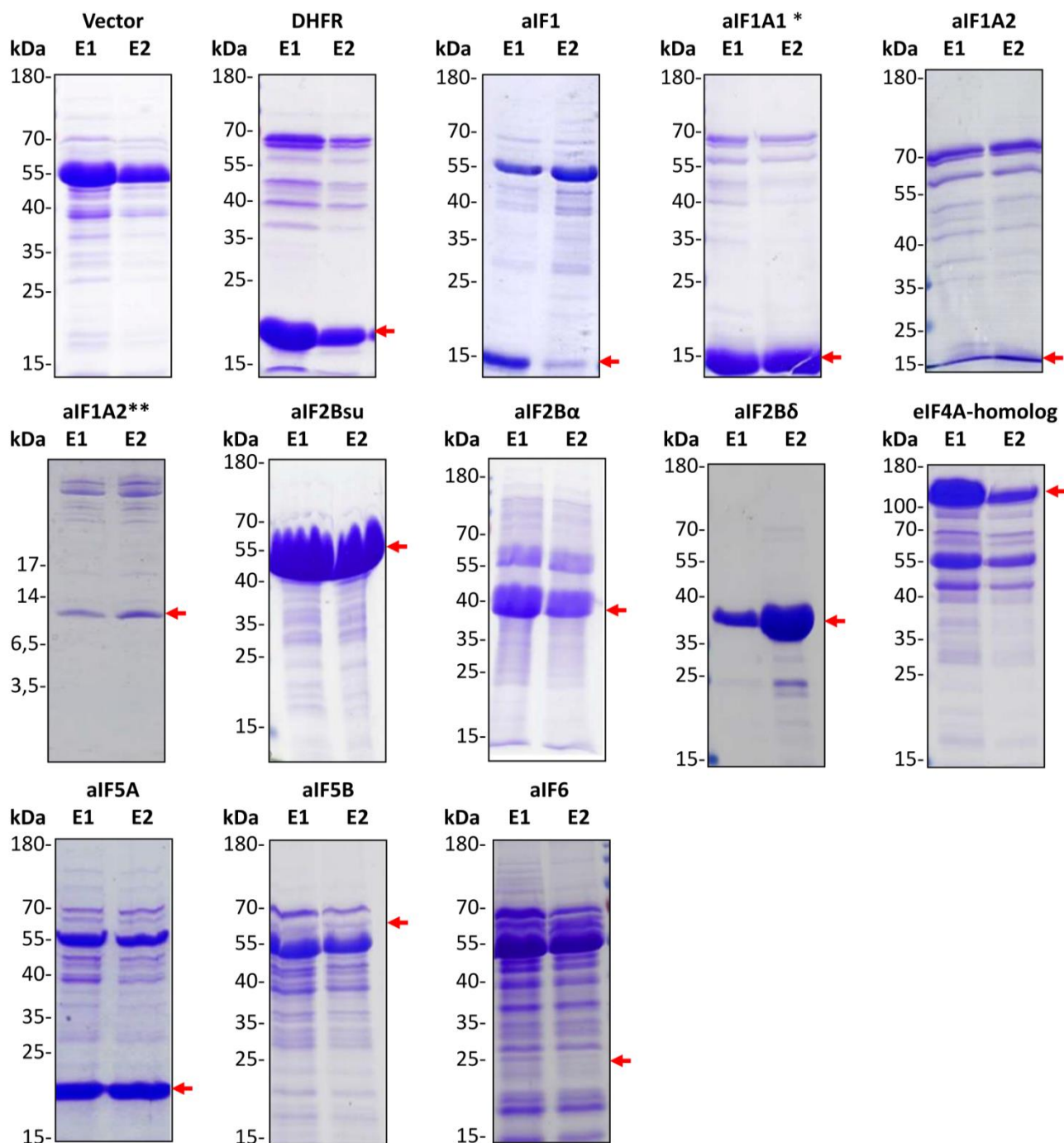


Supplementary Figure 2. Growth curves of aIF deletion mutants and overproduction strains.

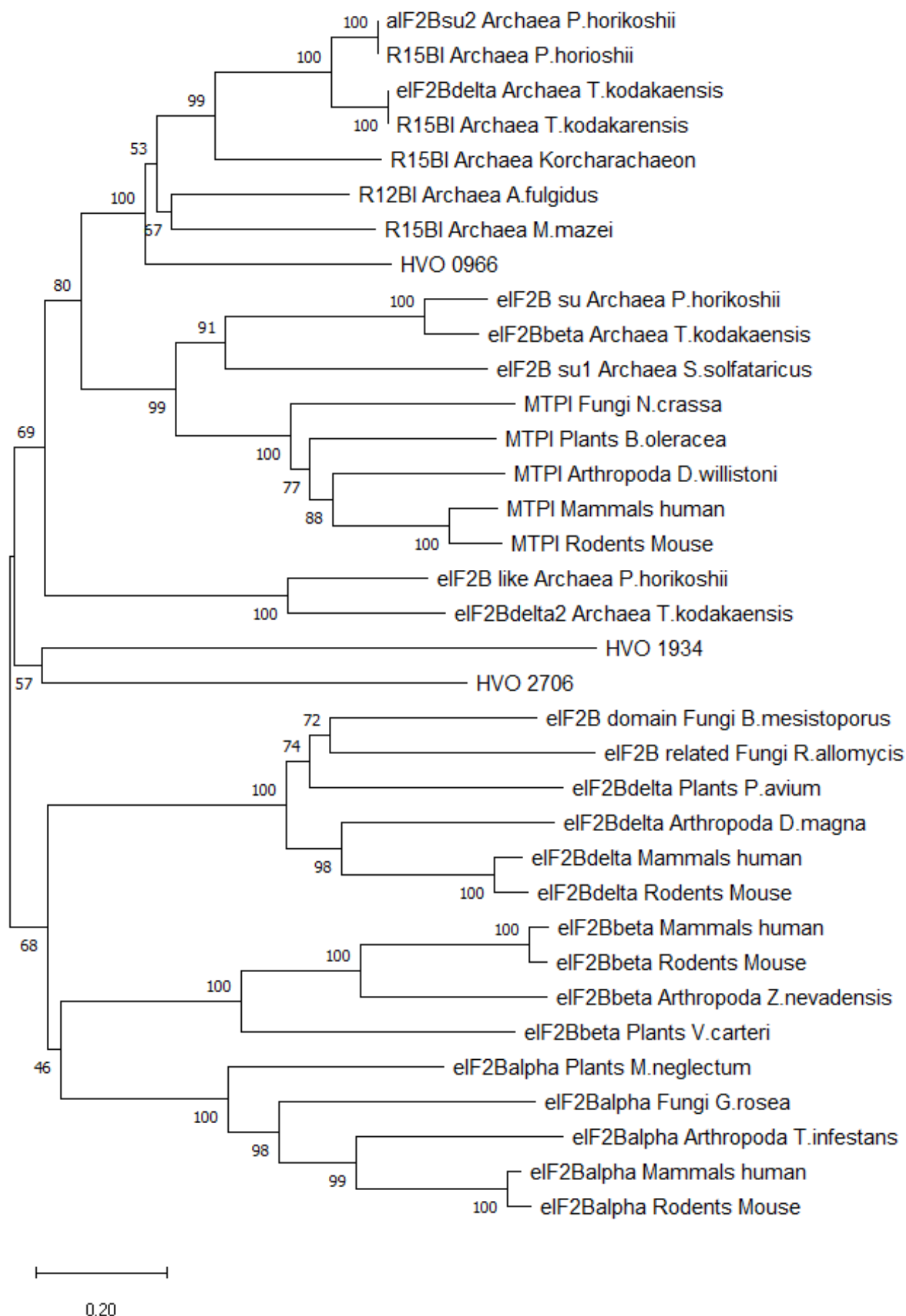
All cells were grown in triplicates under optimal growth conditions in complex media (all vector-containing cultures in the presence of Novobiocin) and in 96-well plates. OD600 was measured frequently, and average values and their standard deviations are shown. Dotted lines – plasmid-free cultures, solid lines – plasmid-containing cultures, red lines – deletion mutants, black lines – wildtype, grey line – wildtype with empty vector, orange line – wildtype with expression plasmid.



