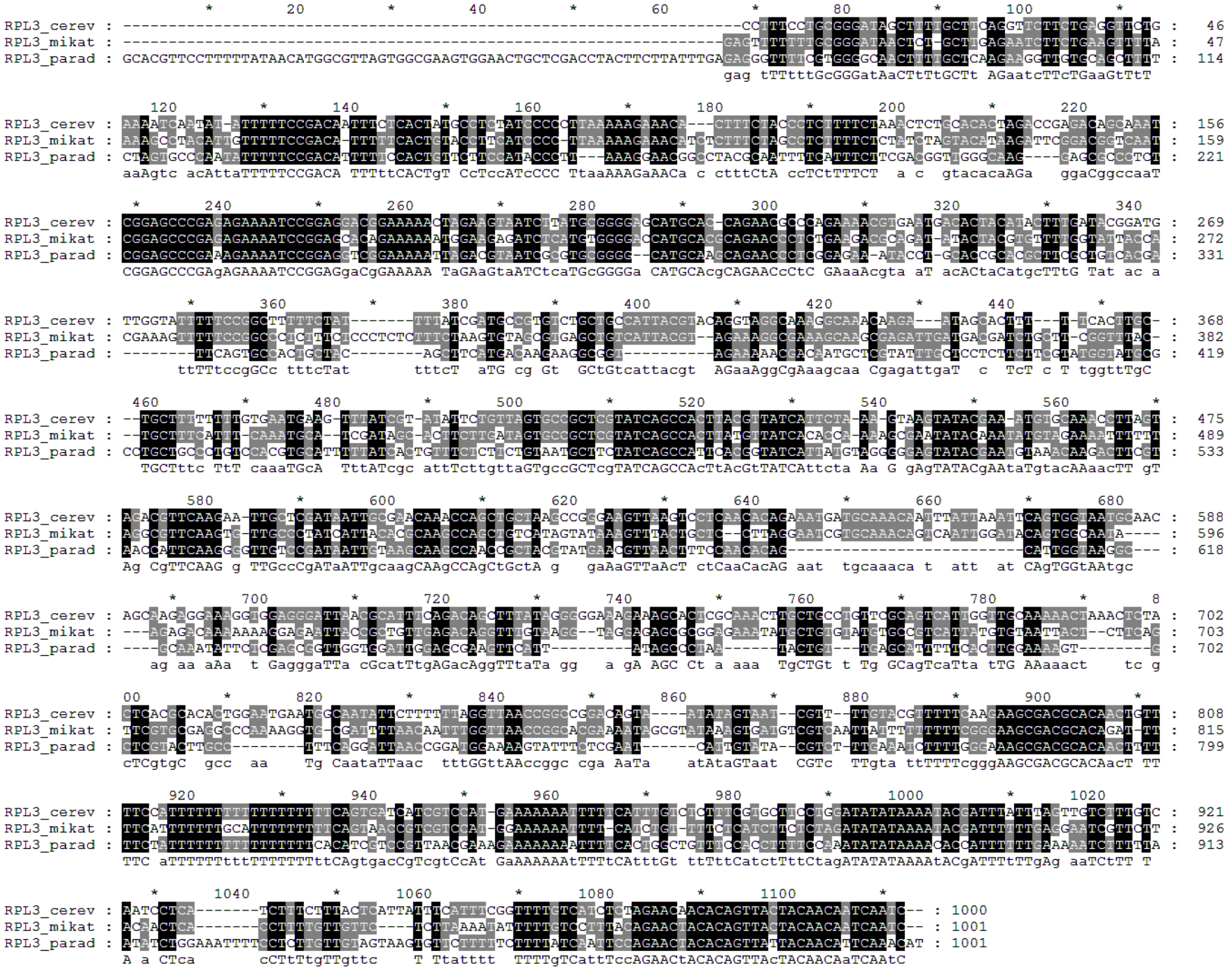
Supplementary figure S1.

Upstream region alignments of Abf1-dependent RP genes considered in this study.

RPL3

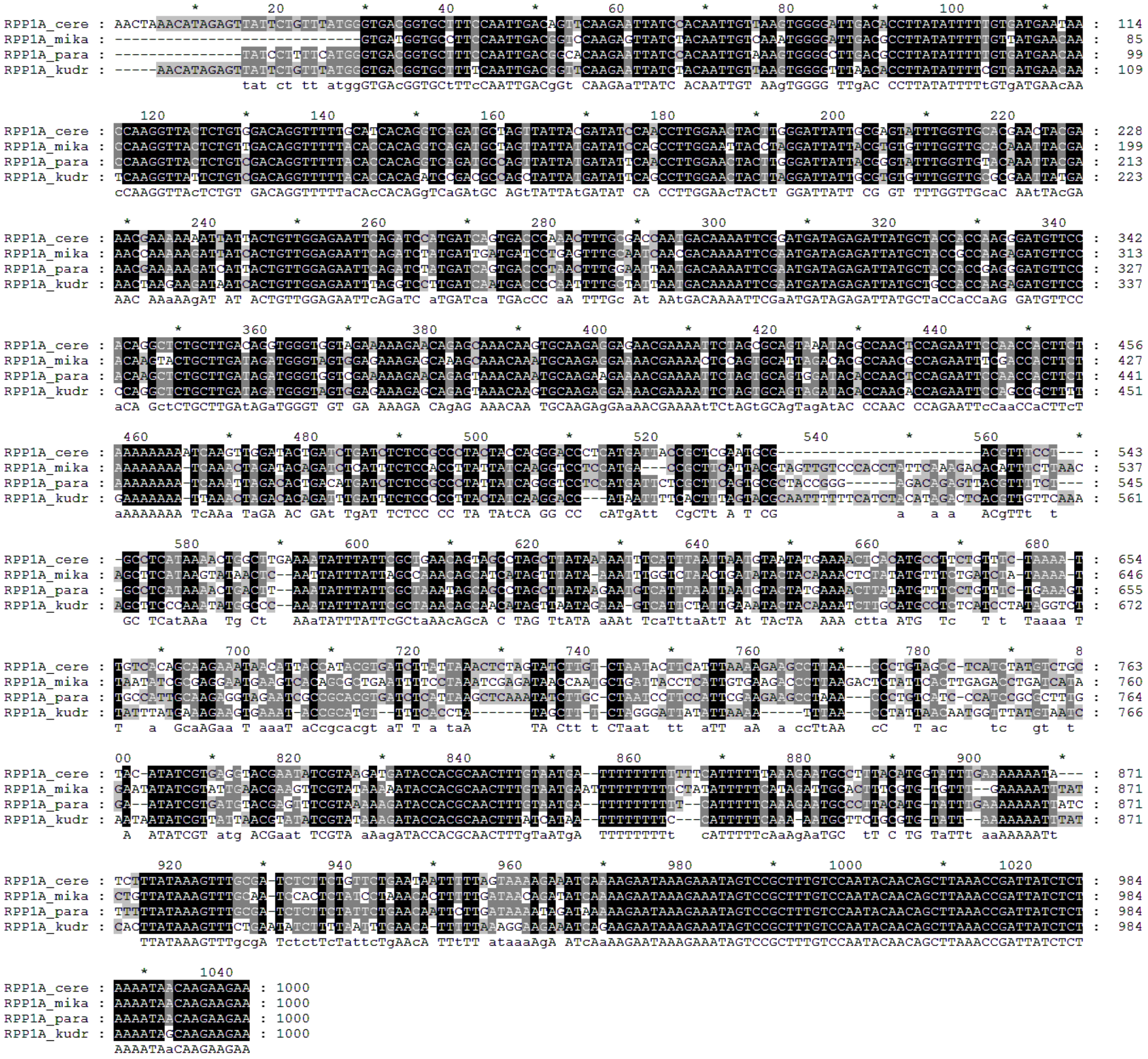


```
                      *        20         *        40         *        60         *        80         *       100         *
RPL3_cerev : --------------------------------------------------------------------CCTTTCCTGCGGGATAGCTTTTGCTTCAGGTTCTTCTGAGGTTCTG :   46
RPL3_mikat : ------------------------------------------------------------------GAGTTTTTTTGCGGGATAACTCT-GCTTGAGAATCTTCTGAAGTTTTA :   47
RPL3_parad : GCACGTTCCTTTTTATAACATGGCGTTAGTGGCGAAGTGGAACTGCTCGACCTACTTCTTATTTGAGAGGGTTTTCGTGGGGCAACTTTTGCTCAAGAAGGTTGTGCAGCTTTT :  114
                                                                               gag tTTtttGcGGGatAaCTtTtGCTt AGaatcTTcTGaaGtTtT

                 120        *        140        *        160        *        180        *        200        *        220
RPL3_cerev : AAAATCAATAT-ATTTTTCCGACAATTTCTCACTATGCCTCTATCCCCCTTAAAAAGAAACA---CTTTCTACCCTCTTTTCTAAACTCTGCACACTAGACCGAGACAGCAAAT :  156
RPL3_mikat : AAAGCCTACATTGTTTTTCCGACA-TTTTTCACTGTACCTTCATCCCC-TTAAAAAGAAACATCTCTTTCTAGCCTCTTTTCTCTATCTAGTACATAAGATTCGGACGGTCAAT :  159
RPL3_parad : CTAGTGCCCAATATTTTTCCGACATTTTTCCACTGTTCTTCCATACCCTT---AAAGGAACGGCCTACGCAATTTTCATTTCTTCGACGGTTGGGCAAG----GAGCGCCCTCT :  221
             aaAgtc acAttaTTTTTCCGACA TTTttCACTgT CcTccATcCCC TtaaAAAGaAACa c ctttCtA ccTCtTTTCT  a c  gtacacaAGa   ggaCggccaaT

              *        240        *        260        *        280        *        300        *        320        *        340
RPL3_cerev : CGGAGCCCGAGAGAAAATCCGGAGGACGGAAAAACTAGAAGTAATCTTATGCGGGGAGCATGCAC-CAGAACGCCCAGAAAACGTGAATGACACTACATACTTTGATACGGATG :  269
RPL3_mikat : CGGAGCCCGAGAGAAAATCCGGAGCACAGAAAAAATGGAAGAGATCTCATGTGGGGACCATGCACGCAGAACCCTCTGAAGACGCAGAT-ATACTACGTGTTTTGGTATTACCA :  272
RPL3_parad : CGGAGCCCGAAAGAAAATCCGGAGGTCGGAAAAATTAGACGTAATCGCGTGCGGGG--CATGCAAGCAGAACCCTCGGAGAA-ATACCT-GCACCGCACGCTTCGCTGTCACGA :  331
             CGGAGCCCGAgAGAAAATCCGGAGgaCgGAAAAA TaGAaGtaATCtcaTGcGGGGa CATGCAcgCAGAACcCtC GAaaAcgta aT acACtaCatgcTTtG Tat ac a

                    *        360        *        380        *        400        *        420        *        440        *
RPL3_cerev : TTGGTATTTTTCCGGCTTTTTCTAT-------TTTATCGATGCCGTGTCTGCTGCCATTACGTACAGGTAGGCAAAGGCAAACAAGA---ATAGCACTTT---T-TCACTTGC- :  368
RPL3_mikat : CGAAAGTTTTTCCGGCCCTCTTTCTCCCTCTCTTTCTAAGTGTACCGTGAGCTGTCATTACGT--AGAAAGGCGAAAGCAAGCGAGATTGATGACGATCTGCTT-CGGTTTAC- :  382
RPL3_parad : --------TTCAGTGCCACTGCTAC--------AGCTTCATGACAAGAAGGCGGT----------AGAAAAACGACAATGCTCGTATTTGCTCCTCTTCTTCGTATGGTATGCG :  419
                   ttTTtccgGCc tttcTat       tttcT  aTG cg Gt  GCtGtcattacgt  AGaaAggCgAaagcaa CgagattgaT  c  TcT c T tggttTgC

               460        *        480        *        500        *        520        *        540        *        560        *
RPL3_cerev : --TGCTTTTTTTTGTGAATGAAG-TTTATCGT-ATATTCTGTTAGTGCCGCTCGTATCAGCCACTTACGTTATCATTCTA-AA-GTAAGTATACGAA-ATGTGCAAACCTTAGT :  475
RPL3_mikat : --TGCTTTCATTT-CAAATGCA--TCGATAGC-ACTTCTTGATAGTGCCGCTCGTATCAGCCACTTATGTTATCACACCA-AAAGCGAATATACAAATATGTAGAAAATTTTTT :  489
RPL3_parad : CCTGCTGCCCTGTCCACGTGCATTTTTATCACTGTTTCTCTTCTGTAATGCTTCTATCAGCCATTCACGGTATCATTATGTAGGGGGAGTATACGAATGTAAACAAGACTTCGT :  533
               TGCTttc TtT caaaTGcA  TttATcgc attTcttgttaGTgccGCTcgTATCAGCCAcTtAcGtTATCAttcta Aa G gAgTATACgAAtaTgtacAAaacTT gT

                     580        *        600        *        620        *        640        *        660        *        680
RPL3_cerev : AGACGTTCAAGAA-TTGCTCGATAATTGCGAACAAACCAGCTGCTAAGCCGGGAAGTTAAGTCCTCAACACAGAAATGATGCAAACAATTTATTAAATTCAGTGGTAATGCAAC :  588
RPL3_mikat : AGGCGTTCAAGTG-TTGCCCTATCATTACACGCAAGCCAGCTGTCATAGTATAAAGTTTACTGCTC--CTTAGGAATCGTGCAAACAGTCAATTGGATACAGTGGCAATA---- :  596
RPL3_parad : AACCATTCAAGGGGTTGTCCGATAATTGTAAGCAAGCCAACCGCTACGTATGAACGTTAACTTTCCAACACAG--------------------------CATTGGTAAGGC--- :  618
             Ag CgTTCAAG g TTGccCgATaATTgcaagCAAgCCAgCtGctA g   gaAaGTTaAcT ctCaaCacAG aat  tgcaaaca t  att  at CAgTGGtAAtgc

                  *        700        *        720        *        740        *        760        *        780        *       8
RPL3_cerev : AGCAAGAGGAAAGGTGGAGGGATTAACGCATTTCAGACAGCTTTATAGGGGGAAAGAAAGCACTCGCAAACTTGCTGCCTGTTCGCAGTCATTGGTTGCAAAAACTAAACTCTA :  702
RPL3_mikat : ---AGAGACAAAAAAAGGAGAATTACCGCTGTTGAGACAGGTTTGTAAGG--TAGGAGAGCGCGGAGAAATATGCTGTGTATGTGCCGTCATTATGTGTAATTACT--CTTCAG :  703
RPL3_parad : ----GCAAATATTCTCGAGCGGTTGGTGGATTGCAGCGAAGTTCATT---------ATAGCCCTAA------TACTGT---TCAGCATTTTTCACTTGGAAAAGT--------G :  702
                ag aa aAa  t GagggaTTa cGcatTtgAGacAggTTtaTa gg   a gA AGC Ct a aaa  TgCTGt t Tg GCagTcaTta tTG AAaaact    tc g

             00         *        820        *        840        *        860        *        880        *        900        *
RPL3_cerev : CTCACGCACACTGGAATGAATGGCAATATTCTTTTTTAGGTTAACCGGCCGGACAGTA----ATATAGTAAT--CGTT--TTGTACGTTTTTCAAGAAGCGACGCACAACTGTT :  808
RPL3_mikat : TTCGTGCGAGGCCCAAAAGGTG-CGATTTTAACAATTTGGTTAACCGGCACGAAAATAGCGTATAAAGTGATGTCGTCAATTATTTTTTTTTCGGGAAGCGACGCACAGAT-TT :  815
RPL3_parad : CTCGTACTTGCC--------TTTCAGGATTAACCGGATGGAAAAGTATTTCTCGAAT------CATTGTATA--CGTCT-TTGAAATCTTTTGGGAAAGCGACGCACAACTTTT :  799
             cTCgtgC  gcc  aa    Tg CaataTTaac  tttGGttAAccggc cga AaTa    atAtaGTaat  CGTc  TTgta ttTTTTcgggAAGCGACGCACAacT TT

                   920        *        940        *        960        *        980        *       1000        *       1020
RPL3_cerev : TTCCATTTTTTTTTTTTTTTTTTCAGTGATCATCGTCCAT-GAAAAAAATTTTTCATTTGTCTCTTTCGTGCTTCCTGGATATATAAAATACGATTTATTTAGTTGTCTTTGTC :  921
RPL3_mikat : TTCATTTTTTGCATTTTTTTTTTCAGTAACCGTCGTCCAT-GGAAAAAAATTT-CATCTGT-TTTCTCATCTTCTCTAGATATATAAAATACGATTTTTTGAGGAATCGTTCTT :  926
RPL3_parad : TTCTATTTTTTTTTTTTTTTTTCACATCGTCCGTTAACGAAAGAAAAAAAATTTTCACTGGCTGTTTCCACCTTTTCCAATATATATAAAACACCATTTTTTGAAAAATCTTTTTA :  913
             TTC aTTTTTTtttTTTTTTTttCAgtgacCgTcgtCcAt GaAAAAAAtTTTtCAtttGt ttTttCatctTttCtagATATATAAAAtACgATTTtTTgAg aaTCtTT T

                *       1040        *       1060        *       1080        *       1100        *
RPL3_cerev : AATCCTCA-------TCTTTCTTTACTCATTATTTCATTTCGGTTTTGTCATCTCTAGAACAACACAGTTACTACAACAATCAATC-- : 1000
RPL3_mikat : ACAACTCA-------CCTTTTGTTGTTC----TCTTAAAATATTTTTGTCCTTTACAGAACTACACAGTTACTACAACAATCAATC-- : 1001
RPL3_parad : ATATCTGGAAATTTTCCTCTTGTTGTAGTAAGTGTTCTTTTTCTTTTATCAATTCCAGAACTACACAGTTATTACAACATTCAAACAT : 1001
             A a CTca       cCTtTtgTTgttc    T Ttatttt TTTTgTCattTccAGAACtACACAGTTAcTACAACAaTCAAtC
```

