```
5msf:S     CGGAGGAUCACCACGG
           ::::::::::::::::
2iz8:R     AUGAGGCUCACCCAUG
```

RMscore=0.83674

Figure S6. *A false positive example of RMalign benchmarking in balance-SCOR.*

5msf:S (yellow) is superposed on 2iz8:R (cyan) by RMalign. These two RNA

structures are very similar (RMscore = 0.837). But they are belonged to two distinct

function classes in FSCOR (Phage_coat_protein_binding,

MS2_phage_coat_protein_binding_stem-loop).