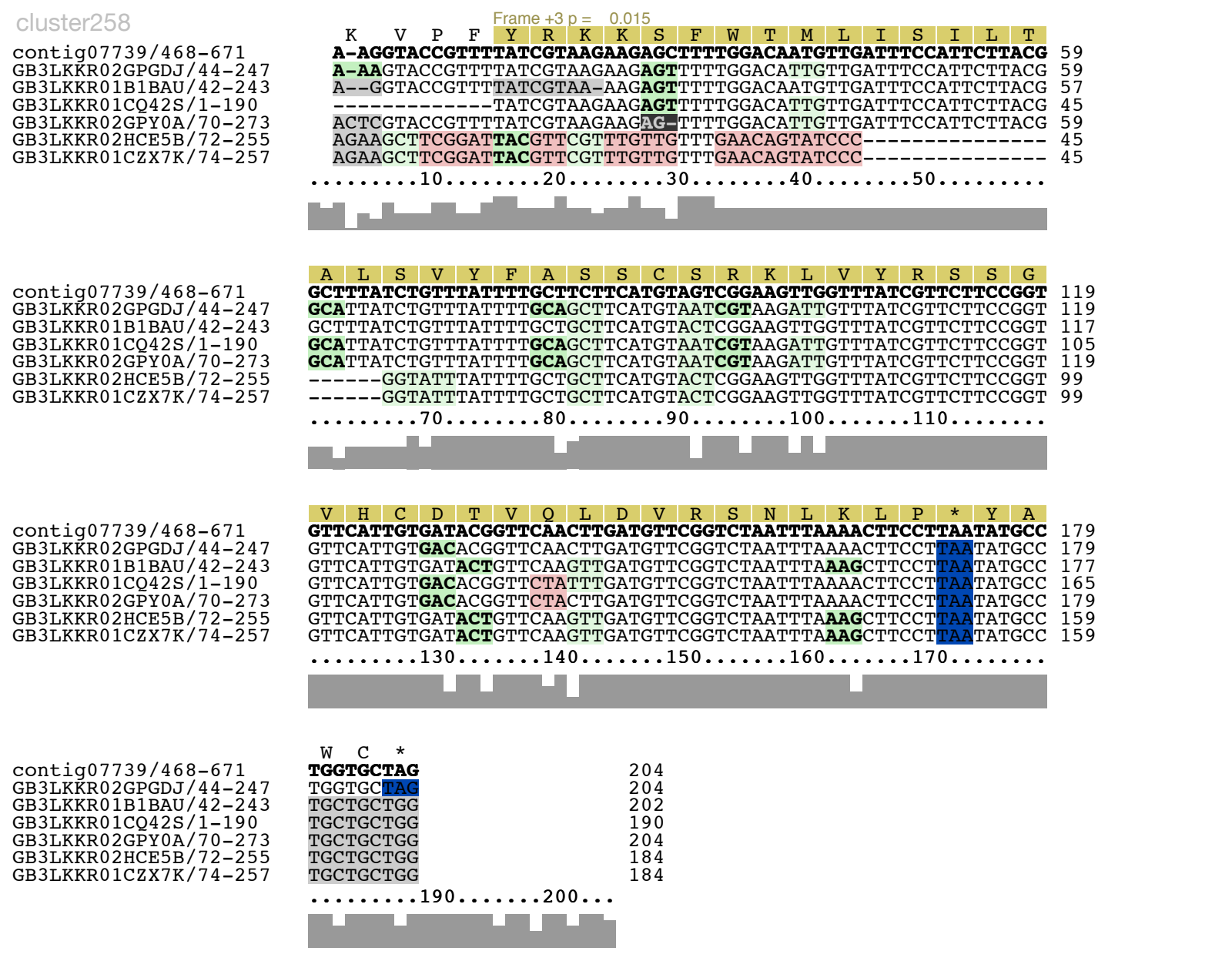


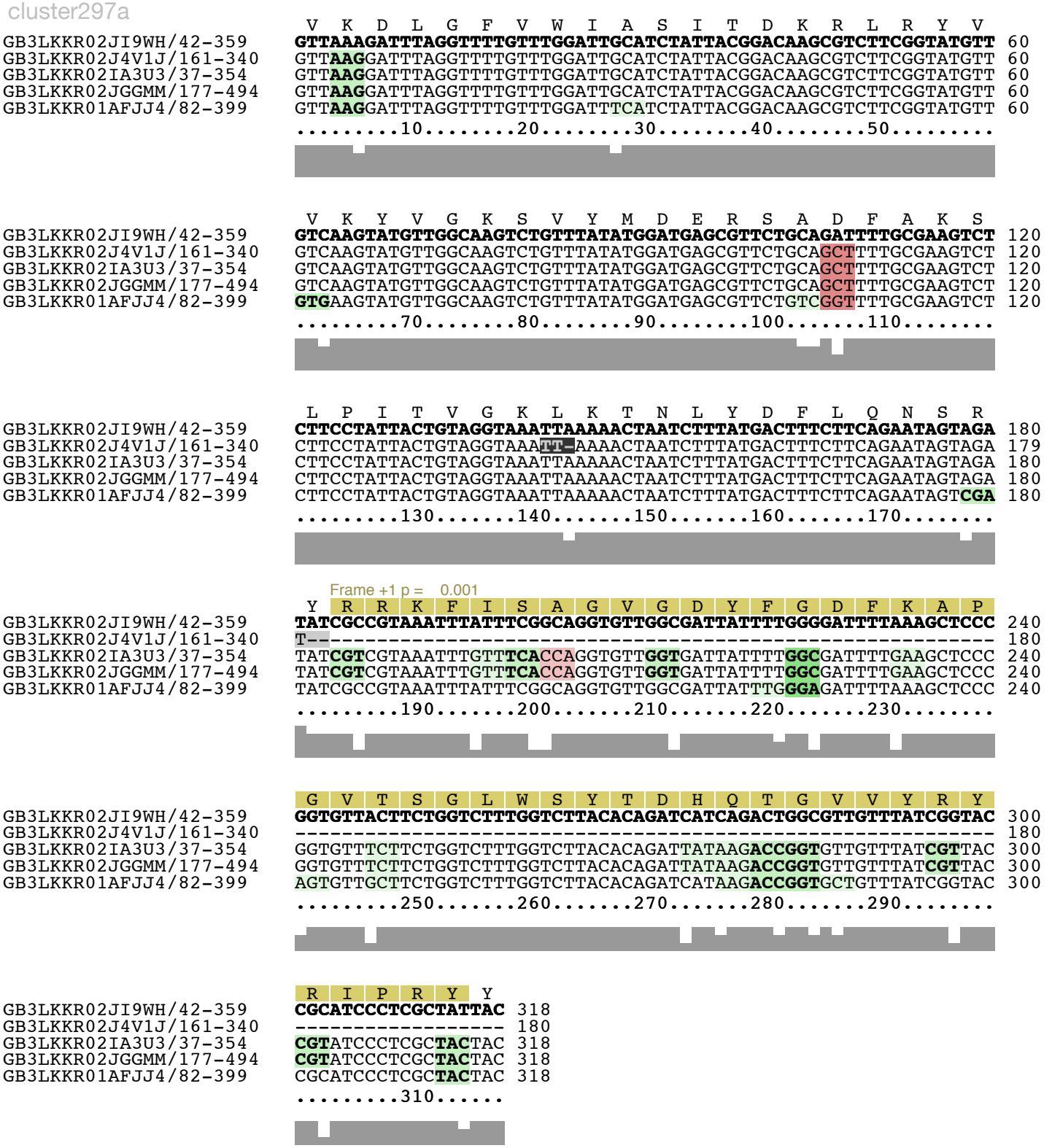

cluster211a
Frame -3 p = 3.9e-06
A V A G G T Y R D W L E T V
GB3LKKR01EWCHU/1-169 GCAGTAGCAGGAGGTAC----------ATACAGGGATTGGTTGGAAACAGTGT 110
GB3LKKR02IEAKO/31-199 GCAGTAGCAGGAGGTAC----------ATACAGGGATTGGTTGGAAACAGTGT 110
GB3LKKR02FP5VJ/14-182 GCAGTAGCAGGAGGTAC----------ATACAGGGATTGGTTGGAAACAGTGT 110
GB3LKKR02F78VO/1-176 ATGCTAAACAGAATTGCAGTAAGCGGTGGAACTTATAGAGATTGGTTAGAAACAGTAT 125
.....10.....20.....30.....40.....50.....
Y T A G K Y L D R P E T P V F I G G M T
GB3LKKR01EWCHU/1-169 ACACAGCAGGAAAATACCTTGACAGGCCCGAAACACCTGTATTTATCGGAGGTATGACAC 50
GB3LKKR02IEAKO/31-199 ACACAGCAGGAAAATACCTTGACAGGCCCGAAACACCTGTATTTATCGGAGGTATGACAC 50
GB3LKKR02FP5VJ/14-182 ACACAGCAGGAAAATACCTTGACAGGCCCGAAACACCTGTATTTATCGGAGGTATGACAC 50
GB3LKKR02F78VO/1-176 ATACGGCAGGAAAATACCTTGACAGACCGGAAACACCGGTATTTATCGGCGGTATGACCC 65
.....70.....80.....90.....100.....110.....
Q Y I E F D E V I S K S A T E S L Q H A
GB3LKKR01EWCHU/1-169 AATATATCGAATTCGACGAAGTGATTTCAAAAAGTGCGACAGAAAGTTTACAACATGCTA 5
GB3LKKR02IEAKO/31-199 AATATATCGAATTCGACGAAGTGATTTCAAAAAGTGCGACAGAAAGTTTACAACATGCTA 5
GB3LKKR02FP5VJ/14-182 AATATATCGAATTCGACGAAGTGATTTCAAAAAGTGCGACAGAAAGTTTACAACATGCTA 5
GB3LKKR02F78VO/1-176 AATATATCGAGTTCGATGAAGTAATTTCAAAATCAGCAACAGAAACAATATACGGC---- 5
.....130.....140.....150.....160.....170.....
K
GB3LKKR01EWCHU/1-169 AA 1
GB3LKKR02IEAKO/31-199 AA 1
GB3LKKR02FP5VJ/14-182 AA 1
GB3LKKR02F78VO/1-176 -- 1
....

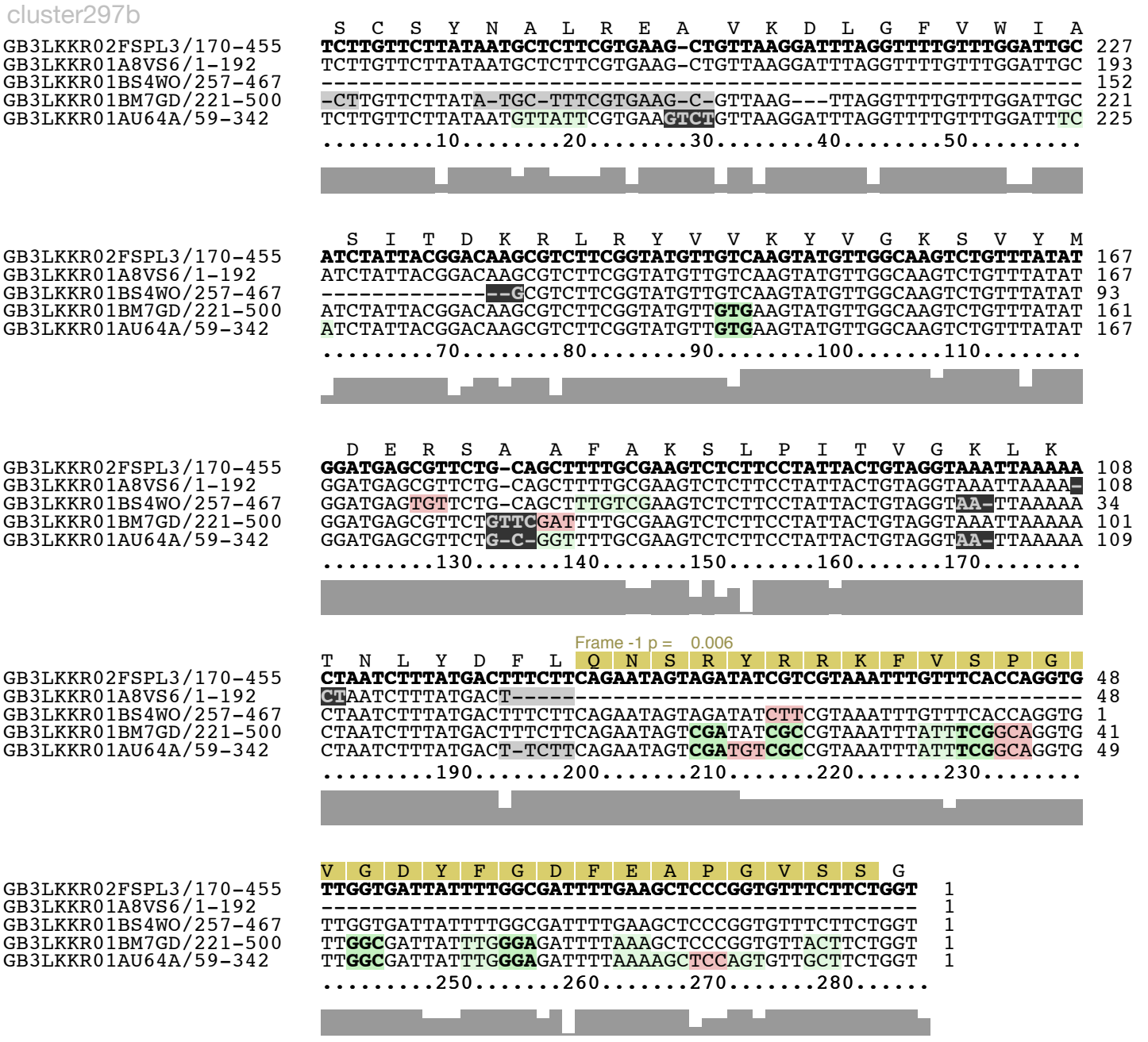

cluster211b
* V N N G R T Q L A
GB3LKKR02FZEFS/108-325 TAAGTTAACAATGGACGCACTCAACTTGCAA 60
GB3LKKR02I4GU4/159-256 TAAGTTAACAATGGACGCACTCAACTTGCAA 60
GB3LKKR01A3RF7/9-215 TAAATTAACAATGGATGCACTCAACTTGCAG 60
GB3LKKR01EE5WR/1-203 GAAATTGACAATGGACGCGCTGAACCTGCAA 44
GB3LKKR02JMT8K/92-304 CAGTCTATCAATGGACGCACTCAACTTAGCA 54
contig03712/344-517 AAAATTAACAATGGATGCGCTAAACCTGCAA 60
GB3LKKR01EP7G6/106-331 AAGAATT-AAGTGAAACAAAGAAAGTTTAGA 59
.....10.....20.....30.....40.....50.....
Frame +3 p = 3.4e-14
T K V Y N M L N R I A V S G
GB3LKKR02FZEFS/108-325 CAA-AAGTTTACAACATGTTAAACAGGATCGCA----------GTAAGTGGT 101
GB3LKKR02I4GU4/159-256 CAAAAAGTT-TCAACATGTTAAACAGGATCGCA----------GTAAGT--- 98
GB3LKKR01A3RF7/9-215 CAAAAAGTTTACAACATGCTAAACAGAATTGCA----------GTAAGCGGT 102
GB3LKKR01EE5WR/1-203 CAGAAAGTTTACAACATGCTAAACAGGATCGCA----------GTATCAGGA 86
GB3LKKR02JMT8K/92-304 CAAAAAGTTTACAACATGTTAAACAGAATTGCA----------GTAAGTGGC 96
contig03712/344-517 CAGAAAGTTTACAACATGCTAAACAGAATCGCA----------GTAGCAGGA 102
GB3LKKR01EP7G6/106-331 AAGGAATACTACTACATGTTCTATGAATTATATACTAAGAGAATGTCAGCA-GAAGCGGT 118
.....70.....80.....90.....100.....110.....
G T Y R D W L E T V Y T A G K Y L D R P
GB3LKKR02FZEFS/108-325 GGAACATATAGGGATTGGCTGGAAACAGTATATACGGCGGGAAAGTACCTTGACAGGCCG 161
GB3LKKR02I4GU4/159-256 ---------- 98
GB3LKKR01A3RF7/9-215 GGAACTTATAGAGATTGGTTAGAAACAGTATATACGGCAGGAAAATACCTTGACAGA-CG 161
GB3LKKR01EE5WR/1-203 GGTACCTACCGAGACTGGCTGGAAACAGTGTATACAGCAGGAAAATATCTTGACAGACCC 146
GB3LKKR02JMT8K/92-304 GGAACATACAGAGACTGGTTAGAAACAGTATTCACAGGCGGAGAATACATGGAAAGATGT 156
contig03712/344-517 GGTACATACAGGGATTGGTTGGAAACAGTGTACACAGCAGGAAAATACCTTGACAGGCCC 162
GB3LKKR01EP7G6/106-331 GGAACTTATAGAGATTGGTTAGAAACAGTATATACGGCAGGAAATAACCTTGACAGACCG 178
.....130.....140.....150.....160.....170.....
E T P V F I G G M T Q Y I E F D E V I
GB3LKKR02FZEFS/108-325 GAAACACCGGTATTTATCGGCGGCATGACTCAATACATTGAATTCGATGAAGTGATC 218
GB3LKKR02I4GU4/159-256 ---------- 98
GB3LKKR01A3RF7/9-215 GAAACACCGGTA-TTATCGGGG-TATGAC-CAATATATCGAGTTCGATG--------- 207
GB3LKKR01EE5WR/1-203 GAAACACCTGTGTTTATCGGAGGTATGACACAATATATCGAATTCGACGAAGTGATC 203
GB3LKKR02JMT8K/92-304 GAAACACCAATATTCGAAGGTGGAACAAGCCAAGAAATTGTATTTCAAGAAGTAATC 213
contig03712/344-517 GAAACACCTGTA---------- 174
GB3LKKR01EP7G6/106-331 GAAACACCGGTATTTATCGGCGGTATGACCCAATATATCGAGTTCGCT--------- 226
.....190.....200.....210.....220.....230.....

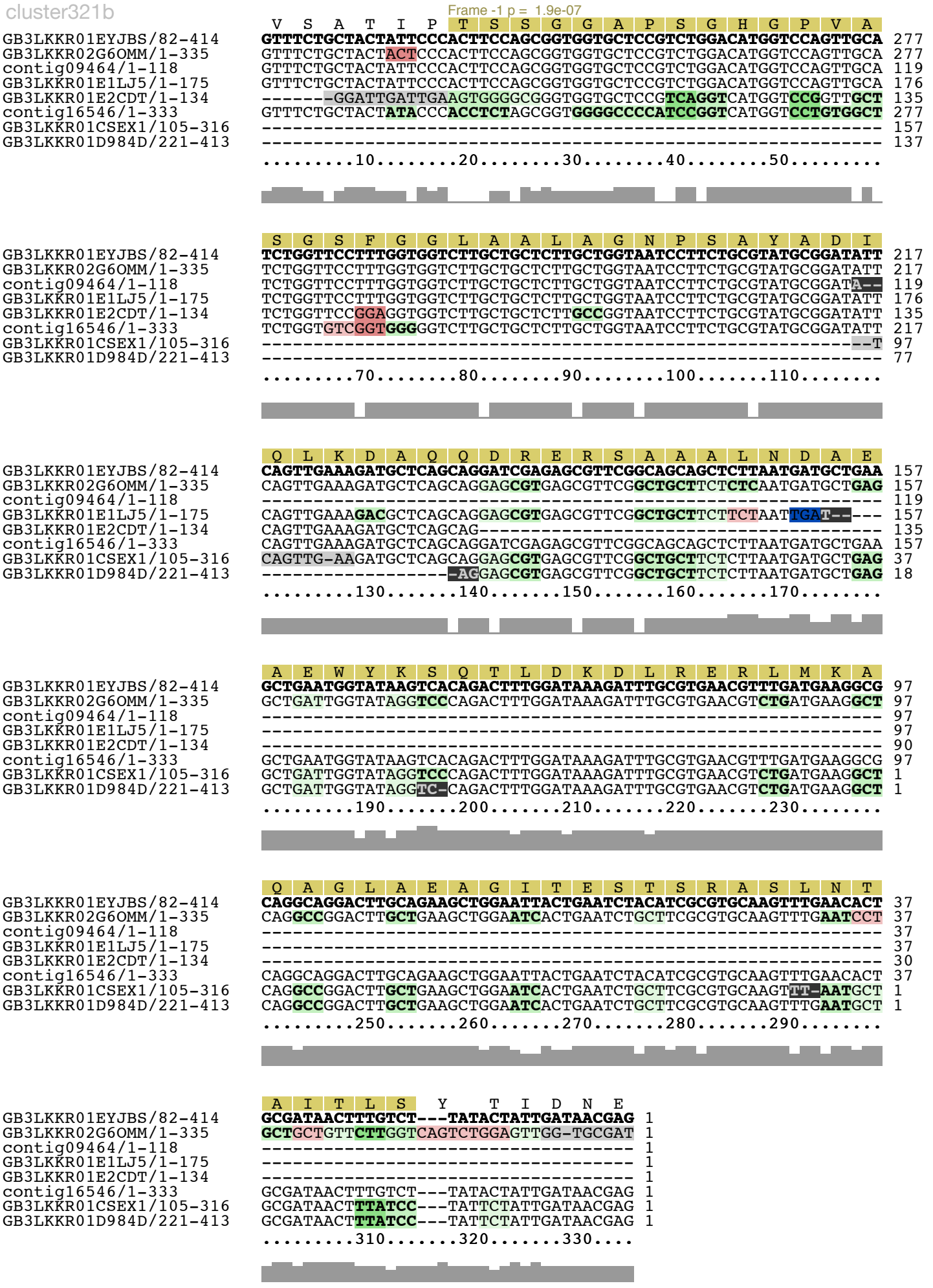

cluster241a
Frame -3 p = 0.002
H Y Q C E E P G Y I M G L M A I T P M
GB3LKKR02IEC5V/306-457 CACTACCAATGCGAAGAGCCGGGATACATTATGGGGCTAATGGCAATCACACCGATGA 95
GB3LKKR01EIO7Z/1-110 CACTACCAATGTGAAGAACCGGGCTACATTATGGGATTAATGGCAATCACACCGATGA 95
GB3LKKR02HOXTL/22-174 CACTACCAATGCGAAGAGCCGGGATACATTATGGGGCTAATGGCAATCACACCGATGA 95
GB3LKKR01DJQRC/358-498 ----------CGAAGAGCCGGGATACATTATGGGGCTAATGGCAATCACACCGATGA 82
GB3LKKR01CUDIG/48-200 AATTACCTATGCGAAGAGCCGGGATACATTATGGGGCTAATGGCAATCACACCGATGA 95
.....10.....20.....30.....40.....50.....
I D Y S Q G N D F D L N L Q T I D D L H
GB3LKKR02IEC5V/306-457 TTGATTATTCACAAGGAAACGACTTTGATCTAAACTTGCAAACAATAGATGATCTGCATA 35
GB3LKKR01EIO7Z/1-110 TTGATTATTCGCAAGGAAACGACTTTGATTTAAACTTGCAAACAATGGAT---------- 35
GB3LKKR02HOXTL/22-174 TTGATTATTCACAAGGAAATGACTTTGATTTAAACTTGCAAACAATGGATGATCTCCATA 35
GB3LKKR01DJQRC/358-498 TTGATTATTCACAAGGAAATGACTTTGATTTAAACTTGCAAACAATGGATGATCTCCATA 22
GB3LKKR01CUDIG/48-200 TTGATTATTCACAAGGAAATGACTTTGATTTAAACTTGCAAACAATGGATGATCTCCATA 35
.....70.....80.....90.....100.....110.....
K P A L D G I G Y Q D
GB3LKKR02IEC5V/306-457 AACCGGCATTAGATGGTATCGGCTACCAGGAT 1
GB3LKKR01EIO7Z/1-110 ------------------------------ 1
GB3LKKR02HOXTL/22-174 AACCGGCACTAGATGGAATTGAAGATTAACAG 1
GB3LKKR01DJQRC/358-498 AACCGGCACTAGATGGAATTGGATACCAAGAC 1
GB3LKKR01CUDIG/48-200 AACCGGCACTAGATGGAATTGGATACCAAGAC 1
.....130.....140.....150..

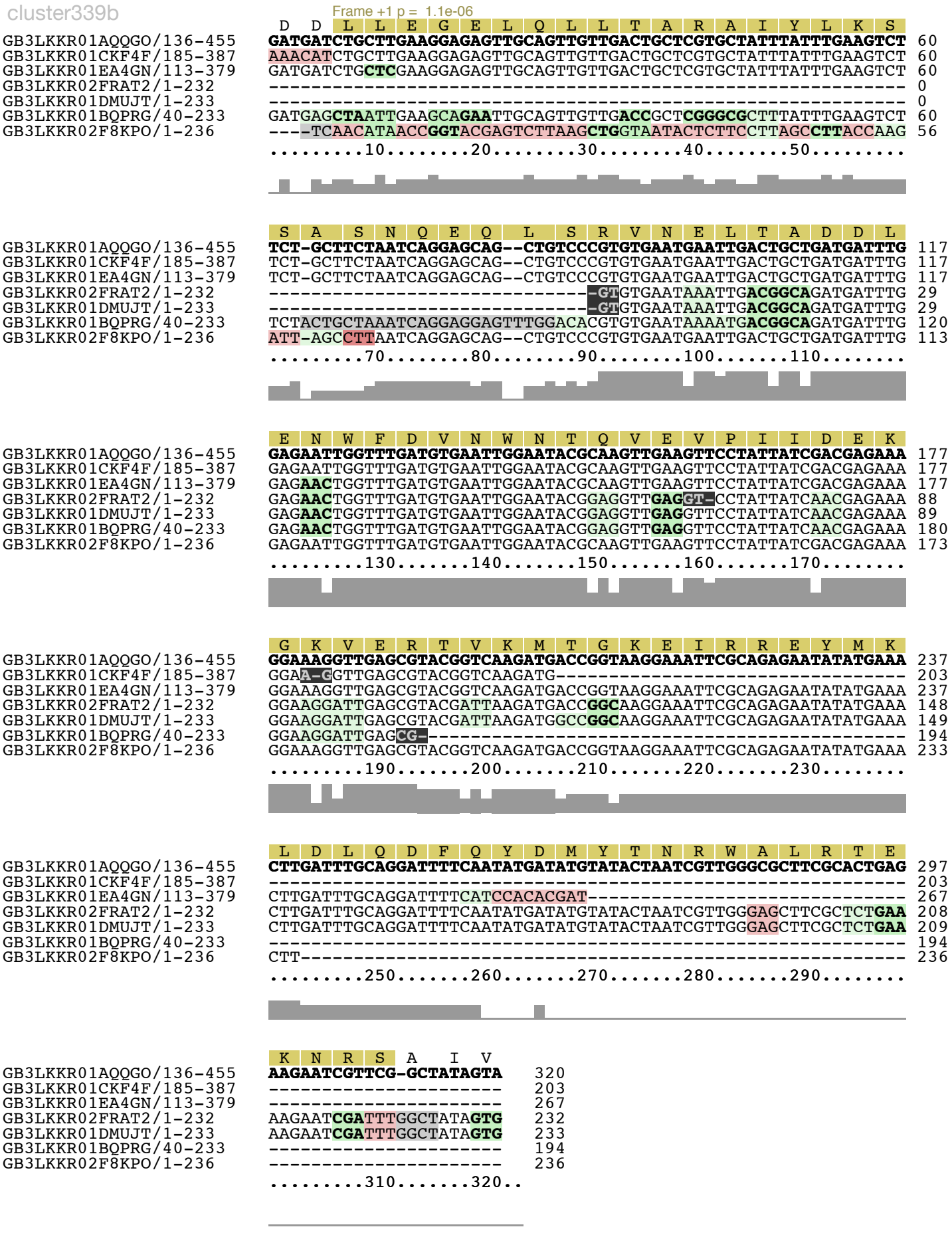

cluster241b
Frame +1 p = 5.5e-06
G G K P M N S G H I H Y Q C E E P
GB3LKKR01C994Z/1-147 ---------GGAGGGAAACCAATGAACAGCGGACATATACACTACCAATGCGAAGAGCCG 51
GB3LKKR01AVTUK/1-175 ATCGGAGGAGGAGG-AAACCAACAAACAGCGGACATATACACTACCAATGTGAAGAACCG 59
GB3LKKR01E2N9H/1-177 ATCCTACGAGGAGGCAAGCCACTAAACAACGGACATATACATTACCAATGCGAGGAACCA 60
GB3LKKR01B1HN4/10-186 ATCGGACGAGGAGGCAAGCCACTAAACAACGGACATATACATTACCAATGCGAGGAACCA 60
GB3LKKR02J46T7/1-166 ----------GAGGGAAACCAATGAACAGCGGGCATATACACTACCAATGCGAAGAGCCG 50
.....10.....20.....30.....40.....50.....
G Y I M G L M A I T P M I D Y S Q G N D
GB3LKKR01C994Z/1-147 GGATACATTATGGGGCTAATGGCAATCACACCGATGATTGATTATTCACAAGGAAATGAC 111
GB3LKKR01AVTUK/1-175 GGCTACATTATGGGATTAATGGCAATCACACCGATGATTGATTATTCGCAAGGA-ACGAC 118
GB3LKKR01E2N9H/1-177 GGATACATCATGGGACTGATGGCTATCACACCGATGATCGACTATTCGCAAGGAAACGAC 120
GB3LKKR01B1HN4/10-186 GGATACATCATGGGACTGATGGCTATCACACCGATGATCGACTATTCGCAAGGCAATGAC 120
GB3LKKR02J46T7/1-166 GGATACATTATGGGGCTAATGGCAAACACACAGGAAAACAAATTCTACATGATCAGT-AA 109
.....70.....80.....90.....100.....110.....
F D L N L Q T M D D L Q
GB3LKKR01C994Z/1-147 TTTGATTTAAACTTGCAAACAATGGATGATCTCCAA 147
GB3LKKR01AVTUK/1-175 TTTGATTTAAACTTGCAAACAATGGATATCTGCAGA 175
GB3LKKR01E2N9H/1-177 TTTGATCTAAACTTGCAAACAATAGATGATCTGCAT 177
GB3LKKR01B1HN4/10-186 TTTGATCTAAACTTGCAAACAATAGATGATCTACAC 177
GB3LKKR02J46T7/1-166 TGTAGGATCAAAACCGACAATCAAAGCCGGTTTCGA 166
.....130.....140.....150.....160.....170.....

