

A

```

1      10     20     30     40     50
Andhra_gp14 MKNIYSNHIKGQKLTGLKPSIDGVVIHNDYGSMTPSQYLNWLYSRFEQNGSYTACWAS...
SAP-2_gp14  .....MKSQQAQDWIKHEGVGVDFDGAYGFQC
GRCS_gp15  .....MKSQAQAKWIKHEGTGVDFDGAYGFQC

60     70     80     90     100    110
Andhra_gp14 VYVNNRNETLWYHPNTNYIEWFCGNNYANSHLIGF...EVCESEFPNHISDETFMKNNEEATF
SAP-2_gp14  MDLAVAYIYIITDGKVRMWGNAKDAINNDFKGLATVYENTSFKPLGDVAVYTNNSQY..
GRCS_gp15  MDLAVAYVYIITDGKVRMWGNAKDAINNDFKGLATVYENTSFKPLGDVAVYTNNSQY..

120    130    140    150    160    170
Andhra_gp14 KVADVMSKSYKLPINRNIVHLHREYFSTSCPHRSWAIVHGVGAPNTRANQLKLIIDYFISR
SAP-2_gp14  GHI.....OCVTSGNLDYYTCLQNNWLNNGGYDGWEK.....ATIRTHYYDYG
GRCS_gp15  GHI.....QCVISGNLDYYTCLQNNWLNNGGYDGWEK.....ATIRTHYYDYG

180    190    200    210    220
Andhra_gp14 ITHYANIGKTPDKPOVSEN..KYVKYNWR...GTF...AHKTNTLPIVPRYDYGMS
SAP-2_gp14  VTHFIRKFSNSESKVLEQN.IQLTNWKKQNYGTYYRNEKATFTCGFLPIFARVC...SP
GRCS_gp15  VTHFIRKFSASNSNVLETSKVNFTFGNWKQNYGTYYRNEATFTCGFLPIFARVVG...SP

230    240    250    260    270    280
Andhra_gp14 AKEVDKDSYIOPNEVYFQTIKDKQAKLWIKFKYAKKGSSKQFYMPITGKIEDKHEKI
SAP-2_gp14  KLSEPNGYWFOPNGYTPYDEVCLS..DGLVWIGYNWQG....TRYLPLVRQWNGKTGNA
GRCS_gp15  KLSEPNGYWFOPNGYTPYDEVCLS..DGLVWIGYNWQG....TRYLPLVRQWNGKTGNS

290
Andhra_gp14 LNEKHLWQKLEVEKHKG
SAP-2_gp14  YSIGVPGVFS.....
GRCS_gp15  YSIGLPGVFS.....

```

B

```

1      10     20     30     40     50
Andhra_gp10 .....MNDKEKIDKFIHSNINDDFGLSVDLVLKVKVGIGRFSAWCGNSSTKIKQVILN
SAP-2_gp10  .....MNDQEKIDKFTHSYINDDFGLTIDQLVLRVKVGYGRFNWVWLGNGNESKIROVILN
GRCS_gp11  MILKRVII MNDQEKIDKFTHSYINDDFGLTIDQLVLRVKVGYGRFNWVWLGNGNESKIROVILK

60     70     80     90     100    110
Andhra_gp10 AVKSIQVSPALFAAYEKNEGYNGSWGWLNHTSPQGNVYLTDAQFVARKLVSQSRQAGTPSW
SAP-2_gp10  AVKSIQVSPTLIAAYEKNEGYNSAGLWLNHTSAQGDYLTDAKFVARKLVSQSRQAGOPSW
GRCS_gp11  AVKSIQVSPTLFAAYEKNEGYNSAGLWLNHTSARGDYLTDAKFVARKLVSQSRQAGOPSW

120    130    140    150    160    170
Andhra_gp10 IDAGNIVDFVFPASVKKRKNYDSSHNMKNKVCRAYIPLTAAATWAAAYPFGIQA SYNKRVQ
SAP-2_gp10  YDAGNIVHFVFPQNVQRKGNADFAKNNKACGTVGRAYIPLTAAATWAAAYPLGIKASYNKRVQ
GRCS_gp11  YDAGNIVHFVFPQNVQRKGNADFAKNNKACGTI GRAYIPLTAAATWAAAYPLGIKASYNKRVQ

180    190    200    210    220
Andhra_gp10 NYGNPFLDAANTIIAGWGGKLDGKGGSSSSSSSGTSG...GLDVAARAFEF LKKVQD
SAP-2_gp10  NYGNPFLDAGANTIIAGWGGKLDGKGGSSSSSSSGSDSGSSLLALAKQAMQEL LKKVQD
GRCS_gp11  NYGNPFLDAGANTIIAGWGGKLDGKGGSSSSSSSGSDSGSSLLALAKQAMQEL LKKVQD

230    240    250    260    270    280
Andhra_gp10 S MOWDHSIGTDKFFSNQMFITKTYNNTYRLNMNQKLLDEMKDLISRIDGGS GN.DTGA
SAP-2_gp10  ALQWDVHSIGSDKFFSNDFYFTLQKTFNNTYHIKMTIGLLDSLKRLIDSVQIDDGGS.SNP
GRCS_gp11  ALQWDVHSIGSDKFFSNDFYFTLQKTFNNTYHIKMTIGLLDSLKRLIDSVQVDSGSSSNP

290    300    310    320    330    340
Andhra_gp10 DSDGDHGGKAGKSVAPNGKSGRIGGNWTVSNLPOKYKDAIEVDFDKYTL..AGSPEV
SAP-2_gp10  TDDGDBHNAIRGKSVKPNGKSGRVIIGGNWTVDQLPEKYKKAIGVPLFKKEYLYKPGNIEP
GRCS_gp11  TDDGDBHKAISGKSVKPNGKSGRVIIGGNWTVADQLPEKYKKAIGVPLFKKEYLYKPGNIEP

350    360    370    380    390    400
Andhra_gp10 NTGDTGQCTELTWAYMHOIWKROPANDNOVTNGQRVWVYRNQGARVTHRPVGYGFSS
SAP-2_gp10  QTGNAGQCTELTWAYMSQLHGKROPDQGOVTNGQRVWVYKRLGAKTTHRPVGYGFSS
GRCS_gp11  QTGNAGQCTELTWAYMSQLHGKROPDQGOVTNGQRVWVYKRLGAKTTHRPVGYGFSS

*
410    420    430    440    450    460
Andhra_gp10 KPNYLQAMLPGVGHTGVVAVRDKDGSFLTANYNVPPYVAPSRVVEALIDGVPENAGDNI
SAP-2_gp10  KPPYLQASIIYGIHTGVVAVRDKDGSFLTANYNVPPYVAPSRVLLYTLINGVPENAGDNI
GRCS_gp11  KPPYLQASIIYGIHTGVVAVRDKDGSFLTANYNVPPYVAPSRVLLYTLINGVPENAGDNI

*
470
Andhra_gp10 MFFSGIK
SAP-2_gp10  VFFSGIA
GRCS_gp11  VFFSGIA

```

Figure S2. Cater et al.