RPL4B

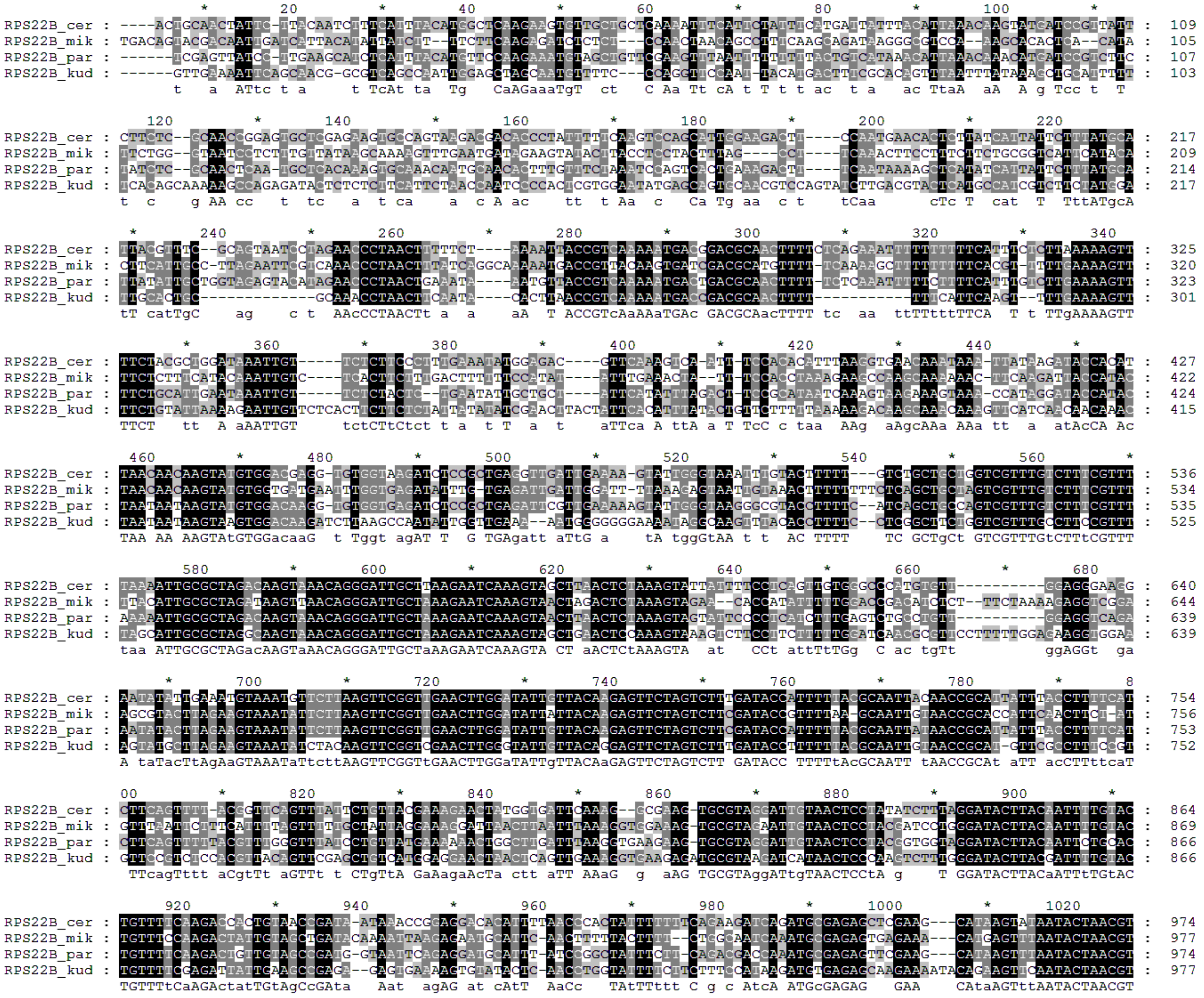
```
                      *        20         *        40         *        60         *        80         *       100         *
RPL4B_cere : -----------------------ATATGATTAACAAAACTTGGTAAATTATCTGGCCTGTCAACCCTTACCTGTCCTGTCCCTTCTTTAGACAAAAGAAAATAAAAAA-TTGG :   90
RPL4B_mika : ------------TTACCTGTTCCATATATCTAACAAAACTAGGTAGATTACCTGGCGTGTCAGCTCCGCTCCCCTTCTTTCTATCTTAGGACAAAAGAAAATAGAGCT--CAAA :  100
RPL4B_para : GTTTCGCATATGTTACCTGTTCCATATGCTTAGCAAAACGGAGTAAATTATCTGGCGTGTCAGTCGTT-----TTGGCCAAAAAC-TAAAACTTGGT----TGGACACACTTGG :  104
RPL4B_kudr : --------------------TCCATATGTTTAACAAAACTTGTTAAATTATCTGGCGTGTCAGCCCTT-----CGGACAAAAAAAATAAAACTTGGACACATGAAGAATCTTTT :   89
                                 tccATATg tTAaCAAAACt ggTAaATTAtCTGGCgTGTCAgccctt              a c Taa AC      a aT  A a   tt

                120         *       140         *       160         *       180         *       200         *       220
RPL4B_cere : ACACAGGAAAACAACAGCCTCCATACCACAGTTTCTGTGTCTTATTCTAT--TTAGGAAGGTCATTCTATATTACTCAAAGGAAAGACATCC----AGTAGAAA--CAATAGTG :  196
RPL4B_mika : ATACAATAAATTGTTTG--TTTATACGGC--TTTCTCTTAGTGATACTAC--CTGAAAGTACCGTTCCTTACTTCTCGAAGAGAAAAGATAC----GACAGATATCCAGTAGAA :  204
RPL4B_para : GCCTACGGCGATTTCTAAGTAGACGGGGAGGCGGTTGTGCATAAATCGAGGGTTACCCTACCCTTTTTGCGTTGCCCAAAAAGAAGACACCC-------AGTGAAAACTGGCG :  211
RPL4B_kudr : TCCTACGGAAACTTCTCAGT----------------GTATTCAATTCGGAAA-------GGCGTTCTTCTATTTCGGGAAAAGAGGACACCCGCCCAGTAGCAGAAAACTGGCG :  180
              c  A g aaa  tct     T  a            tgT     t AttC a    t       cc Tt t tatT C c AA agAagAcA cC       AG   a   A T G g

              *       240         *       260         *       280         *       300         *       320         *       340
RPL4B_cere : TTGCTAAACGGTTAACTTGCCCACTAATGTCTGCTTATA--TTTGCAAATCACTATTGTGGCAAGTCATACCCTGGAGCTTTGTGATTGAACAACATATACTATATTGC-AGCA :  307
RPL4B_mika : AAACTA--CCGTCG-CTAAACAAATGAAATGTCCTATA--ATACCAGTTTAC---TGCCGCAAATCC--------AGCGCGGTGGAGAGCAACGT---CTGAACTAC-ATTA :  298
RPL4B_para : TCGCAAAATCGGTAAAGACCCAACCCACCACGATCTGCAGAATTCAATATAGTAATGGTAGT--ACTAATCCCTAAAAGGCTTTAGTTGGA-ATCATTATTTAAGTTACTATCA :  322
RPL4B_kudr : TCGCTAAACAGGCGAATACCCAATTAACCCGCTTTTGTA---TGCAATTGAAGGATAACAGTGAACCCATTTCCAGAATACTGTGAA-AGA-GGCATAAATGCGATAATTTCGA :  289
             t gCtAaac G   a ta cCaA t A        T tA    T c A  t a  at g  G   aa c    c   A   ctgTg   g a a CaT      t attac a  A

                    *       360         *       380         *       400         *       420         *       440         *
RPL4B_cere : GTATTTTTCAGAAATAATATTCG-AAAGAAGTGAGAACAAGAAATGACCACGATAGATTACAGCTGACCAACTTAGAAAATGAGTAAACTTATT-TTTGTCTTAAGAAGTGCAT :  419
RPL4B_mika : CCGTTTCCCATGCGTAATACTCATAAAAAAATCAGTACTAAAAA--GTTATGAAAAATTATAGTTGATAGAGTTACTAA-----TGAATTCAAT-TTTTCTTAGAGATGTGTAT :  404
RPL4B_para : G--TTTTGGACACCCGCTACA---GCAATATTGAGAAAGGAATGGTGCTCCAGCATATC-----TAGGAGGCATACAAATAGGAAAGTCCGCT-TTTACCCA-GAATATATAT :  424
RPL4B_kudr : AAATTTAGTCAAGTTGTTGTA---AAAATAGCGATACCTGGTGGATAATTTGGTGCATCGCAATTGATAGGGACACGTATAGGTAAGGTCTTTTCTTTATTTATAAATATATAC :  400
                TTT   a a  t  Ta       aaAa A tgAgaac   a       t  g  a AT   a  Tga ag g tAc aA   g   aa t    T TTT     ta a At T tAt

              460         *       480         *       500         *       520         *       540         *       560         *
RPL4B_cere : GCAGCGACCTCTCCCAATTACCAAATTGTAATTTTTTATTATTCTTTTTTT-CTGC-ATAGTTCATTCGACAGCTTGGTTGAAAAGAGTGATAAAAATTTTCTGT-TTTATGAA :  530
RPL4B_mika : ATAA-GACTTGTTCTAAATTCTTAATCGTAGCGTACTATTTTACTTTTCTTATTGCTGTATAAAAATCGATAGGTTGGTACATAAGAGTAGTGAA---TTTTCCT-CTTACAAA :  513
RPL4B_para : ATTG-TACCGTTTCTAGCTATT--ATAATAACTGTATAACATTATTTTCCA-ATGTTAT----CATTC--CTGGC--CTCGAAATATGTTGTGAGCAGT----------ACAGA :  516
RPL4B_kudr : ATTC-TGCCGATTATGGGATTC--TCAACGGTATTCGTTCATCTTCCTTTACACTATGT----TGTTC--TCGATTACTTGAAGAATATGAGGAATACCTTTTCAGCCCACAGA :  505
             at    aCc  Ttcta  t     at  ta    tt tat aT   TttT t    tg t T      atTC     G tt   T gAaaa  gT  tgAa a ttt         Aca A

                    580         *       600         *       620         *       640         *       660         *       680
RPL4B_cere : AAGTTTTCATAACTCTATTAAGGGTTGCACTATAAGA-ACA------TTTCGCAATAAAGCA-ACCCTTATCCGGACCCTAC--ATGTTCCGTAAGTCCTGCCTTATTTTATCG- :  633
RPL4B_mika : AAGCTTCCACAGCTTTATTAAAGGTCACACAATAATA-ACAGCGTTGCTTTTCACCGAAGCA-AACCCTATCCCGACTGAACCTATATTATATAGGT----CTCTATATATCG- :  620
RPL4B_para : CCGCACTG-TAGATATAGCATAACAAGAATATCGCTACGCGCT--------CCAGAAGAGTAGTTCCCAATCCAAGCTGTATCTTTGTTTTACGAGT----CTCACTATACTGC :  617
RPL4B_kudr : CCGCTCCAATAGCTATATTAAATACAGTAAATAGCAATGGACTAACTCACACCTGTAAAATA-TTCCTTATTTGAAACATATCGTTACTTTACGAGC----CCTCATATACAG- :  613
               Gct   atAgcT TAttAaa     g A a     A  ca            Ca  aaAg A   CC tATcc  ac  tA c  T tT ta  aGt     C   aTaTA  G

                  *       700         *       720         *       740         *       760         *       780         *       8
RPL4B_cere : TAACGGTATTCATCTTACAGGAA---TTTTTGAATATAGAT---AACGTT----AGTTTTGATA---------GATTGGAA--CAAATGGGAAAATA--ACAATTTAGAAGCGC :  724
RPL4B_mika : TAGCCCTGTGCAGCACCGGTGAAAGATTTTTGGCAAAAAATTCAAACGCAGTAAAATATTAAGA---------TACTTGAG--TGATTGGTACCATA-CACAATCCAGAAACGG :  722
RPL4B_para : AAAGCTTGCGCATTTTACGAGGATCT---ATCTAGAACGTTTGAAACAATGCTAATTTGTGCCGTTGTAGAAGTTTTTGAAGCTGCTTGATACCA---AGAAATTCAGAAACAT :  725
RPL4B_kudr : AAATCCTG-GTGGTTTACAAGATTTTTAAATCCAAAATATTTGGAC---TGCGAGGATGATTCG-------AATGCCCGAAGCTGGATGAGATCATAAACAAACTTGGAAACGC :  716
              Aa c Tg gca  ttac  Gaa    t    T  a Aa     Tt   Aac  tg   aa tt t          t  t GAa  tg  TG  A cAta      AAtt aGAAaCg

             00         *       820         *       840         *       860         *       880         *       900         *
RPL4B_cere : TTTCCTCAGCGTATCTGAATTATAAAACAAC----TGCGCATAT-TGCTAAG-AACTG-------CACTGAAGGCATGAATT-------GTCTATTCCGTTAGAAATATAATTA :  818
RPL4B_mika : TATTCTTAGTATGCTCTCCCTAT---ATTGA----TGTACATTTCTGGTAGA-ACGGG-------CAATAAGGGCATAAAATAGTAAATGTCTGTTCCATCATAAATATCATAC :  821
RPL4B_para : TTGCCTTAGTGCAATTTCTATGTATGACCATGCATCTCACATATGCTTTAGCCACTTG------CCTTTCCCCACAT--ATCGTGCAGTTTCTGTCCCAT---AA-CATCATGC :  827
RPL4B_kudr : TCTCTTTAGTACACTTCCTGTTTAAGAATGT-CATGTGGTAAATGCTTCGCTTGCTTATAATAACTTTAAAACACGTG-AGCGTATATTTGCTCAGTAAG---AAATATCATGT :  825
             T tccTtAGt  a tt c  T Ta  A            cAtaT    ta   ac tg        c  t a   CaT  A        a t tCT t ccat   AAatATcAT

                    920         *       940         *       960         *       980         *      1000         *      1020
RPL4B_cere : TTTACGAAAGCATCGCGCAGACGCAATTTT-TTTAACATTTTTTTTTTTCAAGTACTCTGGAAAAGTTTT-CATGAAGATCATGAATACGTTACACTACTATTTATTATTGAAA :  930
RPL4B_mika : TTGACGAATCCTTCGCGCAGACGCAATTTTATTTTCATTTTTTTTTTCAAGCACAAGGTGGAATAGATTT-TATGCAGATATTAGATAT-----ACCGCCACTTTAATTGTGT :  929
RPL4B_para : GGCACGATATCATCGCACCGACGCAATTTT-TTTTTTTTTTTTTTTTTCAAGCATAAGTTTAAAAAAATTT-CATCCTAACTTCGAACAG-----TTTAGTTCGTTAACTAT-- :  932
RPL4B_kudr : TTCACGAAACAACTGCAGAGACGCACCGTC-TTTCATAATTTTTTTTTTCAAGCGTACAATGAAGAAAATTTTCAGCCAGATTTTCAATGC-----ATTCCAATTTTAATTGTAA :  933
             tt ACGAaa catcGC caGACGCAattTt TTT   atTTTTTTTTTcaagc tA   Tg AaaA aTTT cAt cagAt tt aAta      a t c a ttTaAtTgt

                *      1040         *      1060         *      1080         *      1100
RPL4B_cere : ATAATATTTCTTTCCTATCAGCAATCGCTTACATATTCATAGTCATTTACTAGGGTA--TATACCAATAATA-- : 1000
RPL4B_mika : ATTGTGCATTTTCAATTAAGAAAATGGTTCACTTATTGATAGTCATCTATCAAAATA--CATACCAATATTAAT : 1001
RPL4B_para : GTAATGCTTTTTGATC--TGGCTCTACTTTACATATCAATAAAAACTAATAAAACAAGCAAATTTATAAT--- : 1001
RPL4B_kudr : GCAGTAGATTATGAATATTGCAATTTGTTTATATATTGGTAATCAACTCATAAAACAAACAAATAAGA------ : 1001
              ta T   TttT a t   g  a T gtTtAcaTATt aTA tcA cTa tAaaa A  cA A  aata t
```