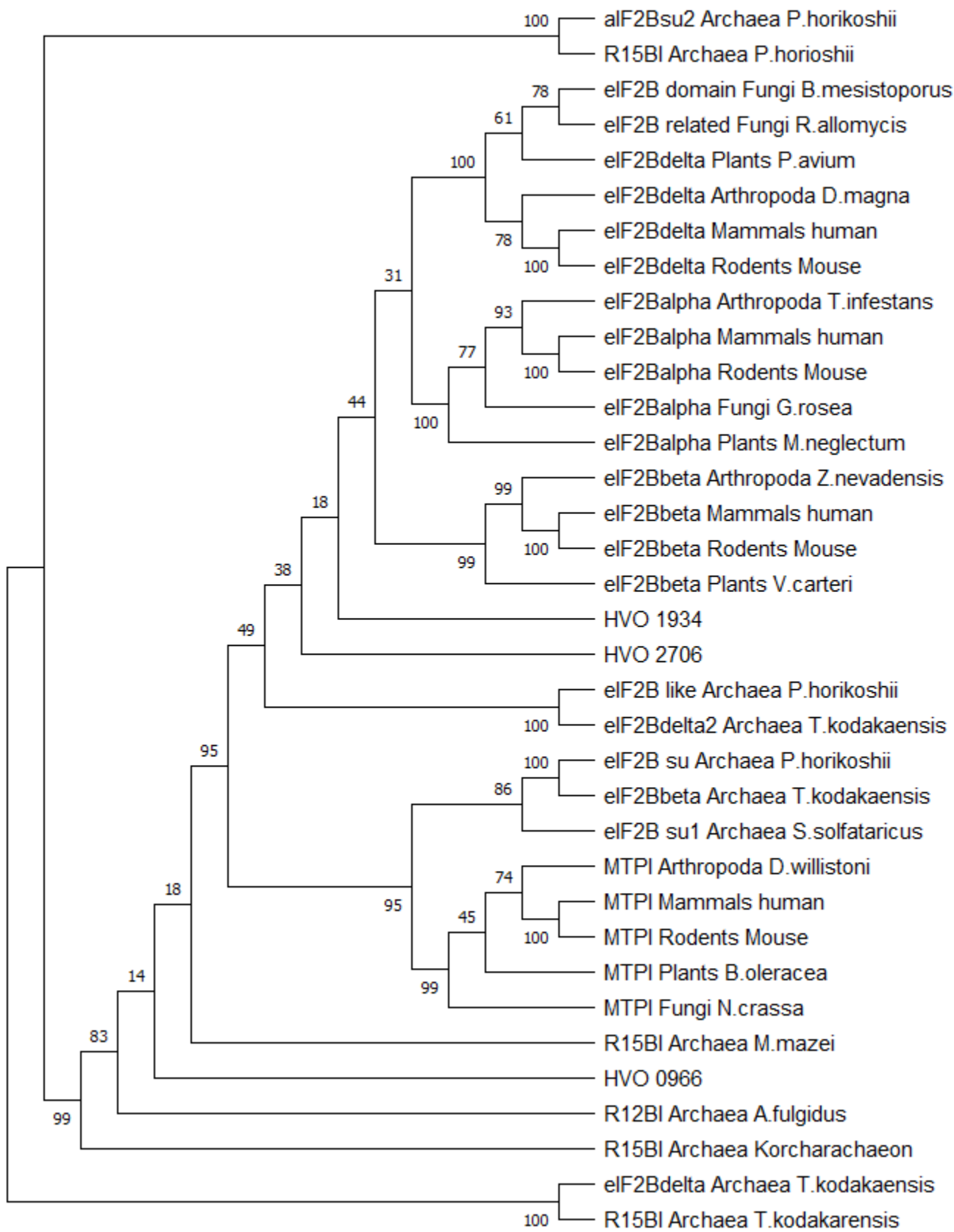
Supplementary Figure 3. SDS-Page of the elution fractions 1 and 2 of His₆-tagged aIFs. The red arrow indicates the overexpressed His₆-tagged bait protein. Examples given are representative for three biological replicates.

*The aIF1A1 overexpression construct contained the native 83 nucleotides long 3'-UTR after the ORF. Without the UTR, aIF1A1 was not detectable after overexpression.

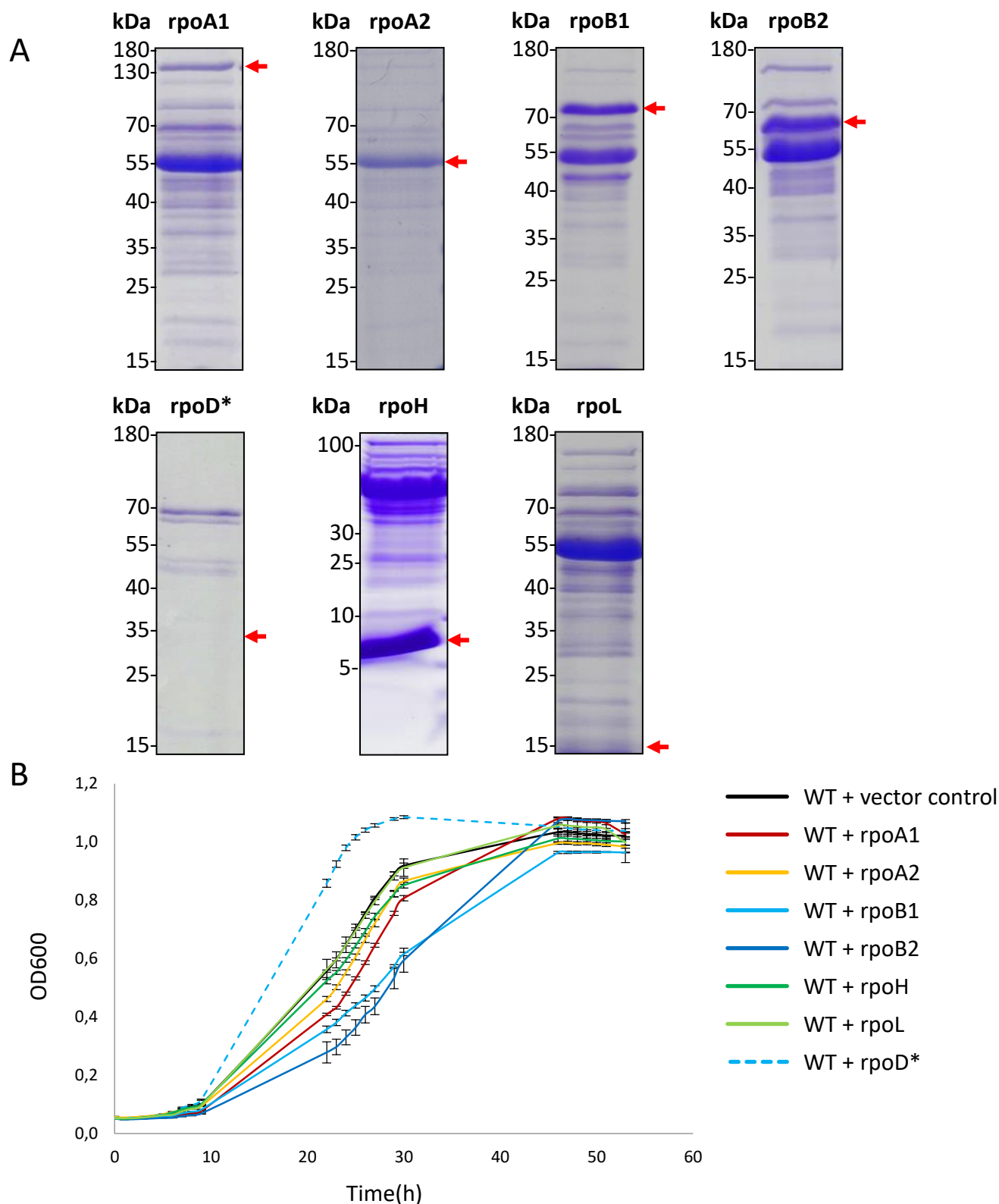
** Here, a Tricine-based gel was used for better visibility of the aIF1A2 protein.



Supplementary Figure 4. Neighbor Joining (NJ) tree with 1000 bootstrap replications. The bootstrap values (%) are shown at each node.



Supplementary Figure 5. Maximal Parsimony (MP) tree with 1000 bootstrap replications. The bootstrap values (%) are shown at each node.



Supplementary Figure 6. Overproduction of His₆-tagged RNA polymerase subunits.

A) SDS-Page of the elution fraction 2 of indicated Rpo subunits. The red arrow indicates the overexpressed His₆-tagged bait protein. Examples given are representative for three biological replicates.

B) Growth curves of cultures of the wildtype and the strains overproducing the indicated Rpo subunit. All cultures were grown in triplicates under optimal growth conditions in complex media (all vector-containing cultures in the presence of Novobiocin) and 96-well plates. OD600 was measured frequently, and average values and their standard deviations are shown.

* RpoD yield after overproduction was very low.

