

Figure S1: Multiple sequence alignment of yeast Trf proteins generated with ClustalW and Boxshade. Species are Scer: *Saccharomyces cerevisiae*, Spar: *S. paradoxus*, Smik: *S. mikatae*, Sbay: *S. bayanus*, Skud: *S. kudriavzevii*, Scas: *S. castellii*, Sklu: *S. kluyveri*, Kpol: *Kluyveromyces polysporus*, Klac: *K. lactis*, Kthe: *K. thermotolerans*, Kwal: *K. waltii*, Cgla: *Candida glabrata*, Cgui: *C. guilliermondii*, Ctro: *C. tropicalis*, Calb: *C. albicans*, Cpar: *C. parapsilosis*, Clus: *C. lusitaniae*, Agos: *Ashbya gossypii*, Zrou: *Zygosaccharomyces rouxii*, Dhan: *Debaryomyces hansenii*, Lelo: *Lodderomyces elongisporus*, Ylip: *Yarrowia lipolytica*, Soct: *Schizosaccharomyces octosporus*, Spom: *Sch. pombe*, Sjap: *Sch. japonicus*

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Trf5Scer      1 -----MTRLKAKYSPTKGRKE-----DKHTKRMR
Trf5Spar      1 -----MTRPKAQYSPSKGRKE-----NKHTKRMR
Trf5Smik      1 -----MTRPKAQYSPSKGKSKE-----NKRIKRMR
Trf5Sbay      1 -----MTRSKAQFSPSKGGKKE-----YKNPKRMR
Trf5Skud      1 -----MKKAKVLFSPSKGGKKE-----NKNPNRMR
Trf5Cgla      1 -----MRGDRSKRKVAKYQKKE-----SARVKRLR
Trf5Kpol      1 -----MSKKRKLK-----IVKPKKLR
Trf5Scas      1 -----MGAPVFLTHFIFMTRNKPKRTHSSPTKKVSKKTHRKIR
Trf4Spar      1 -----MGAKSVTASSS-KKIKNRHNGKVKKSKKIKKVRKPQ
Trf4Smik      1 -----MGAKSIAASST-KKIKKQHNGKVKKSKKIKKVRKSK
Trf4Sbay      1 -----MGVKSITSSS-KKSKKQHNGKVKKKVKKVRKSK
Trf4Skud      1 -----MGAKSIVASSSSKSKKQHNGKMKKKNKIKKVRKSK
Trf4Kpol      1 -----
Trf4Scas      1 -----MATKSTSSIKQKPEIKSKKIEISKGKGMKNS
Trf4Cgla      1 -----MSAAVDDVK-----
TrfKlac       1 -----MSKRPSSGKGVK-PNRNRNKP-----VKQVKKMR
TrfAgos       1 -----MMTASVAGNRSGRSGNIARERSNRSRGAQKSDKERNLSKGSSRPKSNSSRVKKMR
TrfZrou       1 -----
TrfKthe       1 -----MGAKEASKNERAGPKSSSSKSK----PLKNNQRRTKRLR
TrfKwal       1 -----MGVKEGKKTERFGRKSSAKSK----PLKENQQARRLR
TrfSklu       1 -----MGRKKSQSPSLPQGSNSKNSKKLAYPLSAKKKKVKKLR
TrfDhan       1 -----MMVSKRK--RESPPVKLKSQKQKKTSGGIIPIENKY
TrfCgui       1 -----MGNKRK--KEN-----GKNSKPSTTKPG-FVESKNKY
TrfClus       1 -----MRKSTIMGQKRS--NDS-----QPAVTRKKARKTK--KKPQNTF
TrfCtro       1 -----MSGNKR--KGSINSTKPKKKVKSPSVDVQLS--TNN
TrfCalb       1 -----MGTKRK--RENLVGKPRSKRQKDKSLLKVDNASFLEN
TrfCpar       1 -----MGNKRQ--RERSDRKGDQKRQKLNNVVAATTS PKHEN
TrfLelo       1 -----MGSKRKHTKDGSMRDSSKKKRLSTAHGPPVEKRQRTSS
TrfYlip       1 MFSEVLSPMAKRTTKLPPATVATKADLRNRPIAQPVSRRRGQQATPNNANNNSNNNSAED
TrfSoct       1 -----MAKKSTFSKANKANKIKKSKFDEREPLPRRIFKKDDRNR
Cid14Spom     1 -----MGKKSVSFNRRNY----KKRKNERTEPLPRRIFKNDKPSK
TrfSjap       1 -----MSKKKSKDSNSKKNR-PNSSKGESKGLARRIFKRGSKSK

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Trf5Scer 26 KSSFTRTQKMLEVFNDNRSHFNKYESLAIDVEDDDTFGNLVLME--
Trf5Spar 26 KSSFTRTQKMLEVFNDNRSHFNKYESLAIDVDDGTFGNFVLMEND--
Trf5Smik 26 KSSFTRTQKMFVFNENRSHFNKYESLAIDVDDGTGNGFVLMKND--
Trf5Sbay 26 KSSFTRTQKMFVFNENRSHFNKYESLAIDVDDGTGNGFVLMENS--
Trf5Skud 26 KTSFTRTQKMFVFNENRSHFNKYESLAIDIDDDGTGNGFVLMENN--
Trf5Cgla 26 RSSFNALQRNIEVFNDNKEFLNKYENLELDLSDPENRTHLLSEYNDLDTQ--
Trf5Kpol 17 KSSINKIRKFNLFNEIDIDIDNYDKLIDMEKSN--NNRFLVLQD--
Trf5Scas 39 KSSISRIEKQKFNFDNDIDQYNKYENLALDVSDETELLQQDRKGHHFSFIEEDVREEVPG
Trf4Scer 36 KSIISLNDENEVEILPSRNEQETNKLPKDHVTADGILVLEHKSDDDEGFVDYDG--
Trf4Spar 36 KPKSLSDENGVEIVSSRNDQETNTSLKDHVTADGILVLEHKSDDDEGFVDYDG--
Trf4Smik 36 KKSLSDENGAEVTSRSEQDNNKSPDDHVTEDGILVLEHKSDDDEGFDDYDG--
Trf4Sbay 36 KPRSTSDNEAESVVDNEEESKASGDHVTADGILVLENKSDDEGFDDYDG--
Trf4Skud 37 KDTSTSDENEAGNLPKLNQEIKNPDDHVTSDGILVLEKKSDDDEGFDDYDG--
Trf4Kpol 1 --MSTTEKN-----KDIVIINDNVSEENDDYDDYDG--
Trf4Scas 34 SKSKNSKHGKSMRRSKNKNQNNKPPTTVRSTDGITFLESS--ESEGYDDYDG--
Trf4Cgla 10 -----TVEDVADVIAVSS--DSQGDDYDG--
TrfKlac 29 KSSLSRAQKNFVVFQQ-QSHENKYESLQSIIRDGEDAGDEVVFLHDEGKD----LNSDD
TrfAgos 56 KSSLKVKQKNFAVFNDSAHEHNKYETLAVAEADEK----EVILLDEE--
TrfZrou 3 KSSLKAQRNFQVFN--NDHVNQYENLPESAVEDK-----
TrfKthe 35 KSSLKAQRNFVFNKDGAKHINKYENLELDNIESEG--DDGSER--
TrfKwal 35 KSSLKAQRNFVFNKDNHNLKYNENLKMVEIESEG--DNANES--
TrfSklu 39 KSSLKAQRNFVFNKMDHEINKYENLPVDISDEEHNNDNHSKDGNGPSFTHDGMILIDEY
TrfDhan 38 EALPSSDNESDSS----LKFDFKSNREP---EMVFVESDDEEEGVVIVSDDDKPE--
TrfCgui 30 DVLSS---DSDSS----AIFDH---NRKDE---NLVLVDSDDD--IVVESDSENEN--
TrfClus 36 ETLPP---EPQDD----IVLVESGDESHS---DVVVFSDREE--TQETETKEAK--
TrfCtro 35 NFVALQDHVDEDS--DIEVIYEQKPKQE----LVLLDSEEDE-----DEDAENEV--
TrfCalb 37 KFETLQNHLDDES--DSELIYDYDRKKSEELTDDLVLIDSEES-----NDSSD--
TrfCpar 37 NFKLP--HSDDDS--DSDIYFDYSRKQSQP--EKELILVDSDAEK-----NSGDS--
TrfLelo 39 NTYESLYEIDGESSDSEHIFNYDKDTSPEKDNVINLIDSDDED-----KEEKGEEE--
TrfYlip 61 KSNNTNDTKSKDGKEKASKKRRKKNKKSQSGPISQDRRNSGNGYNVLDENDDKSDG
TrfSoct 41 -RFKKNQKRRKSKYPDELEVNNSFLLE-QEQ----GENRKESDG-TQYSQQKNDKND
Cid14Spom 37 FKSRRKEKDKNSDAYDEMLLNNFTLLD-QEEPMEIGSKSRNDNDSEGIIRDKGGVEIS
TrfSjap 40 -RKSSESKKHRTVYDDLSGENNFVLDNQDPDVIKSETEPESSNVSSSTETAVSSDVS