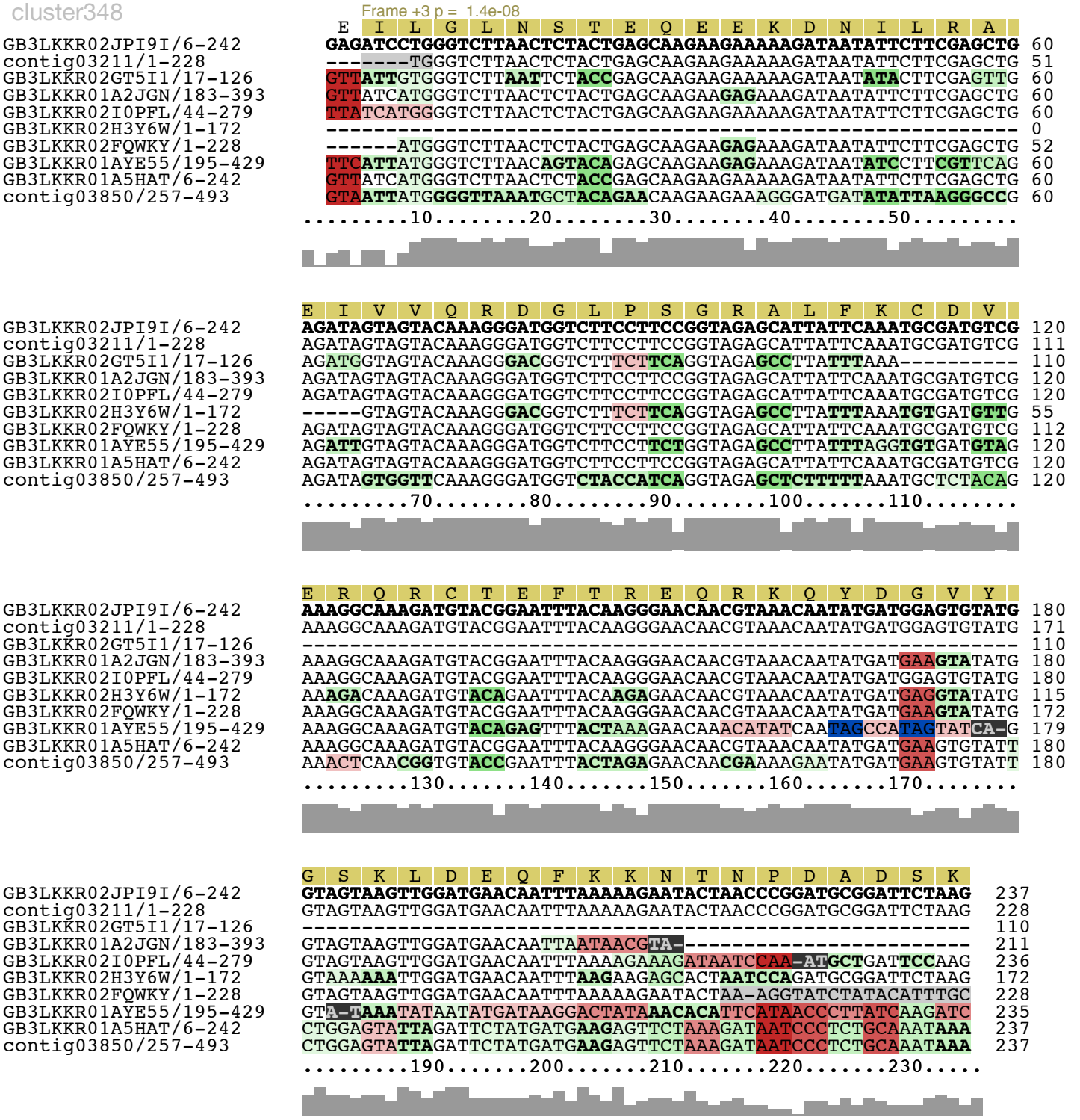

cluster258
Frame +3 p = 0.015
K V P F Y R K K S F W T M L I S I L T
contig07739/468-671 A-AGGTACCGTTTTATCGTAAGAAGAGCTTTTGGACAATGTTGATTTCCATTCTTACG 59
GB3LKKR02GPGDJ/44-247 A-AAGTACCGTTTTATCGTAAGAAGAGTTTTTGGACATTGTTGATTTCCATTCTTACG 59
GB3LKKR01B1BAU/42-243 A--GGTACCGTTTTATCGTAA-AAGAGTTTTTGGACAATGTTGATTTCCATTCTTACG 57
GB3LKKR01CQ42S/1-190 ----------TATCGTAAGAAGAGTTTTTGGACATTGTTGATTTCCATTCTTACG 45
GB3LKKR02GPY0A/70-273 ACTCGTACCGTTTTATCGTAAGAAGAG-TTTTGGACATTGTTGATTTCCATTCTTACG 59
GB3LKKR02HCE5B/72-255 AGAAGCTTCGGATTACGTTCGTTTGTTGTTTGAACAGTATCCC---------- 45
GB3LKKR01CZX7K/74-257 AGAAGCTTCGGATTACGTTCGTTTGTTGTTTGAACAGTATCCC---------- 45
.....10.....20.....30.....40.....50.....
A L S V Y F A S S C S R K L V Y R S S G
contig07739/468-671 GCTTTATCTGTTTATTTTGCTTCTTCATGTAGTCGGAAGTTGGTTTATCGTTCTTCCGGT 119
GB3LKKR02GPGDJ/44-247 GCATTATCTGTTTATTTTGCAGCTTCATGTAATCGTAAGATTGTTTATCGTTCTTCCGGT 119
GB3LKKR01B1BAU/42-243 GCTTTATCTGTTTATTTTGCTGCTTCATGTACTCGGAAGTTGGTTTATCGTTCTTCCGGT 117
GB3LKKR01CQ42S/1-190 GCATTATCTGTTTATTTTGCAGCTTCATGTAATCGTAAGATTGTTTATCGTTCTTCCGGT 105
GB3LKKR02GPY0A/70-273 GCATTATCTGTTTATTTTGCAGCTTCATGTAATCGTAAGATTGTTTATCGTTCTTCCGGT 119
GB3LKKR02HCE5B/72-255 ------GGTATTTATTTTGCTGCTTCATGTACTCGGAAGTTGGTTTATCGTTCTTCCGGT 99
GB3LKKR01CZX7K/74-257 ------GGTATTTATTTTGCTGCTTCATGTACTCGGAAGTTGGTTTATCGTTCTTCCGGT 99
.....70.....80.....90.....100.....110.....
V H C D T V Q L D V R S N L K L P * Y A
contig07739/468-671 GTTCATTGTGATACGGTTCAACTTGATGTTCGGTCTAATTTAAAACTTCCTTAATATGCC 179
GB3LKKR02GPGDJ/44-247 GTTCATTGTGACACGGTTCAACTTGATGTTCGGTCTAATTTAAAACTTCCTTAATATGCC 179
GB3LKKR01B1BAU/42-243 GTTCATTGTGATACTGTTCAAGTTGATGTTCGGTCTAATTTAAGCTTCCTTAATATGCC 177
GB3LKKR01CQ42S/1-190 GTTCATTGTGACACGGTTCTATTTGATGTTCGGTCTAATTTAAAACTTCCTTAATATGCC 165
GB3LKKR02GPY0A/70-273 GTTCATTGTGACACGGTTCTACTTGATGTTCGGTCTAATTTAAAACTTCCTTAATATGCC 179
GB3LKKR02HCE5B/72-255 GTTCATTGTGATACTGTTCAAGTTGATGTTCGGTCTAATTTAAGCTTCCTTAATATGCC 159
GB3LKKR01CZX7K/74-257 GTTCATTGTGATACTGTTCAAGTTGATGTTCGGTCTAATTTAAGCTTCCTTAATATGCC 159
.....130.....140.....150.....160.....170.....
W C *
contig07739/468-671 TGGTGCTAG 204
GB3LKKR02GPGDJ/44-247 TGGTGCTAG 204
GB3LKKR01B1BAU/42-243 TGCTGCTGG 202
GB3LKKR01CQ42S/1-190 TGCTGCTGG 190
GB3LKKR02GPY0A/70-273 TGCTGCTGG 204
GB3LKKR02HCE5B/72-255 TGCTGCTGG 184
GB3LKKR01CZX7K/74-257 TGCTGCTGG 184
.....190.....200...

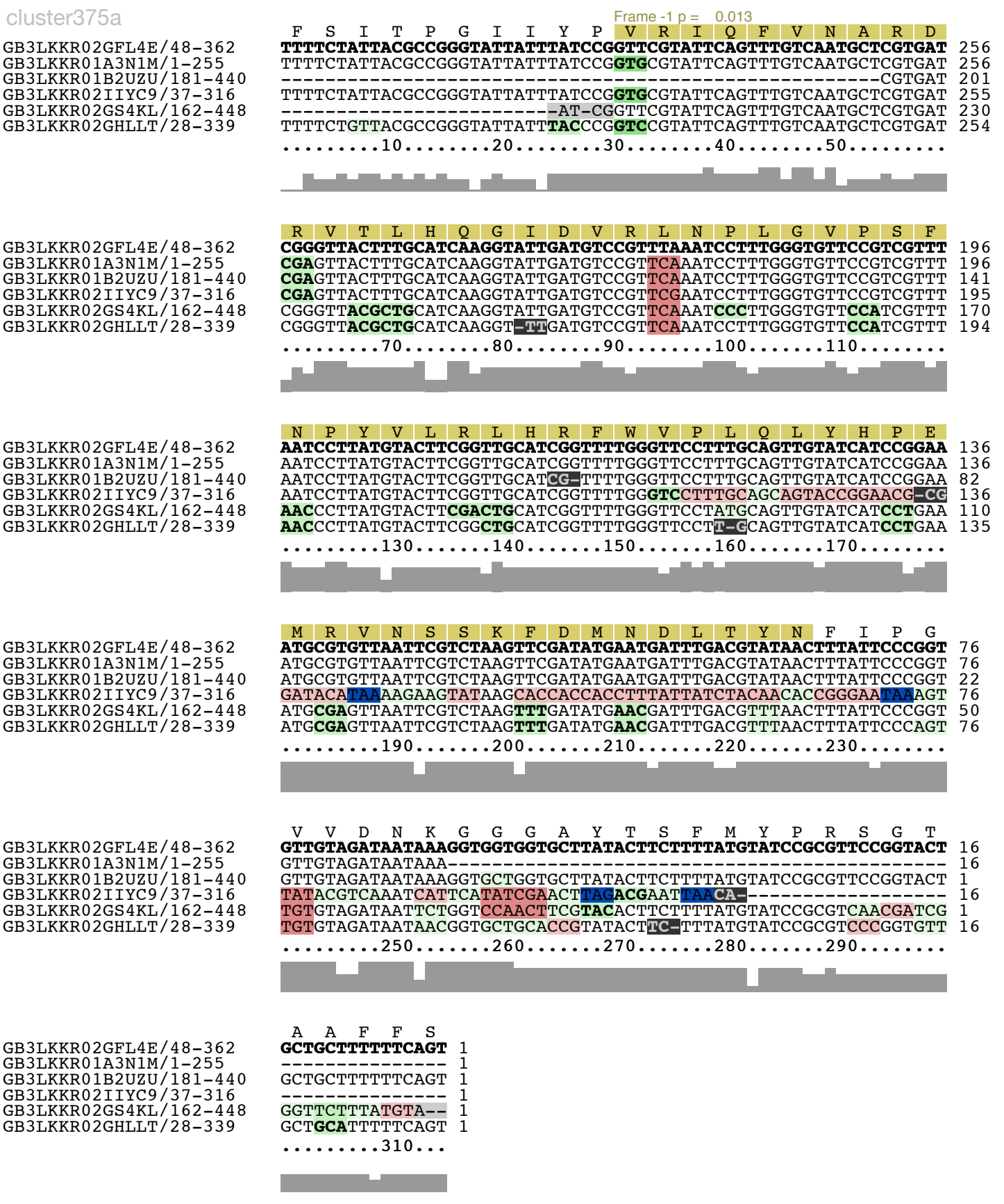

cluster297a
GB3LKKR02JI9WH/42-359
GB3LKKR02J4V1J/161-340
GB3LKKR02IA3U3/37-354
GB3LKKR02JGGMM/177-494
GB3LKKR01AFJJ4/82-399
Frame +1 p = 0.001


cluster297b
S C S Y N A L R E A V K D L G F V W I A
GB3LKKR02FSPL3/170-455 TCTTGTTCTTATAATGCTCTTCGTGAAG-CTGTTAAGGATTTAGGTTTTGTTTGGATTGC 227
GB3LKKR01A8VS6/1-192 TCTTGTTCTTATAATGCTCTTCGTGAAG-CTGTTAAGGATTTAGGTTTTGTTTGGATTGC 193
GB3LKKR01BS4WO/257-467 ---------- 152
GB3LKKR01BM7GD/221-500 -CTTGTTCTTATA-TGC-TTTCGTGAAG-C-GTTAAG---TTAGGTTTTGTTTGGATTGC 221
GB3LKKR01AU64A/59-342 TCTTGTTCTTATAATGTTATTCGTGAAGTCTGTTAAGGATTTAGGTTTTGTTTGGATTTC 225
.....10.....20.....30.....40.....50.....
S I T D K R L R Y V V K Y V G K S V Y M
GB3LKKR02FSPL3/170-455 ATCTATTACGGACAAGCGTCTTCGGTATGTTGTCAAGTATGTTGGCAAGTCTGTTTATAT 167
GB3LKKR01A8VS6/1-192 ATCTATTACGGACAAGCGTCTTCGGTATGTTGTCAAGTATGTTGGCAAGTCTGTTTATAT 167
GB3LKKR01BS4WO/257-467 ----------GCGTCTTCGGTATGTTGTCAAGTATGTTGGCAAGTCTGTTTATAT 93
GB3LKKR01BM7GD/221-500 ATCTATTACGGACAAGCGTCTTCGGTATGTTGTGAAGTATGTTGGCAAGTCTGTTTATAT 161
GB3LKKR01AU64A/59-342 ATCTATTACGGACAAGCGTCTTCGGTATGTTGTGAAGTATGTTGGCAAGTCTGTTTATAT 167
.....70.....80.....90.....100.....110.....
D E R S A A F A K S L P I T V G K L K
GB3LKKR02FSPL3/170-455 GGATGAGCGTTCTG-CAGCTTTTGCGAAGTCTCTTCCTATTACTGTAGGTAAATTAAAAA 108
GB3LKKR01A8VS6/1-192 GGATGAGCGTTCTG-CAGCTTTTGCGAAGTCTCTTCCTATTACTGTAGGTAAATTAAAA- 108
GB3LKKR01BS4WO/257-467 GGATGAGTGTTCTG-CAGCTTTGTCGAAGTCTCTTCCTATTACTGTAGGTAA-TTAAAA 34
GB3LKKR01BM7GD/221-500 GGATGAGCGTTCTGTTCGATTTGCGAAGTCTCTTCCTATTACTGTAGGTAAATTAAAA 101
GB3LKKR01AU64A/59-342 GGATGAGCGTTCTG-C-GGTTTTGCGAAGTCTCTTCCTATTACTGTAGGTAA-TTAAAA 109
.....130.....140.....150.....160.....170.....
Frame -1 p = 0.006
T N L Y D F L Q N S R Y R R K F V S P G
GB3LKKR02FSPL3/170-455 CTAATCTTTATGACTTTCTTCAGAATAGTAGATATCGTCGTAAATTTGTTTCACCAGGTG 48
GB3LKKR01A8VS6/1-192 CTAATCTTTATGACT----------- 48
GB3LKKR01BS4WO/257-467 CTAATCTTTATGACTTTCTTCAGAATAGTAGATATCTTCGTAAATTTGTTTCACCAGGTG 1
GB3LKKR01BM7GD/221-500 CTAATCTTTATGACTTTCTTCAGAATAGTCGATATCGCCGTAAATTTATTTCGGCAGGTG 41
GB3LKKR01AU64A/59-342 CTAATCTTTATGACT-TCTTCAGAATAGTCGATGTCGCCGTAAATTTATTTCGGCAGGTG 49
.....190.....200.....210.....220.....230.....
V G D Y F G D F E A P G V S S G
GB3LKKR02FSPL3/170-455 TTGGTGATTATTTTGGCGATTTTGAAGCTCCCGGTGTTTCTTCTGGT 1
GB3LKKR01A8VS6/1-192 ---------- 1
GB3LKKR01BS4WO/257-467 TTGGTGATTATTTTGGCGATTTTGAAGCTCCCGGTGTTTCTTCTGGT 1
GB3LKKR01BM7GD/221-500 TTGGCGATTATTTGGGAGATTTTAAAGCTCCCGGTGTTACTTCTGGT 1
GB3LKKR01AU64A/59-342 TTGGCGATTATTTGGGAGATTTTAAAAGCTCCAGTGTTGCTTCTGGT 1
.....250.....260.....270.....280.....

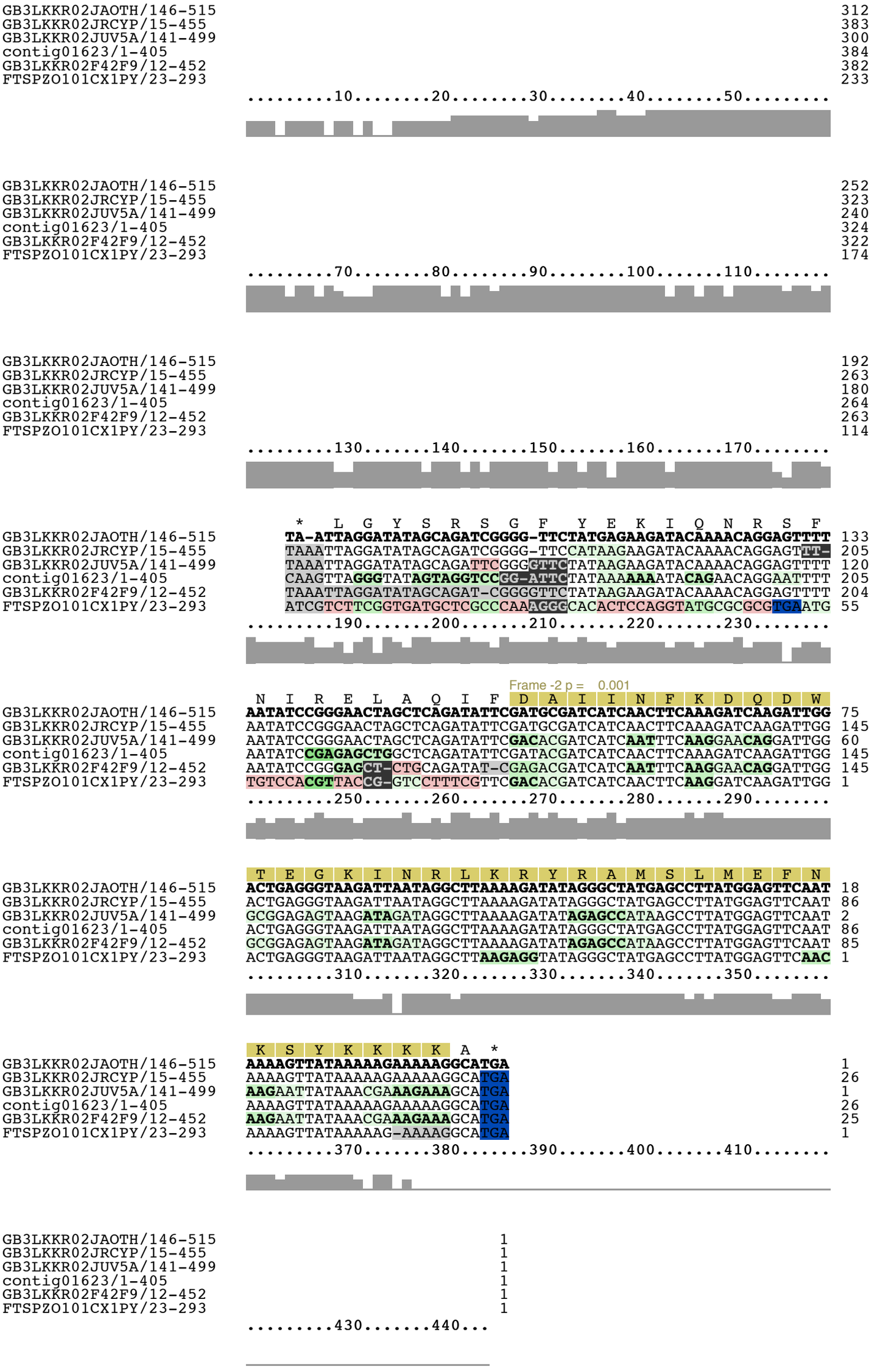

cluster321b
Frame -1 p = 1.9e-07
V S A T I P T S S G G A P S G H G P V A
GB3LKKR01EYJBS/82-414 GTTTCTGCTACTATTCCCACTTCCAGCGGTGGTGCTCCGTCTGGACATGGTCCAGTTGCA 277
GB3LKKR02G6OMM/1-335 GTTTCTGCTACTACTCCCACTTCCAGCGGTGGTGCTCCGTCTGGACATGGTCCAGTTGCA 277
contig09464/1-118 GTTTCTGCTACTATTCCCACTTCCAGCGGTGGTGCTCCGTCTGGACATGGTCCAGTTGCA 119
GB3LKKR01E1LJ5/1-175 GTTTCTGCTACTATTCCCACTTCCAGCGGTGGTGCTCCGTCTGGACATGGTCCAGTTGCA 176
GB3LKKR01E2CDT/1-134 ------GGATTGATTGAAGTGGGGCGGGTGGTGCTCCGTCAGGTCATGGTCCGGTTGCT 135
contig16546/1-333 GTTTCTGCTACTATACCCACCTCTAGCGGTGGGGCCCCATCCGGTCATGGTCCTGTGGCT 277
GB3LKKR01CSEX1/105-316 -- 157
GB3LKKR01D984D/221-413 -- 137
.....10.....20.....30.....40.....50.....
S G S F G G L A A L A G N P S A Y A D I
GB3LKKR01EYJBS/82-414 TCTGGTTCCTTTGGTGGTCTTGCTGCTCTTGCTGGTAATCCTTCTGCGTATGCGGATATT 217
GB3LKKR02G6OMM/1-335 TCTGGTTCCTTTGGTGGTCTTGCTGCTCTTGCTGGTAATCCTTCTGCGTATGCGGATATT 217
contig09464/1-118 TCTGGTTCCTTTGGTGGTCTTGCTGCTCTTGCTGGTAATCCTTCTGCGTATGCGGATA-- 119
GB3LKKR01E1LJ5/1-175 TCTGGTTCCTTTGGTGGTCTTGCTGCTCTTGCTGGTAATCCTTCTGCGTATGCGGATATT 176
GB3LKKR01E2CDT/1-134 TCTGGTTCCGGAGGTGGTCTTGCTGCTCTTGCCGGTAATCCTTCTGCGTATGCGGATATT 135
contig16546/1-333 TCTGGTGTCGGTGGGGGTCTTGCTGCTCTTGCTGGTAATCCTTCTGCGTATGCGGATATT 217
GB3LKKR01CSEX1/105-316 --T 97
GB3LKKR01D984D/221-413 -- 77
.....70.....80.....90.....100.....110.....
Q L K D A Q Q D R E R S A A A L N D A E
GB3LKKR01EYJBS/82-414 CAGTTGAAAGATGCTCAGCAGGAGCGTGAGCGTTCGGCTGCTTCTCTCAATGATGCTGAA 157
GB3LKKR02G6OMM/1-335 CAGTTGAAAGATGCTCAGCAGGAGCGTGAGCGTTCGGCTGCTTCTCTCAATGATGCTGAG 157
contig09464/1-118 -- 119
GB3LKKR01E1LJ5/1-175 CAGTTGAAAGACGCTCAGCAGGAGCGTGAGCGTTCGGCTGCTTCTTCTAATTGAT----- 157
GB3LKKR01E2CDT/1-134 CAGTTGAAAGATGCTCAGCAG-- 135
contig16546/1-333 CAGTTGAAAGATGCTCAGCAGGATCGAGAGCGTTCGGCAGCAGCTCTTAATGATGCTGAA 157
GB3LKKR01CSEX1/105-316 CAGTTG-AAGATGCTCAGCAGGAGCGTGAGCGTTCGGCTGCTTCTCTTAATGATGCTGAG 37
GB3LKKR01D984D/221-413 ----------------AGGAGCGTGAGCGTTCGGCTGCTTCTCTTAATGATGCTGAG 18
.....130.....140.....150.....160.....170.....
A E W Y K S Q T L D K D L R E R L M K A
GB3LKKR01EYJBS/82-414 GCTGAATGGTATAAGTCACAGACTTTGGATAAAGATTTGCGTGAACGTTTGATGAAGGCG 97
GB3LKKR02G6OMM/1-335 GCTGATTGGTATAGGTCCCAGACTTTGGATAAAGATTTGCGTGAACGTCTGATGAAGGCT 97
contig09464/1-118 -- 97
GB3LKKR01E1LJ5/1-175 -- 97
GB3LKKR01E2CDT/1-134 -- 90
contig16546/1-333 GCTGAATGGTATAAGTCACAGACTTTGGATAAAGATTTGCGTGAACGTTTGATGAAGGCG 97
GB3LKKR01CSEX1/105-316 GCTGATTGGTATAGGTCCCAGACTTTGGATAAAGATTTGCGTGAACGTCTGATGAAGGCT 1
GB3LKKR01D984D/221-413 GCTGATTGGTATAGGTC-CAGACTTTGGATAAAGATTTGCGTGAACGTCTGATGAAGGCT 1
.....190.....200.....210.....220.....230.....
Q A G L A E A G I T E S T S R A S L N T
GB3LKKR01EYJBS/82-414 CAGGCAGGACTTGCAGAAGCTGGAATTACTGAATCTACATCGCGTGCAAGTTTGAACACT 37
GB3LKKR02G6OMM/1-335 CAGGCCGGACTTGCTGAAGCTGGAATCACTGAATCTGCTTCGCGTGCAAGTTTGAATCCT 37
contig09464/1-118 -- 37
GB3LKKR01E1LJ5/1-175 -- 37
GB3LKKR01E2CDT/1-134 -- 30
contig16546/1-333 CAGGCAGGACTTGCAGAAGCTGGAATTACTGAATCTACATCGCGTGCAAGTTTGAACACT 37
GB3LKKR01CSEX1/105-316 CAGGCCGGACTTGCTGAAGCTGGAATCACTGAATCTGCTTCGCGTGCAAGTTT-AATGCT 1
GB3LKKR01D984D/221-413 CAGGCCGGACTTGCTGAAGCTGGAATCACTGAATCTGCTTCGCGTGCAAGTTTGAATGCT 1
.....250.....260.....270.....280.....290.....
A I T L S Y T I D N E
GB3LKKR01EYJBS/82-414 GCGATAACTTTGTCT---TATACTATTGATAACGAG 1
GB3LKKR02G6OMM/1-335 GCTGCTGTTCTTGGTCAGTCTGGAGTTGG-TGCGAT 1
contig09464/1-118 ------------------------------------ 1
GB3LKKR01E1LJ5/1-175 ------------------------------------ 1
GB3LKKR01E2CDT/1-134 ------------------------------------ 1
contig16546/1-333 GCGATAACTTTGTCT---TATACTATTGATAACGAG 1
GB3LKKR01CSEX1/105-316 GCGATAACTTTATCC---TATTCTATTGATAACGAG 1
GB3LKKR01D984D/221-413 GCGATAACTTTATCC---TATTCTATTGATAACGAG 1
.....310.....320.....330....