Sac_cerevisiae	MSSDLAELGFDPALKKKKKTKKVIPDDFDAAVNGK-----	36
Dro_melanogaster	---MDAEDGFDPTLLKKKKKKTT-FDLDAALGLEDDTK-----KEDP--QDE----	42
Homo_sapiens	---MSGDEMIFDPTMSKKKKKKKKP-FMLDEEGDTQTEETQPSETKEVEPEPTEDKDLEA	56
Rattus_norvegicus	---MSGDEMIFDPTMSKKKKKKKKP-FMLDEEGDAQTEETQPSETKEVEPEPAEEKDVEA	56
Sul._solfataricus	-----	0
Met._jannaschii	-----	0
Mbc._thermoautotrophicum	-----	0
Pco._furiosus	-----	0
Hfx._volcanii_1	-----	0
Hfx._volcanii_2	-----	0
Hqu._walsbii	-----	0
Nal_madadii	-----	0
Hco_morrhuae	-----	0
Hru_sodomense	-----	0
Sac_cerevisiae	-----ENGSG--GD--DLFAGLKKKKKSKSVSA-----DAAEAEKEPT	69
Dro_melanogaster	---ASAEGGAAAEEDNLDLESFGKKKKKKKKPFNMDEIEAAIPSFSGDDVAASEEPPEEE	99
Homo_sapiens	DEEDTRKKDASDDLDLNFNNKKKKKKTKKIFDIDEAEEGVKDLKIES--DVQEPTEPE	114
Rattus_norvegicus	DEEDSRKKDASDDLDLNFNNKKKKKKTKKIFDIDEAEAAIKDVKIES--DAQEPAEPE	114
Sul._solfataricus	-----	0
Met._jannaschii	-----	0
Mbc._thermoautotrophicum	-----	0
Pco._furiosus	-----	0
Hfx._volcanii_1	-----	0
Hfx._volcanii_2	-----	0
Hqu._walsbii	-----	0
Nal_madadii	-----	0
Hco_morrhuae	-----	0
Hru_sodomense	-----	0
Sac_cerevisiae	DDIAEALGELSLKKKKKTKDSSVDAFEKELAKAGLDNVDAESKEGT---PSANSSIIQ	125
Dro_melanogaster	INLDMDFSMKKKKKSKK-KE-LDELFDQ-----ADDDKSEDKENEDNSSTWFGS	149
Homo_sapiens	DDLDIMLGNKKKKKNVFPD-EDEILEKDEA---LEDEDNKKDDGISFSNQTGPWAGS	170
Rattus_norvegicus	DDLDIMLGNKKKKKNVFPD-EDEILEKDEA---LEDEDSKKDDGISFSNQTGPWAGS	170
Sul._solfataricus	-----M	1
Met._jannaschii	-----MSDLEN	6
Mbc._thermoautotrophicum	-----	0
Pco._furiosus	-----ME	2
Hfx._volcanii_1	-----	0
Hfx._volcanii_2	-----	0
Hqu._walsbii	-----	0
Nal_madadii	-----	0
Hco_morrhuae	-----	0
Hru_sodomense	-----	0
Sac_cerevisiae	EVGLPYSELLSRFFNILRTNNPELAGDRSGPKFRIPPPVCLR-DGKKTIFSNIQDIAEKL	184
Dro_melanogaster	DRDYTYDELLKRVFEIILDKNPDMAAGRK-PKFVMRPPQVLRVGTGKTSFANFMDIAKTL	208
Homo_sapiens	ERDYTYEELLNRVFNIMREKNPDMVAGEK-RKFVMKPPQVVRVGTGKTSFVNFTDICKLL	229
Rattus_norvegicus	ERDYTYEELLNRVFNIMREKNPDMVAGEK-RKFVMKPPQVVRVGTGKTSFVNFTDICKLL	229
Sul._solfataricus	SSEKEYVEMLDRLYSKL---PEKGR-KE-GTQSLPNMIILN-IGNTTIIRNFAEYCDRI	54
Met._jannaschii	IDYYDYKALLKRARSQI---PDYVF-QK-DRFELPEIEILI-EGNRTIIRNFRELAKAV	59
Mbc._thermoautotrophicum	--MDDYEKLLERAIDQL---PPEVF-ET-KRFEVPKAYSVI-QGNRTFIQNFREVADAL	51
Pco._furiosus	IDYYDYKLLLEKAYQEL---PENVKHHK-SRFEVPGALVTI-EGNKTIENFKDIADAL	56
Hfx._volcanii_1	---MDYDDQLDRALSAS---PDVAE-GD-DRFSVPEPTVRQ-EGNVTYENFAATHDRL	50
Hfx._volcanii_2	---MEYQTALDRALNVL---PERNV-EQ-ERLTVDPDPSGET-DGAFTRLTNLGEIADAL	50
Hqu._walsbii	---MDYTESLNRALDEL---PERRD-EE-SRLSIPDPVGET-DGAFTRLTNLGEIADAL	50
Nal_madadii	---MDYESSLDRAMEDV---PDIGG-DE-ERLQIPDAQTQK-DGAFTRFTNLGEIADVL	50
Hco_morrhuae	---MDYEASLDRAMDSV---PDLDT-GD-SRLDVPDAEAQK-DGAFTRLTNLGNVADAL	50
Hru_sodomense	---MDYESSLDRAMDEV---PDLGG-SD-ERLSVPDPPEWQK-DGAFTRLTNLSAIADAL	50
	* * : . * : * * : . :	

Sac_cerevisiae	HRSPHELIQYLFALGLTSGSVDGQKRLVIKGFQSKQMVNLRRYILEYVTCKTCKSINT	244
Dro_melanogaster	HRLPKHLLDFFLLAELGTSGSMDGNQQLIIKGRFQPKQIENVLRRYIKEYVTCHTCSRSPET	268
Homo_sapiens	HRQPKHLLAFLLAELGTSGSIDGNNQLVIKGRFQPKQIENVLRRYIKEYVTCHTCSRSPDT	289
Rattus_norvegicus	HRQPKHLLAFLLAELGTSGSIDGNNQLVIKGRFQPKQIENVLRRYIKEYVTCHTCSRSPDT	289
Sul._solfataricus	RREDKICMKYLLKELAAPGNVDDKGELVIQKGFSSQVINTLMERFLKAYVECSTCKSLDT	114
Met._jannaschii	NRDEEFFAKYLLKETGSAGNLEG-GRLLQRRISPELLKSRINDFLREYVICRECGKPD	118
Mbc._thermoautotrophicum	NRDPQHLLKFLRLRELGTAGNLEG-GRAILQKGFTHFLINERIEDYVNKFVICHECNRPDT	110
Pco._furiosus	NRDPQHLLKFLRLREIATAGTLEG-RRVVVLRGFTPYLIANKLKKYIKEYVICPVCGSPDT	115
Hfx._volcanii_1	AREATHVLKFFQTELGTSAQIDDRGRARFTGEFRQRRIADALDEYVESFVLCSECGSPDT	110
Hfx._volcanii_2	SRTPAHLHSAIQRTLTGTSGQLEG-DRARYSGSFSINDFEEAIDGYVEEYVICSECGLPDT	109
Hqu._walsbii	GRPAEHVHRNVQELGTNGQLED-ERARYNGSFSVADFEAAIDYVIEYVTCTECGLPDT	109
Nal._madadii	SREDEHLHRFVQREMGTSKGKFE-GRGRYNGTFSEQDFNAAVDAYVDEYVLCTECGLPDT	109
Hco._morruhae	SRDPEHLHRVIQRDLGTNGQFSG-DRARYNGTFSGEDFDAIDSYSQEFVICSECGLPDT	109
Hru._sodomense	SRDPEHVHSKIQQELGTAGQYED-GRARYSGNFRERDFQAAIDSYSIESFVTCSECGLPDT	109
	* . . : . . . : : : : : * * * : *	
Sac_cerevisiae	ELKREQSNRLFFMVCKSCGSTRSVSSIKTGFQAVTGKRRRM-----	285
Dro_melanogaster	ILQK--DTRLFFLQCESCGSRCSVASIKSGFQAVTGKRAAIRAKTT-----	312
Homo_sapiens	ILQK--DTRLYFLQCECHSRCSVASIKTGFQAVTGKRAQLRAKAN-----	333
Rattus_norvegicus	ILQK--DTRLYFLQCECHSRCSVASIKTGFQAVTGKRAQLRAKAN-----	333
Sul._solfataricus	ILKK--EKKSWEIVCLACGAQTPVKPL-----	139
Met._jannaschii	KIIK--EGRVHLLKCMACGAIRPIRMI-----	143
Mbc._thermoautotrophicum	RIIR--EGRISLLKCEACGAKAPLKNV----- -----	135
Pco._furiosus	KIIK--RDRFHLKCEACGAETPIQHL-----	140
Hfx._volcanii_1	KLTS--QRGADVLRCDACGALSAPDL-----	135
Hfx._volcanii_2	RLVT--EDGVDMLRCEACGAFRPVQKRSSVSNK-RQREAVEEGRTYEVEITGTGRKGDGV	166
Hqu._walsbii	RLTT--ENGVDMLRCEACGAFRPVQKQTTTQQQSQSGPAVEEGATYEVEITGTGRKGDGV	167
Nal._madadii	RLVR--EDRTPMLRCDACGAFRPVTKRSTSAQQQQQDAVEEGKTYTVEITGTGRKGDGV	167
Hco._morruhae	RLEM--EGRTQMLRCEACGAFRPVEKNTGSQET-EQRPDVEEGRTYEVEITGTGRKGDGV	166
Hru._sodomense	RLET--ENRTPMLRCEACGAFRPVAKQNTSNTQ-RQEEAVESGTTYELEIVGTGRKGDGV	166
	: : * : * : :	
Sac_cerevisiae	-----	285
Dro_melanogaster	-----	312
Homo_sapiens	-----	333
Rattus_norvegicus	-----	333
Sul._solfataricus	-----	139
Met._jannaschii	-----	143
Mbc._thermoautotrophicum	-----	135
Pco._furiosus	-----	140
Hfx._volcanii_1	-----	135
Hfx._volcanii_2	AQRGKYTIFVPGAQEGQTVRIYIKNTSGSLAFARLA-	202
Hqu._walsbii	AEKGKFTIFVSGAEEGQTVRVQIERTSGTLAFAQVI-	203
Nal._madadii	AEKGEYTFVPGAQEGDVVDIYIKNISGNLAFARLD-	203
Hco._morruhae	AEQGYTIFVPGAQEGDVVDIYIENISGTLAFARLA-	202
Hru._sodomense	AERGEYTFVPGAQEGETVTAYIKNVSGNLAFARRED	203