RPP1A



```
                     *        20         *        40         *        60         *        80         *       100         *
RPP1A_cere : AACTAAACATAGAGTTATTCTGTTTATGGGTGACGGTGCTTTCCAATTGACAGTTCAAGAATTATCCACAATTGTTAAGTGGGGATTGACACCTTATATTTTTGTGATGAATAA :  114
RPP1A_mika : -----------------------------GTGATGGTGCCTTCCAATTGACGGTCCAAGAGTTATCTACAATTGTCAAATGGGGATTGACGCCTTATATTTTTGTTATGAACAA :   85
RPP1A_para : ---------------TATCCTTTTCATGGGTGACGGTGCTTTCCAATTGACGGCACAAGAATTATCCACAATTGTAAAGTGGGGCTTGACGCCTTATATTTTTGTGATGAACAA :   99
RPP1A_kudr : -----AACATAGAGTTATTCTGTTTATGGGTGACGGTGCTTTTCAATTGACGGTTCAAGAATTATCTACAATTGTTAAGTGGGGTTTAACACCTTATATTTTCGTGATGAACAA :  109
                            tat ct tt atggGTGAcGGTGCtTTcCAATTGACgGt CAAGAaTTATC ACAATTGT AAgTGGGG TTgAC CCTTATATTTTtGTgATGAACAA

                120         *       140         *       160         *       180         *       200         *       220
RPP1A_cere : CCAAGGTTACTCTGTGGACAGGTTTTTGCATCACAGGTCAGATGCTAGTTATTACGATATCCAACCTTGGAACTACTTGGGATTATTGCGAGTATTTGGTTGCACGAACTACGA :  228
RPP1A_mika : CCAAGGTTACTCTGTTGACAGGTTTTTACACCACAGGTCAGATGCTAGTTATTATGATATCCAGCCTTGGAATTACCTAGGATTATTACGTGTGTTTGGTTGCACAAATTACGA :  199
RPP1A_para : CCAAGGTTACTCTGTCGACAGGTTTTTACACCACAGGTCAGATGCCAGTTATTATGATATTCAACCTTGGAACTACTTGGGATTATTACGGGTATTTGGTTGTACAAATTACGA :  213
RPP1A_kudr : TCAAGGTTATTCTGTCGACAGGTTTTTACACCACAGATCCGACGCCAGCTATTATGATATTCAGCCTTGGAACTACTTAGGATTATTGCGTGTGTTTGGTTGCGCGAATTATGA :  223
             cCAAGGTTAcTCTGT GACAGGTTTTTaCAcCACAGgTCaGAtGC AGtTATTAtGATAT CA CCTTGGAAcTACtT GGATTATT CG GT TTTGGTTGcaC AAtTAcGA

              *       240         *       260         *       280         *       300         *       320         *       340
RPP1A_cere : AACGAAAAAATTATTACTGTTGGAGAATTCAGATCCATGATCAGTGACCCAAACTTTGCGACCAATGACAAAATTCGGATGATAGAGATTATGCTACCACCAAGGGATGTTCC :  342
RPP1A_mika : AACCAAAAGATTATCACTGTTGGAGAATTCAGATCTATGATTGATGATCCTGAGTTTGCAATCAACGACAAAATTCGAATGATAGAGATTATGCTACCGCCAAGAGATGTTCC :  313
RPP1A_para : AACGAAAAGATCATTACTGTTGGAGAATTCAGATCTATGATCAGTGACCCTAACTTTGGAATTAATGACAAAATTCGAATGATAGAGATTATGCTACCACCGAGGGATGTTCC :  327
RPP1A_kudr : AACTAAGAAGATAATCACTGTTGGAGAATTTAGGTCCTTGATCAATGACCCCAATTTTGCTATTAATGACAAAATTCGAATGATAGAGATTATGCTGCCACCAAGAGATGTTCC :  337
             AAC AAaAAgAT AT ACTGTTGGAGAATTcAGaTC aTGATca TGAcCC aA TTTGc At AAtGACAAAATTCGaATGATAGAGATTATGCTaCCaCCaAG GATGTTCC

                    *       360         *       380         *       400         *       420         *       440         *
RPP1A_cere : ACAGGCTCTGCTTGACAGGTGGGTGGTAGAAAAAGAACAGAGCAAACAAGTGCAAGAGGAGAACGAAAATTCTAGCGCAGTAAATACGCCAACTCCAGAATTCCAACCACTTCT :  456
RPP1A_mika : ACAAGTACTGCTTGATAGATGGGTAGTGGAGAAAGAGCAAAGCAAACAAATGCAAGAGGAAAACGAAAACTCCAGTGCATTAGACACGCCAACGCCAGAATTTCGACCACTTCT :  427
RPP1A_para : ACAAGCTCTGCTTGATAGATGGGTGGTCGAAAAAGAACAGAGTAAACAAATGCAAGAAGAAAACGAAAATTCTAGTGCAGTGGATACACCAACTCCAGAATTCCAACCACTTCT :  441
RPP1A_kudr : CCAGGCTCTGCTTGATAGATGGGTAGTGGAGAAAGAGCAGAGTAAACAAGTGCAAGAGGAAAACGAAAATTCTAGTGCAGTAGATACACCAACACCAGAATTCCAGCCGCTTTT :  451
             aCA GctCTGCTTGAtAGaTGGGT GT GA AAAGA CAgAG AAACAA TGCAAGAgGAaAACGAAAAtTCtAGtGCAgTagAtAC CCAAC CCAGAATTcCaaCCaCTTcT

              460         *       480         *       500         *       520         *       540         *       560         *
RPP1A_cere : AAAAAAAAATCAAGTTGGATACTGATCTGATCTCTCCGCCCTACTACCAGGGACCCTCATGATTACCGCTCGAATGCG------------------------ACGTTTCCT--- :  543
RPP1A_mika : AAAAAAAA-TCAAACTAGATACAGATCTCATTTCTCCACCTTATTATCAAGGTCCTCCATGA---CCGCTTCATTACGTAGTTGTCCCACCTATTCAAAGACACATTTCTTAAC :  537
RPP1A_para : AAAAAAAA-TCAAATTAGACACTGACATGATCTCTCCGCCCTATTATCAGGGTCCTCCATGATTCTCGCTTCAGTGCGCTACCGGG------AGACAGAGTTACGTTTTCT--- :  545
RPP1A_kudr : GAAAAAAA-TTAAACTAGACACAGATTTGATTTCTCCCCCTTACTATCAAGGACC---ATAATTTTCACTTTAGTACGCAATTTTTTCATCTACATAGACTCACGTTGTTCAAA :  561
             aAAAAAAA TcAAa TaGA AC GAt TgAT TCTCC CC TA TAtCA GG CC  cATgAtt  CgCTt A T CG               a   a a  ACgTTt  t

                    580         *       600         *       620         *       640         *       660         *       680
RPP1A_cere : -GCCTCATAAAACTGGCTTGAAAATATTTATTCGCTGAACAGTAGCCTAGCTTATAAAAATTTCATTTAATTAATGTAATATGAAAACTCACATGCCTTCTGTTTC-TAAAA-T :  654
RPP1A_mika : AGCTTCATAAGTATAACTC--AATTATTTATTAGCCAAACAGCATCATAGTTTATA-AAATTTGGTCTAACTGATATACTACAAAACTCTATATGTTTCTGATCTA-TAAAA-T :  646
RPP1A_para : -GCCTCATAAAACTGACTT--AAATATTTATTCGCTAAATAGCAGCCTAGCTTATAAGAATGTCATTTAATTAATGTACTATGAAAACTTATATGTTTCCTGTTTC-TGAAAGT :  655
RPP1A_kudr : AGCTTCCCAAATATGGCCC--AAATATTTATTCGCTAAACAGCAACATAGTTAATAGAAA-GTCATTCTATTGAAATACTACAAAATCTTGCATGCCTCTCATCCTATAGGTCT :  672
              GC TCatAAa  Tg Ct   AAaTATTTATTcGCtaAAcAGcA C TAG TtATA aAAt TcaTttaAtT At TAcTA  AAA ctta ATG  Tc   T t  Taaaa T

                  *       700         *       720         *       740         *       760         *       780         *       8
RPP1A_cere : TGTCACAGCAAGAAATAACATTACCATACGTGATCTTATTAAACTCTAGTATCTTGT-CTAATACTTCATTTAAAAGAAGCCTTAA---CCCTGTAGCC-TCATCTATGTCTGC :  763
RPP1A_mika : TAATATCGCGAGGAATGAAGTCACAGCGCTGAATTTTCCTAAATCGAGATAACCAATGCTGATTACCTCATTGTGAAGACCCTTAAGACTCTATTCACTTGAGACCTGATCATA :  760
RPP1A_para : TGCCATTGCAAGAGGTAGAATCGCCGCACGTGATCTCATTAAGCTCAAATATCTTGC-CTAATCCTTCCATTCGAAGAAGCCTAAA---CCCTGTCATC-CCATCCGCGCTTTG :  764
RPP1A_kudr : TATTTATGAAAGAAGTGAAAT-ACCGCATGT--TTTCACCTA-------TAGCTT-T-CTAGGGATTATATTAAAA-----TTTAA---CCTATTAACAATGGTTTATGTAATC :  766
             T   a  GcaAGaa T aaaT aCcgcacgt aT T a taA       TA Ctt t CTaat  tt  aTT  aA  a ccTtAA   cC   T ac      tc   gt  t

             00         *       820         *       840         *       860         *       880         *       900         *
RPP1A_cere : TAC-ATATCGTGAGGTACGAATATCGTAAGATGATACCACGCAACTTTGTAATGA--TTTTTTTTTTTTCATTTTTTAAAGAATGCCTTTACATGGTATTTGAAAAAAATA--- :  871
RPP1A_mika : GAATATATCGTATTGAACGAAGTTCGTATAAAAATACCACGCAACTTTGTAATGAATTTTTTTTTTTTCTATTTTTCATAGATTGCACTTTCGTG-TGTTT--GAAAAATTTAT :  871
RPP1A_para : GA--ATATCGTGATGTACGAGTTTCGTAAAAAGATACCACGCAACTTTGTAATGA--TTTTTTTTTT--CATTTTTCAAAGAATGCCCTTACATG-TATTTGAAAAAAATTATC :  871
RPP1A_kudr : AATAATATCGTTATTAACGTATATCGTATAAAGATACCACGCAACTTTATCATAA--TTTTTTTTC---CATTTTTCAAA-AATGCTTCTGCGTG-TATT--AAAAAAATTTAT :  871
              A  ATATCGT atg ACGaat TCGTA aAagATACCACGCAACTTTgTaATgA  TTTTTTTTt   cATTTTTcAaAgAaTGC  tT C TG TaTTt aaAAAAATt

                  920         *       940         *       960         *       980         *      1000         *      1020
RPP1A_cere : TCTTTATAAAGTTTGCGA-TCTCTTCTGTTCTGAATAATTTTTAGTAAAAGAAATCAAAAGAATAAAGAAATAGTCCGCTTTGTCCAATACAACAGCTTAAACCGATTATCTCT :  984
RPP1A_mika : CTGTTATAAAGTTTGCAA-TCCACTCTATCCTAAACACTTTTTGATAACAGATATCAAAAGAATAAAGAAATAGTCCGCTTTGTCCAATACAACAGCTTAAACCGATTATCTCT :  984
RPP1A_para : TTTTTATAAAGTTTGCGA-TCTCTTCTATTCTGAACAATTCTTGATAAAATAGATAAAAAGAATAAAGAAATAGTCCGCTTTGTCCAATACAACAGCTTAAACCGATTATCTCT :  984
RPP1A_kudr : CACTTATAAAGTTTCTGAATATCTTTTAATTTGAACA-TTTTTAAAGGAAGAAATCAGAAGAATAAAGAAATAGTCCGCTTTGTCCAATACAACAGCTTAAACCGATTATCTCT :  984
                TTATAAAGTTTgcgA TctctTcTattcTgAAcA TTtTT ataaaAgA ATcAaAAGAATAAAGAAATAGTCCGCTTTGTCCAATACAACAGCTTAAACCGATTATCTCT

                *      1040
RPP1A_cere : AAAATAACAAGAAGAA : 1000
RPP1A_mika : AAAATAACAAGAAGAA : 1000
RPP1A_para : AAAATAACAAGAAGAA : 1000
RPP1A_kudr : AAAATAGCAAGAAGAA : 1000
             AAAATAaCAAGAAGAA
```