Trf5Scer 72 -----KSDVDIPVIEEVTSSSEDEQRAESS-----
Trf5Spar 72 -----KGDVDIPVIEENTSSDDEKRIESR-----
Trf5Smik 72 -----KVDVEIPVIEEETSSDEEGQTESR-----
Trf5Sbay 72 -----EGDIDIPVIEEETSDDDETINESL-----
Trf5Skud 72 -----KGDIDIPVIEEDTSDDDKMMKGSR-----
Trf5Cgla 76 -SDGESKADNHNSYDTIPVIDIDSGDEGIVSDIK-----
Trf5Kpol 59 -TDG-----IDKIDEIPIVDIESDTS--NDDID-----
Trf5Scas 99 -----TSDVPIGIFDSENQSSSTETKIDACPT-----
Trf4Scer 89 -----HFDNPTDIPSTT--EESKTPSLAVHG-----
Trf4Spar 89 -----HFDNPTDIPSTT--EESRTPSLAVHG-----
Trf4Smik 89 -----HFDNPTDIPSTT--EGSKTPLLGVHG-----
Trf4Sbay 89 -----HFDNPTDVPSTA--EGSKTPLLVVHG-----
Trf4Skud 90 -----HFDNPTDVPSTT--EENKTPLLTVHG-----
Trf4Kpol 30 -----HIGNPLTISDSS--AESNNGDNKVPK-----
Trf4Scas 86 -----HFDNPTESDKDLKMAKVAVEKVPQ-----
Trf4Cgla 34 -----HNSPKE-----MPI-----
TrfKlac 83 IDEVSVSENDLLEDEEEDDEEGEEEPVGTADGI-----
TrfAgos 99 -----EDTAMTTETKGVHAEETANVTGAEGVN-----
TrfZrou 37 -----
TrfKthe 77 -----TQESSEAPTTEATPESEEPQKEQA-----
TrfKwal 77 -----TKIS--EDEVVNISSGSDENRVSQG-----
TrfSklu 99 DDQDIPNDSIIKDVKEVDVLDLSEENMLNINN-----
TrfDhan 87 -----DSEEPASKKQ-----
TrfCgui 73 -----NSETDTKKRKVSDSNHQPKASKR-----
TrfClus 79 -----AIDSIPETAD-----
TrfCtro 80 -----ETKKSVDQSNPKRRKFDEVNEADD-----
TrfCalb 84 -----GFDDINSESEKKQVLVGN-----
TrfCpar 82 -----DSNESIKDSTESSHENQ-----
TrfLelo 91 -----EEEEEDDDENGSNGENQIEIDGDKVKDKIEISPSDQEKLIESTSTSSST
TrfYlip 121 EGERSSKRRRTAGSAASTTASSDMSSENERSVSTAPTAPAPKPPAD-----
TrfSoct 93 SK--PSLNQSGRVDPLETLEKLDLPEEAIAKKGAPSIIVGLKLLDDKSE-----
Cid14Spom 96 KNKNDPIYIQFGKADPLEPLEKPDLPPEEAIAKRGEPILLGIPKREGR-----
TrfSjap 99 FAEPRAQTHGKVDPLDVLKPDLPDEAIAKRGEPILLGVPKVKKR-----

Trf5Scer 96 -----KRNNSLEDNQDFIAFSDSSEDETEQIKEDDDERSFLLTDEHEVSKLTS--
Trf5Spar 96 -----KRGHSLLEDNHDFIAFSDSSEEEKQIKEDEDERSFLLADQYKSTFSS--
Trf5Smik 96 -----KGDHSLLEDNHDFIAFSDTSEDEKEQKRGEDEEKCDFLSLNQYEISTFGS--
Trf5Sbay 96 -----KNGNSLEDNHDFIAFSESSGDEE-EEERVTEEKSVLLVHDQYEISTVTS--
Trf5Skud 96 -----EKRNSLEDNQDFI PFSDSSEDEQGE EEGNSEGVSGFLMPDQYEITKNNT--
Trf5Cgla 110 -----ISGGKLEDNDDFIAFSSSEDENSGA-ENNESEDYLSSGNTSSD-----
Trf5Kpol 84 -----NLEDSLKDNNDFIAVSSSTSEED-----YDDISEDEDTDGNES-----
Trf5Scas 125 -----LLQLNKLANNDDFIPFASSEDEDEDEGPLNPTINDYGETLANR-----
Trf4Scer 113 -----DEKD-LANNDDFISLSASSEDEQAEQ-EEEREKQELEIKKKEKQK-----
Trf4Spar 113 -----NEKD-LANNDDFISLSASSEDEQAEQ-EEERQKEELEVKKKKQK-----
Trf4Smik 113 -----DEKD-LANNDDFISLSASSEDEHAEQ-EEERQKE-----EKQK-----
Trf4Sbay 113 -----NEND-LANNDDYIALSASSEDEDAKQKEEEKQKKEEELKRRKQK-----
Trf4Skud 114 -----SERD-LANNDDFISLSASSEDEDAKKEEERQKKEAELLRIRQK-----
Trf4Kpol 54 -----LRSD-IDTNDDFIAFSDSSEDEKENDDINEKESK-----DEDA-----
Trf4Scas 111 -----LQNNKLEDNQDFIAFSSSSDEKDIQEKQALEVDEQ--VTKEPT-----
Trf4Cgla 44 -----IDNNQIDENDDFIAFSESSGGE---DGDEAEQEQPQ--AEQEQ-----
TrfKlac 117 -----IGNNSLDANEDFIAFDLSEPEDEHENGFEHSEPETAGKEEIE-----
TrfAgos 126 -----AAANALDDNQDFI FSDSSEEVASGE---ENGADAYA-VEDAE-----
TrfZrou 37 -----NGSLDGNDDFIAFDDSSSEDEGGK---EEQE---TESVE-----
TrfKthe 101 -----QDNALDDNQDYI SLSMSSEEEQESE---EEAPDEAGGEHPGGD-----
TrfKwal 100 -----EENALEDNQDYI SLSMSSDAADVSS---EEEGHSDNVGSDDDY-----
TrfSklu 134 -----NQNALDNNEDFIPFAVSSSEDEEEK---DEHGTYDYDDYDDEYPSKEEE-
TrfDhan 97 -----KFVNNE LAKNQDFIEFGFSSSEEDAPERNDYDDYSDGVLSDDESGETI----
TrfCgui 96 -----KMEYNE LSKNQDFIEFGFSSSE---EANKYDDYSDDGIISDDQSGNR----
TrfClus 89 -----AAPPNL TNNNDYIRLGLSSEDE-----EAEDLSDDGVLSDDESGBR----
TrfCtro 105 -----ITTETNELAKNEDFIEFGFSSSTDEEE---SEGEE-----SEND-----
TrfCalb 103 -----KTPENELANNEDFIEFGFSSSEDDSEEISNSDNDL-----SNGDY----
TrfCpar 99 -----ESNELTTNQDFIQFGFSSSEDEDE--HDEEHD-----SQNTN----
TrfLelo 140 TSSTSSTNLPEANDLAKNDDFIEFGFSSSEDEDEDEDRDDGNGGINSVAEEIIDTTSR----
TrfYlip 168 --SPPPPPPVDPSEWNMNE DVFDFSDGDEDEDEPEEPVRSRKRTEIEVDASS----
TrfSoct 139 -----KPKPEPKNAV DENADYIGFDWNSDEDEVNDTSKDETND-----SGPNNIPGFMQN
Cid14Spom 141 -----KTNPVHDKAVENNSDFIKFDWNSDEDEDSVSNDSKKNNESLKKSSKNEIPGFMQR
TrfSjap 144 -----KSIDGASVEGNADFIKFDFTDDEEEDKEDETSRR-----EKKSAIPAFMQK

