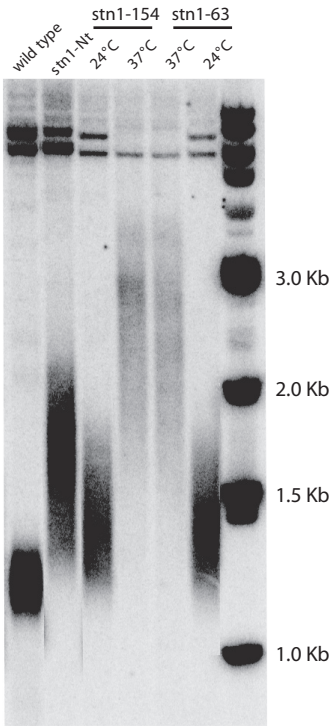
A

```
Sc_Stn1      1 --MDKYGHIAHQEGD-VCYYIPRLFKYNSYVSGTEDVRIFVGDLKYRMRVSLQICEKYYD
KL_stn1      1 MEHHVLGYETSKHGSRYPVFLTQLLPTSKWYGKATSLTIRSIYKNLETSRKWNTEYLIYN
Cgl_Stn1     1 -----------------MEHGELVSEYRCYSERVSRGLYHAEVCMTVRMLHSCLDQSHA
                                     .*.     *.   .  :          .     :
                                                          D>E
Sc_Stn1        RRLS-MLFWKNHPLQQIHLIGCIIGLQFKWIGKQEYIFFQLDDCTSDSSLVGYTSDMRFL
KL_stn1        SSIRDIFLYLNHPITSIKICGLVVGWKWKLIGNEDRAFWYIDDCS------------DTI
Cgl_Stn1       RVLGGKLYWKNRAIRRLKFVGTVIGVKYMWLKGDDYAVIHLDDSS----------DSSIL
                 :   : : *:.:  ::: * ::* ::  :  ::  .  :**.:              :

Sc_Stn1        TCKVKKDSILSWGLNITD-LIGLTLHVYGQASLNYQDLQVEYLRLCYS-LTEDIDHWKIT
KL_stn1        LCQCSKSQLLALNCPLVD-MSGWTLILTGLLDQERVEFKVTQIEVVKN-LKHEIDFWSEA
Cgl_Stn1       KCKCEVNQLNSFGININAGFIGSRVEVCGVYNTEFNDLEVGFIGVLPSTLFSEIEHWRKC
                *: . ..: : .  :   : *  : : *  . :  *::*  : :  . *  **:.*

Sc_Stn1        MNMREQLDTPWSLSDFVIGELFTQEQEWTPETSQIEVVNPDFVGIGYKTPESKRNETTFI
KL_stn1        FDNQKELAIPWEIDPESLNEFYRGKQ-------------------HTPSKSNSNLGNYI
Cgl_Stn1       CLLLRMPDDLTDEELKASGIGDDEMQDGRDSP------------LDEYFSTPPQNKAQFI
                    .      . .    .      *                      . .  *   :*

Sc_Stn1        EQLQ-EERLKDELEIISPYNSTDTSNSVHSLSFRFVSSLKDFPETHFLNSGDQIDNGNDE
KL_stn1        EQLQTIHFQENELLLASPYN-------------GHVSTGMGVWNSDLLQSTLEQDLIEQS
Cgl_Stn1       EKLV-LRDVKDKLEITSPDP--------------VRNESISVVDDTCDNTTLGSNTIDLR
               *:*   .  ::* : **                  .   .. :    ::    :  :

Sc_Stn1        QLKKLEYQSANLPVMIPNRTSAKSNLMLILLGLQMKEISNSDLYKLKEVRSVVTSLASFL
KL_stn1        RLDKTLGG-----QISPNSRKRSSKLSPKQMKREILGVLIEKSMESKVCKIYEPLLSINL
Cgl_Stn1       TAIEPITQPEVSGNDNFYKPATGSTSKRKLYRKLFIAIYLIPEEECTINDLARDIGITSV
                  :                   *.         :  :      : .           :

Sc_Stn1        FQQQNVGVMKSFDSLEKEAFRDLVNRLVSQGLIGLKDKTSETFDLLPLKNLFEVAEKRIS
KL_stn1        GPGGEATDLKTEPVLHLKFYETFLAQLAEMAIITLDSFT---INMTNLHNCYRYIITRFQ
Cgl_Stn1       LKGFLDGQGHISNDDMQIILQEYLSQLITGDVLVITARN--RVSLKKLHALKAYTQKHIN
                        :          .  : :*    :: :   .   ..:  *:    *  .*:.

Sc_Stn1        VLMKLQCYTGTVQLSHVQEKLHLPYITTNGIVDVFKECLKRTKKQYPEVLKNWWIDLDPK
KL_stn1        SLINVQIPQITIKYSEIRNFCKLPLLSKK---LILQMCKHFLNTTHIGNLIDWWVDP---
Cgl_Stn1       LLLKIQALLGTVRYQDVLQSTSMAIPAET------IIDAFKESLRTIDAGVAWFIET---
                *:::*    *:: ..: :   :.  : .             .         *:::

Sc_Stn1        NGMEDQNSGILLHLEYAAAYS-- 494
KL_stn1        --TSEERYKVFFTYSKSK----- 434
Cgl_Stn1       ---HQHSFTIHFTYSQSTQTCNN 436
                   :.   : :  . :
```

B



Puglisi et al., Figure S1