Supplementary Figure 7. Multiple sequence alignment of a/eIF2 β translation initiation factors from selected archaea and eukaryotes, representing various phylogenetic lineages. The alignment was generated using Clustal Omega at the website of the European Bioinformatics Institute (www.ebi.ac.uk). Positions of increasing degrees of conservation are marked with ., :, and *. The four conserved cysteines in two CXXC motifs, which form a zinc finger, are shown in red. The three polylysine stretches confined to eukaryotic proteins are shown in blue. The C-terminal extensions that are found exclusively in halophilic and methanogenic archaea are shown in purple.

Supplementary Table 1. Primers for generating and/or confirming *H. Volcanii* deletion mutants

Name	Sequence
HVO_0136 P1	CCGACGCGCCGCCGACGCTGT
HVO_0136 P2	GCGGAGCTGGTCGGCAAGGTCTCGGCGGCTCTCGTT
HVO_0136 P3	AGCCGCCGAGACCTTGCCGACCAGCTCCGCCGCGAA
HVO_0136 P4	GACGACCTGTCCCTTGTCGTG
HVO_0359 P1	GGTTGAGGGAATCCGCAACG
HVO_0359 P2	GCATCGTTATCGCTCGCTCATTGGTGTGGTCACGC
HVO_0359 P3	ACCACACCAATGAGCGAGCGATAACGATGCAACAGGC
HVO_0359 P4	GTTCCGTCGGGCGATTCTG
HVO_0569 P1	CAGCCGCTCAGTGGATGTGC
HVO_0569 P2	GACGGCGAACTCGTCGGCGACGTTCCGTACCATGC
HVO_0569 P3	GTACGGAACGTCGCCGACGAGTTCGCCGTCTGAGC
HVO_0569 P4	CGTCCCGGCGATGTACCAC
HVO_0699 P1	ACACCAAACCCACCACAAGGTCGATATCTATG
HVO_0699 P2	TTCGCGGTGGTACTCGAGTTCGCCGGGGTCAGGCCA
HVO_0699 P3	GACCCCGGCGAACTCGAGTACCACCGCGAACGCAGC
HVO_0699 P4	GGGTCAGCTCGGCGACGCCC
HVO_1333 P1	ACGCGGGCGAGTCGCTGCC
HVO_1333 P2	GTCAGTCCCAGAAGCCGTCTGGCATCGCCGAGGTTACG
HVO_1333 P3	ATGCCAGACGGCTTCTGGGACTGACGGGGTGGATTCCGGTT
HVO_1333 P4	GTCGCTCGGCTCCGACATCCTCG
HVO_1678 P1	TTCTCGGTTCAAGTCGGCTTGCGG
HVO_1678 P2	TCGTTTTTACAGGTAGTCCATGCGCGGCAGTACG
HVO_1678 P3	GCGCATGGACTACCTGTAAAACGAACGTCCGGCGG
HVO_1678 P4	CGGTCGGCCTCGCCGCCGCCG
HVO_1934 P1	CAGCTGCGAGACAGCGCGACGACG
HVO_1934 P2	GTCGTCCACGCGCGACGTGTGGCATATCGTGACTTACGGC
HVO_1934 P3	GCCACACGTCGCGCGTGGGACGACTGAGTCGGGAGTGC
HVO_1934 P4	CGGTTTCGGGGCTCCGGTCGAGG
HVO_2242 P1	CGTGATTCGTTCCGGCAGCCCG
HVO_2242 P2	GACCGATTGAGGCCATAGGGGTTGAGTGTCTGGC
HVO_2242 P3	CGAACCCTATGGCCTGAATCGGTCGCACGCGTCG
HVO_2242 P4	CGGCTACAAGGCGCTCGACTCC
HVO_2706 P1	CCCATCTGCGAGGCGGGCCAGC
HVO_2706 P2	TCAGAAGTCGATGACGGTCTCGTCTATCATACGAGAAGTCGCCGTATCG
HVO_2706 P3	ATGATAGACGAGACC GTCATCGAGTCTGAGCGGGCGGCG
HVO_2706 P4	TCGGTTCCTCGTCAGTGACCGCGCC
HVO_A0637 P1	GTCCGCTGTTCTGGGAGACGACGTAACCG
HVO_A0637 P2	TACTGAATGTGGCTTCATTTGACGAGGTATCCACGATTCCCCTACAACAC
HVO_A0637 P3	ATGACCTCGTCAAATGAAGGCCACATTCAGTAATCATTTTCTCCGAAAGGAGAG
HVO_A0637 P4	GGGAACCAAGACGGCCGACGACGC
HVO_B0053 P1	GACGCTGGCCGACCGCTATC
HVO_B0053 P2	GGCGTCGTGAAGCGTTCGGAGCGCTTCGAGTTCTGC
HVO_B0053 P3	CTCGAAGCGCTCCGAACGCTTCACGACGCCTTCCC
HVO_B0053 P4	ACGACGCTCCGCCAGACTC
Probe 0359 for	TCAACAAGATGGACGTCGTC
Probe 0359 rev	ACTTCCTCGTGGTGCATCTC
Probe 0569 for	CGTTCCGCCAGCGAGACACC
Probe 0569 rev	GCCGCGTAGGCGTCGGCCAT
Probe 0966 for	CACGAACGGGGGCGCACCGGTC
Probe 0966 rev	GCGGTCGTCCATGCGAGAACTACGGG
Probe 1333 for	ACCCTTCACCCGCTCTCGAACGGCGTAGC
Probe 1333 rev	GCCGTCTGGCATCGCCGAGGTTACG
Probe 1934 for	GCGTGGGACGACTGAGTCGGGAGTGC

Probe 1934 rev	CGGTTTCGGGGCTCCGGTCGAGG
Probe 2242 for	GGACGCGCTCTCGCGGACGC
Probe 2242 rev	CTGCGCGCCGGGCACGAAGA
Probe 2706 for	CCCATCTGCGAGGCGGGCCAGC
Probe 2706 rev	ATACGAGAACGTCGCCGTATCG
Probe A0637 for	ACCCAACGACGAACCGGCGA
Probe A0637 rev	CACGTGCGGTACTTCATGCG
Probe B0053 for	TGAACATCACCGGAACGACC
Probe B0053 rev	CTCCGAGGTCGTCGAGCAGC

Supplementary Table 2. Primers for generating expression vectors with His₆-tagged gene variants.