Trf5Scer 145 -----QQSLNTE SACNVEY PWRNHC HSKQRRIADWLTSEIKDFVHYISP
Trf5Spar 145 -----QHPQNTDSACNTEY PWRNHC HSRQRRIADWLTSEIKDFVHYISP
Trf5Smik 145 -----QYHQDTE SICA NAEY PWRDHC HSSQRRIADWLTLEIKDFVRYISP
Trf5Sbay 144 -----ISHENGDSVCNTEY PWRKDHGHSRQRGIADWLTLEIKDFVHYISP
Trf5Skud 145 -----QSHENTHSTSNTEY PWRNHNHSRQRKIAEWLTSEIKDFVHYISP
Trf5Cgla 153 -----DELAGR RNAERELNADFPWLLNHDH SKQKEISDWLTAEIRDFVAYISP
Trf5Kpol 122 -----HADERTLNTEFPWLLNHDH SKQKEIIDWLTLEIKDFVAYISP
Trf5Scas 170 -----YEYTSVNVVHPWILNHDHTEQRSISAWLTTEIIDFVSYISP
Trf4Scer 155 -----EILNTDYPWILNHDH SKQKEISDWLTFEIKDFVAYISP
Trf4Spar 155 -----EILNTDYPWILNHDH SKQKEISDWLTFEIKDFVAYISP
Trf4Smik 149 -----EILNTDYPWIVNHDH SRQKEISDWLTFEIKDFVAYISP
Trf4Sbay 156 -----EILNTDYPWILNHDH SKQTEISDWLTFEIKDFVAYISP
Trf4Skud 157 -----EILNTDYPWILNHDH SRQKEISDWLTFEIKDFVAYISP
Trf4Kpol 91 -----NILNMDFPWTINRDH SKQKEIADWLTLEIRDFVSYISP
Trf4Scas 153 -----KILKSDYPWILNHDH SKQKEISDWLTLEIADVFVSYISP
Trf4Cgla 82 -----YTDYPWTIDRDYSKEKELADWLN YEILDFVAYISP
TrfKlac 161 -----EGEGDKLR-HNADFPWILNHDH SKQREIADWLTLEIKDFVSYISP
TrfAgos 165 -----DESSEPLP-TNADYPWIQNHDSRQREIADWLTLEIKDFVSYISP
TrfZrou 70 -----ESGEQVLPVTNTDYPWILNHDH SKQREIADWLTLEIRDFVAYISP
TrfKthe 141 -----AAQPTLNNTDYPWILNHDH SKQREIADWLTLEIKDFVAYISP
TrfKwal 140 -----EGVPKTLNTDYPWILNHDH SKQREIADWLTLEIKDFVAYISP
TrfSklu 181 -----EQNAANIAAKRTLNTDYPWVLSHDH SKQKEIADWLTLEIKDFVSYISP
TrfDhan 145 -----HTQTTKSLYPWIKDHDH SKQKEIADWFTMEIKDFVNYISP
TrfCgui 141 -----HTAKEPSSLYPWIKNQDHSKQQEIADWLTLEIKDFVNYISP
TrfClus 131 -----HHSQSATSYPWVKGHDSKQREIADWLTMEIKDFVNYISP
TrfCtro 140 -----DHSGAPNSQYPWIKDHDHSTQKEIADWLTMEIRDFVNYISP
TrfCalb 142 -----AHGETPNSSYPWVKDHDH SKQKEIADWLTLEMKDFVNYISP
TrfCpar 134 -----ELSAEANSSYPWIKDHDHSTQKEIADWLTMEMKDFVRYISP
TrfLelo 196 -----PEDLHTNSQYPWVKNHDH SRQKEIADWLTMEMKDFVNYISP
TrfYlip 222 -----GPASKKQDLEAPWIKSNYHQYDR-VSDWLQEVMDFVKYISP
TrfSoct 188 NGRFFHEANKQNEQSSRKRKR MAYEIDPSSCPW--HRPYKADIEVSRLLHQDITQFVDYITP
Cid14Spom 196 RGRFFHEANEKSD-SNRKRKRQAYELDSQSCPW--HRQYKVEREVSRIHQDILHFIDYITP
TrfSjap 192 MGRFFFRDK-----VSNRKRKR NAMDIEP-ICAW--HKPYPEEPVARLLHQDILNFINYLEP

Trf5Scer 190 SKNEIKCRNRTIDKLRRAVKELWSDADLHVFGSFATDLYLPGSDIDCVVNS-RNRDKEDR
Trf5Spar 190 SKSEIKCRNRTIDKLRQAVKELWSDADLHVFGSFATDLYLPGSDIDCVINS-RNRDKEDR
Trf5Smik 190 SKSEIKCRNRTIDKLRQAVKELWRDADLHVFGSFATDLYLPGSDIDCVINS-RNRDKEDR
Trf5Sbay 189 SKAEIKCRNRTIDKLRQAVKELWSDADLHVFGSFATDLYLPGSDIDCVINS-RNRDKEDR
Trf5Skud 190 SKSEIKCRNRTIDKLRQAVKQLWSDADLHVFGSFATDLYLPGSDIDCVINS-RHHDKEDR
Trf5Cgla 201 SREEIETRNTIAKIRRSVKRLWTDADLQVFGSYATDMYLPGSDIDCVVNS-KSGDKENR
Trf5Kpol 164 SKEEIEIRNVTISKIRNSLKEWSDSDLHVFGSYATDLYLPGSDIDCVVNS-ENGDKENR
Trf5Scas 212 SKDEIHTRNRTLARLRKAVSEQWKDASLHVFGSYATDLYLPGSDIDCAVIS-RNRDKDRR
Trf4Scer 193 SREEIEIRNQTISTIREAVKQLWPDADLHVFGSYSTDLYLPGSDIDCVVTS-ELGGKESR
Trf4Spar 193 SREEIEIRNQTISSIREAVKQLWPDADLHVFGSYSTDLYLPGSDIDCVVTS-ELGGKESR
Trf4Smik 187 SREEIEIRNQTISTIREAVRQLWPDADLHVFGSYSTDLYLPGSDIDCVVNS-ELGGKESR
Trf4Sbay 194 SREEIEVRNQTISTIREAVKQLWSDADLHVFGSYSTDLYLPGSDIDCVVNS-ELGGKESR
Trf4Skud 195 SREEIEIRNQTISTIREALKQLWPDADLHVFGSYSTDLYLPGSDIDCVVNS-ELGGKESR
Trf4Kpol 129 NRKEIELRNQTIGKLRDAVQHHPDANLHVFGSYATDLYLPGSDIDCVVNS-KAGDKQSR
Trf4Scas 191 SREEIESRNQTISKVRNAVQQLWPDADLHVFGSYATDLYLPGSDIDCVINS-KAGDKENR
Trf4Cgla 117 SKEEIEETRNTIGSIRSAVKELWPDADLHVFGSYATDLYLPGSDIDCVVNS-KQGDKQSR
TrfKlac 205 NRQEI EQRNQAI AKLKEAVVELWPDSSLNCFGSYATDLYLPGSDIDCVVNS-ASGDKENR
TrfAgos 209 NKTEIQLRNDLKRIRDVAQFQWPDANLHCFGSYATDLYLPGSDIDCVVNS-KSGDKDNK
TrfZrou 115 SRQEI EILRNKTI RTRLRHAVRKLWPGADLQVFGSYATDLYLPGSDIDCVINS-KTGDKENR
TrfKthe 183 SQEIEIRVRNSTISKIRNAVKDLWPDADLHVFGSFATDLYLPGSDIDCVINS-SSGDKENR
TrfKwal 182 SQEIEIRVRNSTISTIRAAVRELWPDADLLVFGSFATDLYLPGSDIDCVINS-TKGDKQNR
TrfSklu 229 SREEIETRNFITISKVRDAVQQLWSDADLHVFGSFATDLYLPGSDIDCVVNS-RSGDKENR
TrfDhan 186 SEAEIMTRNRVNVQLKQQIGQFWPATELHVFGSCATDLYLPGSDIDMVVNS-ETGDYHR
TrfCgui 182 SKLEITRNNVIGRLKSTIKFQWPDTEVHVFGSSATDLYLPGSDIDMVVIS-RDGDREQR
TrfClus 172 SKEEIVVRNTVIRLKRRIAEFQWPDQAHVFGSCATDLYLPGSDIDMVVIS-TGDIYQR
TrfCtro 181 SDEEII TRNKVIAALKKSISDFWPGTTVHVFGSCATDLYLPGSDIDMVVNS-DTGSYENA
TrfCalb 183 SSEEIVTRNNVISTLKKEIGKFWPGTEHVFGSCATDLYLPGSDIDMVVNS-ETGDYENR
TrfCpar 175 SKAEIITRNNVIN TLKKEISSFWPGTEAHVFGSCATDLYLPGSDIDMVVIS-STGDYENR
TrfLelo 237 SSEEIVIRNKVVNTLKTQIALFWPGTEAHVFGSSATDLYLPGSDIDMVVLS-DTGDYENR
TrfYlip 263 TQSEIKARQDLVERVRGAVNGLWGDVHVHLSFTTNMHLPSDIDLVVCS-PHGHYGER
TrfSoct 248 TPEEHAVRKSLSIRINNAVVKWPDVSVYVFGSFETRLLYPTSDLDLVIISPETHYRGTK
Cid14Spom 255 TPEEHAVRKSLSIRINQAVLQWPDVSVYVFGSFETRLLYPTSDLDLVIISPETHYRGTK
TrfSjap 246 TPQEHAVRKSLSITKLDRAIRAKWPEVTVYVFGSFETRLLYPTSDLDLVIISPETHYRGTK