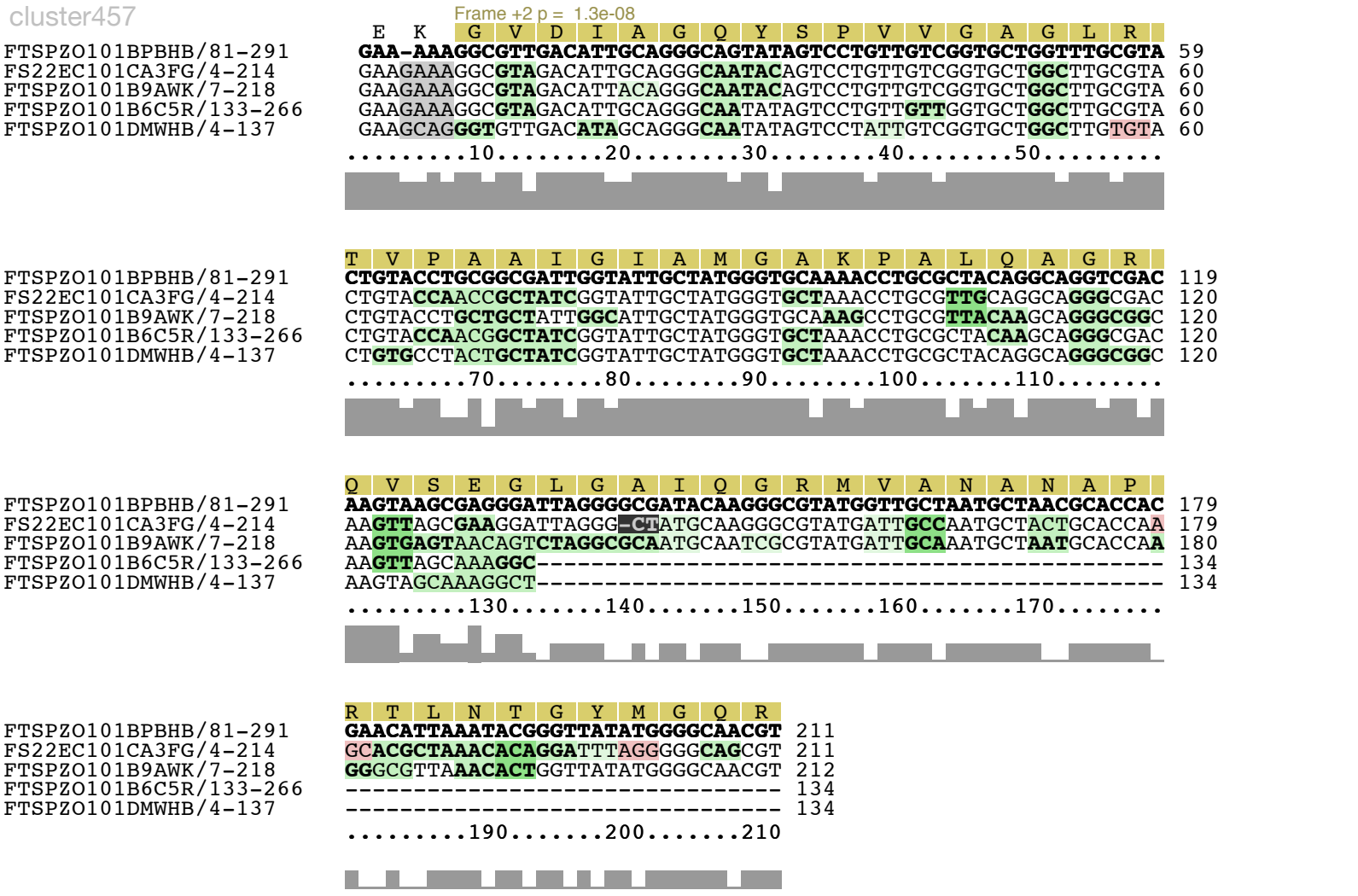

cluster339b
Frame +1 p = 1.1e-06
D D L L E G E L Q L L T A R A I Y L K S
GB3LKKR01AQQGO/136-455 GATGATCTGCTTGAAGGAGAGTTGCAGTTGTTGACTGCTCGTGCTATTTATTTGAAGTCT 60
GB3LKKR01CKF4F/185-387 AAACATCTGCTTGAAGGAGAGTTGCAGTTGTTGACTGCTCGTGCTATTTATTTGAAGTCT 60
GB3LKKR01EA4GN/113-379 GATGATCTGCTCGAAGGAGAGTTGCAGTTGTTGACTGCTCGTGCTATTTATTTGAAGTCT 60
GB3LKKR02FRAT2/1-232 ---------- 0
GB3LKKR01DMUJT/1-233 ---------- 0
GB3LKKR01BQPRG/40-233 GATGAGCTAATTGAAGCAGAATTGCAGTTGTTGACCGCTCGGGCGCTTTATTTGAAGTCT 60
GB3LKKR02F8KPO/1-236 ----TCAACATAACCGGTACGAGTCTTAAGCTGGTAATACTCTTCCTTAGCCTTACCAAG 56
.....10.....20.....30.....40.....50.....
S A S N Q E Q L S R V N E L T A D D L
GB3LKKR01AQQGO/136-455 TCT-GCTTCTAATCAGGAGCAG--CTGTCCCGTGTGAATGAATTGACTGCTGATGATTTG 117
GB3LKKR01CKF4F/185-387 TCT-GCTTCTAATCAGGAGCAG--CTGTCCCGTGTGAATGAATTGACTGCTGATGATTTG 117
GB3LKKR01EA4GN/113-379 TCT-GCTTCTAATCAGGAGCAG--CTGTCCCGTGTGAATGAATTGACTGCTGATGATTTG 117
GB3LKKR02FRAT2/1-232 ----------GTGTGAATAAATTGACGGCAGATGATTTG 29
GB3LKKR01DMUJT/1-233 ----------GTGTGAATAAATTGACGGCAGATGATTTG 29
GB3LKKR01BQPRG/40-233 TCTACTGCTAAATCAGGAGGAGTTTGGACACGTGTGAATAAAATGACGGCAGATGATTTG 120
GB3LKKR02F8KPO/1-236 ATT-AGCCTTAATCAGGAGCAG--CTGTCCCGTGTGAATGAATTGACTGCTGATGATTTG 113
.....70.....80.....90.....100.....110.....
E N W F D V N W N T Q V E V P I I D E K
GB3LKKR01AQQGO/136-455 GAGAATTGGTTTGATGTGAATTGGAATACGCAAGTTGAAGTTCCTATTATCGACGAGAAA 177
GB3LKKR01CKF4F/185-387 GAGAATTGGTTTGATGTGAATTGGAATACGCAAGTTGAAGTTCCTATTATCGACGAGAAA 177
GB3LKKR01EA4GN/113-379 GAGAACTGGTTTGATGTGAATTGGAATACGCAAGTTGAAGTTCCTATTATCGACGAGAAA 177
GB3LKKR02FRAT2/1-232 GAGAACTGGTTTGATGTGAATTGGAATACGGAGGTTGAGGT-CCTATTATCAACGAGAAA 88
GB3LKKR01DMUJT/1-233 GAGAACTGGTTTGATGTGAATTGGAATACGGAGGTTGAGGTTCCTATTATCAACGAGAAA 89
GB3LKKR01BQPRG/40-233 GAGAACTGGTTTGATGTGAATTGGAATACGGAGGTTGAGGTTCCTATTATCAACGAGAAA 180
GB3LKKR02F8KPO/1-236 GAGAATTGGTTTGATGTGAATTGGAATACGCAAGTTGAAGTTCCTATTATCGACGAGAAA 173
.....130.....140.....150.....160.....170.....
G K V E R T V K M T G K E I R R E Y M K
GB3LKKR01AQQGO/136-455 GGAAAGGTTGAGCGTACGGTCAAGATGACCGGTAAGGAAATTCGCAGAGAATATATGAAA 237
GB3LKKR01CKF4F/185-387 GGAA-GGTTGAGCGTACGGTCAAGATG---------- 203
GB3LKKR01EA4GN/113-379 GGAAAGGTTGAGCGTACGGTCAAGATGACCGGTAAGGAAATTCGCAGAGAATATATGAAA 237
GB3LKKR02FRAT2/1-232 GGAAGGATTGAGCGTACGATTAAGATGACCGGCAAGGAAATTCGCAGAGAATATATGAAA 148
GB3LKKR01DMUJT/1-233 GGAAGGATTGAGCGTACGATTAAGATGGCCGGCAAGGAAATTCGCAGAGAATATATGAAA 149
GB3LKKR01BQPRG/40-233 GGAAGGATTGAGCG-- 194
GB3LKKR02F8KPO/1-236 GGAAAGGTTGAGCGTACGGTCAAGATGACCGGTAAGGAAATTCGCAGAGAATATATGAAA 233
.....190.....200.....210.....220.....230.....
L D L Q D F Q Y D M Y T N R W A L R T E
GB3LKKR01AQQGO/136-455 CTTGATTTGCAGGATTTTCAATATGATATGTATACTAATCGTTGGGCGCTTCGCACTGAG 297
GB3LKKR01CKF4F/185-387 ---------- 203
GB3LKKR01EA4GN/113-379 CTTGATTTGCAGGATTTTCATCCACACGAT---------- 267
GB3LKKR02FRAT2/1-232 CTTGATTTGCAGGATTTTCAATATGATATGTATACTAATCGTTGGGAGCTTCGCTCTGAA 208
GB3LKKR01DMUJT/1-233 CTTGATTTGCAGGATTTTCAATATGATATGTATACTAATCGTTGGGAGCTTCGCTCTGAA 209
GB3LKKR01BQPRG/40-233 ---------- 194
GB3LKKR02F8KPO/1-236 CTT---------- 236
.....250.....260.....270.....280.....290.....
K N R S A I V
GB3LKKR01AQQGO/136-455 AAGAATCGTTCG-GCTATAGTA 320
GB3LKKR01CKF4F/185-387 ---------- 203
GB3LKKR01EA4GN/113-379 ---------- 267
GB3LKKR02FRAT2/1-232 AAGAATCGATTTGGCTATAGTG 232
GB3LKKR01DMUJT/1-233 AAGAATCGATTTGGCTATAGTG 233
GB3LKKR01BQPRG/40-233 ---------- 194
GB3LKKR02F8KPO/1-236 ---------- 236
.....310.....320..

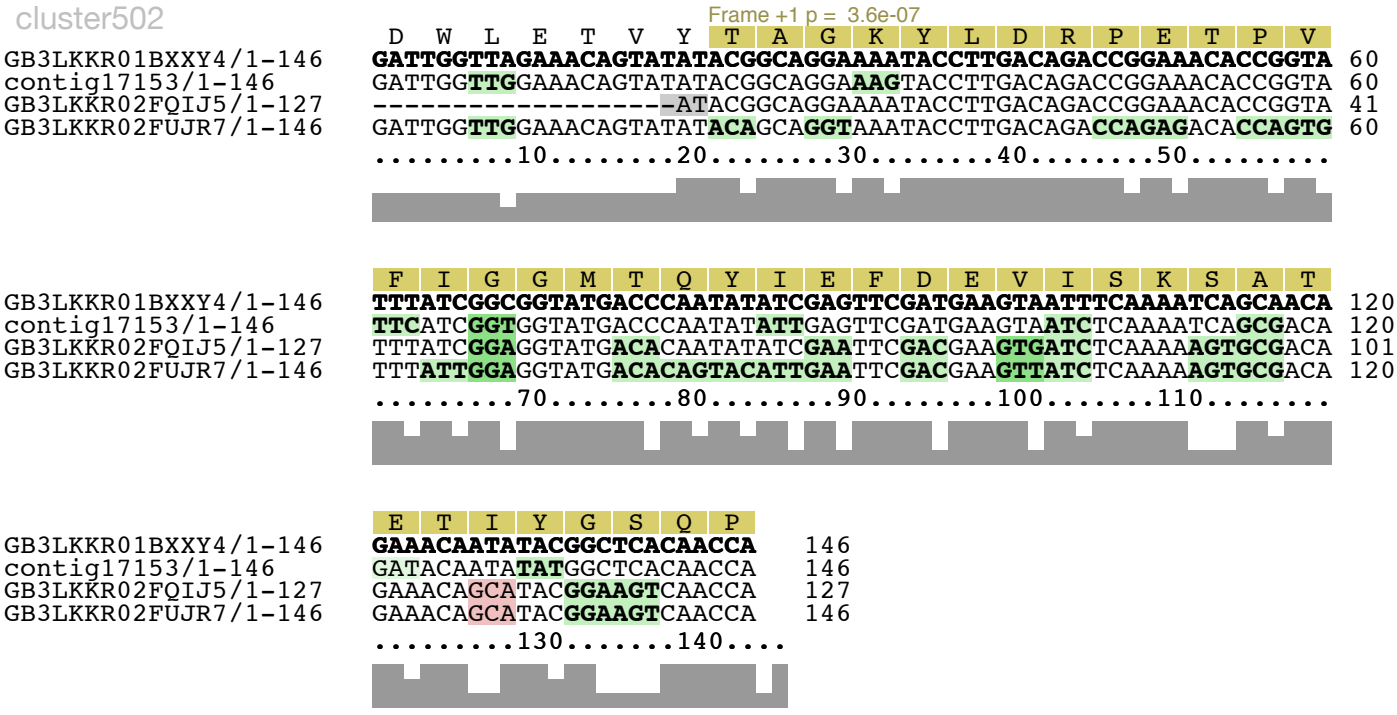

cluster348
Frame +3 p = 1.4e-08
E I L G L N S T E Q E E K D N I L R A
GB3LKKR02JPI9I/6-242 GAGATCCTGGGTCTTAACTCTACTGAGCAAGAAGAAAAAGATAATATTCTTCGAGCTG 60
contig03211/1-228 -------TGGGTCTTAACTCTACTGAGCAAGAAGAAAAAGATAATATTCTTCGAGCTG 51
GB3LKKR02GT5I1/17-126 GTTATTGTGGGTCTTAATTCTACCGAGCAAGAAGAAAAAGATAATATACTTCGAGTTG 60
GB3LKKR01A2JGN/183-393 GTTATCATGGGTCTTAACTCTACTGAGCAAGAAGAGAAAGATAATATTCTTCGAGCTG 60
GB3LKKR02I0PFL/44-279 TTATCATGGGGTCTTAACTCTACTGAGCAAGAAGAAAAAGATAATATTCTTCGAGCTG 60
GB3LKKR02H3Y6W/1-172 -- 0
GB3LKKR02FQWKY/1-228 ------ATGGGTCTTAACTCTACTGAGCAAGAAGAGAAAGATAATATTCTTCGAGCTG 52
GB3LKKR01AYE55/195-429 TTCATTATGGGTCTTAACAGTACAGAGCAAGAAGAGAAAGATAATATCCTTCGTTCAG 60
GB3LKKR01A5HAT/6-242 GTTATCATGGGTCTTAACTCTACCGAGCAAGAAGAAAAAGATAATATTCTTCGAGCTG 60
contig03850/257-493 GTAATTATGGGGTTAAATGCTACAGAACAAGAAGAAAGGGATGATATATTAAGGGCCG 60
.....10.....20.....30.....40.....50.....
E I V V Q R D G L P S G R A L F K C D V
GB3LKKR02JPI9I/6-242 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 120
contig03211/1-228 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 111
GB3LKKR02GT5I1/17-126 AGATGGTAGTACAAAGGGACGGTCTTTCTTCAGGTAGAGCCTTATTTAAA---------- 110
GB3LKKR01A2JGN/183-393 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 120
GB3LKKR02I0PFL/44-279 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 120
GB3LKKR02H3Y6W/1-172 -----GTAGTACAAAGGGACGGTCTTTCTTCAGGTAGAGCCTTATTTAAATGTGATGTTG 55
GB3LKKR02FQWKY/1-228 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 112
GB3LKKR01AYE55/195-429 AGATTGTAGTACAAAGGGATGGTCTTCCTTCTGGTAGAGCCTTATTTAGGTGTGATGTAG 120
GB3LKKR01A5HAT/6-242 AGATAGTAGTACAAAGGGATGGTCTTCCTTCCGGTAGAGCATTATTCAAATGCGATGTCG 120
contig03850/257-493 AGATAGTGTGGTTCAAAGGGATGGTCTACCATCAGGTAGAGCTCTTTTTAAATGCTCTACAG 120
.....70.....80.....90.....100.....110.....
E R Q R C T E F T R E Q R K Q Y D G V Y
GB3LKKR02JPI9I/6-242 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGGAGTGTATG 180
contig03211/1-228 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGGAGTGTATG 171
GB3LKKR02GT5I1/17-126 -- 110
GB3LKKR01A2JGN/183-393 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGAAGTATATG 180
GB3LKKR02I0PFL/44-279 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGGAGTGTATG 180
GB3LKKR02H3Y6W/1-172 AAAGACAAAGATGTACAGAATTTACAAGAGAACAACGTAAACAATATGATGAGGTATATG 115
GB3LKKR02FQWKY/1-228 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGAAGTATATG 172
GB3LKKR01AYE55/195-429 AAAGGCAAAGATGTACAGAGTTTACTAAAGAACAAACATATCAATAGCCATAGTATCA-G 179
GB3LKKR01A5HAT/6-242 AAAGGCAAAGATGTACGGAATTTACAAGGGAACAACGTAAACAATATGATGAAGTGTATT 180
contig03850/257-493 AAACTCAACGGTGTACCGAATTTACTAGAGAACAACGAAAAGAATATGATGAAGTGTATT 180
.....130.....140.....150.....160.....170.....
G S K L D E Q F K K N T N P D A D S K
GB3LKKR02JPI9I/6-242 GTAGTAAGTTGGATGAACAATTTAAAAAGAATACTAACCCGGATGCGGATTCTAAG 237
contig03211/1-228 GTAGTAAGTTGGATGAACAATTTAAAAAGAATACTAACCCGGATGCGGATTCTAAG 228
GB3LKKR02GT5I1/17-126 -- 110
GB3LKKR01A2JGN/183-393 GTAGTAAGTTGGATGAACAATTAATAACGTA-------------------------- 211
GB3LKKR02I0PFL/44-279 GTAGTAAGTTGGATGAACAATTTAAAAGAAAGATAATCCAA-ATGCTGATTCCAAG 236
GB3LKKR02H3Y6W/1-172 GTAAAAAATTGGATGAACAATTTAAGAAGAGCACTAATCCAGATGCGGATTCTAAG 172
GB3LKKR02FQWKY/1-228 GTAGTAAGTTGGATGAACAATTTAAAAAGAATACTAA-AGGTATCTATACATTTGC 228
GB3LKKR01AYE55/195-429 GTA-TAAATATAATATGATAAGGACTATAAACACATTCATAACCCTTATCAAGATC 235
GB3LKKR01A5HAT/6-242 CTGGAGTATTAGATTCTATGATGAAGAGTTCTAAAGATAATCCCTCTGCAAATAAA 237
contig03850/257-493 CTGGAGTATTAGATTCTATGATGAAGAGTTCTAAAGATAATCCCTCTGCAAATAAA 237
.....190.....200.....210.....220.....230.....

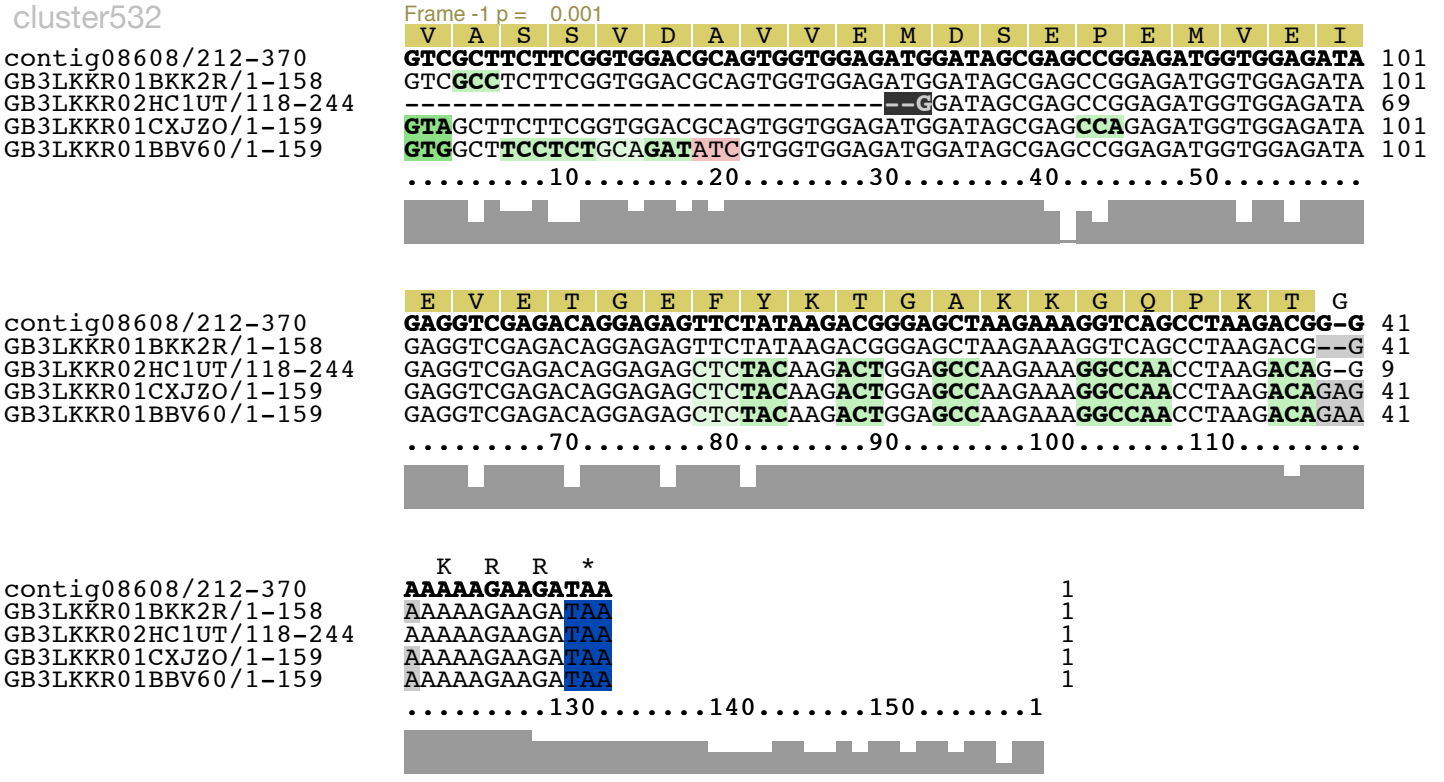

cluster375a
Frame -1 p = 0.013
F S I T P G I I Y P V R I Q F V N A R D
GB3LKKR02GFL4E/48-362 TTTTCTATTACGCCGGGTATTATTTATCCGGTTCGTATTCAGTTTGTCAATGCTCGTGAT 256
GB3LKKR01A3N1M/1-255 TTTTCTATTACGCCGGGTATTATTTATCCGGTGCGTATTCAGTTTGTCAATGCTCGTGAT 256
GB3LKKR01B2UZU/181-440 ----------CGTGAT 201
GB3LKKR02IIYC9/37-316 TTTTCTATTACGCCGGGTATTATTTATCCGGTGCGTATTCAGTTTGTCAATGCTCGTGAT 255
GB3LKKR02GS4KL/162-448 -----------------------AT-CGGTTCGTATTCAGTTTGTCAATGCTCGTGAT 230
GB3LKKR02GHLLT/28-339 TTTTCTGTTACGCCGGGTATTATTTACCCGGTCCGTATTCAGTTTGTCAATGCTCGTGAT 254
.....10.....20.....30.....40.....50.....
R V T L H Q G I D V R L N P L G V P S F
GB3LKKR02GFL4E/48-362 CGGGTTACTTTGCATCAAGGTATTGATGTCCGTTTAAATCCTTTGGGTGTTCCGTCGTTT 196
GB3LKKR01A3N1M/1-255 CGAGTTACTTTGCATCAAGGTATTGATGTCCGTTCAAATCCTTTGGGTGTTCCGTCGTTT 196
GB3LKKR01B2UZU/181-440 CGAGTTACTTTGCATCAAGGTATTGATGTCCGTTCAAATCCTTTGGGTGTTCCGTCGTTT 141
GB3LKKR02IIYC9/37-316 CGAGTTACTTTGCATCAAGGTATTGATGTCCGTTCGAATCCTTTGGGTGTTCCGTCGTTT 195
GB3LKKR02GS4KL/162-448 CGGGTTACGCTGCATCAAGGTATTGATGTCCGTTCAAATCCCTTGGGTGTTCCATCGTTT 170
GB3LKKR02GHLLT/28-339 CGGGTTACGCTGCATCAAGGT-TTGATGTCCGTTCAAATCCTTTGGGTGTTCCATCGTTT 194
.....70.....80.....90.....100.....110.....
N P Y V L R L H R F W V P L Q L Y H P E
GB3LKKR02GFL4E/48-362 AATCCTTATGTACTTCGGTTGCATCGGTTTTGGGTTCCTTTGCAGTTGTATCATCCGGAA 136
GB3LKKR01A3N1M/1-255 AATCCTTATGTACTTCGGTTGCATCGGTTTTGGGTTCCTTTGCAGTTGTATCATCCGGAA 136
GB3LKKR01B2UZU/181-440 AATCCTTATGTACTTCGGTTGCATCG-TTTTGGGTTCCTTTGCAGTTGTATCATCCGGAA 82
GB3LKKR02IIYC9/37-316 AATCCTTATGTACTTCGGTTGCATCGGTTTTGGGTCCTTTGCAGCAGTACCGGAACG-CG 136
GB3LKKR02GS4KL/162-448 AACCCTTATGTACTTCGACTGCATCGGTTTTGGGTTCCTATGCAGTTGTATCATCCTGAA 110
GB3LKKR02GHLLT/28-339 AACCCTTATGTACTTCGGCTGCATCGGTTTTGGGTTCCTT-GCAGTTGTATCATCCTGAA 135
.....130.....140.....150.....160.....170.....
M R V N S S K F D M N D L T Y N F I P G
GB3LKKR02GFL4E/48-362 ATGCGTGTTAATTCGTCTAAGTTCGATATGAATGATTTGACGTATAACTTTATTCCCGGT 76
GB3LKKR01A3N1M/1-255 ATGCGTGTTAATTCGTCTAAGTTCGATATGAATGATTTGACGTATAACTTTATTCCCGGT 76
GB3LKKR01B2UZU/181-440 ATGCGTGTTAATTCGTCTAAGTTCGATATGAATGATTTGACGTATAACTTTATTCCCGGT 22
GB3LKKR02IIYC9/37-316 GATACATAAAAGAAGTATAAGCACCACCACCTTTATTATCTACAACACCGGGAATAAAGT 76
GB3LKKR02GS4KL/162-448 ATGCGAGTTAATTCGTCTAAGTTTGATATGAACGATTTGACGTTTAACTTTATTCCCGGT 50
GB3LKKR02GHLLT/28-339 ATGCGAGTTAATTCGTCTAAGTTTGATATGAACGATTTGACGTTTAACTTTATTCCCAGT 76
.....190.....200.....210.....220.....230.....
V V D N K G G G A Y T S F M Y P R S G T
GB3LKKR02GFL4E/48-362 GTTGTAGATAATAAAGGTGGTGGTGCTTATACTTCTTTTATGTATCCGCGTTCCGGTACT 16
GB3LKKR01A3N1M/1-255 GTTGTAGATAATAAA---------- 16
GB3LKKR01B2UZU/181-440 GTTGTAGATAATAAAGGTGCTGGTGCTTATACTTCTTTTATGTATCCGCGTTCCGGTACT 1
GB3LKKR02IIYC9/37-316 TATACGTCAAATCATTCATATCGAACTTAGACGAATTAACA-- 16
GB3LKKR02GS4KL/162-448 TGTGTAGATAATTCTGGTCCAACTTCGTACACTTCTTTTATGTATCCGCGTCAACGATCG 1
GB3LKKR02GHLLT/28-339 TGTGTAGATAATAACGGTGCTGCACCGTATACTTC-TTTATGTATCCGCGTCCCGGTGTT 16
.....250.....260.....270.....280.....290.....
A A F F S
GB3LKKR02GFL4E/48-362 GCTGCTTTTTTCAGT 1
GB3LKKR01A3N1M/1-255 --------------- 1
GB3LKKR01B2UZU/181-440 GCTGCTTTTTTCAGT 1
GB3LKKR02IIYC9/37-316 --------------- 1
GB3LKKR02GS4KL/162-448 GGTTCTTTATGTA-- 1
GB3LKKR02GHLLT/28-339 GCTGCATTTTTCAGT 1
.....310...

