Fig. S10A

```
# 1: A_Sequence: Btr2 (2.A.76.1.2 homologue)
# 2: B_Sequence: Cba1 (5.A.1.2.1 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 196
# Identity:      52/196 (26.5%)
# Similarity:    90/196 (45.9%)
# Gaps:          24/196 (12.2%)
# Score: 134.0
#=======================================
                                                   2
A_Sequence         1 YVCRKAMADSRRNAMLGALGIALG--VGFWAVIVLFGLT--FLNHTIPNF     46
                     |:    : :  ::  | ||   ||  :||  : ::||:   |:      :
B_Sequence         1 YITGTTLEEELQDKKLFALSRTLGFVLGFTIIFMIFGILAGFVGQAFIRY     50
                                                   2

                                  3
A_Sequence        47 QFYLMLLGGSYLAYCGIKMVQVRKSVEIDENLKSQANEKSPL----W-KE     91
                     :  |  :||  :   |: || : |     | |  | | :||     |
B_Sequence        51 RNVLTKIGGIIIVLFGLNMVGLLKL----EFLNKQRNVRSPKEVKNWFSS     96
                                  3

                         4                                          5
A_Sequence        92 ILGGLAINLS-NPKVVVFFSSVL--AGYVANISAFKDILAVLAILMGSTL    138
                     || |:|      | :     ::|   |  | :|  | |: :||  :|
B_Sequence        97 ILMGMAFAAGWTPCIGPVLGTILIYVGTTATVS--KGIILLLAYSIG-LA    143
                         4                                          5

                                                           6
A_Sequence       139 IWFWTVAILFSQNKIRRFYAKNNR---YLDNAAGVVFILFGLKLIY    181
                     | |   |:|   |:  :|  |: :   |:   :||| |: |: :::
B_Sequence       144 IPFLLTALLI--NQFSKFLMKSEKVLPYIVKISGVVIIVVGVLIVF    187
                                                           6

#---------------------------------------

============ FINISHED =============
Average Quality (AQ)     23.74 +/- 7.86
Standard score (Z):      14.0
Precise score (Z):  14.0
```

Fig. S10B

```
# 1: A_Sequence = Sne3 (2.A.106.1.2 homologue)
# 2: B_Sequence = Orf5 (5.A.1.2.1 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 161
# Identity:      52/161 (32.3%)
# Similarity:    82/161 (50.9%)
# Gaps:          22/161 (13.7%)
# Score: 130.0
#=======================================



                         1                                          2
A_Sequence         1 LLGIILAFLIVDGIAILAGEWITDIAPRELIKMLSGAIFI-IFGLVTLIF     49
                     |:|  : |: :   : | | :      ::|:: : ||||| ||||: | |
B_Sequence         1 LVGFSVIFIFLGYSSSLVGTFFYQY--QDLLRQI-GAIFIVIFGLMILGF     47
                         2                                          3
                                                   3
A_Sequence        50 RNKREEIK-TKYHFEN-P--FYSGFI--LIFVSEWGDKTQIATG---LFA     90
                        :  :|  |  |:| |  ::  |:  | | : |   |   ||   : |
B_Sequence        48 FTPKFLMKEKKLQFKNRPAGYFGTFLIGLAFAAGWTPCTGPITGAVFMMA     97
                                                   4
                                          4
A_Sequence        91 TQYNG------LMVLTGVIIALSLLSVIAIYSGKFISDKVTRETLTKLTG    134
                      |  |      |: : |  |   |||:  |   |:|  |  | |:||: |
B_Sequence        98 AQNPGSGMWYMLVYVLGFAIPFFLLSIF-ITRVKWI-QKYNR-TITKVGG    144
                                  5
                         5
A_Sequence       135 FLFISMGVLFF    145
                     :| |::|:| |
B_Sequence       145 YLMIALGILLF    155
                         6
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     26.20 +/- 7.85
Standard score (Z):      13.0
Precise score (Z):  13.2
```

Fig. S10C

```
# 1: A_Sequence: Cac1 (2.A.107.2.1 homologue)
# 2: B_Sequence: Dsp2 (5.A.1.2.1 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 154
# Identity:      47/154 (30.5%)
# Similarity:    79/154 (51.3%)
# Gaps:          14/154 ( 9.1%)
# Score: 146.0
#=======================================
                          2                                 3
A_Sequence         1 FAISFGFFQFLCTFIGAYSGFLFNTYITYVPQIIGGMIIAFVGAFM---I     47
                     | : |    |   |  :: |  |: |   : :::||::|| :| ||   |
B_Sequence         1 FILGFSIIFFALGFSASWVGSFFSEYRDLI-RMLGGVLIAVMGLFMLGLI     49
                          2                                 3
                                                   4
A_Sequence        48 KEGFDNKEEKLLLNFKMYFVLGISVSIDAAVVGFT-MFNKISSNYVILGD     96
                     | ||  ||::| :  | :  || ||   |   |:|     |  : : |
B_Sequence        50 KPGFMMKEKRLEVGRKRWGYLGSSVIGMAFAAGWTPCVGPILVSVLALAA     99
                                                   4
                                  5                                 6
A_Sequence        97 S------VFIGIVTLILSIIAFIISRYLKRIQLVCKYADYI---GGIILV    137
                     |       :|   ||  :|  ||:: :| | : : ||:: :   || ::|
B_Sequence       100 SNPSAGLAYITAYTLGFAIPFFIMAFFLGRTRWILKYSNSLMKAGGALMV    149
                                  5                                 6


A_Sequence       138 IFGL    141
                     :||:
B_Sequence       150 VFGV    153

#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     28.64 +/- 7.96
Standard score (Z):      15.0
Precise score (Z):  14.7
```