Trf5Scer 249 NYIYELARHLKNGGLAIRMEVIVKTRVPIIKFIEPQSQLHIDVSFERTNGLEAAKLIREW
Trf5Spar 249 NYIYELARYLKNKGLAIRMEVIVKTRVPIIKFIEPQSQLHIDVSFERTNGLEAAKLIREW
Trf5Smik 249 NYIYELARYLKTGGLAIRMEVIVKTRVPIIKFIEPQSQLHIDVSFERTNGLEAAKLIREW
Trf5Sbay 248 NYIYELARHLKNQGLAIRMEVIVRTRVPIIKFIEPQSQLHIDVSFERTNGLEAAKLIREW
Trf5Skud 249 NYIYELARYLKNNEGLAIRMEVIVRTRVPIIKFIEPLSQLHIDVSFERTNGLEAARLIREW
Trf5Cgla 260 QYLYELARHLKNDGLATRVEVI AKSRVPIIKFVEPESDIHIDVSFERSNGLEAAKLIREW
Trf5Kpol 223 NDLYSLATHFKRNLAIQVEVI AKARVPIIKFVEPNSKLIHIDISFERLNGLVAKI IREW
Trf5Scas 271 QCLYDLAKSLKQKGLATHLEVI AKARVPIIKFVEPRSKIHIDVSFEKTNGEAACLIREW
Trf4Scer 252 NNLYSLASHLKKKNLATEVEVAKARVPIIKFVEPHSGIHIDVSFERTNGLEAAKLIREW
Trf4Spar 252 NNLYSLASHLKKKNLATEVEVAKARVPIIKFVEPHSGIHIDVSFERTNGLEAAKLIREW
Trf4Smik 246 TNLYSLASHLKKKNLATEIEVAKARVPIIKFVEPHSGIHIDVSFERTNGLEAAKLIREW
Trf4Sbay 253 NNLYSLASHLKKKNLATEIEVAKARVPIIKFVEPHSGIHIDVSFERTNGLEAAKLIREW
Trf4Skud 254 NNLYSLASHLKKKNLATEIEVAKARVPIIKFVEPHSRIHIDVSFERTNGLEAAKLIREW
Trf4Kpol 188 NCLYSLASHLKKKGLAEDIEI AKARVPIIKFVEPLSKIHVDSFERTNGLEAAKLIRGW
Trf4Scas 250 NSLYSLASFLLKQGLATQIEVI AKTRVPIIKFVEPESNIHIDVSFERTNGLEAAKLIREW
Trf4Cgla 176 NNLYKLANFLKKEIATEIEVAKARVPIIKFVEVESRTHMDSFERLNGLAACLIRDW
TrfKlac 264 NALYSLASFLLKRRQLATQVEVI AKARVPIIKFVEPESKIHIDVSFERTNGLEAARVIRGW
TrfAgos 268 NALYSLASYLKRNLATQVSVIAKARVPIIKFVEPASQIHIDLSFERTNGVEAAKI IRGW
TrfZrou 174 SSLYELAHFLKRNRLATQVEVI AKARVPIIKFVEPTSQIHVDVSFERTNGLEAAKLIRSW
TrfKthe 242 NCLYSLASFLLKRRKLATQVEVI SKARVPIIKFVEPISQIHIDISFERVNGLEAARVIRGW
TrfKwal 241 NCLYSLASFLLKRNKLATQVEVI SKARVPIIKFVEPSSQIHIDISFERVNGVEAARI IRGW
TrfSklu 288 NALYSLASFLLKRRKLATQVEVI SARVPIIKFVEPESGIHIDVSFERTNGLEAARI IRNW
TrfDhan 245 SRLYQLSSFLRNKLLAKNIEVI AKAKVPIIKFVDPDSNIHIDVSFERTNGIDAACKIRRW
TrfCgui 241 SRLYQLSTHLRSKLLAKNIEVI AKAKVPIIKFVDPDSNIHIDVSFERSNGIDAAIKIREW
TrfClus 231 GKLYQLSSFLRTNKLAKNIEVIATAKVPIIKFVDPQYNIHVDSIFERTNGLEAARRIRKW
TrfCtro 240 SRLYQLSTFLRTNKLATEVEVIAHAKVPIIKFVDPKSRLHIDVSFERTNGIDAACKIRRW
TrfCalb 242 SRLYQLSTFLRTKLLAKNVEVIAAKVPIIKFVDPVSELHIDVSFERTNGLEAACKIRRW
TrfCpar 234 SRLYQLSSFLRVKNLAKNVEVIANAKVPIIKFVDPDSNLPVDISFERTNGLEAARRIRKW
TrfLelo 296 SRLYQLSSFLKAKKLATNVEVIAAKVPIIKFVDPDSNIHVDSIFERKNGLEAARRIRRW
TrfYlip 322 ACIYQLSSVIRSRMKVAELQTI TKARVPIIKFIDSRITGVHVDISFEKDGGIKTASTITKW
TrfSoct 308 KDMFVLAHHLRKSVAETDIQVITANVPIIKFVDPITKIHVDVSFNQAGGLKTCLVVNGF
Cid14Spom 315 KDMFVLAHHLKLLKLAASEVQVITANVPIIKFVDPITKIVHVDISFNQPGGLKTCLVVNGF
TrfSjap 306 KHMYSLARHLKKNCKLATEIQVITANVPIIKFVDPFTRIHVDVSFNQPGGLKTCLVVNGF

