Fig. S7A

```
# 1: A_Sequence: Spl1 (2.A.75.1.1 homologue)
# 2: B_Sequence: Ogr1 (2.A.95.1.3 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 157
# Identity:      50/157 (31.8%)
# Similarity:    74/157 (47.1%)
# Gaps:          14/157 ( 8.9%)
# Score: 124.0
#========================================
                          1                        2
A_Sequence         1 LIVAIGAQNTFV-LTQGIRKQHRFVVALICSL-CDAFLISAGVAG--LGS      46
                     :|  ||    || ||||:  : |  :|:  :|   | |::  | |  |  
B_Sequence         1 IIDPIGLTPLFVALTQGMPDRQRRAIAVRATLVAVAVLLAFAVFGEALLG      50
                          1                        2

                                  3
A_Sequence        47 LIEQSPTLLRLAGGGGALFLFIYGLKCLFSALQAEQELGETESNPTSRRQ      96
                      :  |    |:|||   : ||:  |  ||   || :|  :|  :||    
B_Sequence        51 FVGISMAAFRIAGG---VLLFLTALDMLFQRRQARRE--DTADDPTEDPS      95
                                  3

                           4                                        5
A_Sequence        97 VILTILAI-TLCNPNVYLDTVVLLGGISATFVGQGRYLFGAGAISMSFIW     145
                     |    |||  |  |   : |::|| | | :  |    | |     :: ::
B_Sequence        96 VF--PLAIPLLAGPGA-IATIILLTGQSESVAGFAAVL-GVMVAVLTIVF     141
                           4                                        5

A_Sequence       146 FFILSYG    152
                      | |: |
B_Sequence       142 LFFLAAG    148
#----------------------------------------
============ FINISHED =============
Average Quality (AQ)      20.31 +/- 7.39
Standard score (Z):       14.0
Precise score (Z):  14.0
```

Fig. S7B

```
# 1: A_Sequence = Pag1 (2.A.76.1.2 homologue)
# 2: B_Sequence = Cba1 (2.A.95.1.4 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 167
# Identity:      44/167 (26.3%)
# Similarity:    79/167 (47.3%)
# Gaps:          15/167 ( 9.0%)
# Score: 115.0
#=======================================
                          1                                 2
A_Sequence         1 ALVHLVALMSP-GPDFFFVS-QTAASRSRKEAMMGVLGITLGIVVWAGV-     47
                     : : |:||::| |   ||:|  |  :   |   : :  |::  ||  |:
B_Sequence         1 SFISLLALINPIGAIPFFISLTTQQTEEEKRHTIKIAAISVATVV--GIS     48
                          1                                 2

                                           3
A_Sequence        48 ALMGLHLILEKMAWLHQVIMVGGGLYLLWMGWQLMCSARQRHKQPQQDEP     97
                     ||:|   |:|        : ||||| :: |   :: :   | |   ::|
B_Sequence        49 ALLG-QQIIEFFNISVASLQVGGGLIMIMMAMNMLNAQTSRTKATPEEED     97
                                           3

                                    4
A_Sequence        98 VVELPKRGMSFLKGLLTNLSNPKAIIYFGSVFSLFVGDDVGSAERWGLFL    147
                       |  |  :: :   |  |: |      ||: :: |    |  : |   |
B_Sequence        98 EAE-AKASIAVVPLALPLLTGP------GSISTVIV--YAGKTQHWYQLL    138
                                    4

                          5
A_Sequence       148 LIIGETFAWFALVAAIF    164
                     :::|   |  |:|  :|
B_Sequence       139 ILVGIGVALGAVVYIVF    155
                          5
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     17.31 +/- 6.50
Standard score (Z):      15.0
Precise score (Z):  15.0
```