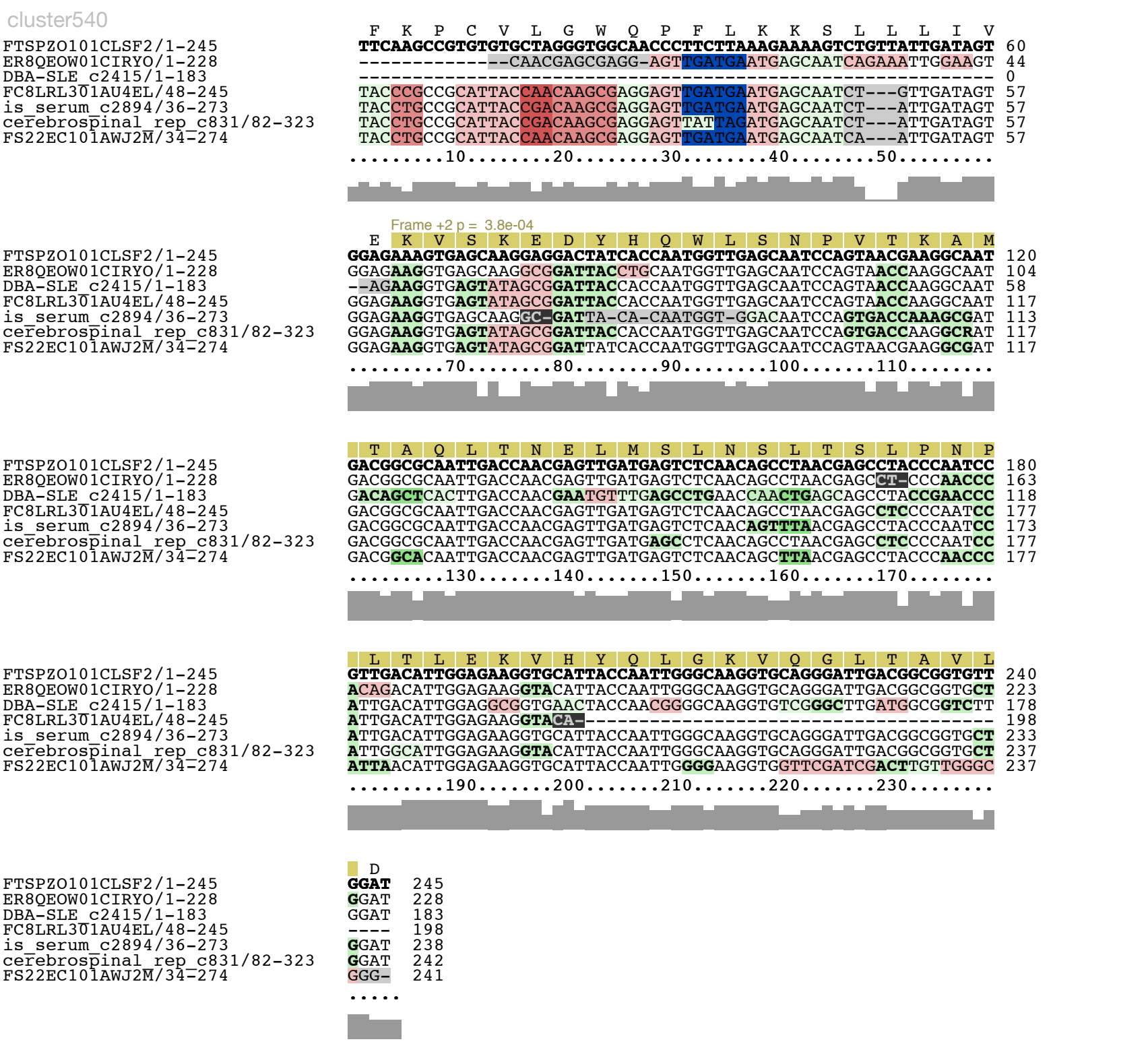
cluster406b

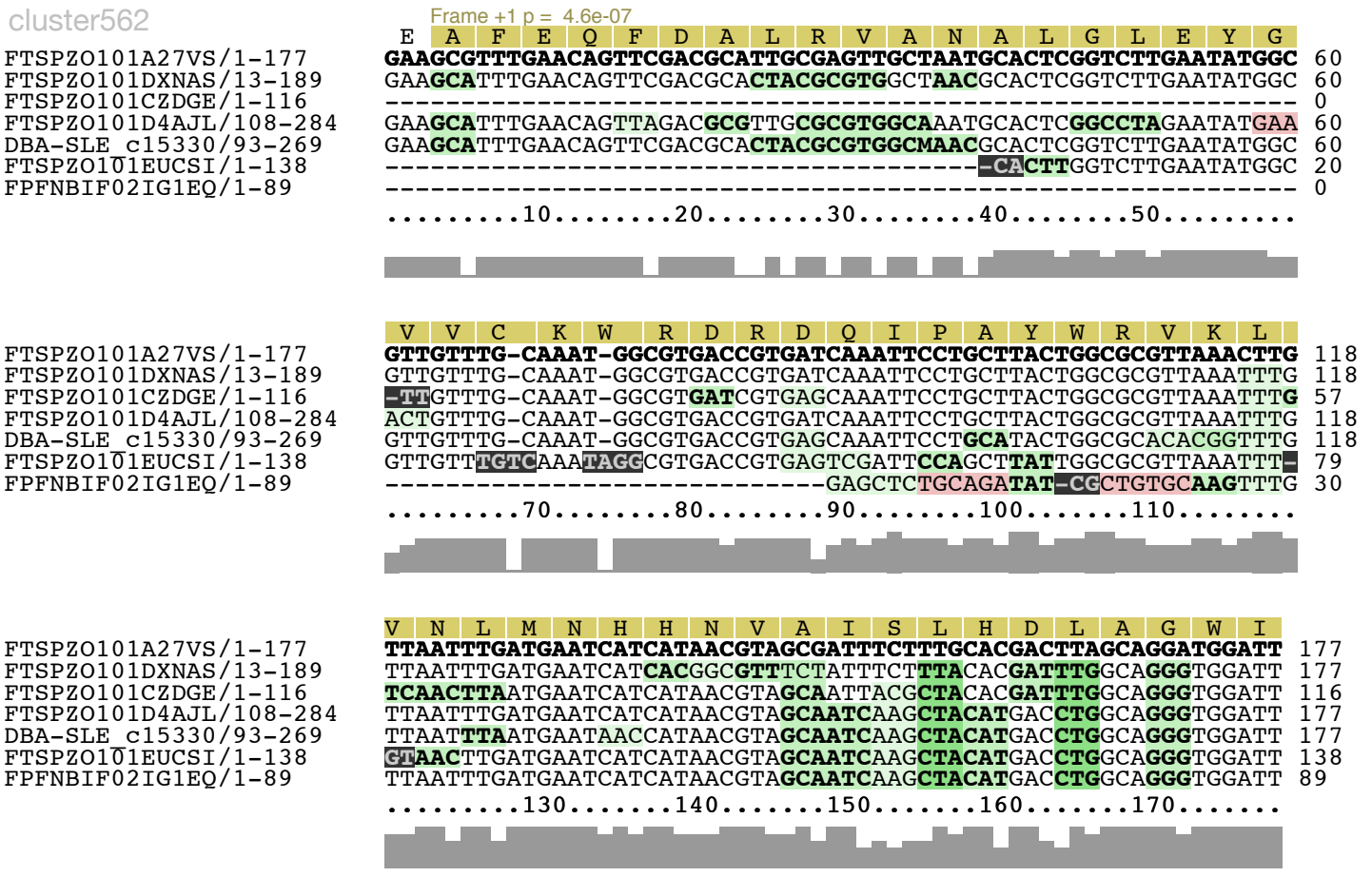


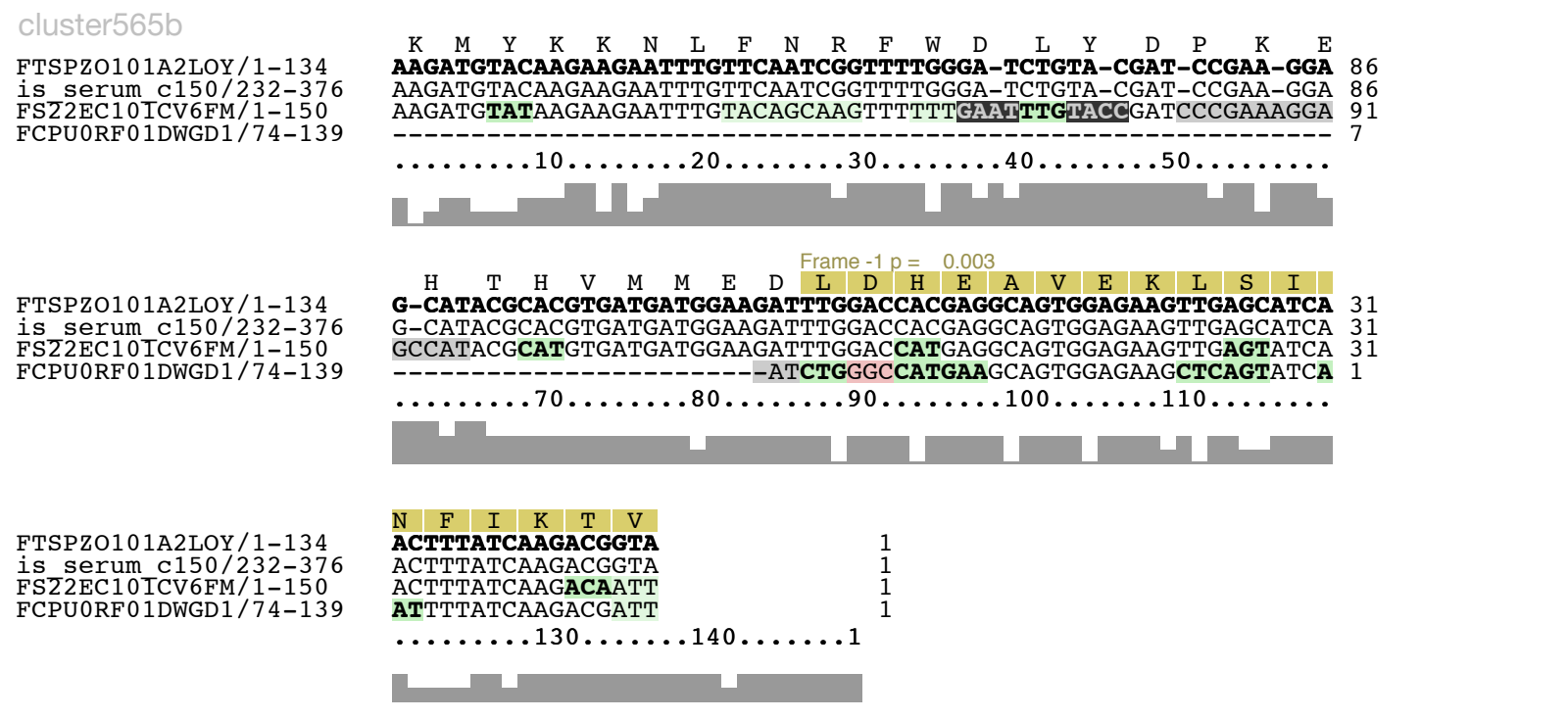

cluster457
Frame +2 p = 1.3e-08
E K G V D I A G Q Y S P V V G A G L R
FTSPZO101BPBHB/81-291 GAA-AAAGGCGTTGACATTGCAGGGCAGTATAGTCCTGTTGTCGGTGCTGGTTTGCGTA 59
FS22EC101CA3FG/4-214 GAAGAAAGGCGTAGACATTGCAGGGCAATACAGTCCTGTTGTCGGTGCTGGCTTGCGTA 60
FTSPZO101B9AWK/7-218 GAAGAAAGGCGTAGACATTACAGGGCAATACAGTCCTGTTGTCGGTGCTGGCTTGCGTA 60
FTSPZO101B6C5R/133-266 GAAGAAAGGCGTAGACATTGCAGGGCAATATAGTCCTGTTGTTGGTGCTGGCTTGCGTA 60
FTSPZO101DMWHB/4-137 GAAGCAGGGTGTTGACATAGCAGGGCAATATAGTCCTATTGTCGGTGCTGGCTTGTGTA 60
.....10.....20.....30.....40.....50.....
T V P A A I G I A M G A K P A L Q A G R
FTSPZO101BPBHB/81-291 CTGTACCTGCGGCGATTGGTATTGCTATGGGTGCAAAACCTGCGCTACAGGCAGGTCGAC 119
FS22EC101CA3FG/4-214 CTGTACCAACCGCTATCGGTATTGCTATGGGTGCTAAACCTGCGTTGCAGGCAGGGCGAC 120
FTSPZO101B9AWK/7-218 CTGTACCTGCTGCTATTGGCATTGCTATGGGTGCAAAGCCTGCGTTACAAGCAGGGCGGC 120
FTSPZO101B6C5R/133-266 CTGTACCAACGGCTATCGGTATTGCTATGGGTGCTAAACCTGCGCTACAAGCAGGGCGAC 120
FTSPZO101DMWHB/4-137 CTGTGCCTACTGCTATCGGTATTGCTATGGGTGCTAAACCTGCGCTACAGGCAGGGCGGC 120
.....70.....80.....90.....100.....110.....
Q V S E G L G A I Q G R M V A N A N A P
FTSPZO101BPBHB/81-291 AAGTAAGCGAGGGATTAGGGGCGATACAAGGGCGTATGGTTGCTAATGCTAACGCACCAC 179
FS22EC101CA3FG/4-214 AAGTTAGCGAAGGATTAGGG-CTATGCAAGGGCGTATGATTGCCAATGCTACTGCACCAA 179
FTSPZO101B9AWK/7-218 AAGTGAGTAACAGTCTAGGCGCAATGCAATCGCGTATGATTGCAAATGCTAATGCACCAA 180
FTSPZO101B6C5R/133-266 AAGTTAGCAAAGGC---------- 134
FTSPZO101DMWHB/4-137 AAGTAGCAAAGGCT---------- 134
.....130.....140.....150.....160.....170.....
R T L N T G Y M G Q R
FTSPZO101BPBHB/81-291 GAACATTAAATACGGGTTATATGGGGCAACGT 211
FS22EC101CA3FG/4-214 GCACGCTAAACACAGGATTTAGGGGGCAGCGT 211
FTSPZO101B9AWK/7-218 GGGCGTTAAACACTGGTTATATGGGGCAACGT 212
FTSPZO101B6C5R/133-266 ---------- 134
FTSPZO101DMWHB/4-137 ---------- 134
.....190.....200.....210

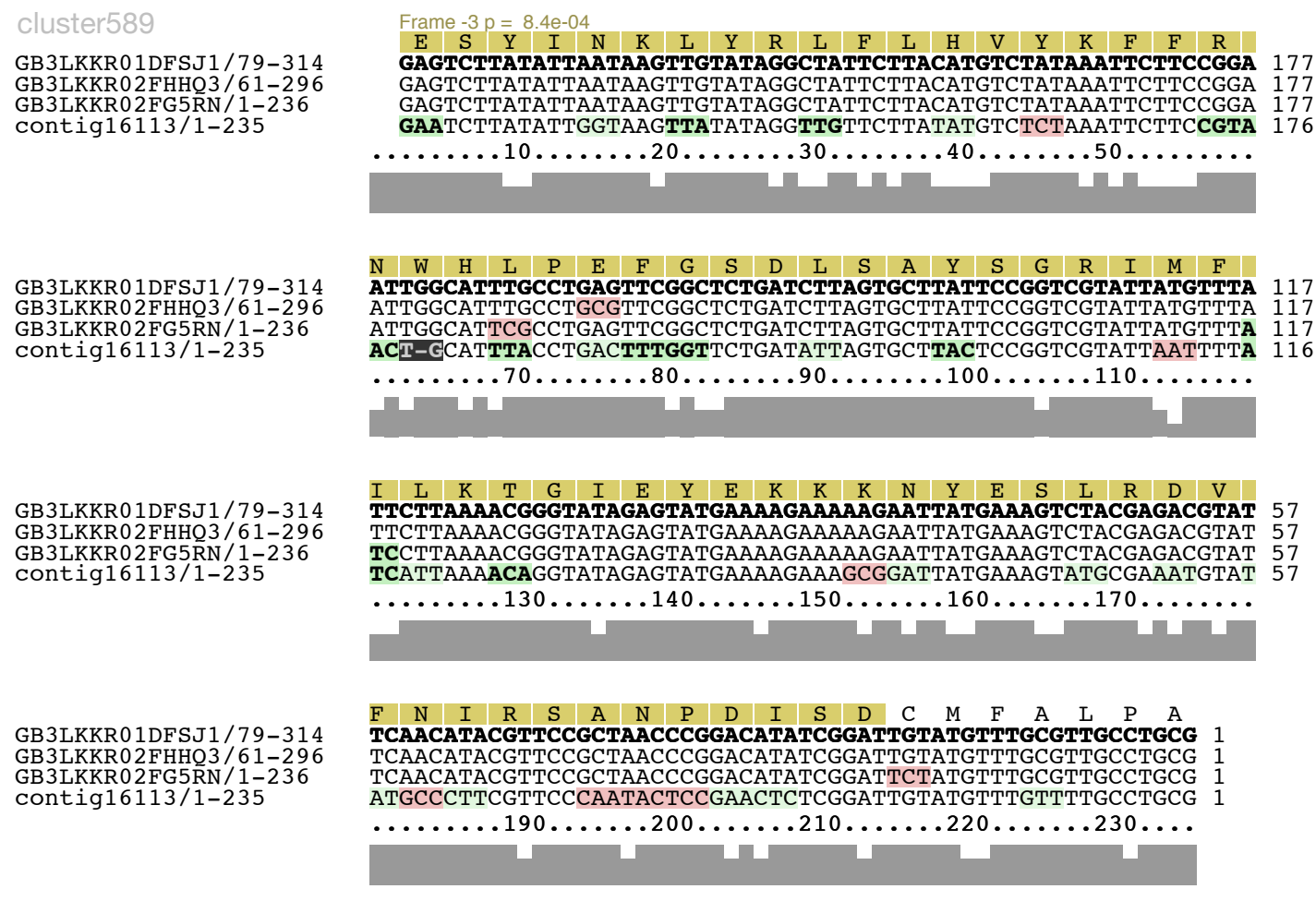

cluster502
Frame +1 p = 3.6e-07
D W L E T V Y T A G K Y L D R P E T P V
GB3LKKR01BXXY4/1-146 GATTGGTTAGAAACAGTATATACGGCAGGAAAATACCTTGACAGACCGGAAACACCGGTA 60
contig17153/1-146 GATTGGTTGGAAACAGTATATACGGCAGGAAAGTACCTTGACAGACCGGAAACACCGGTA 60
GB3LKKR02FQIJ5/1-127 -----------------ATACGGCAGGAAAATACCTTGACAGACCGGAAACACCGGTA 41
GB3LKKR02FUJR7/1-146 GATTGGTTGGAAACAGTATATACAGCAGGTAAATACCTTGACAGACCAGAGACACCAGTG 60
.....10.....20.....30.....40.....50.....
F I G G M T Q Y I E F D E V I S K S A T
GB3LKKR01BXXY4/1-146 TTTATCGGCGGTATGACCCAATATATCGAGTTCGATGAAGTAATTTCAAAATCAGCAACA 120
contig17153/1-146 TTCATCGGTGGTATGACCCAATATATTGAGTTCGATGAAGTAATCTCAAAATCAGCGACA 120
GB3LKKR02FQIJ5/1-127 TTTATCGGAGGTATGACACAATATATCGAATTCGACGAAGTGATCTCAAAAAGTGCGACA 101
GB3LKKR02FUJR7/1-146 TTTATTGGAGGTATGACACAGTACATTGAATTCGACGAAGTTATCTCAAAAAGTGCGACA 120
.....70.....80.....90.....100.....110.....
E T I Y G S Q P
GB3LKKR01BXXY4/1-146 GAAACAATATACGGCTCACAACCA 146
contig17153/1-146 GATACAATATATGGCTCACAACCA 146
GB3LKKR02FQIJ5/1-127 GAAACAGCATACGGAAGTCAACCA 127
GB3LKKR02FUJR7/1-146 GAAACAGCATACGGAAGTCAACCA 146
.....130.....140....

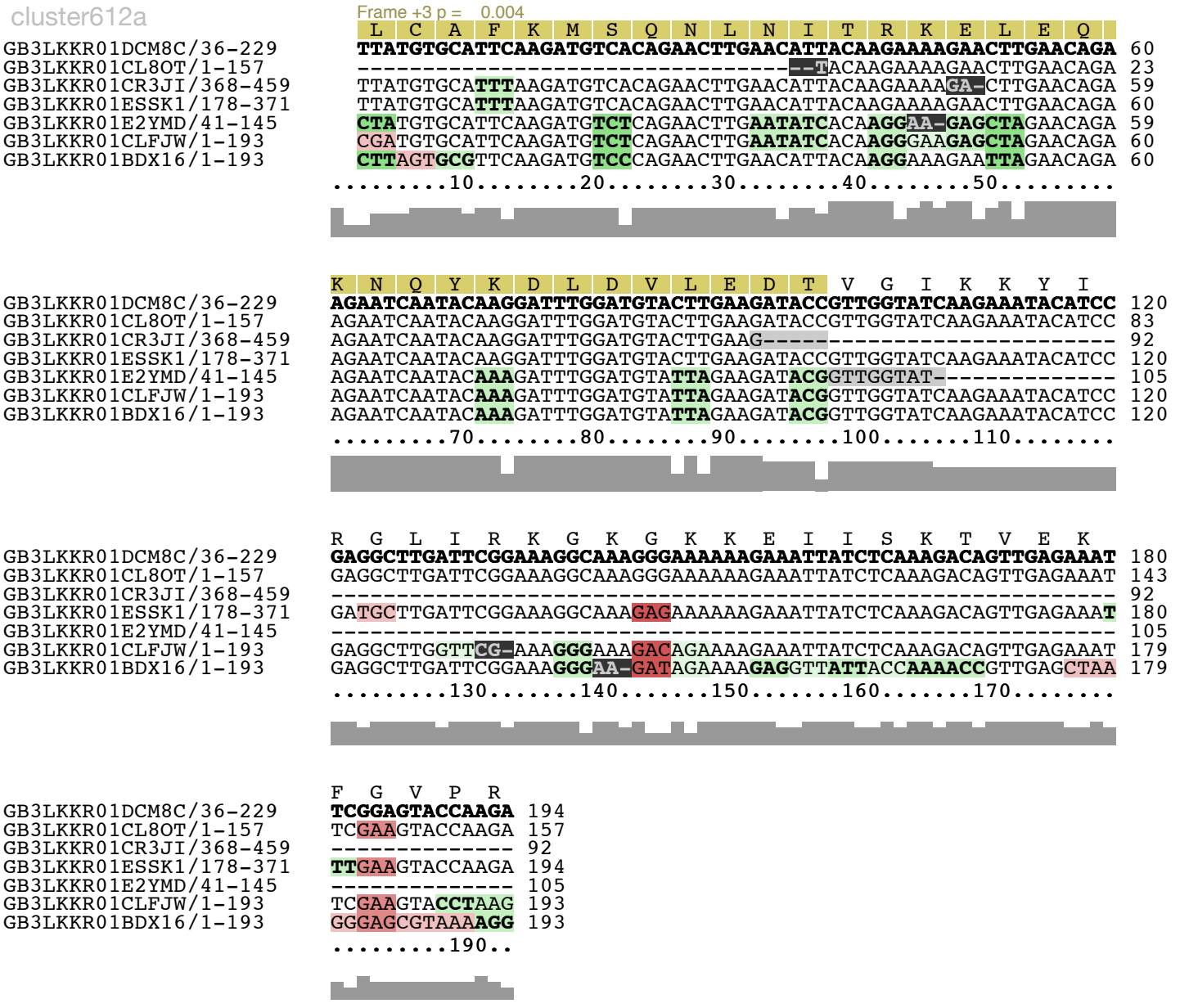

cluster532
Frame -1 p = 0.001
V A S S V D A V V E M D S E P E M V E I
contig08608/212-370 GTCGCTTCTTCGGTGGACGCAGTGGTGGAGATGGATAGCGAGCCGGAGATGGTGGAGATA 101
GB3LKKR01BKK2R/1-158 GTCGCCTCTTCGGTGGACGCAGTGGTGGAGATGGATAGCGAGCCGGAGATGGTGGAGATA 101
GB3LKKR02HC1UT/118-244 ----------G GATAGCGAGCCGGAGATGGTGGAGATA 69
GB3LKKR01CXJZO/1-159 GTAGCTTCTTCGGTGGACGCAGTGGTGGAGATGGATAGCGAGCCAGAGATGGTGGAGATA 101
GB3LKKR01BBV60/1-159 GTGGCTTCCTCTGCAGATATCGTGGTGGAGATGGATAGCGAGCCGGAGATGGTGGAGATA 101
.....10.....20.....30.....40.....50.....
E V E T G E F Y K T G A K K G Q P K T G
contig08608/212-370 GAGGTCGAGACAGGAGAGTTCTATAAGACGGGAGCTAAGAAAGGTCAGCCTAAGACGG-G 41
GB3LKKR01BKK2R/1-158 GAGGTCGAGACAGGAGAGTTCTATAAGACGGGAGCTAAGAAAGGTCAGCCTAAGACG--G 41
GB3LKKR02HC1UT/118-244 GAGGTCGAGACAGGAGAGCTCTACAAGACTGGAGCCAAGAAAGGCCAACCTAAGACAG-G 9
GB3LKKR01CXJZO/1-159 GAGGTCGAGACAGGAGAGCTCTACAAGACTGGAGCCAAGAAAGGCCAACCTAAGACAGAG 41
GB3LKKR01BBV60/1-159 GAGGTCGAGACAGGAGAGCTCTACAAGACTGGAGCCAAGAAAGGCCAACCTAAGACAGAA 41
.....70.....80.....90.....100.....110.....
K R R *
contig08608/212-370 AAAAAGAAGATAA 1
GB3LKKR01BKK2R/1-158 AAAAAGAAGATAA 1
GB3LKKR02HC1UT/118-244 AAAAAGAAGATAA 1
GB3LKKR01CXJZO/1-159 AAAAAGAAGATAA 1
GB3LKKR01BBV60/1-159 AAAAAGAAGATAA 1
.....130.....140.....150.....1


cluster540
F K P C V L G W Q P F L K K S L L L I V
FTSPZO101CLSF2/1-245 TTCAAGCCGTGTGTGCTAGGGTGGCAACCCTTCTTAAAGAAAAGTCTGTTATTGATAGT 60
ER8QEOW01CIRYO/1-228 ----------CAACGAGCGAGG-AGTTGATGAATGAGCAATCAGAAATTGGAAGT 44
DBA-SLE_c2415/1-183 ---------- 0
FC8LRL301AU4EL/48-245 TACCCGCCGCATTACCAACAAGCGAGGAGTTGATGAATGAGCAATCT---GTTGATAGT 57
is_serum_c2894/36-273 TACCTGCCGCATTACCGACAAGCGAGGAGTTGATGAATGAGCAATCT---ATTGATAGT 57
cerebrospinal_rep_c831/82-323 TACCTGCCGCATTACCGACAAGCGAGGAGTTATTAGATGAGCAATCT---ATTGATAGT 57
FS22EC101AWJ2M/34-274 TACCTGCCGCATTACCAACAAGCGAGGAGTTGATGAATGAGCAATCA---ATTGATAGT 57
.....10.....20.....30.....40.....50.....
Frame +2 p = 3.8e-04
E K V S K E D Y H Q W L S N P V T K A M
FTSPZO101CLSF2/1-245 GGAGAAAGTGAGCAAGGAGGACTATCACCAATGGTTGAGCAATCCAGTAACGAAGGCAAT 120
ER8QEOW01CIRYO/1-228 GGAGAAGGTGAGCAAGGCGGATTACCTGCAATGGTTGAGCAATCCAGTAACCAAGGCAAT 104
DBA-SLE_c2415/1-183 --AGAAGGTGAGTATAGCGGATTACCACCAATGGTTGAGCAATCCAGTAACCAAGGCAAT 58
FC8LRL301AU4EL/48-245 GGAGAAGGTGAGTATAGCGGATTACCACCAATGGTTGAGCAATCCAGTAACCAAGGCAAT 117
is_serum_c2894/36-273 GGAGAAGGTGAGCAAGGC-GATTA-CA-CAATGGT-GGACAATCCAGTGACCAAAGCGAT 113
cerebrospinal_rep_c831/82-323 GGAGAAGGTGAGTATAGCGGATTACCACCAATGGTTGAGCAATCCAGTGACCAAGGCRAT 117
FS22EC101AWJ2M/34-274 GGAGAAGGTGAGTATAGCGGATTATCACCAATGGTTGAGCAATCCAGTAACGAAGGCGAT 117
.....70.....80.....90.....100.....110.....
T A Q L T N E L M S L N S L T S L P N P
FTSPZO101CLSF2/1-245 GACGGCGCAATTGACCAACGAGTTGATGAGTCTCAACAGCCTAACGAGCCTACCCAATCC 180
ER8QEOW01CIRYO/1-228 GACGGCGCAATTGACCAACGAGTTGATGAGTCTCAACAGCCTAACGAGCCT-CCCAACCC 163
DBA-SLE_c2415/1-183 GACAGCTCACTTGACCAACGAATGTTTGAGCCTGAACCAACTGAGCAGCCTACCGAACCC 118
FC8LRL301AU4EL/48-245 GACGGCGCAATTGACCAACGAGTTGATGAGTCTCAACAGCCTAACGAGCCTCCCCAATCC 177
is_serum_c2894/36-273 GACGGCGCAATTGACCAACGAGTTGATGAGTCTCAACAGTTTAACGAGCCTACCCAATCC 173
cerebrospinal_rep_c831/82-323 GACGGCGCAATTGACCAACGAGTTGATGAGCCTCAACAGCCTAACGAGCCTCCCCAATCC 177
FS22EC101AWJ2M/34-274 GACGGCACAATTGACCAACGAGTTGATGAGTCTCAACAGCTTAACGAGCCTACCCAACCC 177
.....130.....140.....150.....160.....170.....
L T L E K V H Y Q L G K V Q G L T A V L
FTSPZO101CLSF2/1-245 GTTGACATTGGAGAAGGTGCATTACCAATTGGGCAAGGTGCAGGGATTGACGGCGGTGTT 240
ER8QEOW01CIRYO/1-228 ACAGACATTGGAGAAGGTACATTACCAATTGGGCAAGGTGCAGGGATTGACGGCGGTGCT 223
DBA-SLE_c2415/1-183 ATTGACATTGGAGGCGGTGAACTACCAACGGGGCAAGGTGTCGGGCTTGATGGCGGTCTT 178
FC8LRL301AU4EL/48-245 ATTGACATTGGAGAAGGTACA---------- 198
is_serum_c2894/36-273 ATTGACATTGGAGAAGGTGCATTACCAATTGGGCAAGGTGCAGGGATTGACGGCGGTGCT 233
cerebrospinal_rep_c831/82-323 ATTGGCATTGGAGAAGGTACATTACCAATTGGGCAAGGTGCAGGGATTGACGGCGGTGCT 237
FS22EC101AWJ2M/34-274 ATTAACATTGGAGAAGGTGCATTACCAATTGGGGAAGGTGGTTCGATCGACTTGTTGGGC 237
.....190.....200.....210.....220.....230.....
D
FTSPZO101CLSF2/1-245 GGAT 245
ER8QEOW01CIRYO/1-228 GGAT 228
DBA-SLE_c2415/1-183 GGAT 183
FC8LRL301AU4EL/48-245 ---- 198
is_serum_c2894/36-273 GGAT 238
cerebrospinal_rep_c831/82-323 GGAT 242
FS22EC101AWJ2M/34-274 GGG- 241
.....