Trf5Scer 309 LRDS PGLRELVLIIKQFLHSRRLNNVHTGGLGGFTVICLVYSFLNMHPRIKSNIDVLDN
Trf5Spar 309 LRDS PGLRELVLIIKQFLHSRRLNNVHTGGLGGFTVICLVYSFLNMHPRIKSNIDAPDN
Trf5Smik 309 LRDS QGLRELVLIIKQFLHSRRLNNVHTGGLGGFTVICLVYSFLNMHPRIKSNIDALDN
Trf5Sbay 308 LDS PGLRELVLVIKQFLHSRRLNNVHTGGLGGFTVICLVYSFLNMHPRIKSNIDAPDN
Trf5Skud 309 LRDS PGLRELVLIIKQFLHSRRLNNVHTGGLGGFTVICLVYSFLNMHPRIKSNIDTPDN
Trf5Cgla 320 IGDTPGLRELTLVVKQFLHARRLNDVHTGGLGGFSIICLVFSFLRLHPRIITGDI DPLDN
Trf5Kpol 283 LDDTPGLRELVLIVKQFLAARRLNNVHTGGLGGLSIICLVYSFLKLPRIITNDIDPIDN
Trf5Scas 331 IKDTPGLRELVLVLKQFLAVKRLNEVVNGGLGGFSIICLVYAFLRMHPRIKAGEIDPMKN
Trf4Scer 312 LDDTPGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVFSFLHMPRIITNEIDPKDN
Trf4Spar 312 LNDTPGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVFSFLHMPRIITNEIDPKDN
Trf4Smik 306 LNDTPGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVFSFLHMPRIITNEIDPKDN
Trf4Sbay 313 LNDTPGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVFSFLHMPRIITREIDPKDN
Trf4Skud 314 LNDTPGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVFSFLHMPRIITKEIDSKDN
Trf4Kpol 248 LDSTNGLRELVLIVKQFLQARRLNKVHTGGLGGFSIICLVYSFLHLHPRILANEINPIEN
Trf4Scas 310 LQDTPGLRELVLIIKQFLHSRRLNNVHTGGLGGFSIICIVFSFLQMPRIITNEIDPMEN
Trf4Cgla 236 LASTPGLRELVLVVKQFLHSRRLNNVHSGGLGGFSIICLVYSFLRMHPRIITAEIDPLEN
TrfKlac 324 LEEQPGLRELVLIVKQFLHARRLNNVHTGGLGGYSIICLVYTFKLHPRVLTGDI DPLEN
TrfAgos 328 LHDTPGLRELVLIVKQFLHARRLNDVHTGGLGGFSIICLVYAFILMYHFLRLHPRIICRDI EPLQN
TrfZrou 234 LQQT PGLRELVLIVKQFLHARRLNNVHTGGLGGFSIICLVYAFNLHPRIIVTGEIDARYN
TrfKthe 302 LKETPGLRELVLIVKQFLAARRLNVHTGGLGGFSIICLVYAFQLHPRVISSIDSMEN
TrfKwal 301 LNDTPGLRELVLIVKQFLAARRLNVHTGGLGGFSIICLVYSFLQLHPRVISSIDSMEN
TrfSklu 348 LDETPGLRELVLIVKQFLSARRLNNVHTGGLGGFSIICLVYSFLQLHPRIITNDINSLN
TrfDhan 305 LSTTPGLRELVLIVKQFLRSRRLNNVHVGGLGGYSTIILCYHFLKLPRLSTKNMAVLDN
TrfCgui 301 LASTPGLRELVLIVKQFLRSRRLNNVHVGGLGGYSTIILCYHFLKLPRVATENMSILDN
TrfClus 291 LDSMPGLRELVLIVKQFLRSRRLNNVHVGGLGGYATIILMYHFLRLHPRVSTGNISVMEN
TrfCtro 300 LVSTPGLRELVLIVKQFLRTRRLNNVHVGGLGGYATIIMCYHFLRLHPKITTDAMSALDN
TrfCalb 302 LISTPGLRELVLIVKQFLRSRRLNNVHVGGLGGYATIIMCYHFLRLHPKLS TSSMDALDN
TrfCpar 294 LLATPGLRELVLIVKQFLRSRRLNNVHVGGLGGYATIIMCYHFMQLHPKISTNTMDAPDN
TrfLelo 356 LASTPGLRELVLIVKQFLRSRRLNNVHVGGLGGYATIIMCYHFLRLHPKLS TESMSSLDN
TrfYlip 382 SKSMPALRPLVLIVKQFLSSRRLNEVFTGGLGGFSVICMVYSFLIQHPRISTGDISPMDN
TrfSoct 368 LKKYPALRPLVLI IKHYLNMRALNEVFLGGLSSYAIIVCLVVSFLQLHPRLSTGSMIREEDN
Cid14Spom 375 MKKY PALRPLVLI IKHFLNMRALNEVFLGGLSSYAIIVCLVVSFLQLHPRLSTGSMIREEDN
TrfSjap 366 LKKFPAVRPLTMLVKHFLNMRALNEVFLGGLSSYAIIVCLVVSFLQMPRLSTSSVRQEDN

Trf5Scer 369 LGVLLIDFFELYGKNFGYDDVAISIS--DGYASYIPKSCWRTLEPS-RSKFSLAIQDPGD
Trf5Spar 369 LGVLLIDFFELYGKNFGYDDVAISIS--DGYPSYIPKSCWRTLEPS-RSKFSLAIQDPGD
Trf5Smik 369 LGVLLIDFFELYGKNFGYDDVAISIS--DGYPSYIPKSYWKTLEPS-RSKFSLAIQDPGD
Trf5Sbay 368 LGVLLIDFFELYGKNFGYDDVAISNS--DGYPSYIPKSYWKTLEPS-RGRFSLAIQDPGD
Trf5Skud 369 LGVLLIDFFELYGKNFGYDDVAISIS--DDHPSYIPKSHWKTLELS-RSKFSLAIQDPGD
Trf5Cgla 380 LGVLLIEFFELYGKNFAYDDVAICVD--DSRATYKPKTSCRFPYPPA-RTSF TLAIQDPGD
Trf5Kpol 343 LGVLLIDFFELYGKNFAYDDVAISFL--DGRTSYMPKSEFKQFPV-RNPFSLAIQDPND
Trf5Scas 391 LGVLLIEFFELYGKNFSYDRVAISIS--NGVASYIPRKEWKDLLSN---KDR IAIQDPGD
Trf4Scer 372 LGVLLIEFFELYGKNFGYDDVALGSS--DGYPVYFPKSTWSAIQPI-KNPFSLAIQDPGD
Trf4Spar 372 LGVLLIEFFELYGKNFGYDDVALGSS--DGYPVYFPKSAWSAIQPI-KNPFSLAIQDPGD
Trf4Smik 366 LGVLLIEFFELYGKNFGYDDVALGSS--DGYPVYFPKLAWSAI LPI-KNPFSLAIQDPGD
Trf4Sbay 373 LGVLLIEFFELYGKNFGYDDVALGSS--DGYPVYFPKSTWNAIQPI-KNPF TLAIQDPGD
Trf4Skud 374 LGVLLIEFFELYGKNFGYDDVALGSS--DGYPIYFPKSSWSAIQPI-KNPFSLAIQDPGD
Trf4Kpol 308 LGVLLIDFFELYGKNFGYDHVALSVM--NGKATYLPKSNWKE LHPI-KSTFQLAIQDPGD
Trf4Scas 370 LGVLLIEFFELYGKNFGYDDVAISVT--DGYPSYLPKSSWKG LQQT-RGSFSLAIQDPGD
Trf4Cgla 296 LGVLLIEFFELYGKNFGYDDVAIGVQ--DGSPIYMAKRWSKSL EQN-RGSFNLAIQDPGD
TrfKlac 384 LGVLLIDFFELYGKNFGYDDVIGSVS--EHEARYIPKNEHPDLSAG-RPRFSLI IQDPGD
TrfAgos 388 LGVLLIDFFELYGKNFGYDDVGI AVS--EGDASYINKKEYPELTRNL RGT FNLIQDPGD
TrfZrou 294 LGVLLIDFFELYGKNFGYDDVAVVVA--DQRPCYMHKSDWLDLRLSGGGSFTLAIQDPGD
TrfKthe 362 LGILLIDFFELYGKNFGYDHVAISVT--DSGARYLSKELYGSLQNP-RTSFALAIQDPGD
TrfKwal 361 LGILLIDFFELYGKNFGYDHVAIAVS--DTGARYLPKQFHASM QHP-RTSFALAIQDPGD
TrfSklu 408 LGVLLIDFFELYGKNFGYDDVAISVQ--DGQVGYLPKDECPALQNP-RSTFSLAIQDPGD
TrfDhan 365 LGSLLIEFFELYGRNFSYDNLIIAIDTETDLPKYLLKRKHVP LNNTS-RNPFSLI IQDPSPD
TrfCgui 361 LGSLLIEFFELYGRNFSYDNLIIAIDSRDTPKYLKRHYPELNAS-KNPF SIVIQDPSPD
TrfClus 351 LGTLLIEFFELYGRNFSYDHLIVALANGED-PRYLLKSRNHVLTAG-RGQFSIVVQDPSPD
TrfCtro 360 LGVLLIEFFELYGRNFSYDDLVALALDPENEEPKYVRKSKSPLQ HSA-RSSF AII IQDPAD
TrfCalb 362 LGVLLIEFFELYGRNFSYDNLIIISLDRDTEEPREYKKG NHPILNTA-RNTFSIVIQDPAD
TrfCpar 354 LGVLLIEFFELYGRNFSYDNLIIISIDPETQLPRYLLKGRHPIL STA-RNTFSIVVQDPAD
TrfLelo 416 LGVLLIEFFELYGRNFSYDNLIIISLDPKTEEPRYLPKGRYSV LNNTA-RNTFAIVVQDPAD
TrfYlip 442 LGVLLIEFFELYGVNFYERVALNMD--GNCGYLSKRLYPDL IGR--NPF AVAIRDPDD
TrfSoct 428 YGVLLLELLELYGKRFHYDAVGI AVH---NGGFYFSKKKQGWLRPN--QPYLLS IMDPVE
Cid14Spom 435 FGVLLLEFLLELYGKQFYDAVGI AVH---NGGFYFSKKKMGWLKPN--QPYLLS IQDPVD
TrfSjap 426 LGVLFLEFLLELYGKRYNYDAVGI AVH---NGGFYFSKKKMGWVKPS--QPYLLS IQDPVD