Fig. S7C

```
# 1: A_Sequence: Msp1 (2.A.77.1.4 homologue)
# 2: B_Sequence: Orf7 (2.A.95.1.4 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 152
# Identity:      42/152 (27.6%)
# Similarity:    68/152 (44.7%)
# Gaps:           9/152 ( 5.9%)
# Score: 97.0
#=======================================
                     1                             2
A_Sequence         1 FLLAAFFANPEFRAKDVVLGQYLGFIVLLT--ISSLAYFVQF--IIPSNW     46
                     ||      ||: | |         |:|| |  |:    |  |   :|:
B_Sequence         1 FLAVTTGQNPQKRRKTARKASLTAFVVLTTFAIAGTFIFKMFGITLPAFE     50
                     1                             2
                         3                                          4
A_Sequence        47 ISLLGVIPIMIGIRSFLHLKK-PQTDYSGENRDFSKYKEGQMMLPVTLVT     95
                     |:  ||| ::||:   |  |: |  : |||  : :  ||   ::|: :
B_Sequence        51 IA-GGVILLLIGL-DMLEAKRSPTQESSGETAEAAS-KEDVGIVPLGIPM     97
                         3                                          4
                                                   5
A_Sequence        96 LANGGDNLGVYMPLFASMGPFDL-FLTAIIFLIMVGVWCFLGYKLVNNRV    144
                     ||  |    | : :  :  |: :  : | | :  |  :  ||      |:
B_Sequence        98 LAGPGAITSVMVLVGQAQNPWQVGTIIAAIAITAVSCYVVLGAATRVARI    147
                                                   5

A_Sequence       145 LG    146
                     ||
B_Sequence       148 LG    149
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     13.03 +/- 5.85
Standard score (Z):      14.0
Precise score (Z):  14.4
```

Fig. S7D

```
# 1: A_Sequence: Asu1(2.A.107.2.1 homologue)
# 2: B_Sequence: Csh1(2.A.95.1.5 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 124
# Identity:      33/124 (26.6%)
# Similarity:    64/124 (51.6%)
# Gaps:           6/124 ( 4.8%)
# Score: 108.0
#=======================================
                                  3                                 4
A_Sequence         1 YISEFDHWIA-FALLCVIGINMIKMSVTNENSDDDPSD--FSL-RHLTML      46
                     ::||    ||   :| :| : |:     : |  | |:|  | :   : ::
B_Sequence         1 HLSETSLGIAGGVILFLIALRMV-FPAPHGNGADHPADEPFVVPLAIPLI      49
                                  3                                 4

                                                   5
A_Sequence        47 GVATSIDALAMGVSFAFLKVNIWTAAAIIGITTTILSL-FGVKAGHWLGD      95
                        :::  : : ||    ::  | ||  : :    |:| |  |  ||||:
B_Sequence        50 AGPSALATVLLLVSREPARLWEWVAALALTMVVCALTLAFAEKISHWLGE      99
                                                   5

                                  6
A_Sequence        96 RIHKQAELLGGIILIAMGVKVLIE    119
                     |:    | | |::| |: |::|::
B_Sequence       100 RVTTAFERLMGLVLTAIAVQMLLD    123
                                  6
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)      16.70 +/- 6.06
Standard score (Z):       15.0
Precise score (Z):  15.1
```

Fig. S7E

```
# 1: A_Sequence: Gka1 (2.A.109.1.5 homologue)
# 2: B_Sequence: Dgi1 (2.A.95.1.5 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 106
# Identity:      29/106 (27.4%)
# Similarity:    52/106 (49.1%)
# Gaps:           6/106 ( 5.7%)
# Score: 93.0
#=======================================
                        1                                 2
A_Sequence        1 LIIGIDVILGGDNAVVIALAS-RNLPEQKRNVAIIVGTALAIAVRIVLTV     49
                    | : : :|: |   | : ::  |  | :::   |      |:|: |:
B_Sequence        1 LAVPLFLIMDGLGNVPVCMSMLRRFPPRRQQRIIFRELCFALAISILFCF     50
                        1                                 2
                                         3
A_Sequence       50 AVVWLLTI----P-FLQLAGGVVLFWIALKLIGQKDEKPTMIKAEPSLWK     94
                       |||      |  |:|||||||| |:::::   : | |    :||
B_Sequence       51 FGDWLLKFLGLGPSTLRLAGGVVLFVISMRMVFPDESKETADPEDPSALA    100
                                         3
                        4
A_Sequence       95 AIQTIV    100
                    | :  :
B_Sequence      101 AEEPFI    106
                        4
#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     12.39 +/- 5.29
Standard score (Z):      15.0
Precise score (Z):  15.2
```