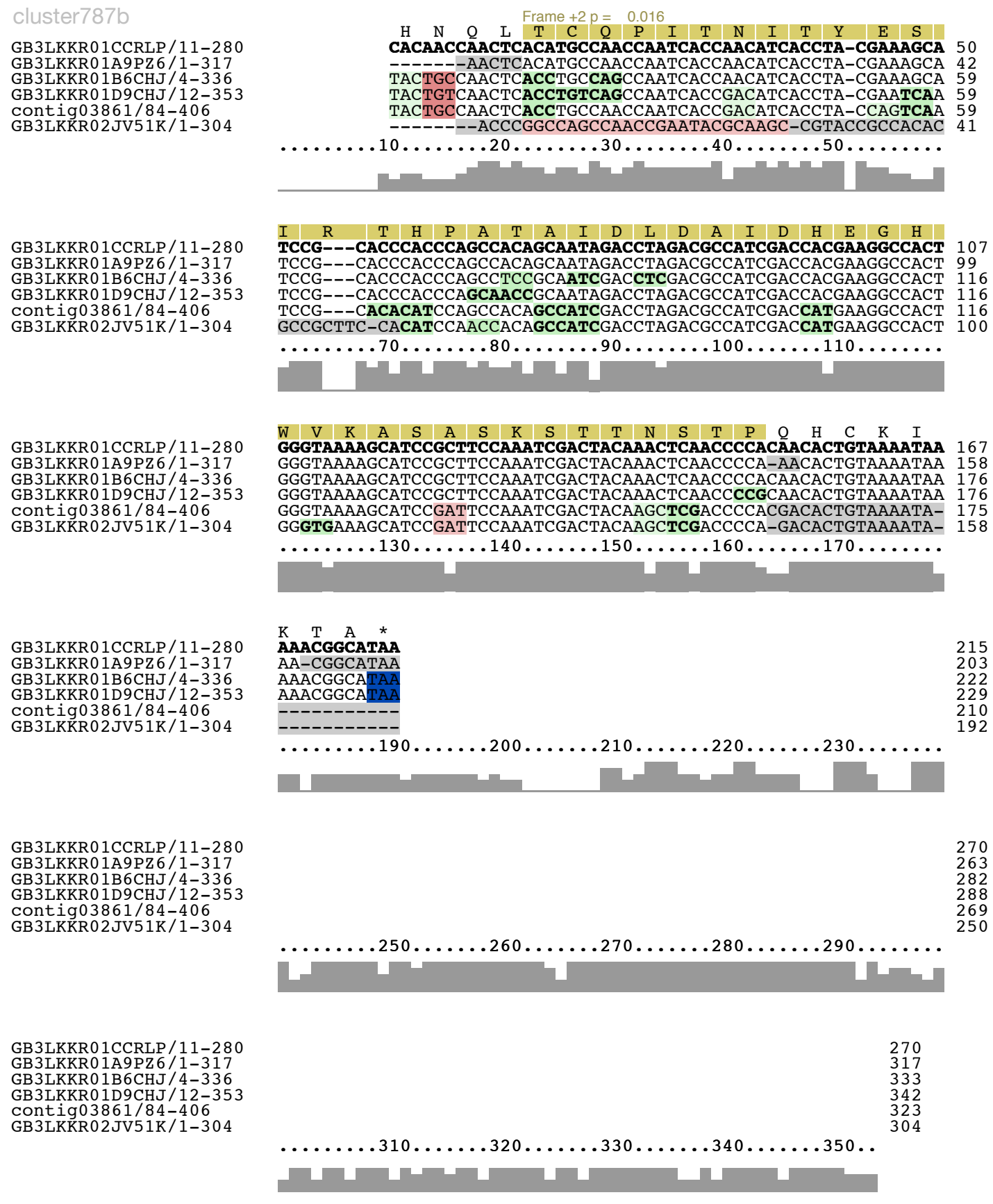

cluster562
Frame +1 p = 4.6e-07
E A F E Q F D A L R V A N A L G L E Y G
FTSPZO101A27VS/1-177 GAAGCGTTTGAACAGTTCGACGCATTGCGAGTTGCTAATGCACTCGGTCTTGAATATGGC 60
FTSPZO101DXNAS/13-189 GAAGCATTTGAACAGTTCGACGCACTACGCGTGGCTAACGCACTCGGTCTTGAATATGGC 60
FTSPZO101CZDGE/1-116 0
FTSPZO101D4AJL/108-284 GAAGCATTTGAACAGTTAGACGCGTTGCGCGTGGCAAATGCACTCGGCCTAGAATATGAA 60
DBA-SLE_c15330/93-269 GAAGCATTTGAACAGTTCGACGCACTACGCGTGGCMAACGCACTCGGTCTTGAATATGGC 60
FTSPZO101EUCSI/1-138 -CACTTGGTCTTGAATATGGC 20
FPFNBIF02IG1EQ/1-89 0
.....10.....20.....30.....40.....50.....
V V C K W R D R D Q I P A Y W R V K L
FTSPZO101A27VS/1-177 GTTGTTTG-CAAAT-GGCGTGACCGTGATCAAATTCCTGCTTACTGGCGCGTTAAACTTG 118
FTSPZO101DXNAS/13-189 GTTGTTTG-CAAAT-GGCGTGACCGTGATCAAATTCCTGCTTACTGGCGCGTTAAATTTG 118
FTSPZO101CZDGE/1-116 -TTGTTTG-CAAAT-GGCGTGATCGTGAGCAAATTCCTGCTTACTGGCGCGTTAAATTTG 57
FTSPZO101D4AJL/108-284 ACTGTTTG-CAAAT-GGCGTGACCGTGATCAAATTCCTGCTTACTGGCGCGTTAAATTTG 118
DBA-SLE_c15330/93-269 GTTGTTTG-CAAAT-GGCGTGACCGTGAGCAAATTCCTGCATACTGGCGCACACGGTTTG 118
FTSPZO101EUCSI/1-138 GTTGTTTGTCAAATAGGCGTGACCGTGAGTCGATTCCAGCTTATTGGCGCGTTAAATTT- 79
FPFNBIF02IG1EQ/1-89 -----------------------------GAGCTCTGCAGATAT-CGCTGTGCAAGTTTG 30
.....70.....80.....90.....100.....110.....
V N L M N H H N V A I S L H D L A G W I
FTSPZO101A27VS/1-177 TTAATTTGATGAATCATCATAACGTAGCGATTTCTTTGCACGACTTAGCAGGATGGATT 177
FTSPZO101DXNAS/13-189 TTAATTTGATGAATCATCACGGCGTTTCTATTTCTTTACACGATTTGGCAGGGTGGATT 177
FTSPZO101CZDGE/1-116 TCAACTTAATGAATCATCATAACGTAGCAATTACGCTACACGATTTGGCAGGGTGGATT 116
FTSPZO101D4AJL/108-284 TTAATTTGATGAATCATCATAACGTAGCAATCAAGCTACATGACCTGGCAGGGTGGATT 177
DBA-SLE_c15330/93-269 TTAATTTAATGAATAACCATAACGTAGCAATCAAGCTACATGACCTGGCAGGGTGGATT 177
FTSPZO101EUCSI/1-138 GTAACTTGATGAATCATCATAACGTAGCAATCAAGCTACATGACCTGGCAGGGTGGATT 138
FTSPZO101EUCSI/1-89 TTAATTTGATGAATCATCATAACGTAGCAATCAAGCTACATGACCTGGCAGGGTGGATT 89
.....130.....140.....150.....160.....170.....

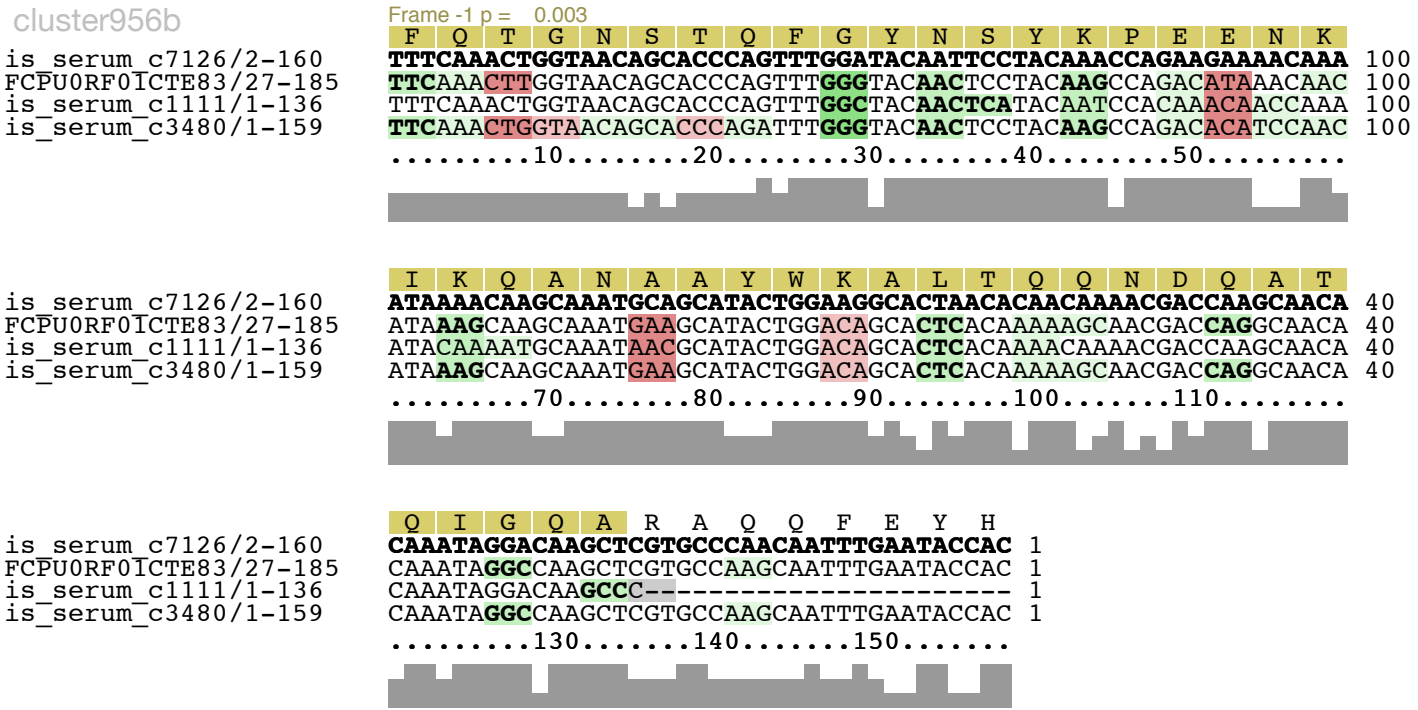

cluster565b
K M Y K K N L F N R F W D L Y D P K E
FTSPZO101A2LOY/1-134 AAGATGTACAAGAAGAATTTGTTCAATCGGTTTTGGGA-TCTGTA-CGAT-CCGAA-GGA 86
is_serum_c150/232-376 AAGATGTACAAGAAGAATTTGTTCAATCGGTTTTGGGA-TCTGTA-CGAT-CCGAA-GGA 86
FS22EC10TCV6FM/1-150 AAGATGTATAAGAAGAATTTGTACAGCAAGTTTTTTGAATTGTACCGATCCCGAAAGGA 91
FCPU0RF01DWGD1/74-139 -- 7
.....10.....20.....30.....40.....50.....
Frame -1 p = 0.003
H T H V M M E D L D H E A V E K L S I
FTSPZO101A2LOY/1-134 G-CATACGCACGTGATGATGGAAGATTTGGACCACGAGGCAGTGGAGAAGTTGAGCATCA 31
is_serum_c150/232-376 G-CATACGCACGTGATGATGGAAGATTTGGACCACGAGGCAGTGGAGAAGTTGAGCATCA 31
FS22EC10TCV6FM/1-150 GCCATACGCATGTGATGATGGAAGATTTGGACCATGAGGCAGTGGAGAAGTTGAGTATCA 31
FCPU0RF01DWGD1/74-139 ----------------------ATCTGGGCCATGAAGCAGTGGAGAAGCTCAGTATCA 1
.....70.....80.....90.....100.....110.....
N F I K T V
FTSPZO101A2LOY/1-134 ACTTTATCAAGACGGTA 1
is_serum_c150/232-376 ACTTTATCAAGACGGTA 1
FS22EC10TCV6FM/1-150 ACTTTATCAAGACAATT 1
FCPU0RF01DWGD1/74-139 ATTTTATCAAGACGATT 1
.....130.....140.....1

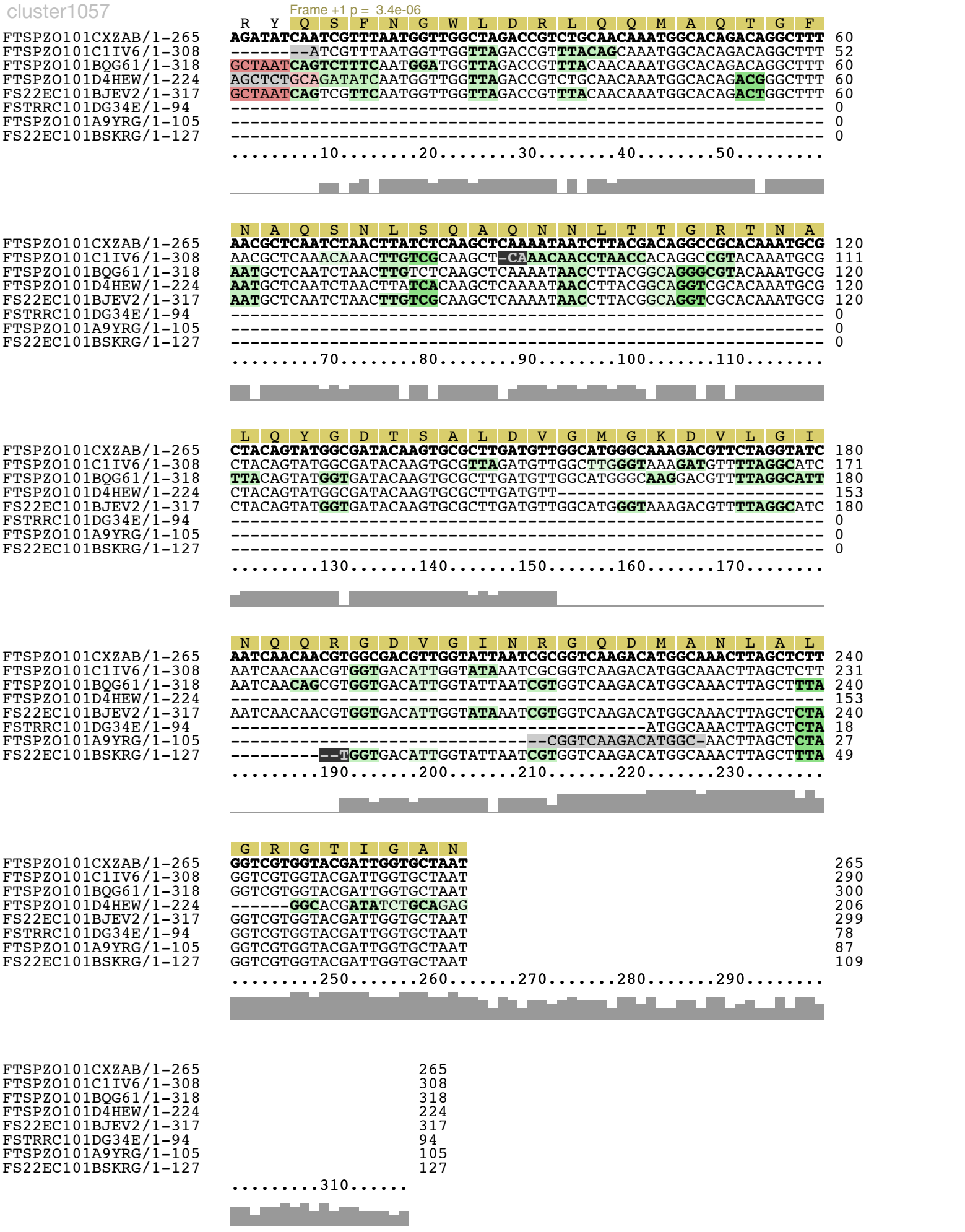

cluster589
Frame -3 p = 8.4e-04
E S Y I N K L Y R L F L H V Y K F F R
GB3LKKR01DFSJ1/79-314 GAGTCTTATATTAATAAGTTGTATAGGCTATTCTTACATGTCTATAAATTCTTCCGGA 177
GB3LKKR02FHHQ3/61-296 GAGTCTTATATTAATAAGTTGTATAGGCTATTCTTACATGTCTATAAATTCTTCCGGA 177
GB3LKKR02FG5RN/1-236 GAGTCTTATATTAATAAGTTGTATAGGCTATTCTTACATGTCTATAAATTCTTCCGGA 177
contig16113/1-235 GAATCTTATATTGGTAAGTTATATAGGTTGTTCTTATATGTCTCTAAATTCTTCCGTA 176
.....10.....20.....30.....40.....50.....
N W H L P E F G S D L S A Y S G R I M F
GB3LKKR01DFSJ1/79-314 ATTGGCATTTGCCTGAGTTCGGCTCTGATCTTAGTGCTTATTCCGGTCGTATTATGTTTA 117
GB3LKKR02FHHQ3/61-296 ATTGGCATTTGCCTGCGTTCGGCTCTGATCTTAGTGCTTATTCCGGTCGTATTATGTTTA 117
GB3LKKR02FG5RN/1-236 ATTGGCATTCGCCTGAGTTCGGCTCTGATCTTAGTGCTTATTCCGGTCGTATTATGTTTA 117
contig16113/1-235 ACT-GCATTTACCTGACTTTGGTTCTGATATTAGTGCTTACTCCGGTCGTATTAATTTTA 116
.....70.....80.....90.....100.....110.....
I L K T G I E Y E K K K N Y E S L R D V
GB3LKKR01DFSJ1/79-314 TTCTTAAAACGGGTATAGAGTATGAAAAGAAAAAGAATTATGAAAGTCTACGAGACGTAT 57
GB3LKKR02FHHQ3/61-296 TTCTTAAAACGGGTATAGAGTATGAAAAGAAAAAGAATTATGAAAGTCTACGAGACGTAT 57
GB3LKKR02FG5RN/1-236 TCCTTAAAACGGGTATAGAGTATGAAAAGAAAAAGAATTATGAAAGTCTACGAGACGTAT 57
contig16113/1-235 TCATTAAAACAGGTATAGAGTATGAAAAGAAAGCGGATTATGAAAGTATGCGAAATGTAT 57
.....130.....140.....150.....160.....170.....
F N I R S A N P D I S D C M F A L P A
GB3LKKR01DFSJ1/79-314 TCAACATACGTTCCGCTAACCCGGACATATCGGATTGTATGTTTGCGTTGCCTGCG 1
GB3LKKR02FHHQ3/61-296 TCAACATACGTTCCGCTAACCCGGACATATCGGATTGTATGTTTGCGTTGCCTGCG 1
GB3LKKR02FG5RN/1-236 TCAACATACGTTCCGCTAACCCGGACATATCGGATTCTATGTTTGCGTTGCCTGCG 1
contig16113/1-235 ATGCCCTTCGTTCCCAATACTCCGAACTCTCGGATTGTATGTTTGTTTTGCCTGCG 1
.....190.....200.....210.....220.....230....

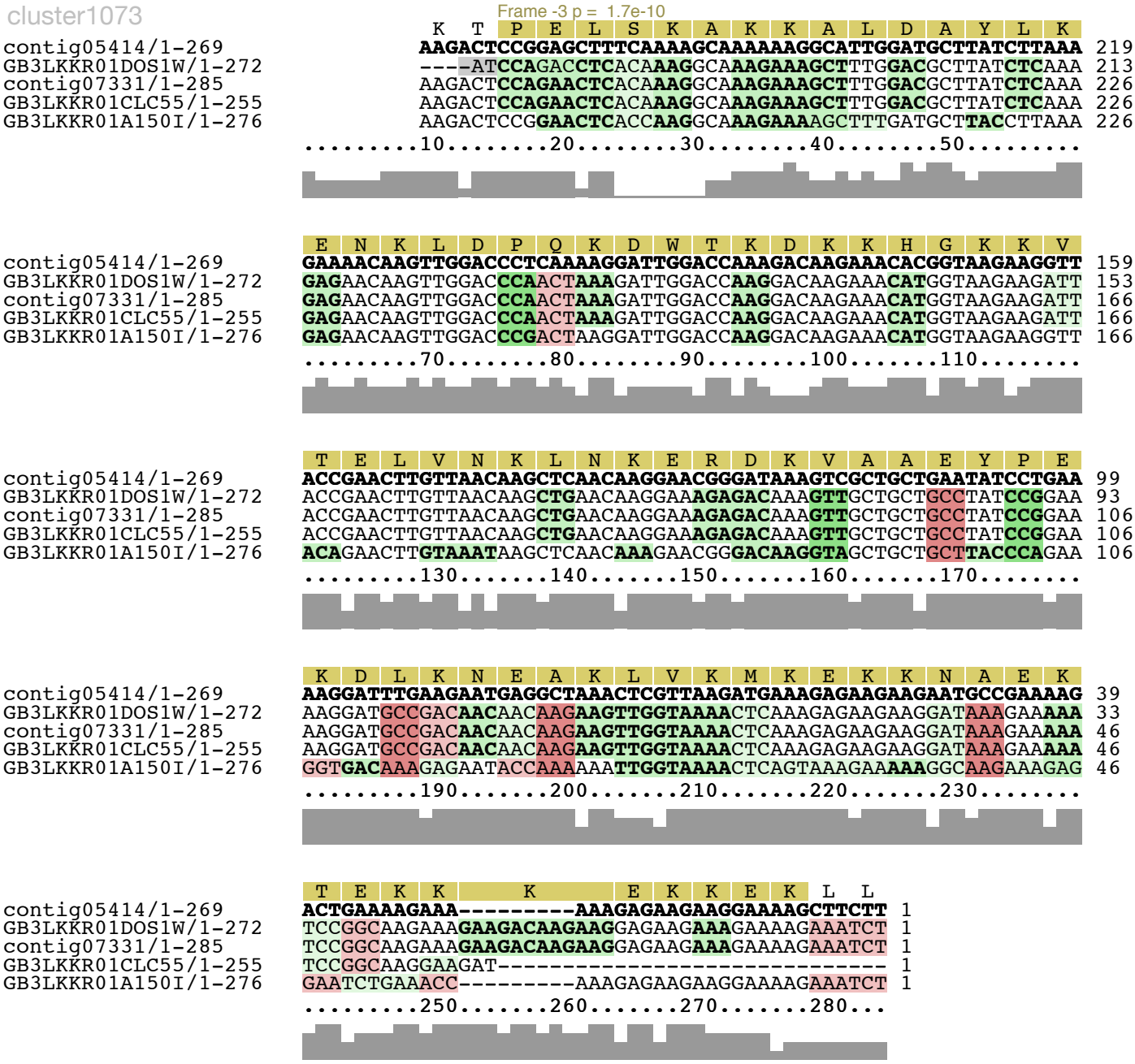

cluster612a
Frame +3 p = 0.004
L C A F K M S Q N L N I T R K E L E Q
GB3LKKR01DCM8C/36-229 TTATGTGCATTCAAGATGTCACAGAACTTGAACATTACAAGAAAAGAACTTGAACAGA 60
GB3LKKR01CL8OT/1-157 --TACAAGAAAAGAACTTGAACAGA 23
GB3LKKR01CR3JI/368-459 TTATGTGCATTTAAGATGTCACAGAACTTGAACATTACAAGAAAAGA-CTTGAACAGA 59
GB3LKKR01ESSK1/178-371 TTATGTGCATTTAAGATGTCACAGAACTTGAACATTACAAGAAAAGAACTTGAACAGA 60
GB3LKKR01E2YMD/41-145 CTATGTGCATTCAAGATGTCTCAGAACTTGAATATCACAAGGAA-GAGCTAGAACAGA 59
GB3LKKR01CLFJW/1-193 CGATGTGCATTCAAGATGTCTCAGAACTTGAATATCACAAGGGAAGAGCTAGAACAGA 60
GB3LKKR01BDX16/1-193 CTTAGTGCGTTCAAGATGTCCCAGAACTTGAACATTACAAGGAAAGAATTAGAACAGA 60
.....10.....20.....30.....40.....50.....
K N Q Y K D L D V L E D T V G I K K Y I
GB3LKKR01DCM8C/36-229 AGAATCAATACAAGGATTTGGATGTACTTGAAGATACCGTTGGTATCAAGAAATACATCC 120
GB3LKKR01CL8OT/1-157 AGAATCAATACAAGGATTTGGATGTACTTGAAGATACCGTTGGTATCAAGAAATACATCC 83
GB3LKKR01CR3JI/368-459 AGAATCAATACAAGGATTTGGATGTACTTGAAG----------92
GB3LKKR01ESSK1/178-371 AGAATCAATACAAGGATTTGGATGTACTTGAAGATACCGTTGGTATCAAGAAATACATCC 120
GB3LKKR01E2YMD/41-145 AGAATCAATACAAAGATTTGGATGTATTAGAAGATACGGTTGGTAT----------105
GB3LKKR01CLFJW/1-193 AGAATCAATACAAAGATTTGGATGTATTAGAAGATACGGTTGGTATCAAGAAATACATCC 120
GB3LKKR01BDX16/1-193 AGAATCAATACAAAGATTTGGATGTATTAGAAGATACGGTTGGTATCAAGAAATACATCC 120
.....70.....80.....90.....100.....110.....
R G L I R K G K G K K E I I S K T V E K
GB3LKKR01DCM8C/36-229 GAGGCTTGATTCGGAAAGGCAAAGGGAAAAAAGAAATTATCTCAAAGACAGTTGAGAAAT 180
GB3LKKR01CL8OT/1-157 GAGGCTTGATTCGGAAAGGCAAAGGGAAAAAAGAAATTATCTCAAAGACAGTTGAGAAAT 143
GB3LKKR01CR3JI/368-459 ----------92
GB3LKKR01ESSK1/178-371 GATGCTTGATTCGGAAAGGCAAAGAGAAAAAAGAAATTATCTCAAAGACAGTTGAGAAAT 180
GB3LKKR01E2YMD/41-145 ----------105
GB3LKKR01CLFJW/1-193 GAGGCTTGGTTCG-AAAGGGAAAGACAGAAAAGAAATTATCTCAAAGACAGTTGAGAAAT 179
GB3LKKR01BDX16/1-193 GAGGCTTGATTCGGAAAGGGAA-GATAGAAAAGAGGTTATTACCAAAACCGTTGAGCTAA 179
.....130.....140.....150.....160.....170.....
F G V P R
GB3LKKR01DCM8C/36-229 TCGGAGTACCAAGA 194
GB3LKKR01CL8OT/1-157 TCGAAGTACCAAGA 157
GB3LKKR01CR3JI/368-459 ---------- 92
GB3LKKR01ESSK1/178-371 TTGAAGTACCAAGA 194
GB3LKKR01E2YMD/41-145 ---------- 105
GB3LKKR01CLFJW/1-193 TCGAAGTACCTAAG 193
GB3LKKR01BDX16/1-193 GGGAGCGTAAAAGG 193
.....190..