Name	Sequence
Oligo-His-Tag_for	CATGGGCCACCACCACCACCACGC
Oligo-His-Tag_rev	CATGGCGTGGTGGTGGTGGTGGCC
NcoI_His_0117_for	TGATGCCCATGGGCCACCACCACCACCACGCCACTTCGCGCCTCCTT
KpnI_0117_rev	GAATTGGGTACCTCAGTCGATGTAATCGAG
HVO_0136_His_NheI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGAGCGACGACGAGAACGAG
HVO_0136_KpnI_rev	CGAATTGGGTACCGCTTACTGGATGTGACCTTCG
NcoIH0136mit3UTRKpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCCAGCGACGACGAGAACGAGAG
NcoIH0136mit3UTRKpnI_rev	GAATTGGGTACCGGCGAGATGAAAAGGGCACAGG
HVO_0699_His_NheI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGAAGTACAGCGGATGGCCT
HVO_0699_KpnI_rev	CGAATTGGGTACCGTTACTCTTCGTCGCCGCTGC
NcoI_His_0966_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGGACGACCGCGTA
NcoI_His_0966_KpnI_rev	CGAATTGGGTACCGCTACGGTTCGGCCCGCGGC
NcoI_1333_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGCCAGACGCGGAGGCCGC
NcoI_1333_KpnI_rev	CGAATTGGGTACCGTCAGTCCCAGAACGACTGG
HVO_1678_His_NheI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGGACTACGACGACCAACTG
HVO_1678_KpnI_rev	CGAATTGGGTACCGTTACAGATCGGGAATCGCTG
NdeI_His_1901_for	ACTAGGACCATATGCACCACCACCACCACCACGTGACGAAAAACCCACAA
1901_KpnI_rev	GGCGAATTGGGTACCTCACTTGAGCGTCCC
NcoI_His_1934_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGCCACACGTGCCACCGT
NcoI_His_1934_KpnI_rev	CGAATTGGGTACCGTCAGTCGTCCACGCCGCC
NcoI_His_1946_KpnI_for	TGATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGTCGGAAGTCTGCTCGA
NcoI_His_1946_KpnI_rev	CGAATTGGGTACCGTCACGCGACGTTGAACCCC
NheI_1963_KpnI_for	ACCACCACGCTAGCGGCATGTCCGACACTGATT
NheI_1963_KpnI_rev	CGAATTGGGTACCGCTATTTGCCCCAGAAGGGG
HVO_2242_His_NheI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGAGTATCAGACTGCGCTCGACCGA
HVO_2242_KpnI_rev	CGAATTGGGTACCTCAGGCGAGTCGCGCGAACGC
NcoI_His_2300_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGGCGAAAGAGCAGAAGCA
NcoI_His_2300_KpnI_rev	CGAATTGGGTACCGTTAGACGATCTTTCGCTGG
NcoI_His_2706_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGATAGACGAGACCATCGA
NcoI_His_2706_KpnI_rev	CGAATTGGGTACCGTCAGAACTCGATGACGCC
NcoIHis_A0637_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCCAGTAAAAATCAAGGGCGTCG
NcoIHis_A0637_KpnI_rev	CGAATTGGGTACCTTACTGAATGTGGCCTTCGCGCCGAA
NcoI_H0346_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCGTAGACGTAAAGCCAACACAA
NcoI_H0346_KpnI_rev	CGAATTGGGTACCGTCATTCAATCACCAGTCGGTATACGACT
NcoI_His_0347_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGAACCGACAAGCG
NcoI_His_0347_KpnI_rev	CGAATTGGGTACCGTTAGTCGTCCGCGGGTGCG
NcoI_H0348_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCGCTCAGGCACAGCGAGA
NcoI_H0348_KpnI_rev	CGAATTGGGTACCGTTAGACCGCGTCCTTCAGTTCG
NcoI_His_0349_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGTCAATGCAGACA
NcoI_His_0349_KpnI_rev	CGAATTGGGTACCGTCAGTCATCGGATTTCGACC
NcoI_His_0350_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCATGACTGATACCGAC
NcoI_His_0350_KpnI_rev	CGAATTGGGTACCGTCAGTCGTCGGACGGTTCG
NcoI_H1042_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCGAACTGCGGGTCATCGA
NcoI_H1042_KpnI_rev	CGAATTGGGTACCGTTACGCGTCGATACCGGCGCGG
NcoI_H2781_KpnI_for	GATGCCCATGGGCCACCACCACCACCACCACGCTAGCGGCGTAAACGACTTCCAGGTCGA
NcoI_H2781_KpnI_rev	CGAATTGGGTACCGTTTAAACTTACAGTGCAGCTTCTCTTC

Supplementary Table 3. Co-isolated proteins with aIF2 subunits.

MW [kDa]	Group	Specification	Genloci	Accession	Description	Bait			
						aIF2 α	aIF2 β -1	aIF2 β -2	aIF2 γ
29.5	Translation	aIFs	HVO_0699	D4GT46	aIF2 α	bait	+	+	+
14.9	Translation	aIFs	HVO_1678	D4GZP2	aIF2 β -1		bait		
22.2	Translation	aIFs	HVO_2242	L9VAS4	aIF2 β -2			bait	+
43.9	Translation	aIFs	HVO_1901	D4GTD4	aIF2 γ	+	+	+	bait
34.9	Translation	aIFs	HVO_0966	L9USK7	aIF2B α	+			+
65.3	Translation	aIFs	HVO_1963	D4GTJ2	aIF5B	+		+	+
45.6	Translation	aEFs	HVO_2413	L9V6J4	aEF1 α	+		+	+
57.8	Translation	aEFs	HVO_2575	L9V605	aEF1 α -like protein	+			
80.4	Translation	aEFs	HVO_0356	L9UK07	aEF2	+		+	+
24.8	Translation	30S rpS	HVO_1145	D4GWA5	30S rpS3Ae			+	
23.3	Translation	30S rpS	HVO_2544	D4GTX6	30S rpS5	+			
13.4	Translation	30S rpS	HVO_2782	L9V5R1	30S rpS11			+	
23.1	Translation	50S rpL	HVO_2757	P41199	50S rpL1	+			
25.6	Translation	50S rpL	HVO_2561	D4GTZ3	50S rpL2			+	+
37.2	Translation	50S rpL	HVO_2564	L9V5K9	50S rpL3			+	
27	Translation	50S rpL	HVO_2563	D4GTZ5	50S rpL4			+	
36.9	Translation	50S rpL	HVO_2756	P41198	50S rpL10	+			
19.8	Translation	50S rpL	HVO_0484	D4GS24	50S rpL10e	+			
22.5	Translation	50S rpL	HVO_0561	L9UPT6	50S rpL15e	+			
20.2	Translation	50S rpL	HVO_2545	P50563	50S rpL18			+	
12.7	Translation	50S rpL	HVO_2779	D4GWY3	50S rpL18e			+	
16.9	Translation	50S rpL	HVO_2559	L9V5K3	50S rpL22			+	
17.1	Translation	50S rpL	HVO_2543	L9V5X1	50S rpL30	+		+	
81.2	Translation	transferase	HVO_2736	D4GW73	tRNA(Met) cytidine acetyltransferase TmcA	+			
108.8	Transcription	RNAP-subunits	HVO_0349	D4GZX6	rpoA1	+			
46.1	Transcription	RNAP-subunits	HVO_0350	D4GZX7	rpoA2	+			
58.9	Transcription	RNAP-subunits	HVO_0347	L9UK99	rpoB2	+			+
11.7	Transcription	regulator	HVO_1133	D4GW85	HTH domain protein				+
23.8	Transcription	regulator	HVO_A0121	D4GQF3	HTH-10 family transcription regulator	+			
28	Transcription	regulator	HVO_2108	D4GUQ5	IcIR family transcription regulator	+	+	+	
18.1	Transcription	regulator	HVO_1792	D4GSB6	Lrp/AsnC family transcription regulator	+			
8.3	Transcription	regulator	HVO_2723	D4GW47	RNA-binding protein Lsm	+			
19.9	Transcription	regulator	HVO_1727	L9VGC6	TATA-box-binding protein	+			
19.8	Transcription	regulator	HVO_0163	L9UFW5	Transcriptional regulator	+			
28	Transcription	regulator	HVO_0179	L9UGU5	Transcriptional regulator				+
27.5	Transcription	regulator	HVO_2928	L9UK32	Transcriptional regulator	+	+		
30.9	Transcription	regulator	HVO_2636	L9V878	Transcriptional regulator	+			
15.2	Protein folding	chaperone	HVO_0450	D4GRZ1	Hsp20-type molecular chaperone	+			
37.3	Replication and Repair	repair	HVO_0104	Q48328	DNA repair and recombination protein RadA	+			
24.6	Replication and Repair	repair	HVO_2383	L9V6G6	DNA repair and recombination protein RadB	+			
69.6	Replication and Repair	replication	HVO_0415	D4GRV6	Repair helicase UvrD	+			
34.6	Replication and Repair	replication	HVO_0292	L9JUJ8	Replication factor A	+			
87.4	Replication and Repair	replication	HVO_1571	L9VEG4	Type 2 DNA topoisomerase 6 subunit B	+			
23.2	RNA turnover	ribonuclease	HVO_2438	L9V6L9	Ribonuclease H I	+			
50.1	RNA turnover	ribonuclease	HVO_2724	L9V5P6	Ribonuclease J			+	
59.3	Protein turnover	thermosome	HVO_0455	Q30560	Thermosome subunit 2	+		+	
55.2	Protein turnover	thermosome	HVO_0778	Q9HHA2	Thermosome subunit 3	+		+	

Supplementary Table 4. The aIF-aIF interaction network.