Trf5Scer 426 PNNNISRGSFNMKDIKKAFAGAFELLVNKWELNSATFKDRVG-----KSILGNVIKYRG
Trf5Spar 426 PNNNISRGSFNMKDIKKAFAGAFELLVNKWELDSATFKDRVG-----KSILGNVIKYRG
Trf5Smik 426 PSNNISRGSFNMKDIKKAFAGAFELLTNKCWELDSATFKDRVG-----KSILGNVIKYSG
Trf5Sbay 425 PNNNISRGSFNMKDIKKAFAGAFELLVNKWELDSATFKDRLG-----KSILGNVIKYRG
Trf5Skud 426 PNNNISRGSFNMKDIKKAFAGAFELLVNKWELDSATFKDRVG-----KSILGNVIKYRG
Trf5Cgla 437 PTNNLSRGSFNVVDIKKSFSGAFDLLVNKCFELDAATFKNRVG-----KSILGNVIKYRG
Trf5Kpol 400 PYNNISRGSFNLRDIKKAFSGAFDLLTNVCFEMDFATFKDRVG-----RSILGNVIKYRG
Trf5Scas 446 PSNNIARSSKNLQGIKKAFSSAFDLLVNQCFELDTATFKDRVG-----KSILGNVIKYRG
Trf4Scer 429 ESNNISRGSFNIRDIKKAFAGAFDLLTNRCFELHSATFKDRLG-----KSILGNVIKYRG
Trf4Spar 429 ESNNISRGSFNIRDIKKAFAGAFDLLTNRCFELHSATFKDRLG-----KSILGNVIKYRG
Trf4Smik 423 ESNNISRGSFNIRDIKKAFAGAFDLLTNRCFELHSATFKDRLG-----KSILGNVIKYRG
Trf4Sbay 430 EANNISRGTFNIRDIKKAFAGAFDLLTNRCFELHSATFKDRLG-----KSILGNVIKYRG
Trf4Skud 431 ESNNISRGSFNIRDIKKAFAGAFDLLTNRCFELHSATFKDRLG-----KSILGNVIKYRG
Trf4Kpol 365 ATNNISRGSFNIRDIKKAFAGAFDLLTNRCFELHRAKLDKDRQG-----CSILGNVIKYRG
Trf4Scas 427 ETNNISRGSFNLRDIKKGFAGAFDLLTNRCFELDQT SFKQVRG-----KSILGNVIKYRG
Trf4Cgla 353 VTNNISRGSFNLRDIKKAFAGAFDLLTNKCFELNSISIKERYG-----KTILGNI IKYHG
TrfKlac 441 PSNNISRGSFNLRDIKKGFAGAFDLLANRCFELDSATFKDRIG-----SSILGNVIKYKG
TrfAgos 446 PANNISRGSFNIRDIKKAFAGAFDLLTNRCFELDAATFKHRVG-----KSILGNVIKYRG
TrfZrou 352 SSNNISRSSFNLRDIKKAFAGGF DLLTNRCFELDAATFKDRVG-----KSILGNVIKYRG
TrfKthe 419 KDNNISRGSFNIRDIKKAFAGAFDLLTNRCFELDAATFKDRVG-----KSILGNVIKYRG
TrfKwal 418 KENNISRGSFNIRDVKKAFAGAFDLLTNRCFELDAATFKDRVG-----KSILGNVIKYRG
TrfSklu 465 SSNNISRGSFNLRDIKKAFAGAFDLLTNKCFELDAATFKDRLG-----KSILGNVIKYRG
TrfDhan 424 PANNITRSSYNLRDLKKAFFGAFQLLVDKCYELNGASYKSRI G-----QSILGDI IKYRG
TrfCgui 420 PSNNITRSSYNLRDVKKAFFGAYQILIDKCYELHSATYRARI G-----QSILGDI IKYKG
TrfClus 409 PANNITRSSYNLRDLKKAFFGAYQLLVEKCYELHAASYKNRI G-----QSILGDI IKYRG
TrfCtro 419 PSNNITRSSYNLRDLKKAFFGAYQLLSEKCYQLNAASYKERL G-----SSILGDI IKYTG
TrfCalb 421 TTNNITRSSYNLRDLKKAFFGAYQLLVEKCYQLNAASYKQRL G-----QSILGDI IKYNG
TrfCpar 413 SSNNITRSSYNLRDLKKAFFGAYQLLVAKCYELNAAPYRERL G-----KSILGDI IKYKG
TrfLelo 475 PNNNITRSSYNLRDLKKAFFGAYQLLVAKCYELHAASYRARL G-----QLILGDI IKYKG
TrfYlip 497 HENNISQGT FNMRN IKRAFSGAFQLLSGKCLDMNKTGYKGRQ G-----KSLLTSI IKLKG
TrfSoct 483 FSNDRVSKSRGLLRVKATLNGFDLLTNELFALASRIEREGSRRISDFPSILGSI ISVDE
Cid14Spom 490 FQNDVSKSRGLLRVKATFANGFDLLTSKLYALASRIEREGVNRVKDFPSILSTI LSVDE
TrfSjap 481 YNDISKSSRGI LRVKATLNGSFDLLTSELYSLAARIEREGHLHILKDEKSLLSICI GIDD