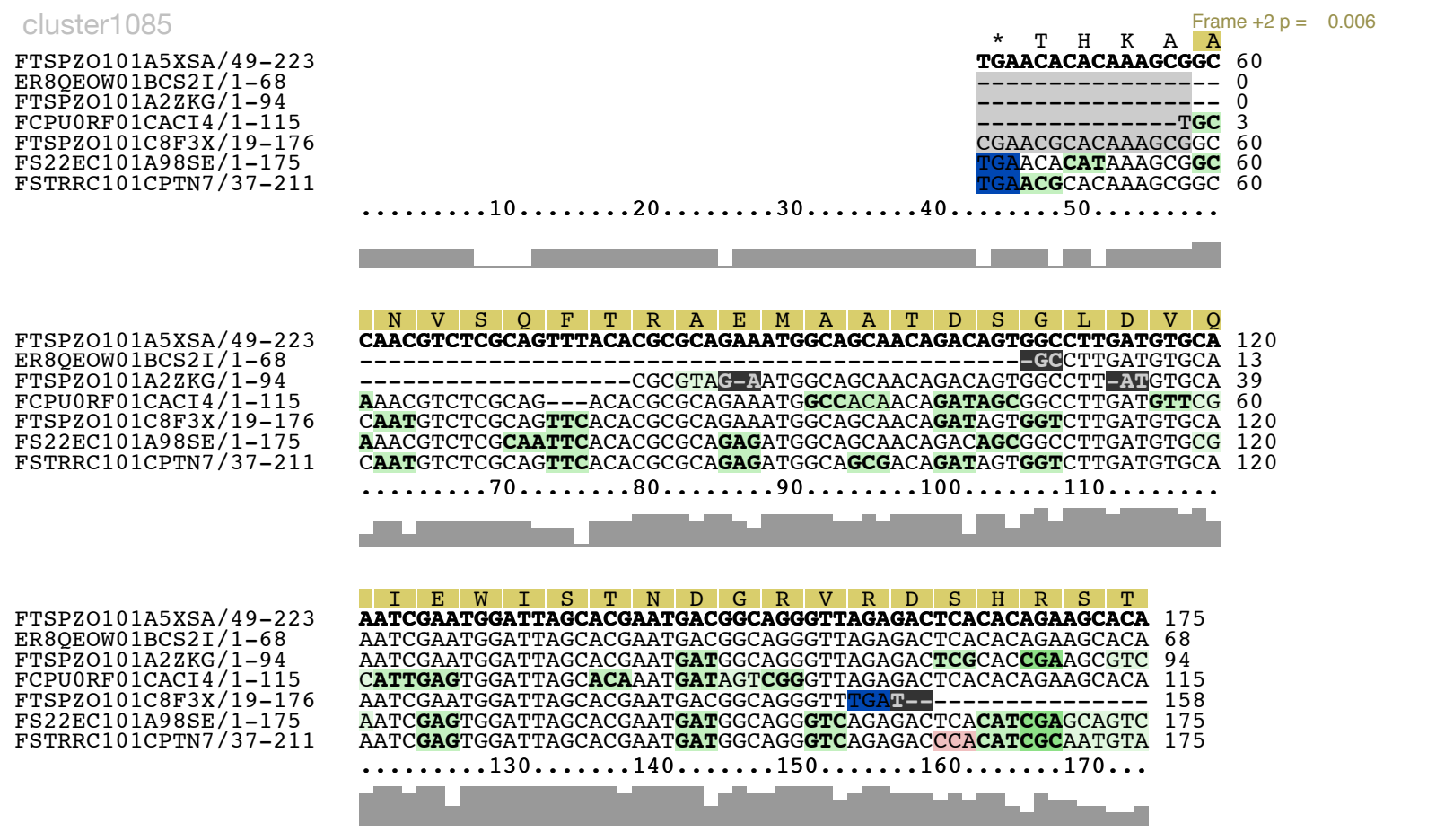
cluster787b

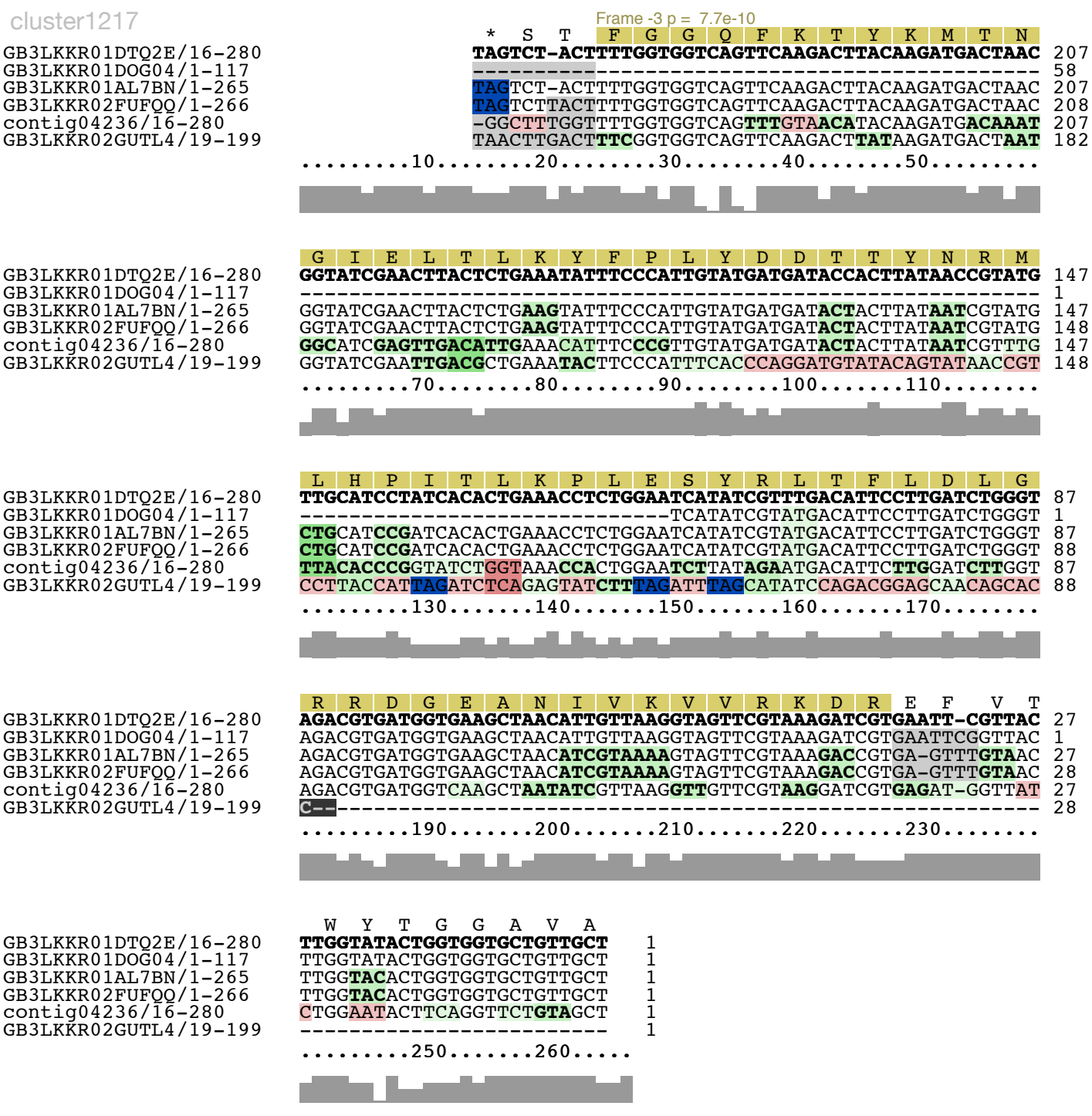


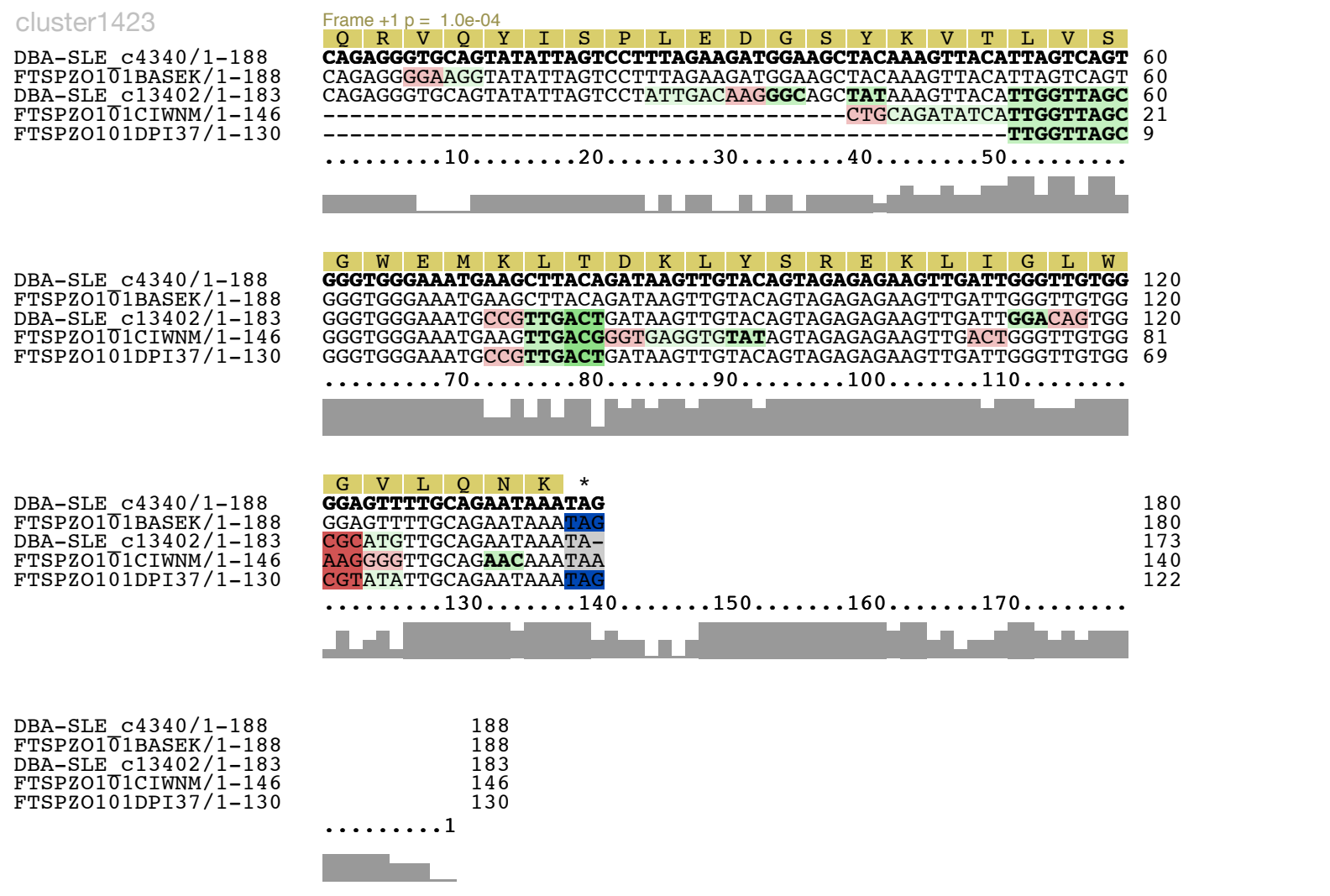

cluster956b
Frame -1 p = 0.003
F Q T G N S T Q F G Y N S Y K P E E N K
is_serum_c7126/2-160 TTTCAAACTGGTAACAGCACCCAGTTTGGATACAATTCCTACAAACCAGAAGAAAACAAA 100
FCPU0RF01CTE83/27-185 TTCAAACTTGGTAACAGCACCCAGTTTGGGTACAACTCCTACAAGCCAGACATAAACAAC 100
is_serum_c1111/1-136 TTTCAAACTGGTAACAGCACCCAGTTTGGCTACAACTCATACAATCCACAAACAACCAAA 100
is_serum_c3480/1-159 TTCAAACTGGTAACAGCACCCAGATTTGGGTACAACTCCTACAAGCCAGACACATCCAAC 100
.....10.....20.....30.....40.....50.....
I K Q A N A A Y W K A L T Q Q N D Q A T
is_serum_c7126/2-160 ATAAAACAAGCAAATGCAGCATACTGGAAGGCACTAACACAACAAAACGACCAAGCAACA 40
FCPU0RF01CTE83/27-185 ATAAAGCAAGCAAATGAAGCATACTGGACAGCACTCACAAAAAGCAACGACCAGGCAACA 40
is_serum_c1111/1-136 ATACAAAATGCAAATAACGCATACTGGACAGCACTCACAAAACAAAACGACCAAGCAACA 40
is_serum_c3480/1-159 ATAAAGCAAGCAAATGAAGCATACTGGACAGCACTCACAAAAAGCAACGACCAGGCAACA 40
.....70.....80.....90.....100.....110.....
Q I G Q A R A Q Q F E Y H
is_serum_c7126/2-160 CAAATAGGACAAGCTCGTGCCCAACAATTTGAATACCAC 1
FCPU0RF01CTE83/27-185 CAAATAGGCCAAGCTCGTGCCAAGCAATTTGAATACCAC 1
is_serum_c1111/1-136 CAAATAGGACAAGCCC----------------------- 1
is_serum_c3480/1-159 CAAATAGGCCAAGCTCGTGCCAAGCAATTTGAATACCAC 1
.....130.....140.....150.....


cluster1057
Frame +1 p = 3.4e-06
R Y Q S F N G W L D R L Q Q M A Q T G F
FTSPZO101CXZAB/1-265 AGATATCAATCGTTTAATGGTTGGCTAGACCGTCTGCAACAAATGGCACAGACAGGCTTT 60
FTSPZO101C1IV6/1-308 -------ATCGTTTAATGGTTGGTTAGACCGTTTACAGCAAATGGCACAGACAGGCTTT 52
FTSPZO101BQG61/1-318 GCTAATCAGTCTTTCAATGGATGGTTAGACCGTTTACAACAAATGGCACAGACAGGCTTT 60
FTSPZO101D4HEW/1-224 AGCTCTGCAGATATCAATGGTTGGTTAGACCGTCTGCAACAAATGGCACAGACGGGCTTT 60
FS22EC101BJEV2/1-317 GCTAATCAGTCGTTCAATGGTTGGTTAGACCGTTTACAACAAATGGCACAGACTGGCTTT 60
FSTRRC101DG34E/1-94 -- 0
FTSPZO101A9YRG/1-105 -- 0
FS22EC101BSKRG/1-127 -- 0
.....10.....20.....30.....40.....50.....
N A Q S N L S Q A Q N N L T T G R T N A
FTSPZO101CXZAB/1-265 AACGCTCAATCTAACTTATCTCAAGCTCAAAATAATCTTACGACAGGCCGCACAAATGCG 120
FTSPZO101C1IV6/1-308 AACGCTCAAACAAACTTGTCGCAAGCT-CAAACAACCTAACCACAGGCCGTACAAATGCG 111
FTSPZO101BQG61/1-318 AATGCTCAATCTAACTTGTCTCAAGCTCAAAATAACCTTACGGCAGGGCGTACAAATGCG 120
FTSPZO101D4HEW/1-224 AATGCTCAATCTAACTTATCACAAGCTCAAAATAACCTTACGGCAGGTCGCACAAATGCG 120
FS22EC101BJEV2/1-317 AATGCTCAATCTAACTTGTCGCAAGCTCAAAATAACCTTACGGCAGGTCGCACAAATGCG 120
FSTRRC101DG34E/1-94 -- 0
FTSPZO101A9YRG/1-105 -- 0
FS22EC101BSKRG/1-127 -- 0
.....70.....80.....90.....100.....110.....
L Q Y G D T S A L D V G M G K D V L G I
FTSPZO101CXZAB/1-265 CTACAGTATGGCGATACAAGTGCGCTTGATGTTGGCATGGGCAAAGACGTTCTAGGTATC 180
FTSPZO101C1IV6/1-308 CTACAGTATGGCGATACAAGTGCGTTAGATGTTGGCTTGGGTAAAGATGTTTTAGGCATC 171
FTSPZO101BQG61/1-318 TTACAGTATGGTGATACAAGTGCGCTTGATGTTGGCATGGGCAAGGACGTTTTAGGCATT 180
FTSPZO101D4HEW/1-224 CTACAGTATGGCGATACAAGTGCGCTTGATGTT---------------------------- 153
FS22EC101BJEV2/1-317 CTACAGTATGGTGATACAAGTGCGCTTGATGTTGGCATGGGTAAAGACGTTTTAGGCATC 180
FSTRRC101DG34E/1-94 -- 0
FTSPZO101A9YRG/1-105 -- 0
FS22EC101BSKRG/1-127 -- 0
.....130.....140.....150.....160.....170.....
N Q Q R G D V G I N R G Q D M A N L A L
FTSPZO101CXZAB/1-265 AATCAACAACGTGGCGACGTTGGTATTAATCGCGGTCAAGACATGGCAAACTTAGCTCTT 240
FTSPZO101C1IV6/1-308 AATCAACAACGTGGTGACATTGGTATAAATCGCGGTCAAGACATGGCAAACTTAGCTCTT 231
FTSPZO101BQG61/1-318 AATCAACAGCGTGGTGACATTGGTATTAATCGTGGTCAAGACATGGCAAACTTAGCTTTA 240
FTSPZO101D4HEW/1-224 -- 153
FS22EC101BJEV2/1-317 AATCAACAACGTGGTGACATTGGTATAAATCGTGGTCAAGACATGGCAAACTTAGCTCTA 240
FSTRRC101DG34E/1-94 --ATGGCAAACTTAGCTCTA 18
FTSPZO101A9YRG/1-105 ----------------------------------CGGTCAAGACATGGC-AACTTAGCTCTA 27
FS22EC101BSKRG/1-127 ---------TGGTGACATTGGTATTAATCGTGGTCAAGACATGGCAAACTTAGCTTTA 49
.....190.....200.....210.....220.....230.....
G R G T I G A N
FTSPZO101CXZAB/1-265 GGTCGTGGTACGATTGGTGCTAAT 265
FTSPZO101C1IV6/1-308 GGTCGTGGTACGATTGGTGCTAAT 290
FTSPZO101BQG61/1-318 GGTCGTGGTACGATTGGTGCTAAT 300
FTSPZO101D4HEW/1-224 ------GGCACGATATCTGCAGAG 206
FS22EC101BJEV2/1-317 GGTCGTGGTACGATTGGTGCTAAT 299
FSTRRC101DG34E/1-94 GGTCGTGGTACGATTGGTGCTAAT 78
FTSPZO101A9YRG/1-105 GGTCGTGGTACGATTGGTGCTAAT 87
FS22EC101BSKRG/1-127 GGTCGTGGTACGATTGGTGCTAAT 109
.....250.....260.....270.....280.....290.....
FTSPZO101CXZAB/1-265 265
FTSPZO101C1IV6/1-308 308
FTSPZO101BQG61/1-318 318
FTSPZO101D4HEW/1-224 224
FS22EC101BJEV2/1-317 317
FSTRRC101DG34E/1-94 94
FTSPZO101A9YRG/1-105 105
FS22EC101BSKRG/1-127 127
.....310.....

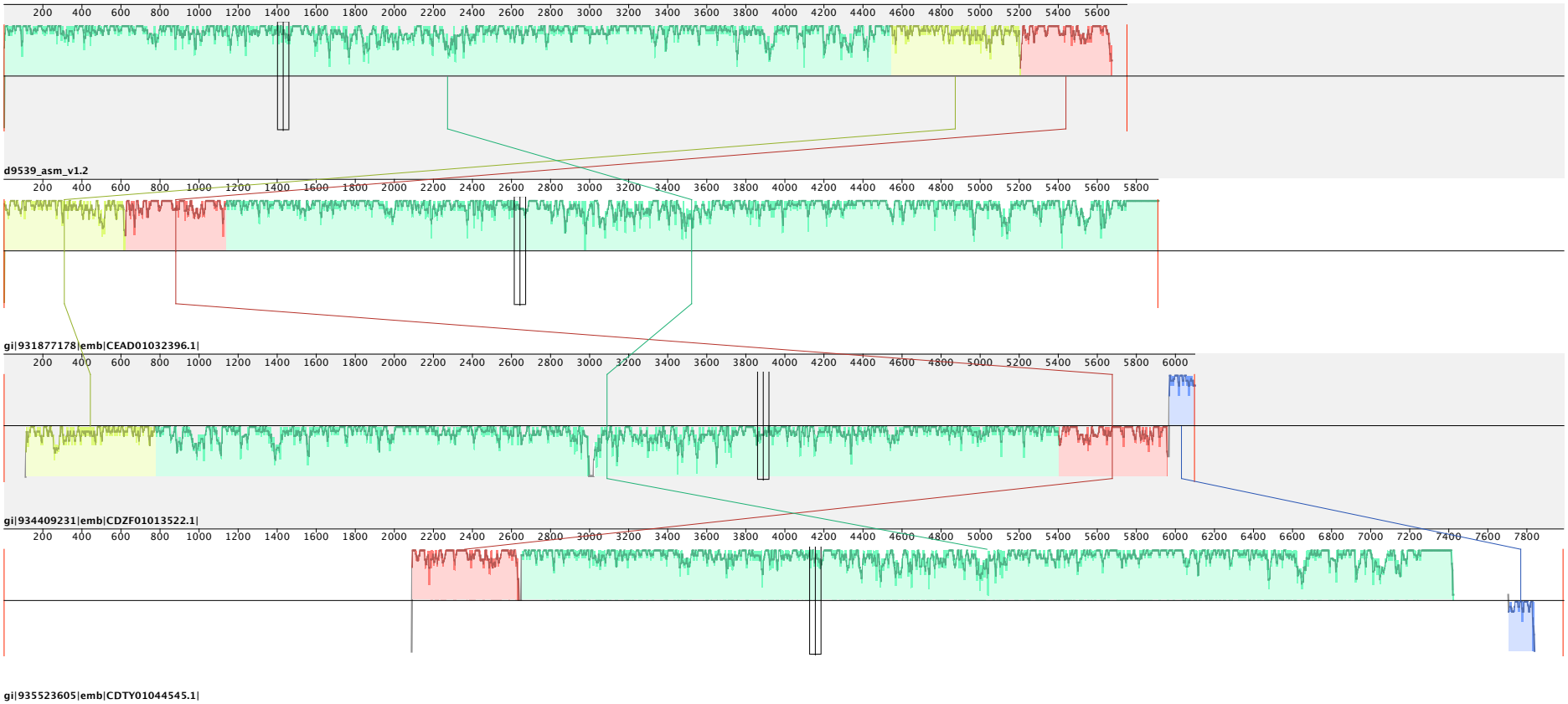

cluster1073
Frame -3 p = 1.7e-10
K T P E L S K A K K A L D A Y L K
contig05414/1-269 AAGACTCCGGAGCTTTCAAAAGCAAAAAAGGCATTGGATGCTTATCTTAAA 219
GB3LKKR01DOS1W/1-272 ---ATCCAGACCTCACAAAGGCAAAGAAAGCTTTGGACGCTTATCTCAAA 213
contig07331/1-285 AAGACTCCAGAACTCACAAAGGCAAAGAAAGCTTTGGACGCTTATCTCAAA 226
GB3LKKR01CLC55/1-255 AAGACTCCAGAACTCACAAAGGCAAAGAAAGCTTTGGACGCTTATCTCAAA 226
GB3LKKR01A150I/1-276 AAGACTCCGGAACTCACCAAGGCAAAGAAAAGCTTTGATGCTTACCTTAAA 226
.....10.....20.....30.....40.....50.....
E N K L D P Q K D W T K D K K H G K K V
contig05414/1-269 GAAAACAAGTTGGACCCTCAAAAGGATTGGACCAAAGACAAGAAACACGGTAAGAAGGTT 159
GB3LKKR01DOS1W/1-272 GAGAACAAGTTGGACCCAACTAAAGATTGGACCAAGGACAAGAAACATGGTAAGAAGATT 153
contig07331/1-285 GAGAACAAGTTGGACCCAACTAAAGATTGGACCAAGGACAAGAAACATGGTAAGAAGATT 166
GB3LKKR01CLC55/1-255 GAGAACAAGTTGGACCCAACTAAAGATTGGACCAAGGACAAGAAACATGGTAAGAAGATT 166
GB3LKKR01A150I/1-276 GAGAACAAGTTGGACCCGACTAAGGATTGGACCAAGGACAAGAAACATGGTAAGAAGGTT 166
.....70.....80.....90.....100.....110.....
T E L V N K L N K E R D K V A A E Y P E
contig05414/1-269 ACCGAACTTGTTAACAAGCTCAACAAGGAACGGGATAAAGTCGCTGCTGAATATCCTGAA 99
GB3LKKR01DOS1W/1-272 ACCGAACTTGTTAACAAGCTGAACAAGGAAAGAGACAAAGTTGCTGCTGCCTATCCGGAA 93
contig07331/1-285 ACCGAACTTGTTAACAAGCTGAACAAGGAAAGAGACAAAGTTGCTGCTGCCTATCCGGAA 106
GB3LKKR01CLC55/1-255 ACCGAACTTGTTAACAAGCTGAACAAGGAAAGAGACAAAGTTGCTGCTGCCTATCCGGAA 106
GB3LKKR01A150I/1-276 ACAGAACTTGTAAATAAGCTCAACAAAGAACGGGACAAGGTAGCTGCTGCTTACCCAGAA 106
.....130.....140.....150.....160.....170.....
K D L K N E A K L V K M K E K K N A E K
contig05414/1-269 AAGGATTTGAAGAATGAGGCTAAACTCGTTAAGATGAAAGAGAAGAAGAATGCCGAAAAG 39
GB3LKKR01DOS1W/1-272 AAGGATGCCGACAACAACAAGAAGTTGGTAAAACTCAAAGAGAAGAAGGATAAAGAAAAA 33
contig07331/1-285 AAGGATGCCGACAACAACAAGAAGTTGGTAAAACTCAAAGAGAAGAAGGATAAAGAAAAA 46
GB3LKKR01CLC55/1-255 AAGGATGCCGACAACAACAAGAAGTTGGTAAAACTCAAAGAGAAGAAGGATAAAGAAAAA 46
GB3LKKR01A150I/1-276 GGTGACAAAGAGAATACCAAAAAATTGGTAAAACTCAGTAAAGAAAAAGGCAAGAAAGAG 46
.....190.....200.....210.....220.....230.....
T E K K K E K K E K L L
contig05414/1-269 ACTGAAAAGAAA---------AAAGAGAAGAAGGAAAAGCTTCTT 1
GB3LKKR01DOS1W/1-272 TCCGGCAAGAAAGAAGACAAGAAGGAGAAGAAAGAAAAGAAATCT 1
contig07331/1-285 TCCGGCAAGAAAGAAGACAAGAAGGAGAAGAAAGAAAAGAAATCT 1
GB3LKKR01CLC55/1-255 TCCGGCAAGGAAGAT---------- 1
GB3LKKR01A150I/1-276 GAATCTGAAACC---------AAAGAGAAGAAGGAAAAGAAATCT 1
.....250.....260.....270.....280...


cluster1085
Frame +2 p = 0.006
* T H K A A
FTSPZO101A5XSA/49-223 TGAACACACAAAGCGGC 60
ER8QEOW01BCS2I/1-68 ---------- 0
FTSPZO101A2ZKG/1-94 ---------- 0
FCPU0RF01CACI4/1-115 ----------TGC 3
FTSPZO101C8F3X/19-176 CGAACGCACAAAGCGGC 60
FS22EC101A98SE/1-175 TGAACACATAAAGCGGC 60
FSTRRC101CPTN7/37-211 TGAACGCACAAAGCGGC 60
.....10.....20.....30.....40.....50.....
N V S Q F T R A E M A A T D S G L D V Q
FTSPZO101A5XSA/49-223 CAACGTCTCGCAGTTTACACGCGCAGAAATGGCAGCAACAGACAGTGGCCTTGATGTGCA 120
ER8QEOW01BCS2I/1-68 ----------GCCTTGATGTGCA 13
FTSPZO101A2ZKG/1-94 ----------CGCGTAG-AATGGCAGCAACAGACAGTGGCCTT-ATGTGCA 39
FCPU0RF01CACI4/1-115 AAACGTCTCGCAG---ACACGCGCAGAAATGGCCACAACAGATAGCGGCCTTGATGTTCG 60
FTSPZO101C8F3X/19-176 CAATGTCTCGCAGTTCACACGCGCAGAAATGGCAGCAACAGATAGTGGTCTTGATGTGCA 120
FS22EC101A98SE/1-175 AAACGTCTCGCAATTCACACGCGCAGAGATGGCAGCAACAGACAGCGGCCTTGATGTGCG 120
FSTRRC101CPTN7/37-211 CAATGTCTCGCAGTTCACACGCGCAGAGATGGCAGCGACAGATAGTGGTCTTGATGTGCA 120
.....70.....80.....90.....100.....110.....
I E W I S T N D G R V R D S H R S T
FTSPZO101A5XSA/49-223 AATCGAATGGATTAGCACGAATGACGGCAGGGTTAGAGACTCACACAGAAGCACA 175
ER8QEOW01BCS2I/1-68 AATCGAATGGATTAGCACGAATGACGGCAGGGTTAGAGACTCACACAGAAGCACA 68
FTSPZO101A2ZKG/1-94 AATCGAATGGATTAGCACGAATGATGGCAGGGTTAGAGACTCGCACCGAAGCGTC 94
FCPU0RF01CACI4/1-115 CATTGAGTGGATTAGCACAAATGATAGTCGGGTTAGAGACTCACACAGAAGCACA 115
FTSPZO101C8F3X/19-176 AATCGAATGGATTAGCACGAATGACGGCAGGGTTTGAT--------------- 158
FS22EC101A98SE/1-175 AATCGAGTGGATTAGCACGAATGATGGCAGGGTCAGAGACTCACATCGAGCAGTC 175
FSTRRC101CPTN7/37-211 AATCGAGTGGATTAGCACGAATGATGGCAGGGTCAGAGACCCACATCGCAATGTA 175
.....130.....140.....150.....160.....170...