[illegible]

Supplementary Table 5. Overview of ribosomal proteins co-isolated with aIFs.

[illegible]

Supplementary Table 6. All (non-metabolic) proteins co-purified with aIFs.

					Bait														
MW [kDa]	Group	Genloci	Accession	Description	aIF1	aIF1A-1	aIF1A-2	aIF2α	aIF2β-1	aIF2β-2	aIF2γ	aIF2βsu	aIF2Bα	aIF2Bβ	aIF4A-hom	aIF5A	aIF5B	aIF6	
10.8	Translation	HVO_1946	D4GTH5	aIF1	bait														
11.5	Translation	HVO_0136	D4GZ79	aIF1A-1		bait													
11.2	Translation	HVO_A0637	D4GRU5	aIF1A-2	+		bait												
29.5	Translation	HVO_0699	D4GT46	aIF2α				bait	+	+	+		+			+			
14.9	Translation	HVO_1678	D4GZP2	aIF2β-1					bait										
22.2	Translation	HVO_2242	L9VAS4	aIF2β-2				+		bait	+		+						
43.9	Translation	HVO_1901	D4GTD4	aIF2γ				+	+	+	bait		+						
43.2	Translation	HVO_1934	D4GTG3	aIF2Bsu								bait							
34.9	Translation	HVO_0966	L9USK7	aIF2Bα	+	+	+	+			+	+	bait		+	+	+	+	
30.7	Translation	HVO_2706	L9V7F9	aIF2Bβ									+	bait					
104.5	Translation	HVO_1333	D4GKK1	eIF4A-hom.											bait				
14.2	Translation	HVO_2300	L9V7A1	aIF5A												bait			
65.3	Translation	HVO_1963	D4GTJ2	aIF5B	+	+	+	+		+	+	+	+		+	+	bait	+	
23	Translation	HVO_0117	L9UI67	aIF6														bait	
45.6	Translation	HVO_2413	L9V6J4	aEF1α	+	+	+	+		+	+	+	+		+	+	+	+	
57.8	Translation	HVO_2575	L9V605	aEF1α-like protein	+			+				+				+	+	+	
80.4	Translation	HVO_0356	L9UK07	aEF2	+	+		+		+	+	+	+		+	+	+	+	
28.3	Translation	HVO_2773	L9V5L7	30S rpS2									+						
33.4	Translation	HVO_2558	D4GTZ0	30S rpS3	+								+		+				
24.8	Translation	HVO_1145	D4GWA5	30S rpS3Ae						+			+						
26.6	Translation	HVO_2552	L9V7Y2	30S rpS4e	+								+		+	+			
23.3	Translation	HVO_2544	D4GTX6	30S rpS5				+							+				
22.6	Translation	HVO_0354	L9UJR0	30S rpS7	+								+		+				
11.5	Translation	HVO_0360	L9ULL7	30S rpS10	+												+		
13.4	Translation	HVO_2782	L9V5R1	30S rpS11						+			+						
18.9	Translation	HVO_2784	L9V5M6	30S rpS13	+								+						
17.5	Translation	HVO_1148	L9UVI2	30S rpS15									+						
12.7	Translation	HVO_2555	D4GTY7	30S rpS17									+						
16	Translation	HVO_2560	L9V6S9	30S rpS19P	+	+							+						
11.6	Translation	HVO_1896	D4GTC9	30S rpS24e	+														
23.1	Translation	HVO_2757	P41199	50S rpl1	+			+				+	+	+	+	+	+	+	
25.6	Translation	HVO_2561	D4GTZ3	50S rpl2	+	+				+	+	+	+		+		+	+	
37.2	Translation	HVO_2564	L9V5K9	50S rpl3	+					+			+		+	+		+	
27	Translation	HVO_2563	D4GTZ5	50S rpl4	+	+				+			+		+			+	
19.6	Translation	HVO_2548	L9V5X7	50S rpl6									+		+				
36.9	Translation	HVO_2756	P41198	50S rpl10	+			+					+		+				
19.8	Translation	HVO_0484	D4GS24	50S rpl10e				+											
16	Translation	HVO_2778	D4GWY1	50S rpl13	+														
22.5	Translation	HVO_0561	L9UPT6	50S rpl15e				+											
20.2	Translation	HVO_2545	P50563	50S rpl18						+			+						
12.7	Translation	HVO_2779	D4GWY3	50S rpl18e	+					+			+						
16.9	Translation	HVO_2559	L9V5K3	50S rpl22	+					+		+	+		+		+		
13.4	Translation	HVO_2553	L9V5Y5	50S rpl24		+													
17.1	Translation	HVO_2543	L9V5X1	50S rpl30	+	+		+		+		+	+		+		+		
25.8	Translation	HVO_2547	D4GTX9	50S rpl32e	+														
81.2	Translation	HVO_2736	D4GW73	tRNA(Met) cytidine acetyltransferase TmcA	+			+							+				
40.5	Translation	HVO_0911	D4GUZ0	GTP-binding protein Drg									+						