RPS22B

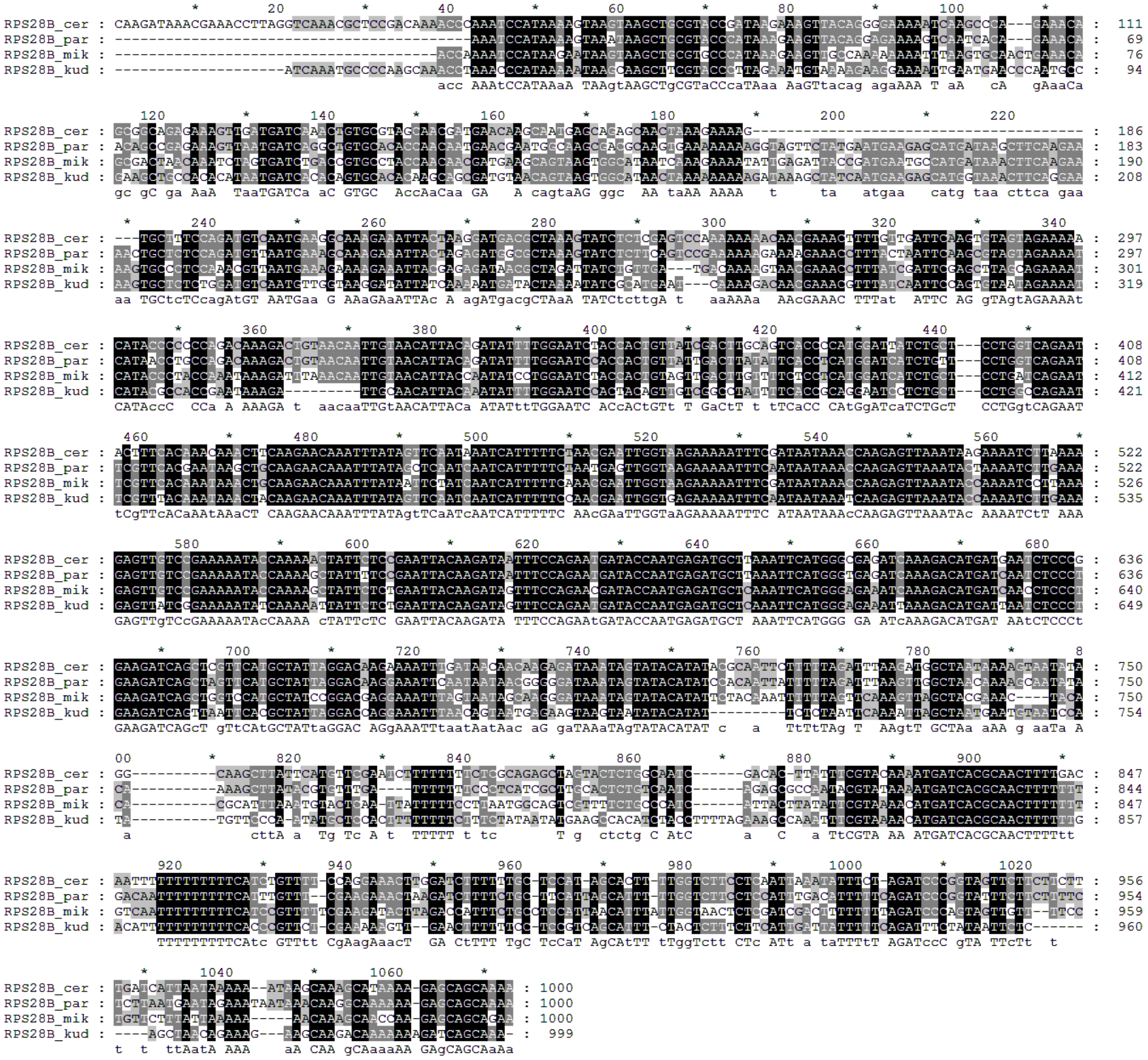


```
                      *        20         *        40         *        60         *        80         *       100         *
RPS22B_cer : ----ACTGCAACTATTC-TTACAATCTTTCATTTACATGGCTCAAGAAGTGTTGCTGCTCAAAATTTCATTCTATTTCATGATTATTTACATTAAACAAGTATGATCCGTTATT :  109
RPS22B_mik : TGACAGTACGACAATTGATCATTACATATTATCTT--TTCTTCAAGAGATCTCTCT---CCAACTAACAGCCTTTCAAGCAGATAAGGGCGTCCA--AAGCACACTCA--CATA :  105
RPS22B_par : ------TCGAGTTATCC-TTGAAGCATCTCATTTACATGTTCCAAGAAATGTAGCTGTTCGAAGTTTAATTTTTTTTTACTGTCATAAACATTAAACAAACATGATCCGTCTTC :  107
RPS22B_kud : ------GTTGAAAATTCAGCAACG-GCGTCAGCCAATTGGAGCTAGCAATGTTTTC---CCAGGTTCCAAT-TACATGACTTTCGCACAGTTTAATTTATAAAGCTGCATTTTT :  103
                   t   a  ATtc t a     t TcAt ta  Tg   CaAGaaaTgT  ct   C Aa Tt cA t T t t ac  t a   ac TtaA aA  A g Tcc t  T

                120         *       140         *       160         *       180         *       200         *       220
RPS22B_cer : CTTCTC--GCAACCGGAGTGCTCGAGAAGTGCCAGTAAGACGACACCCTATTTTTCAAGTCCAGCATTGGAAGACTT----CCAATGAACACTCTTATCATTATTCTTTATGCA :  217
RPS22B_mik : TTCTGG--GTAATCCTCTTTGTTATAAGCAAAAGTTTGAATGATAGAAGTATACTTACCTCCTACTTTAG----CCT----TCAAACTTCCTTTCTTCTGCGGTCATTCATACA :  209
RPS22B_par : TATCTC--GCAACTCAA-TGCTCACAAAGTGCAAACAATGCAACACTTTGTTTCTAAATCCAGTCACTGAAAGACTT----TCAATAAAAGCTCATATCATTATTCTTTATGCA :  214
RPS22B_kud : TCACAGCAAAAAGCCAGAGATACTCTCTCTTCATTCTAACCAATCCCCACTCGTGGAATATGAGCAGTGCAACGTCCAGTATCTTGACGTACTCATGCCATCGTCTTCTATGGA :  217
             t  c    g  AA cc  t  tc   a  t ca    a  c A ac    tt  t Aa  c   Ca Tg aa  c t    tCaa      cTc T  cat  T  TttATgcA

              *       240         *       260         *       280         *       300         *       320         *       340
RPS22B_cer : TTACGTTTC--GCAGTAATCCTAGAACCCTAACTTTTTCT----AAAATTACCGTCAAAAATGACGGACGCAACTTTTCTCAGAAATTTTTTTTTTCATTTCTCTTAAAAAGTT :  325
RPS22B_mik : CTTCATTGCC-TTAGAATTCGTCAAACCCTAACTTTATCAGGCAAAAATGACCGTTACAAGTGATCGACGCATGTTTT-TCAAAAGCTTTTTTTTTCACGT-TTTTGAAAAGTT :  320
RPS22B_par : TTATATTGCTGGTAGAGTACATAGAACCCTAACTGAAATA----AATGTTACCGTCAAAAATGACTGACGCAACTTTT-TCTCAAATTTTTCTTTTCATTTGTCTTGAAAAGTT :  323
RPS22B_kud : TTGCACTGC-------------GCAAACCTAACTTCAATA----CACTTAACCGTCAAAAATGACCGACGCAACTTTT-----------TTTCATTCAAGT--TTTGAAAAGTT :  301
             tT catTgC    ag    c t  AAcCCTAACTt a  a    aA  T ACCGTcAaAAaTGAc GACGCAacTTTT tc  aa  ttTTtttTTCA  T t TTgAAAAGTT

                    *       360         *       380         *       400         *       420         *       440         *
RPS22B_cer : TTCTACGCTGGATAAATTGT-----TCTCTTCCCTTTGAAATATGGAGAC----GTTCAAAGTCA-ATT-TCCACACATTTAAGGTGAACAAATAAA-TTATAAGATACCACAT :  427
RPS22B_mik : TTCTCTTTCATACAAATTGTC----TCACTTCTTTGACTTTTTTCCATAT----ATTTGAAACTA--TT-TCCACCTAAAGAAGCCAAGCAAAAAAC-TTCAAGATTACCATAC :  422
RPS22B_par : TTCTGCATTGAATAAATTGT-----TCTCTACTC--TGAATATTGCTGCT----ATTCATATTTAGACT-TCCGCATAATCAAAGTAAGAAAGTAAA-CCATAGGATACCATAC :  424
RPS22B_kud : TTCTGTATTAAAAGAATTGTTCTCACTTCTTCTCTATTATATATCGAACTTACTATTCACATTTATACTGTTCTTTTTAAAAAGACAAGCAAACAAAGTTCATCAACAACAAAC :  415
             TTCT   tt  A aAATTGT     tctCTtCtct t a  t T  a  t    aTTca A ttA a T TcC c taa  AAg  aAgcAAa AAa tt  a  atAcCA Ac

              460         *       480         *       500         *       520         *       540         *       560         *
RPS22B_cer : TAACAACAAGTATGTGGACGAGG-TGTGGTAAGATCTCCGCTGAGGTTGATTGAAAA-GTATTGGGTAAATTTGTACTTTTT---GTCTGCTGCTGGTCGTTTGTCTTTCGTTT :  536
RPS22B_mik : TAACAACAAGTATGTGGTGATGAATTTGGTGAGATATTTG-TGAGATTGATTGGATT-TTAAAGAGTAATTGTAAACTTTTTTTTCTCAGCTGCTAGTCGTTTGTCTTTCGTTT :  534
RPS22B_par : TAATAATAAGTATGTGGACAAGG-TGTGGTGAGATCTCCGCTGAGATTCGTTGAAAAAGTATTGGGTAAGGGCGTACCTTTTC--ATCAGCTGCCAGTCGTTTGTCTTTCGTTT :  535
RPS22B_kud : TAATAATAAGTAAGTGGACAAGATCTTAAGCCAATATTGCTTGAAA--AATGCGGGGGAAAATAGCCAAGTTTACACCTTTTC--CTCGGCTTCTGGTCGTTTGCCTTCCGTTT :  525
             TAA AA AAGTAtGTGGacaaG  t Tggt agAT T  G TGAgatt aTtG a    tA tggGtAA t t  AC TTTT    TC GCTgCt GTCGTTTGtCTTtCGTTT

                    580         *       600         *       620         *       640         *       660         *       680
RPS22B_cer : TAAAATTGCGCTAGACAAGTAAACAGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCCTCAGTTGTGGCCCATGTGTTT----------GGAGGGAACG :  640
RPS22B_mik : TTACATTGCGCTAGATAAGTTAACAGGGATTGCTAAAGAATCAAAGTAACTAGACTCTAAAGTAGAA--CACCATATTTTTGGACCGACATCTCT--TTCTAAAAGAGGTCGGA :  644
RPS22B_par : AAAAATTGCGCTAGACAAGTAAACAGGGATTGCTAAAGAATCAAAGTAACTTAACTCTAAAGTAGTATTCCCCTCATCTTTGAGTCTGCCTGTT----------GGAGGTCAGA :  639
RPS22B_kud : TAGCATTGCGCTAGGCAAGTAAACAGGGATTGCTAAAGAATCAAAGTAGCTGAACTCCAAAGTAAAGTCTTCCTTCTTTTTGGATCAACGCGTTCCTTTTTGGAGAAGGTGGAA :  639
             taa ATTGCGCTAGacAAGTaAACAGGGATTGCTaAAGAATCAAAGTA CT aACTCtAAAGTA  at   CCt attTtTGg  C ac tgTt          ggAGGt  ga

                  *       700         *       720         *       740         *       760         *       780         *       8
RPS22B_cer : AATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAACTTGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATTATTTACCTTTTCAT :  754
RPS22B_mik : AGCGTACTTAGAAGTAAATATTCTTAAGTTCGGTTGAACTTGGATATTATTACAAGAGTTCTAGTCTTCGATACCGTTTTAA-GCAATTGTAACCGCACCATTCAACTTCT-AT :  756
RPS22B_par : AATATACTTAGAAGTAAATATTCTTAAGTTCGGTTGAACTTGGATATTGTTACAAGAGTTCTAGTCTTCGATACCATTTTTACGCAATTATAACCGCATTATTTACCTTTTCAT :  753
RPS22B_kud : AGTATGCTTAGAAGTAAATATCTACAAGTTCGGTCGAACTTGGGTATTGTTACAGGAGTTCTAGTCTTTGATACCTTTTTTACGCAATTGTAACCGCAT-GTTCGCCTTTCCGT :  752
             A taTacTtAgAaGTAAATaTtcttAAGTTCGGTtGAACTTGGaTATTgTTACAaGAGTTCTAGTCTT GATACC TTTTtAcGCAATT tAACCGCAt aTT acCTTttcaT

             00         *       820         *       840         *       860         *       880         *       900         *
RPS22B_cer : CTTCAGTTTT-ACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGTGATTCAAAG--GCGAAG-TGCGTAGGATTGTAACTCCTATATCTTTAGGATACTTACAATTTTGTAC :  864
RPS22B_mik : GTTTAATTCTTTCATTTTAGTTTTTGCTATTAGGAAAGGATTAACTTAATTTAAAGGTGGAAAG-TGCGTAGAATTGTAACTCCTACGATCCTGGGATACTTACAATTTTGTAC :  869
RPS22B_par : CTTCAGTTTTTACGTTTGGGTTTATCCTGTTATGAAAAAACTGGCTTGATTTAAGGTGAAGAAG-TGCGTAGGATTGTAACTCCTACGGTGGTAGGATACTTACAATTCTGCAC :  866
RPS22B_kud : GTTCCGTCTCCACGTTACAGTTCGAGCTGTCATGGAGGAACTAACTCAGTTGAAAGGTGAAGAGATGCGTAAGATCATAACTCCCAAGTCTTTGGGATACTTACGATTTTGTAC :  866
              TTcagTttt aCgtTt aGTTt t CTgTtA GaAagaAcTa ctt aTT AAaG  g  aAG TGCGTAggATtgTAACTCCtA g    T GGATACTTACaATTtTGtAC

                  920         *       940         *       960         *       980         *      1000         *      1020
RPS22B_cer : TGTTTTCAAGACCACTGTAACCGATA-ATAAACCGGAGGACACATTTTAACCCACTATTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAG---CATAAGTATAATACTAACGT :  974
RPS22B_mik : TGTTTCCAAGACTATTGTAGCTGATACAAAATTAAGAGAATGCATTC-AACTTTTTACTTTT--CTGGCAATCAAATGCGAGAGTGAGAAA---CATGAGTTTAATACTAACGT :  977
RPS22B_par : TGTTTTCAAGACTGTTGTAGCCGATG-GTAATTCAGAGGATGCATTT-ATCCGGCTATTTCTT-CAGACGACCAAATGCGAGAGTTCGAAG---CATAAGTTTAATACTAACGT :  974
RPS22B_kud : TGTTTTCGAGATTATTGAAGCCGAGA--GAGTGAAAAGTGTATACTC-AACCTGGTATTTTCTTCTTTCCATAAGATGTGAGAGCAAGAAAATACAGAAGTTCAATACTAACGT :  977
             TGTTTtCaAGActatTGtAgCcGAta   Aat  agAG at cAtT  AaCc   TAtTTttt C g c AtcA ATGcGAGAG   GAA    CAtaAGTttAATACTAACGT
```