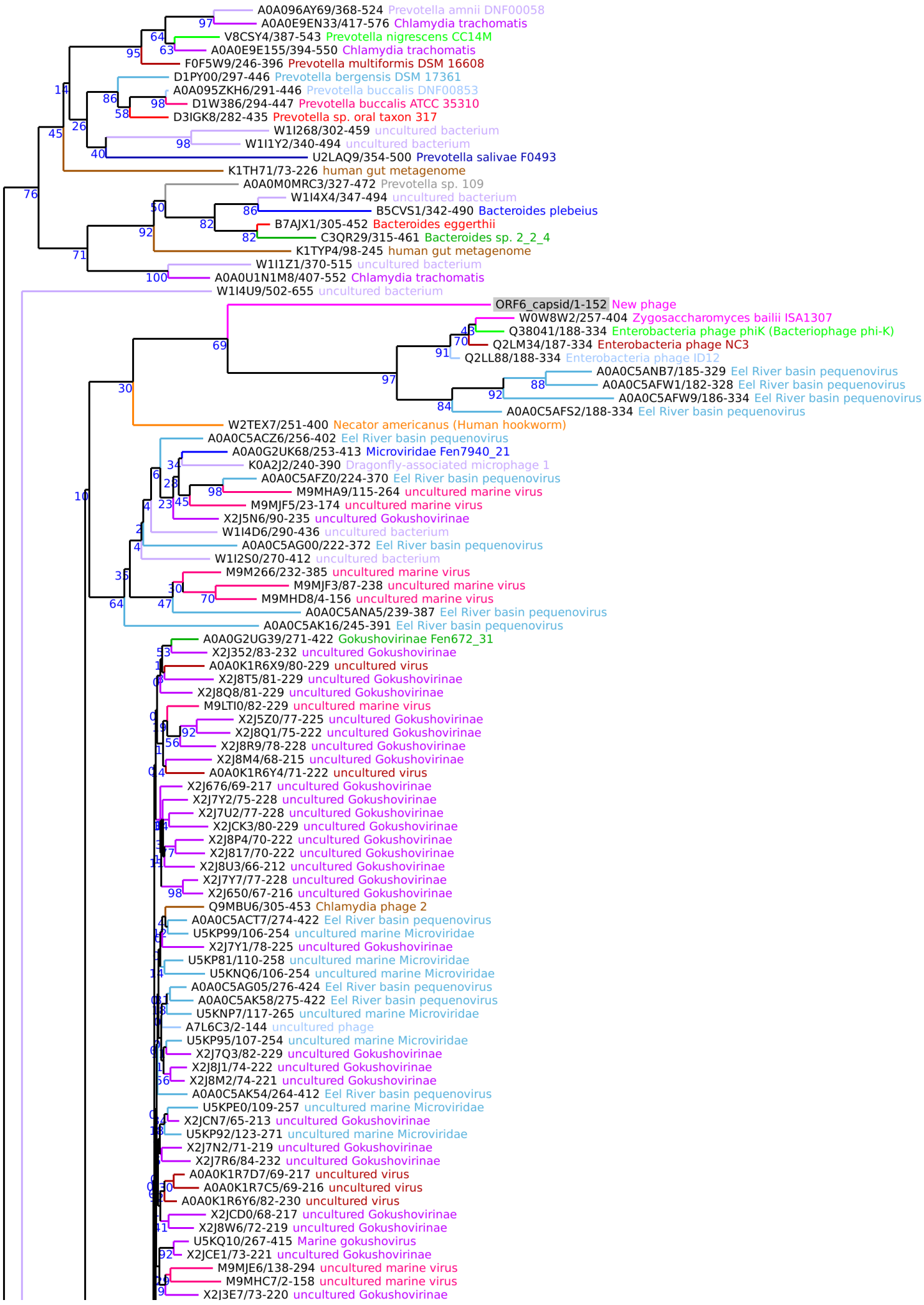

cluster1217
Frame -3 p = 7.7e-10
* S T F G G Q F K T Y K M T N
GB3LKKR01DTQ2E/16-280 TAGTCT-ACTTTTGGTGGTCAGTTCAAGACTTACAAGATGACTAAC 207
GB3LKKR01DOG04/1-117 ---------- 58
GB3LKKR01AL7BN/1-265 TAGTCT-ACTTTTGGTGGTCAGTTCAAGACTTACAAGATGACTAAC 207
GB3LKKR02FUFQQ/1-266 TAGTCTTACTTTTGGTGGTCAGTTCAAGACTTACAAGATGACTAAC 208
contig04236/16-280 -GGCTTTGGTTTTGGTGGTCAGTTTGTAACATACAAGATGACAAAT 207
GB3LKKR02GUTL4/19-199 TAACTTGACTTTCGGTGGTCAGTTCAAGACTTATAAGATGACTAAT 182
.....10.....20.....30.....40.....50.....
G I E L T L K Y F P L Y D D T T Y N R M
GB3LKKR01DTQ2E/16-280 GGTATCGAACTTACTCTGAAATATTTCCCATTGTATGATGATACCACTTATAACCGTATG 147
GB3LKKR01DOG04/1-117 ---------- 1
GB3LKKR01AL7BN/1-265 GGTATCGAACTTACTCTGAAGTATTTCCCATTGTATGATGATACTACTTATAATCGTATG 147
GB3LKKR02FUFQQ/1-266 GGTATCGAACTTACTCTGAAGTATTTCCCATTGTATGATGATACTACTTATAATCGTATG 148
contig04236/16-280 GGCATCGAGTTGACATTGAAACATTTCCCGTTGTATGATGATACTACTTATAATCGTTTG 147
GB3LKKR02GUTL4/19-199 GGTATCGAATTGACGCTGAAATACTTCCCATTTCACCCAGGATGTATACAGTATAACCGT 148
.....70.....80.....90.....100.....110.....
L H P I T L K P L E S Y R L T F L D L G
GB3LKKR01DTQ2E/16-280 TTGCATCCTATCACACTGAAACCTCTGGAATCATATCGTTTGACATTCCTTGATCTGGGT 87
GB3LKKR01DOG04/1-117 ----------TCATATCGTATGACATTCCTTGATCTGGGT 1
GB3LKKR01AL7BN/1-265 CTGCATCCGATCACACTGAAACCTCTGGAATCATATCGTATGACATTCCTTGATCTGGGT 87
GB3LKKR02FUFQQ/1-266 CTGCATCCGATCACACTGAAACCTCTGGAATCATATCGTATGACATTCCTTGATCTGGGT 88
contig04236/16-280 TTACACCCGGTATCTGGTAAACCACTGGAATCTTATAGAATGACATTCTTGGATCTTGGT 87
GB3LKKR02GUTL4/19-199 CCTTACCATTAGATCTCAGAGTATCTTTAGATTTAGCATATCCAGACGGAGCAACAGCAC 88
.....130.....140.....150.....160.....170.....
R R D G E A N I V K V V R K D R E F V T
GB3LKKR01DTQ2E/16-280 AGACGTGATGGTGAAGCTAACATTGTTAAGGTAGTTCGTAAAGATCGTGAATT-CGTTAC 27
GB3LKKR01DOG04/1-117 AGACGTGATGGTGAAGCTAACATTGTTAAGGTAGTTCGTAAAGATCGTGAATTCGGTTAC 1
GB3LKKR01AL7BN/1-265 AGACGTGATGGTGAAGCTAACATCGTAAAAGTAGTTCGTAAAGACCGTGA-GTTTGTAAC 27
GB3LKKR02FUFQQ/1-266 AGACGTGATGGTGAAGCTAACATCGTAAAAGTAGTTCGTAAAGACCGTGA-GTTTGTAAC 28
contig04236/16-280 AGACGTGATGGTCAAGCTAATATCGTTAAGGTTGTTCGTAAGGATCGTGAGAT-GGTTAT 27
GB3LKKR02GUTL4/19-199 C---------- 28
.....190.....200.....210.....220.....230.....
W Y T G G A V A
GB3LKKR01DTQ2E/16-280 TTGGTATACTGGTGGTGCTGTTGCT 1
GB3LKKR01DOG04/1-117 TTGGTATACTGGTGGTGCTGTTGCT 1
GB3LKKR01AL7BN/1-265 TTGGTACACTGGTGGTGCTGTTGCT 1
GB3LKKR02FUFQQ/1-266 TTGGTACACTGGTGGTGCTGTTGCT 1
contig04236/16-280 CTGGAATACTTCAGGTTCTGTAGCT 1
GB3LKKR02GUTL4/19-199 ---------- 1
.....250.....260.....

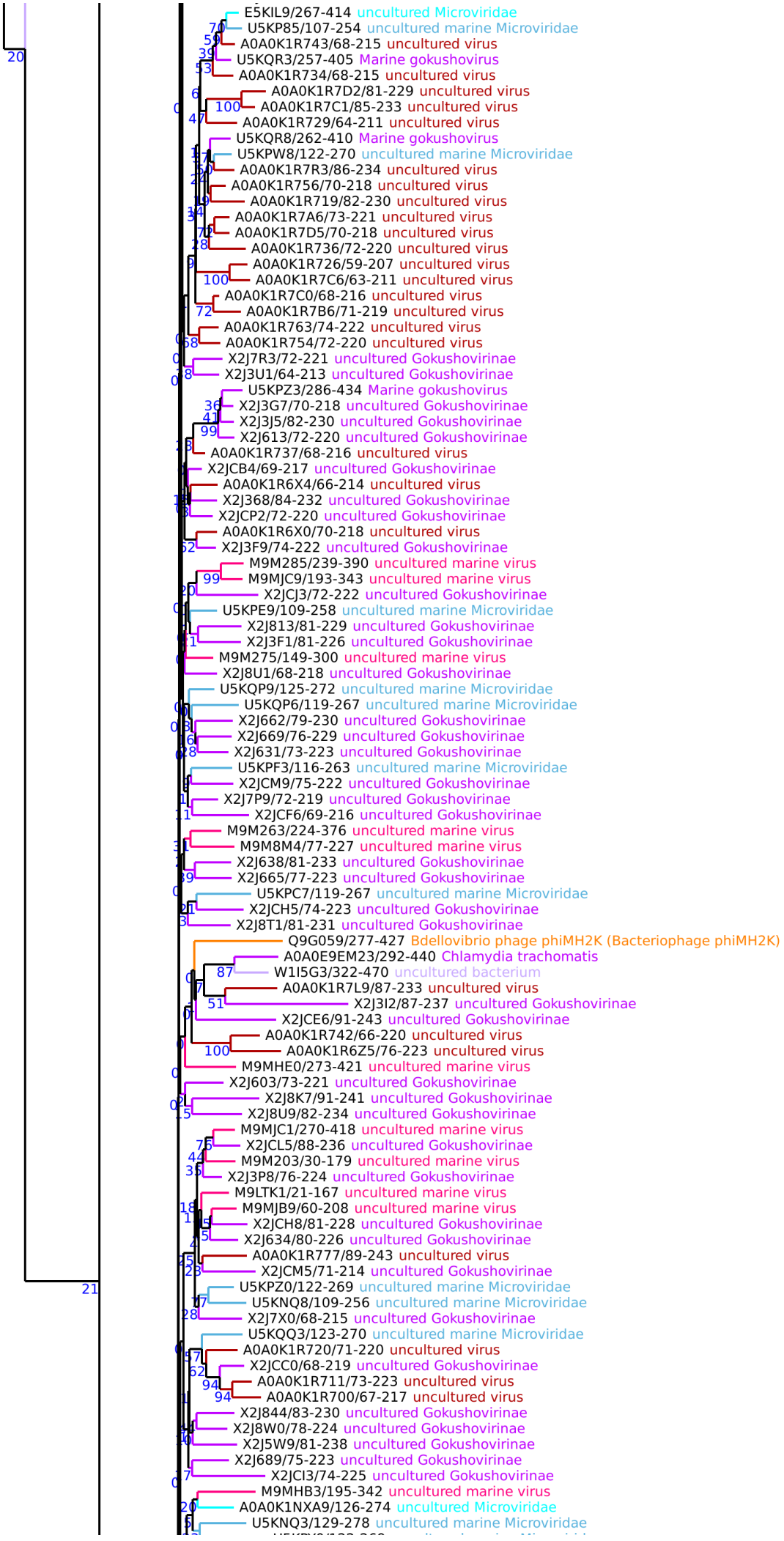

cluster1423
Frame +1 p = 1.0e-04
Q R V Q Y I S P L E D G S Y K V T L V S
DBA-SLE_c4340/1-188 CAGAGGGTGCAGTATATTAGTCCTTTAGAAGATGGAAGCTACAAAGTTACATTAGTCAGT 60
FTSPZO101BASEK/1-188 CAGAGGGGAAGGTATATTAGTCCTTTAGAAGATGGAAGCTACAAAGTTACATTAGTCAGT 60
DBA-SLE_c13402/1-183 CAGAGGGTGCAGTATATTAGTCCTATTGACAAGGGCAGCTATAAAGTTACATTGGTTAGC 60
FTSPZO101CIWNM/1-146 ----------CTGCAGATATCATTGGTTAGC 21
FTSPZO101DPI37/1-130 ----------TTGGTTAGC 9
.....10.....20.....30.....40.....50.....
G W E M K L T D K L Y S R E K L I G L W
DBA-SLE_c4340/1-188 GGGTGGGAAATGAAGCTTACAGATAAGTTGTACAGTAGAGAGAAGTTGATTGGGTTGTGG 120
FTSPZO101BASEK/1-188 GGGTGGGAAATGAAGCTTACAGATAAGTTGTACAGTAGAGAGAAGTTGATTGGGTTGTGG 120
DBA-SLE_c13402/1-183 GGGTGGGAAATGCCGTTGACTGATAAGTTGTACAGTAGAGAGAAGTTGATTGGACAGTGG 120
FTSPZO101CIWNM/1-146 GGGTGGGAAATGAAGTTGACGGGTGAGGTGTATAGTAGAGAGAAGTTGACTGGGTTGTGG 81
FTSPZO101DPI37/1-130 GGGTGGGAAATGCCGTTGACTGATAAGTTGTACAGTAGAGAGAAGTTGATTGGGTTGTGG 69
.....70.....80.....90.....100.....110.....
G V L Q N K *
DBA-SLE_c4340/1-188 GGAGTTTTGCAGAATAAATAG 180
FTSPZO101BASEK/1-188 GGAGTTTTGCAGAATAAATAG 180
DBA-SLE_c13402/1-183 CGCATGTTGCAGAATAAATA- 173
FTSPZO101CIWNM/1-146 AAGGGGTTGCAGAACAAATAA 140
FTSPZO101DPI37/1-130 CGTATATTGCAGAATAAATAG 122
.....130.....140.....150.....160.....170.....
DBA-SLE_c4340/1-188 188
FTSPZO101BASEK/1-188 188
DBA-SLE_c13402/1-183 183
FTSPZO101CIWNM/1-146 146
FTSPZO101DPI37/1-130 130
.....1

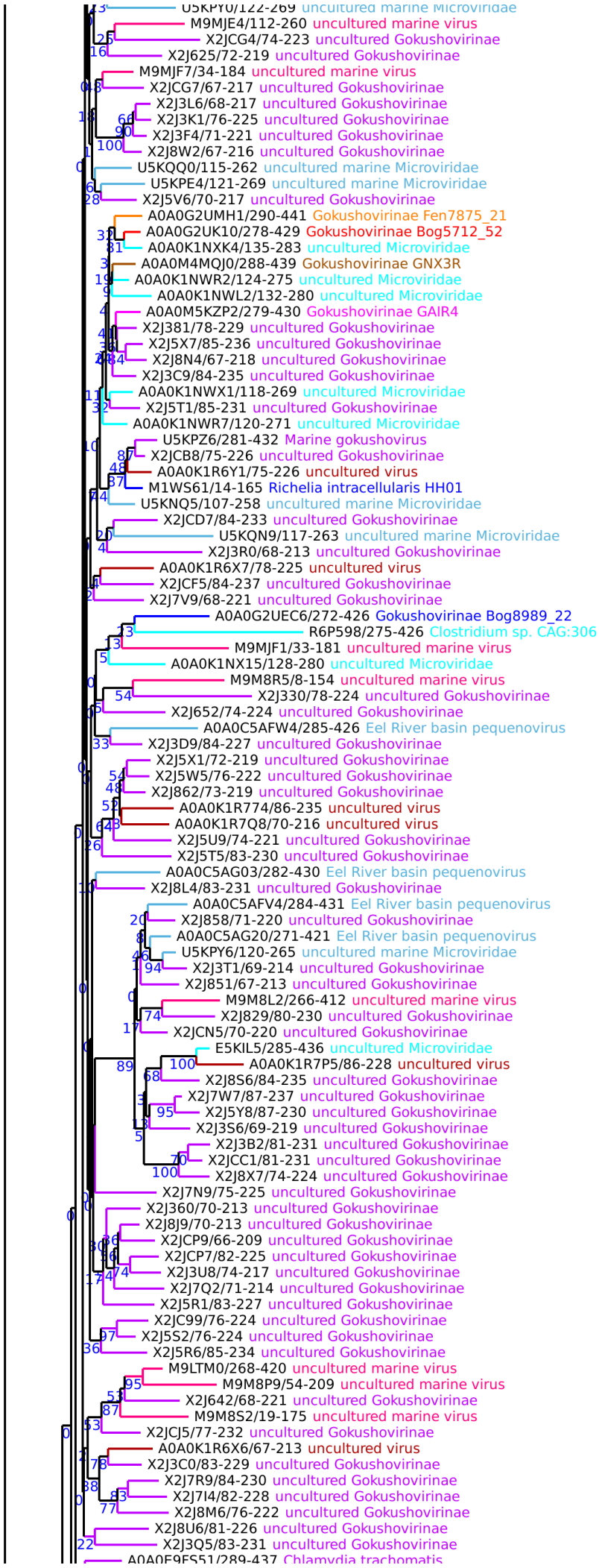
Supplementary Figure S3. Whole genome comparison of the bacteriophage HFM assembly with three metagenomic contigs from the NCBI env_nt database using Mauve[1]. The sequence of the selected env_nt contigs corresponds mostly to our assembled circular genome. Assuming the contigs are derived from closely related bacteriophages, differences in the order of the conserved blocks (in different colors) may be attributed to different cut points during the linearization of the circular genome, rearrangements, or possible misassemblies. The middle sections of the contigs are well conserved between the different contigs, but the flanking regions differ considerably. Corresponding segments in different contigs are connected with lines in the same colour.

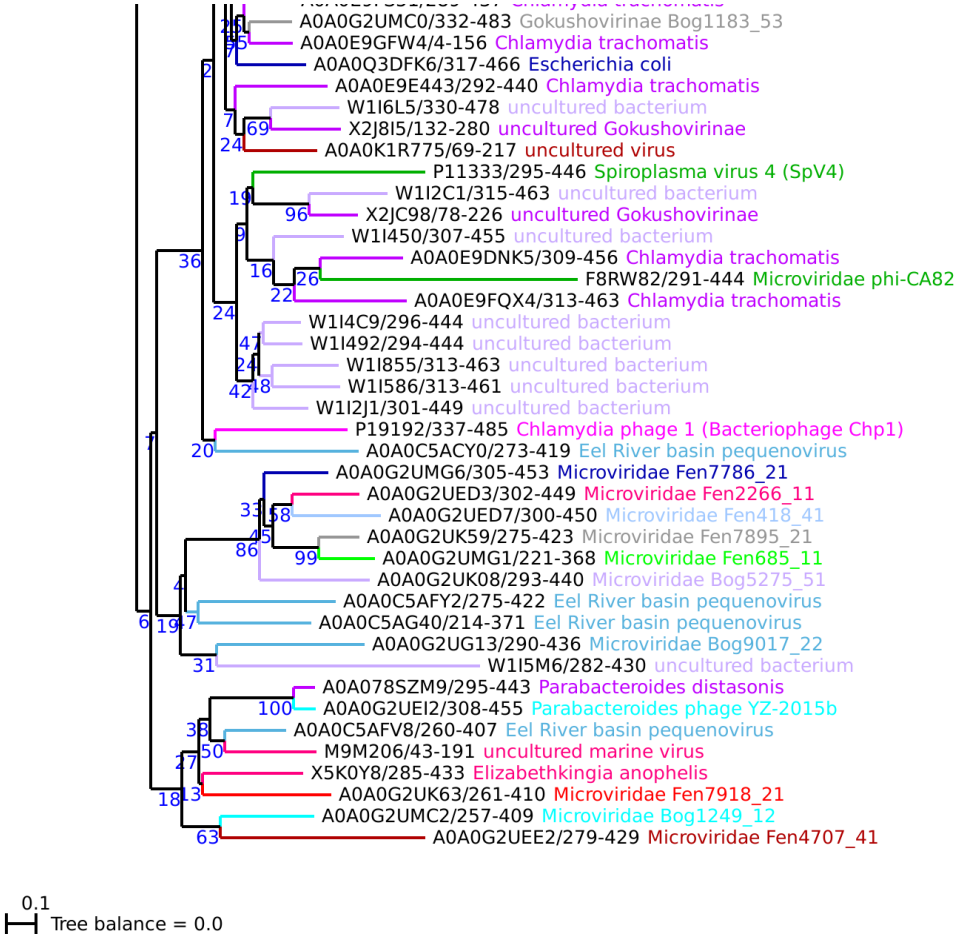

d9539_asm_v1.2
gi|931877178|emb|CEAD01032396.1|
gi|934409231|emb|CDZF01013522.1|
gi|935523605|emb|CDTY01044545.1|

Supplementary Figure S4. Neighbour-joining tree of 331 phage capsid F proteins from Uniprot, as well as bacteriophage HFM ORF6 (highlighted in gray). Tree nodes are marked with bootstrap support as percentages. The species as listed in Uniprot is shown to the right and colour coded. Note however that in many cases the listed species is the host in which the phage was found. This will happen for proteins from e.g. “Unassembled WGS sequence” entries.


A0A096AY69/368-524 Prevotella amnii DNF00058
A0A0E9EN33/417-576 Chlamydia trachomatis
V8CSY4/387-543 Prevotella nigrescens CC14M
A0A0E9E155/394-550 Chlamydia trachomatis
F0F5W9/246-396 Prevotella multiformis DSM 16608
D1PY00/297-446 Prevotella bergensis DSM 17361
A0A095ZKH6/291-446 Prevotella buccalis DNF00853
D1W386/294-447 Prevotella buccalis ATCC 35310
D3IGK8/282-435 Prevotella sp. oral taxon 317
W1I268/302-459 uncultured bacterium
W1I1Y2/340-494 uncultured bacterium
U2LAQ9/354-500 Prevotella salivae F0493
K1TH71/73-226 human gut metagenome
A0A0M0MRC3/327-472 Prevotella sp. 109
W1I4X4/347-494 uncultured bacterium
B5CVS1/342-490 Bacteroides plebeius
B7AJX1/305-452 Bacteroides eggerthii
C3QR29/315-461 Bacteroides sp. 2_2_4
K1TYP4/98-245 human gut metagenome
W1I1Z1/370-515 uncultured bacterium
A0A0U1N1M8/407-552 Chlamydia trachomatis
W1I4U9/502-655 uncultured bacterium
ORF6_capsid/1-152 New phage
W0W8W2/257-404 Zygosaccharomyces bailii ISA1307
Q38041/188-334 Enterobacteria phage phiK (Bacteriophage phi-K)
Q2LM34/187-334 Enterobacteria phage NC3
Q2LL88/188-334 Enterobacteria phage ID12
A0A0C5ANB7/185-329 Eel River basin pequenovirus
A0A0C5AFW1/182-328 Eel River basin pequenovirus
A0A0C5AFW9/186-334 Eel River basin pequenovirus
A0A0C5AFS2/188-334 Eel River basin pequenovirus
W2TEX7/251-400 Necator americanus (Human hookworm)
A0A0C5ACZ6/256-402 Eel River basin pequenovirus
A0A0G2UK68/253-413 Microviridae Fen7940_21
K0A2J2/240-390 Dragonfly-associated microphage 1
A0A0C5AFZ0/224-370 Eel River basin pequenovirus
M9MHA9/115-264 uncultured marine virus
M9MJF5/23-174 uncultured marine virus
X2J5N6/90-235 uncultured Gokushovirinae
W1I4D6/290-436 uncultured bacterium
A0A0C5AG00/222-372 Eel River basin pequenovirus
W1I2S0/270-412 uncultured bacterium
M9M266/232-385 uncultured marine virus
M9MJF3/87-238 uncultured marine virus
M9MHD8/4-156 uncultured marine virus
A0A0C5ANA5/239-387 Eel River basin pequenovirus
A0A0C5AK16/245-391 Eel River basin pequenovirus
A0A0G2UG39/271-422 Gokushovirinae Fen672_31
X2J352/83-232 uncultured Gokushovirinae
A0A0K1R6X9/80-229 uncultured virus
X2J8T5/81-229 uncultured Gokushovirinae
X2J8Q8/81-229 uncultured Gokushovirinae
M9LTI0/82-229 uncultured marine virus
X2J5Z0/77-225 uncultured Gokushovirinae
X2J8Q1/75-222 uncultured Gokushovirinae
X2J8R9/78-228 uncultured Gokushovirinae
X2J8M4/68-215 uncultured Gokushovirinae
A0A0K1R6Y4/71-222 uncultured virus
X2J676/69-217 uncultured Gokushovirinae
X2J7Y2/75-228 uncultured Gokushovirinae
X2J7U2/77-228 uncultured Gokushovirinae
X2JCK3/80-229 uncultured Gokushovirinae
X2J8P4/70-222 uncultured Gokushovirinae
X2J817/70-222 uncultured Gokushovirinae
X2J8U3/66-212 uncultured Gokushovirinae
X2J7Y7/77-228 uncultured Gokushovirinae
X2J650/67-216 uncultured Gokushovirinae
Q9MBU6/305-453 Chlamydia phage 2
A0A0C5ACT7/274-422 Eel River basin pequenovirus
U5KP99/106-254 uncultured marine Microviridae
X2J7Y1/78-225 uncultured Gokushovirinae
U5KP81/110-258 uncultured marine Microviridae
U5KNQ6/106-254 uncultured marine Microviridae
A0A0C5AG05/276-424 Eel River basin pequenovirus
A0A0C5AK58/275-422 Eel River basin pequenovirus
U5KNP7/117-265 uncultured marine Microviridae
A7L6C3/2-144 uncultured phage
U5KP95/107-254 uncultured marine Microviridae
X2J7Q3/82-229 uncultured Gokushovirinae
X2J8J1/74-222 uncultured Gokushovirinae
X2J8M2/74-221 uncultured Gokushovirinae
A0A0C5AK54/264-412 Eel River basin pequenovirus
U5KPE0/109-257 uncultured marine Microviridae
X2JCN7/65-213 uncultured Gokushovirinae
U5KP92/123-271 uncultured marine Microviridae
X2J7N2/71-219 uncultured Gokushovirinae
X2J7R6/84-232 uncultured Gokushovirinae
A0A0K1R7D7/69-217 uncultured virus
A0A0K1R7C5/69-216 uncultured virus
A0A0K1R6Y6/82-230 uncultured virus
X2JCD0/68-217 uncultured Gokushovirinae
X2J8W6/72-219 uncultured Gokushovirinae
U5KQ10/267-415 Marine gokushovirus
X2JCE1/73-221 uncultured Gokushovirinae
M9MJE6/138-294 uncultured marine virus
M9MHC7/2-158 uncultured marine virus
X2J3E7/73-220 uncultured Gokushovirinae