					Bait													
MW [kDa]	Group	Genloci	Accession	Description	aiF1	aiF1A-1	aiF1A-2	aiF2a	aiF2b-1	aiF2b-2	aiF2y	aiF2bsu	aiF2Ba	aiF2B6	aiF4A-hom	aiF5A	aiF5B	aiF6
108.8	Transcription	HVO_0349	D4GZX6	rpoA1	+	+		+					+		+	+	+	
46.1	Transcription	HVO_0350	D4GZX7	rpoA2	+			+					+					
67.7	Transcription	HVO_0348	L9UJM2	rpoB1	+													
58.9	Transcription	HVO_0347	L9UK99	rpoB2	+						+		+		+	+	+	
28.1	Transcription	HVO_2781	L9V5W2	rpoD	+								+					
13.6	Transcription	HVO_2748	D4GWA3	rpoF									+					
8.5	Transcription	HVO_0346	D4GZX3	rpoH									+					
10.4	Transcription	HVO_1042	D4GVL8	rpoL	+													
16.9	Transcription	HVO_2029	L9VBJ7	AsnC family transcriptional regulator		+							+					
13.5	Transcription	HVO_A0135	D4GQG4	HTH domain protein	+													
11.7	Transcription	HVO_1133	D4GW85	HTH domain protein	+	+					+	+	+		+			
23.4	Transcription	HVO_1695	D4H040	HTH domain protein	+	+									+			
23.8	Transcription	HVO_A0121	D4GQF3	HTH-10 family transcription regulator	+			+							+		+	
28	Transcription	HVO_1501	D4GYE7	HTH-type transcriptional regulator GlpR	+												+	
28.4	Transcription	HVO_B0114	D4GPB5	IcIR family transcription regulator	+								+		+		+	+
28.1	Transcription	HVO_B0201	D4GPK2	IcIR family transcription regulator													+	
27.9	Transcription	HVO_A0583	D4GRP3	IcIR family transcription regulator	+										+		+	
28	Transcription	HVO_2108	D4GUQ5	IcIR family transcription regulator	+	+	+	+	+	+		+	+		+	+	+	+
18.5	Transcription	HVO_B0066	D4GP68	Lrp/AsnC family transcription regulator	+			+	+				+	+		+	+	+
18.1	Transcription	HVO_1792	D4GSB6	Lrp/AsnC family transcription regulator	+		+	+				+	+		+		+	+
16.9	Transcription	HVO_0240	D4GZ15	Lrp/AsnC family transcription regulator									+					
11.4	Transcription	HVO_2869	D4GXH6	PadR family transcription regulator	+							+			+			
13.6	Transcription	HVO_0730	D4GT98	PadR family transcription regulator RosR									+					
13.1	Transcription	HVO_1090	D4GW09	Putative transcription factor									+					
8.3	Transcription	HVO_2723	D4GW47	RNA-binding protein Lsm	+			+										+
25.1	Transcription	HVO_0819	D4GUE2	SirR/DtxR family transcription regulator SirR	+										+	+	+	+
19.9	Transcription	HVO_1727	L9VGC6	TATA-box-binding protein	+			+					+		+			
20.3	Transcription	HVO_0158	D4GZA2	TATA-box-binding protein 1									+					
23.7	Transcription	HVO_2067	D4GU80	TetR family transcription regulator	+													
21.6	Transcription	HVO_A0161	L9V4Z6	TetR family transcriptional regulator	+													
19.8	Transcription	HVO_0163	L9UFW5	Transcriptional regulator			+	+				+	+		+	+	+	+
28	Transcription	HVO_0179	L9UGU5	Transcriptional regulator	+						+	+	+		+	+	+	+
27.5	Transcription	HVO_2928	L9UK32	Transcriptional regulator	+	+	+	+	+			+	+	+	+		+	+
39	Transcription	HVO_0568	L9UN99	Transcriptional regulator	+													
30.9	Transcription	HVO_2636	L9V878	Transcriptional regulator				+										
15.2	Transcription	HVO_1360	D4GXQ1	TrmB family transcription regulator	+													
39.3	Transcription	HVO_2688	D4GVQ2	TrmB family transcription regulator TrmB									+					
20.6	Transcription	HVO_1174	L9UT88	Transcription factor E	+								+					
35	Protein folding	HVO_0329	L9UK29	Branched-chain amino acid aminotransferase									+					
67.2	Protein folding	HVO_1590	L9VEI0	Chaperone protein DnaK	+										+			
15.2	Protein folding	HVO_0450	D4GRZ1	Hsp20-type molecular chaperone				+										
46.6	Protein folding	HVO_0321	D4GZV0	Peptide chain release factor subunit 1	+										+			
48.1	Replication and Repair	HVO_0853	D4GUK0	DNA double-strand break repair protein Mre11	+												+	+
100	Replication and Repair	HVO_0854	D4GUK1	DNA double-strand break repair Rad50 ATPase	+											+	+	+
78.7	Replication and Repair	HVO_0551	L9UMB1	DNA mismatch repair protein MutL	+								+					
99.2	Replication and Repair	HVO_0552	D4GSE9	DNA mismatch repair protein MutS	+								+		+	+	+	
37.3	Replication and Repair	HVO_0104	Q48328	DNA repair and recombination protein RadA	+			+				+			+	+	+	+
24.6	Replication and Repair	HVO_2383	L9V6G6	DNA repair and recombination protein RadB	+	+		+				+	+	+	+	+	+	+
76.8	Replication and Repair	HVO_1723	L9VE99	Putative DNA helicase Rad25	+								+		+	+	+	+
94.8	Replication and Repair	HVO_1573	D4GZ02	DNA gyrase subunit A	+								+		+			
150.5	Replication and Repair	HVO_0858	L9US19	DNA polymerase B1	+								+					
26.7	Replication and Repair	HVO_0175	D0VWY8	DNA polymerase sliding clamp									+					
108.6	Replication and Repair	HVO_0393	L9UJ16	Excinuclease ABC subunit A									+					
76.3	Replication and Repair	HVO_0283	L9UK77	Helicase AshA									+					
42.4	Replication and Repair	HVO_1537	D4GY11	Orc1-type DNA replication protein	+													+
42.2	Replication and Repair	HVO_0194	L9UGW2	ORC1-type DNA replication protein	+							+	+		+		+	
24	Replication and Repair	HVO_3014	D4GYC9	Origin-associated GTP-binding protein	+								+					
69.6	Replication and Repair	HVO_0415	D4GRV6	Repair helicase UvrD				+					+					
34.6	Replication and Repair	HVO_0292	L9UJU8	Replication factor A				+					+					
53.4	Replication and Repair	HVO_2427	D4GSN1	Replication factor C large subunit									+					
36.2	Replication and Repair	HVO_0203	L9UG08	Replication factor C small subunit									+					
51	Replication and Repair	HVO_0519	D4GS55	Replication protein A									+					
41.8	Replication and Repair	HVO_1570	L9VEU6	Type 2 DNA topoisomerase 6 subunit A	+								+		+			
87.4	Replication and Repair	HVO_1571	L9VEG4	Type 2 DNA topoisomerase 6 subunit B				+					+		+			
75.4	RNA turnover	HVO_0783	L9UNA4	ATP-dependent protease Lon											+			
23.2	RNA turnover	HVO_2438	L9V6L9	Ribonuclease H I				+										
50.1	RNA turnover	HVO_2724	L9V5P6	Ribonuclease J	+	+				+			+					
25.6	RNA turnover	HVO_1094	D4GW15	Ribonuclease P protein component 3	+											+		+
50.3	RNA turnover	HVO_0388	L9UJ19	Ribonuclease R	+							+	+		+	+	+	
34.1	RNA turnover	HVO_0144	L9UJH9	Ribonuclease Z	+		+								+		+	+
67.4	Protein turnover	HVO_0829	D4GUG3	Peptidase S9 family protein	+								+					+
27.6	Protein turnover	HVO_1091	Q9V2V6	Proteasome subunit alpha 1									+					
26.7	Protein turnover	HVO_2923	Q9V2V5	Proteasome subunit alpha 2									+					
26	Protein turnover	HVO_1562	L9VFN7	Proteasome subunit beta										+				
48.7	Protein turnover		L9UQ37	Proteasome-activating nucleotidase												+		
59.3	Protein turnover	HVO_0455	Q30560	Thermosome subunit 2	+	+		+		+		+	+	+	+	+	+	+
55.2	Protein turnover	HVO_0778	Q9HHA2	Thermosome subunit 3	+			+		+		+	+	+	+	+	+	+

Supplementary Table 7. The RNA polymerase subunits interaction network.
RpoD is shown in brackets as the yield after overproduction was very low.

MW [kDa]	Genloci	Accession	Description	Bait						
				rpoA1	rpoA2	rpoB1	rpoB2	(rpoD)	rpoH	rpoL
108.8	HVO_0349	D4GZX6	rpoA1	bait	+	+	+	+	+	+
46.1	HVO_0350	D4GZX7	rpoA2	+	bait	+	+	+	+	+
67.7	HVO_0348	L9UJM2	rpoB1	+	+	bait	+		+	+
58.9	HVO_0347	L9UK99	rpoB2	+	+	+	bait	+	+	+
28.1	HVO_2781	L9V5W2	rpoD	+	+	+	+	bait	+	+
8.5	HVO_0346	D4GZX3	rpoH	+	+	+	+		bait	+
10.4	HVO_1042	D4GVL8	rpoL	+	+	+	+		+	bait
7.3	HVO_2776	D4GWX5	rpoN	+	+	+	+		+	+
5.1	HVO_0653	L9UMK6	rpoP	+		+	+		+	+
13.6	HVO_2748	D4GWA3	rpoF						+	

Supplementary Table 8. Overview of aIFs co-isolated with RNA polymerase subunits.
RpoD is shown in brackets as the yield after overproduction was very low.

MW [kDa]	Genloci	Accession	Description	Bait						
				rpoA1	rpoA2	rpoB1	rpoB2	(rpoD)	rpoH	rpoL
10.8	HVO_1946	D4GTH5	aIF1							
11.5	HVO_0136	D4GZ79	aIF1A-1							
11.2	HVO_A0637	D4GRU5	aIF1A-2							
29.5	HVO_0699	D4GT46	aIF2 α						+	
14.9	HVO_1678	D4GZP2	aIF2 β -1							
22.2	HVO_2242	L9VAS4	aIF2 β -2							
43.9	HVO_1901	D4GTD4	aIF2 γ							
43.2	HVO_1934	D4GTG3	aIF2B _{su}				+			
34.9	HVO_0966	L9USK7	aIF2B α	+	+	+	+	+	+	+
30.7	HVO_2706	L9V7F9	aIF2B δ							
104.5	HVO_1333	D4G XK1	eIF4A-hom.							
14.2	HVO_2300	L9V7A1	aIF5A							
65.3	HVO_1963	D4GTJ2	aIF5B	+	+	+	+		+	+
22.98	HVO_0117	D4GYW3	aIF6							

Supplementary Table 9. Overview of RNA polymerase subunits co-isolated with aIFs.

[illegible]

Supplementary Table 10. All (non-metabolic) proteins co-purified with RNA polymerase proteins.

Transcription factors that were also co-isolated with aIFs as baits are marked grey-blue.