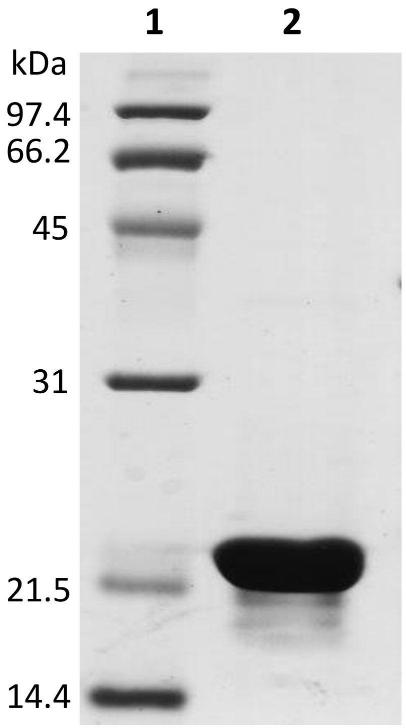
RPS28A

```
                      *        20         *        40         *        60         *        80         *       100         *
RPS28A_cer : ------------------TTGTGGGTTTTCACCCACTTTATGCAAATCACCTAGGAAACCTTCATTGAACATAGTCCTCTTTGGACCGGATGATGCAGAATTATCAGAACTCTT :   96
RPS28A_par : -----------GGTAAGCTTGTGGATTCTCACCCACTTTATGCAAATCACCTAGGAAACCTTCATTGAACATAGTCCTCTTTGGACCGGATGCTGTAGAAGTATCGGAGCTCTT :  103
RPS28A_mik : -----------------CTTGTGGATTTTCACCAACTTTATGCAAATCACCTAGAAAACCTTCATTAAACATGGTCCTCTTTGGATCAGATGACGTAGCATCATTAGAACTTTT :   97
RPS28A_kud : CATTAGCTCTGGATAAGCTTGTGGGTTTTCGCCAACTTTATGTAAATCCTTCAAGAAACCTTCATTGAACATGGTTCTCTTTGGGTCGGATAAGGTGGGACTATCAGGACTTTT :  114
                              cTTGTGG TTtTCaCC ACTTTATGcAAATCacctAggAAACCTTCATTgAACAT GTcCTCTTTGGa CgGATga GtaG A tATcaGaaCT TT

                120         *       140         *       160         *       180         *       200         *       220
RPS28A_cer : CTTGGCAGAATTGGTTTTCTTCTTTTCATTATTCTTGGTCTTCTTCTTGATTAAGTCTCTCTCATCCTTTGGACCCAAAAGTTTTAAGACTTCTTGGTCGATAATTGGCTTGAA :  210
RPS28A_par : CTTGGTAGAATTAGTCTTCTTCTTTTCATTATTCTTGGTCTTCTTCTTGATTAAGTCTCTCTCATCCTTTGGACCCAAAAGCTTTAAGACTTCTTGATCGATGATTGGCTTGAA :  217
RPS28A_mik : CTTTGTAGAAGATGTCTTCTTTTTTTCATTGTTCTTGGTTTTCTTTTTGAGCAAGTCTCTTTCATCCTTTGGACCCAAGAGCTTTAAAATTTCTTGGTCAATAATTGGCTTAAA :  211
RPS28A_kud : CTTGGCAGGAGTGGCTTTTTTCTTTTCGTTGTTTTAGTCTTTTTTTTTGACCAGGTCTCTCTCATCCTTTGGGCCTAGGAGCTTCAAAATTTCTTGGTCGATGATCGGCTTAAA :  228
             CTTgG AGaA t Gt TTcTTcTTTTCaTT TTcTTgGTcTTcTT TTGA  AaGTCTCTcTCATCCTTTGGaCCcAa AGcTTtAA A TTCTTGgTCgAT ATtGGCTT AA

              *       240         *       260         *       280         *       300         *       320         *       340
RPS28A_cer : ACTACGTGGATCGGCCCACTTCAGCTCCTTTAAGTTTTTAACATCGGCAAAAATACCTGGCACCAGTTTATAGCGTTCAGTTAAAATTCTTTCCTTGTTTTCTTGAATGTACTG :  324
RPS28A_par : ACTGCGTGGATCAGCCCACTTAAGCTCCTTTAAATTCTTAACATCCGCAAAAATACCTGGTACTAGTTTATAACGTTCTTTCAAAATTTTTTTCTTGTTTTCTTGAATGTATTG :  331
RPS28A_mik : ACTACGTGGATCCGCCCATTTAAGTTCCTTTAAGTTCTTAACATCTGCAAATATTCCTGGCACTAACTTATAACGTTCTTTCAATATTTTTTCCTTGTTTTCTTGAATATATTG :  325
RPS28A_kud : ACTACGTGGATCGGCCCATTTTAGCTCCTTCAAGTTTTTAACATCAGCAAAAATGCCTGGTACTAACTTATAACGTTCTTTTAAAATTCTTTCTTTATTTTCCTGAACGTATTG :  342
             ACTaCGTGGATC GCCCA TT AGcTCCTTtAAgTT TTAACATC GCAAAaAT CCTGG ACtA  TTATAaCGTTCttT AAaATT TTTC TTgTTTTCtTGAAtgTAtTG

                    *       360         *       380         *       400         *       420         *       440         *
RPS28A_cer : CATGACGTAATTTCTAACCTGATCCTCTGTAATCTCAATACCAACACCAGAGTTTTCATTCATACCCATTTTGGTGGATGCCTCGCCATTAGCCTTTACATATTTAAATGCGGC :  438
RPS28A_par : CATGACATAATTTCTAACCTGATCCTCAGTAATCTCAATACCAACTCCAGAGTTTTCGTTCATGCCCTCTTTGGTAGATGCATCGCCATTAGCCTTTACATATTTAAATGCTGC :  445
RPS28A_mik : CATGACATAATTTCTAACCTGATCCTCAGTTATTTCAATACCCACTCCAGAGTTTTCGTTCATACCCTCCTTGGTAGATGCATCGCCGTTTGCCTTTACATATTTGAAGGCGGC :  439
RPS28A_kud : CATGACGTAATTCCTGACTTGATCCTCAGTGATCTCAATACCCACACCAGAGTTTTCGTTCATGCCCTCCTTGGTGGATGCGTCGCCGTTAACCTTCACATATTTGAATGCGGC :  456
             CATGAC TAATTtCTaACcTGATCCTCaGT ATcTCAATACC AC CCAGAGTTTTCgTTCAT CCCtc TTGGT GATGC TCGCC TTagCCTTtACATATTT AAtGCgGC

              460         *       480         *       500         *       520         *       540         *       560         *
RPS28A_cer : ATCGACTTGCAGAGATGTCTTCAAATCACCATTAATGATGCCGTTAACAATTAATTCAGACTTGGGTAGATCTGTACCTTTGACAAAAGATGCCAGGTTGTGTACTAGCGCTCT :  552
RPS28A_par : ATTTACTTGCAAAGATGTCTTCAAGTCACCGTTAATGATACCGCTAACGATCAATTCGGACCTGGGAAGATTTGCACCTTTGACAAAAGATGCTAAGTTATGTACTAGCGCTCT :  559
RPS28A_mik : ATTGACTTGTAGGGATGTCTTCAAGTCACCGTTAATGATACCGTTAACAACCAATTCAGAATTAGGAAGATCCGCACCTTTGATAAAAGAAGCTAGGTTATGTACCAGTGCTCT :  553
RPS28A_kud : ATCGACTTGCAAAGATGTCTTCAAGTCACCGTTGATGATACCGTCAACAATCAATTCAGACTTGGGAAGATCTGCACCTTTGATGAAGGAAGCTAAGTTGTGTACTAACGCTCT :  570
             AT gACTTGcA aGATGTCTTCAAgTCACCgTTaATGATaCCGttAACaAtcAATTCaGActTgGGaAGATctGcACCTTTGA aAAaGA GCtA GTT TGTACtAgcGCTCT

                    580         *       600         *       620         *       640         *       660         *       680
RPS28A_cer : AGTAGATTTGTTCCATTGATAGTCCGAAGGAGTCTCCTTAATCAATTTGTAAAGTGAATCAGAAACCTTTTTATTCTTGACAATCTCCTTCACCTTTTTATCTTCAAACCCAAC :  666
RPS28A_par : GGTAGATTTGTTCCATTGATAATCCGAAGGTGTTTCCTTAATCAATTTGTAAAGTGAATCGGAAACCTTTTTATTCTTGACAATCTCCTTGACCTTGTTATCTTCGAACCCAAC :  673
RPS28A_mik : AGTAGATTTATTCCATTGGTAACCTGAAGGTGTCTCTTTAATCAATTTGTATAGTGAATCTGAAACCTTTTTATTCTTGACAATCTCTTTAACCTTATTGTCTTCAAACCCAAC :  667
RPS28A_kud : GCTGGATTTATCCCATCGATTATCGGAGGGTGTGTTCTTTATTAATTCGTAAAGAGAATCGGAAACCTTTTTATTTTTGACAATCTCCTTGATTTTGTTATCTTCAAACCCAAT :  684
              gTaGATTT TtCCATtGaTaatC GAaGGtGT TccTTaATcAATTtGTAaAGtGAATC GAAACCTTTTTATTcTTGACAATCTCcTT AccTT TTaTCTTCaAACCCAAc

                  *       700         *       720         *       740         *       760         *       780         *       8
RPS28A_cer : CTGTGAAAACAGCTGAGTCAATTCTTCTACAGAAGAC---ATTTTAATATATT-----GACGTTATTATACTCCTGATATTTTTTTCTCATTAAAACAAGCATCAAATCCCTTT :  772
RPS28A_par : TTGTGAAAACAGCTGAGTCAGTTCTTCTACAGACGAC---ATTTTACTATATT-----GACGTTGCTATACTCCTGGTACT---CTCCTATCAGAACAATAACCAAATCCCTTT :  776
RPS28A_mik : TTGCGAAAACAGCTGAGTTAATTCTTCTACCGACGACGACATCTTACTGTATC-----GGTGTTGCTCTACTTCTGTAATT---CTCCTAGTAGATCACTAATCTTATCCCCTT :  773
RPS28A_kud : CTGTGAAAACAGTTTAGTCAATTCTTCCACAGACGAC---ATTTTATTGTATTTTTCCGGCGTTGTTGTGCGCTTAATACC----ACCTGTTGGTGCTATG--CATATCC-TTC :  788
              TGtGAAAACAGcTgAGTcAaTTCTTCtACaGAcGAC   ATtTTA T TATt     G cGTTg T TaCtccTg tA t    tCctattaga Caat a Ca ATCCctTt

             00         *       820         *       840         *       860         *       880         *       900         *
RPS28A_cer : TAAGCATATCAATCCCAATCTTTATACC-CTGCGATGTCAAATTTTTCATTTGTACAGACGCGGCCGTCTAGAGTGACC-ACGCACTTTTTT---GATAAATTTTTTTTTTCTT :  881
RPS28A_par : TAAGCATATCAATCCCAATCTTTATACC-CAGCGATGACAAATTTTTCATTTGCACAGACGCTGCCGTGTAGAGTGACC-ACGCACTTTTTTT--GATAAATTTTTTTT--CTT :  884
RPS28A_mik : TTAAACTGCCAATCTCAATCTTTTTATCTCAGCGATGACAAATTTTTCATTTACACAGACGCAGCCGTGTATAATGACC-ACGCACTTTTTTTTTGACAAAATTTTTTT---CT :  883
RPS28A_kud : TAATCACATCAATCTCAATCTTTT-------GCGATGACAAATTTTTCGTTTCCACAGACGCTGCCGTGTTGAGTGACCCACGCACTTTTTTC--GCCAAATTTTTTTT----T :  889
             TaA catatCAATC CAATCTTT ta c c GCGATGaCAAATTTTTCaTTT cACAGACGC GCCGTgTagAgTGACC ACGCACTTTTTT   Ga AAAtTTTTTTT    T

                  920         *       940         *       960         *       980         *      1000         *      1020
RPS28A_cer : GGTCGTTGAACTACTTGGAATAAAGAAAATGAAATTTCAGTCTAATAGATGATTTATTGTAAATTACAGTTGTGTTCGTTTTCGATTCTTCTCAAAAGCAGAAAACCAAGCTAG :  995
RPS28A_par : GGTCGTTGAACTATTTGGAATGA--AAAATGAAATTTTAGTCTAATTGATGATTTATTATCAGTTACAGGTGCGTTCGATTTC-ACTTTGCTTCAAACCTAGAAACCAAGCTAG :  995
RPS28A_mik : GGTCGTTGAACTATTTGTATTAA--AAAATGAAATTTCAATCTAATTATTGACTTATTGCCAGTTGTGACTACTATCTATTTTATTTTGTTTCAAAGCCAGGAAACCAAGCCAG :  995
RPS28A_kud : GATCGTTGAATAATTTGCAATAAAAAAAATAAAATTTCAATCTTATTAATGATTTATTGCCAGATGGGATT--------TTTAACTTTGTTTCAAGGCCAGGAAACCAAGCTAG :  995
             GgTCGTTGAActAtTTG AaTaA  AAAATgAAATTTcA TCTaATt aTGAtTTATTg cAgtT     T    tc  TTT   tTt t TcaAa cCaggAAACCAAGCtAG

               *
RPS28A_cer : CAATC : 1000
RPS28A_par : CAATC : 1000
RPS28A_mik : CAATC : 1000
RPS28A_kud : CAAAC : 1000
             CAAtC
```