E5KIL9/267-414 uncultured Microviridae
U5KP85/107-254 uncultured marine Microviridae
A0A0K1R743/68-215 uncultured virus
U5KQR3/257-405 Marine gokushovirus
A0A0K1R734/68-215 uncultured virus
A0A0K1R7D2/81-229 uncultured virus
A0A0K1R7C1/85-233 uncultured virus
A0A0K1R729/64-211 uncultured virus
U5KQR8/262-410 Marine gokushovirus
U5KPW8/122-270 uncultured marine Microviridae
A0A0K1R7R3/86-234 uncultured virus
A0A0K1R756/70-218 uncultured virus
A0A0K1R719/82-230 uncultured virus
A0A0K1R7A6/73-221 uncultured virus
A0A0K1R7D5/70-218 uncultured virus
A0A0K1R736/72-220 uncultured virus
A0A0K1R726/59-207 uncultured virus
A0A0K1R7C6/63-211 uncultured virus
A0A0K1R7C0/68-216 uncultured virus
A0A0K1R7B6/71-219 uncultured virus
A0A0K1R763/74-222 uncultured virus
A0A0K1R754/72-220 uncultured virus
X2J7R3/72-221 uncultured Gokushovirinae
X2J3U1/64-213 uncultured Gokushovirinae
U5KPZ3/286-434 Marine gokushovirus
X2J3G7/70-218 uncultured Gokushovirinae
X2J3J5/82-230 uncultured Gokushovirinae
X2J613/72-220 uncultured Gokushovirinae
A0A0K1R737/68-216 uncultured virus
X2JCB4/69-217 uncultured Gokushovirinae
A0A0K1R6X4/66-214 uncultured virus
X2J368/84-232 uncultured Gokushovirinae
X2JCP2/72-220 uncultured Gokushovirinae
A0A0K1R6X0/70-218 uncultured virus
X2J3F9/74-222 uncultured Gokushovirinae
M9M285/239-390 uncultured marine virus
M9MJC9/193-343 uncultured marine virus
X2JCJ3/72-222 uncultured Gokushovirinae
U5KPE9/109-258 uncultured marine Microviridae
X2J813/81-229 uncultured Gokushovirinae
X2J3F1/81-226 uncultured Gokushovirinae
M9M275/149-300 uncultured marine virus
X2J8U1/68-218 uncultured Gokushovirinae
U5KQP9/125-272 uncultured marine Microviridae
U5KQP6/119-267 uncultured marine Microviridae
X2J662/79-230 uncultured Gokushovirinae
X2J669/76-229 uncultured Gokushovirinae
X2J631/73-223 uncultured Gokushovirinae
U5KPF3/116-263 uncultured marine Microviridae
X2JCM9/75-222 uncultured Gokushovirinae
X2J7P9/72-219 uncultured Gokushovirinae
X2JCF6/69-216 uncultured Gokushovirinae
M9M263/224-376 uncultured marine virus
M9M8M4/77-227 uncultured marine virus
X2J638/81-233 uncultured Gokushovirinae
X2J665/77-223 uncultured Gokushovirinae
U5KPC7/119-267 uncultured marine Microviridae
X2JCH5/74-223 uncultured Gokushovirinae
X2J8T1/81-231 uncultured Gokushovirinae
Q9G059/277-427 Bdellovibrio phage phiMH2K (Bacteriophage phiMH2K)
A0A0E9EM23/292-440 Chlamydia trachomatis
W1I5G3/322-470 uncultured bacterium
A0A0K1R7L9/87-233 uncultured virus
X2J3I2/87-237 uncultured Gokushovirinae
X2JCE6/91-243 uncultured Gokushovirinae
A0A0K1R742/66-220 uncultured virus
A0A0K1R6Z5/76-223 uncultured virus
M9MHE0/273-421 uncultured marine virus
X2J603/73-221 uncultured Gokushovirinae
X2J8K7/91-241 uncultured Gokushovirinae
X2J8U9/82-234 uncultured Gokushovirinae
M9MJC1/270-418 uncultured marine virus
X2JCL5/88-236 uncultured Gokushovirinae
M9M203/30-179 uncultured marine virus
X2J3P8/76-224 uncultured Gokushovirinae
M9LTK1/21-167 uncultured marine virus
M9MJB9/60-208 uncultured marine virus
X2JCH8/81-228 uncultured Gokushovirinae
X2J634/80-226 uncultured Gokushovirinae
A0A0K1R777/89-243 uncultured virus
X2JCM5/71-214 uncultured Gokushovirinae
U5KPZ0/122-269 uncultured marine Microviridae
U5KNQ8/109-256 uncultured marine Microviridae
X2J7X0/68-215 uncultured Gokushovirinae
U5KQQ3/123-270 uncultured marine Microviridae
A0A0K1R720/71-220 uncultured virus
X2JCC0/68-219 uncultured Gokushovirinae
A0A0K1R711/73-223 uncultured virus
A0A0K1R700/67-217 uncultured virus
X2J844/83-230 uncultured Gokushovirinae
X2J8W0/78-224 uncultured Gokushovirinae
X2J5W9/81-238 uncultured Gokushovirinae
X2J689/75-223 uncultured Gokushovirinae
X2JCI3/74-225 uncultured Gokushovirinae
M9MHB3/195-342 uncultured marine virus
A0A0K1NXA9/126-274 uncultured Microviridae
U5KNQ3/129-278 uncultured marine Microviridae


U5KPY0/122-269 uncultured marine Microviridae
M9MJE4/112-260 uncultured marine virus
X2JCG4/74-223 uncultured Gokushovirinae
X2J625/72-219 uncultured Gokushovirinae
M9MJF7/34-184 uncultured marine virus
X2JCG7/67-217 uncultured Gokushovirinae
X2J3L6/68-217 uncultured Gokushovirinae
X2J3K1/76-225 uncultured Gokushovirinae
X2J3F4/71-221 uncultured Gokushovirinae
X2J8W2/67-216 uncultured Gokushovirinae
U5KQQ0/115-262 uncultured marine Microviridae
U5KPE4/121-269 uncultured marine Microviridae
X2J5V6/70-217 uncultured Gokushovirinae
A0A0G2UMH1/290-441 Gokushovirinae Fen7875_21
A0A0G2UK10/278-429 Gokushovirinae Bog5712_52
A0A0K1NXK4/135-283 uncultured Microviridae
A0A0M4MQJ0/288-439 Gokushovirinae GNX3R
A0A0K1NWR2/124-275 uncultured Microviridae
A0A0K1NWL2/132-280 uncultured Microviridae
A0A0M5KZP2/279-430 Gokushovirinae GAIR4
X2J381/78-229 uncultured Gokushovirinae
X2J5X7/85-236 uncultured Gokushovirinae
X2J8N4/67-218 uncultured Gokushovirinae
X2J3C9/84-235 uncultured Gokushovirinae
A0A0K1NWX1/118-269 uncultured Microviridae
X2J5T1/85-231 uncultured Gokushovirinae
A0A0K1NWR7/120-271 uncultured Microviridae
U5KPZ6/281-432 Marine gokushovirus
X2JCB8/75-226 uncultured Gokushovirinae
A0A0K1R6Y1/75-226 uncultured virus
M1WS61/14-165 Richelia intracellularis HH01
U5KNQ5/107-258 uncultured marine Microviridae
X2JCD7/84-233 uncultured Gokushovirinae
U5KQN9/117-263 uncultured marine Microviridae
X2J3R0/68-213 uncultured Gokushovirinae
A0A0K1R6X7/78-225 uncultured virus
X2JCF5/84-237 uncultured Gokushovirinae
X2J7V9/68-221 uncultured Gokushovirinae
A0A0G2UEC6/272-426 Gokushovirinae Bog8989_22
R6P598/275-426 Clostridium sp. CAG:306
M9MJF1/33-181 uncultured marine virus
A0A0K1NX15/128-280 uncultured Microviridae
M9M8R5/8-154 uncultured marine virus
X2J330/78-224 uncultured Gokushovirinae
X2J652/74-224 uncultured Gokushovirinae
A0A0C5AFW4/285-426 Eel River basin pequenovirus
X2J3D9/84-227 uncultured Gokushovirinae
X2J5X1/72-219 uncultured Gokushovirinae
X2J5W5/76-222 uncultured Gokushovirinae
X2J862/73-219 uncultured Gokushovirinae
A0A0K1R774/86-235 uncultured virus
A0A0K1R7Q8/70-216 uncultured virus
X2J5U9/74-221 uncultured Gokushovirinae
X2J5T5/83-230 uncultured Gokushovirinae
A0A0C5AG03/282-430 Eel River basin pequenovirus
X2J8L4/83-231 uncultured Gokushovirinae
A0A0C5AFV4/284-431 Eel River basin pequenovirus
X2J858/71-220 uncultured Gokushovirinae
A0A0C5AG20/271-421 Eel River basin pequenovirus
U5KPY6/120-265 uncultured marine Microviridae
X2J3T1/69-214 uncultured Gokushovirinae
X2J851/67-213 uncultured Gokushovirinae
M9M8L2/266-412 uncultured marine virus
X2J829/80-230 uncultured Gokushovirinae
X2JCN5/70-220 uncultured Gokushovirinae
E5KIL5/285-436 uncultured Microviridae
A0A0K1R7P5/86-228 uncultured virus
X2J8S6/84-235 uncultured Gokushovirinae
X2J7W7/87-237 uncultured Gokushovirinae
X2J5Y8/87-230 uncultured Gokushovirinae
X2J3S6/69-219 uncultured Gokushovirinae
X2J3B2/81-231 uncultured Gokushovirinae
X2JCC1/81-231 uncultured Gokushovirinae
X2J8X7/74-224 uncultured Gokushovirinae
X2J7N9/75-225 uncultured Gokushovirinae
X2J360/70-213 uncultured Gokushovirinae
X2J8J9/70-213 uncultured Gokushovirinae
X2JCP9/66-209 uncultured Gokushovirinae
X2JCP7/82-225 uncultured Gokushovirinae
X2J3U8/74-217 uncultured Gokushovirinae
X2J7Q2/71-214 uncultured Gokushovirinae
X2J5R1/83-227 uncultured Gokushovirinae
X2JC99/76-224 uncultured Gokushovirinae
X2J5S2/76-224 uncultured Gokushovirinae
X2J5R6/85-234 uncultured Gokushovirinae
M9LTM0/268-420 uncultured marine virus
M9M8P9/54-209 uncultured marine virus
X2J642/68-221 uncultured Gokushovirinae
M9M8S2/19-175 uncultured marine virus
X2JCJ5/77-232 uncultured Gokushovirinae
A0A0K1R6X6/67-213 uncultured virus
X2J3C0/83-229 uncultured Gokushovirinae
X2J7R9/84-230 uncultured Gokushovirinae
X2J7I4/82-228 uncultured Gokushovirinae
X2J8M6/76-222 uncultured Gokushovirinae
X2J8U6/81-226 uncultured Gokushovirinae
X2J3Q5/83-231 uncultured Gokushovirinae
A0A0F9FS51/289-437 Chlamydia trachomatis



0.1

Tree balance = 0.0

Supplementary Figure S5. PHACTS [2] prediction on the bacteriophage HFM predicted ORFs. PHACTS uses a machine learning approach based on protein sequences to classify if a phage is more likely to be temperate or lytic and whether it has a gram-positive or gram-negative host preference. The results do not yield information about the lifestyle of the phage, but they suggest that the phage is likely to invade gram-negative hosts

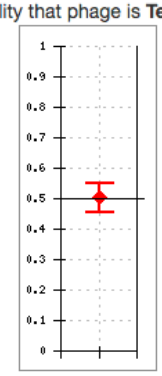
✔ Lifestyle:

Analysis Statistics

Ten iterations of PHACTS were performed using the default settings. The phage was **non-confidently** predicted as having a **Temperate lifestyle**.

Predicted Class	Averaged Probability	Standard Deviation
Temperate	0.503	0.048

Probability that phage is **Temperate**



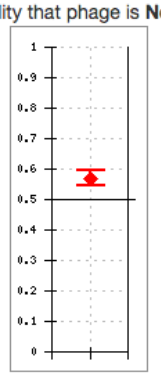
✔ Gram-stain of host:

Analysis Statistics

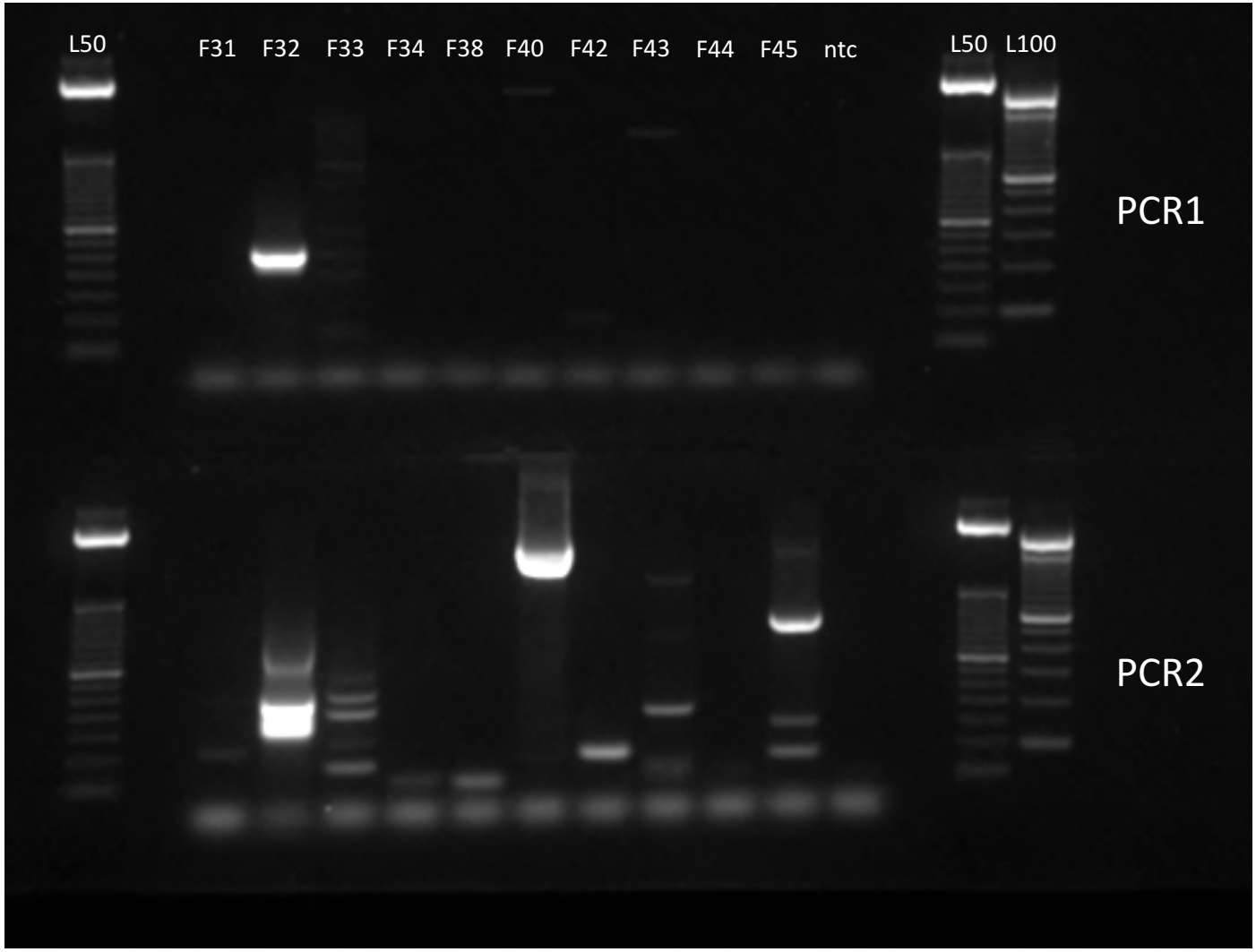
Ten iterations of PHACTS were performed using the default settings. The phage was **confidently** predicted as infecting a **Gram Negative** host.

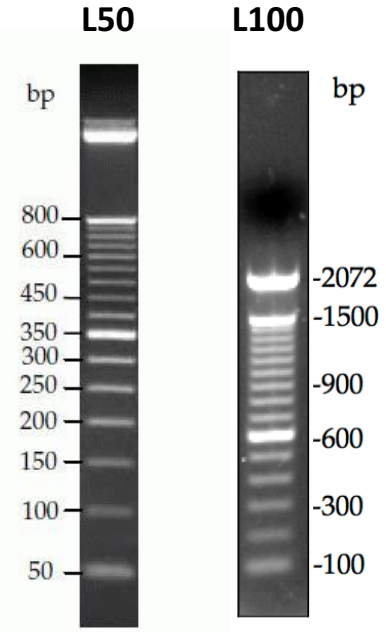
Predicted Class	Averaged Probability	Standard Deviation
Negative	0.57	0.025

Probability that phage is **Negative**



Supplementary Figure S6. Results from two separate Bacteriophage HFM PCRs from the the same set of samples. The main image shows one complete gel. The two smaller gel images show the sizes of the bands in the two size markers used in the main gel, see below for description. We have chosen an image where all bands are clearly distinguishable, despite variations in intensities. The PCR amplifications are of bacteriophage HFM in individual FESC D samples. Bands of the expected size were only observed in sample F32, where DNA fragments of 267 bp and 155 bp were obtained in PCR 1 and 2, respectively. Ntc, L50 and L100 refer to non-template control, 100 bp DNA Ladder (ThermoFisher Scientific, cat.no. 15628050) and 50 bp DNA Ladder (ThermoFisher Scientific, cat.no. 10416014).


L50
F31
F32
F33
F34
F38
F40
F42
F43
F44
F45
ntc
L50
L100
PCR1
PCR2


L50
L100
bp
800
600
450
350
300
250
200
150
100
50
bp
-2072
-1500
-900
-600
-300
-100

Supplementary Table S1 - Description of viral metagenomics libraries

library_id	sample_type	nucleic_acid	platform	reads	avg_read_len
ER8QEOW01	nasopharyngeal swabs	DNA	GS	160,120	99.6
ER8QEOW02	nasopharyngeal swabs	RNA	GS	138,941	102.8
FC8LRL301	nasopharyngeal swabs	DNA	GS FLX	165,715	185.9
FC8LRL302	nasopharyngeal swabs	RNA	GS FLX	239,014	208.1
FCPU0RF01	serum	DNA	GS FLX	177,184	143.7
FCPU0RF02	serum	RNA	GS FLX	113,542	140.5
FPFNBIF01	serum	DNA	GS FLX	25,767	170.1
FPFNBIF02	serum	RNA	GS FLX	305,191	199.1
FSTRRC101	serum	DNA	GS FLX	28,217	177.9
FS22EC101	serum	DNA	Titanium	256,310	193.2
FS22EC102	serum	RNA	Titanium	189,704	187.6
FTSPZO101	cerebrospinal fluid	DNA	Titanium	158,065	220.1
FTSPZO102	cerebrospinal fluid	RNA	Titanium	51,683	134.5
GB7HT0Z01	nasopharyngeal & throat swabs	DNA	Titanium	199,388	258.8
GB7HT0Z02	nasopharyngeal & throat swabs	RNA	Titanium	233,531	264.4
GB3LKKR01	feces	DNA	Titanium	723,577	327.0
GB3LKKR02	feces	RNA	Titanium	736,239	323.7
			OVERALL	3,902,188	

Supplementary Table S2 - Summary of predicted families hits to different databases

Cluster	sample_origin	RNAcode_pvalue	composite score	hits_to
1217	feces	7.70E-10	7.57	env_nt;metahit_2014_cds;metahit_2014_pep;nr;env_nr
339b	feces	1.07E-06	7.52	metahit_2014_cds;env_nt;metahit_2014_pep
211b	feces	3.36E-14	7.49	env_nt;metahit_2014_cds;metahit_2014_pep
562	CSF;serum	4.59E-07	7.39	
297a	feces	0.001	7.38	metahit_2014_cds;env_nt;metahit_2014_pep;
457	CSF;serum	1.35E-08	7.32	env_nt
348	feces	1.42E-08	7.32	env_nt;metahit_2014_cds;metahit_2014_pep;
502	feces	3.60E-07	7.3	metahit_2014_cds;env_nt;metahit_2014_pep;
540	CSF;mucus;serum	3.76E-04	7.24	env_nt
241b	feces	5.54E-06	7.24	env_nt;metahit_2014_cds;metahit_2014_pep;
179a	feces	0.005	7.23	metahit_2014_cds;env_nt;metahit_2014_pep;
406b	CSF;feces	0.001	7.21	env_nt;metahit_2014_cds;metahit_2014_pep
1073	feces	1.66E-10	7.19	metahit_2014_cds;env_nt;metahit_2014_pep
211a	feces	3.90E-06	7.17	metahit_2014_cds;env_nt;metahit_2014_pep;
589	feces	8.36E-04	7.12	metahit_2014_cds;env_nt;metahit_2014_pep;
375a	feces	0.013	7.09	metahit_2014_cds;env_nt;metahit_2014_pep;
182a	feces	5.23E-04	7.05	env_nt;metahit_2014_cds;metahit_2014_pep;
1423	CSF;serum	1.00E-04	7.01	
258	feces	0.015	6.99	env_nt;metahit_2014_cds;metahit_2014_pep;
297b	feces	0.006	6.99	metahit_2014_cds;env_nt;metahit_2014_pep;
1057	CSF;serum	3.44E-06	6.99	
241a	feces	0.002	6.94	env_nt;metahit_2014_cds;metahit_2014_pep;
956b	serum	0.003	6.94	nr
321b	feces	1.88E-07	6.93	metahit_2014_cds;env_nt;metahit_2014_pep;
182b	feces	1.54E-04	6.9	metahit_2014_cds;env_nt;metahit_2014_pep;
532	feces	0.001	6.79	metahit_2014_cds;env_nt;metahit_2014_pep;nr
787b	feces	0.016	6.78	env_nt;metahit_2014_pep;

565b	CSF;serum	0.003	6.74	nr
1085	CSF;mucus;serum	0.006	6.73	metahit_2014_pep
612a	feces	0.004	6.56	metahit_2014_cds;env_nt;metahit_2014_pep;
179b	feces	0.01	6.54	metahit_2014_cds;env_nt;
113b	feces	0.008	6.32	metahit_2014_cds;env_nt;metahit_2014_pep;

Supplementary Table S3 - Summary of hits of protein families to MetaHIT database. "n" stands for the CDS version, "p"stands for the protein version of the database

Cluster	composite score	sample_origin	MetaHIT
1217	7.57	feces	2014_n;2014_p
339b	7.52	feces	2014_n;2014_p
211b	7.49	feces	2014_n;2014_p
562	7.39	CSF;serum	
297a	7.38	feces	2014_n;2014_p
457	7.32	CSF;serum	
348	7.32	feces	2014_n;2014_p
502	7.3	feces	2014_n;2014_p
241b	7.24	feces	2014_n;2014_p
540	7.24	CSF;mucus;serum	
179a	7.23	feces	2014_n;2014_p
406b	7.21	CSF;feces	2014_n;2014_p
1073	7.19	feces	2014_n;2014_p
211a	7.17	feces	2014_n;2014_p
589	7.12	feces	2014_n;2014_p
375a	7.09	feces	2014_n;2014_p
182a	7.05	feces	2014_n;2014_p
1423	7.01	CSF;serum	
1057	6.99	CSF;serum	
297b	6.99	feces	2014_n;2014_p
258	6.99	feces	2014_n;2014_p
241a	6.94	feces	2014_n;2014_p
956b	6.94	serum	
321b	6.93	feces	2014_n;2014_p
182b	6.9	feces	2014_n;2014_p

532	6.79	feces	2014_n;2014_p
787b	6.78	feces	2014_p
565b	6.74	CSF;serum	
1085	6.73	CSF;mucus;serum	2014_p
612a	6.56	feces	2014_n;2014_p
179b	6.54	feces	2014_n
113b	6.32	feces	2014_n;2014_p

Supplementary Table S4 - Summary of hits of protein families to the NCBI environmental databases. (n) stands for env_nt,(p) for env_nr

Cluster	composite score	sample_origin	env_hits
1217	7.57	feces	marine sediment (p);gut (n)
339b	7.52	feces	gut (n)
211b	7.49	feces	gut (n)
562	7.39	CSF;serum	
297a	7.38	feces	gut (n)
457	7.32	CSF;serum	wastewater (n)
348	7.32	feces	gut (n)
502	7.3	feces	Human gut (n)
241b	7.24	feces	gut (n)
540	7.24	CSF;mucus;serum	wastewater (n)
179a	7.23	feces	gut (n)
406b	7.21	CSF;feces	gut (n)
1073	7.19	feces	gut (n)
211a	7.17	feces	gut (n)
589	7.12	feces	gut (n)
375a	7.09	feces	gut (n)
182a	7.05	feces	Human gut (n)
1423	7.01	CSF;serum	
1057	6.99	CSF;serum	
297b	6.99	feces	gut (n)
258	6.99	feces	gut (n)
241a	6.94	feces	gut (n)
956b	6.94	serum	
321b	6.93	feces	gut (n)
182b	6.9	feces	Human gut (n)

532	6.79	feces	Human gut (n)
787b	6.78	feces	Human gut (n)
565b	6.74	CSF;serum	
1085	6.73	CSF;mucus;serum	
612a	6.56	feces	gut (n)
179b	6.54	feces	gut (n)
113b	6.32	feces	Gut (n)

Supplementary methods

Protein family construction

We employed RNAcode's evolutionary model to distinguish between coding and non-coding sequences. However, because RNAcode depends on long, high-quality multiple alignments for its predictions, it has previously been impossible to use this method for gene prediction from short read metagenomics datasets. We have addressed this issue by adding several filtering steps. In short, we generated candidate protein families by building high-quality multiple sequence alignments from clusters of similar sequences. Subsequently, we calibrated the RNAcode thresholds to detect coding sequences in short reads, and combined these with sequence-based measures like ORF length and sequence complexity and to select high-confidence candidate protein families. These steps are outlined in Figure 1.

Clustering

To build the multiple sequence alignments, we began by clustering sequences by similarity with the MCL Algorithm[3]. This procedure yielded a total of 248,813 raw clusters, of which 13,861 had between 3 and 250 sequences (Supplementary Figure 1a) and were selected for building multiple sequence alignments. However, closer examination of these clusters revealed that many of them contained sequences with very high identity. Considering that RNAcode has been reported to perform poorly on alignments with low sequence diversity[4], we opted to sub-cluster sequences with more than 95% identity within each cluster, using a single-linkage approach, and replaced them with a single representative copy. We hypothesized that these highly similar sequences had likely originated from the same source, and thus could confound RNAcode, which would consider them two independent proteins. Supplementary Figure 1b shows the cluster size distributions before and after sub-clustering. The increase in the number of small clusters, and specifically the large fraction (64%) of clusters were reduced to one or two sequences after sub-clustering, strengthens our hypothesis that most initial clusters included nearly identical sequences, thus validating our strategy. It is possible that some of the singletons are true ORFans, but this cannot be determined without additional homologous sequences.

Multiple sequence alignment of clusters

It is well known that multiple sequence alignment quality has a large effect on bioinformatics tools that use them as input[5]. RNAcode is no exception, and unfortunately, viral-enriched metagenomics data is close to a worst-case scenario for a multiple sequence alignment. Factors such as variable coverage, population variability, and sequence quality of next-generation sequencing (NGS) data could lead to clusters composed of sequences of different lengths, which in turn will result in alignments with a large number of gaps. Under these circumstances, RNAcode could erroneously predict mostly-gapped regions to have high coding potential, due to the low effective number of triplets that can be scored (S. Washietl, personal communication). In order to overcome this problem, we used a codon-aware aligner, MACSE, which takes possible frameshifts and stop codons into account[6], coupled with manual inspection and removal of low-coverage regions and poorly-aligning sequences. In the absence of an accurate automated solution, we found this to be the most effective way to ensure that RNAcode would not erroneously predict coding potential due to poor alignment quality. To ensure high quality, we here focus on clusters of more than 8

sequences. 456 clusters were aligned, of which 209 low quality alignments (e.g. poor overlap) were discarded.

Selection of high-confidence protein families

As RNAcode was originally designed to work with longer alignments, we carried out a calibration procedure using simulated reads of varying lengths from coding and non-coding regions to optimize it for shorter alignments. The results of this calibration procedure suggest that the tool can accurately separate true ORFs from non-coding regions for alignment lengths as short as 50 nt, using a p-value threshold of 0.15 (Supplementary Figure 1c). Based on these findings, we applied the $P \leq 0.15$ threshold to the remaining clusters, resulting in the exclusion of 154 families predicted to not have significant coding potential.

RNAcode does not take sequence complexity into account when assessing coding potential, and thus may yield low p-values for short tandem amino-acid repeats. Since such repeats often appear in non-coding regions, we applied the seg algorithm[7] to identify and exclude low-complexity candidates, complementing RNAcode's predictions. In total, an additional 61 clusters were excluded based on low complexity.

Finally, to rank our resulting families in terms of coding potential, we calculated a composite score that combines the RNAcode score, sequence complexity, and ORF length. Although *ad hoc*, in our experience the composite score is a convenient heuristic that was more useful than simply evaluating the p-value alone, since it integrates external, biologically relevant information that RNAcode does not consider.

From the original set of 456 clusters selected for further analysis, our approach identified 32 high-confidence candidate novel ORFan protein families, which we ranked by our ad-hoc composite score. Their final trimmed and filtered alignments were composed of a median of 6 sequences and have a predicted ORF length between 30 and 130 amino acids (Figures 3a and 3b). The coding potential was assessed using RNAcode as described in the previous sections, and the RNAcode p-value distribution for the 32 clusters ranged from very confident predictions with p-values around 10^{-10} to values close to 0.02 (Figure 2a). The RNAcode output for cluster 457 is shown in Figure 3d, and RNAcode predictions for all 32 families are available in Supplementary Fig. S2.

Phylogenetic tree construction

The ORF6 protein sequence and all 1657 sequences in the Pfam full alignment of Phage_F (PF02305) were aligned to the Pfam HMM with hmmalign. Unalignable regions in the N- and C-terminus were removed, keeping a conserved core region of about 150 residues. Sequences with >50% gap residues were removed, and sequences >90% identical to other sequences were removed, leaving 331 representative and non-redundant sequences. The tree was built with the Neighbor Joining method using Scoredist distance correction using Belvu[8], with 1000 bootstraps

References

1. Darling, A. C. E., Mau, B., Blattner, F. R. & Perna, N. T. Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res.* **14,** 1394–403 (2004).
2. McNair, K., Bailey, B. A. & Edwards, R. A. PHACTS, a computational approach to classifying the lifestyle of phages. *Bioinformatics* **28,** 614–618 (2012).
3. Enright, A. J., Van Dongen, S. & Ouzounis, C. A. An efficient algorithm for large-scale detection of protein families. *Nucleic Acids Res.* **30,** 1575–1584 (2002).
4. Washietl, S. *et al.* RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data. *RNA* **17,** 578–94 (2011).
5. Blackburne, B. P. & Whelan, S. Measuring the distance between multiple sequence alignments. *Bioinformatics* **28,** 495–502 (2012).
6. Ranwez, V., Harispe, S., Delsuc, F. & Douzery, E. J. P. MACSE: Multiple alignment of coding SEquences accounting for frameshifts and stop codons. *PLoS One* **6,** (2011).
7. Wootton, J. C. & Federhen, S. Analysis of compositionally biased regions in sequence databases. *Methods Enzymol.* **266,** 554–571 (1996).
8. Sonnhammer, E. L. & Hollich, V. Scoredist: a simple and robust protein sequence distance estimator. *BMC Bioinformatics* **6,** 108 (2005).