Trf5Scer 481 QKRDFNDERDLVQNKAI IENERYHKK-RTRIVQEDLFINDTEDLPVEE IYKLEDEPAKKKQ
Trf5Spar 481 QKRNFKDERDLVENKAI IENERYHKK-RTRIQEDLFINDI DELPVEE IYKLEDEPLKKKR
Trf5Smik 481 QTRDFKDERGLVENKAI IENERYHKK-RTRIVHEDVFINDTE DLPAAE IYKLEDEPPKKKR
Trf5Sbay 480 QQRDFKDERDLVENKAI IENERYHKK-RTRIVHEDMFINDTE DLPVED IYKLEDEPLKKKR
Trf5Skud 481 QKRDFKDERDLVENKAI IENERYHKK-RTRIVHEDVFINDTE DLPAAE IYKLEDEPPKKKR
Trf5Cgla 492 APRDFNDERALVENRAI IENEHYHKK-RARVHAD-----DEDTSDEDDMF-INISA
Trf5Kpol 455 EKRDFFKDERDLIENAA ILTNEEYHKK-RSRI VHEDI FLDTT DSEPD LDEEQ DMYHIDI PV
Trf5Scas 501 AMRNF RDERHLVNVRAI IENENFYRE-LEDKKRKEKAEKEEMFL NPSSDEA ELDEALLGE
Trf4Scer 484 KARDFKDERGLV LNKAI IENENYHKK-RSRI IHDEDFAE DTVTSTATATTT DDDYEIT--
Trf4Spar 484 KARDFKDERGLV LNKAI IENENYHKK-RSRI IHDEDFTE ETATSTATATTT DDDYEIT--
Trf4Smik 478 KARDFKDERGLV LNKAI IENENYHKK-RSRI IHDEEFTEDTVTSTAT----DDYEI I--
Trf4Sbay 485 KARDFKDERGLV LNKAI IENENYHKK-RSRI IHDEEFAE DITVSTATASTT DDDYDII--
Trf4Skud 486 KARDFKDERGLV LNKAI IENENYHKK-RSRI IHDEEFTEDTATS--TATTT DDDYEI I--
Trf4Kpol 420 KARDF RDERGLVENKAI IENENYHKK-RSRI IHGSDNEEEEEEE--ESDKEDDPYNI E--
Trf4Scas 482 KERDFKDE RSLVNVKAI IVENEKYHKK-RSRI VHKNVPDEVSQ TVEVVAE DDDGDDMYIVE
Trf4Cgla 408 KRDF RDERGLVQNKAI IENESYHKK-RSRI IMH----GELSAVNGKRSADDES N-----
TrfKlac 496 TKRDFNDERDLV IENAI IQENEKYHKN-RGRIVHDDL F----TDISDIEAEE E IYQVQEP P
TrfAgos 501 AKRDFKDERAL I VNKAI IQENEEFHQR-RGRIVHRDTA----EFIN--ISDDDDYELQPPP
TrfZrou 407 KLRDFNDDRDLVANS AI IENEKYHKK-RSRI VHDNDE----VFIDPSESENE-----
TrfKthe 474 KQRDFKDERNLV VNKAI IENET YHKK-RGRIVHEEVF----TDVSDGEKEDDIYTVVEEP--
TrfKwal 473 KQRDFKDERDLV VNRAI IENEKYHKK-RGRIVHQEVF----TDASDGEKEDDIYTVAE P--
TrfSklu 520 KQRDFKDE RSLVINKAI IVENEQYHKK-RGRIVKGEIF----TDVSDNENEEDLYKVEGP--
TrfDhan 479 KERDFNDDRHKVTNDAL INHEEENEGN--DDDES DGANGNNKYYFSDMTVSE EDTTFA--
TrfCgui 475 KERDFNDERHMVVNQAMV TDDPTPAI--TDES DGHNGNDKYYFSDMTVSE EDDTFTAN--
TrfClus 464 KDRDFNDDRDKVVNSAL I SHLDDE----DDDES DGADGNDKYYLSDMTSE-EEETV VAP--
TrfCtro 474 KERNFSDRRHKVVNHAL VKHDDDDDGQEDDAESD GQNGNDKYYFSDMTDES DE-PYVPSV
TrfCalb 476 KERDFNDDRHKVVNHAL I SHEEITDD----ESDGLDGNDKYYFSDMTVESNEDEYVP--
TrfCpar 468 KERNFVDERHLVRNDAL IHHEEHPNT-EQDLES DGLEGNDKYYFSDMTVSE EE-EYTPLP
TrfLelo 530 KERHFRDERHMVVNEAL ISHEEETS--LDGKKIVTKSNDEFYFSDMTDSDE TBEYKQPL
TrfYlip 552 PVRDQTPDAITEPLKY TGGDEFKIP--QDAVYNSVLMNDEDEDEKAKQAE DADKTKRRA
TrfSoct 543 GVRKRVHMLNCFNEHP IALEPMVDVEQLSSI DVDR LPTENVDLQFVEDES DSDEVEQET
Cid14Spom 550 GVRQHRHEHMLKCYKNNP VPLEPLVEVDALAS I DVDKLPLQDVGLQYVEDES DSDETDAK
TrfSjap 541 NITKREHIQCYACDPVPLEPLTSIQNLTS I DVDAVQLPAMELEFVEGESE SDDVAEVA

Trf5Scer 540 KAKKDKREGE-----IKKSAIPSPPPDFGVSRSKLKRKVKKTQGS
 Trf5Spar 540 KVTKDKRKGR-----IKKSAIPSPPPDIAVSKRKIQGKVEVDHGS
 Trf5Smik 540 KATKHKREGK-----TKKSAIPSPPELAVNKNKRQLEKKDTGPGS
 Trf5Sbay 539 KGKKDKKERK-----TKERTVSPASEAAVKKSKRQHQAADLSP
 Trf5Skud 540 KAKKDKKERS-----TKESAI P S P P P E L T V T K T K R K H K K T V T A G S
 Trf5Cgla 542 NEE-ETEEM Y-----KVEKVEKVVKKR-KIAKADTNTKTKTCTK
 Trf5Kpol 514 PKKRKVQKER-----TINPAILLAQKRSKLSKSSKSDSKSEKPNK
 Trf5Scas 560 RAEDIYK LDR-----PLKRTKNDKHKHKHKHKHTNTDKNTKKEKV
 Trf4Scer 541 -----NPPAKKAKIEEKPE---
 Trf4Spar 541 -----NPPTKKAKIEAEPK---
 Trf4Smik 531 -----RPPAKKAKMEVLEPGFI
 Trf4Sbay 542 -----EPPTKKAKTKFSEPEAK
 Trf4Skud 541 -----EPPTKRARTETVKPQPK
 Trf4Kpol 475 -----EPPMKKLKRSSSIK---
 Trf4Scas 541 -----EPPSKRKKKS NKA---
 Trf4Cgla 457 -----EHHDDTQNKK---
 TrfKlac 551 TKKTKKDKSKEKKERKEKRREKRKKQQLKENTERVQEEVEDNYDPTEAII V N D E P S E Q E D
 TrfAgos 554 -----KRAR-----VPAPAPAPADNVVVLDDP---AD
 TrfZrou 454 -----ALKEEQDSYLIQEPEQPPK
 TrfKthe 528 -----AKKKPKKAKKAKKAKK
 TrfKwal 527 -----AKKKSKKAKKAKKAKK
 TrfSklu 574 -----ARKKKK--KKTQKVKK
 TrfDhan 535 -----QEIK
 TrfCgui 532 -----KKEVS
 TrfClus 518 -----EHKQP
 TrfCtro 533 -----AKPTP-----TPLTK
 TrfCalb 529 -----EKKRT-----TPVTN
 TrfCpar 526 -----TKPTLVSKQ--TPITN
 TrfLelo 588 -----LKVKSHKTI SPTPVTN
 TrfYlip 610 AQREEQKKK-----ELTASDDKIPKGPAAADRNPQKADQRKMSK
 TrfSoct 603 DDLIKK-----KGLNDLQNTNHN-EGLS
 Cid14Spom 610 DDLFKVNESI-----ETNGHENFQKQALTSTGEQ
 TrfSjap 601 APSKIAN-----RMIHSIENEK

Trf5Scer 581 LLHQNNLSIDDLMGLSENDQESDQDQKGRD-----TPSGQDEKSP
 Trf5Spar 581 PPHQKNLSIDDLMGLSENDQESDQDQKEKD-----TPPGQDEEPP
 Trf5Smik 581 LPHHNNLRIDDLMGLSENEEESHQKESD-----ISFGQDGKPP
 Trf5Sbay 580 IPHHDNPSIDALMGLSDNDEGSDQDRRGSG-----IQPGQDGKQP
 Trf5Skud 581 FTQRGNLSIDALMGLSDNDEGSGDQDRGSE-----VSLGQDEKQP
 Trf5Cgla 579 AKARNHTSIDQLMGIPEDEEPPVIQERE-----
 Trf5Kpol 553 KKQLPDKFIDSLMGLVSDDEQEEGEKGNSIKQKISGHSRSKDNKKYETTTDYN SDEEKI
 Trf5Scas 600 EKVKTNLKVAKSQS I I T S K N R T I D I L K G L A K G -----TNTKISGDEMI IDESTA
 Trf4Scer 555 SEPAKRNSGETY I T V S S E - D D -----
 Trf4Spar 555 I E P A K E E S G E T H I I I S S E - D D D -----
 Trf4Smik 548 SEPSKEKSGETHI T I S S E N D D D -----
 Trf4Sbay 559 KEPLKEKSEETY I T I S S G D D D C -----
 Trf4Skud 558 SEPSEKKSEESHIT I S S D D D D D D D E -----
 Trf4Kpol 489 EDDGNAKKKPRKERNRRQKEDQD-----
 Trf4Scas 555 EKIKKKKTVDSYMLPSE-----
 Trf4Cgla 467 QKVN-----DYD-----
 TrfKlac 611 DYDPSKPSVDDYMLPEENNNDENDKDTKEEARTPV-----INLIEDENGASDDSN S D P K
 TrfAgos 578 DYVPAQP-VDKLMGLDDT-----DDYLPAPASPTDTPK
 TrfZrou 473 KRRQTKS-VDELMGVPNEDEE-----DDYNPLNRETDESIT
 TrfKthe 544 ETKASSSSVDTLMGLDTQDDADEGDYDPSN-----EAPSTLAELEARS DI
 TrfKwal 543 DPKPSTKTME S L M G L E ---ESDDDGYDPSN-----EAPATLVSEDSKSDI
 TrfSklu 588 D---NAKVVNQLMGIN---DEEDDYNPVQ-----TNMNEEGDDYNPEE
 TrfDhan 539 PEDPNKKKVADFM S I N V P S E D -----EEDDPKE-----KKEEDTETQDSD
 TrfCgui 537 AKD-NEEKISGLLGIKNENE-----ADEVSETNEDD
 TrfClus 523 QKNENKASV E S F M G I Q -----SESEEEEE
 TrfCtro 543 KPKDTKKLIESMLSLNNSSD-----EDKGSKE-----ENEYVPTVGTK
 TrfCalb 539 KAKDTKKLVESFLSLEDSSDVEELSAKDVAGF-----EDEPYIPKL--K
 TrfCpar 540 KAKDTKKLVESYLSLESSPEAQEKTRDDDDAAAAPA-----TTAATEPKPKL
 TrfLelo 604 KAKDTKKLVESFLGLEKSED-----ENNVNND-----DLEYDPEKLLPP
 TrfYlip 650 DRAAARAAAREVMEI S S D D D D G S D S K N G G A K S N -----PIDLSSDEEKG
 TrfSoct 625 NVSDARMNAKDLFNI DEESSEY-----EKNDNDFK
 Cid14Spom 639 SSSNSRANPSKLFNI S S D D S E -----DEVPII
 TrfSjap 618 N--ESAYSSQEFFSMNEASFDDG-----NSPENAVL