MW [kDa]	Genloci	Accession	Description	Bait						
				rpoA1	rpoA2	rpoB1	rpoB2	(rpoD)	rpoH	rpoL
108.8	HVO_0349	D4GZX6	DNA-directed RNA polymerase subunit A1	+	+	+	+	+	+	+
46.1	HVO_0350	D4GZX7	DNA-directed RNA polymerase subunit A2	+	+	+	+	+	+	+
67.7	HVO_0348	L9UJM2	DNA-directed RNA polymerase subunit B1	+	+	+	+		+	+
58.9	HVO_0347	L9UK99	DNA-directed RNA polymerase subunit B2	+	+	+	+	+	+	+
28.1	HVO_2781	L9V5W2	DNA-directed RNA polymerase subunit D	+	+	+	+		+	+
8.5	HVO_0346	D4GZX3	DNA-directed RNA polymerase subunit H	+	+	+	+		+	+
10.4	HVO_1042	D4GVL8	DNA-directed RNA polymerase subunit L	+	+	+	+		+	+
7.3	HVO_2776	D4GWX5	DNA-directed RNA polymerase subunit N	+	+	+	+		+	+
5.1	HVO_0653	L9UMK6	DNA-directed RNA polymerase subunit P	+		+	+		+	+
13.6	HVO_2748	D4GWA3	DNA-directed RNA polymerase subunit F						+	
29.5	HVO_0699	D4GT46	Translation initiation factor 2 subunit alpha						+	
43.2	HVO_1934	D4GTG3	Translation initiation factor aIF-2B alpha subunit				+			
34.9	HVO_0966	L9USK7	Translation initiation factor IF-2B subunit delta	+	+	+	+	+	+	+
65.3	HVO_1963	D4GTJ2	Translation initiation factor aIF5B	+	+	+	+		+	+
28.3	HVO_2110	L9V9M0	ArcR family transcription regulator	+						
67.2	HVO_1590	L9VEI0	Chaperone protein DnaK					+		
17.7	HVO_0766	L9UNS7	Hsp20-type molecular chaperone	+						
12.6	HVO_1116	D4GW55	HTH domain protein			+		+		
11.7	HVO_1133	D4GW85	HTH domain protein	+		+	+	+	+	+
13.8	HVO_0962	D4GV69	HTH domain protein						+	
23.4	HVO_1695	D4H040	HTH domain protein	+		+	+		+	+
23.8	HVO_A0121	D4GQF3	HTH-10 family transcription regulator	+						
28	HVO_1501	D4GYE7	HTH-type transcriptional regulator GlpR	+					+	+
15.2	HVO_0450	D4GRZ1	Hsp20-type molecular chaperone						+	
28	HVO_2108	D4GUQ5	IcIR family transcription regulator	+	+	+	+	+	+	+
27.9	HVO_A0583	D4GRP3	IcIR family transcription regulator	+					+	
28.4	HVO_B0114	D4GPB5	IcIR family transcription regulator	+	+	+	+		+	+
28.1	HVO_B0201	D4GPK2	IcIR family transcription regulator	+			+	+		
18.1	HVO_1792	D4GSB6	Lrp/AsnC family transcription regulator	+		+	+	+	+	+
18.5	HVO_B0066	D4GP68	Lrp/AsnC family transcription regulator						+	
11.4	HVO_2869	D4GXH6	PadR family transcription regulator	+			+			+
25.1	HVO_0819	D4GUE2	SirR/DtxR family transcription regulator SirR	+		+	+		+	+
19.8	HVO_0163	L9UFW5	Transcriptional regulator	+		+	+	+	+	+
28	HVO_0179	L9UGU5	Transcriptional regulator	+		+	+		+	+
15.2	HVO_1360	D4GXQ1	TrmB family transcription regulator						+	
39	HVO_0568	L9UN99	Transcriptional regulator	+						
27.5	HVO_2928	L9UK32	Transcriptional regulator	+		+	+	+	+	+
30.9	HVO_2636	L9V878	Transcriptional regulator						+	
48.1	HVO_0853	D4GUK0	DNA double-strand break repair protein Mre11	+			+		+	
100	HVO_0854	D4GUK1	DNA double-strand break repair Rad50 ATPase	+		+	+	+	+	+
94.8	HVO_1573	D4GZ02	DNA gyrase subunit A						+	+
99.2	HVO_0552	D4GSE9	DNA mismatch repair protein MutS	+		+	+		+	+
150.5	HVO_0858	L9US19	DNA polymerase B1	+						
37.3	HVO_0104	Q48328	DNA repair and recombination protein RadA	+	+	+	+	+	+	+
24.6	HVO_2383	L9V6G6	DNA repair and recombination protein RadB	+	+	+	+	+	+	+
53.2	HVO_A0441	L9VPT6	DNA repair helicase Rad25	+						
76.8	HVO_1723	L9VE99	Putative DNA helicase Rad25	+		+	+	+		+

33.4	HVO_2558	D4GTZ0	30S ribosomal protein S3						+	
26.6	HVO_2552	L9V7Y2	30S ribosomal protein S4e	+	+	+	+		+	
23.3	HVO_2544	D4GTX6	30S ribosomal protein S5			+				
13.6	HVO_2373	D4GWM1	30S ribosomal protein S8e					+		
11.5	HVO_0360	L9ULL7	30S ribosomal protein S10	+		+			+	
18.9	HVO_2784	L9V5M6	30S ribosomal protein S13				+			
16	HVO_2560	L9V659	30S ribosomal protein S19P			+	+		+	
11.6	HVO_1896	D4GTC9	30S ribosomal protein S24e					+		
23.1	HVO_2757	P41199	50S ribosomal protein L1	+		+	+	+	+	+
25.6	HVO_2561	D4GTZ3	50S ribosomal protein L2	+		+	+	+	+	+
37.2	HVO_2564	L9V5K9	50S ribosomal protein L3	+		+	+	+	+	+
27	HVO_2563	D4GTZ5	50S ribosomal protein L4			+	+			
36.9	HVO_2756	P41198	50S ribosomal protein L10			+	+		+	
19.8	HVO_0484	D4GS24	50S ribosomal protein L10e			+				
16.8	HVO_2758	P41200	50S ribosomal protein L11	+		+	+	+		+
17.8	HVO_2542	L9V7W8	50S ribosomal protein L15			+				
22.5	HVO_0561	L9UPT6	50S ribosomal protein L15e	+		+	+		+	+
16.9	HVO_2559	L9V5K3	50S ribosomal protein L22	+	+	+	+		+	+
13.4	HVO_2553	L9V5Y5	50S ribosomal protein L24					+		
17.1	HVO_2543	L9V5X1	50S ribosomal protein L30	+		+	+		+	+
25.8	HVO_2547	D4GTX9	50S ribosomal protein L32e			+	+	+		
57.8	HVO_2575	L9V605	Elongation factor aEF-1 subunit alpha-like protein	+		+	+		+	+
45.6	HVO_2413	L9V6J4	Elongation factor 1-alpha	+	+	+	+		+	+
80.4	HVO_0356	L9UK07	Elongation factor 2	+	+	+	+	+	+	+
28.9	HVO_1284	D4GXB4	GTP cyclohydrolase III	+		+	+			+
33.5	HVO_2348	D4GWJ7	GTP cyclohydrolase MptA							+
67.4	HVO_0829	D4GUG3	Peptidase S9 family protein	+					+	
48.7		L9UQ37	Proteasome-activating nucleotidase						+	
46.6	HVO_0321	D4GZV0	Peptide chain release factor subunit 1	+		+			+	+
23.6	HVO_1931	D4GTG0	Probable GTP-binding protein EngB	+			+			+
8.3	HVO_2723	D4GW47	RNA-binding protein Lsm	+					+	
59.3	HVO_0455	O30560	Thermosome subunit 2	+	+	+	+	+	+	+
55.2	HVO_0778	Q9HHA2	Thermosome subunit 3	+		+	+	+	+	
14.3	HVO_3013	D4GYC7	Origin-associated protein						+	
42.2	HVO_0194	L9UGW2	ORC1-type DNA replication protein	+		+	+		+	+
42.4	HVO_1537	D4GYI1	Orc1-type DNA replication protein				+			
86.6	HVO_1703	D4H048	Putative DEAD/DEAH box helicase	+						
23.2	HVO_2438	L9V6L9	Ribonuclease H I	+			+	+	+	+
50.1	HVO_2724	L9V5P6	Ribonuclease J	+		+				+
25.6	HVO_1094	D4GW15	Ribonuclease P protein component 3	+			+	+	+	+
50.3	HVO_0388	L9UJI9	Ribonuclease R	+		+	+		+	+
34.1	HVO_0144	L9UJH9	Ribonuclease Z	+		+	+		+	+
19.9	HVO_1727	L9VGC6	TATA-box-binding protein			+	+	+	+	