```
         ....|....| ....|....| ....|....| ....|....| ....|....|
              10         20         30         40         50
Rab1a|   MSSMNPEYDY LFKLLLIGDS GVGKSCLLLR FADDTYTESY ISTIGVDFKI
Rab1b|   ---MNPEYDY LFKLLLIGDS GVGKSCLLLR FADDTYTESY ISTIGVDFKI
Rab11a|  MGTRDDEYDY LFKVVLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT
Rab11b|  MGTRDDEYDY LFKVVLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT


         ....|....| ....|....| ....|....| ....|....| ....|....|
              60         70         80         90        100
Rab1a|   RTIELDGKTI KLQIWDTAGQ ERFRTITSSY YRGAHGIIVV YDVTDQESFN
Rab1b|   RTIELDGKTI KLQIWDTAGQ ERFRTITSSY YRGAHGIIVV YDVTDQESYA
Rab11a|  RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY YRGAVGALLV YDIAKHLTYE
Rab11b|  RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY YRGAVGALLV YDIAKHLTYE


         ....|....| ....|....| ....|....| ....|....| ....|....|
             110        120        130        140        150
Rab1a|   NVKQWLQEID RYASENVNKL LVGNKCDLTT KKVVDYTTAK EFADSLGIPF
Rab1b|   NVKQWLQEID RYASENVNKL LVGNKSDLTT KKVVDNTTAK EFADSLGIPF
Rab11a|  NVERWLKELR DHADSNIVIM LVGNKSDLRH LRAVPTDEAR AFAEKNGLSF
Rab11b|  NVERWLKELR DHADSNIVIM LVGNKSDLRH LRAVPTDEAR AFAEKNNLSF


         ....|....| ....|....| ....|....| ....|....| ....|....|
             160        170        180        190        200
Rab1a|   LETSAKNATN VEQSFMTMAA EIKKRMGPGA TAGGAEK--- ---SNVKIQS
Rab1b|   LETSAKNATN VEQAFMTMAA EIKKRMGPGA ASGG-ER--- ---PNLKIDS
Rab11a|  IETSALDSTN VEAAFQTILT EIYRIVSQKQ MSDRRENDMS PSNNVVPIHV
Rab11b|  IETSALDSTN VEEAFKNILT EIYRIVSQKQ IADRAAHDES PGNNVVDISV


         ....|....| ....|...
             210
Rab1a|   TP----VKQS GGGCC---
Rab1b|   TP----VKPA GGGCC---
Rab11a|  PPTTEN--KP KVQCCQNI
Rab11b|  PPTTDGQKPN KLQCCQNL
```

S2.1 Fig. Multiple sequence alignment of Rab1 and Rab11 sequences. Residues that are conserved in all sequences are highlighted in yellow and residues that are conserved in two or more sequences are highlighted in green.

```
                                    G1                              G2
              10          20          30          40          50
Rab11a|   MGTRDDEYDY LFKVVLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT
Rab11b|   MGTRDDEYDY LFKVVLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT


                               G3
              60          70          80          90          100
Rab11a|   RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY YRGAVGALLV YDIAKHLTYE
Rab11b|   RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY YRGAVGALLV YDIAKHLTYE


                                          G4
             110         120         130         140         150
Rab11a|   NVERWLKELR DHADSN-IVI MLVGNKSDLR HLRAVPTDEA RAFAEKNGLS
Rab11b|   NVERWLKELR DHADSN-IVI MLVGNKSDLR HLRAVPTDEA RAFAEKNNLS


          G5
             160         170         180         190         200
Rab11a|   FIETSALDST NVEAAFQTIL TEIYRIVSQK QMSDRRENDM SPSNNVVPIH
Rab11b|   FIETSALDST NVEEAFKNIL TEIYRIVSQK QIADRAAHDE SPGNNVVDIS


             210
Rab11a|   VPPTTENKP- -KVQCCQNI
Rab11b|   VPPTTDGQKP NKLQCCQNL
```

S2.2 Fig. Pairwise sequence alignment of Rab11a and Rab11b. The G loops are colored in red. The amino acid variations in Rab11b sequence compared to those of Rab11a are highlighted in green.