Trf5Scer 621 LETKTVDAQTRRDYWLSKGQAL-----
Trf5Spar 621 LETKTVDAQTRRDYWLSKGQAL-----
Trf5Smik 621 LETQTVDAQTRRDYWLSKGRAL-----
Trf5Sbay 620 LKTQTVDAQTRRDYWLSKGQAL-----
Trf5Skud 621 LELQTVDAQTRRDYWLSKGQAL-----
Trf5Cgla 607 --KKSLSMQDKRDYWLSKGQAL-----
Trf5Kpol 613 ELKKKVDAQTRRDYWLSKGQSMSTIATT-----
Trf5Scas 649 LQNTKVDAQTRRDYWLSKGVLSGTGGLGPEKTTV
Trf4Scer 576 -----DEDGYNPYTL-----
Trf4Spar 577 -----DEDGYNPYTL-----
Trf4Smik 571 -----DEDGYNPYTL-----
Trf4Sbay 581 -----DEDGYNPYSL-----
Trf4Skud 583 -----DEDGYNPYSL-----
Trf4Kpol 512 -----DEEEEDDYNPLKR-----
Trf4Scas 577 -----EKEDEDDYNPTLLR-----
Trf4Cgla 478 -----DAEEEDDYDPLA-----
TrfKlac 665 MQ--LVDKQTKRDYWLSKGQAM-----
TrfAgos 610 L-----DKAAKRNYWLSKGQTM-----
TrfZrou 508 LKNFTVDAQTKRDYWLNKGNMSMN-----
TrfKthe 589 RKK-SVDAQTKRDYWLSKGQAL-----
TrfKwal 585 RKK-SVDAQTRRDYWLSKGQAL-----
TrfSklu 626 DKKNYVDKRTKRDYWLSKGQNL-----
TrfDhan 579 KQKNNLDKDIKRDYWRQKGLGL-----
TrfCgui 567 KQKSNLDKNIKRDYWRQKGLEL-----
TrfClus 546 KVRTNLDKDVKREYWRSKGLEI-----
TrfCtro 582 KPKNLDKDVRDYWRQKGLDL-----
TrfCalb 582 KSKSNLDKDIKRDYWRQKGLDL-----
TrfCpar 587 PRKPVVDKDFKRDYWRSKGFDM-----
TrfLelo 643 KPKNLDKDVKRDYWRQKGLEL-----
TrfYlip 694 RSDIKKDPsAKRFWQKGLDY-----
TrfSoct 656 RDIQRSDEEESRATKVRKKTR-----
Cid14Spom 666 EDTTASDEE-SRAKKIRKRF-----
TrfSjap 647 VDDE--EEEEERASSLGKRRRTD-----

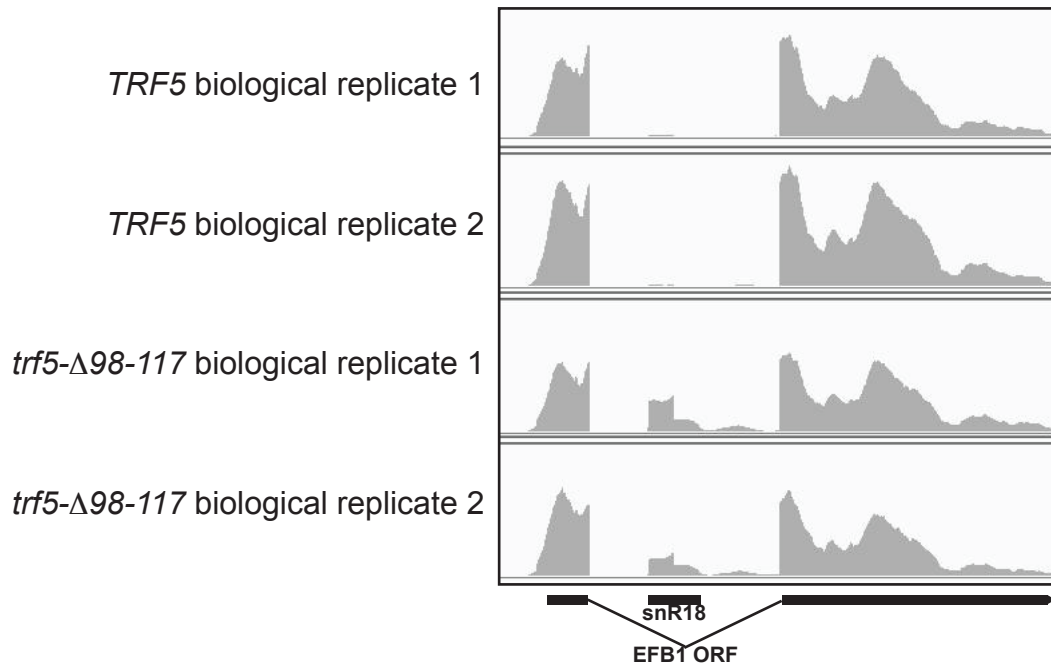


Figure S2: Transcriptome sequencing from duplicate cultures of *TRF5* and *trf5-Δ98-117* strains is highly reproducible. Shown is the region that includes *snR18* snoRNA and *EFB1* mRNA as an example.

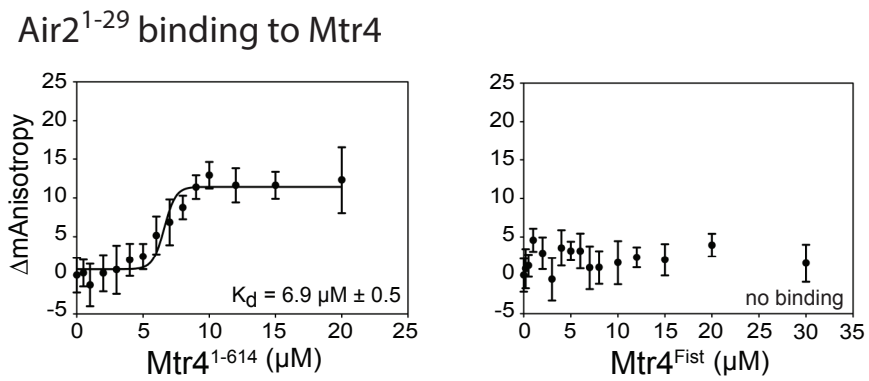


Figure S3: The Air2 N-terminal peptide binds to a truncated recombinant Mtr4 that contains only the two RecA domains, but not to the isolated fist domain. Fluorescent anisotropy measurements were performed as in figure 2.