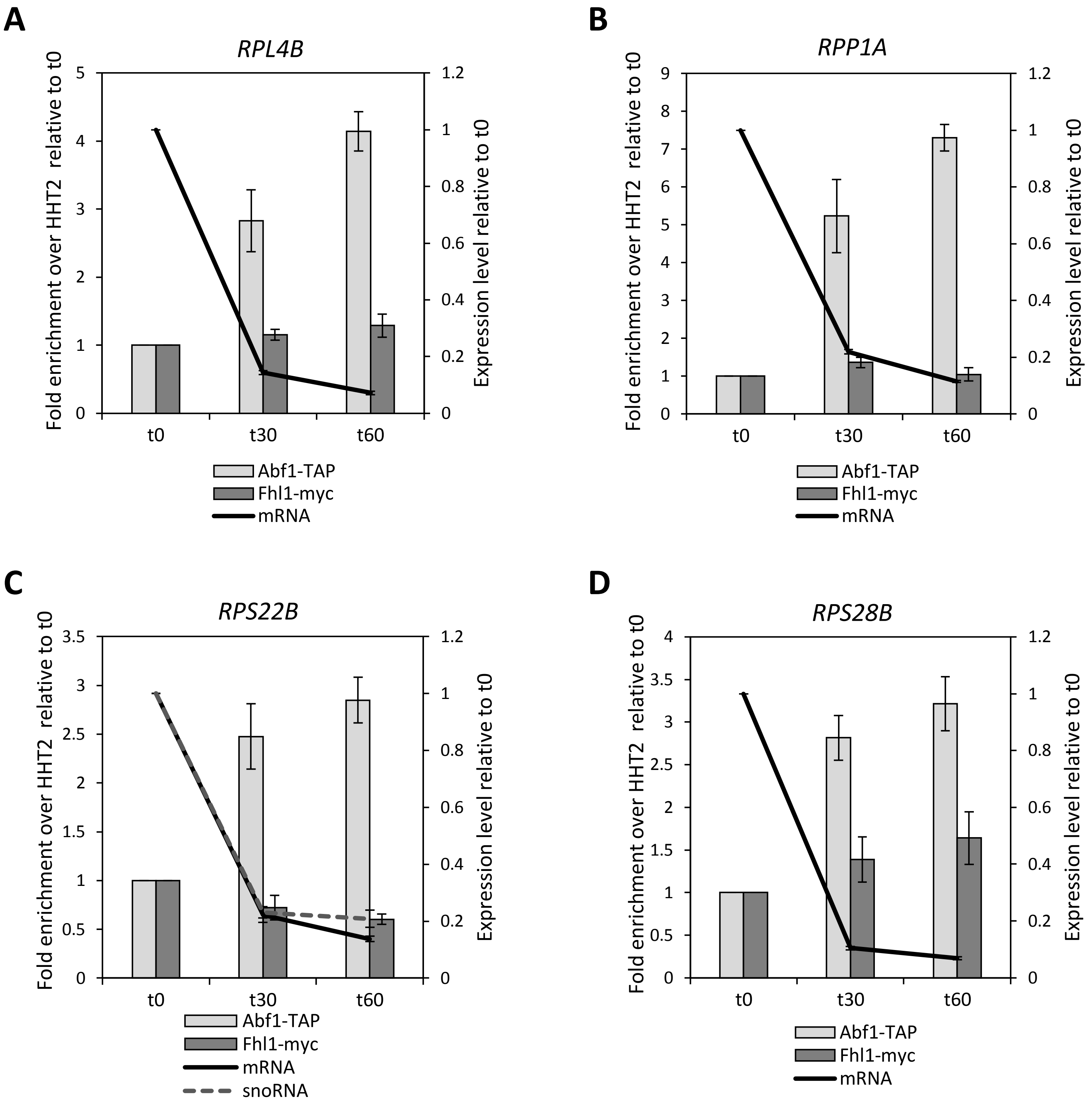
RPS28B



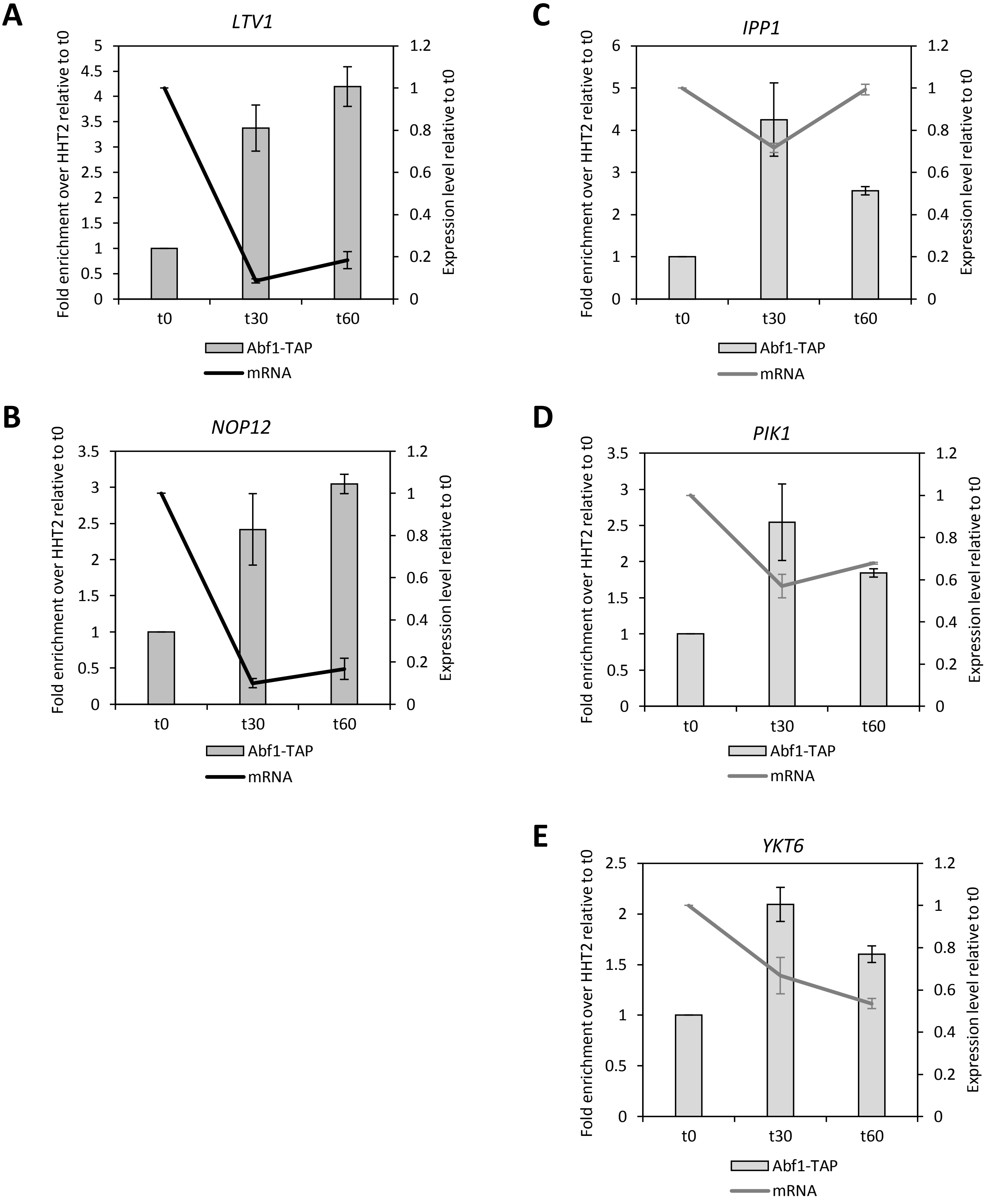
```
                      *        20         *        40         *        60         *        80         *       100         *
RPS28B_cer : CAAGATAAACGAAACCTTAGGTCAAACGCTCCGACAAAACCCAAATCCATAAAAGTAAGTAAGCTGCGTACCGATAAGAAAGTTACAGGGAAAAATCAAGCCCA---GAAACA :  111
RPS28B_par : ------------------------------------------AAATCCATAAAAGTAAATAAGCTGCGTACCCATAAAGAAGTTACAGGAGAAAAGTCAATCACA---GAAACA :   69
RPS28B_mik : ---------------------------------------ACCAAATCCATAAGAATAAGTAAGCTGCGTGCCCATAAAGAAGTTGCCAAAAAAAATTTAAGTGCAACTGAAACA :   76
RPS28B_kud : --------------------ATCAAATGCCCCAAGCAAACCTAAACCCATAAAAATAAGCAAGCTTCGTACCCTTAGAAATGTAAAAGAAGGAAAATTGAATGAACCCAATGCC :   94
                                                    acc AAAtCCATAAaA TAAgtAAGCTgCGTaCCcaTAaa AaGTtacag agaAAA T aA   cA   gAaaCa

                120         *       140         *       160         *       180         *       200         *       220
RPS28B_cer : GCGGCAGAGAAAGTTGATGATCAAACTGTGCGTAGCAACGATGAACAAGCAATGAGCAGAGCAACTAAAGAAAAG--------------------------------------- :  186
RPS28B_par : ACAGCCGAGAAAGTTAATGATCAGGCTGTGCACACCAACAATGAACGAATGGCAAGCGACGCAAGTGAAAAAAAAGGTAGTTCTATGAATGAAGAGCATGATAAGCTTCAAGAA :  183
RPS28B_mik : GCGACTAACAAATCTAGTGATCTGACCGTGCCTACCAACAACGATGAAGCAGTAAGTGGCATAATCAAAGAAAATATTGAGATTACCGATGAATGCCATGATAAACTTCAAGAA :  190
RPS28B_kud : GAAGCTGCCACACATAATGATCACACAGTGCACACAAGCAGCGATGTAACAGTAAGTGGCATAACTAAAAAAAAAGATAAAGCTATCAATGAAGAGCATGGTAAACTTCAGGAA :  208
             gc gC ga AaA  TaaTGATCa aC GTGC  AccAaCaa GA   A cagtaAG ggc  AA taAA AAAA   t     ta   atgaa   catg taa cttca gaa

              *       240         *       260         *       280         *       300         *       320         *       340
RPS28B_cer : ---TGCTTTCCAGATGTCAATGAAGGCAAAGAAATTACTAAGGATGACGCTAAAGTATCTCTCGAGTCCAAAAAAAACAACGAAACTTTGTTGATTCAAGTGTAGTAGAAAAA :  297
RPS28B_par : AACTGCTCTCCAGATGTTAATGAAAGCAAAGAAATTACTAGAGATGGCGCTAAAGTATCTCTTCAGTCCGAAAAAAGAAAAGAAACCTTTACTAATTCAAGCGTAGTAGAAAAT :  297
RPS28B_mik : AAGTGCCCTCCAAACGTTAATGAAAGAAAAGAAATTACGAGAGATAACGCTAGATTATCTGTTGA---TGACAAAAGTAACGAAACCTTTATCGATTCGAGCTTAGCAGAAAAT :  301
RPS28B_kud : AAGTGCTCTCTGGATGTCAATGTTGGTAAGGATATTATCAAAAATGATACTAAAATATCGCATGAAT---CAAAAGACAACGAAACGTTTATCAATTCCAGTGTAATAGAAAAT :  319
             aa TGCtcTCcagAtGT AATGaa G AAaGAaATTAc A agATgacgCTAaA TATCtcttgA t   aaAAAa  AAcGAAAC TTTat  ATTC AG gTAgtAGAAAAt

                    *       360         *       380         *       400         *       420         *       440         *
RPS28B_cer : CATACCCCCCAGACAAAGACTGTAACAATTGTAACATTACAGATATTTTGGAATCTACCACTGTTATCGACTTGCAGTCACCCCATGGATTATCTGCT---CCTGGTCAGAAT :  408
RPS28B_par : CATAACCTGCCAGACAAAGACTGTAACAATTGTAACATTACAGATATTTTGGAATCCACCACTGTTATTGACTTATATTCACCTCATGGATCATCTGTT---CCTGGTCAGAAT :  408
RPS28B_mik : CATACCCTACCAAATAAAGATTTAAACAATTGTAACATTACCAATATCCTGGAATCTACCACTGTAGTTGACTTGTTTTCTCCTCATGGATCATCTGCT---CCTGATCAGAAT :  412
RPS28B_kud : CATACGCCACCGAATAAAGA---------TTGCAACATTACAAATATTTTGGAATCCACTACAGTTGTCGGCCTATTTTCACCGCAGGAATCCTCTGCT---CCTGGCCAGAAT :  421
             CATAccC  CCa A AAAGA t  aacaaTTGtAACATTACa ATATttTGGAATC ACcACtGTt T GaCtT t tTCaCC CAtGgATcaTCTGcT   CCTGgtCAGAAT

              460         *       480         *       500         *       520         *       540         *       560         *
RPS28B_cer : ACTTTCACAAACAAACTTCAAGAACAAATTTATAGTTCAATAAATCATTTTTCTAACGAATTGGTAAGAAAAAATTTCGATAATAAACCAAGAGTTAAATAAGAAAATCTTAAAA :  522
RPS28B_par : TCGTTCACGAATAAGCTGCAAGAACAAATTTATAGCTCAATCAATCATTTTTCTAATGAGTTGGTAAGAAAAAATTTCAATAATAAACCAAGAGTTAAATACTAAAATCTTGAAA :  522
RPS28B_mik : TCGTTCACAAATAAACTGCAAGAACAAATTTATAATTCTATCAATCATTTTTCAAACGAATTGGTAAGAAAAAATTTCGATAATAAACCAAGAGTTAAATACCAAAATCCTTAAA :  526
RPS28B_kud : TCGTTTACAAATAAACTACAAGAACAAATTTATAGTTCAATCAATCATTTTTCCAACGAATTGGTGAGAAAAAATTTCAATAATAAATCAAGAGTTAAATACCAAAATCTTGAAA :  535
             tCgTTcACaAAtAAaCT CAAGAACAAATTTATAgtTCaATcAATCATTTTTC AAcGAaTTGGTaAGAAAAAATTTC ATAATAAAcCAAGAGTTAAATAc AAAATCtT AAA

                    580         *       600         *       620         *       640         *       660         *       680
RPS28B_cer : GAGTTGTCCGAAAAATACCAAAAACTATTCTCCGAATTACAAGATAATTTCCAGAATGATACCAATGAGATGCTTAAATTCATGGCGAGATCAAAGACATGATGAATCTCCCG :  636
RPS28B_par : GAGTTGTCCGAAAAATACCAAAAGCTATTTTCCGAATTACAAGATAATTTCCAGAATGATACCAATGAGATGCTTAAATTCATGGTGAGATCAAAGACATGATCAATCTCCCT :  636
RPS28B_mik : GAGTTGTCCGAAAAATACCAAAAGCTATTCTCTGAATTACAAGATAGTTTCCAGAACGATACCAATGAGATGCTCAAATTCATGGAGAAATCAAAGACATGATCAACCTCCCT :  640
RPS28B_kud : GAGTTATCGGAAAAATATCAAAAATTATTCTCTGAATTACAAGATAGTTTCCAGAATGATACCAATGAGATGCTCAAATTCATGGAGAAATTAAAGACATGATTAATCTCCCT :  649
             GAGTTgTCcGAAAAATAcCAAAA cTATTcTC GAATTACAAGATA TTTCCAGAAtGATACCAATGAGATGCT AAATTCATGGG GA ATcAAAGACATGAT AAtCTCCCt

                  *       700         *       720         *       740         *       760         *       780         *       8
RPS28B_cer : GAAGATCAGCTCGTTCATGCTATTAGGACAAGAAAATTTGATAACAACAAGAGATAAATAGTATACATATACGCAATTCTTTTTAGATTTAAGATGGCTAATAAAAGTAATATA :  750
RPS28B_par : GAAGATCAGCTAGTTCATGCTATTAGGACAAGGAAATTCAATAATAACGGGGATAAATAGTATACATATCCACAATTATTTTTAGATTTAAGTTGGCTAACAAAAGCAATATA :  750
RPS28B_mik : GAAGATCAGCTGGTCCATGCTATCCGGACGAGGAAATTTAGTAATAGCAAGGGATAAATAGTATACATATTCTACAAATTTTTTAGTTCAAAGTTAGCTACGAAAC----TACA :  750
RPS28B_kud : GAAGATCAGTTAATTCACGCTATTAGGACCAGGAAATTTAACAGTAATGAGAAGTAAGTAATATACATAT---------TCTCTAATTCAAAATTAGCTAATGAATGTAATCCA :  754
             GAAGATCAGcT gTtCAtGCTATtaGGAC AGgAAATTtaatAatAac aG gaTAAaTAgTATACATAT c   a   TtTtTAg T  AAgtT GCTAa aAA g aaTa A

             00         *       820         *       840         *       860         *       880         *       900         *
RPS28B_cer : GG----------CAAGCTTATTCATGTTCGAATCTTTTTTTCTCGCAGAGCTAGTACTCTGGCAATC------GACAC-TTATTTCGTACAAAATGATCACGCAACTTTTGAC :  847
RPS28B_par : CA----------AAAGCTTATACGTGTTTGA----TTTTTTTCCCTCATCGCTTGCACTCTGTCAATC------AGAGCGCCAATACGTATAAAATGATCACGCAACTTTTTTT :  844
RPS28B_mik : CA----------CGCATTTAAATGTACTCAA-TTATTTTTCCTTAATGGCAGTCGTTTTCTGCCCATC------ATTACTTATATTCGTAAAACATGATCACGCAACTTTTTTT :  847