Fig. S10D

```
# 1: A_Sequence: Pfu1 (2.A.95.1.4 homologue)
# 2: B_Sequence: Dto1 (5.A.1.2.1 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 213
# Identity:      57/213 (26.8%)
# Similarity:   104/213 (48.8%)
# Gaps:          25/213 (11.7%)
# Score: 140.0
#=======================================
                         1                                          2
A_Sequence         1 GLFAITNP--IGAVPVFIAVTRNLSPEKRKEIARKTSTTVMVTLLVFALV     48
                     || :  :|  :  :| : :    || :: ||  |:|   | ::  || :
B_Sequence         1 GLLSFFSPCILPLIPAYFSFITGLSLDELKENKRQTRQKVFLS-TVFYVA     49
                         1                                          2
                                                           3
A_Sequence        49 G-EWIFKFFGASTDAFS------------IAGGIILFRMSLEMLSGKLSS     85
                     |  :||  ||||                 | |||||    | :| | ::
B_Sequence        50 GFSFIFILFGASASFLGGLASQYAWVVRYIGGGIILV-FGLHLL-GIINI     97
                                                           3
                                                   4
A_Sequence        86 VKIS-EEEEHISEEAVTLEEVAIIPLAIPLLSGP--GAITTTMLYMAKSS    132
                        : |:: |: |: : |    :| :|      |  | :  ::| :| :
B_Sequence        98 KGFNFEKKIHVKEKPLHLMGTFVIGMAFGAGWSPCIGPLLGSILIVAGNQ    147
                                                   4
                                  5
A_Sequence       133 TMIEKSIVLLVVVAIGITV-WIILSA-ANRIHQ--KLGTIGIKVMTRMMG    178
                       : | : || | : |: | ::|||   | | :  |  |  |:|: :: |
B_Sequence       148 ETVLKGVFLLAVYSAGLAVPFLILSVFINSILEIMKRATKFIRVLNKISG    197
                                  5
                         6
A_Sequence       179 LILASMAVQMVIN    191
                     ::| :: : :| :
B_Sequence       198 ILLIAIGLLLVFD    210
                         6
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     22.82 +/- 7.67
Standard score (Z):      15.0
Precise score (Z):  15.3
```

Fig. S10E

```
# 1: A_Sequence: Sni1 (2.A.116.1.4 homologue)
# 2: B_Sequence: Psp5 (5.A.1.2.1 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 194
# Identity:      46/194 (23.7%)
# Similarity:    97/194 (50.0%)
# Gaps:          15/194 ( 7.7%)
# Score: 117.0
#=======================================
                                  2                                 3
A_Sequence         1 KPRPTSLAFLAGWVVGLVGLTVVFIEASSLAGGEQHTRPAWMSWVRIILG     50
                     |  |  |  ::  |: ::| :::|:                |  |: | |
B_Sequence         1 KNSPNKLTVISQTVLFILGFSILFVLLGISVSTVSRLLSEHMRLVQQIGG     50
                                  2                                 3

                                                             4
A_Sequence        51 AALIVFGVYRF-VTRHR--HTEQPRWMRPFAKLTPG-RAG--LTGVAVAV     94
                     | ::|||::   : | :  ::|: |:: |    :|| :||  : |:| ||
B_Sequence        51 ALIVVFGLHMTGLLRIKLLYSEK-RYL-PSG--SPGKKAGALVLGMAFAV     96
                                                             4

                                                                    5
A_Sequence        95 VRPEVLALVATAGLEIGAGGLSTAGAWTCGVLFIAVAASTVAIPVLAYAI    144
                          :  : :: | | || ::| |    ||| ::: |  :|:| |  |:
B_Sequence        97 GWTPCIGPILSSIL-IYAGSMATLGK---GVLLLSMYALGLAVPFLLSAV    142
                                                                    5

                                                   6
A_Sequence       145 AGERLDPTMARIKDWMDRNLGAMEAVVLVVIGLMVIEKGISSLS    188
                       : |   : ::   : : :     ||::::|::|    :   |
B_Sequence       143 LIDNLTAYLRKVTKHLPK-ISVASGVVMMLMGVLVFTNQLEVFS    185
                                                   6

#---------------------------------------
============ FINISHED =============
Average Quality (AQ)      21.78 +/- 7.27
Standard score (Z):       13.0
Precise score (Z):  13.1
```