RPS28B_kud : TA----------TGTTCCCA-ATATGCTCCACTTTTTTTTCTTTCTATAATATGAAGCCACATCTACCTTTTAGAAAGCCAAATTTCGTAAAACATGATCACGCAACTTTTTTG :  857
              a              cttA a  Tg Tc A t  TTTTT t tc        T g  ctctg C AtC       a   C   a TtCGTA AA ATGATCACGCAACTTTTtt

                  920         *       940         *       960         *       980         *      1000         *      1020
RPS28B_cer : AATTTTTTTTTTTTCATCTGTTTT-CCAGGAAACTTGGATCTTTTTTGC-TCCAT-AGCACTT-TTGGTCTTCCTCAATTAAATATTTCT-AGATCCCGGTAGTTCTTCTTCTT :  956
RPS28B_par : GACAATTTTTTTTTCATTTGTTT--CGAAGAAACTAAGATCTTTTCTGC-TTCATTAGCATTT-TTGGTCTTCCTCCATTTGACATTTTTCAGATCCCGGTATTTCTTCTTTTC :  954
RPS28B_mik : GTCAATTTTTTTTTCATCCGTTTTTCGAAGATACTTAGACCATTTCTGCCTCCATTAACATTTATTGGTAACTCTCGATCGACTTTTTTTAGATCCCAGTAGTTGTT--TTCC :  959
RPS28B_kud : ACATTTTTTTTTTTCACCCGTTCT-CGAAAAAGTT--GAACTTTTTTCC-TCCGTCAGCATTT-CTACTCTTTCTTCATTGATTATTTTTCAGATTTCTATAATTCTC------ :  960
                  TTTTTTTTTCAtc GTTtt CgAagAaacT  GA CtTTT TgC TcCaT AgCAtTT tTggTctt CTc ATt a taTTTtT AGATccC gTA TTcTt  t

                *      1040         *      1060         *
RPS28B_cer : TGATCATTAATAAAAA--ATAAGCAAAGCATAAAA-GAGCAGCAAAA : 1000
RPS28B_par : TCTTAATGAATAGAAATAATAAACAAGGCAAAAAA-GAGCAGCAAAA : 1000
RPS28B_mik : TGTTCTTTATTAAAAA-----AACAAAGCAACCAA-GAGCAGCAGAA : 1000
RPS28B_kud : ----AGCTAACAGAAAG---AAGCAAGACAAAAAAAGATCAGCAAA- :  999
             t  t ttAatA AAA    aA CAA gCAaaaAA GAgCAGCAaAa
```


1
2
kDa
97.4
66.2
45
31
21.5
14.4

Supplementary Figure S2.
SDS-PAGE analysis on a 12% polyacrylamide denaturing gel of the purified His-tagged Fhl1 forkhead domain (FHD). Lane 1) protein markers; lane 2) His6-tagged FHD. Gel was stained with Coomassie blue dye.

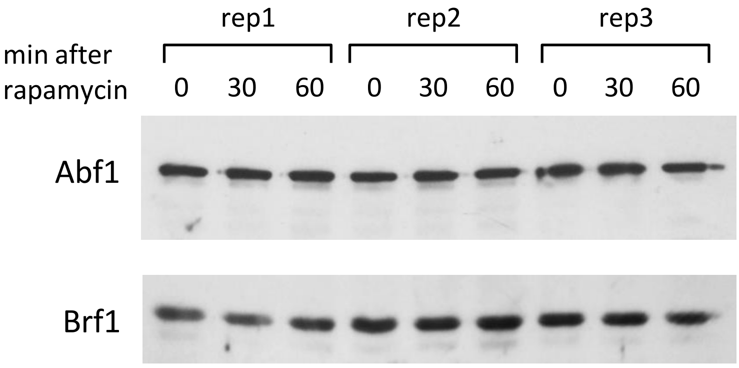


Supplementary Figure S3.
Abf1 and Fhl1 association with RPG promoters and expression level analysis after rapamycin treatment. Exponentially growing *ABF1* TAP-tagged or *FHL1* myc-tagged cells were treated with rapamycin (200 ng/ml). After 30 or 60 min of incubation, cells were collected for expression and ChIP analyses of *RPL4B* (*A*), *RPP1A* (*B*), *RPS22B* (*C*) and *RPS28B* (*D*) genes. Left *y* axis, Abf1 and Fhl1 enrichment (light grey and dark grey bars, respectively); right *y* axis, gene expression levels (black line; dotted grey line in panel C indicates *SNR44* expression level) are reported as relative to untreated cells (t0). Data were collected from three independent replicates and are presented as mean value ±SEM.



Supplementary Figure S4.

Abf1 association with Ribi and RP-unrelated promoters and expression level analysis after rapamycin treatment. Exponentially growing *ABF1* TAP-tagged cells were treated with rapamycin (200 ng/ml). After 30 or 60 min of incubation, cells were collected for expression and ChIP analyses of two Ribi genes, *LTV1* (*A*) and *NOP12* (*B*), and of three RP-unrelated Abf1 targets, *IPP1* (*C*), *PIK1* (*D*), *YKT6* (*E*). Both Abf1 enrichment (left *y* axis) and gene expression levels (right *y* axis) are reported as relative to untreated cells (t0). Data were collected from three independent replicates and are presented as mean value ±SEM.



Supplementary Figure S5.

Abf1 protein levels remain unaltered upon rapamycin treatment. Exponentially growing cells (Abf1-TAP strain) were treated with rapamycin (200 ng/ml). After 30 or 60 min of incubation, whole cell extracts were subjected to SDS-PAGE fractionation (8% polyacrylamide), followed by Western blotting using either anti-Abf1 polyclonal antibodies (yC-20, Santa Cruz Biotechnology) or anti-yeast Brf1 antiserum (provided by F. Pugh, The Pennsylvania State University). The results of hybridizations perfomed on the same nitrocellulose blot are shown. Rep1-3 refer to three independent rapamycin-treated cultures.

Supplementary Table S1. *S. cerevisiae* strains used in this study.

Strain	**Relevant genotype**	**Source**
BY4741	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*	Open Biosystems
Abf1-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6*	Open Biosystems
Tbf1-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6*	Open Biosystems
Fhl1-13myc	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 FHL1-13MYC-KANMX6*	This study
ΔRPL4B	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPL4B::URA3*	This study
RPL4B Amut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPL4B Abf1 bs mut YEplac 181*	This study
RPL4B Fmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPL4B Fhl1 bs mut YEplac 181*	This study
RPL4B AFmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPL4B Abf1 bs mut Fhl1 bs mut YEplac 181*	This study
ΔRPP1A	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPP1A::URA3*	This study
RPP1A Amut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPP1A Abf1 bs mut YEplac 181*	This study
RPP1A Fmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPP1A Fhl1 bs mut YEplac 181*	This study
RPP1A AFmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPP1A Abf1 bs mut Fhl1 bs mut YEplac 181*	This study
ΔRPS22B	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B::URA3*	This study
RPS22B Amut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B Abf1 bs mut YEplac 181*	This study
RPS22B Fmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B Fhl1 bs mut YEplac 181*	This study
RPS22B Tmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B Tbf1 bs mut YEplac 181*	This study
RPS22B AFmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B Abf1 bs mut Fhl1 bs mut YEplac 181*	This study
RPS22B TAFmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS22B Abf1 bs mut Fhl1 bs mut Tbf1 bs mut YEplac 181*	This study
ΔRPS28B	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS28B::URA3*	This study
RPS28B Amut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS28B Abf1 bs mut YEplac 181*	This study
RPS28B Fmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS28B Fhl1 bs mut YEplac 181*	This study
RPS28B AFmut	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ABF1-TAP-HIS3MX6 RPS28B Abf1 bs mut Fhl1 bs mut YEplac 181*	This study

Supplementary Table S2. Oligonucleotides used in this study.

Name	**Sequence (from 5')**	**Use**
Fhl1_F2	GGGTATCACTGAAGTAAATGTATCCCTTGAGGAAAAACTTCGGATCCCCGGGTTAATTAA	*FHL1* tagging
Fhl1_R2	AAGATTTATGCTTCTACTTCGAATATGCTAATACTATTATGAATTCGAGCTCGTTTAAAC	*FHL1* tagging
RPL4B::URA3_fw1	GGTATTCATCTTACAGGAATTTTTGAGAGCTCGTTTTATTTAGG	Gene disruption
RPL4B::URA3_rev1	CAGCCTTTTCAGAAACAGCGTAAGCGATCCCAATACAACAGAT	Gene disruption
RPL4B::URA3_fw2	TAAGTCCTGCCTTATTTATCGTAACGGTATTCATCTTACAGGAATTTTTG	Gene disruption
RPL4B::URA3_rev2	CAGGATTCAGCGGAGGTTTGGTGACCAGCCTTTTCAGAAACAGCG	Gene disruption
RPP1A::URA3_fw1	GAAGCCTTAACCCTGTAGCCTCATCAGAGCTCGTTTTATTTAGG	Gene disruption
RPP1A::URA3_rev1	AAGCCTTAGCAAAAATATCAGCCCAGATCCCAATACAACAGAT	Gene disruption
RPP1A::URA3_fw2	ATCTTGTCTAATACTTCATTTAAAAGAAGCCTTAACCCTGTAGCC	Gene disruption
RPP1A::URA3_rev2	AAGTCCTTCAAGTTTTGGCCGTCCAAAGCCTTAGCAAAAATATCA	Gene disruption
RPS22B::URA3_fw1	CGCAGTAATCCTAGAACCCTAACTTTTTCAGAGCTCGTTTTATTTAGG	Gene disruption
RPS22B::URA3_rev1	CCGAACTTAAGAACATTTACATTTCAATATGATCCCAATACAACAGAT	Gene disruption
RPS22B::URA3_fw2	TCATTATTCTTTATGCATTACGTTTCGCAGTAATCCTAG	Gene disruption
RPS22B::URA3_rev2	CTCTTGTAACAATATCCAAGTTCAACCGAACTTAAGAAC	Gene disruption
RPS28B::URA3_fw1	GCTAGTACTCTGGCAATCGACACTTAGAGCTCGTTTTATTTAGG	Gene disruption
RPS28B::URA3_rev1	CTTCACGTTCAGATTCCATCAAGACGATCCCAATACAACAGAT	Gene disruption
RPS28B::URA3_fw2	TCGAATCTTTTTTTTCTCGCAGAGCTAGTACTCTGGCAATCG	Gene disruption
RPS28B::URA3_rev2	ATATACCTTTAACGCAAACGACGAGCTTCACGTTCAGATTCCATC	Gene disruption
RPL4B fw	GCATAGTTCATTCGACAGCTTGG	Gene replacement/ pGEM cloning
RPL4B rev	GCAGTAGCAGCAATAGCAGAAGC	Gene replacement/ pGEM cloning
RPL4B Abf1mut fw	TCCGTTAGAAATCGACTTATTTCCTAAAGCATCGC	Gene replacement
RPL4B Abf1mut rev	GCGATGCTTTAGGAAATAAGTCGATTTCTAACGGA	Gene replacement
RPL4B Fhl1mut fw	AAAGCATCGCGCAGCCTCGATTTTTTTAACATTTT	Gene replacement
RPL4B Fhl1mut rev	AATGTTAAAAAAATCGAGGCTGCGCGATGCTTT	Gene replacement
RPP1A fw	CGAATGCGACGTTTCCTGCC	Gene replacement/ pGEM cloning
RPP1A rev	GTCGTCATCGGATTCTTCTTTAGC	Gene replacement/ pGEM cloning
RPP1A Abf1mut fw	GTCTGCTACATCGCCTGAGGTCCTAATATCGTAAG	Gene replacement
RPP1A Abf1mut rev	CTTACGATATTAGGACCTCAGGCGATGTAGCAGAC	Gene replacement
RPP1A Fhl1mut fw	ATCGTAAGATGATACCTCTCGACTTTGTAATGATT	Gene replacement
RPP1A Fhl1mut rev	AATCATTACAAAGTCGAGAGGTATCATCTTACGAT	Gene replacement
RPS22B fw	CAAGTATGATCCGTTATTCTTCTCG	Gene replacement/ pGEM cloning
RPS22B rev	TATTATCGGTTACAGTGGTCTTGAAAA	Gene replacement/ pGEM cloning
RPS22B Abf1mut fw	CTAAAATTACACTAAAAAATATCGGACGCAACT	Gene replacement
RPS22B Abf1mut rev	AGTTGCGTCCGATATTTTTTAGTGTAATTTTAG	Gene replacement
RPS22B Fhl1mut fw	TCAAAAATGACGGCCTCGACTTTTCTCAGAAATT	Gene replacement
RPS22B Fhl1mut rev	AATTTCTGAGAAAAGTCGAGGCCGTCATTTTTGA	Gene replacement
RPS22B Tbf1mut fw	GTAATCCTAGAAACAGATCTTTTTCTAAAATTAC	Gene replacement
RPS22B Tbf1mut rev	GTAATTTTAGAAAAAGATCTGTTTCTAGGATTAC	Gene replacement

RPS22B Abf1mut Fhl1mut fw	TTCTAAAATTACACTAAAAAATATCGGCCTCGACT	Gene replacement
RPS22B Abf1mut Fhl1mut rev	AGTCGAGGCCGATATTTTTTAGTGTAATTTTAGAA	Gene replacement
RPS28B fw	CAGAATGATACCAATGAGATGC	Gene replacement/ pGEM cloning
RPS28B rev	TGTTTAGATGAGCTTACCAACG	Gene replacement/ pGEM cloning
RPS28B Abf1mut fw	CGACACTTATTTAGGACAAAAGGCACACGCAACTT	Gene replacement
RPS28B Abf1mut rev	AAGTTGCGTGTGCCTTTTGTCCTAAATAAGTGTCG	Gene replacement
RPS28B Fhl1mut fw	TTTCGTACAAAATGATCTCTCGACTTTTGACAATT	Gene replacement
RPS28B Fhl1mut rev	AATTGTCAAAAGTCGAGAGATCATTTTGTACGAAA	Gene replacement
RPS28B Abf1mut Fhl1mut fw	TTTAGGACAAAAGGCACTCTCGACTTTTGACAATT	Gene replacement
RPS28B Abf1mut Fhl1mut rev	AATTGTCAAAAGTCGAGAGTGCCTTTTGTCCTAAA	Gene replacement
RPL3_fw_ChIP	GGCCGGACAGTAATATAGTAATCG	ChIP-qPCR
RPL3_rev_ChIP	TTTTCATGGACGATGATCACTG	ChIP-qPCR
RPL4B_fw_ChIP	GAAGGCATGAATTGTCTATTCCG	ChIP-qPCR
RPL4B_rev_ChIP	CATGAAAACTTTTCCAGAGTACTTGA	ChIP-qPCR
RPP1A_fw_ChIP	CCCTGTAGCCTCATCTATGTCTG	ChIP-qPCR
RPP1A_rev_ChIP	TTCAAATACCATGTAAAGGCATTC	ChIP-qPCR
RPS22B_fw_ChIP	GTTTCGCAGTAATCCTAGAACCC	ChIP-qPCR
RPS22B_rev_ChIP	TCCAGCGTAGAAAACTTTTTAAGAG	ChIP-qPCR
RPS28A_fw_ChIP	TCCCAATCTTTATACCCTGCGA	ChIP-qPCR
RPS28A_rev_ChIP	TCCAAGTAGTTCAACGACCAAGA	ChIP-qPCR
RPS28B_fw_ChIP	GCTAGTACTCTGGCAATCGACAC	ChIP-qPCR
RPS28B_rev_ChIP	GGAGCAAAAAAGATCCAAGTTTC	ChIP-qPCR
FLR1_ChIP_fw	GGAGCAATAACAGTGCGAAA	ChIP-qPCR
FLR1_ChIP_rev	TTATCCCGCCCATTAGTCAG	ChIP-qPCR
LTV1_ChIP_fw	GCTTCTTGCGTCTATTTCTGC	ChIP-qPCR
LTV1_ChIP_rev	TCAGTCGCGTTATACGGATTAG	ChIP-qPCR
RPL28_ChIP_fw	ATTTTTCCTATTTTTCCTCTGGCG	ChIP-qPCR
RPL28_ChIP_rev	GATGAAAGGTTTGAACCTATCTGGG	ChIP-qPCR
NOP12_ChIP_fw	CACGTACTGTCCTTCCTGATTCG	ChIP-qPCR
NOP12_ChIP_rev	CTGAAACATCAGGTTTGCTTGCT	ChIP-qPCR
IPP1_ChIP_fw	CGCAGACGCTAAGGTTGTTG	ChIP-qPCR
IPP1_ChIP_rev	AACTAACCTTCCTAACTTCGACGC	ChIP-qPCR
PIK1_ChIP_fw	CGTACTTGATAGCGTGTATAACAGGG	ChIP-qPCR
PIK1_ChIP_rev	GGTAGGGTTCTTTTGTTTCAGTGC	ChIP-qPCR
YKT6_ChIP_fw	GTGTTCCACAATTTCAGCATTATATG	ChIP-qPCR
YKT6_ChIP_fw	GTGCTTGCTCTTGATTTCACACC	ChIP-qPCR
HHT2_RT_fw	TCAATCTTCTGCTATCGGTGCTT	ChIP-qPCR/ expression analysis
HHT2_RT_rev	GCGTGAATAGCAGCCAGATTAGT	ChIP-qPCR/ expression analysis
TAF10_exp_fw	ACCTTTTCCATCGGTTGCG	expression analysis
TAF10_exp_rev	CCATCATCCACTACAGCCTCTCTC	expression analysis
ALG9_exp_fw	AATCAAGGTGGTGTGAAGGCAC	expression analysis
ALG9_exp_rev	GATTATCTGGCAGCAGGAAAGAAC	expression analysis

RPL4B_exp_fw	CCTTGAAGCATGACTAGAATTTATAGT	expression analysis
RPL4B_exp_rev	GAAAACAAAAAGGTTTGATTAAAGAC	expression analysis
RPP1A_exp_fw	GTCCAATACAACAGCTTAAACCG	expression analysis
RPP1A_exp_rev	CAAGGCGGCGTAAGACAAAG	expression analysis
RPS22B_exp_fw	GACTCGCTCTTCCGTTTTAGC	expression analysis
RPS22B_exp_rev	GGTCTCAATAGAACCTGACGTTTAC	expression analysis
SNR44_fw	CCGGGCTGATAACTAGATGG	expression analysis
SNR44_rev	TCCATAACCGTGTAAGAAGCA	expression analysis
RPS28B_exp_fw	TGGTCTTGATGGAATCTGAACG	expression analysis
RPS28B_exp_rev	CAATGCTCGAAGAGCACCAATAG	expression analysis
LTV1_exp_fw	GTTCCTGTCTCCAATCCAAATAAAA	expression analysis
LTV1_exp_rev	AGCCCTCCTACCCTTTGGTTT	expression analysis
NOP12_exp_fw	CACGTACTGTCCTTCCTGATTCG	expression analysis
NOP12_exp_rev	CTGAAACATCAGGTTTGCTTGCT	expression analysis
IPP1_exp_fw	CCTTCCACGACATTCCCTTG	expression analysis
IPP1_exp_rev	CCTTGGTGATTTCTAACTTGGCG	expression analysis
PIK1_exp_fw	CTTCATGGAATGGCAGGTGAG	expression analysis
PIK1_exp_rev	CGTATCCTCTCTTTCTTGGTAGCC	expression analysis
YKT6_exp_fw	GGCAGATGTGACTGAGACCAATG	expression analysis
YKT6_exp_rev	TGATAGCGTCAGCCTGTGAAG	expression analysis
Fhl1FHD_NheI_fw	GCTAGCAAGCCACCGAAAATACCA	FHD sequence cloning
Fhl1FHD_HindIII_rev	AAGCTTTTATTTTTTGCCCCTCTGCGG	FHD sequence cloning

Supplementary Table S3. Oligonucleotide primers and templates used to generate radiolabelled EMSA probes.

Probe	Probe length	Template	Primers name	Primers sequence
RPL4B wt	188 bp	pGEM::RPL4B_wt	RPL4B_promoter_fw	GAACTGCACTGAAGGCATGA
			RPL4B_ promoter_rev	GCGATTGCTGATAGGAAAGAA
RPL4B Fmut	188 bp	pGEM::RPL4B_Fmut	RPL4B_ promoter_fw	GAACTGCACTGAAGGCATGA
			RPL4B_ promoter_rev	GCGATTGCTGATAGGAAAGAA
RPP1A wt	172 bp	pGEM::RPP1A_wt	RPP1A_ promoter_fw	GCCTTAACCCTGTAGCCTCA
			RPP1A_ promoter_rev	TCAGAACAGAAGAGATCGCAAA
RPP1A Fmut	172 bp	pGEM::RPP1A_Fmut	RPP1A_ promoter_fw	GCCTTAACCCTGTAGCCTCA
			RPP1A_ promoter_rev	TCAGAACAGAAGAGATCGCAAA
RPS22B wt	151 bp	pGEM::RPS22B_wt	RPS22B_ promoter_fw	CATTATTCTTTATGCATTACGTTTCG
			RPS22B_ promoter_rev	GAAGAGAACAATTTATCCAGCGTAG
RPS22B Fmut	151 bp	pGEM::RPS22B_Fmut	RPS22B_ promoter_fw	CATTATTCTTTATGCATTACGTTTCG
			RPS22B_ promoter_rev	GAAGAGAACAATTTATCCAGCGTAG
RPS28B wt	161 bp	pGEM::RPS28B_wt	RPS28B_ promoter_fw	GGCAAGCTTATTCATGTTCG
			RPS28B_ promoter_rev	CCAAAAGTGCTATGGAGCAA
RPS28B Fmut	161 bp	pGEM::RPS28B_Fmut	RPS28B_ promoter_fw	GGCAAGCTTATTCATGTTCG
			RPS28B_ promoter_rev	CCAAAAGTGCTATGGAGCAA
RPL28	165 bp	pGEM::RPL28	RPL28_ EMSA_fw	CCAGGGACCCACACATTAC
			RPL28_ ChIP_rev	GATGAAAGGTTTGAACCTATCTGGG
FLR1	157 bp	pGEM::FLR1	FLR1_ EMSA_fw	ATGAAAGAAGACAAATGCAAAG
			FLR1_ EMSA_rev	CTGTTCCCCTTTTACCTGAC